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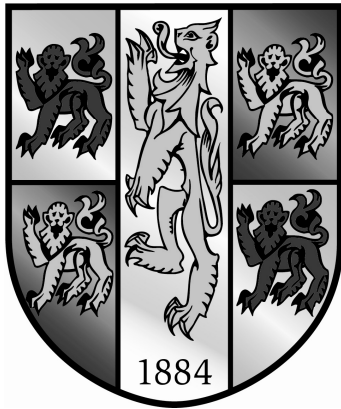
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Fisheries-induced evolution: a genetic approach using selection experiments on *Poecilia reticulata*

A thesis submitted to Bangor University for the degree of
Doctor of Philosophy

By Serinde Joy van Wijk
Oktober 2011
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*How fleeting are the wishes and efforts of man! How short his time!
and consequently how poor will his products be, compared with those
accumulated by Nature*

Charles Darwin, 1859

To my brother, who taught me to appreciate every step on the way

ABSTRACT

Increasing evidence suggests that size-selective mortality imposed by commercial fishing results in directional changes in life histories of exploited species, including effects on maturation age, growth rate and body size. Whether these changes are the result of fisheries-induced evolution or other selective pressures in the natural environment and/or phenotypic plasticity continues to be the subject of much debate. Currently, molecular genetic data revealing fisheries-induced shifts at candidate loci are lacking.

Here, the hypothesis that harvesting can induce genetic change over few generations was tested directly by subjecting laboratory-reared offspring of wild-caught Trinidadian guppies, *Poecilia reticulata*, to divergent, size-specific selection over three generations. The smallest/ largest/ random twenty percent of males was selected each generation and changes in standard length, as well as in the frequencies of alleles at neutral microsatellite loci and putative candidate genes for selection were recorded.

Significant divergence between differently selected lines was observed for male standard length ($\pm 7\%$), size ($\pm 8-12\%$) and age ($\pm 4-6\%$) at maturation, compared to only 1% change in standard length over generations in the random breeding control line. Significant drift between lines, but no genetic erosion or inbreeding, was apparent over generations at microsatellite markers. Signatures of selection and significant genetic divergence between selected lines were detected at five out of 17 putative candidate loci (Pr39, M9, M30, M987 and prolactin) which confirmed strong Y-linkage of genes underlying male body size in guppies, as indicated by the phenotypic data. Additionally, significant genotype-phenotype associations were obtained for twelve of the candidate genes. For two of these loci (M30 and M1046) an association between the same single nucleotide polymorphism and a QTL for standard length had been observed previously.

To our knowledge, this is the first study where selection on body size with known intensity and direction has been compared directly with both a phenotypic response and changes at individual genetic marker loci. Hereby, this study forms one of the first pieces of molecular genetic evidence for fisheries-induced evolution: by demonstrating that phenotypic shifts in body size resulting from size-selective harvesting, comparable to commercial fisheries in principle, are underlain by quantifiable genetic change.

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GLOSSARY

AMOVA	Analysis of molecular variance
ANOVA	Analysis of variance
AT	Annealing temperature
BLAST	Basic Logical Alignment Search Tool
bp	Basepair
cDNA	Complementary DNA
cds	Coding sequence
CTAB	Hexadecyltrimethylammomium Bromide
d	Darwins
DNA	Deoxyribonucleic acid
dNTP	Deoxynucleoside triphosphate
FAO	Food and Agriculture Organization
FBPase	fructose-1,6-bisphosphatase 1
FIE	Fisheries-induced evolution
GH	Growth hormone
h^2	Heritability
H_o	Observed heterozygosity
H_s	Expected heterozygosity
HW	Hardy Weinberg
i	Selection intensity
IGF	Insulin growth factor
Indel	Insertion-deletion
LD	Linkage disequilibrium
MC4R	Melanocortin-4 receptor
MgCl₂	Magnesium Chloride
NGS	Next generation sequencing
ORF	Open reading frame
PCR	Polymerase chain reaction
PMRN	Probabalistic maturation reaction norm
QTL	Quantitative trait loci
R	Selection response
RAD	Restriction site-associated DNA
RIPL1	rab interacting lysosomal-like protein-1
S	Selection differential
S.E.	Standard error of the mean
SL	Standard length
SNP	Single nucleotide polymorphism
St. dev.	Standard deviation
V_A	Additive genetic variance
V_P	Phenotypic variance

1. GENERAL INTRODUCTION

1.1 LIFE HISTORY EVOLUTION AND NATURAL SELECTION IN THE WILD

1.1.1 Adaptation to changing environments

Individuals adapt differently to different environments. Understanding the rate and mechanisms by which populations adapt to changing environments touches on the very basis of evolutionary biology and has been the focus of frontline research for decades. It was Darwin's personal observations of local adaptation of beak shape of Galapagos finches on different islands, which led directly to the theory of evolutionary change by natural selection (Darwin 1859). Since this early work, a vast amount of understanding of fundamental evolutionary processes and the dynamic interactions of populations and their environment has been achieved by studying local adaptation and life history evolution in the wild (Endler 1986; Hendry et al. 2011).

What is adaptation? It is important to have a good understanding and precise definition of this deceptively straightforward term. Throughout the present study, adaptation is regarded as a process that increases fitness in any given environment (modified from Hendry et al. 2011). Using this basic definition it becomes instantly clear that traits closely related to fitness, such as life history traits, should be strong targets of selection and thus, changes in life history traits will often be involved in adaptation. It is also important to emphasise that this definition includes both genetic and non-genetic adaptations, implying that not only evolution in a strict, genetic, sense but also phenotypic plasticity (Stearns 1989; Ghalambor et al. 2007) can underlie adaptation. In contrast, throughout this thesis, only genetic change is meant when discussing evolutionary change.

At a phenotypic level, adaptation through genetic change and phenotypic plasticity may have similar outcomes and can be hard to distinguish, for example when countergradient variation is present (Conover and Present 1990; Conover and Schultz 1995) or when environmental change over the study period results in cryptic evolution (Merilä et al. 2001a). From an evolutionary perspective however, the difference between genetic and plastic change is crucial and it can be appreciated

only by an understanding of the mechanisms underlying adaptations (Vasemägi and Primmer 2005; Latta et al. 2007; Gienapp et al. 2008). Understanding the (genetic) basis of adaptations can yield insights into speciation processes, the heritability of adaptations, (that is; whether they will be passed on to future generations), if adaptations are reversible and whether adapted individuals and populations are likely to be able to cope with further changing environments.

1.1.2 Understanding adaptation

To appreciate the mechanisms involved in local adaptation, an understanding is needed of the ecological context of-, or differences between-, contrasting habitats and localities of interest. Furthermore, the genetic differences between, and colonisation history of, the study populations should be assessed. It is the combination of these factors, which often interact in a complex fashion, that shapes population differentiation and determines the rate and nature of adaptation (Shaw et al. 1994; Li & Merilä 2001; Merilä et al. 2001b; Hilborn et al. 2003; Garant et al. 2005).

Molecular techniques are indispensable tools to uncover and understand adaptation processes and to predict how and when populations will adapt to changing environments (Garant and Kruuk 2005; Hendry et al. 2011; Le Rouzic et al. 2011). Neutral molecular genetic markers, such as microsatellites, have provided information on population structure and differentiation in a vast range of species, from skin colour in humans (Jablonski 2004), to local adaptation in seemingly unstructured habitats like the sea (Hansen et al. 2001; Nielsen et al. 2009a).

Recently, technological advances at a quantitative and molecular level have further enhanced our understanding of evolutionary change and the genetic basis of adaptation (Box 1). Until recently, by far the majority of such work has been performed on model organisms, where a wealth of genetic resources and the availability of inbred lines and long-standing selection experiments facilitate powerful associations and genetic scans (Kadarmideen and Janss 2007; Burke et al. 2010). However, next generation sequencing technologies and advanced molecular

techniques are aiding the discovery of genes and genomic regions under selection in a vast range of species (Reusch and Wood 2007; Stapley et al. 2010). Thus, the ultimate goal of characterising the nature and diversity of adaptive genetic variation and the genetic basis of fitness differences between individuals in different environments, is becoming feasible for an increasing number of species (Luikart et al. 2003; Ellegren and Sheldon 2008; Stinchcombe and Hoekstra 2007; Tenaillon and Tiffin 2008). A renewed interest into functional genetic differences between populations has arisen as we can now finally begin to appreciate truly how traits evolve and what genetic correlations and constraints shape the evolution of (life history) traits (Vasemägi & Primmer 2005; Slate et al. 2008; Nielsen et al. 2009a).

For example, different modes of selection at polymorphic sites in the rhodopsin gene have been demonstrated to act in gobies (*Pomatoschistus minutes*) inhabiting water bodies that differ in turbidity and vision (Larmuseau et al. 2009); differences in gene expression profiles explain colonisation patterns in butterflies (Wheat et al. 2011); genome scans have allowed for detecting candidate loci involved in freshwater adaptation in stickleback (Hohenlohe et al. 2010) and horn morphology in wild Soay sheep (Johnston et al. 2011); they are but a few of the breadth of excellent studies in recent years that have made use of molecular tools to answer fundamental questions in evolutionary biology.

1.2 CONTEMPORARY EVOLUTION

Whilst initially regarded as a slow process taking many millions of years or hundreds of generations (Darwin 1859; Wells et al. 1934; Mayr 1966), the realisation has risen that evolution can happen quickly in response to rapidly changing environments (Hendry and Kinnison 2001; Reznick and Ghalambor 2001; Reznick and Ghalambor 2005b). Numerous examples exist that demonstrate adaptation can be a rapid process (Endler 1980; Reznick et al. 1990; Avilés et al. 2006; Palkovacs et al. 2008; Barrett et al. 2010). This understanding has been further fuelled by investigations of how the natural world is affected by human activities and disturbances. Adaptive responses to, for example, pollution (Kettlewell 1955, 1973) fisheries (Sharpe and Hendry 2009), hunting (Coltman et al. 2003); insect control (McKenzie and

Batterham 1994; Raymond et al. 2001) and pesticide resistance (Heap 1997) have demonstrated unequivocally that human activities affect habitats worldwide at a pace rarely observed in history (Palumbi 2001; Hendry et al. 2008).

In particular, human harvesting is a selective force far more direct and consistent than many natural selective drivers (Coltman et al. 2003; Allendorf et al. 2008; Coltman 2008; Darimont et al. 2009) and, in order to safeguard biodiversity and yield, there is an urgent need to understand how and at what rate human disturbances affect ecosystem stability and resilience (Scheffer et al. 2001), species distribution, (Møller and Mousseau 2008, 2009) population dynamics, trophic interactions (Estes et al. 1998; Lande 1998) and evolution of traits (Stockwell et al. 2003).

BOX 1. STRATEGIES FOR IDENTIFYING THE GENETIC BASIS TO ADAPTATION AND FITNESS-RELATED TRAITS

Recently, major technological advances have been made aiding the identification of genetic variation and loci underlying functionally important traits in non-model organisms. Such endeavours are important, as they contribute to our understanding of fundamental evolutionary processes and allow us to predict the long-term consequences of human disturbances. In particular, the possibility to create and access vast amounts of genetic and genomic resources has improved our understanding of these processes. Here, these tools are briefly summarised.

Broadly, approaches for identifying functionally important genetic variation can be classified in two main groups. Firstly, bottom up approaches do not require any *a priori* knowledge on the function and properties of genes of interest and use genome-wide detection techniques (Storz 2005; Butlin 2010) that create and screen large amounts of random markers for F_{ST} outliers in individuals from contrasting environments (e.g. Bonin et al. 2006). This approach yields information on genomic regions putatively under selection, which can then be investigated in more detail to identify loci, and ultimately genes likely to be involved in adaptation (e.g. Wood et al. 2008). Alternatively, when pedigrees are available, associations with phenotypic traits of interest on a high-density linkage map can be made directly (e.g. Rogers and Bernatchez 2005; Johnston et al. 2011).

Secondly, when prior knowledge convincingly suggests that specific loci are likely to be involved in the trait(s) of interest, a top down approach may be preferred, in which the genes of interest are investigated directly for polymorphisms and, if found, followed by exploration of the associations of polymorphisms with relevant phenotypes (Piertney and Webster 2010). When sequence information on the target gene is available for the species of interest, obtaining primer information can be straightforward (e.g. Hemmer-Hansen et al. 2011; this study) but alternatively, published sequences from related species can be used to design primers in conserved regions that cross-amplify in the study species (Primmer et al. 2002; Aitken et al. 2004).

Both approaches have profited immensely from recent advances in sequencing technology allowing for large numbers of markers to be identified and/ or genotyped simultaneously (Mardis 2008; Stapley et al. 2010). Cost-effectively, these approaches are more worthwhile in studies where few individuals and large numbers of markers per individual are required, such as mapping studies or cases where pooled population samples can be used (Burke et al. 2010). When investigating allele frequencies for numerous samples, next generation sequencing still is very costly. A promising new approach in this context is restriction-site associated DNA (RAD) tagging, where numerous SNPs are detected and sequenced simultaneously for large samples in a single sequencing run (Baird et al. 2008). Especially when a reference genome is available, SNP discovery can be realised with relatively light sequencing effort. Additionally, the approach can be used to confirm the role of candidate loci from mapping studies (Holenhohe et al. 2010). Even without the availability of a sequenced genome, the approach is still very powerful in locating functional regions of differentiation from other genomic sources and/ or crosses (Baird et al. 2009; Rowe et al. 2011).

The applications of next generation sequencing (NGS) in recent years predict a surge in knowledge on the genetic basis of fitness variation in the wild. With third generation sequencing close behind it, providing longer read lengths and increased flexibility in *de novo* assembly of genomic data (Stapley et al. 2010), adaptation genomics are expected to become accessible for a rapidly increasing number of natural populations.

1.2.1 Harvesting of marine resources

With respect to yield, fisheries occupy a unique position between other harvested resources, as fish are the only commercial food source that is harvested in the wild on a large scale (as opposed to small scale harvesting such as wild fungi). The tremendous catches by commercial fisheries embody the single largest mortality factor on marine fish post larval stages. Global catches peaked in 1996 with 86.3 million tons of fish. 79.5 Million tons were caught in 2008 and almost 50% of the world's population consumes 15% of their animal protein by eating fish (FAO 2010). In the last century, fisheries have resulted in overexploitation over 30% of commercially valuable fish species with another 50% being exploited up to the limits of their sustainable maxima (FAO 2010).

Fisheries are the single largest mortality factor on adults of harvested stocks, and as such, fisheries form one of the strongest selective forces on wild fish populations observed in the last 100 years (Fenberg and Roy 2008). An increasing body of evidence shows that selection by fishing has negative impacts not only on yield and population sizes (Heino 1998; Law and Grey 1989; Conover and Munch 2002; Ernande et al. 2004) but also life history traits (Jorgensen et al. 2007) and there is an urgent need to understand what adaptations are taking place in harvested species in response to fisheries, both at a phenotypic and a genetic level. In addition to affecting target species, fisheries affect their communities (Jennings et al. 1999; Shackell et al. 2009), resulting in additional loss of recovery potential (Hutchings 2000), resilience (Hsieh et al. 2006) and ecosystem productivity (Worm et al. 2006). Collapses of fish stocks (Beverton 1990; Myers et al. 1997; Hutchings 2000; Dulvy et al. 2003; FAO 2010; Pinsky et al. 2011) combined with globally declining catches (Myers and Worm 2003; Pauly et al. 2003; FAO 2010) show that our understanding of the impact of fisheries on marine resources has been insufficient for their descent management.

The reason for this failure to understand – and predict – the dynamics of marine resources lies partly in the short-sighted vision of some fisheries managers that seem

incapable of safeguarding yield for themselves or future generations¹ (Rutter 1902; Hardin 1968; Botsford 1997; Beverton 1998). Secondly, its explanation lies in the difficulties involved in studying dynamics of underwater populations with very large census sizes, high juvenile mortality and large inter-annual variation in recruitment, survival and population sizes (Winemiller and Rose 1992; Hedgecock 1994; Iles and Beverton 2000; Berkeley et al. 2004). Life history strategies of many harvested marine fish are iteroparous, so-called “bet-hedging” strategies: where reproductive success is highly variable and spread out over a long reproductive period following maturation late in life (Fogarty et al. 1991; Winemiller and Rose 1992). Furthermore, it is often the older and larger individuals that produce the most viable offspring (Trippel 1995; Walsh et al. 2006; Johnson et al. 2011). For the majority of harvested fish species however, detailed information on reproductive behaviour, stock identity and connectivity, migration, compensatory and depensatory processes and trophic interactions is rare at best (Conover et al. 2006; Liermann and Hilborn 2001; Rose et al. 2001). However, all these factors can greatly influence recruitment and survival; violation of assumptions on any on these processes will affect the reliability of predictions of current and future stock sizes (Fogarty et al. 1991; Botsford 1997; Rijnsdorp et al. 2007). Although considerable effort is being made to infer historic population sizes from historical data (Jackson 2001; Lotze and Worm 2009) such information is seldom available – nor used as a baseline reference, even if accessible (Pauly 1995). As research surveys typically date from after the beginning of industrial fisheries, perhaps most complicating of all challenges in fisheries science may therefore be the fact that for the great majority of stocks, no reference data are available for pre-fisheries population sizes and dynamics. Consequently, the impact of harvesting can only be inferred or estimated, and not fully quantified. Research is heavily dependent on landing data from commercial fishing vessels, and vast discards at sea, illegal fishing activities and unreported landings all greatly affect the reliability

¹ Rutter wrote in 1902: “A large fish is worth more on the markets than a small fish; but so is large cattle worth more on the market than small cattle, yet, a stock-raiser would never think of selling his fine cattle and keeping only the runts to breed from. It would be better for the salmon as a species, and therefore better for the salmon industry, if the present minimum net-mesh were made the maximum.” (Rutter 1902, p 134).

and accuracy of fisheries data and complicate its interpretation to aid successful management of stocks (Myers et al. 1997; Watson and Pauly 2001).

The failure to understand the effects of harvesting on population dynamics is reflected in the number of collapsed stocks and declining catches as well as the lack of recovery of stocks after exploitation has stopped (Myers et al. 1997; Hutchings 2000; Petitgas et al. 2010). In some stocks that have been severely diminished by exploitation, recruitment is now so low that it is not sufficient to allow populations to return to their previous abundance levels, even after fishing has been brought to halt (Hutchings 2000). While it is always true that zero spawners will produce zero recruits, more than zero spawners do not always result in viable recruits and for some stocks at least, population dynamics at low levels of abundance seem to be different from those at healthy population sizes. Although conclusive evidence for such compensatory processes is rare (Myers et al. 1995; Liermann and Hilborn 2001), the reasons for an observation of reduced recruitment could further lie in changes in trophic interactions and community structure (de Roos et al. 2006), the age structure of the remnant populations (Berkeley et al. 2004), or increased natural mortality (Swain et al. 2007; Swain 2011).

1.2.2 Fishing as a selective force

Fishing mortality is non-random. The type of gear and mesh size used, depth, season and area targeted affect the catchability of different fish (Swain 1993; Arreguín-Sánchez 1996; Heino and Godo 2002; Kuparinen et al. 2009) and imply that some individuals are more likely to get caught than others. Fisheries are, for example, selective on behaviour, as active fish are more likely to get caught than cautious fish (Heino and Godo 2002; Biro and Post 2008). If such differences exist between sexes, for example differences in mating behaviour or time spent in a high-risk fishing ground, fishing can be selective on sex and result in biased sex ratios (for example in plaice *Pleuronectes platessa*; Solmundsson et al. 2003). Strong schooling fish are most likely to be caught by nets, whilst bold fish are more frequently caught on baited lines (Fernö and Olsen 1994). Depending on depth differently aged fish can be accessed (Swain 1993); fishing on spawning grounds targets solely adult individuals,

whereas catch is irrespective of maturity status on feeding grounds. By varying net mesh size, only the largest or intermediate size classes can be targeted, which can drive selection on growth (Reis and Pawson 1999; Swain et al. 2007). The intricate ways in which fishing acts as a selective force are the subject of decades of study and are discussed in some excellent reviews (Arreguín-Sánchez 1996; Heino and Godo 2002). Here, we focus on a specific aspect of fishing: selection on body size and its consequences for life histories of exploited species.

1.2.3 Fisheries-induced change in life history traits

Selection on body size can affect life history in several ways, which are not mutually exclusive and can be hard to disentangle. Most importantly, the underlying mechanisms of a response can be very different in nature and hard to unravel. Body size is the complex end product of a suite of individual characteristics including life history trade-offs, genetic make-up, and a range of physical factors such as temperature and salinity (Ricker et al. 1978; Conover and Present 1990; Krohn et al. 1997) and biological parameters such as density (Lorenzen and Enberg 2002), food availability (Krohn et al. 1997; Brander 2007) and trophic interactions (Steingrund and Gaard 2005) affecting size at birth, survival, growth and maturation. By definition, increased mortality goes hand in hand with a reduction in population size and associated changes in density-dependent processes and competition for resources. Especially in fish, the most phenotypically plastic of all vertebrates (Rochet 1998), changes in growth and faster maturation may be a phenotypically plastic response to such changes in the environment. In many species, so-called compensatory growth (Policansky 1993) has been observed, where per capita growth increases at low levels of abundance as a plastic response to (harvesting induced) low densities, reduced competition and higher per capita food levels (Policansky 1993; Trippel 1995; Heino and Godo 2002; Engelhard and Heino 2004a). The required size of maturation is then reached at an earlier age.

Amongst others, natural populations of cod (Olsen et al. 2004; Swain et al. 2007), plaice (Rijnsdorp 1993; Grift et al. 2003, 2007), herring (Engelhard and Heino 2004a, 2004b), grayling (Haugen and Vollestad 2001) and salmon (Ricker et al. 1978; Ricker

1981; Hard et al. 2008) have been observed to mature at a younger age and attain smaller body sizes after decades of intense and size-selective harvesting (see for more references Jorgensen et al. 2007).

However, although some of the observed changes can be explained by faster maturation resulting from compensatory growth (Engelhard and Heino 2004a; Hilborn and Minto-Vera 2008), size (Ricker et al. 1978) and growth rate (Swain et al. 2007) actually decreased for several stocks as well, despite favourable conditions. In these stocks, a solely plastic response is insufficient to explain the trends in maturation and body size and genetic adaptation to harvesting offers a potential explanation.

The response of life history traits to such a high, and selective form of mortality like fishing would be expected from life history theory, which states that investments in reproduction are likely to increase at the cost of investments in growth under high predation (Law 1979; Magnhagen 1991; Roff 1991). Harvesting selectively removes older and larger individuals from populations and increases reproductive opportunities for small and early maturing fish. Thereby, fishing enhances fitness for fish that allocate relatively more resources to reproduction at an early age. Provided that growth and maturation traits have a genetic basis, it follows that the frequency of early maturing genotypes will increase under harvesting pressure (Law 2000).

1.2.4 Fisheries induced evolution?

For evolutionary change induced by fishing to take place, two basic requirements must be met that apply to all occurrences of adaptation in nature: firstly, the trait must be heritable, that is; a proportion of the observed trait variance must result from additive genetic variation (Falconer and Mackay 1996) and second, there must be a mismatch between the fitness of the current trait value and the optimal trait distribution (Hendry et al. 2011). For fisheries-induced selection in particular, this means that selection by harvesting must be of such magnitude that it outpaces possible natural selection acting on the same trait in another direction (Conover 2007; Edeline et al. 2007; Stenseth and Dunlop 2009).

Substantial evidence exists that indicates the presence of heritable genetic variation in life history traits in fishes: the presence of countergradient variation for life history traits over environmental gradients (Conover and Present 1990; Conover and Schultz 1995; Conover and Baumann 2009) and successful selective breeding achievements in the aquaculture industry (Jonasson et al. 1997; De-Santis & Jerry 2007) provide strong evidence for a quantitative genetic basis and heritable genetic variation of life history traits (Law 2000).

A mismatch between population mean values for body size and maturation age, and those optimal under fishing pressure is also evident because of the non-random nature of fishing, targeting – in most cases – larger and older individuals. Similarly, large fish are favoured by natural selection in cases where fecundity increases with age and size (Trippel 1995; Walsh et al. 2006; Fenberg and Roy 2008; Johnson et al. 2011) and when fish can outgrow natural predation risk (Heino and Godo 2002; Conover 2007; Edeline et al. 2007). Additionally, fisheries selection, expressed as a high and selective mortality, embodies a much stronger selective force than natural selection for large size and late maturation (Law 2000). Especially on feeding grounds and in heavily exploited stocks, mortality is of such magnitude that fish are often caught before attaining their reproductive age. In cod the age of 50% maturity was around five years in the mid 1990s (Olsen et al. 2004), but cod were caught as young as three years of age (Myers et al. 1997). In some fisheries, mortality is so high, that it affects all adult size classes, virtually removing the size selective component and it can be hard to distinguish whether selection or “simply” increased mortality is the cause of observed declines (Jackson 2001; Fenberg and Roy 2008; Swain 2011). Even in the absence of a size selective component to fishing, or without immature individuals being caught, a decrease in maturation age would still be expected from life history theory, since increased mortality translates to a reduction in lifetime reproductive success and favours an early onset of the reproductive lifespan (Roff 1992).

Less clear than determining a mismatch between optimal and observed trait values, is to establish whether observed changes match selection differentials imposed by

fishing (Kuparinen and Merilä 2007; Law 2000, 2007). The nature and timing of fisheries harvesting greatly affect the intensity and direction of selection it embodies, and plasticity and compensatory growth can obscure selection for reduced growth and small size (Rochet 1998; Heino and Godo 2002; Nusslé et al. 2011). In relation to this, growth at early ages in fish is to a large extent dependent on environmental variables and can determine size later in life, thereby either obscuring or reinforcing evolutionary trends (Letcher et al. 2011). As many species have indeterminate growth (Heino and Kaitala 1999), reductions in size can also be the result of a truncated age structure (Hsieh et al. 2006) and do not necessarily represent phenotypic shifts in size-at-age. Correlations between life history traits further complicate the inference of selection differentials as it is hard to distinguish between traits under selection and co-evolving traits (Heino and Godo 2002; Funk et al. 2005; Munch et al. 2005). Harvesting is seldom the only selective force working on exploited populations over time and other (environmental) factors need to be considered that could explain observed trends in life history traits and phenotypes of exploited stocks (Daufresne et al. 2009).

Such complexities make it difficult to reliably estimate an evolutionary response to fishing and to compare quantitative estimates of selection differentials from fishing with observed phenotypic shifts (Law 2000, 2007). Fortunately, an increasing body of research is dedicated to this matter and realistic estimates of heritability and quantitative genetic parameters in wild populations are becoming more readily available (Jonasson et al. 1997; Haugen and Vollestad 2001; Funk et al. 2005; DiBattista et al. 2009; Nusslé et al. 2009) although direct links between estimates of quantitative parameters and fishing pressure are still scarce.

1.2.5 Discriminating between evolutionary change and phenotypic plasticity

Evidence of fisheries induced changes of life history traits dates from as early as the 1950s (Miller, 1957) but has been largely ignored by the scientific community until empirical studies demonstrated declines in growth, age and size of maturation in harvested stocks a few decades later (Handford et al. 1977; Bigler et al. 1996; Ricker 1981; Rijnsdorp 1993). Even then, a proper scientific debate did not ensue (but see

Stokes et al. 1993; Rochet 1998) until the 21st century (Browman et al. 2000; Law 2000; Kuparinen and Merilä 2007; Zhou et al. 2010). The field of “Darwinian fisheries science” as coined by Conover (Conover 2000) has become a rapidly growing field of study: a European research network dedicated entirely to Fisheries-Induced Evolution (FinE: www.iiasa.ac.at/research/EEP/fine/home.html) began in late 2007 and a brief search on Web of Knowledge for “Fisheries (-) induced evolution” and “Darwinian fisheries” yields 112 of 142 hits published from 2007 onwards, compared to no hits before the 1990s (Fig. 1.1).

This increasing interest in selective effects of fisheries, and in particular its possible evolutionary consequences, is explained by an increasing concern over the potential negative effects of evolutionary change on harvested stocks and yield (Browman et al. 2000; Law 2007; Fenberg and Roy 2008). If selective fishing has evolutionary consequences on the reproductive and physiological characteristics of harvested species, understanding these effects is of critical importance, since evolutionary change in life history traits may irreversibly affect a fisheries yield. In the long run (Law 2000, 2007) genetic erosion may lead to a loss in adaptive potential (Smith et al. 1991; Hauser et al. 2002; Hoarau et al. 2005); changes in life history traits may be hard to reverse if strong selection for large body size is lacking.

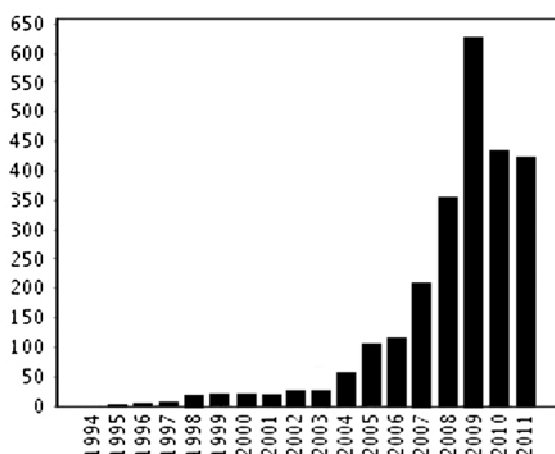


Fig. 1.1. Citation report of the number of studies citing 142 studies on: “fisheries(-) induced evolution” or “Darwinian fisheries”. Created from Web of Knowledge: <http://apps.webofknowledge.com>.

Further debate focuses on the strength of the – mostly phenotypic – data in providing evidence for fisheries induced genetic change (Browman et al. 2000; Hilborn 2006; Hilborn and Minte-Vera 2008; Kuparinen et al. 2008).

One of the earliest and still most convincing examples on fisheries induced evolution comes from Ricker

et al. (Ricker et al. 1978) who demonstrated reductions in size of Pacific Salmon *Oncorhynchus gorbuscha* to be associated with fishing pressure. As these fish almost always mature at 2 years of age, plastic components affecting maturity could be eliminated as a cause of reduced growth, and temperature and salinity trends could explain only part of the observed declines in size. Furthermore, feeding conditions had actually improved over the study period, and a plastic response to environmental changes would have been expected to cause directional change in size in the opposite direction from what was observed. These factors altogether strongly suggest there was a genetic response to harvesting, causing reduced growth. Ricker (1981) demonstrated comparable trends in other species of salmon and considerable work has been done on the effects of fishing on salmon life history traits since then, demonstrating heritable components to body size (Jonasson et al. 1997; Smoker et al. 2000; Funk et al. 2005) and confirming substantial fisheries selection (reviewed in Hard et al. 2008), although, like elsewhere, only phenotypic data is available to infer evolutionary change.

1.2.6 The use of probabilistic reaction norms for inferring genetic change

Examples such as Ricker et al. 1978 are rare and by far the majority of evidence so far is provided by studies using probabilistic maturation reaction norms (PMRN, (Stearns and Koella 1986; Heino et al. 2002), which have been very useful in clarifying the most important drivers behind observed life history shifts (Dieckmann and Heino 2007). The method plots the probability of maturation as a function of age and size (Fig. 1.2). By focusing on the maturation process itself, the approach attempts to disentangle the environmental processes affecting growth and survival from the genetic component determining whether attaining a certain age or size makes maturation likely (Rijnsdorp 1993; Heino et al. 2002). The method has the advantage of relatively straightforwardly visualising trends in maturation independent of environmentally-induced variation in growth, using data readily available from survey and catch data of most exploited stocks. It has been criticised however, for being too reliant on maturation being a function of just age and size and requiring trait variation to be due to environmental factors only (Kuparinen and Merilä 2007; Morita et al. 2009).

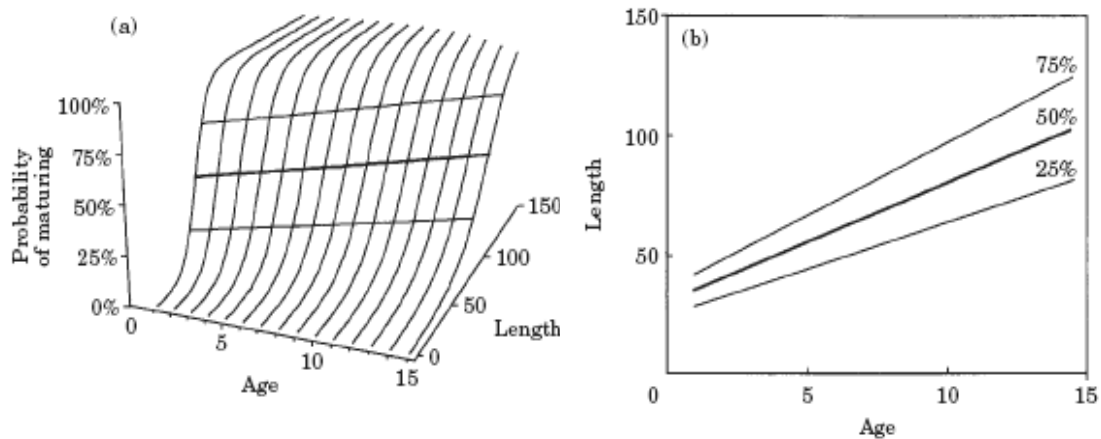


Fig. 1.2. (a) Reaction norms for age and size at maturation describing the probability of immature individuals to mature as a function of size and age. (b) Projection of the 50% midpoints and width of the range of reaction norms on a plain, results in a 2-dimensional representation of the probability of maturation at a certain age-size combination. Figure from: Heino et al. 2002.

If this requirement is not met, PMRNs may be more representative of genetic variation in other traits affecting maturation than of phenotypic plasticity in maturation age and length. Exactly this shortcoming of the reaction norm approach has received criticism from peers: it assumes that maturation is a mere function of current age and size, and that genetic components of traits such as body condition and growth rate leave the maturation probability unaffected (Kuparinen and Merilä 2007). However, in salmon for example, there is evidence that recent growth history is a greater indicator of maturation probability than age or size (Morita and Fukawaka 2006). Barot et al. (2005) found similar reaction norms for different American plaice stocks with different fisheries selection pressures, indicating factors other than fisheries' selection contributed to the norm in some way. Transplant experiments with charr (*Salvelinus leucomaenis*) also demonstrated the PRMN has a plastic component (Morita et al. 2009). In Atlantic cod, *Gadus morhua*, some of the change in age and size of maturation suggested to be a response to harvesting using a reaction norm approach (Olsen et al. 2004) took place in cohorts that were present before a change in exploitation regime occurred. Such an observation implies that environmental change is a more likely explanation for observed changes than genetic adaptations to harvesting (Kuparinen and Merilä 2007; Law 2007).

Multidimensional reaction norms offer a promising means to surmount some of these problems and three dimensional reaction norms have been obtained amongst others for cod (Baulier et al. 2006) sole (Mollet et al. 2006) and plaice (Grift et al. 2007; Kraak 2007), and included body condition and/or temperature as variables. These studies found that the third dimension could explain part of the trends initially attributed to evolutionary effects of fishing but that this contribution was small (e.g. 3-8% in Grift et al. 2007), and a large part remained unexplained. In theory, the reaction norm model can be extended with an unlimited number of axes, including any environmental or physiological parameters on which sufficient data are available. Such multidimensional models are increasingly hard to interpret, however, and reaction norms with more than three dimensions are, to our knowledge, currently nonexistent.

1.2.7 The missing link: conclusive evidence of genetic change

It is not that critics consider the process of fisheries-induced evolution (FIE) to be unlikely; they question the claim that phenotypic data provide conclusive evidence on evolutionary change by selective harvesting (Kuparinen and Merilä 2007; Law 2007; Morita et al. 2009) and the magnitude of FIE as claimed by some (Conover and Munch 2002; Jorgensen et al. 2007). There is ample evidence demonstrating life history changes in exploited species (e.g. reviewed in Jorgensen et al. 2007), but at best very little quantitative or direct molecular genetic evidence is available to support hypotheses on the impact of selective fishing on the genetic composition of populations (Kuparinen and Merilä 2007; Law 2007).

Studies demonstrating a genetic response to fishing are rare for obvious reasons: disentangling genetic effects from phenotypic plasticity can be notoriously difficult, as described in 1.2.5. Secondly, numerous selection pressures operate simultaneously on wild populations, hindering the unequivocal association of a selection pressure with specific phenotypic shifts or individual genetic loci. Thirdly, life history traits, and body size in particular, are quantitative traits of which the genetic basis is still poorly understood. Numerous loci are likely to affect trait distributions due to their polygenic nature. Consequentially, a substantial amount of

non-additive genetic variance contributes to variance of polygenic traits, and phenotypic change is typically much larger than measurable change at individual loci (Falconer and Mackay 1996).

One notable exception is a recent study by Jakobsdóttir et al. (Jakobsdóttir et al. 2011) who examined allele distributions at the *Pantophysin* locus (*Pan 1*) in a temporal data series (1948 – 2002) of Icelandic cod. Their analyses showed a strong decrease in the frequency of the *Pan 1*^{BB} genotype over time, which also had significantly higher frequencies in older fish within single cohorts. Their data suggest strongly that this allele was associated with low fishing pressure and late maturing fish, and demonstrate the value of complementary research strategies; using temporal series of both phenotypic and genetic data at neutral and putative candidate loci. Although the authors do not claim it as such, this study is to the best of my knowledge the only available study to demonstrate fisheries induced changes at a specific locus.

There is an urgent need for studies providing conclusive quantitative- (i.e. matches of observed phenotypic changes with likely heritabilities and fishing selection differentials) and qualitative genetic evidence (i.e. molecular signatures of selection) that can examine whether fisheries selection on body size is responsible for observed trends, and whether this is the result of evolutionary change or phenotypic plasticity. The present study responds to this call by quantifying the selective response to harvesting in experimental populations of Trinidadian guppies (*Poecilia reticulata* Peters). By means of a size selective breeding regime of known intensity and over multiple generations, closely monitoring both phenotypic shifts in life history traits and genetic dynamics, we test directly the hypothesis that harvesting causes genetic change, and whether it is possible to identify potential candidate loci.

1.3 SELECTION EXPERIMENTS AND THE STUDY OF ADAPTATION

1.3.1 Advantages and limitations to the use of selection experiments

Selection experiments allow genetic and environmental aspects of adaptation to be experimentally investigated (Fuller et al. 2005; Conover and Baumann 2009). Experiments form one of the only means to directly test evolutionary hypotheses; to couple a selective agent directly to its response, removing concealing effects of environmental variation and other selective pressures that are likely to be present in the wild. They allow the magnitude of the response to selection in traits of interest and correlated traits to be quantified. Hereby, the extent to which genetic correlations shape and constrain the evolution of traits can be revealed. Furthermore, experiments are the only means to confirm an actual heritable component to any trait by eliminating potentially confounding environmental variables and trends (Conover and Baumann 2009).

There is a large body of scepticism towards experimental approaches to the study of adaptation in the wild. Simplification of natural systems in laboratory environments could affect heritability estimates and alter the nature of the response to selection compared to natural environments (Holloway et al. 1990; Hoffmann and Merilä 1999 but see for example the studies by Weigensberg and Roff 1996; St. Juliana and Janzen 2007). Any gene x environment interactions present in the wild but not in the laboratory will further distort h^2 estimates and complicate the translation of experimental results to the wild (Hoffmann and Merilä 1999; Ellegren and Sheldon 2008). Furthermore, there is often a taxonomic bias towards short-lived species with fast reproductive cycles, which cannot necessarily be compared directly with species of interest in the wild. For example, such fast-reproducing species are often characterised by large census and effective population sizes, which according to Fisher's Fundamental Theorem (Fisher 1930), should elevate the adaptive evolutionary potential compared to species with smaller population sizes.

Despite these limitations, selection experiments have been immensely fruitful in providing insights into the nature of- and correlations between traits responding to

selection (Swallow et al. 1998; Garland et al. 2002) as well as in some major evolutionary processes, such as the strength of genetic correlations (Beldade et al. 2002); the generality of trade-offs (Rose et al. 2005); the relative importance of phenotypic plasticity and genetic composition (Scheiner 2002) and the identification of genomic regions under selection through quantitative trait locus (QTL)-mapping (Rand et al. 2010). However, examples of artificial selection experiments combining quantitative and molecular approaches in non-model organisms are still rare (Fidler et al. 2007).

1.3.2 Experimental studies on fisheries-induced evolution

At least four previous experimental studies have investigated fisheries-induced evolution, though none of these studies utilised molecular genetic markers to explore the nature and extent of genetic change.

Silliman (1975) used an admixture population of *Tilapia mossambicus* (*Oreochromis mossambicus*) and harvested 10-20% of individuals every few months, using body thickness as selection criterion, by harvesting only those fish that were capable of swimming through a defined width between two rods. It took around six generations to observe a strong reduction in yield and male growth.

Edley and Law (1988) performed repeated episodes of harvesting on different size classes of mixed clonal lines of *Daphnia magna*. Every few days, 40% of individuals in the vulnerable size classes were culled and an increase in frequency of slow growing clones in large-harvested lineages, compared to small harvested replicate populations, was recorded. Additionally, divergence in life history traits other than growth rate (age and size at maturation) was observed.

Thirdly, an artificial selection experiment on Atlantic silversides *Menidia menidia* (Conover and Munch 2002) demonstrated a very rapid response of life-history traits to four generations of selection on adult body size. Not only body size responded to selection but a range of life history, physiological and behavioural traits co-evolved and changed significantly as a result of the selection regime (Walsh et al. 2006).

Finally, natural selection experiments on Trinidadian guppies (Reznick et al. 1990, 1997) showed rapid and strong evolutionary responses in life history parameters to relaxed predation pressure (further explained in 1.4.3). The guppy experiment is of particular interest here as it is one of the strongest examples known to date of life history evolution due to size-selective harvesting in the wild. There is a large body of previous- and ongoing work on adaption of guppies to environments with different size-selective predation regimes (Magurran 2005), making these fish an informative model for studying FIE and the ecology and evolution of life-history strategies in general.

1.4 THE TRINIDADIAN GUPPY, *POECILIA RETICULATA*, AS A MODEL SPECIES

1.4.1 *Poecilia reticulata* as a research model

The Trinidadian guppy (*Poecilia reticulata* Peters, Poeciliidae, Cyprinodontiformes, Actinopterygii) is a small, lecithotrophic, viviparous freshwater fish native to Venezuela, Guyana, Suriname and the Caribbean islands of Trinidad and possibly Tobago. On Trinidad, it is by far the most widespread and abundant fish species, and it can be found in most freshwater bodies on the island (Haskins and Haskins 1951; Magurran and Phillip 2001). It has been introduced throughout the world for mosquito control (Courtenay and Meffe 1989) and can now be found throughout the Caribbean and the Americas, parts of Africa, Southeast Asia and Oceania. Escapees from the aquarium trade have even succeeded in establishing successful populations in warm effluent waters of power plants in temperate countries (Fig. 1.3).



Fig. 1.3. Worldwide distribution of *Poecilia reticulata* showing native range (black) and invasive distribution (dark grey). Native distributions are taken from Magurran (2005), invasive distributions from: www.fishbase.org and may be incomplete. With the exception of Russia (Moskou only) distribution of *P. reticulata* may vary within countries, which is not indicated on the map. Inset shows the island of Trinidad with the three Northern river drainages and the Tacarigua River (Ta).

Although the species has gained tremendous popularity through domestication and breeding of strains for the aquarium trade, for which a variety of guppy strains is being used worldwide, it is the original Trinidadian guppy that still is by far the most popular subject of research. This is a result of the fact that much of the geographic variation in behaviour, morphology, and life history traits can be related to a key selective force (predation) and can be interpreted in relation to corresponding fitness variation (see 1.4.3).

The earliest known papers on the species date back to the second half of the 19th century (Peters 1859; Günther 1866) but its popularity for evolutionary studies began over 50 years later with work on sperm competition (Schmidt 1919; Winge 1922a; Winge 1937) and sexual selection (Haskins & Haskins 1949). However, it was not until the work of Endler and Reznick, who disclosed the importance of predation intensity on morphology and life history (Endler 1980, 1988; Reznick and Endler 1982), that the guppies' popularity as a model organism truly exploded. Since then, the species has gained increasing popularity with around 95% of papers being published since 1990. The species is a popular model organism for the study of life history (Reznick et al. 1992; Reznick et al. 2001a), sperm competition and sexual selection (Matthews et al. 1997; Evans and Magurran 2001), population genetics (Shaw et al. 1994; Carvalho et al. 1996); conservation biology (van Oosterhout et al. 2007a), senescence (Reznick 1997; Reznick et al. 2001b; Reznick et al. 2004), behaviour (Magurran et al. 1995; Croft et al. 2009), parasitology (Cable and van Oosterhout 2007) and fisheries-induced evolution (Reznick and Ghalambor 2005a), to name but a few out of the breadth of fields that have benefitted from the extraordinary research qualities of this small fish.

The reasons for such attention are multiple. A good model species can be studied both in its natural habitat and in manipulated environments or laboratories. It responds quickly to manipulations in a measurable way, is easy to breed and has sufficiently short generation times to allow studies over multiple generations within the timeframe of standard research projects. Ideally, a model species' biology is well documented in the literature and it can be found across diverse ecological conditions

in the wild within a small geographical distance, allowing for the assessment of different environmental factors on the species' characteristics. Guppies have all such attributes (Magurran 2005) and in addition, have several of the specific qualities that are required for specialist models of specific fields of research: their sexual polymorphism in colour and heritable colour pattern variations make them ideal for studying sexual selection (Houde 1997); the possibility of controlled mating and artificial insemination (Evans et al., 2003), combined with the ability of females to store sperm (Winge, 1922a, 1937) and multiple paternity within broods provide a convenient setup for testing hypothesis on sperm competition and pre- and post copulatory female choice (Evans and Magurran, 2000); it is possible to tag and mark fish individually for monitoring of social interactions and survival in the wild (Reznick et al. 1996; Croft et al. 2003a, 2003b); their tolerance to a range of temperatures, water qualities and toxic substances, makes guppies a popular subject in toxicological studies (Haubruge et al., 2000; Magurran and Phillip, 2001). Furthermore, guppies show a range of interesting behaviours as reproductive, feeding and predator avoidance strategies and are extremely popular in behavioural research (Magurran and Seghers 1991; Godin and Briggs 1996; Laland and Williams 1997). Last, but by no means least, guppies owe their popularity to the fact that throughout the rivers in the Northern Mountain ranges of Trinidad, marked differences in phenotypic variation at morphological, behavioural and life history traits is repeatedly associated with variation in predation levels between stream parts.

1.4.2 Population distribution; phylogenetic history and connectivity

The Trinidadian mountains host many parallel rivers running down into two main drainages: the Caroni drainage to the West of the island and the Oropuche to the East (Fig. 1.3). These drainages have been separated for at least 600,000 years (Carvalho et al. 1991) and are host to highly divergent clades of guppies (Carvalho et al. 1991; Fajen and Breden 1992; Breden et al. 1999; Alexander et al. 2006; Schories et al. 2009; Willing et al. 2010). In addition, seven notable rivers run down the Northern slopes of the mountains directly into the sea. These were initially believed to be colonised from the Caroni drainage (Carvalho et al. 1991; Fajen and Breden

1992), but more recent analyses suggest that these comprise a third phylogenetic lineage (Suk and Neff 2009; Willing et al. 2010). Guppies can be found mostly in smaller pools, streams and tributaries, rather than in fast flowing or deep bodies of water throughout the three drainages with exception of some of the Northern rivers, which guppies have failed to colonise, most likely due to their isolation rather than unsuitability of habitat (Magurran and Phillip 2001).

Genetic analysis has revealed a clear pattern of differentiation between populations within streams, between rivers and between drainages (Carvalho et al. 1991; Shaw et al. 1991; Shaw et al. 1994; Barson et al. 2009; Willing et al. 2010). Within rivers, upland populations typically depict low levels of local genetic diversity, whereas fish further downstream have more genetic variability and are often an admixture of populations upstream as well as neighbouring rivers. It follows from this that the highest levels of differentiation between rivers can be expected between upland populations; as supported by genetic data (Shaw et al. 1991; Crispo et al. 2006; Barson et al. 2009). Limited gene flow upstream due to barrier waterfalls and strong currents flushing fish downstream during heavy rainfall, explain this source-sink pattern of differentiation (Shaw et al. 1991; Crispo et al. 2006; Barson et al. 2009). The strongest divergence is observed however between drainages (Carvalho et al. 1991; Willing et al. 2010).

The parallel population distributions of guppies in multiple rivers provides a unique system for studying effects of stochastic differentiation, colonisation history and ecological effects on dispersal, population distribution and persistence (Magurran 2005 and references therein). Furthermore, and of particular relevance to the present study, is the fact that predation levels vary between up- and lowland river parts and have shaped the life history of guppies repeatedly, and in similar ways, throughout the river basins.

1.4.3 Predation and life history strategies

Throughout the lower parts of the rivers, guppies share their habitat with different predatory fish communities. Predators such as *Crenicichla alta*, *Hoplias malabaricus*,

Aequidens pulcher and *Astyanax bimaculatus*, can be found in high numbers and are fervent guppy predators (Magurran and Phillip 2001), in particular of adult individuals. Further upstream, the distribution of these predatory fish is limited by waterfalls, which form barriers to their dispersal (Endler 1978). Predation on guppies in upper parts of streams is mainly by the killifish *Rivulus hartii* but only large individuals of this species are capable of feeding on adult guppies and *Rivulus* is mainly a threat to smaller and juvenile guppies only (Mattingly and Butler 1994). Initially, it was thought that the predation difference between the different communities results from a difference in predation intensity as a function of body size; mortality is notably higher for larger individuals in “high predation” sites, but not for juveniles. Later analyses showed that this is not the case, but an overall difference in mortality characterises the two predation regimes (Mattingly and Butler 1994; Reznick et al. 1996).

Although the importance of predation on life history evolution is extremely well studied, surprisingly little is known about the feeding patterns of the different predatory fish and which species actually prey on *P. reticulata* as a major part of their diet (Haskins et al. 1961; Endler 1987; Fraser et al. 1995). The impact of avian predators and invertebrates is also poorly quantified (Endler 1983; Rodd and Reznick 1991). What is evident however, is that predation intensity is much lower, both on adults and juveniles, in the upland communities compared to populations further downstream (Mattingly and Butler 1994; Reznick et al. 1996). This is also true for populations in the rivers North of the mountains, though the species composition of the predatory community is different; the main piscivores are gobies (*Eleotris pisionis*) (Reznick and Bryga 1996).

Endler (1980, 1983) first investigated the role of predation in the evolution of guppies in contrasting habitats, demonstrating colour variation to be the result of sexual selection for brightly coloured males and natural selection for colours that do not stand out from their surroundings in heavily predated areas. Subsequent experiments demonstrated that predation level does not only affect male colour patterns, but affects a whole range of life-history traits in a manner in agreement

with life-history theory (Reznick and Endler 1982; Reznick et al. 1996). Where mortality is high, individuals produce more offspring more frequently and start reproduction at an earlier age, whereas under low predation pressure – where individuals can be expected to have a longer reproductive lifespan – relatively more resources are allocated to growth as opposed to reproduction. The differences persisted over two generations of breeding under common garden conditions, confirming these consistent differences to have a genetic basis (Reznick 1982; Reznick and Bryga 1996). No less than 50 traits, ranging from life history traits such as reproductive allotment and timing of maturation, to sex ratios, colour patterns, behaviour strategies and levels of genetic variation, have been repeatedly found to co-vary with predation regime in different rivers (Endler 1995; Reznick et al. 1996; Magurran 2005) as well as growth rate (Arendt and Reznick 2005), parasite resistance (Cable and van Oosterhout 2007) and morphometrics (Palkovacs et al. 2011).

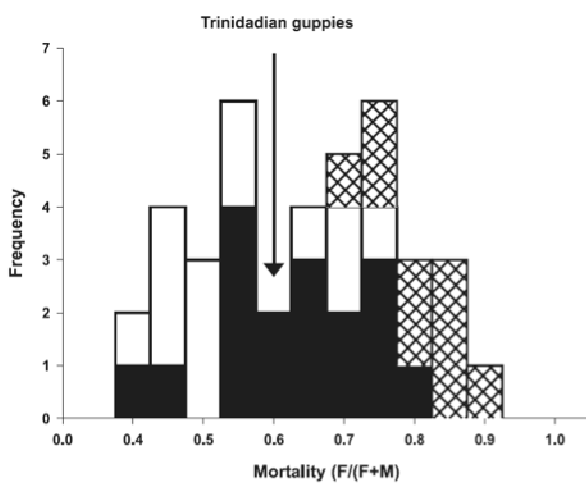


Fig. 1.4. Frequency distribution of mortality values of guppies and exploited marine species, expressing fishing mortality F as a proportion of total mortality $F+M$. Fish species are divided over three categories: pelagics (open bars), heavily exploited groundfish (cross-hatched) and other species (black). Data for guppies comes from Reznick et al. 1996, marine species from Mertz and Meyers 1998. Figure from: Reznick and Ghalambor 2005a.

Using mark-recapture data from previous work (Reznick et al. 1996), Reznick and Ghalambor (Reznick & Ghalambor 2005a) expressed differential mortality of high- and low predation populations as a proportion F of total mortality ($F+M$), a common expression of fishing mortality in fisheries science, and showed that this mortality falls in the middle of the range of fishing mortality levels experienced by marine exploited fish species (Fig. 1.4). Direct comparisons of harvesting-induced life history shifts of marine species and heavily

predated guppy populations are therefore possible and seem relevant.

1.4.4 Transplant experiments

Perhaps most convincing in demonstrating the role of predation in life history evolution, are a series of natural selection experiments where “high predation” guppies (originating from an environment with prominent guppy predators such as *C. alta*) were introduced to a “low predation” environment (with only the weak predator *R. hartii* present) in a tributary of the Aripo River (Endler 1980) and the Guanopo River (El Cedro) (Reznick and Bryga 1987). Over the course of 11 years and 7.5 years respectively, life histories of the introduced fish changed rapidly and significantly, increasingly resembling low predation guppies over time: having large body size with late onset of maturation; producing fewer, large offspring; males displaying bright colour patterns. These differences persisted under several generations of common garden rearing, confirming a genetic basis, rather than phenotypic plasticity driving the observed shifts (Reznick and Bryga 1987; Reznick et al. 1990). In a third, more recent introduction experiment (1996), guppies from a high predation site in the Yarra River on the Northern Slopes, were introduced into a low predation environment of the neighbouring Damier River (Karim et al. 2007). The introduced fish colonised high predation sites further downstream and over less than ten years, developed colour patterns and life history traits different from their ancestral population, as well as different between habitats with different predation regimes in the Damier river (Karim et al. 2007; Gordon et al. 2009).

1.4.5 Environmental differences between upland and lowland habitats

Predation pressure has repeatedly demonstrated to be of great importance in shaping the life history evolution of guppies (see 1.4.3-1.4.4) and makes guppies a useful model to study effects of harvesting predation on exploited fish species (Reznick & Ghalambor 2005a). However, predation is not the only factor that differs between up- and downstream river parts and like for marine fish, environmental factors other than predation may affect growth in guppies.

Although physical properties of the water (temperature, water quality, pH) are no different between sites, canopy cover and population density differ can vary considerably within and between rivers. In areas with low canopy cover, light

availability is significantly higher than in areas with dense forest cover result in elevated primary productivity of algae – the primary food source for wild guppies. Consequently, food availability differs between sites, which in turn affects guppy growth (Grether et al. 2001; Reznick et al. 2001a; Schwartz and Hendry 2010). For example, algal availability and canopy cover can explain the majority of variation in growth rates between different low predation sites (Grether et al. 2001). As canopy cover typically is lower at high predation localities, the early maturation and small body size of guppies at such localities may thus as well be partially an effect of compensatory growth resulting from higher food availability.

Guppy population density is another factor that varies greatly between sites, although in a much more erratic pattern than vegetation. In terms of biomass, low predation sites seem to have higher densities of guppies (Reznick et al. 2001a) but greater schooling at high predation sites may affect density, resource availability and competition locally (Rodd and Reznick 1997). These complex dynamics are still poorly understood (Magurran 2005) but in general, resource availability seems to be higher in open streams and high predation sites leading to faster growth rates and larger asymptotic body size (Reznick et al. 2001a). Additionally, parasite load and resistance to parasites (van Oosterhout et al. 2003, 2007b) is higher in high predation environments and may affect growth and survival. Furthermore, year to year variation is considerable due to seasonal variation (Reznick 1989), flooding (Grether et al. 2001) and external influences such as human disturbance, which can affect population dynamics in a dramatic though unpredictable fashion (Magurran 2005; Schwartz and Hendry 2010).

1.4.6 Predator introduction experiment

To circumvent such co-varying environmental factors that could explain part of the changes observed after the transplant experiment, *C. alta* was introduced into a river stretch of the Aripo River that was previously only inhabited by guppies and *R. hartii* (Reznick 1997). All other environmental factors thus remained equal except predation regime, which increased after the introduction of the predatory fish. After five years, fish in the introduction size were intermediate between control sites up-

and downstream for both age and size of maturation (males) and first parturition (females), although only female age at first parturition was significantly different from the low predation control and the authors fail to report whether these data are obtained from wild-caught fish or from their offspring, reared under common garden conditions (Reznick 1997; Reznick and Ghalambor 2005a). This lack of a response may be evidence of the importance of environmental factors other than predation in determining guppy life history. The experiment is ongoing however and, when compared to the earlier transplant experiments (Reznick and Bryga 1987; Reznick et al. 1990), seems indicative of an ongoing evolutionary response to increased predation. In light of our own experiments, this work is of particular interest as it directly quantifies the effect of increased predation on life history traits. Quantification of such an effect in the wild in this way is, to our knowledge, currently non-existent.

1.4.7 *Poecilia reticulata* as a genetic and genomic model

The body of research dedicated to unravelling the eco-evolutionary dynamics of Trinidadian guppies and the contributions this work has made to our understanding of life history evolution and natural selection in general is impressive. However, the genetic basis of the traits studied is thus far poorly understood and *P. reticulata* as a genetic and genomic model seems to be still in its infancy, although a significant amount of genetic data has been published in recent years (e.g. Dreyer et al. 2007; Willing et al. 2010; Fraser et al. 2011).

Early work using genetic markers focused on clarifying population structure using allozymes (Carvalho et al. 1991; Shaw et al. 1994); phylogeography of guppies in Trinidad has been further studied more recently using microsatellites (Suk and Neff 2009) and single nucleotide polymorphisms (SNPs) (Willing et al. 2010) as is discussed in 1.4.2. Microsatellite development (Becher et al. 2002; Watanabe et al. 2003; Olendorf et al. 2004; Paterson et al. 2005; Shen et al. 2007a) has greatly aided the study of population genetics (Barson et al. 2009; Suk and Neff 2009) sexual selection and inbreeding (van Oosterhout et al. 2003) and allowed for paternity analyses to be used in mate choice studies (Evans and Magurran 2000; Becher and

Magurran 2004). These and other markers also enabled the development of modest linkage maps (Khoo et al. 2003; Watanabe et al. 2004; Shen et al. 2007b; Tripathi et al. 2009a) giving insights into chromosome number (23) and marker distributions, as well as information on physical correlation between traits and the location of the sex locus and sex-linked traits (Tripathi et al. 2009a, 2009b).

However, knowledge on functional genetic variation has, with few exceptions (Brooks 2000) had to wait for the more recent advances in genomic research that allows investigation of the genetic basis of the traits that have been studied for so long. An extensive database of 18,000 expressed sequence tags (ESTs) was developed in 2007 (Dreyer et al. 2007), marking the onset of the genomic age in guppy research. SNP polymorphisms from 224 of these EST-linked markers and a further 819 BAC-linked markers were subsequently used to map colour pattern (size, area, intensity, hue and centre of mass position) and body characteristics (measurements of- and ratios between width and length of morphometric reference distances) of male guppies (Tripathi et al. 2009a). These authors located putative genomic regions for selection in the wild and made a major step forward towards identifying genes that determine male colouration and body size. Already this work has generated valuable insights into functional genetic variation in the wild (Willing et al. 2010), the genetic basis of important traits such as body size (the present study), orange preference by females (Watson et al. 2011) and spine deformities (Gorman et al. 2011). Recently, a full transcriptome of male and female guppies has been sequenced using 454 GS FLX technology (Fraser et al. 2011); candidate genes and polymorphisms for selection were identified, as well as insights gained into (sex specific) gene expression variation (Fraser et al. 2011). Furthermore, the sequencing of the entire guppy genome is expected to commence in 2011 (Dreyer, pers. comm.).

With such major molecular advances, the Trinidadian guppy joins only a handful of species for which we have such well documented knowledge on life history, behaviour and eco-evolutionary- and population dynamics in the wild, as well as the amenability to experimental manipulations and access to extensive genomic resources.

1.5 AIMS OF THE STUDY AND OUTLINE OF EXPERIMENTS

1.5.1 Aims and objectives

In this thesis, artificial selection experiments on the Trinidadian guppy are used to investigate the genetic basis of a response to size selective harvesting, to contribute to the understanding of life history evolution in guppies, fisheries-induced evolution and the genetic basis of body size variation in fish. Specifically, this thesis is aimed at answering the following question:

Can directional size-selective harvesting cause detectable genetic change and phenotypic shifts in life history traits of captive populations of Trinidadian guppies over few generations?

This work addresses the above question by means of four explicit objectives:

1. To quantify the correlated responses of life history traits to size-selective harvesting in guppies
2. To characterise the rate at, and direction in which these traits may change under strong directional selection
3. To monitor the genetic dynamics of neutral microsatellite loci in small, captive breeding fish populations
4. To identify polymorphisms in putative candidate genes associated with phenotypic shifts and a selection response

1.5.2 Underlying rationale

As explained earlier, substantial advances have been made in recent years in our understanding of the circumstances that promote rapid evolution of life history traits in fishes, the rate at which human harvesting can cause phenotypic shifts in commercially exploited species and the genetic basis of adaptation in the wild. However, a conceptual framework in which the knowledge from these advances can be combined to determine the genetic basis of rapid phenotypic shifts in response to human exploitation and disturbance is still lacking. The challenges herein for wild

populations lie in the reliable quantification of selection differentials, which often vary over time, and secondly in convincingly establishing a causal relationship between a selective agent and observed trends (Law 2000, 2007). Supporting such a relationship with an associated genetic trend, in particular at specific loci of known function, is even more challenging and we know of only one example of a study that has succeeded in doing so in marine fish (Jakobsdóttir et al. 2011).

Artificial selection experiments, as used in the present study, maximise control and minimise environmental variation (Fuller et al. 2005). Thereby, they provide a strong method to simplify the complexities involved in disentangling different selective pressures, environmental and genetic change in the wild. Using two different selection regimes of known intensity and direction, in conjunction with neutral microsatellite markers and candidate genes for which substantial support suggests a role in body size (e.g. Tripathi et al. 2009a), the quantitative- and molecular genetic components of a response to harvesting can thus be quantified. Replication within each selection regime will further provide insights into the generality of the response observed.

We have chosen the Trinidadian guppy as a model for its ease of breeding and experimental manipulations and because it is one of a very few species for which the effects of ecology and natural selection on life history have been studied in detail and for which a suit of genetic and genomic tools is available (see 1.4). It is truly a “non model-model organism” and one of the best-known examples of life history evolution in the wild. However, information on the genetic basis of the distinctive traits characterising fish from high and low predation environments is lacking.

This work represents the first time that selection on body size in guppies, as so well-documented to be a major driver of differentiation of wild guppy populations, has been mimicked under controlled conditions. Hereby, the present study contributes directly to our understanding of the genetic basis of life history traits and genetic dynamics of small captive populations. Comparing the outcomes of this work with

observations from the field will further provide insights into the importance of size-selective harvesting as a driver of life history evolution in wild populations.

The intensity of the selection here imposed is strong, but not unrealistic for some semelparous harvested species like salmon where up to 80-90% of individuals can get caught (Ricker et al. 1978; Hard et al. 2008). Fig. 1.5 gives an example of how artificial, knife-edge, selection may differ from that by fisheries on wild populations. The absence of a gradual size range over which fish are more or less vulnerable may have a considerable effect on the intensity of selection and is unrealistic for natural populations. However, such intensity is required to observe a response within the timeframe of an experiment. Furthermore, results can be translated to be relevant for more natural populations, as done by (Brown et al. 2008) for selection experiments on Atlantic silverside (Conover and Munch 2002). Our aim is to contribute to the understanding and identification of the evolutionary processes and

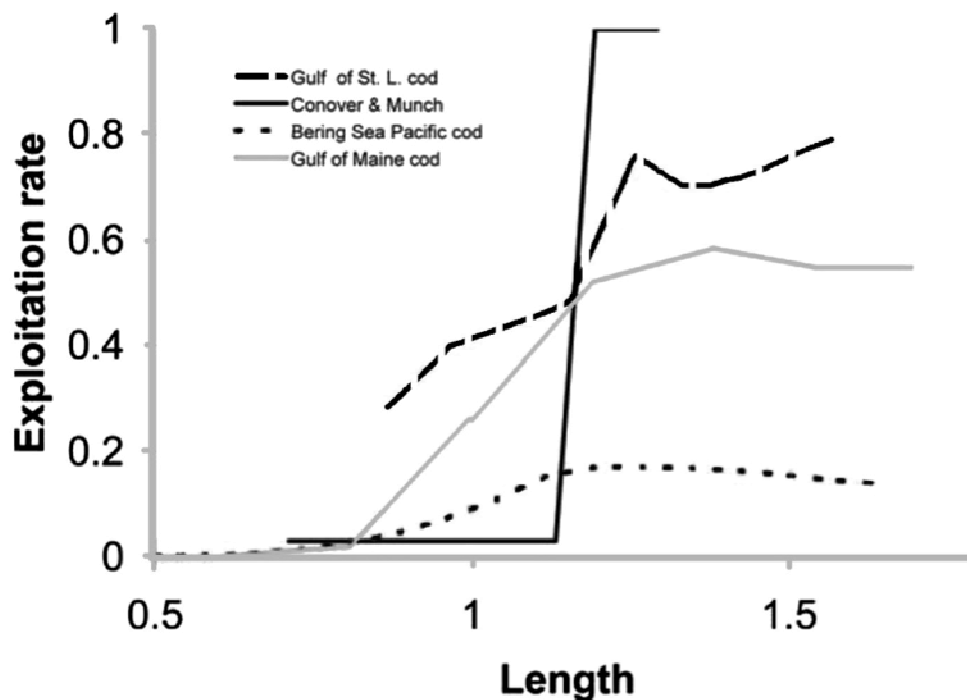


Fig. 1.5. Comparison between artificial selection regime on Atlantic Silversides (Conover & Munch, black solid line) and annual exploitation rates for Southern Gulf of Saint Lawrence cod (black broken line), Gulf of Maine cod (grey solid line), and Bering Sea Pacific cod (black dotted line). Length is plotted relative to a “standardized” length corresponding roughly to 50% vulnerability to the fishing gear and here demonstrates the difference in vulnerability to selection between experimental and natural populations. From: Hilborn and Minte-Vera 2008.

genes involved in a rapid response to selection. To our knowledge, this work represents the first case where artificial selection experiments in fish have been combined with measurements of both neutral genetic diversity at microsatellite loci and putative candidate loci. We hope that these findings will aid the understanding of contemporary evolution and adaptation of natural populations in general.

1.5.3 Outline of the experiments and thesis

This work comprises three main data chapters. Firstly, I describe the phenotypic response to selection experiments on wild-caught Trinidadian guppies and infer heritability of traits and rates of evolution from the data obtained (Chapter 2). Next, I reveal the genetic dynamics of microsatellite loci and quantify stochastic effects and drift between selection lines and over generations (Chapter 3). Finally, I explore the effects of selection at putative candidate genetic markers (Chapter 4)

2.

PHENOTYPIC DIVERGENCE OF MALE
***P. RETICULATA* IN RESPONSE TO THREE**
GENERATIONS OF ARTIFICIAL SELECTION
ON MALE STANDARD LENGTH

2.1 INTRODUCTION

2.1.1 Phenotypic change and micro-evolution in natural populations

The fact that evolution can be a rapid process, taking place over brief time periods and few generations, has become more widely acknowledged and accepted in recent years (Endler 1986; Hendry and Kinnison 1999; 2001; Kingsolver et al. 2001). Several different lines of evidence support the potentially rapid pace of evolutionary change. Firstly, long-term monitoring studies (Grant and Grant 2002; Avilés et al. 2006; Gratten et al. 2008) and manipulations (Endler 1980; Reznick et al. 1990) of wild populations are becoming more common and provide increasing support for natural selection affecting trait distributions on contemporary, ecological, timescales. Secondly, instances of rapid divergence and parallel evolution between populations only recently isolated from each other provide information on the pace adaptation can take in contrasting environments (Stearns 1983; Hendry 2000; Bell et al. 2004). Thirdly, common garden experiments and selection experiments have convincingly demonstrated the genetic basis of, and presence of genetic variation for, fitness-related traits and the capacity hereof to respond rapidly to intense selection (Conover and Present 1990; Houle-Leroy et al. 2003; Barrett et al. 2010). Finally, the increasing influence of human activities on natural populations provides a unique opportunity to study adaptation to environmental change in wild populations, and provides some of the strongest cases demonstrating rapid evolution (Kettlewell 1973; Heap 1997; Lee 2002).

Whether human activities increase the pace of evolutionary change in the wild, or whether they merely direct our attention more towards mapping such changes, in order to understand the magnitude of our impact on the natural environment, is as yet undecided (Carroll et al. 2007). The fact is that the ever-increasing demand for resources by man has affected the majority of ecosystems and species globally (Palumbi 2001; Stockwell et al. 2003; Darimont et al. 2009). Of particular interest here, from both a conservation- and a management perspective (Fenberg and Roy 2008), is the impact of size-selective fishing on exploited marine fish species. Phenotypic shifts in a range of (life history) traits have been reported for several fish

species that have been exposed to intense harvesting pressures (Jorgensen et al. 2007; Sharpe and Hendry 2009) and evolutionary change has been suggested as an explanatory underlying process. As discussed in 1.2.5, the majority of evidence for fisheries-induced evolutionary change (FIE) is based on phenotypic data and indirect measurements of evolutionary change, and care should be taken when interpreting phenotypic change as genetic change. For example, in their analysis of studies on climate change adaptation in birds, Gienapp et al. (2008) found that in only 40% of studies reporting selection on heritable traits, selection actually resulted in a measureable response in the expected direction. Furthermore, from the studies reporting both phenotypic and (quantitative) genetic trends associated with climate change, a majority (64%) of the phenotypic trends were not consistent with the genetic trends reported (Gienapp et al. 2008). Similarly, Hilborn and Minte-Vera (2008) found no correlation between the intensity of fishing and the magnitude of change in weight gain observed in their meta-analysis of 73 exploited stocks. Furthermore, they regularly observed increases in mass at age in exploited stocks as well; representing a response to selection in the opposite direction of what one would theoretically expect. Whether this represents the difficulties involved in detecting genetic change of highly plastic traits under weak selection, biased trait estimates due to the challenges involved in measuring quantitative traits in the wild, or a lack of genetic support for phenotypic trends, remains largely unresolved.

2.1.2 The required evidence for quantifying fisheries-induced evolution

Although the range of studies suggesting FIE is impressive, conclusions on the magnitude and importance of FIE have been criticised on the grounds that (1) phenotypic evidence alone cannot be regarded as conclusive evidence for evolutionary change and (2) careful assessment of the importance of FIE to fisheries management should be made, rather than making premature claims on its impact on yield and the health of stocks (Hilborn 2006; Kuparinen and Merilä 2007; Law 2007; Hilborn and Minte-Vera 2008).

In order to respond to such criticisms, several key pieces of information are required: firstly, in order for the rate of fisheries-induced change to be quantified, reliable

estimates of fisheries selection differentials and heritabilities (Box. 2.1) in harvested populations have to be compared with observed phenotypic shifts. Given the intensity of fishing mortality and the convincing indications available for considerable heritability of body size (Stokes and Law 2000), significant differentials can be expected. However, exact estimates are still rare and hard to obtain: estimating fisheries selection differentials requires information on catch data as well as on that of the remaining individuals, in addition to an opportunity to disentangle fisheries from other selective pressures in the wild. Estimates have been made for body size in cod (Swain et al. 2007) and pike (Edeline et al. 2007) and growth in several species of whitefish (Nusslé et al. 2011) and indeed suggest significant differentials imposed by fishing. Direct estimates of heritability of traits are still harder to obtain in the wild since they require trait values from both offspring and parents, something which is unfeasible for most marine fish species. Successful attempts by Funk et al. (2005) & Smoker et al. (2000) on salmon however, indicate a heritable component to body size of around 0.3, which is in correspondence with observations from experiments and other species (Law 2000; Conover and Munch 2002).

In addition to verifying any correspondence between fisheries selection pressure and observed phenotypic shifts, the molecular genetic basis of this response and of the traits concerned, like body size and the maturation process, needs to be better understood. Only empirically-derived genetic data can provide the conclusive evidence to demonstrate whether current and past selection by size-selective harvesting can induce genetic change over short periods of time. As explained in 1.2.7, such data are still rare and hard to obtain in the wild, although considerable effort is being made (Nielsen et al. 2009b; Jakobsdóttir et al. 2011). Currently however, studies on exploited fish species combining quantitative and molecular genetic data with phenotypic shifts and likely estimates of fisheries selection differentials are absent.

2.1.3 Artificial selection experiments for studying fisheries-induced evolution

In light of the above, artificial selection experiments are an important tool for disentangling genetic and environmental components of phenotypic change (Brakefield 2003; Fuller et al. 2005; Conover and Baumann 2009). By minimising environmental variation, a genetic basis to traits of interest can be verified and estimated. The nature of the response can be precisely quantified and correlations between traits investigated (Chippindale et al. 1997; Houle-Leroy et al. 2003). Careful design of experiments allows for replication and the investigation of the generality of the response (Rose et al. 2005). Comparisons of experiments to wild populations facilitate valuable inferences on the selective forces shaping evolution in the wild (Korsten et al. 2010; Rand et al. 2010). Despite limitations of laboratory-based experiments, often caused by practical restrictions to the number of generations investigated, population sizes and the limited species suitable for such manipulations, these advantages make selection experiments extremely valuable for evolutionary studies. For the study of FIE in particular, experiments are of great value as they can combine the three different components to a holistic assessment of FIE by: (1) knowledge of- and control over selection differentials, (2) the possibility to accurately estimate heritability and quantitative genetic parameters and (3) the opportunity to monitor genetic change over generations at loci of interest in parallel with phenotypic shifts.

Here we present the response to artificial selection on standard length in replicate selection lines of the Trinidadian guppy, *Poecilia reticulata* L. descended from a wild-caught guppy population, as a model to study evolutionary effects of fishing. To our knowledge, this is the first time that selection on body size, as so well documented to be a major driver of differentiation of wild guppy populations (see 1.4), has been imitated under controlled conditions for this species. The results of the experiments conducted here therefore provide a valuable contribution to our understanding of the strength of selection by predation in wild guppies and fish species in general, and to our understanding of the complexity of selective forces that shape life history evolution in the wild. Trinidadian guppies have a unique niche as one of the best-known examples of life history evolution in the wild (Magurran 2005). Due to the

intrinsic qualities of the species as a model species (see 1.4.1) and its capacity to respond quickly, and in a predictable fashion, to selection in the wild, we can investigate the underlying genetic mechanisms in more detail to elucidate the rate of evolution, genetic basis and heritability of body size in these extraordinary little fish.

In this chapter, the phenotypic response to selection on body size is addressed. We use the results of our experiments to make inferences on heritability of this ecologically important trait and provide estimates of quantitative genetic variation and rates of evolution. The molecular genetic response to selection in our experiments will be discussed in Chapters 3 and 4.

BOX 2.1. TERMINOLOGY IN QUANTITATIVE GENETICS

ADDITIVE GENETIC VARIANCE

The proportion of the genetic variation that is derived from paternally and maternally inherited genes: the heritable amount of genetic variation in the narrow sense.

RESIDUAL VARIANCE

The non-additive component of phenotypic variation, comprised of environmental variance and non-additive genetic variance

NON-ADDITIVE GENETIC VARIANCE

Dominance: Interaction between alleles at the same locus or between loci (epistasy) where one allele conceals the expression of another

Pleiotropy: Phenomenon where one gene affects multiple traits

Linkage Disequilibrium: The correlation of allele frequencies at two (or more) polymorphic loci

HERITABILITY (h^2)

Narrow sense: The proportion of phenotypic variance present for a trait which is attributable to additive genetic variance. In other words: the proportion of the phenotype determined by the genes inherited from the parents, or the degree of resemblance between related individuals.

Broad sense: The proportion of variance present for a trait which is genetically determined, comprising both additive and non-additive genetic variance.

SELECTION DIFFERENTIAL (S)

The difference between the mean phenotypic value of the population as a whole and the mean of the selected parents. It is equivalent to the selection intensity i multiplied by the phenotypic standard deviation σ_p .

SELECTION RESPONSE (R)

The change in mean phenotypic value between the mean phenotypic value of the population as a whole and the mean of the offspring. It depends on both heritability (h^2) and the selection differential (S).

BREEDER'S EQUATION

The relationship between the response to selection R , the selection differential S , and the narrow-sense heritability h^2 :

$$R = h^2 S$$

ADAPTIVE GENETIC VARIANCE

Heritable phenotypic variation that is influenced predominantly by natural selection, so enhancing fitness in specific environments (Carvalho et al. 2003).

Unless stated otherwise, definitions are obtained from Falconer and Mackay (1996)

2.2 EXPERIMENTAL DESIGN

2.2.1 Rationale behind chosen selection regime

For the purpose of this study, a selection regime was required that was: (1) straightforward to execute and manipulate; (2) constant for all generations and insensitive to potential slight variations in generation time and to expected differences in body size, growth rate and maturation between lines; (3) controllable for- and excluding as much as possible – complicating factors like maternal effects and reproductive variance; (4) severe enough to likely give a response within three generations of selection and (5) maintainable by one person for multiple generations of fish within a single aquarium system. For these reasons, it was decided to perform mass selection experiments in which selected individuals were allowed to breed freely amongst themselves for a fixed amount of time, after which a cut-off selection regime based on adult (maximum) male standard length (SL) was used to select individuals for breeding subsequent generations.

2.2.2 Minimising effects of drift and sexual selection

The choice of population used in our experiments was motivated by three main points: (1) ensure high levels of genetic variation in the baseline population; (2) minimise reduction of neutral genetic variation over generations and (3) ensure sufficient offspring to facilitate short generation times and minimal age-related variation in body size.

In order to maximise genetic variation in the starting population, fish from a single high predation population were used as the starting material for selection, as high predation populations have naturally higher levels of genetic variation (Shaw et al. 1994; Suk and Neff 2009). Furthermore, female guppies are capable of storing sperm and broods from high predation populations have high levels of multiple paternity compared to low predation populations (Kelly et al. 1999). Sampling of gravid females therefore ensured greater variation in the F1 generation than the wild-caught sample.

In order to decrease reproductive skew resulting from female choice and sexual selection, and to maximise the likelihood of a large number of males fathering in each generation, male competition was reduced by having a female-biased sex ratio of 1.5. Houde (1997) observed that naïve, virgin females are more responsive and less discriminating towards approaching males than experienced females. Rearing the sexes separately in our experiments may thus result in less pronounced effects of sexual selection on reproductive variance than expected under more natural rearing conditions. Furthermore, males from high predation localities perform higher frequencies of sneaky matings (Matthews et al. 1997) than their low predation counterparts and the use of a high predation population therefore may have reduced female choice even further.

The Lower Tacarigua was ultimately chosen for its abundance of fish, thereby not likely to be negatively affected by our sampling of individuals, the easy access for sampling and its prolific breeding properties (out of four sampled populations it produced easily the most offspring).

2.2.3 Minimising maternal effects and inbreeding

In order to remove maternal effects (Box 2.2) and to ensure effects of environmental variation on body size were minimised and standardised for all fish, two generations of random breeding were allowed prior to selection. For selection, a cut-off selection regime was used with an intensity of 20%. This percentage was chosen as we considered it sufficient to provoke a response to selection within the planned number of generations but not as severe as used by others, which has been criticised for being unrealistically high and knife-edged; selecting every individual above a single cut-off size (Brown et al. 2008; Hilborn and Minte-Vera 2008). Although in natural systems, selection is not likely to be as knife-edge as imposed here, such high levels of exploitation mortality do occur in harvested populations (Mertz and Myers 1998, Fig. 1.4).

The decision to use random females and only select on adult male body size was driven by the need to minimise inbreeding levels and variation in maternal effects between lines. Using differently sized females for breeding in the different lines could increase the impact of maternal effects, as female body size is known to affect offspring quality (Reznick et al. 2001b). Secondly, as males virtually stop growth after maturation (Reznick 1990) selection on adult male body size can ensure individuals are chosen based on their genetically-determined body size. Female guppies on the other hand continue growth throughout their adult life and selecting females based on their size would only ensure same-aged, and therefore more likely to be related, individuals to be selected. This could increase inbreeding within selection lines and is therefore undesirable.

BOX 2.2. MATERNAL EFFECTS

Maternal effects are a specific source of environmental variation that affects a female's offspring, causing resemblance between offspring and their mother or between offspring of the same mother, and thereby can be mistaken for inherited genetic variance (Falconer and Mackay 1996). Most maternal effects are pre- and post-natal nutritional effects on offspring depending on the mother's body condition. For example, larger mice providing more milk to their young, increasing weaning weight (Young et al. 1965) and older female guppies give birth to smaller fry (Reznick et al. 2001b). Alternatively, maternal effects can arise from the fact that a mother's offspring share a common environment, resulting in resemblance between offspring traits but not necessarily depending on the condition of the mother. Effects of egg incubation temperature on duckling size (Hepp et al. 2006) provide an example.

Maternal effects can bias experimental results considerably (Falconer 1953) and if left unaccounted for can be of great concern in interpreting experimental results and be of effect even over two generations (so grandmaternal effects on grandoffspring, Kirkpatrick and Lande 1989). In many cases however, (except when one performs selection on maternal effects themselves for example) maternal effects can be standardised between experimental groups by rearing individuals for one or two generations in a common environment.

2.3 MATERIAL AND METHODS

2.3.1 Sampling and transport of fish to the Bangor University aquarium facility

Ninety male and 90 female guppies were collected from the Lower Tacarigua River (10°38'49.5"N, 61°22'47.2"W, grid reference 677228E/117420N). Fish were caught using a 1m² fine meshed net (4mm²) net and hand nets, maintained alive in 20L buckets and transported to the aquarium facility at the University of the West Indies in Tunapuna, where male and female fish were kept in separate 50L aquaria for 48 hours. Fish were transported to the UK in groups of 9-10 fish per 1.5L bag, filled with 0.5L of water and pure oxygen. Upon arrival at Bangor University, males and females were divided equally between two 140L (122 x 30.5 x 38.1 cm) tanks with gravel substrate and artificial vegetation. Only 2 fish died during transport and all fish were in the new aquarium facility within 48hrs.

2.3.2 Health monitoring

Throughout the experiment water quality and health of fish were monitored closely. Unhealthy looking fish were immediately removed from the stock tanks and treated with methylene blue or antibiotics. If no improvement was observed over a seven-day period, the individual was killed humanely using an overdose of MS222 (tricaine methane sulphonate, 2.5ml/L) followed by destruction of the brain. Dead males were placed in 100% ethanol and stored at room temperature. If improvement was seen, the fish was kept in isolation for a further seven days after symptoms had disappeared and then returned to its original tank.

2.3.3 Rearing protocol

Fish were kept in a controlled temperature environment with 12:12 hour light cycles. Water temperatures ranged from 24.5-25.2°C and pH was 7-7.3. Fish were fed *ad libitum* live brine shrimp (*Artemia artemia*) nauplii in the afternoon, except during some weekends and Bank Holidays, when they were fed commercial flake food. Tanks were inspected for fry daily and fry were immediately transferred to separate tanks where they were reared in densities up to 2.08 fry/L. When the oldest fish had

reached 21 days of age and onwards, juveniles were checked for maturity status daily and maturing individuals were removed to an identical separate, single-sex 120L aquarium with densities up to 1.25 individuals/L. Males and females were separated well before reaching sexual maturity and kept in single-sex tanks until all had been sexually mature for at least 30 days, at which all fish was measured for standard length (SL). At the end of the breeding period in each generation except the F6, all parental fish were measured again. Of all male fish still alive at the end of the breeding period, tissue samples were taken in addition to size measurements, placed directly in 100% ethanol and stored at room temperature until DNA extraction.

2.3.4 Rearing of random breeding generations: removal of maternal effects and increasing population size in generations F1-F2

For the first generation of breeding in the aquarium, fry (F1) were collected for 60 days in separate 105L (91.5 x 30.5 x 38.1 cm) aquaria and a total of 313 fry were collected and reared to maturity. From these, 50 males and 50 females were chosen at random and used to parent the F2 generation. In total, 1017 F2 fry were collected over a 90-day period. From these, a random fraction of 97 fry were taken to estimate maturation age and size (see further 2.3.7). A further 250 males and 375 females were reared to maturity, randomly divided into five groups of 50 males and 75 females, placed in five 140L aquaria and used to parent the F3 generation. F3 were produced over a 60-day period and 1200 individuals were reared to sexual maturity. These fish were used to set up the experimental selection lines S1, S2 (selection for small male body size) L1, L2 (selection for large male body size) and a random mating control line (C).

2.3.5 Establishing selection lines in generation F3

All fish used in selection lines were kept at constant 12:12hr light cycles in identical 120L aquaria (60 x 50 x 40 cm) over 2 levels in a continuous flow-through system with coral sand substrate and artificial vegetation. Breeding and rearing tanks from all treatments were distributed at random throughout the bank, water temperatures ranged from 24.5-25.2 °C and pH was constant at 7.2-7.5.

When all males had been mature for at least 30 days, 50 mature males were randomly chosen out of 550 mature F3 males, measured and designated to the random breeding control line (from now on referred to as C). The remaining 500 mature males were all measured and the 20% extreme percentiles of the obtained normal distribution were determined as the selection cut-off size. The 20% smallest and 20% largest male fish were selected subsequently by aligning individual fish to a chart on which the cut-off size was outlined (Fig. 2.1). When the number of selected fish did not match the required sample size of 50 individuals, previously discarded or selected fish (depending on whether too many or too few fish were selected initially) were rechecked until the required number of fish was obtained. In all cases, the difference between determined size and the number of fish initially selected was always less than nine individuals, even when size differences between fish were

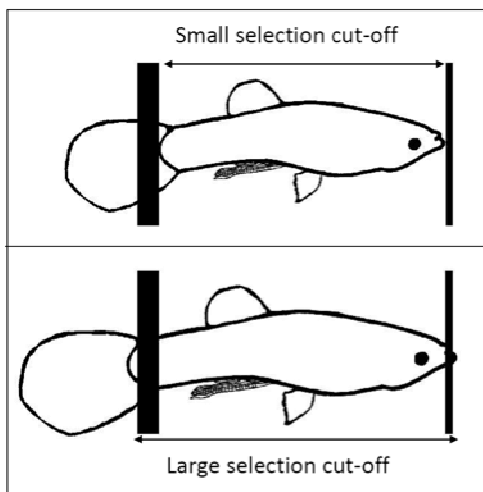


Fig. 2.1. Representation of knife-edge selection procedure, using a chart with two bars. Males falling within the two bars were selected for breeding in S-lines, fishing falling outside both bars for breeding in L-lines. All other fish were discarded.

around 0.1 mm, which strengthens confidence in the accuracy of our measurements.

The selected small and large fish were each randomly divided over two groups, resulting in four groups of 50 males each, two of which consisting out of the smallest 20% of males (from now on referred to as S1 and S2) and two out of the largest 20% of males (from now on referred to as L1 and L2). Each group of males was partnered with a group of 75 randomly chosen F3 females to parent the F4 generation.

2.3.6 Maintenance of selection lines in generation F4-F6

Selected F3 individuals were left to breed at will for 30 days and any fry observed during this period discarded. After this period, F4 fry were collected daily for 60 days. At irregular intervals but at least once weekly, fry were measured immediately after collection until between 100 and 150 fry per line were measured for size at birth. Fry

were kept in identical 120L aquaria and the F4 was reared as described previously, in separate aquaria for males and females until all males were mature for at least 30 days.

When all males had been mature for at least 30 days, 75 F4 females were chosen at random from each line and measured. Per line, 250 F4 males were selected at random and photographed in the same manner. For these male fish, the size distributions obtained were used to determine the selection cut-off size, which was decided upon such that only the smallest/ largest 20% of males (50 fish) were retained. For the control line, 50 fish were selected at random from the pool of 250 males and measured again.

All selected F4 fish were left to mate freely for 30 days to produce the F5, which were reared and of which 50 mature males and 75 females per line were selected to produce the F6 in the same way. For the F6, a random fraction of 100 fry per line was taken to estimate maturation age and size (see 2.3.7) and approximately 100 males and 100 females were reared in the main experiment as for previous generations. When all F6 males were mature for at least 30 days, all fish were measured and the experiments terminated. A schematic overview of the experiments is provided in Fig. 2.2.

2.3.7 Estimation of maturation age and size in the F2 and F6 generations

In the F2 and F6 fry, a random fraction of fry was captured daily and placed in 4 L plastic sweet jars. Up to six fry born on the same day were placed in a jar. All jars were aerated and kept in a controlled temperature environment at 25°C. They were fed *ad libitum* brine shrimp daily and a full water change was performed once per week, at which point each jar was moved to a randomly chosen location within the controlled temperature room. Randomisation was done by collecting all jars on the floor and replacing them at will throughout the room, in order to randomise any effects of microclimate on maturation. Furthermore, in the F2 generation, SL of all fish was measured weekly by taking the average of three measurements using electronic callipers.

Maturity status was confirmed daily by visual inspection of all fish over 14 days of age. If a fish was female, recognisable by black pigment speckling in the anal area, she was removed from the experiment. If a male, recognisable by the onset of gonopodium development, the fish was kept in the jar and reared to maturity. A maximum of five males were reared in any one jar. Upon reaching sexual maturity,

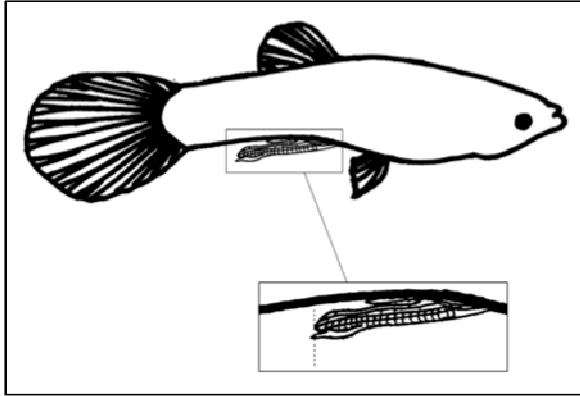


Fig. 2.3. Mature male guppy, as indicated by the developmental stage of the gonopodium: maturation is defined as the fleshy hood extending beyond the tip of the gonopodium (inset).

as indicated by the fleshy hood extending beyond the gonopodium tip (Fig. 2.3, Houde 1997), the male was photographed and in the F6 generation a tissue sample was taken after which he was removed from the experiment. In the F2, males were kept in jars for a further 30 days to obtain a complete representation of male growth in relation to maturity status.

2.3.8 Measurements

Fish were measured by photographing them in a small Petri dish with mm scale on a lighted surface. Pictures were analysed using Adobe Photoshop® to obtain standard length of all individual fish. Accuracy and repeatability of measurements was verified using a set of 50 males for which three pictures were taken for each male and in addition three measurements of standard length were made using electronic callipers. Repeatability was calculated as: $\sum_{1-50} (1 - (\sigma_k^2 / \sigma_t^2)) / 50$, in which σ_k is the standard deviation between repeated measures of the k^{th} fish and σ_t the standard deviation over all measurements (Lynch and Walsh 1998). Repeatability among measurements was high; $0.98 (\pm 0.026 \text{ st. dev.})$ for caliper measurements and $0.95 (\pm 0.050 \text{ st. dev.})$ for photographic measurements. Despite their slightly lower repeatability, photographs were used for the majority of the measurement in this study because of the flexibility allowed in the timing of analysis of the photographs and secondly, because the pictures can be stored and thereby it was possible to recheck them for possible erroneous measurements at a later time.

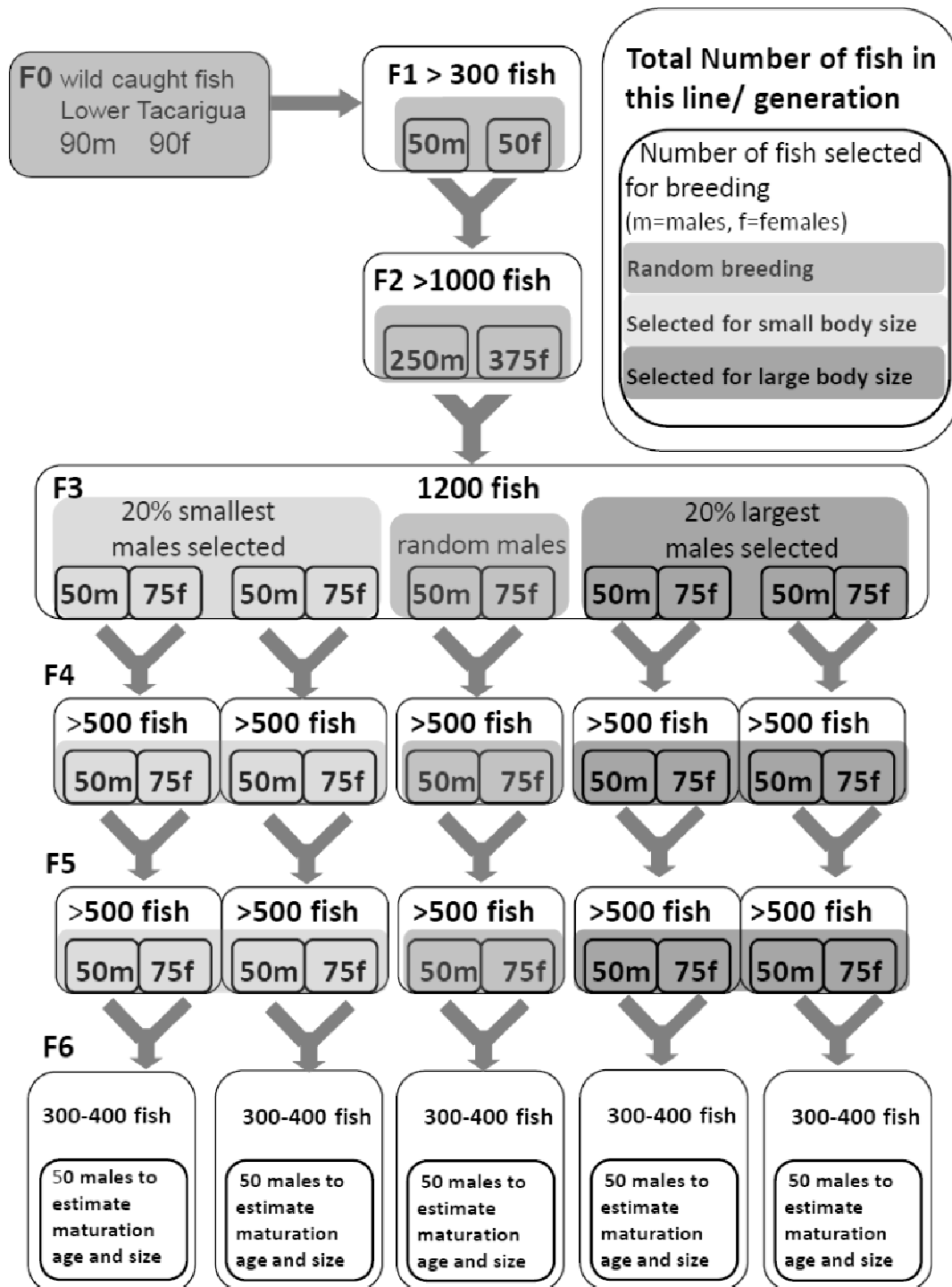


Fig. 2.2. Schematic representation of selection experiments, showing the number of fish reared in the different generations F0-F6. Numbers of fish selected and used for breeding the next generation are indicated in grey, the different shades indicating the different treatments: light grey for small-selected lines, dark grey for large-selected lines and intermediate shading for random breeding generations.

2.3.9 Statistical analyses

PASW Statistics 18.0.3 for Mac was used to test for differences in standard length, age and size of maturation between the selection lines and control line, using single-factor nested analysis of variance (ANOVA), with treatment as fixed factor and replicate line as random factor nested within treatment. Bonferroni post hoc tests were used to reveal which comparisons were significant. Tests were done on both male and female traits and for each generation independently.

Linear regression was used to investigate changes in standard length over generations, except in cases where only two values were compared. In these cases, permutation tests were performed, using Rndom Pro 3.14 (Jadwiszczak 2009) with 10000 permutations.

Quantitative genetic parameters were estimated following Falconer and Mackay (1996), (see Box. 2.1) using the standard relationships $V_A = h^2V_P$ and $R = h^2S$. The selection differential S was calculated for each generation as the difference between mean SL of the population before selection, and mean SL of the selected parents. Response to selection R was calculated as the difference between mean SL of the population before selection and mean SL in the next generation. Heritability was estimated from the slope of the linear regression of the cumulative response to selection over generations; R/S . In order to correct for the fact that selection was performed on a single sex only, which implies the relation between heritability, selection differential and response to selection is; $h^2=2RS^{-1}$, heritability equals twice the slope of this regression. Note that this will inflate the error variance and could lead to an overestimation of actual heritability if some of the response to selection is mediated to Y-linked genes (Winge 1922b; Houde 1992; van Oosterhout et al. 2003).

2.4 RESULTS

2.4.1 Breeding efficacy

The first F1 fry were observed immediately after transport of wild-caught fish and breeding commenced directly. Throughout all generations, fry were typically found at least 30 days after breeding commenced, confirming gestation times found elsewhere (Evans and Magurran 2000).

The number of fry observed varied considerably between days, lines and generations. The maximum range difference in mean number of fry observed per line within a single generation was 15.4 / day in the F5 (the most prolific generation) and generation means ranged from 4.4 – 31.5 fry collected per day over all lines and generations. While reproductive output of females may have varied between lines and generations, different levels of cannibalism are also likely to have caused the variation, as fry were collected only once daily and females were regularly observed chasing newborns as soon as they left their hiding places. The main aquarium facility

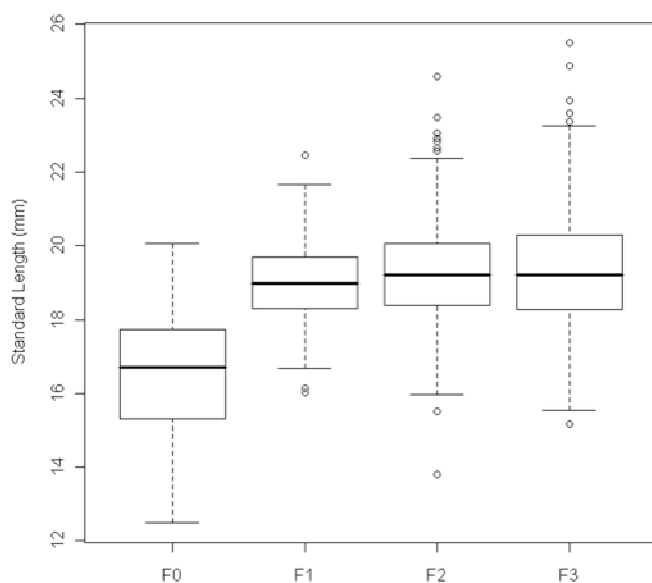


Fig.2.4. Box plot of standard length in mm of wild-caught males (F0) and the first three generations produced by random breeding (F1-F3). Differences in standard length are significant only between F0 and F1 males ($p = 0.001$). Sample sizes were $N = 84, 49, 252$ and 542 individuals respectively for the subsequent generations.

where the fish were housed contained multiple other experimental aquaria and disturbance by human presence cannot be excluded from having caused stress in the fish, increasing cannibalism amongst females. As reproductive output as such has not been quantified for individual females here, we refrained from making any further conclusions on the reasons behind the observed variation in offspring number.

2.4.2 Experimental results – random breeding generations

Standard length

Rearing fish in the aquarium yielded larger fish than those caught in the wild (Fig. 2.4). The first generation of breeding in the lab yielded significantly larger males than those observed in the wild-caught sample (two-sample randomisation test with 10000 randomisations, $p = 0.0001$). Two more generations of random breeding in the lab did however not result in changes in standard length of male fish ($p = 0.122$ and 0.647 for the F1-F2 and F2-F3 comparisons respectively). Linear regression on standard length in generations F1-F3 confirmed this ($R^2 = 0.003$, $F_{1,841} = 2.289$, $p = 0.131$). These results provide strong support for the assumption that optimal rearing conditions and *ad libitum* feeding in the aquarium environment resulted in maximal growth of fish and minimised the effects of variation in rearing environment and feeding levels on standard length.

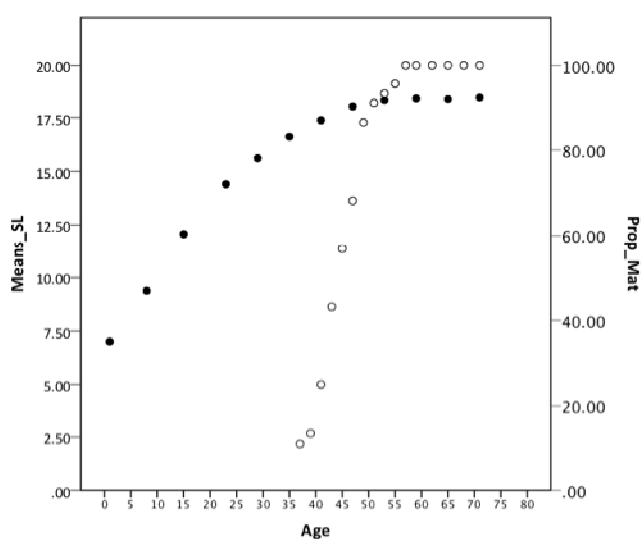


Fig. 2.5: Growth and maturation in the F2 generation. Closed circles show mean standard length (mm) and open circles the proportion of males mature at a certain age (in days). Females were removed from the experiment as soon as they could be identified (14-21 days of age) but data points for juveniles include both male and female measurements. Growth follows a logarithmic model: $(SL = 3.0963 * \ln(\text{age}) + 5.301)$. $R^2 = 0.920$, $F_{1,10} = 115.188$ $p = 0.000$

Growth rate

Growth rate was estimated in the F2 generation and showed a logarithmic growth pattern: ($R^2 = 0.920$, $F_{1,10} = 115.188$, $p = 0.000$). Between 47 and 53 days of age, growth virtually stopped and all fish were mature at 57 days of age (Fig. 2.5). These data strongly support our assumption that the selection cut-off size in our experiments, which is defined when all males have been mature for 30 days, was determined on fully grown males and no males were selected that had not yet attained their maximum size.

2.4.3 Experimental results – response to selection

Response to selection in male standard length

Twenty percent selection on male standard length resulted in strong divergence in length between treatments, but not between replicate selection lines within treatments (Fig. 2.6). A significant divergence in SL was observed between treatments after one generation of selection (nested ANOVA, $F_{2,2.092} = 87.016$, $p = 0.010$). A Bonferroni post hoc test revealed all treatments were significantly different from each other ($p = 0.000$ for S-L and C-L and $p = 0.023$ for S-C). Replicate lines within treatments did not differ significantly from each other ($F_{2,1.211} = 1.041$, $p = 0.354$). After two generations of selection (in F5 males), this pattern was repeated ($F_{2,1985} = 412.277$, $p = 0.003$ between treatments, $F_{2,1.230} = 1.037$, $p = 0.335$ within treatments). For the F6, the variance in sample size between lines was greater than in previous generations (Table 2.1) and the design was therefore unbalanced. Creating a balanced design by sampling 68 individuals per line at random demonstrated significant differences between treatments ($F_{2,2.800} = 14307.362$, $p = 0.000$) but not within treatments between lines ($F_{2,336} = 0.008$, $p = 0.992$).

Table 2.2. Summary of linear regression analysis for males in individual breeding lines of the F3-F6 generations. The slope of the regression is shown, as well as the R^2 , F coefficient and p values.

	S1	S2	C	L1	L2
Slope	-0.495	-0.463	0.007	0.616	0.614
R²	0.13	0.113	0	0.151	0.133
F	$F_{1,1158} 172.948$	$F_{1,1144} 145.471$	$F_{1,1145} 0.030$	$F_{1,1142} 203.001$	$F_{1,1103} 169.456$
p	0	0	0.863	0	0

Table 2.3. Summary of linear regression analysis for females in individual breeding lines for the F3-F6 generations. The slope of the regression is shown, as well as the R^2 , F coefficient and p values.

	S1	S2	C	L1	L2
Slope	0.686	0.514	0.704	0.643	0.653
R²	0.099	0.058	0.102	0.083	0.087
F	$F_{1,594} 65.066$	$F_{1,598} 36.495$	$F_{1,592} 67.304$	$F_{1,595} 54.115$	$F_{1,595} 56.671$
p	0.000	0.000	0.000	0.000	0.000

Table. 2.1. Overview of standard length, standard deviation and population size of selection lines and control line in generations F3-F6. Due to time limitations, the experiment was halted in the F6, resulting in fewer samples and greater variation in population size than in previous generations.

		S1	S2	C	L1	L2
F3	SL (mm)	19.30				
	St. dev.	1.49				
	N	542				
F4	SL (mm)	18.88	18.92	19.22	20.24	20.06
	St. dev.	1.32	1.39	1.60	1.53	1.57
	N	244	245	232	248	247
F5	SL (mm)	18.09	18.25	19.52	20.82	20.74
	St. dev.	1.15	1.08	1.64	1.44	1.60
	N	244	245	249	249	249
F6	SL (mm)	18.02	18.05	19.12	20.77	20.73
	St. dev.	1.16	1.05	1.37	1.47	1.26
	N	130	114	124	105	68

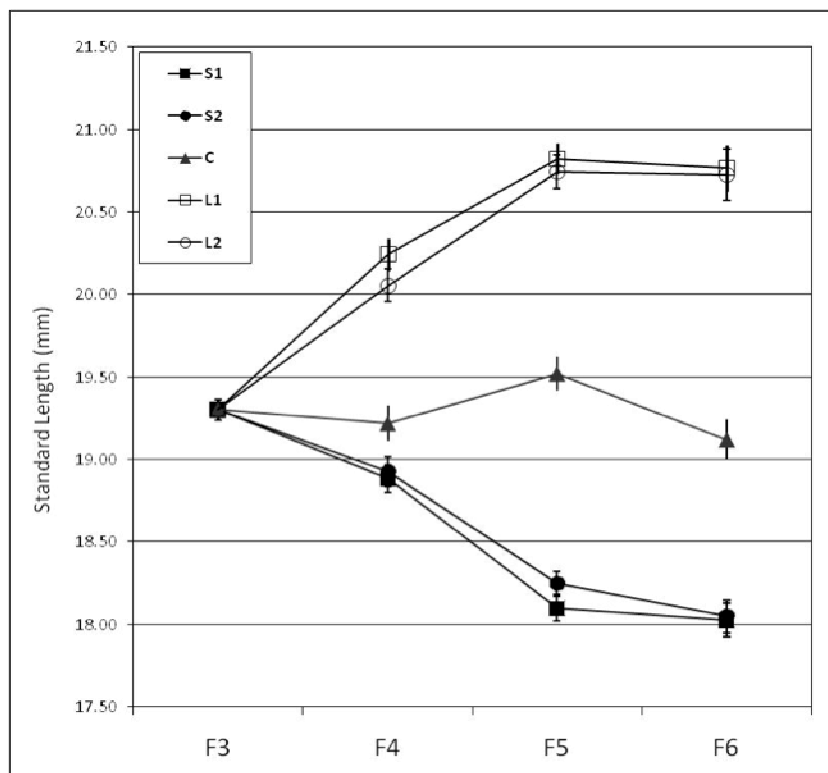


Fig. 2.6. Standard length in mm of selection lines and random breeding control line in generations F3-F6. Open circles and squares are replicate lines selected for large standard length, closed circles and squares for small standard length and the control line is given by closed triangles. Error bars indicate standard errors of the mean.

Linear regression revealed standard length declined significantly in both small selected lines and increased significantly in both large selected lines. No change in standard length was observed for the control line (Table 2.2).

Response to selection in females

No response to selection was observed in females. Female SL was much more variable than male SL and varied between lines and generations (Fig. 2.7). No significant difference between treatments was observed for the F4 ($F_{2,1.997} = 0.859$, $p = 0.538$) but differences between lines within treatments were significant ($F_{2,368} = 3.315$, $p = 0.037$) indicating that environmental heterogeneity was greater than the effect of directional selection, and that the response to selection in males was largely the result of selecting genetic variation at Y-linked genes. For the F6, a similar conclusion can be drawn ($F_{2,2.001} = 0.032$, $p = 0.969$ between, and $F_{2,366} = 3.639$, $p = 0.027$ within treatments). For the F5, significant differences between treatments were observed ($F_{2,2.115} = 10.546$, $p = 0.079$), which, a Bonferroni post hoc analysis revealed, were caused by the control being larger than both S-lines and L-lines ($p = 0.000$ and $p = 0.027$ respectively).

Although regression analysis did indicate a significant increase in SL of females over generations (Table 2.3), Fig 2.7 shows that this is not in a unidirectional pattern, nor consistent with the selection regime and therefore is unlikely to be a result of selection on standard length in males. As no trend was observed over generations and since the few significant differences observed were not in agreement with the direction of imposed selection, changes in female standard length are not likely to be the result of directional selection, nor likely to have had a reinforcing impact on the response to selection in males by consequential maternal effects. The variation in female size is most likely the result of stochastic variation in age distributions of the randomly chosen females. Female guppies have indeterminate growth and a significant correlation was observed between standard length and mean age of females at the time of measurement over generations (Pearson's correlation = 0.315, $p = 0.000$, Fig. 2.7).

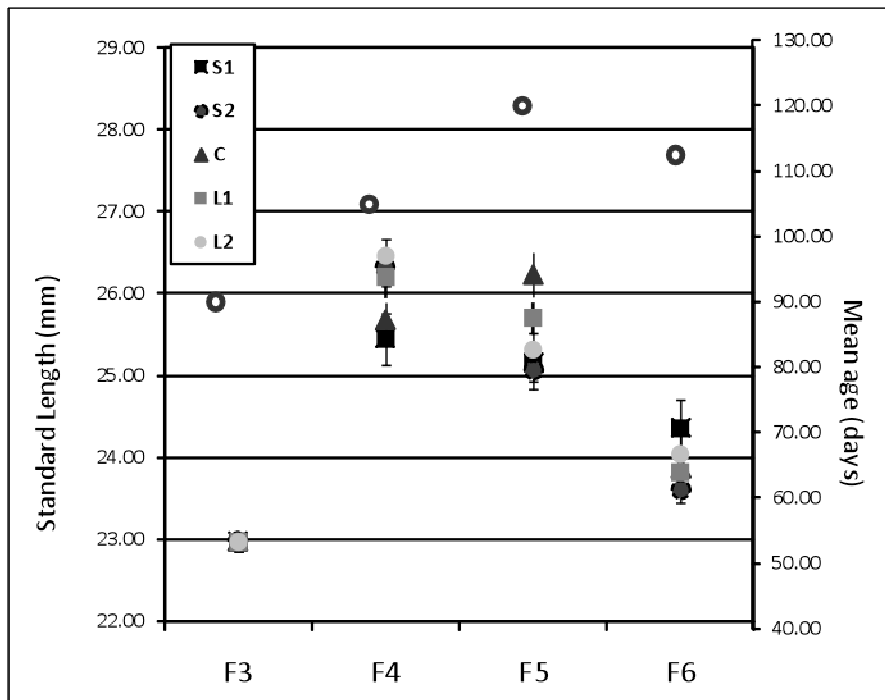


Fig. 2.7. Standard length of females in generations F3-F6 for selection lines and control line plotted with mean age of females per generation (large open circles). Grey circles and squares represent replicate lines selected for large standard length, dark circles and squares for small standard length and the control line is given by closed triangles. Error bars represent standard errors of the mean.

Size at birth

No significant difference in size at birth was observed between treatments in the F6 (nested ANOVA, $F_{1,2.002} = 5544$, $p = 0.143$ between treatments and $F_{2,368} = 1.647$ $p = 0.194$ within treatments).

Size and age of maturation

Size and age of maturation were estimated prior to setting up selection lines, in the F2 generation, and for each selection line independently in the final generation (F6).

In the F2, maturation age (Age_{mat}) and standard length ($Size_{mat}$) were 46.44 days (± 9.37 st. dev) and 18.03 mm (± 1.03 st. dev) respectively. This was significantly smaller than the mean standard length in the main F2 tanks (19.23 mm ± 1.49 st. dev). Even when allowing for an additional 0.5mm of growth after maturation, (as can be expected, see Fig. 2.5), the difference in standard length between fish used for the

maturation experiment and those in the main breeding tanks was still significant. However, complications were encountered with maintaining a constant room temperature where the maturation tanks were housed. Although no significant trend for reduced age or size of maturation over time was observed, ($R^2 = 0.057$, $F_{1,42} = 2.558$, $p = 0.117$) room temperatures up to 2°C above the desired temperature of 25°C were regularly observed and cannot be excluded from having resulted in reduced maturation sizes, resulting in smaller fish than those observed in the main experiment.

In the F6 generation, such complications were absent and $Size_{mat}$ was not significantly different from mean standard length in the control line, or from the F2. Furthermore, no significant difference was found between the F2 and F6_C main breeding tanks.

Maturation age and size were highly correlated in the F2 ($r = 0.651$, $p = 0.000$) and the F6 ($r = 0.799$, $p = 0.000$ over all data and $r = 0.495$, 0.683 , 0.795 , 0.806 and 0.585 for S1, S2, C, L1 and L2 respectively). Both Age_{mat} and $Size_{mat}$ diverged significantly in the F6 generations between treatments ($F_{2,1902} = 28.574$, $p = 0.038$, for Age_{mat} and $F_{2,1895} = 51.284$, $p = 0.022$ for $Size_{mat}$) and both within-treatment comparisons were non-significant ($F_{2,228} = 1.429$, $p = 0.242$, for Age_{mat} and $F_{2,228} = 1.337$, $p = 0.265$ for $Size_{mat}$). The high p -value in these comparisons can be mainly explained by heterogeneity between lines in the S-treatment (Fig. 2.8). A Bonferroni post hoc test on a one-way ANOVA revealed that, whilst both L-lines were almost identical for both traits ($p = 1.000$) and highly differentiated from both S-lines and the control ($p < 0.001$ for all comparisons), S2 was not significantly different from the S1 ($p = 1.000$ for both traits) and the control ($p = 0.962$ for Age_{mat} and $p = 0.460$ for $Size_{mat}$).

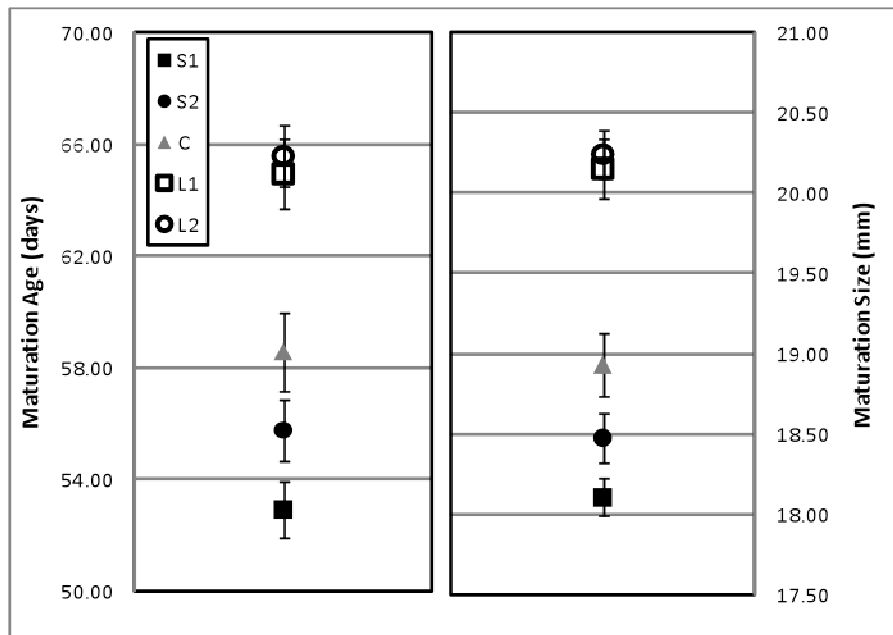


Fig. 2.8. Size (SL in mm) and age (days) of maturation of selection lines and random breeding control line in the F6 generation. Open circles and squares are replicate lines selected for large standard length, closed circles and squares for small standard length and the control line is given by closed triangles. Error bars indicate standard errors of the mean.

2.4.4 Estimates of heritability and quantitative genetic parameters

Heritability

Realised heritability (h^2) was estimated using the breeder's equation $R=h^2S$ (Falconer and Mackay 1996) from the cumulative response to selection R over the cumulative selection differential S . Linear regression through R/S over all selection lines explained the majority of variation between data points (Fig. 2.9, $R^2 = 0.960$, $F_{1,14} = 335.230$, $p = 0.000$) and thereby provides support for a heritable component to SL and for a symmetrical response to selection. As selection was done on a single sex only, h^2 equals the slope of the regression multiplied by two, yielding in this particular case: $h^2 = 2*0.258 = 0.518$, with standard error estimated as twice the standard error of the slope; $2*0.14 = 0.28$. However, when estimated for small and large lines independently, the slope of the regression, i.e. heritability, did differ slightly between the different treatments and suggests a slightly larger h^2 for small body size (Table 2.4). However this difference is not significant (independent sample

t-test, using variances computed from the standard error of h^2 for $n=7$: $T_{(2),11} = 1.31$, $p = 0.218$). Although these two independent estimates did not differ significantly from each other, the low number of data points used for estimating h^2 resulted in low power to test for statistical significance (effect size: 0.698, actual power: 0.225) and the lack of significance between these estimates is therefore more likely the result of a lack of power rather than the absence of actual significance.

Since reliable estimates of maturation age and size were obtained in one generation only, consequently the response to selection of these traits could not be measured, nor could heritabilities reliably be estimated. For these reasons, it was not possible to make inferences on genetic correlations between standard length, size and age of maturation.

Table 2.4. Estimates of heritability (h^2) based on linear regression of R/S for small and large standard length independently. Slope of the regression, R^2 , F - and p value are given for each regression.

	S-Lines	L-lines
R^2	0.933	0.808
$F_{1,5}$	69.487	20.974
p	0.000	0.006
slope	0.269	0.199
S.E.	0.032	0.043
h^2	0.538	0.398
S.E. of h^2	0.064	0.086

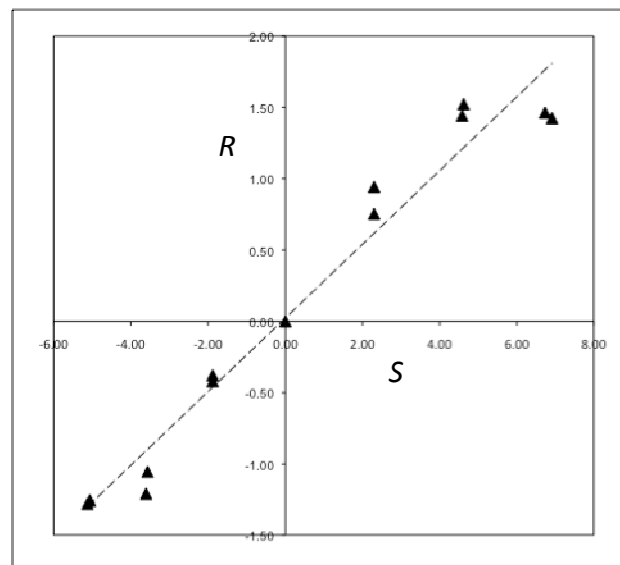


Fig. 2.9. Cumulative response to selection plotted against cumulative selection differential (S) in mm. The linear regression through these data – dotted line – is an estimate of heritability, indicating symmetrical heritability of standard length. Slope = 0.258, $R^2 = 0.960$, $F_{1,14} = 335.230$, $p = 0.000$.

Quantitative variance components of selection lines over generations

Using the estimates of heritability from Table 2.4, the additive genetic variance present in the different selection lines and generations can be estimated, following: $V_A = h^2 V_P$, where V_A is the level of additive genetic variation, and V_P the phenotypic variance, comprised of both genetic (additive and non-additive) and environmental variation (Falconer and MacKay 1996). Although heritability estimates for up- and down selection were not significantly different, the h^2 estimates for S- and L-lines independently (Table 2.4) were used for the calculations of V_A for both directions of selection separately, as these estimates more closely resemble the actual changes in V_A than a global estimate. As no selection was performed on the random breeding control line, and therefore no R/S regression was available, the global estimate of h^2 (0.518) from the regression was used to calculate V_A in this line.

Fig. 2.10 shows the phenotypic variation (V_P) and its additive genetic component (V_A) for all generations and breeding lines. Significant differences in V_P were found only between treatments in the F4 (ANOVA; $F_{2,2} = 20.730, 14.450, 2.739$ and $p = 0.046, 0.065$ and 0.267 for the F4, F5 and F6 respectively. Due to a lack of degrees of

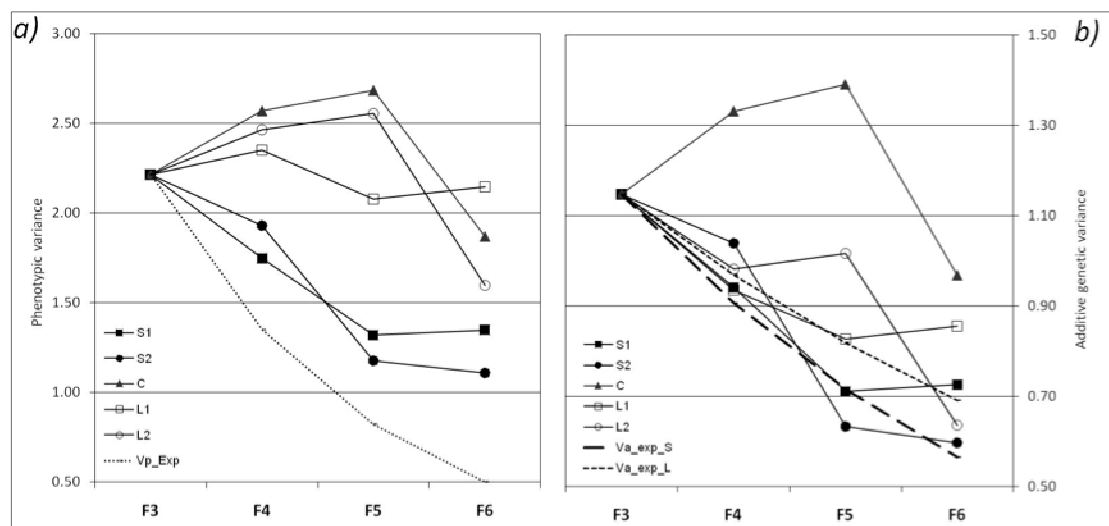


Fig 2.10. Expected and observed phenotypic variance V_P (graph *a*) and its additive genetic component V_A (graph *b*) as estimated using: $V_A = h^2 V_P$, calculated for selection lines and random control independently. Expected V_P and V_A of selection lines were calculated according to Falconer and MacKay (1996) for 20% selection and $i = 0.5 \cdot 1.4$. Heritability estimates from Table 2.4 were used for S- and L- selected lines. For the F3 in the S- and L- lines and for F3-F6 in the control line, the overall estimate of h^2 from the regression in Fig. 2.9 was used.

freedom, within-treatment comparisons and post hoc tests could not be performed). V_A did not differ significantly between treatments (nested ANOVA; $F_{2,2} = 17.618$, 16.436, 1.953 and $p = 0.054$, 0.057 and 0.339 for the F4, F5 and F6 respectively).

Furthermore, the two variance components did not portray the same trend of change over generations. V_p declined significantly over generations only in the S-Lines (logarithmic regression, $R^2 = 0.930$, $F_{1,5} = 32.183$, $p = 0.002$) and did not change in either L-lines or control line ($p > 0.149$ for all models). V_A did decline significantly in both directions of selection, (logarithmic regression, $R^2 = 0.921$, $F_{1,5} = 28.018$, $p = 0.003$ for S-lines and $R^2 = 0.820$, $F_{1,5} = 10.268$, $p = 0.024$ for L-lines), but not in the control line ($p > 0.149$ for all models).

Using the observed values of V_p and the intensity of selection, the expected reduction in V_p and V_A can be calculated following: $V_p^* = V_p (1-k)$ and: $V_A^* = V_A (1-h^2k)$ where V_p^* and V_A^* are the respective variance components in the next generation and k is a constant depending on the selection intensity i . Here $i = 1.4$ and k equals 0.7812, divided by two to account for selection on a single sex only, yields $k = 0.3905$ (Falconer and MacKay 1996). Observed levels of V_p are higher than expected for both directions of selection but the difference is much more pronounced in L-lines than in S-Lines (Fig. 2.10). The observed reduction in V_A is very similar to that expected in S-lines and slightly higher than expected for L-lines.

2.4.5 Rate of evolution

Based on our results, the evolutionary rate of change in standard length was estimated in darwins and haldanes (Table 2.5). Both measures allow the comparison of the amount of phenotypic change in our experiments to measures of contemporary evolution elsewhere. The difference between the two measures lies in the parameter used for scaling evolutionary change. Darwins (d) measure change on an absolute timescale in millions of years. Haldanes depict evolutionary change as the change in standard deviation units per generation, thereby allowing for comparisons between species with contrasting life histories and generation times.

Table 2.5. Evolutionary rate based on three generations of selection on male standard length with $i = 0.2$.

Rate in darwins was calculated as $(\ln X_2 - \ln X_1)/\Delta t$, with X_2 the mean standard length of the F6 and X_1 of the F3. For darwins, t is originally calculated in 10^6 years. However, because of the temporal scale of our experiments, t here was calculated in years and evolutionary rates are shown as 10^3 Darwins (d). Rate in haldanes was calculated as: $((X_2 / S_p) - (X_1 / S_p)) / g$. S_p being the pooled standard deviation $((n_1 - 1)S_1 + (n_2 - 1)S_2) / ((n_1 - 1) + (n_2 - 1))$ and g the number of generations (3). Formulas obtained from Hendry and Kinnison (1999).

	S1	S2	C	L1	L2
10³ Darwins	-51.51	-50.51	7.11	54.94	53.51
Haldanes	-0.299	-0.296	-0.041	0.329	0.324

2.5 CONCLUSIONS AND DISCUSSION

2.5.1 Response to selection

Here we reported on selection experiments in Trinidadian guppies. Six non-overlapping generations of fish were reared in a common and constant environment and we demonstrated a rapid response to selection of male body size. Environmental variation in standard length was successfully standardised in the first two generations of breeding in the laboratory, indicated by an initial increase in standard length but no further change in size in generations F1-F3. After only three generations of selection, a decrease of 6.5-6.6 % and an increase of 7.4-7.6 % of standard length were observed in up- and down selected lines respectively. Laboratory rearing conditions resulted in an increase in standard length of fish. Over generations F3-F6 however, the random control line exhibited less than 1 % (0.94%) change. These results provide strong evidence for micro-evolutionary change in- and a heritable component to standard length in male guppies.

Furthermore, size and age of maturation diverged significantly between treatments. Relative to the age and size of maturation in the F6 generation of the random control, maturation age increased by 10.9 and 12% in L1 and L2 and maturation size by 6.4 and 6.9% respectively. In small selected lines, the response in maturation was slightly smaller for the S1 (-9.6% in maturation age and -4.4% in size) and much smaller in the S2 (-4.8 and -2.4% respectively). The greater response in large selected lines reflects the likewise greater response observed in standard length in L-lines, but the difference between both S-lines is not reflected in the response of standard length in these lines. It cannot be excluded that the rearing conditions in the individual rearing tanks of the maturation experiment affected the S2 fish in a way that resulted in increased standard length of these fish. This is unlikely however, as the largest individuals from the S2 were all born on different days, in different tanks in the randomised design, and not treated any different than jars from the S1 or other treatments. Alternatively, it may be that the genetic basis of the response to selection is more variable in S-lines than in L-lines, causing greater variation in phenotypes between S-lines, an explanation which is clarified further in 2.5.3.

No divergence in standard length between selection treatments was observed in newborn fish. This may be explained by the measurements not having a sufficiently fine resolution to detect differences of such small magnitude. Alternatively, the results could reflect a true lack of response to selection of size at birth. This may indicate that differences in standard length of male guppies are a result of differences in growth rate, rather than physiological differences in body-plan or absolute growth. Furthermore, because no response to selection was observed in females, results indicate that the majority of the response is a result of Y-linked variation. As such variation does not necessarily get expressed in juveniles, a response to selection in juveniles may be absent. Alternatively, since juvenile measurements were done on both males and females, a response to selection in juvenile males may be concealed. However, as only adult standard length, and not growth rate was measured, these alternative explanations could not be tested here.

No response to selection was observed in female fish. On the contrary, although SL varied between generations as a result of variation in the mean age of females, mean SL was remarkably similar between the different selection lines, with the exception of a significant difference between the control and selection lines in the F5. This difference might indicate the process of selection itself, as opposed to random selecting the control, resulting in reduced female body size, possibly by increased inbreeding as a result of selection (van Oosterhout et al. 2007a). However, a difference between the control and treatments was observed in one generation only and is not confirmed by microsatellite data (see Chapter 3). More likely is, although levels of phenotypic variation were higher in females, and therefore small differences between lines would have been harder to detect, that such a lack of response to selection in females indicates strong Y-linkage of the genes underlying the response to selection observed in males. The findings by Tripathi et al. (2009a), who detected major QTLs for male size traits on the sex chromosome of their linkage map of guppies, support this.

Silliman (1975) also reported a response to selection in *Tilapia mossambica* males only: growth rate in males declined significantly over six generations of selective harvesting selection, but no response was evident in females. Furthermore, a delay in the response of females to changes in predation regime was also reported by Reznick and colleagues for their transplant experiments (Reznick and Bryga 1987; Reznick et al. 1997). Like the present study, these authors concluded that strong Y-linkage could explain the observed differences in response rate between the sexes, or alternatively that there might be actual differences in levels of genetic variance for this trait in males and females, or genetic covariance between body size and life history traits. Due to the nature of their experiment, they could not discriminate between the effects of selection on different (co-varying) aspects of life history and therefore could not explain or quantify the (lack of) response to selection on female body size directly. However, as only body size was under selection in the present study and environmental variation was minimal, the present study corroborates their suggestion of y-linkage of the genetic basis of body-size in male guppies.

2.5.2 Heritability of standard length

Heritability estimates here were high; 0.518 overall and 0.538 and 0.398 for S-lines and L-lines independently and are comparable to estimates reported elsewhere. Inconveniently, in many studies addressing fisheries-induced evolution (e.g. Law 2000; Conover and Munch 2002; Law 2007), body length is treated as a life history trait whilst in meta-analyses of heritability in the wild, it is regarded as a morphological characteristic (Houle 1992; Weigensberg and Roff 1996; Kinnison and Hendry 2001). This complicates the transparent comparison of data. As body size affects fitness in many organisms and is closely related to size and age of maturation, fecundity and other such components of life history, it is understandable to regard body size itself as a life history characteristic. Strictly speaking however, it is a morphological trait.

The heritability estimates for standard length in this study are higher than those for life history traits as estimated in the meta-analysis of Weigensberg & Roff (1996), which were 0.268-0.323 on average. Estimated heritabilities for cod and salmonids

(including body length) were around the same magnitude (± 0.3 ; Law 2000), and body length in Pacific Salmon was estimated at 0.4 (Funk et al. 2005). Heritability of morphological traits in Weigensberg & Roff (1996) was estimated at 0.501-0.562, which is similar to the estimates here. Reznick et al. (1997) estimated heritability of body size in male guppies (mg) at 0.88-0.998 which is much higher than our own estimates. Similar estimates (0.9 ± 0.31 s. e.) were found by Reynolds & Gross (1992) and compared to other estimates in guppies our estimates of heritability are therefore low. The reasons for the discrepancies in h^2 estimates between current findings and these two prior studies may lie in population-specific differences in levels of y-linkage or otherwise be an effect of different rearing conditions in our respective experimental designs (D. N. Reznick, pers. comm.). Both Reznick et al. (1997) and Reynolds & Gross (1992) reared fish on food levels measured for each fish individually, while here we provided *ad libitum* amounts of food for whole tanks. Such free access to food may have induced differences in food intake between individual fish and consequently led to higher environmental variation.

However, the heritabilities estimated here are still likely to be exaggerated because our results and those elsewhere (Reynolds and Gross 1992; Reznick et al. 1997) indicate that male body size is, at least partially, Y-linked. Therefore, true heritability is probably lower since the correction for selecting on a single-sex is not necessary for fully Y-linked traits. For the same reason, Houde (1992) obtained extremely high estimates for heritability ($h^2 > 1$) for orange colouration in guppies. Since we do not know the extent of Y-linkage of standard length in selection lines precisely, we cannot quantify such an effect, but it should be kept in mind that true h^2 is likely to be lower than estimated here. Consequently, values of V_A may be overestimated. In addition, heritabilities from this experiment may be somewhat overestimated since no correction has been applied to account for the Bulmer effect (Bulmer 1971). This effect is the result of mass selection reducing variance between families, but not within families, caused by the “joined disequilibrium” of QTLs between related individuals (Bulmer 1971; Hill and Caballero 1992). Not accounting for this effect results in an upward bias of heritability estimated under strong selection. For the above reasons, the actual heritabilities observed here may be closer to those of life

history traits as estimated by e.g. Weigensberg and Roff (1996). However, as the effects of possible Y-linkage and the Bulmer effect have not been quantified here, this remains speculative.

2.5.3 Variance components and their response to selection

Regardless of the possibility of heritability being overestimated in this study, notable differences in h^2 were observed between up- and down selected lines. The explanation for this might be found in several different directions.

Heritability represents a link between additive genetic and phenotypic variation. It cannot be excluded that discrepancies in the accuracy of measurements and the selection procedure resulted in mismatches between observed and expected levels of variance reduction. Additionally, the consistent slower than expected rate of decline in V_p in selection lines in both directions indicates some source of V_p is unaccounted for in our results. However, this cannot explain the strong difference in observed levels of phenotypic variation between S- and L-lines. Therefore, reduced heritability in L-lines indicates either lower V_A or higher levels of V_R (Falconer and MacKay 1996) compared to S-lines. As V_A was similar to- or even slightly higher than expected and no decrease in V_p was observed in L-lines, the lower h^2 in these lines is most likely the result of elevated levels of V_R . Although all fish shared the same environment and were reared under identical conditions, some source of environmental variation may differ between treatments that may explain the higher environmental variation for L-lines than for S-lines. For example, slight variations in density or proportionally higher intake of food of the largest individuals in L-lines may have accentuated differences in food intake between fish in these lines. Therefore, although this is a speculative argument, this elevated environmental variation may account for some of the difference in V_p levels between S- and L-lines.

Alternatively, levels of non-additive genetic variation may be different for the differently selected lines, i.e. dominance and interaction variance. In particular the combined observation of high V_p and higher than expected V_A in L-lines, compared to the resemblances in observed and expected levels of V_A in S-lines, may reflect

changes in levels of dominance variance in L-lines. Dominance variation can be expected to differ between up- and down selected fish, and this can be explained by the possible differences between the genetic bases of large and small body size.

As a quantitative trait, the genetic basis of body size is the product of many genes and therefore non-additive genetic variation can be expected to contribute to trait variation through dominance and epistatic effects. It is not possible here to make any inferences on the effect of genetic interactions between loci on our results. However, large body size is often more closely related to fitness, for example due to improved body condition (Brown et al. 1993) or female choice (Barbosa and Magurran 2006). Although evidence for female preference for large males is inconclusive in guppies (e.g. Reynolds and Gross 1992; Endler and Houde 1995; Evans et al. 2003; Magellan et al. 2005) the observation of increased male size in the absence of predation at least suggest that guppies are no exception to this rule and large male body size may be closer related to fitness than small size, as field experiments show (Reznick et al. 1997).

In his meta-analysis of evolvabilities of traits, Houle (1992) observed higher levels of residual variance for traits closely related to fitness. Such traits, he reasoned, are the combined result of all the selective forces acting on their lower-level components. Consequentially, a larger number of interactions and variables will affect such fitness-related traits. However, being closer related to fitness, large body size is also more likely to be the specific end product of a confined number of pathways, whilst small body size can be achieved through more diverse ways, since reduced size is a more general effect of recessive mutations (Wright 1977; Charlesworth and Charlesworth 1999). Reduced body size as a result of inbreeding for example, has been reported for a range of species (see e.g. Falconer and MacKay 1996 for references) including guppies (van Oosterhout et al. 2007a) and in lake whitefish species (*Coregonus* spp.), markedly lower levels of heterozygosity were observed for dwarf phenotypes than normal-sized fish (Renaut et al. 2011). Such a broader genetic basis to small size may also explain the greater variation in the selection response of maturation between S-lines compared to L-lines.

At least two different processes may therefore contribute to explaining the increased V_R in large, but not in small fish in the present study. First of all, the closer association with fitness of large body size may contribute to elevated levels of V_R in large fish. Secondly, small body size can be expected to be associated with higher levels of recessive homozygotes than large size, and consequently reduced dominance effects. Following the same rationale, if large body size is associated with elevated levels of heterozygosity, this should maximise V_D and contribute to the high variance observed in L-lines. Both rationales, as well potential variation in V_R between lines due to birth rates and food competition, can explain our data and the observation of elevated levels of non-additive variation in L-lines compared to S-lines.

2.5.4 Evolutionary rate of standard length

Natural rates of microevolution

How do the observed rates of evolvability compare to those observed elsewhere? Compared to estimates from wild populations, the estimates of evolutionary rate from our experiments ($50\text{-}55 \times 10^3$ d or 0.2-0.3 haldanes) are very fast. Kinnison and Hendry (2001) observed median rates of 0.035 haldanes in their meta-analysis of studies on contemporary evolution spanning less than 80 generations. Over their entire analysis (over 2000 estimates from studies spanning up to 140 generations) average evolutionary rates were 0.0058 haldanes and 1.2×10^3 d; our rates are ten times higher when calculated in haldanes for the short-generation time studies and around 45 (darwins) and 35-50 (haldanes) times higher when compared to their entire study. Of a greater magnitude than those from Kinnison and Hendry's meta-analysis, were the rates observed after transplant experiments with wild guppies: male size (mg) changed at a rate of $5.3\text{-}27.1 \times 10^3$ d over 7-18 generations (Reznick et al. 1997) or 0.106 haldanes (Reznick and Ghalambor 2005a): 0.2-0.5 times the rate we observed. Darimont et al. (2009) estimated different evolutionary rates for anthropogenically perturbed and naturally evolving systems, and found that the

former increased evolutionary rates by 50-300%. Rates in 10^3 d averaged at 12.06 (\pm 10.45 st.dev) and were highest for marine harvested fish species.

Experimental rates of microevolution

When comparing our results to other instances of artificial selection, the results are very similar. Gingerich (1983) reported an average evolutionary rate of 58.7×10^3 d (range 12-200 $\times 10^3$) from artificial selection experiments, which is close to what was observed in the present study. Using the figures in their publication, we estimated the rate of evolutionary change in darwins for the selection experiments by Conover and Munch (2002). Mean weight of harvested fish (g) increased at a rate in the order of 156×10^3 , and decreased at approximately 95×10^3 d (using an estimated generation time of 235 days). As their selection intensity was much higher (10% of individuals and on both sexes) these double-to-triple rates of evolution when compared to our own work are in the line of what one would expect.

Reasons for high observed rates of evolution

Our high evolutionary rates can in the first place be explained by the high selection intensity and non-overlapping generations that are intrinsic to the experimental design. Furthermore, generation time in the present study was short (6 months) and rates of evolution observed tend to be higher for studies with short generation time (Kinnison and Hendry 2001) or those estimated over brief time periods (Gingerich 1983). Another possibility is that the constant environment in our experiments resulted in high h^2 and consequently rapid evolution of traits. However, although theory suggests h^2 to be affected by environmental conditions (Falconer and Mackay 1996; Hoffmann and Merilä 1999), a considerable body of empirical data suggests h^2 does not differ between laboratory and natural conditions (Weigensberg and Roff 1996; Stokes and Law 2000; Conover and Munch 2002). The even higher heritability for body size in guppies observed by Reynolds & Gross (1992) and Reznick et al. (1997) suggest furthermore that our estimates are not extreme. I am therefore inclined to regard the differences in evolutionary rate observed between our work and natural systems as an effect of the selection intensity employed, rather than of elevated levels of V_A of the trait under selection in our work compared to others.

The evolutionary rates observed here thus are similar to those reported for other artificial selection systems, but much higher than those observed in natural systems. However, our estimates are less than five times as high than those for human-harvested systems estimated by Darimont et al. (2009) which is, considering the strong selection regime imposed here, painfully illustrative of the potential impact human harvesting can have on natural systems.

2.5.5 Overall conclusions

The work reported here has demonstrated that size-selective harvesting is capable of inducing rapid shifts in correlated morphological and life history traits in guppies and provides further advances in our understanding of life history evolution in general. It was known already from field experiments (Endler 1980; Reznick and Bryga 1987; Reznick et al. 1990) that guppies are capable of rapid adaptation to a release of size-selective predation. The present experiments confirm this observation. Furthermore, as a high predation population was used to establish our selection lines, and based on the symmetrical nature of the response, the present study demonstrates that a history of high predation and adaptation hereto in the wild has not deprived guppies of additive genetic variation for life history traits. Although only a single wild population was used, and therefore care must be taken with inferring general conclusions from our observations, we have demonstrated a considerable additive genetic component to variation in standard length and confirmed that the rapid response to selection is at least partially due to Y-linkage of size-related traits in male guppies. Furthermore, our data suggests that large body size in guppies is partially governed by dominance variation at the underlying loci, whilst small fish possess less non-additive genetic variation and are more likely to be the result of greater occurrence of recessive homozygotes.

To what extent can the present study inform on fisheries-induced evolution? Previous experimental work (Conover & Munch 2002) with the same aim has been scrutinised for having unrealistically strong selection intensities. In addition, non-overlapping generations, the knife-edged aspect of the experimental design and the absence of compensatory processes made the observed response not directly

comparable to commercial fisheries (Hilborn and Minte-Vera 2008). Similar criticisms can be justly delivered here: our system is simplified and does not incorporate realistic fishing pressures or compensatory processes. However, we maintain that our findings do nevertheless make a valuable contribution to the ongoing debate on the importance of fisheries-induced evolution for various reasons.

Firstly, the knife-edge selection regime was required here to make it feasible to obtain a response within the duration of this study. Whilst unrealistic in its current form, it is possible to transform the data obtained here to more realistic time spans and selective pressures (Brown et al. 2008).

Secondly, some of the most convincing examples on fisheries-induced evolution come from semelparous Pacific salmon (Ricker 1981) and there is substantial concern over the evolutionary effects of fishing on salmon stocks, with fishing mortalities as high as 70% (Ricker et al. 1978) and 80-90% (Hard et al. 2008) reported. The evolutionary rates observed here may therefore be directly comparable to rates observed in salmon and provide support for the occurrence of evolutionary change in exploited salmon stocks. In addition, the symmetry of the response we observed from a population that had a history of intense size-selective predation in the wild bodes well for the reversibility of an evolutionary response to selection, though empirical testing is required here.

Thirdly, whilst the absence of realistic density- and compensatory processes in our design is likely to have affected the results, this simplified design maximises the likelihood of picking up a genetic response to selection and sheds light on the genetic basis of body size and the dynamics between selection intensity and its genetic and phenotypic response. In light of fisheries-induced evolution, the principles shown here demonstrate the directionality and potential for selection on body size to induce detectable genetic change over few generations of selection. We have clearly demonstrated that there is an important interplay between the selection intensity, phenotypic and genetic change and it is highly likely that this is at least partially illustrative of the dynamics of fish and fisheries on a greater scale.

3.

GENETIC DYNAMICS OF

SELECTION LINES OF *P. RETICULATA* I:

GENETIC VARIATION AT NEUTRAL

MICROSATELLITE LOCI AND DRIFT BETWEEN

SELECTION LINES

3.1 INTRODUCTION

3.1.1 The use of microsatellites for studying genetic diversity of exploited fish species

Microsatellite markers have been used widely to answer an array of questions on the dynamics and connectivity of wild populations (Awise 2004). For aquatic species in particular, whose migratory behaviour and intraspecific interactions occur under water, and whose abundance can easily conceal complex structure (Conover et al. 2006), molecular markers are of great use. For example, neutral microsatellite markers have been previously used in guppies (see 1.4.2) and a wide range of marine and freshwater fish species to assess levels of genetic variation (DeWoody and Awise 2000), expose spawning competition (Bekkevold et al. 2002) and correlations between offspring and parental traits through paternity analysis (Johnson et al. 2011), reveal population structure (Ruzzante et al. 2000; Bernal-Ramírez et al. 2003) and migration patterns (Hendry 2000; Ruzzante et al. 2006). In addition, microsatellites have been very valuable for population assignment of mixed stocks (Nielsen et al. 2001) and estimating effective population sizes (Hauser et al. 2002; Poulsen et al. 2006), which, molecular markers revealed, can be orders of magnitude lower than census sizes. More recently, dense mapping of microsatellites and the design of expressed sequence tag (EST)-linked microsatellites has provided evidence of putative non-neutrality and selective responses of microsatellites (Nielsen et al. 2006; Larsson et al. 2007), making them useful markers in adaptation studies using genome scans and outlier analyses (Hansen et al. 2010; Martínez et al. 2011).

Microsatellite markers have also proven useful for studying evolutionary effects of fishing (Hauser and Seeb 2008), although this field has, with few exceptions (Carvalho and Pitcher 1994; Park and Moran 1994), only emerged recently. The majority of genetic work in fisheries, besides advances in the genetics of aquaculture breeding (De-Santis and Jerry 2007), has focused on estimating effects of exploitation on neutral genetic diversity, and reductions in effective population size (N_e) have been associated with harvesting pressure (Hauser et al. 2002; Hutchinson et al. 2003; Hoarau et al. 2005).

Such reductions in neutral genetic diversity associated with fishing pressure, are virtually the only genetic data currently available in support of fisheries-induced evolution. However, in most exploited species, even very low $N_e:N$ ratios still imply thousand(s) or more breeding individuals, and such skewed ratios are observed in combination with temporal stability of allele frequencies (Poulsen et al. 2006; Cuveliers et al. 2011). Loss of neutral genetic diversity through drift therefore may not be an immediate concern for many intensely harvested stocks (Poulsen et al. 2006, Cuveliers et al. 2011). In large marine fish populations, drift typically operates at much lower rates than selection (Wright 1951). Therefore, neutral genetic variation may be especially unsuitable as a measure of evolutionary change as specific traits affected by fisheries selection, such as growth and aspects of life history, are likely to evolve at rates that differ from those of neutral genetic markers (Merilä and Crnokrak 2001; McKay and Latta 2002; Luttikhuizen et al. 2003; Hutchings et al. 2007). In light of fisheries-induced evolution (FIE), neutral genetic markers may therefore be best suited as a genetic baseline to compare putative candidate markers to. This was, for example, done by Jakobsdóttir et al. (2011), who observed temporal stability at six microsatellite loci, compared to strong changes in allele frequencies at the *Pan I* locus that could be associated with both fishing pressure and changes in age structure in cod. Comparing such baseline variation to candidate gene frequencies offers an opportunity for assessing the effects of selection at a molecular level (Hemmer-Hansen et al. 2007; Hansen et al. 2010; Tonteri et al. 2010). Moreover, monitoring of neutral genetic diversity over time or across generations can reveal information on mating patterns and inbreeding.

3.1.2 The use of microsatellites for studying genetic diversity in artificial selection experiments

In contrast to many natural fish populations, drift may be of considerable importance in small confined populations, e.g. captive populations and selection lines, where furthermore inbreeding and mating patterns may greatly affect levels of genetic variation. For this reason, neutral genetic variation needs to be monitored, quantified and valued correctly.

Surprisingly however, with the exception of studies focusing on bottleneck effects on genetic diversity (Montgomery et al. 2000; England et al. 2003) only few studies have specifically monitored neutral genetic variation in artificial selection experiments (Morgan et al. 2003; Barrett et al. 2010) and even fewer have done so in combination with exploring putative candidate gene frequencies. Numerous experimental studies use molecular markers for e.g. QTL-mapping or genome scans to identify candidate loci of interest (Sørensen et al. 2007; Rand et al. 2010; Svetec et al. 2011), but I found none that actually compared the dynamics of neutral and putative selected loci directly. By far the majority of studies focuses solely on candidate loci and fails to report comparisons with neutral loci (Tao and Boulding 2003; Belter et al. 2004; Fidler et al. 2007). However, high levels of drift and/ or loss of genetic variability in selection lines can be a concern since high levels of genetic erosion and drift could lead to a loss in adaptive variation and/ or conceal the effects of selection (Hartl and Clark 1989). Several studies have concluded that selective breeding, even in small groups (<15 breeding pairs per generation), did not lead to a loss in genetic variability at neutral microsatellites loci over few generations, but did however result in significant drift of allele frequencies between selection lines and within the same line over generations (Morgan et al. 2003; Simões et al. 2008a, 2008b, 2010). Considering the extent of work that has been building on selection experiments (Chippindale 2006), endeavours towards a thorough understanding of molecular genetic dynamics of both neutral markers and putative candidates for selection in experiments, seem justified.

For the present study, microsatellites were used to contribute to two different aspects of genetic assessment: (1) to provide a baseline to compare putative candidate gene frequencies to and (2) to quantify the effects of drift and artificial selection in small, captive breeding populations and selection lines on supposedly neutral marker loci.

3.2 MATERIAL AND METHODS

3.2.1. Origin of fish and rearing protocol

All males used for breeding in the F0-F5 generations (50 males per line and generation) and those used for estimating maturation size and age in the F6 generation were used for genetic analysis. Rearing- and selection protocols can be found in section 2.3.

3.2.2. DNA extraction

Genomic DNA was extracted using hexadecyltrimethylammonium bromide (CTAB) according to the following protocol: 2-3 mm² of tissue was incubated overnight at 60°C in 350µl 2% CTAB buffer (100mM Tris-HCl pH 8.0; 1.4M NaCl; 20mM EDTA pH 8.0; 2% CTAB; 0.2% 2-mercaptoethanol) with 20µl proteinase K solution (QIAGEN). For the extraction, 300µl chloroform: isoamyl alcohol (24:1) was added, mixed for 5 min using an automated rotator and then centrifuged at 13.000rpm for 5min. The supernatant was transferred to a new 1.5ml tube and the extraction step repeated, after which 660µl 100% ethanol and 30µl 3M NaAc pH4.8 were added to the retained supernatant. This solution was mixed for 3 min, left to stand for 10 min and then centrifuged at 13.000rpm for 10 min, after which the supernatant was discarded and 500µl 70% ethanol was added to the pellet. This was centrifuged for 5 min to wash the pellet and the supernatant was discarded again. Pellets were left to dry in a 37°C cabinet and re-suspended in 100µl H₂O.

DNA concentrations were quantified using a NanoDrop® ND-1000 spectrophotometer (NanoDrop Technologies) and ranged from 6-157ng/µl. A working solution of DNA was stored at 4°C and diluted to a volume of 50µl at 10ng/µl for samples with initial DNA concentrations over 10ng/µl. Remaining DNA was kept at extraction concentration and stored at -20°C.

3.2.3 Microsatellite marker choice and PCR protocols

To monitor neutral genetic dynamics in selection lines over generations, male fish were genotyped at 10 microsatellite loci: Pr39, Pr92 (Becher et al. 2002), Pret-32,

Pret-69, Pret-77 (Watanabe et al., 2003), AGAT11 (Olendorf et al. 2004), Hull70-2 (van Oosterhout et al. 2006a), G82, G102 and G289 (Shen et al. 2007a). Markers were chosen such that the entire marker set comprised markers with different numbers of alleles and minimal overlap of allelic ranges with other chosen loci. Forward primers were extended with an 8bp tail, complementary to a FAM/NED/VIC/PET fluorescent dye-labelled universal primer following Schuelke (2000; Tysklind 2009) and amplified using QIAGEN Multiplex PCR kit. All primer sequences are given in Appendix I.

Annealing temperatures (AT) were 53° for Pret-69, Pret-77, Pr39, G102, Hull70-2 and AGAT11 and 58° for Pret-32, G82, Pr92 and G289 and primers with the same AT were amplified in a single 10µl reaction: 6µl Multiplex mix, 1µl Q solution, 1µl H₂O, 1µl DNA at 10ng/µl and 1µl primer mix (containing a mix of equal volumes of forward primers at 1µM and reverse primers and dye-labelled universal primers at 10µM concentrations). PCR products were obtained using a Tetrad2 Peltier thermal cycler (BIO-RAD) and the following program: 95°C 15m; 94°C 30s, AT 90s, 72°C 90s for 12 cycles; 94°C 30s, 50°C 90s, 72°C 90s for 30cycles; 60°C 30m.

PCR products were resolved on a 3130xl Genetic Analyzer (Applied Biosystems) using GeneScan™ LIZ® 500 as an internal size standard and genotyped using GeneMapper® Software v.4.0 (Applied Biosystems). Genotyping accuracy was verified by re-analysing several individuals in multiple runs and by running negative controls on each plate.

3.2.4 Genetic analyses

Terminology

All genetic analyses were performed for each generation and for each selection line independently. In the F3 generation, all sampled individuals were part of the same breeding group, i.e. they were reared under identical conditions and shared the

same parents. However, as the samples were divided over lines in a non-random fashion (one randomly selected line and four lines consisting of the extreme 20% percentiles of the generation, see 2.3.5), the five lines of the F3 generation were treated as separate breeding groups like all selection lines from the F4-F6 generations throughout the analyses. Thus, in total, 23 different breeding groups were analysed (F0 – F1 – F2 – 5 x F3 – 5 x F4 – 5 x F5 – 5 x F6) which from now on will be referred to as either lines (over generations) or populations (within generations).

Null alleles, Hardy-Weinberg equilibrium and linkage

All microsatellites were checked for null alleles using MICRO-CHECKER version 2.2.3 (van Oosterhout et al. 2004) and confirmed by G_{IS} p -values, obtained using 9999 permutations. Benjamini & Hochberg (B-H) corrections for multiple tests were performed using SGoF+ (Carvajal-Rodríguez et al. 2009) here and throughout the analyses.

Conformity to Hardy-Weinberg (HW) equilibrium was tested at each locus in each population and for each generation independently, using the Hardy-Weinberg probability test in Genepop version 4.0.10 (Raymond and Rousset 1995; Rousset 2008) using 10.000 batches and 10.000 iterations per batch. Results were corrected for multiple tests as above.

Genotypic linkage disequilibrium (LD) was tested for using Genepop's log likelihood ratio statistic for each pair of loci in each population. LD was only tested for in the wild-caught (F0) fish because (artificial) selection increases the relatedness between individuals, and thereby affects the independent inheritance of alleles between individuals. This affects all alleles, and is not restricted to alleles at loci that are physically linked (Falconer and Mackay 1996). Hence, artificial selection is predicted to increase LD irrespective of the genomic distance between marker loci. In other words, physically linked loci are expected to remain in LD throughout the experiment, whereas alleles of unlinked loci may become in LD without any physical (genomic) linkage in later generations.

Genetic diversity

Using GenoDive (Meirmans and van Tienderen 2004), the following parameters were obtained for each selection line and for each generation independently, per locus and over all loci; number of alleles A , observed heterozygosity H_o , expected heterozygosity H_s , and inbreeding coefficient G_{IS} (Nei 1987). Standard errors over all loci were obtained through jackknifing over loci and p -Values for G_{IS} were obtained using 9999 permutations.

Allelic Richness A_R (El Mousadik and Petit 1996) was calculated per locus based on a minimum sample size of $N=32$ (F1), using FSTAT version 2.9.3.2 (Goudet 1995). Significant differences in A_R within generations were tested for using nested ANOVA (PASW Statistics 18.0.3). To test for significant changes in A_R over generations, randomisation tests with 10.000 randomisations were performed using Rndom Pro 3.14 (Jadwiszczak 2009).

Genetic Structure

To examine whether variation between populations was more likely to be a result of selection or random drift between lines, hierarchical analyses of molecular variance (AMOVA) were performed for each generation independently, using Arlequin version 3.5.1.2 (Excoffier et al. 2005). AMOVAs were carried out for each generation (F3-F6) independently in a hierarchical fashion using the following levels: (1) within lines, (2) within treatments-between replicate lines, and (3) between treatments. These hierarchical levels are equivalent to F_{ST} , F_{SC} and F_{CT} respectively. In addition, an AMOVA was carried using the following hierarchical levels: within lines within generations (F_{ST}), within lines between generations (F_{SC}) and between lines (F_{CT}). This hierarchy was used to examine whether temporal differentiation within lines or differentiation between lines explained most of the variation.

In addition, both pairwise F_{ST} estimator θ (Weir and Cockerham 1984) and standardised fixation index G''_{ST} (Meirmans and Hedrick 2011) were calculated per generation for each locus for within-treatment comparisons (S1-S2 and L1-L2),

between-treatment comparisons (S1-L1, S1-L2, S2-L1 and S2-L2) and comparisons with the control line. (C-S1, C-S2, C-L1 and C-L2) using GenoDive. *P*-Values were obtained for pairwise F_{ST} comparisons over all loci only, using 9999 permutations, for testing significance between treatments by nested ANOVA and over generations by randomisation tests (10.000 randomisations).

3.2.5 Paternity analysis

To estimate the number of fathers and male reproductive variance in each population, paternity of males was reconstructed using CERVUS version 3.0.3 (Marshall et al. 1998; Kalinowski et al. 2007). Only father-son pairs that were assigned with strict (95%) confidence and no mismatching loci were considered and used for estimating male reproductive success and father-offspring regression of standard length. The slope of the linear relationship between the deviation of offspring standard length from population means on father standard length from population means, is furthermore an estimate of heritability (Falconer and Mackay 1996).

3.3 RESULTS

3.3.1 Loci amplification

All ten microsatellite loci amplified in all selection lines. For locus AGAT11, a variable number of individuals was observed with three clear peaks of almost identical height in seven out of the 23 populations tested. Re-amplification of PCR products and re-genotyping yielded the same results. The third peak was not consistently the same allele in different individuals, nor linked to one other specific allele, although most of the individuals with three peaks carried an allele at 332bp. Re-analysing the data set without allele 332 resulted in high deficiencies in heterozygosity in most of the samples. Paternity analysis indicated that the third allele was inherited (most three-peak individuals had a father with three alleles as well) but a straightforward inheritance pattern could not be identified. The frequency of individuals with three alleles in lines with the allele present varied from 6-14%, but an individual with more than three peaks was never observed. In all likelihood, AGAT11 is located on the (pseudo) y-chromosome and some males may carry an additional copy of this locus. Although no genetic samples for females are available, and sex-linked inheritance could therefore not be tested, this would explain the lack of individuals with four alleles for this locus. Although none of the populations with three-peak individuals had significant deviations from HW-equilibrium, the locus was excluded from further analyses.

3.3.2 Null alleles, Hardy-Weinberg equilibrium and linkage

Null alleles

For three out of nine loci, MICRO-CHECKER indicated that null alleles could explain observed homozygote excess in one out of 23 tests per locus (Hull70-2 in the F2, G102 in F3_L2 and Pret-77 in F6_C). For locus Pret-32, null alleles were indicated as explanations for HW-deviations in the F1 and F4_S2 populations. For one locus, G82, null alleles were highlighted as explaining homozygote excess in three tests (F2, F5_L1 and F6_C). However, the homozygote excess in these populations was not

supported by significant values of G_{IS} after B-H correction (see G_{IS} section below). Furthermore, all 23 populations were derived from the same gene pool very recently and null alleles present in one population should therefore be expected to be present in a majority of the populations. Finally, one of the assumptions of MICRO-CHECKER was violated from the F3 onwards, since artificial selection was done, which could result in deviation from HW-equilibrium. Therefore, the observed homozygote excess is more likely the result of stochastic variation in allele frequencies over generations and an inflated type I error rate due to multiple tests, rather than an indication that null alleles were present at these loci.

Hardy-Weinberg equilibrium

Tests for HW-equilibrium indicated deviations in 8 out of 30 tests in the random breeding generations (F0-F2) and 22 out of 200 tests in selection lines (F3-F6). After Benjamini-Hochberg correction, a highly significant ($p < 0.001$), heterozygote excess remained only for locus Pr39 in F5_L2, F6_L1 and F6_L2 and this locus was removed from further analysis with neutral microsatellite loci. However, due to the consistency of this deviation with the selection regime (L-lines only), which may indicate selection is acting at this locus or a closely linked locus, locus Pr39 was further analysed with the putative candidate loci and is discussed in Chapter 4.

Linkage Disequilibrium

Four out of 36 tests demonstrated significant ($p < 0.05$) linkage disequilibrium between loci (Pret-32 with locus G102 and G82 and locus Pr92 with locus G289 and G82). However, none of these were significant after B-H corrections for multiple tests.

G_{IS}

G_{IS} was calculated per locus and over all loci (Fig. 3.1) for each population independently. Per locus, 34 out of 207 tests yielded significant deviations of G_{IS} from zero. After B-H corrections, only locus Pr39 in the F6_L1 remained significant ($G_{IS} = -0.381$). G_{IS} values therefore do not support the conclusion of null alleles by homozygote excess from MICRO-CHECKER, lending further support to my

interpretation that the type I error rate was inflated due to performing multiple tests with MICRO-CHECKER. Over all loci, 6 out of 23 (including Pr39) and 4 out of 23 (excluding Pr39) tests had significant values of G_{IS} , none of which were significant after B-H corrections.

3.3.3 Genetic diversity

Heterozygosity

Genetic diversity within samples was moderate to high with heterozygosity levels ranging from 0.7-0.78. Only slight variations in heterozygosity estimators were observed between populations, both between treatments and lines, and over generations (Fig. 3.1), and these were not significant ($p > 0.171$ and $p > 0.09$ for all within-generation nested ANOVA comparisons of H_O and H_S , and $p > 0.243$ for all regressions over generations, either over all lines or within lines). In generations F5 and F6, a general excess of heterozygotes was observed in both S- and L-lines, but not in the control (Fig. 3.1), but this excess was not significant (see G_{IS} above). A summary of population genetic parameters is given in Table 3.1. A table of allele frequencies at microsatellite loci can be found in Appendix II.

Allelic Richness

The numbers of alleles ranged from 3-29 depending on the locus (Table 3.2) and did not differ between selection lines (nested ANOVA over all loci per generation, $p > 0.789$ for each generation). Allelic Richness (A_R , Fig. 3.2) was significantly higher in the F0-F1 generations (10.5-10.35) than in the captive-bred generations F2-F6 (mean $A_r = 8.44$, randomisation test, $p = 0.032$). No significant decline in A_R was observed in generations F2-F6 (logarithmic regression, $R^2 = 0.026$, $F_{1,134} = 3.593$, $p = 0.06$) over all treatments, or in the random breeding control line ($R^2 = 0.054$, $F_{1,38} = 2.151$, $p = 0.15$). Furthermore, for selection lines in generations F3-F6, no decline in A_R was observed ($p = 0.52, 0.57, 0.58$ and 0.45 for the S1, S2, L1 and L2 respectively).

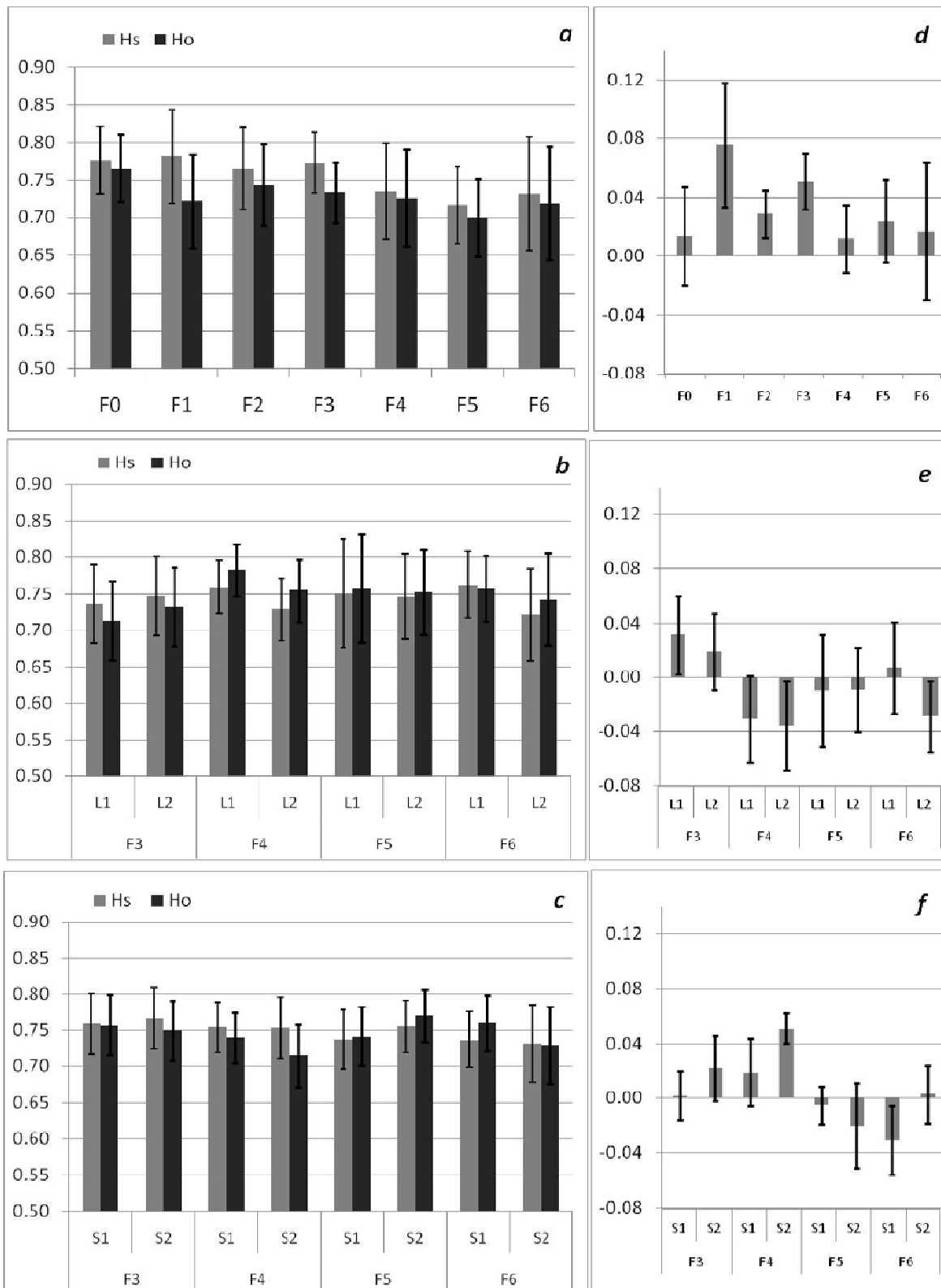


Fig. 3.1. Expected (H_s , grey bars) and observed (H_o , black bars) heterozygosity per generation over eight microsatellite loci for the random breeding control line (a), L-lines (b) and S-lines (c). Frames d-f provide G_S estimates for C-, L- and S-lines respectively. Error bars indicate standard errors, obtained through jackknifing over loci. None of the G_S values were significantly higher than zero after Benjamini-Hochberg correction.

Table. 3.1. Overview of population genetic parameters observed heterozygosity (H_o), expected heterozygosity (H_s) and inbreeding coefficient G_{IS} , number of alleles per locus (A) and Allelic Richness (A_R) over eight microsatellite loci. Standard errors were obtained through jackknifing over loci. S-lines are indicated by light grey shading, L-lines by dark grey, and random breeding populations are white.

Population	N	$H_o \pm St. err$	$H_s \pm St. err.$	$G_{IS} \pm St. err.$	$A \pm St. dev.$	$A_R \pm St. dev.$
F0	46	0.7658 \pm 0.044	0.7762 \pm 0.044	0.014 \pm 0.039	11.50 \pm 5.63	10.35 \pm 4.92
F1	32	0.7227 \pm 0.062	0.7814 \pm 0.042	0.076 \pm 0.042	10.50 \pm 4.54	10.50 \pm 4.54
F2	192	0.7435 \pm 0.054	0.7657 \pm 0.047	0.029 \pm 0.016	11.88 \pm 5.44	9.56 \pm 4.19
F3_S1	52	0.7572 \pm 0.042	0.7589 \pm 0.047	0.002 \pm 0.018	9.63 \pm 4.10	8.87 \pm 3.74
F3_S2	45	0.7500 \pm 0.042	0.7668 \pm 0.042	0.022 \pm 0.024	9.88 \pm 3.91	9.19 \pm 3.56
F3_C	47	0.7336 \pm 0.040	0.7729 \pm 0.045	0.051 \pm 0.019	9.50 \pm 5.04	9.01 \pm 4.38
F3_L1	49	0.7143 \pm 0.054	0.7366 \pm 0.058	0.031 \pm 0.029	9.63 \pm 4.34	8.87 \pm 3.94
F3_L2	50	0.7325 \pm 0.054	0.7467 \pm 0.052	0.019 \pm 0.028	9.75 \pm 4.40	8.96 \pm 3.91
F4_S1	50	0.7400 \pm 0.035	0.7543 \pm 0.037	0.019 \pm 0.025	8.75 \pm 4.17	8.08 \pm 3.59
F4_S2	50	0.7150 \pm 0.043	0.7533 \pm 0.049	0.051 \pm 0.011	9.75 \pm 4.33	8.90 \pm 3.97
F4_C	48	0.7266 \pm 0.064	0.7350 \pm 0.054	0.012 \pm 0.023	8.75 \pm 3.88	8.15 \pm 3.50
F4_L1	49	0.7830 \pm 0.036	0.7598 \pm 0.046	-0.031 \pm 0.032	8.88 \pm 3.44	8.38 \pm 3.26
F4_L2	49	0.7551 \pm 0.043	0.7290 \pm 0.053	-0.036 \pm 0.033	9.38 \pm 4.21	8.64 \pm 3.76
F5_S1	46	0.7418 \pm 0.041	0.7380 \pm 0.042	-0.005 \pm 0.014	8.38 \pm 3.78	7.80 \pm 3.46
F5_S2	43	0.7703 \pm 0.036	0.7554 \pm 0.051	-0.020 \pm 0.031	9.75 \pm 4.80	9.12 \pm 4.28
F5_C	43	0.6998 \pm 0.051	0.7171 \pm 0.054	0.024 \pm 0.028	8.38 \pm 3.85	8.01 \pm 3.53
F5_L1	46	0.7582 \pm 0.075	0.7510 \pm 0.050	-0.010 \pm 0.041	8.38 \pm 3.25	7.94 \pm 2.88
F5_L2	49	0.7526 \pm 0.058	0.7462 \pm 0.047	-0.009 \pm 0.031	8.88 \pm 3.83	8.27 \pm 3.45
F6_S1	50	0.7600 \pm 0.039	0.7373 \pm 0.043	-0.031 \pm 0.025	8.38 \pm 3.89	7.84 \pm 3.55
F6_S2	50	0.7300 \pm 0.0533	0.7321 \pm 0.051	0.003 \pm 0.021	8.63 \pm 3.25	7.97 \pm 2.98
F6_C	50	0.7196 \pm 0.075	0.7323 \pm 0.053	0.017 \pm 0.047	8.38 \pm 3.66	7.87 \pm 3.19
F6_L1	50	0.7575 \pm 0.045	0.7627 \pm 0.049	0.007 \pm 0.034	8.50 \pm 3.46	8.08 \pm 3.26
F6_L2	50	0.7425 \pm 0.063	0.7221 \pm 0.058	-0.029 \pm 0.026	8.13 \pm 3.31	7.67 \pm 3.22

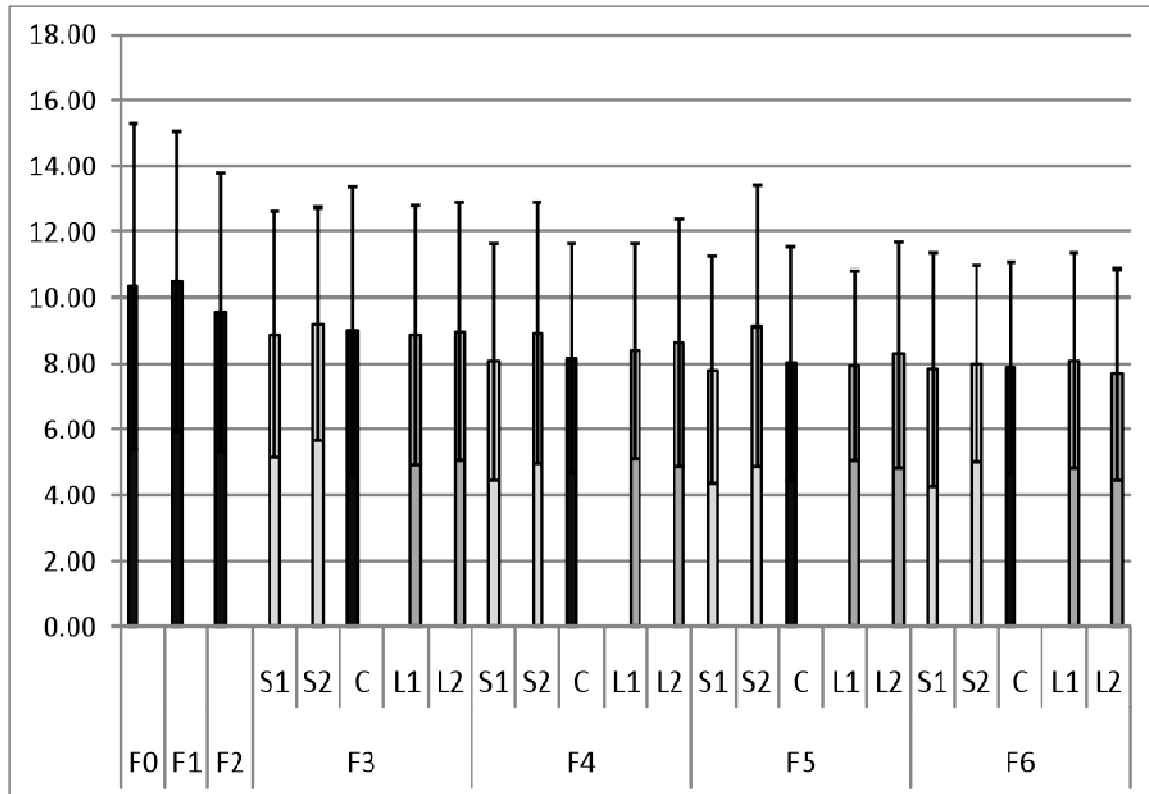


Fig. 3.2. Allelic Richness over eight loci for each generation and selected line independently (random breeding populations black bars, S-line light grey bars, L-line dark grey bars), calculated using a minimum sample size of N=32 (F1). Error bars represent standard deviations from averages over all loci. Allelic Richness was significantly higher in the F0 and F1 generations than the generations being bred in the lab, but no further decline over generations was observed, except for the control line, for which Allelic Richness significantly declined over generations F3-F6.

Table 3.2. Number of alleles observed for each locus in each generation for random breeding lines (white), S-lines (light grey) and L-lines (dark grey). Mean number of alleles over all loci and range of number of alleles per locus over all populations are given as standard deviations.

n genotyped/ n breeding	F0	F1	F2	F3					F4				
	46/90	32/50	192/250	52/52	45/50	47/50	49/50	50/50	50/50	50/50	48/50	49/50	49/50
	S1	S2	C	L1	L2	S1	S2	C	L1	L2			
Pret69	15	12	14	10	13	13	13	12	6	12	12	11	11
Pret77	9	12	12	10	8	7	10	10	8	11	8	10	9
Pr39	10	8	10	8	8	8	7	7	8	8	8	6	8
Hull70-2	20	18	21	15	15	18	16	16	16	17	14	14	16
G102	8	7	9	7	8	6	7	7	7	6	6	7	6
Pret32	16	12	15	14	13	12	11	12	13	13	10	11	12
G82	3	4	4	3	4	3	3	3	4	4	3	3	3
Pr92	7	6	6	6	6	5	5	5	6	6	5	6	6
G289	14	13	14	12	12	12	12	13	11	9	12	9	12
Over all loci	11.33	10.22	11.67	9.44	9.67	9.33	9.33	9.44	8.78	9.56	8.67	8.56	9.22
St. dev.	5.29	4.32	5.12	3.88	3.71	4.74	4.15	4.22	3.83	4.10	3.64	3.36	3.96

n genotyped/ n breeding	F5					F6					Over all populations	
	46/50	43/50	43/50	46/50	49/50	50/50	50/50	50/50	50/50	50/50	range	st. dev
	S1	S2	C	L1	L2	S1	S2	C	L1	L2		
Pret69	8	11	10	10	11	7	10	9	11	10	6-15	2.13
Pret77	7	10	7	8	9	9	8	8	7	8	7-12	1.50
Pr39	6	8	7	5	7	7	8	8	6	8	5-10	1.16
Hull70-2	14	18	15	14	14	15	14	14	14	13	13-21	2.10
G102	7	6	6	7	6	6	6	6	7	5	5-9	0.88
Pret32	13	14	10	10	12	11	11	12	11	9	9-15	1.69
G82	3	3	3	3	3	3	4	3	3	3	3-4	0.45
Pr92	5	6	5	6	5	5	6	5	6	6	5-6	0.57
G289	10	10	11	9	11	11	10	10	9	11	9-15	1.53
Over all loci	8.11	9.56	8.22	8.00	8.67	8.22	8.56	8.33	8.22	8.11		
St. dev.	3.62	4.53	3.63	3.24	3.64	3.67	3.05	3.43	3.35	3.10		

3.3.4 Genetic structure

AMOVA

A hierarchical AMOVA indicated that the majority of molecular variation was attributable to variation within lines in generations F3-F5 but that this proportion was declining over generations with a simultaneous increase in variation between lines within treatments (Fig 3.3). Total variance however increased over generations and absolute values of both variance components increased accordingly (Table 3.3). Variation between treatments was smallest and decreased over generations, both proportionally and absolute, revealing that variation was not a result of selection

regime, but rather a stochastic process resulting in increasing divergence between lines over generations.

A temporal hierarchical AMOVA of among lines (F_{CT}), among lines between generations (F_{SC}), and within lines within generations (F_{ST}), revealed that the increasing variance between lines over generation was foremost the result of variation within lines within generations (98.27% of variation, $F_{ST} = 0.0172$, $p = 0.000$) and increasing differentiation between lines (1.41% of variation, $F_{CT} = 0.014$, $p = 0.000$) rather than of temporal variation within lines (0.31% of variation, $F_{SC} = 0.0032$, $p = 0.0001$). Full AMOVA tables per locus can be found in Appendix III.

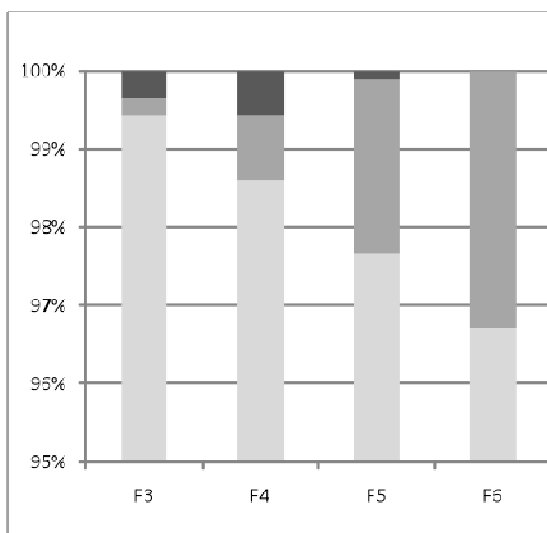


Table 3.3. F_{CT} , F_{SC} , and F_{ST} values accompanying Fig. 3.3. Significance levels are indicated as: ns (not significant), * ($p < 0.05$) and *** ($p < 0.001$).

	Among treatments (F _{CT})	Among lines within treatment (F _{SC})	Within lines (F _{ST})
F3	0.00349 ns	0.00219 ns	0.00567 ***
F4	0.00577 *	0.00832 ***	0.01404 ***
F5	0.00114 ns	0.02242 ***	0.02353 ***
F6	-0.00476 ns	0.03293 ***	0.02833 ***

Fig. 3.3. Hierarchical analysis of molecular variance of eight microsatellite loci (a) among treatments (black) among lines within treatment (dark grey) within lines (light grey), showing an increasing contribution of among lines-within treatment variance at the cost of variation within lines and among treatments.

Pairwise differentiation

Pairwise tests of differentiation revealed significant differentiation between lines at microsatellite loci, and increasing differentiation over generations. In the F3, only F_{ST} values of the S1-L1 and S1-L2 comparisons were significant after B-H corrections. All F_{ST} estimates in the F4 to F6 had p -values < 0.0001 and were highly significant, although this skew in the p -value distribution did not allow SGoF+ to provide corrected p -values. Pairwise F_{ST} revealed an increase in differentiation between lines over generations but no apparent trend of greater differentiation among treatments

than within treatments was observed (Fig. 3.4). This observation was supported by an ANOVA of both F_{ST} and G''_{ST} of within treatment variation, variation among treatments and comparisons with the control line. The only significant difference observed was in the F4 among within-treatment comparisons (S_1-S_2 , L_1-L_2) and comparisons to the control line ($F_{2,7} = 8.661$ and 10.439 , $p = 0.013$ and 0.008 for F_{ST} and G''_{ST} respectively). Differentiation between lines was thus not affected by selection. This is in agreement with the pattern obtained from the AMOVA analysis that showed that little variance can be attributed to variation among treatments.

Pairwise G''_{ST} revealed a similar trend of increasing differentiation over generations and no clear pattern of increased differentiation between treatments, but the range of G''_{ST} values observed was much greater than that of F_{ST} values (per locus maximum G''_{ST} was twice the maximum F_{ST} (0.41 and 0.20 , respectively), and over all loci this difference was more than threefold (0.14 and 0.04 , respectively)). This can be explained by the generally high level of heterozygosity of microsatellite markers, which affects corrected G''_{ST} but not F_{ST} (Meirmans and Hedrick 2011). Whilst it is not of great interest here for investigating differentiation between lines, G''_{ST} is useful for comparing microsatellite differentiation to that of SNP markers in Chapter 4. Full tables of F_{ST} and G''_{ST} estimates per locus can be found in Appendix IV.

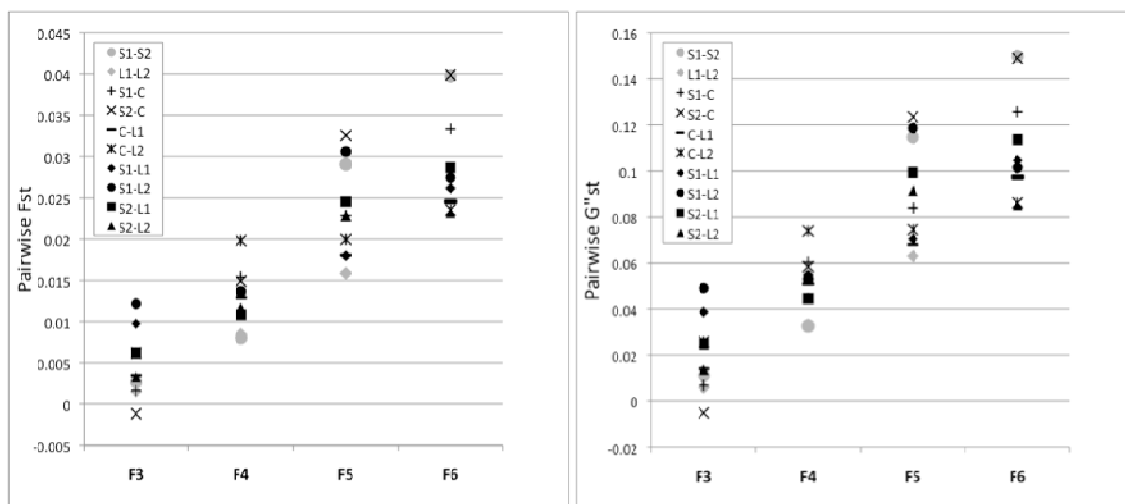


Fig. 3.4. Pairwise differentiation between selection lines estimates as F_{ST} (a) and G''_{ST} (b), showing increasing differentiation over four generations but no apparent effect of selection regime on the amount of differentiation. Grey markers indicate within-treatment comparisons, black markers comparisons between selection lines and cross and line markers comparisons between selection lines and control line.

3.3.5 Paternity reconstruction

Paternity reconstruction using all ten microsatellite loci was successful and 88% (± 0.068 st. dev.) of males could be assigned to a father in the F3-F6 generations. When correcting for missing samples in the parent generation, this proportion was even higher, at 92% (± 0.058 st. dev.). On average, 51% of males fathered 1.7-2.7 male offspring that were retained in the next generation. Out of the wild caught males (F0) genotyped, only 9% fathered F1 males. This low value can partly be explained by missing samples (DNA was only obtained for 46 out of 90 F0 males and 32 out of 50 F1 males) but also reflects that F0 females were gravid when caught. It can therefore be expected that a substantial proportion of F1 offspring were sired by non-sampled males, as well as by new fertilisations using stored sperm. In the F2 and F3, only a low number of individuals could successfully be assigned a father as well (43-44%). Here, this is likely the result of missing samples, as only 32 out of 50 F1, and 192 out of 250 F2 males were genotyped (Table 3.4).

Using the paternity data and standard length of all males, a parent-offspring regression was performed to investigate whether father size was a predictor of male offspring size. Fig. 3.5 shows the relationship between father standard length and offspring standard length, as a deviation from population means, over all samples with fathers in generations F2-F5 and is highly significant ($R^2 = 0.311$, $F_{1,580} = 262.049$, $p = 0.000$). Fathers in the F0 and F1 and their offspring were excluded from this analysis, because maternal effects and effects from variable rearing conditions in the wild may have affected standard length in these populations.

The slope of the regression is an estimate of half the narrow sense heritability h^2 , implying a $h^2 > 1$ when estimated over all samples and assuming no y-linked genetic variation. This estimate is no different when obtained for the control line independently (two-sample t-test, $T_{(2),422} = 0.24$, $p = 0.807$), but is lower and weaker for the L-lines (slope = 0.3, $R^2 = 0.03$ and $p = 0.016$) and not significant for the S-lines using this method (Table 3.5). Between generations, the slope for the regression did not differ ($p > 0.369$) with exception of the F5-F6: no significant slope was observed for the parent offspring regression in this generation. Further analysis revealed that

this is the result of both selection treatments, and a significant slope was present in the F6_C ($R^2 = 0.239$, $F_{1,36} = 11.294$, $p = 0.002$, slope = 0.489 ± 0.146). This indicates a reduced h^2 of standard length as a result of selection, but not of random breeding.

Table. 3.4. Summary of paternity reconstruction of fish in each generation and selection line. Proportion of males fathering and mean number of offspring per father are shown for each generation, as well as the percentage of offspring that was confidently assigned (95% confidence and no mismatching loci). Based on the proportion of males fathering, the number of missing samples and the percentage of confidently assigned offspring, a final estimate of confidently assigned offspring is provided as: *No of conf. assigned offspring + (prop. of sampled males fathering x no. of missing samples x mean no. of offspring per father)*.

	F0	F1	F2	F3				
				S1	S2	C	L1	L2
N genotyped/ N breeding	46/90	32/50	192/250	52/52	45/50	47/50	49/50	50/50
Prop of sampled males fathering	0.07	0.75	0.33	0.38	0.53	0.45	0.37	0.34
Mean offspring / father	1.00	3.46	1.68	2.40	1.96	1.95	2.22	2.65
St. dev.	0.00	3.87	1.10	1.57	1.30	1.36	1.17	2.98
% confidently assigned	0.09	0.43	0.44	0.92	0.94	0.85	0.82	0.92
"" incorporating % of missing males	0.20	0.68	0.57	0.96	1.04	0.91	0.83	0.92

	F4					F5				
	S1	S2	C	L1	L2	S1	S2	C	L1	L2
N genotyped/ N breeding	50/50	50/50	48/50	49/50	49/50	46/50	43/50	43/50	46/50	49/50
Prop of sampled males fathering	0.44	0.34	0.46	0.37	0.51	1.54	0.44	0.56	0.41	0.49
Mean offspring / father	1.79	2.29	1.82	2.50	1.84	1.92	1.79	1.71	2.32	1.92
St. dev.	1.14	1.16	1.37	2.04	1.28	1.53	1.03	1.12	1.29	1.21
% confidently assigned	0.93	0.91	0.93	0.98	0.94	0.96	0.68	0.82	0.88	0.92
"" incorporating % of missing males	0.93	0.91	0.97	1.00	0.96	1.04	0.79	0.95	0.96	0.94

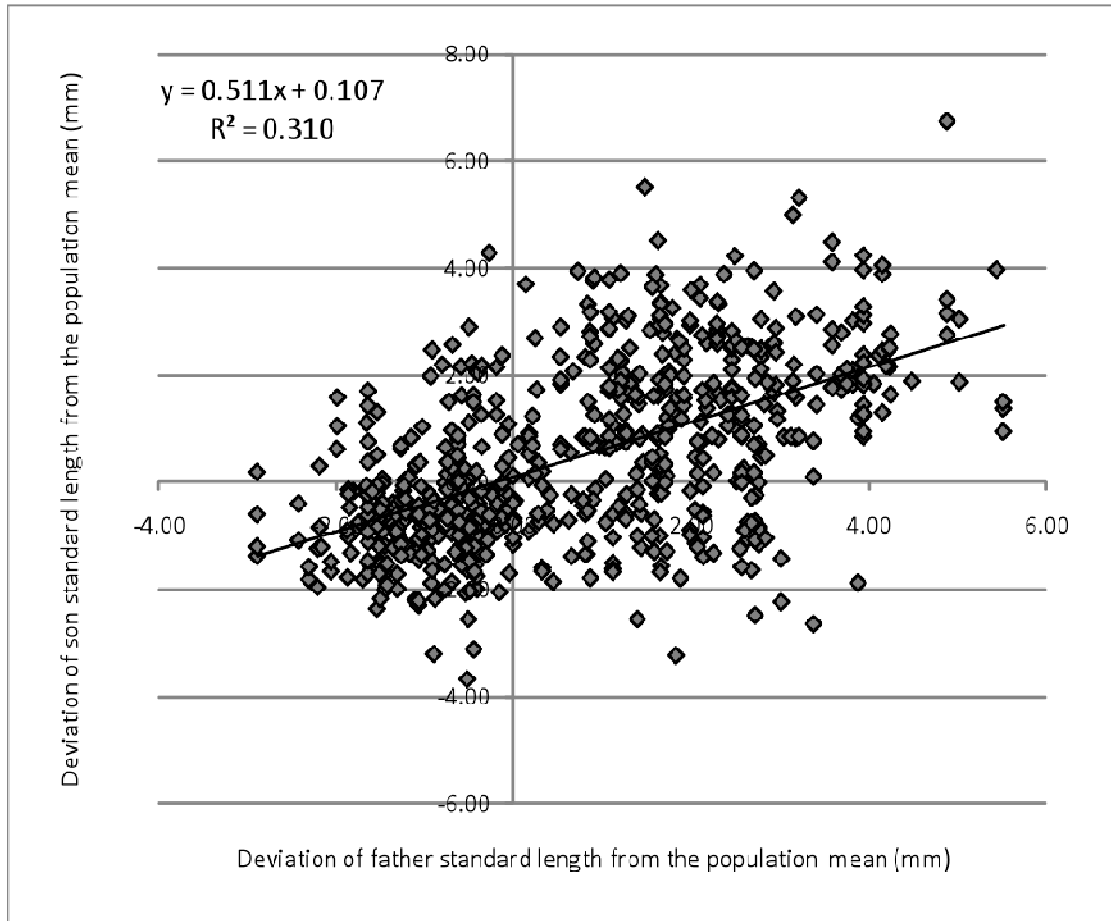


Fig. 3.5. Father-son regression of standard length over all males and all generations, showing linear relationship as: $y = 0.511X + 0.107$ and $R^2 = 0.310$.

Table. 3.5. Relevant values from the father-son regression of standard length over all treatments and for each treatment and generation independently, showing R^2 and slope of the regression, and standard error of the slope. The slope of the regression is an estimate of the narrow sense heritability.

	F2-F5 Fathers	F2 Fathers	F3 fathers	F4 Fathers	F5 fathers	Control line	L-lines	S-Lines
R^2	0.311	0.297	0.622	0.572	0.008	0.234	0.030	0.001
p	0.000	0.000	0.000	0.000	0.238	0.000	0.016	0.588
N	582	84	174	151	173	256	189	212
slope	0.515	0.699	0.671	0.730	-0.065	0.499	0.300	0.052
st. error	0.032	0.119	0.040	0.052	0.055	0.057	0.124	0.095

3.4 CONCLUSIONS AND DISCUSSION

3.4.1 The effect of selection on neutral microsatellite loci

Here, we reported on neutral genetic diversity at eight microsatellite loci over six generations of captive breeding of guppy selection lines, and have demonstrated that three generations of divergent selection did not significantly affect neutral genetic diversity among treatments, although selection was intense (only 20% of males retained) and breeding population sizes finite and relatively small (50 males, 75 females). No deviations from HW-equilibrium were observed, and no significant inbreeding resulted from the breeding regime. No trends over generations, or significant differences between treatments, were observed for Allelic Richness, H_o or H_s , indicating that selection was not the cause of variation in genetic diversity at microsatellite loci between lines. However, Allelic Richness was significantly higher in the F0 and F1 than in later generations. The main difference between the F0 and F1 and the other generations, lies in the fact that F0 are the offspring of wild fish, and a considerable proportion of the F1 are sired by wild males through sperm storage mechanisms, as supported by the paternity analysis. The high allelic diversity seen in these generations therefore likely reflects the wild gene pool of the sampling site in the Tacarigua River more closely than the generations with only laboratory-born parents.

AMOVA in generations F3-F6 revealed genetic variation was mostly partitioned within- and among lines, the contribution of the latter proportionally increasing over generations, and among-treatment variation contributed very little to none to total variation. Therefore, the analysis confirms that drift seems the most likely explanation of the observed genetic differences between lines, rather than selection affecting microsatellite loci. Additionally, a temporal AMOVA showed that variation within lines over generations did not majorly contribute to the total variation observed, implying that over generations, selecting only 20% of individuals for breeding in each generation did not result in marked changes in neutral genetic diversity. Pairwise differentiation, as measured by F_{ST} and G''_{ST} , confirms the pattern

obtained from the AMOVA: a steady increase in differentiation between lines was observed over generations, but no pattern between treatments was detected.

3.4.2 The magnitude of drift through captive breeding

Over three generations of captive breeding, divergence among lines was considerable: mean pairwise F_{ST} and G_{ST} increased on average from 0.0046 to 0.029 and variation observed between lines from 0.57% to 3.31%; a 6.3 and 5.8-fold increase respectively. The lack of concordance of this increase with the selection regime indicates that drift, rather than divergent selection caused divergence between lines at microsatellite loci.

How strong is drift here, compared to drift observed in other experiments? Simões et al. (2008a, 2008b) observed no significant F_{ST} values after three generations of laboratory breeding of *Drosophila* lines introduced from the wild, but they used much larger populations (600-1200 individuals) which obviously would have reduced drift compared to our lines (Montgomery et al. 2000). F_{ST} between lines was significant after 14 generations however (0.026-0.064) and of similar magnitude to mean pairwise F_{ST} observed in the F6 here (0.029). Also after 14 generations, Morgan et al. (2003) observed mean within-treatment F_{ST} values of 0.149 in an AMOVA of six microsatellite loci in mice selection lines, consisting of 13 breeding pairs each; 2-6 times the estimate of Samões et al. but only five times our own estimate after three generations of selection, which seems therefore reasonably comparable in magnitude. However, the design of Morgan et al. controlled for within-family matings, which maximises heterozygosity and is something we did not control for. The above two studies give an indication of the magnitude of drift observed in laboratory breeding lines, but direct comparisons are difficult, because of differences in experimental design and number of generations. As mentioned in 3.1.2, few studies have investigated and quantified the effect of selection on neutral genetic diversity in an experimental context and those who did so, reported on different numbers of generations and selection intensity. Three generations of laboratory breeding is sometimes even regarded as the baseline differentiation level (Samoies et al. 2008a) whilst here it is the endpoint of the experiments.

These examples highlight the difficulties of comparing genetic data between different experiments, and suggest even greater challenges may exist when comparing genetic data from artificial selection experiments to genetic dynamics of wild populations, in particular wild fish populations with large census sizes. However, the above also emphasises the unique nature of our study, which is, to our knowledge, the only study available to look at microsatellite diversity between selection lines over so few generations. This work has demonstrated that, even with such an intense selection regime as imposed here, neutral genetic diversity is unaffected in the short term. Therefore, the data presented here provides a useful baseline model to better understand the effects of selection in Chapter 4. The proportional change between putatively neutral loci and candidate genes not only allows for inferences on demographic events underpinning selection, but also yields information on the likelihood and magnitude of a selective response.

3.4.3 Paternity reconstruction

Variance in male reproductive success

Paternity analysis indicated that the 20% of males retained in each generation were fathered by, on average, 50% of the males breeding in each preceding generation. Assuming an equal number of female as male offspring for each father, and extrapolating this figure of 50% of putative fathers being represented in 10% of the produced offspring (the 20% selected males that were genotyped in each generation), it can be reasonably concluded that all, or close to 100% of breeding males successfully fathered offspring in each generation. Therefore, sexual selection and female choice were successfully minimised by our experimental design (enforcing a female-biased sex ratio and using virgin females from a high-predation population). Although sexual selection can be a considerable factor influencing reproductive success in male guppies (Houde 1997) it thus is unlikely to have significantly reduced the genetic variance in our lines.

Since no information is available on brood sizes in our experiments, comparing these estimates to those of male reproductive success elsewhere is difficult. A crude estimate of the number of fathers per brood can be made, however, with the knowledge that around 500 fry were produced over 60 days. Assuming a gestation time of 30-40 days, this implies 1-2 broods per female, with an average number of 3.33-6.67 surviving fry per brood and an average of 1.5-3 fathers per brood. This number is comparable to the results of Evans & Magurran (2000) whose conservative estimate (non-assigned offspring was removed) for the Lower Tacarigua was 1.62 sires per brood; Becher and Magurran (2004), who observed a median of two fathers per brood and a great majority of broods having 1-3 fathering males and Neff and colleagues (Neff et al. 2008) who observed a mean of three sires per brood in high predation populations from the Caroni drainage.

Reasons for unassigned paternity cases

Paternity assignment was not 100% successful and in total in the F3-F6, 73 fish could not be assigned a father, for which several alternative explanations are possible.

Firstly, due to some undocumented mortality and DNA extraction failures, most populations had at least some missing genotypes. It is likely that a fraction of the unassigned individuals has been sired by these males.

Secondly, it could be argued that contamination between lines or samples resulted in non-assignment of individuals to their respective breeding lines. In order to test for this, all mismatching samples in the F4-F6 were analysed in Cervus against all males in the paternal generation, not only those of the own line. Only five out of 73 males were confidently assigned to a father in another line. However, each of these putative fathers was from a different line and the tanks with the putative contaminating fathers were not adjacent to the breeding tanks of the original lines. This makes contamination an unlikely cause of the low paternity assignments.

Alternatively, failure to separate males and females in time before sexual maturation could have resulted in premature matings, and sperm storage could then have

allowed fry of non-selected fathers to contribute to the next generation. Although mature males were not observed in female rearing tanks, the specific observation of low paternity in the F5_S2 (16 non-assigned F6_S2) combined with several large and late maturing F6_S2 males (Fig. 2.8) raises suspicion that an unselected male may have fathered offspring in this tank. Although unfortunate, if contamination by unselected males occurred, this could only result in our estimate of the response to selection being a conservative one.

Fourth, although it is unlikely, it cannot be excluded that genotyping error resulted in mismatches between father and offspring fish. For the F0-F2, it is not possible to obtain a reliable estimate of genotyping error, due to the large number of missing genotypes in these generations. However, the 73 unassigned fish in the F4-F6 had a total of 98 mismatching genotypes with their most likely father. Out of a total of 966 genotyped fish x 10 loci, this would imply a genotyping error of 1.0%, which seems a reasonable estimate of error, whilst at the same time sufficiently low not to give rise to concerns about the reliability of the data presented here.

Finally, a small number of mismatches can probably be assigned to novel mutations of microsatellite alleles, which have been shown to explain considerable mismatches in paternity analyses elsewhere, occurring at rates as high 3.1×10^{-3} (Jones et al. 1999).

3.4.4 Heritability of standard length

Paternity analysis revealed a strong correlation between father and son standard length, and resulted in high estimates of heritability. When estimated for treatments independently, the regression did not yield unequivocal h^2 estimates for the independent treatments. The estimate for the control line was not different from the overall estimate, but no significant slope was observed in the S-lines and the slope for the L-lines was, even though significant, much lower (0.3) and support weaker ($R^2 = 0.03$). The lack of support for a relationship between father and son standard length in the selection lines, can best be explained by the fact that the sons

in the S- and L-lines represent a non-random sample of the distribution of offspring sizes, including only the sons on the negative side of the mean for the S-lines and the sons on the positive side of the mean for the L-lines. Consequentially, any relationship between offspring and father size will be much weaker than when a full spectrum of offspring sizes is present as in the control line.

When full y-linkage of standard length is assumed, h^2 estimated from parent-offspring regression still is 0.515, and thus provides a minimum estimate of h^2 which is strikingly similar to the estimate assuming no y-linkage in 2.4.4; 0.518. What can explain this two-fold discrepancy?

Firstly, individuals which could not be assigned a father with confidence, or for which no size data was available (i.e. fish that died before the end of the experiment and from which DNA was taken from the corps, rather than from a tissue sample combined with a size measurement) were excluded from the parent-offspring analysis, which may have affected the slope of the regression to some extent.

Secondly, the different generations yielded similar estimates of h^2 , with exception of the F5-F6, where no significant slope was detected over all treatments, but a significant slope was present for the control line. This is in agreement with the results from the selection experiments, which showed no response to selection in the F6 (Fig. 2.6, 2-sample randomisation test, 10000 randomisations: $p > 0.11$ for each of the L- and S- selected lines). A lower response to selection in the F6 is expected, as additive genetic variation is decreasing over generations and consequentially reduces the response to selection (Fig. 2.10). Consequentially, h^2 estimates for the R/S regression are biased downwards by the F6. Analysis of the R/S regression without the F6 yielded a slightly higher estimate of h^2 at $2 \times 0.315 = 0.63$ ($R^2 = 0.989$, $F_{1,9} = 802.447$, $p = 0.000$, slope = 0.315 ± 0.011). However, 0.315 is still considerably lower than 0.515 as estimated in 3.3.5.

Thirdly, and most importantly, it was shown here that the estimate from the parent-offspring regression could not be used to estimate h^2 for selected lines, and the

response to selection could not be used to estimate h^2 for the control line. Consequentially, the data points on which each regression is based are different: control line data is excluded from the analysis in 2.4.4 and selection line data contribute little to the estimate in 3.3.5. For this reason, it could be argued that the two estimates can be considered independent and a much higher h^2 for random breeding fish than those under selection could be concluded. Reduced heritability can be expected as a result of selection, by the Bulmer effect, changes in gene frequencies at underlying loci and effects of selection on variance (Falconer and Mackay 1996; Fig. 2.10). The response to selection may therefore be a less accurate estimate of h^2 in the original population than the estimate from the parent-offspring regression of the control line.

3.4.5 Overall conclusions

In summary, the data presented here provides substantial support for the hypothesis that neutral genetic diversity is not significantly affected by the selection regime. In addition, these results indicate that selection and captive breeding have not resulted in significant levels of inbreeding in selection lines nor affected levels of neutral genetic variation. Rather, we have demonstrated through hierarchical AMOVA that drift between lines had a significant effect on genetic variation, but that within lines no major stochastic changes in microsatellite genetic variation occurred over generations.

Considerable discrepancies were observed between the h^2 estimates from the regression in Chapter 2 and the estimate from the parent-offspring regression here. Heritability in the control line, as estimated from the parent-offspring regression (0.499-0.998), is twice that estimated in Chapter 2 (0.258-0.518). This indicates a greater reduction in additive genetic variance (V_A) by the selection regime than initially estimated in 2.3.5. However, the microsatellite data show that this difference in V_A between selection- and control lines is not reflected in levels of microsatellite genetic diversity, as these were not different between selection and control lines. Thereby, these results provide indirect support that neutral genetic

variation is not a suitable estimator of quantitative genetic variation (Merilä and Crnokrak 2001; McKay and Latta 2002; Luttikhuisen et al. 2003; Hutchings et al. 2007). In addition, these results thus confirm that the microsatellite loci used are not affected by selection and provide a suitable baseline to compare changes at putative candidate loci to. Furthermore, the absence of significant inbreeding levels or major declines in neutral genetic variation, indicate that the breeding regime and experimental design used were successful in maintaining genetic variation over generations and genetic erosion has not likely affected the response to selection in our experiments.

4.

GENETIC DYNAMICS OF
SELECTION LINES OF *P. RETICULATA* II:
IDENTIFICATION OF A RESPONSE TO
SELECTION AT CANDIDATE LOCI

4.1 INTRODUCTION

The ultimate challenge for understanding evolution lies in revealing the genetic basis and pathways underpinning phenotypic variation, thereby identifying the constraints on evolution and the correlations between traits (Lewontin 1974; Stinchcombe and Hoekstra 2007). The aim of the present study is to identify genetic changes associated with phenotypic shifts in response to strong directional selection on body size in Trinidadian guppies. In previous chapters, I have demonstrated a rapid phenotypic response to selection and revealed the presence of additive genetic variation for standard length in male guppies. Furthermore, I demonstrated that neutral genetic variation measured at microsatellite loci did not change in response to selection. Here, patterns of genetic variation at specific candidate loci², are investigated more closely to see whether a response to selection can be observed at individual loci.

4.1.1 A candidate gene approach to identifying functional genetic variation

As summarised in Box 1, several different approaches are available for identifying genes and gene regions under selection in contrasting environments. Such approaches have benefitted greatly from recent developments in sequencing technology. With the candidate gene approach, knowledge on gene function, structure and chromosomal location is utilised, and the spectrum of putative gene associations with trait variation is smaller than with high-throughput sequencing approaches. In particular, the candidate gene approach maximises efficiency of use of available genomic resources and expands our understanding of additional species using relatively low sequencing effort (Piertney and Webster 2010).

² A candidate gene is defined by (Fitzpatrick et al. 2005) as: “any gene that has been identified in one organism and is predicted to have a similar phenotype in another”. De-Santis and Jerry (2007) make a further distinction between candidate genes and major genes: a candidate gene being a gene of which the physiological function is known and its direct effect on the expression of a trait quantifiable. A major gene is a gene or marker of which the exact physiological role is uncertain but a strong association of the gene with trait variation is observed. Both major genes and candidates are included in the present study when candidate genes are being referred to.

For example, comparison of a QTL region to which coat colour polymorphism in soay sheep (*Ovis aries*) was mapped with the cattle genome allowed the identification of a candidate gene for coat colour (Beraldi et al. 2006; Gratten et al. 2007). Subsequent work revealed a significant association with a non-synonymous substitution (single nucleotide polymorphism SNP) at this locus likely to be causal in coat colour variation (Gratten et al. 2007).

Owing to their role in immune response and pathogen resistance, genes from the major histocompatibility complex (MHC) have been repeatedly characterised and demonstrated to be targets of selection. Successful associations with e.g. parasite load and reproductive success have been identified in a range of non-model species (Bernatchez and Landry 2003; Lukas et al. 2004; Oliver et al. 2009), including guppies (Sato et al. 1995; van Oosterhout et al. 2006b; Fraser et al. 2009, 2010).

Fidler et al. (2007) sequenced a dopamine receptor to investigate its role in novelty seeking behaviour in great tits (*Parus major*). The birds were the result of four generations of selective breeding on exploratory behaviour and polymorphisms in the candidate gene were associated with the different selection regimes. In a subsequent study, they identified variation in behavioural phenotypes in the wild source population and confirmed one of the genetic associations (Korsten et al. 2010), providing further support for a functional role of the gene and associated polymorphism in behavioural phenotypes. These examples highlight the usefulness of selection experiments for investigating the genetic basis of ecologically relevant traits and Fidler et al. (2007) is to my knowledge the only study doing so for an experimental design comparable to our own.

In previous chapters, I have discussed the work on the *Pan I* locus in cod (*Gadus morhua*), which provides an informative case study for the use of candidate genes in identifying the genetic response to selective pressures in the wild (Pogson 2001; Jónsdóttir et al. 2008; Árnason et al. 2009; Jakobsdóttir et al. 2011).

Genes involved in growth have been a particular target of research in fishes, as a result of the rapid development of the aquaculture industry and the associated increase in interest in marker-assisted breeding techniques (Jackson et al. 1998; De-Santis and Jerry 2007). With rising concerns for genetic changes in growth and reproduction by selective fishing (see 1.2.3 and 1.2.4), this interest has expanded beyond the aquaculture industry and considerable effort is targeted at characterising growth- and reproduction related genes for exploited fish species. For example, Tao and Boulding (2003) identified SNPs in ten growth-related candidate genes in Arctic charr (*Salvelinus alpinus*) and observed an association between early growth and one of these markers. Hemmer-Hansen et al. (2011) used a candidate gene approach to scan 18 growth- and reproduction-related genes for polymorphism in cod and identified over 30 observed polymorphisms between five cod populations. Such efforts deliver useful tools for analysing both contemporary and historic samples and yield empirical opportunities to assess fisheries induced evolution (FIE).

BOX 4. CANDIDATE GENES FOR GROWTH AND REPRODUCTION

For investigating the genetic basis of body size, genes of several different pathways are of particular interest, which are summarised briefly below.

Growth axis

The growth axis, or somatotropic axis, is the main pathway regulating somatic growth and consists of growth hormone (GH) in the pituitary gland, which stimulates the production of insulin-growth factors (IGF) that stimulate metabolic processes and tissue growth (Moriyama et al. 2000, Florini et al. 1996). The pathway consists of GH and IGF-I and II, and associated releasing hormones (GHRH), inhibitors (GHIH or somatostatin), receptors (GHR, IGFR), binding proteins (IGFBP) and carriers (GHC). All these genes have been associated with variations in weight and size of various fish species (e.g. Tao and Boulding 2003; Ryyanen and Primmer 2004; Almuly et al. 2005). The majority of these associations however are concerned with intronic point mutations or microsatellites, and do not represent causal mutations explaining variations in growth and size.

Transforming growth factors

Myogenic regulatory factors (MRF; myogenin, the MyoD complex, myf-5 and myf-6) and growth factors (GF) are part of the transforming growth factor superfamily and mediate the hormone signal sent by the pituitary gland and structural growth at the muscle tissue level (Atchley et al. 1994). Myostatin (MSTN) is a specific growth factor and inhibition of this gene has been reported to improve growth in mice with up to 30% (McPherron et al. 1997). Since then, polymorphisms in MSTN have been associated with growth differences in a range of species. In mammals, MSTN is expressed exclusively in skeletal muscles and inhibits muscle development but in fish it has been reported in other tissues as well, including gills and gonadal tissue, suggesting a more general role of MSTN in physiological development in fish.

BOX 4. (CONTINUED)

Maturation; hypothalamic-pituitary-gonadal (HPG) axis

Genes involved in maturation and reproduction are of interest in light of FIE because of the proposed selective effects of fishing on maturation and because of the trade-offs between growth and reproduction-related traits and strong linkage between the two. Major candidates involved in the maturation process are aromatase, which controls the androgen/oestrogen ratio (Kroon et al. 2005), and the gonadotropins follicle-stimulating hormone and luteinizing hormone (FSH and LH), which regulate egg/ sperm production, with associated releasing- and receptor genes. Other genes connected to the HPG axis and the maturation process are leptin, melanocortin-4 receptor and steroidogenic factor genes.

Food intake and metabolism

Leptin, which is thought to be also minorly involved in GH regulation (Heiman et al 1998), has been associated with food intake and metabolism in fishes (Johnson et al. 2000).

Grehlin is an important hormone affecting food intake in fish, and is also involved in regulation of pituitary hormones like GH and prolactin (Unniappan and Peter 2005).

The melanocortin-4 receptor (MC4-R) gene, is a candidate gene that has been shown to affect body size through both regulation of the energy budget affecting food intake and through leptin regulation and gonadotropin production (Martin et al. 2006), affecting the onset of maturation. In platyfish *Xiphophorus* spp. this gene is found on the sex-chromosome and copy number variation in alleles is a major candidate for the P-locus, which is known to underlie different male size morphs by determining the timing of maturation (Kallmann 1983; Lampert et al. 2010).

Other putative candidates

Jun transcription factors are genes involved in regulating gene activity following the primary growth factor response (Schlingensiepen et al. 1994).

Parvalbumins (PVALB-I and II) are involved in fibre relaxation and calcium binding in muscle tissue and a microsatellite polymorphisms within the PVALB-I gene has been associated with weight in seabass (*Lates calcarifer*) (Xu et al. 2006).

Pituitary adenylate cyclase-activating polypeptide (PACAP) is found on the same mRNA precursor as GHRH and stimulates the release of GH, prolactin, adrenocorticotrophic hormone (ACTH) and luteinizing hormone (LH) (Miyata et al, 1989). A SNP in this gene (intron) has been associated with growth in charr (Tao and Boulding 2003).

Prolactin is a hormone for which a range of effects has been described in vertebrates, including effects on growth and development (Bole-Feysot et al. 1998). Perhaps most known in fishes is its role in osmoregulation and freshwater adaptation (Manzon et al. 2002; Blel et al. 2010). Its inhibitor, dopamine, is furthermore involved in light adaptations (Witkovsky 2004)

Somatolactin is a pituitary hormone related to growth hormone and prolactin and involved in gonadal maturation and spawning in fish (Ono et al. 1990; Rand-Weaver et al. 1992).

PIT-1 is a pituitary-specific activator of GH and thus involved in regulating somatic growth (Tuggle and Trenkle, 1996).

Furthermore, genes involved in a general stress response, such as heat shock proteins (HSP) may be expected to respond to adaptations to the experimental laboratory environment (Parsell and Lindquist 1993).

4.1.2 A context for the identification of polymorphisms and genetic association studies

Despite the increasing availability of gene associations with phenotypic variation in ecologically relevant traits, it is important to realise that the identification of polymorphisms and association studies are only a first step towards understanding the genetic basis of the traits in question. How polymorphisms translate into variation at the phenotypic level, by altering gene transcription and physiological processes, is an important sequel to candidate gene analysis (Vasemägi and Primmer 2005; Stinchcombe and Hoekstra 2007). However, how such functional genomic mechanisms occur is still rarely explained, given the large number of studies that report traits associated with synonymous or intronic polymorphisms (e.g. in DeSantis & Jerry 2007).

4.1.3 A candidate gene approach to investigating the response to selection on body size

The present study utilises candidate genes for growth and body size, in an attempt to characterise some of the variation that may underlie the response to selection observed in our experiments. The choice of a candidate gene approach, rather than a genome-wide search for putative candidates, was fuelled by feasibility in light of limitations to resources and time, but especially by the fact that for guppies, a plethora of genetic resources is available and a candidate gene approach makes optimal use of these resources.

Candidate genes for investigating a genetic response to selection in the present study were obtained from two different sources. Firstly, six SNP markers and their flanking regions that were identified to be in tight linkage with a major QTL for male body length on the sex chromosome in the linkage map of colour and male size traits by Tripathi et al. (2009a). Secondly, genes for which existing knowledge from other species suggests a role in growth and size determination (Box. 4) and for which sequences of *P. reticulata* were available on GenBank. These markers were used for the identification of polymorphisms and a range of genetic analyses was used to identify signatures of selection at individual marker loci.

Table 4.1 Candidate genes for standard length in male *P. reticulata* investigated in the present study. The top box lists markers obtained from Tripathi et al. 2009 (M9-M1078); the bottom box candidate genes obtained from a *P. reticulata*-specific query on GenBank are listed. Query term, putative functions of obtained markers, GenBank association number and DNA type of sequences are given. If SNPs were successfully developed for the marker/ gene in question, SNP marker names are provided in the final column. Markers named *_Dreyer are the same SNP markers as used by Tripathi et al. 2009a for that specific marker.

Query	<i>P. reticulata</i> sequence obtained / putative function	GenBank No.	Sequence	SNP Marker name(s)
M009	Rab interacting lysosomal protein-like 1	ES375672	cDNA	M9_indel, M9_403
M030	Fructose-1,6-bisphosphatase 1	ES382008	cDNA	M30_Dreyer
M061	Ectodermal-neural cortex 1 ENC1	ES379217	cDNA	---
M155	Splicing factor, arginine/serine-rich	ES385036	cDNA	---
M380	Medaka Chrom. 15, in scaffold91_contig45820	FH889280	BAC genomic	---
M987	---	FH893254	BAC genomic	M987_indel
M1046	Melanocortin 4 Receptor	FI236224	mRNA, partial cds	M1046_Dreyer, M1046_2
M1078	Insulin growth factor 1	FI236241	Intron	---
Steroidogenic factor	SF1 nuclear receptor 5A1 steroidogenic factor	FI236230	mRNA, partial cds	SF1
Insulin growth factor	Insulin growth factor 2	DQ337476	mRNA, complete cds	---
IGF-Binding protein	IGF-Binding Protein 1	FI236240	mRNA, partial cds	---
Growth hormone	Growth hormone	U63805	partial cds	GH1, GH2_60, GH2_74, GH2_165, GH2_211
---	putative GH-regulated TBC protein	ES386819	cDNA	TBC1
Heat Shock Protein	similar to Heat-shock protein beta-1 (Hspb1)	ES385844	cDNA	---
Myostatin	similar to myostatin; isoform II	ES380902	cDNA	Myostatin
Pit-I	similar to PIT54 (Gallus gallus)	ES377286	cDNA	---
Transcription factor	Transcription factor JunB	EF408832	cDNA, partial cds	---
Prolactin	similar to prolactin 1	ES374674	cDNA	Prolactin_1, Prolactin_2

4.2 MATERIALS AND METHODS

4.2.1 DNA Sampling and extraction

Sample preparation and DNA extraction protocols are provided in 2.3 and 3.2.

4.2.2 Candidate marker choice

QTL-mapped markers

Six markers were screened that were previously found to be in close linkage with a major QTL for male standard length (M0009, M0030, M0061, M0155 M0380 and M0987; Tripathi et al. 2009a). Two further SNP markers from this study were used; M1046, the partial coding sequence (cds) of the melanocortin 4 receptor (MC4R) and M1078, the intronic sequence of insulin-like growth factor 1 (IGF1).

Growth-related genes

A list of 31 genes and gene families was assembled that can reasonably be expected to be involved in growth- and maturation-related pathways, based on knowledge of gene function in other (fish) species. A search was performed in the GenBank NCBI nucleotide collection (nr/nt) for published sequences of *P. reticulata* for any of these genes (Table 4.1). Sequences were aligned with sequences from other species using BLASTn (Altschul et al. 1997) to identify conserved regions. Primers were designed within both conserved and non-conserved regions using Primer3 (Rozen and Skaletsky 2000). Since most sequences were cDNA sequences and no information was available on the position of intron/exon boundaries, primers were designed for products with a maximum size of around 500 bp. The presence of an intron within the amplification region would thus not necessarily result in lengthy fragments, which could reduce amplification success and be difficult to sequence. A total of 17 primer pairs were designed for ten genes (Table 4.1).

Microsatellite marker Pr39

Microsatellite locus Pr39 (Becher et al. 2002) was included in the candidate gene analyses. This locus has been used by others for population genetic studies in the

wild (van Oosterhout et al. 2006a; Barson et al. 2009; Suk & Neff 2009) but in our experiments, putative linkage of this marker to a locus under selection in L-lines was suggested by HW-deviations of Pr39 observed in L-lines only (see 3.3.2).

4.2.3 Sequencing reactions and PCR protocols

For the QTL-linked markers, the same primers were used for amplification as those used by Tripathi et al. (2009a), except for M1078, for which a new primer pair was designed using Primer3 (Rozen and Skaletsky 2000).

All QTL map primers amplified at 56°C annealing temperature (AT) and PCR products were obtained using a 10µl reaction (4.4µl H₂O, 1.5µl MgCl₂, 1µl colourless GoTaq® Flexi buffer, 1µl 10mM dNTPs, 0.5µl F primer, 0.5µl R primer and 1µl DNA, GoTaq® Flexi DNA polymerase (PROMEGA). PCR products were obtained using a Tetrad2 Peltier thermal cycler (BIO-RAD) using the following program: 95°C 5m; 95°C 1m, 56°C 1m, 72°C 1m for 35 cycles, 72°C 10m. Unless stated otherwise, all primers were at 10mM concentrations and product amplification was verified on a 1% agarose gel.

The amplification success of primers designed from sequences obtained from GenBank was tested using a gradient PCR and a 10µl reaction (4.4µl H₂O, 1.5µl MgCl₂, 1µl colourless GoTaq® Flexi buffer, 1µl 10mM dNTPs, 0.5µl F primer, 0.5µl R primer, 0.1µl DNA, GoTaq® Flexi DNA polymerase (PROMEGA), on a thermal cycler using the following program: 95°C 5m; 95°C 1m, AT 1m, 72°C 1m for 35 cycles, 72°C 10m).

PCRs for sequencing were conducted in 20µl reactions (8.8µl H₂O, 3µl MgCl₂, 2µl colourless GoTaq® Flexi buffer, 2µl 10mM dNTPs, 1µl F primer, 1µl R primer, 0.2µl DNA, GoTaq® Flexi DNA polymerase (PROMEGA) for: 95°C 5m; 95°C 1m, AT 1m, 72°C 1m for 35 cycles, 72°C 10m. Successful amplification was verified on 1% agarose gel and products were cleaned using 0.1µl Exonuclease I, 0.2µl Thermo sensitive alkaline phosphate (TSAP) and 0.7µl H₂O per reaction in a thermal cycler for 37°C 15m, 74°C

15m. All sequencing reactions were performed by MACROGEN Korea (<http://www.macrogen.com>).

4.2.4 SNP discovery

In order to screen for polymorphisms of interest within markers, amplicons derived from PCR with eight primer pairs obtained from Tripathi et al. (2009a) were sequenced for the six smallest and six largest F3 individuals. Subsequently, marker M987, for which an insert was observed that was present only in S1 individuals of the first screening, was sequenced for the ten smallest and largest individuals in the F3 and F4 generation. Four further markers showing putative segregating polymorphisms between treatments (M9, M380, M1046, M30) were sequenced for the eight smallest/ largest individuals respectively of the S1 and S2 and L1 and L2 lines in the F4 generation.

Fourteen successfully amplifying primer pairs (Table 4.1) for the growth-related genes obtained from GenBank and M1078, the IGF1 intron obtained from Tripathi et al. (2009a) (obtained with new primer pairs), were sequenced for two F6 individuals from each selection line (the smallest two individuals of the S1 and S2 and the largest two individuals of the L1 and L2). In addition, a sample consisting of the pooled DNA of the ten smallest/ largest individuals of each line was sequenced for each primer pair.

Sequences were aligned using Geneious Pro 4.8.5 and manually inspected for polymorphisms. Only polymorphisms present in both directions of at least two individuals in high-quality sequences were considered reliable. In total, in addition to the two insertions/ deletions, 14 SNPs of interest were detected within eight markers (Table 4.1) and sent to KBioscience (<http://www.kbioscience.co.uk>) for genotyping.

Candidate marker genotyping

All breeding males from generation F0, F2, F5 and the males used for estimating maturation age in the F6 were genotyped for all candidate markers, thus providing marker frequencies in pre- and post selection samples. Insertions/ deletions (indels)

were observed in M9 and M987, which were incorporated in the microsatellite 58°C multiplex panel, using new primer pairs designed in Primer3 to create appropriate product sizes. For these markers, and microsatellite marker Pr39, genotypes were obtained for additional populations (all generations for Pr39, all but the F1 for M987 and all but the F1 and F3 for M9). Where appropriate, these data are included in the analysis. All primer sequences and SNP markers with flanking regions, used for genotyping assays by KBioscience, are listed in Appendix I.

4.2.5 Genetic diversity and Linkage disequilibrium

Using GenoDive (Meirmans and van Tienderen 2004), the following parameters were obtained per locus for each selection line and for each generation independently: observed heterozygosity H_O , expected heterozygosity H_S , and inbreeding coefficient G_{IS} (Nei 1987). Because for the identification of putative candidates for selection, the signal of each marker needs to be evaluated independently, summary statistics over all loci were not calculated. Instead, only values for those loci showing deviations from predicted values, or interesting patterns between lines or treatments are shown.

Genotypic linkage disequilibrium (LD) was tested for using Genepop's log likelihood ratio statistic for each pair of loci in each population. As with neutral microsatellite loci, LD was tested for in the wild-caught (F0) fish only because small breeding groups and selection may affect the non-random inheritance of loci, even when not physically linked.

4.2.6 Rationale underlying candidate marker analysis

For the purpose of detecting loci under selection, several different methods can be used, based on different properties of loci. A multi-disciplinary approach to detecting selection is important, since selection may act upon different levels, i.e. Hardy-Weinberg equilibrium, heterozygosity or allele frequencies. Marker loci may reveal a signal at one level, but evidence of selection may not necessarily be detectable at another level. For example, a single allele may show an association with body size whilst heterozygosity levels remain unchanged. Outlier analysis, based on F_{ST} or

heterozygosity, would not detect such a signal. Alternatively, heterozygosity may be under selection, which is not necessarily revealed by analysis of allele frequencies (Schlötterer 2003; Martínez et al. 2011).

Furthermore, a distinction can be made between associations of population gene frequencies and selection treatment, or associations of individual genotypes and standard length. Both can be indicative for selection at a candidate locus, but the underlying tests are different and provide support for a role of the candidate locus in the response to selection, or in the genetic basis to standard length respectively. These are two tightly linked concepts, but intrinsically different, because an association of a certain allele with standard length can be expected to be the same in all populations, whilst outlier- and frequency-based analyses are expected to result in differences between treatments for successful candidate loci.

Following Vasemagi and Primmer (2005), the analyses in this chapter are classified into four categories:

1) Single-locus tests for neutrality - deviations from Hardy-Weinberg equilibrium.

- a. Despite suffering from low power (Lewontin & Cockerham 1959) and potentially being biased by genotyping errors (Hosking et al. 2004), deviations from HW-equilibrium, or a significant inbreeding coefficient F_{IS} , indicates higher/ lower frequencies of certain genotypes than expected under random mating and can thus be indicative of selection (Watterson 1977, 1978; Lachance 2009). Here, deviations from HW-equilibrium were estimated for each locus in each population and for each generation independently, using a Hardy-Weinberg probability test for 10.000 batches and 10.000 iterations per batch in Genepop version 4.0.10 (Raymond and Rousset 1995; Rousset 2008). All p-values were subsequently corrected for multiple tests using Benjamini-Hochberg corrections in the program SGoF+ (Carvajal-Rodríguez et al. 2009).
- b. Both drift and selection can result in significant differences in allele frequencies at candidate loci between populations. However, when these

differences are consistent between treatments, this may indicate selection for certain alleles in different selection regimes and associations with different phenotypes (Fidler et al. 2007; Jakobsdóttir et al. 2011). Using Genepop version 4.0.10 (Raymond and Rousset 1995; Rousset 2008) a log-likelihood based exact test with 10.000 batches and 10.000 iterations per batch was used to estimate genotypic differentiation at each candidate locus between all pairs of populations in generation F5 and F6. Results were corrected for multiple tests using Benjamini-Hochberg corrections in SGoF+.

2) **AMOVA.** The hierarchical partitioning of molecular variation between and within treatments can be indicative of selection, when variation between treatments is greater than between lines within treatments. AMOVAs were carried out using Arlequin version 3.5.1.2 (Excoffier et al. 2005) for generation F5 and F6 independently using the following hierarchical levels: (1) within lines, (2) within treatments-between replicate lines, and (3) between treatments. These hierarchical levels are equivalent to F_{ST} , F_{SC} and F_{CT} respectively. Additionally, the same hierarchical analysis was performed on both generations combined.

3) **Outlier analyses; multiple-marker-based neutrality tests**

a. Pairwise differentiation, as measured by F_{ST} and G''_{ST} , can be compared between neutral and putatively selected loci. Higher/lower divergence than expected under neutrality can be indicative of selection at outlier loci. Several widely used methods incorporate this principle for detecting selection (see above). However, these methods are based on F_{ST} and heterozygosity, which may differ between loci depending on the number of alleles and not necessarily only as a result of selection (Meirmans and Hedrick 2011). Therefore, standardised pairwise differentiation, as estimated by G''_{st} , is used here as well to provide an additional measure of differentiation useful for comparing different types of markers (i.e. microsatellites and SNPs). However, due to the large number of tests involved, this method suffers from low power and therefore a lack of significance of outlier loci may be expected.

- b. The *fdist* outlier method (Beaumont and Nichols 1996) compares a plot of heterozygosity and F_{ST} of marker loci to a simulated neutral distribution of these parameters. Based on the principle of increased genetic differentiation between loci under divergent selection, loci with greater differentiation than the computed neutral space are candidates for divergent selection, and those falling below the neutral distribution for balancing selection. Here, LOSITAN – Selection Workbench (Antao et al. 2008) was used to estimate outlier loci from the entire set of 25 markers (microsatellites and candidate loci), using 10.000 simulations, an infinite alleles model and a forced neutral mean F_{ST} . Additional simulations were run in cases where 10.000 simulations were inconclusive in determining whether a locus was under selection or not; i.e. when they were positioned on the neutral-selection interface in the plot. The analyses were performed on the entire dataset of microsatellite- and candidate loci between all pairs of populations, between all treatment pairs and over all populations in the F5 and F6 separately, as well in the F5 and F6 combined.
- c. The third outlier method used is the heterozygosity-based selective sweep method (Schlötterer 2002). This method is based on elevated rates of loss of heterozygosity of loci under selection, compared to populations where the locus is not under selection. It has been demonstrated (Schlötterer 2002; Kauer et al. 2003) that the natural logarithm of the ratio of expected heterozygosity in two populations ($\ln RH$) follows a normal distribution and can be expected, after normalisation to mean=0 and SD=1, to fall between -1.96 and 1.96. Outlier loci from this distribution are candidates for selection. $\ln RH$ was calculated here for each locus (both microsatellites and candidate loci) and each population pair within generation F5 and F6 (all within- and between-treatment comparisons), and normalised over all loci per population pair. Subsequently, outlier values were detected manually from the obtained distribution.
- 4) **Association analysis.** Using the online program SNPStats (Solé et al. 2006), associations between male standard length and genotype were tested for each candidate locus in the F5 and F6 independently, in all control

populations combined (F0, F2, F5, F6) and in a global test over all populations and generations F0, F2, F5 and F6. Each analysis was corrected for multiple testing using Benjamini-Hochberg corrections in SGoF+. The most likely model of inheritance was inferred based on the lowest p -value and lowest value for the Akaike Information Criterion (AIC) and congruence between results of different analyses. Locus M987 and Pr39, which have more than two alleles, were converted to bi-allelic loci based on putative associated alleles from other analyses (see section 4.3.3 below): the absence/ presence of an insert for M987, and the absence/ presence of allele “174” for Pr39. Five different inheritance models were considered: co-dominance, dominance, over-dominance, recessive and a log-additive model. Interactions between loci were not considered.

4.3 RESULTS

4.3.1 SNP discovery and genotyping success rate

QTL-linked markers

All eight QTL-linked markers amplified successfully in our selection lines (using new primers for M1078). From the SNPs described in Tripathi et al. (2009a), putative segregating SNPs were observed only in M9, M30, M380, M987 and M1046. Additionally, M987 and M9 both contained an indel that appeared to have different frequencies in different lines, based on the sequencing of the smallest and largest F3 and F4 individuals. For M987, four alleles were present: one without an insert, and three with an insert, each one basepair different in size. In addition to the two indels, two of the originally designed SNPs (M30_Dreyer, M1046_Dreyer) and two additional SNPs (M9_403, M1046_2) were ultimately selected for large-scale genotyping.

Candidate genes

Sequence hits for specific gene queries for *P. reticulata* were found for ten genes (Table 4.1) for which a total of 16 primer pairs were designed. From these, three did not amplify (primers for partial sequences of GH, myostatin and HSP), leaving 13 successful amplifying primer pairs. Two of these sequences were of insufficient quality to allow further analysis (IGF-II and a partial sequence of TBC1). A considerable proportion of the other sequences was also difficult to read and failed to provide data of sufficient quality to reliably mine for SNPs in at least one sequencing direction (5' → 3' or 3' → 5'). This is probably a result of genomic DNA being sequenced in a single reaction, rather than as isolated alleles through cloning. Any size variation between alleles (e.g. due to indels in intronic sequences) would have resulted in inconsistencies between base calling peaks and unreadable fragments in one direction of the sequence. Although this limited the data available for SNP mining, we judged this method preferable in terms of speed and cost. From the readable sequences, six were monomorphic (IGF-I, IGFBP, the second part of HSP, JunB and both parts of Pit54). The remaining five sequences yielded ten

putative SNPs: five in GH, two in prolactin, and one each in myostatin, TBC1 and SF1. Together with the four SNPs from the QTL-linked markers, 15 putative candidate SNPs were thus genotyped in a total of eight genes for all F0, F2, F5 and F6 samples.

Table. 4.2. Allele frequencies for all candidate markers showing frequencies of allele-specific nucleotides for SNP markers and number of basepairs for indels and microsatellite Pr39.

Locus	Allele	F0	F2	F5_S1	F5_S2	F5_C	F5_L1	F5_L2	F6_S1	F6_S2	F6_C	F6_L1	F6_L2
M9_403	A	27.91	29.95	25.56	38.10	24.42	8.89	12.24	26.53	41.84	40.00	14.00	15.00
	G	72.09	70.05	74.44	61.90	75.58	91.11	87.76	73.47	58.16	60.00	86.00	85.00
M1046_Dreye	T	36.36	30.11	31.11	39.29	34.88	22.73	36.96	32.65	43.00	36.00	30.61	28.00
	C	63.64	69.89	68.89	60.71	65.12	77.27	63.04	67.35	57.00	64.00	69.39	72.00
M1046_2	A	19.32	14.17	17.39	13.41	9.52	14.13	18.37	23.00	17.00	13.00	18.37	17.00
	G	80.68	85.83	82.61	86.59	90.48	85.87	81.63	77.00	83.00	87.00	81.63	83.00
M30_Dreyer	T	62.50	52.67	50.00	29.76	54.76	63.04	66.67	54.08	26.53	73.00	71.43	69.00
	C	37.50	47.33	50.00	70.24	45.24	36.96	33.33	45.92	73.47	27.00	28.57	31.00
GH1	T	63.95	67.96	63.04	58.33	53.85	65.12	68.37	73.00	51.00	55.32	65.31	66.00
	G	36.05	32.04	36.96	41.67	46.15	34.88	31.63	27.00	49.00	44.68	34.69	34.00
GH2_60	A	61.11	42.20	56.82	65.00	54.76	43.18	50.00	44.90	63.00	58.16	40.00	38.00
	G	38.89	57.80	43.18	35.00	45.24	56.82	50.00	55.10	37.00	41.84	60.00	62.00
GH2_74	G	71.59	83.69	77.17	72.62	84.52	84.44	78.72	77.00	79.00	82.29	84.00	86.00
	C	28.41	16.31	22.83	27.38	15.48	15.56	21.28	23.00	21.00	17.71	16.00	14.00
GH2_165	T	41.67	61.29	54.35	40.24	61.63	61.11	53.13	60.42	34.00	61.00	65.00	61.00
	G	58.33	38.71	45.65	59.76	38.37	38.89	46.88	39.58	66.00	39.00	35.00	39.00
GH2_211	A	30.68	22.99	24.44	35.37	29.76	21.59	26.53	21.88	42.86	29.00	21.74	30.00
	C	69.32	77.01	75.56	64.63	70.24	78.41	73.47	78.13	57.14	71.00	78.26	70.00
Myostatin	A	84.52	75.41	73.91	79.27	71.43	72.22	65.63	75.51	69.39	79.00	75.51	72.00
	C	15.48	24.59	26.09	20.73	28.57	27.78	34.38	24.49	30.61	21.00	24.49	28.00
Prolactin_1	A	41.11	35.90	28.89	35.71	40.48	52.22	48.96	28.00	30.00	52.04	63.00	46.00
	G	58.89	64.10	71.11	64.29	59.52	47.78	51.04	72.00	70.00	47.96	37.00	54.00
Prolactin_2	A	42.39	50.53	44.19	44.05	41.67	54.35	59.18	54.00	44.90	57.45	66.00	59.18
	G	57.61	49.47	55.81	55.95	58.33	45.65	40.82	46.00	55.10	42.55	34.00	40.82
TBC_1	T	46.67	48.14	42.05	50.00	65.12	42.39	43.75	50.00	52.00	70.41	41.00	34.00
	G	53.33	51.86	57.95	50.00	34.88	57.61	56.25	50.00	48.00	29.59	59.00	66.00
SF1	A	88.64	85.26	85.23	95.24	80.49	78.26	83.67	79.17	94.00	88.00	77.00	87.00
	T	11.36	14.74	14.77	4.76	19.51	21.74	16.33	20.83	6.00	12.00	23.00	13.00
M9_indel	270	85.56	85.05	84.78	81.40	88.37	92.39	94.90	86.00	97.00	88.00	98.00	92.00
	273	14.44	14.95	15.22	18.60	11.63	7.61	5.10	14.00	3.00	12.00	2.00	8.00
M987	307	14.44	29.08	18.48	30.23	39.53	46.74	50.00	20.00	44.00	23.00	55.00	49.00
	316	6.67	1.90	2.17	1.16		7.61	8.16				5.00	2.00
	317	77.78	60.05	78.26	53.49	53.49	43.48	34.69	74.00	35.00	71.00	39.00	44.00
	318	1.11	8.97	1.09	15.12	6.98	2.17	7.14	6.00	21.00	6.00	1.00	5.00
Pr39	168	1.09	0.53										
	174	2.17	7.67	9.78	11.63	23.26	39.13	37.76	8.00	2.00	12.00	43.00	36.00
	176	5.43	5.56	1.09	3.49	1.16			5.00	2.00	7.00		1.00
	178	54.35	42.86	43.48	58.14	46.51	26.09	36.73	34.00	66.00	51.00	29.00	41.00
	180	7.61	11.38	23.91	9.30	15.12	8.70	11.22	34.00	14.00	6.00	6.00	8.00
	182	13.04	16.93	7.61	4.65	4.65	20.65	6.12	8.00	3.00	5.00	11.00	3.00
	184		0.26										
	190	1.09											
	202	7.61	8.99	14.13	4.65	6.98	5.43	5.10	10.00	1.00	14.00	10.00	5.00
	204	5.43	3.97		6.98	2.33			1.02	1.00	11.00	4.00	2.00
	218	2.17	1.85		1.16				2.04		1.00	1.00	4.00

Genotyping success

Genotyping success rates were high, with only 182 out of 9971 genotypes missing (1.83% failure). With the exception of SF1 which had a minor allele frequencies of 4.8% in S2_F5, no minor allele frequencies < 5% were observed. Allele frequencies per population for all candidate loci are given in Table 4.2

4.3.2 Genetic diversity and linkage disequilibrium

Linkage disequilibrium

Out of 17 loci compared, eight combinations revealed significant linkage disequilibrium after B-H corrections (Table 4.3). The majority of these were between SNPs within the same marker, e.g. the two SNPs within prolactin. Remarkably however, not all SNPs within the same locus showed statistically significant linkage: the two SNPs within the melanocortin-4 receptor (M1046) were not statistically significantly linked, nor were all markers within the growth hormone. Most notably, GH2_74 and GH2_60 were not significantly linked, despite being only 14bp apart and despite significant linkage of both markers with GH2_165, 100bp further on in the gene. Closer investigation of the five SNPs within the growth hormone revealed that a minimum of nine distinct haplotypes are present for the growth hormone sequence comprising these five SNPs (Appendix V).

Table 4.3. Benjamini-Hochberg corrected *p*-values for significant linkage between candidate markers in the wild-caught (F0) males.

GH1 & GH2_60	0.0029
GH1 & GH2_211	0.0000
GH2_60 & GH2_165	0.0000
GH2_60 & GH2_211	0.0403
GH2_74 & GH2_165	0.0168
GH2_165 & GH2_211	0.0029
M987 & M1046_Dreyer	0.0123
Prolactin1 & 2	0.0000

Genetic diversity

Genetic diversity within samples was moderate and lower for candidate markers than microsatellites: ranging from 0.38-0.47 to 0.40-0.49 over all loci excluding and including microsatellite locus Pr39 respectively (Table 4.4). Measured over all loci, no significant differences in H_0 or H_s were observed

between lines or treatments within generations or over the F5 and F6 combined (nested ANOVA, $p > 0.152$). Over generations, neither H_0 nor H_s changed significantly

in the control line (linear regression. $R^2 = 0.017$ and 0.000 , $F_{1,62} = 1.05$ and 0.014 and $p = 0.309$ and 0.907 for H_0 and H_S respectively). Furthermore, between the F5 and F6 generations, no significant differences were observed between H_0 and H_S in selection lines (2-sample randomisation test with 10.000 randomisations, $p = 0.440$; 0.841 for H_0 and 0.910 ; 0.692 for H_S in small- and large selection treatments respectively).

Table. 4.4. Observed (H_0) and expected (H_S) heterozygosity for candidate loci in generations F0, F2, F5 and F6. H_0 and H_S are shown per line and generation per locus and over all loci. Standard errors over all loci are obtained through jackknifing over loci. Over all loci estimates are provided both including and excluding locus Pr39, since this locus has many more alleles than SNP markers and may thereby disproportionately affect the estimate of the mean.

	F0		F2		F5_S1		F5_S2		F5_C		F5_L1		F5_L2	
	H_0	H_S	H_0	H_S	H_0	H_S	H_0	H_S	H_0	H_S	H_0	H_S	H_0	H_S
MB_403	0.279	0.409	0.467	0.421	0.244	0.386	0.476	0.477	0.349	0.374	0.133	0.164	0.204	0.217
M1046_Dreyer	0.686	0.456	0.462	0.422	0.356	0.434	0.5	0.483	0.512	0.459	0.273	0.356	0.478	0.471
M1046_2	0.295	0.316	0.251	0.244	0.304	0.29	0.268	0.235	0.143	0.175	0.152	0.246	0.357	0.302
M30_Dreyer	0.477	0.474	0.487	0.5	0.378	0.507	0.548	0.422	0.667	0.499	0.609	0.47	0.583	0.448
GH1	0.395	0.457	0.464	0.437	0.609	0.47	0.595	0.481	0.564	0.503	0.419	0.46	0.51	0.436
GH2_60	0.467	0.481	0.5	0.489	0.662	0.494	0.55	0.46	0.619	0.5	0.5	0.496	0.66	0.504
GH2_74	0.386	0.412	0.273	0.274	0.37	0.366	0.452	0.402	0.262	0.265	0.311	0.265	0.383	0.338
GH2_165	0.5	0.492	0.505	0.476	0.522	0.501	0.561	0.486	0.535	0.478	0.378	0.482	0.646	0.502
GH2_211	0.386	0.431	0.385	0.355	0.4	0.373	0.561	0.462	0.452	0.423	0.341	0.342	0.49	0.393
Myostatin	0.214	0.265	0.276	0.372	0.261	0.391	0.317	0.393	0.381	0.413	0.378	0.406	0.498	0.456
Prolactin_1	0.511	0.489	0.463	0.461	0.489	0.415	0.571	0.463	0.619	0.486	0.467	0.505	0.479	0.505
Prolactin_2	0.457	0.494	0.468	0.501	0.279	0.502	0.548	0.498	0.5	0.492	0.565	0.501	0.408	0.489
TBC_1	0.4	0.505	0.527	0.501	0.568	0.492	0.512	0.506	0.512	0.459	0.674	0.492	0.458	0.498
SF1	0.182	0.204	0.274	0.252	0.205	0.255	0.095	0.092	0.341	0.318	0.391	0.343	0.286	0.276
M987	0.356	0.374	0.489	0.548	0.413	0.356	0.581	0.607	0.721	0.557	0.804	0.59	0.918	0.621
M9	0.244	0.25	0.255	0.255	0.304	0.26	0.372	0.306	0.233	0.208	0.152	0.142	0.102	0.098
Over all	0.387	0.408	0.409	0.407	0.399	0.405	0.469	0.42	0.463	0.413	0.409	0.391	0.463	0.41
St. err. through jackknifing over all loci	0.0305	0.0245	0.0261	0.0256	0.0349	0.0217	0.0348	0.0312	0.0413	0.0285	0.0477	0.033	0.0477	0.0351
Pr39	0.696	0.676	0.768	0.758	0.739	0.726	0.698	0.636	0.814	0.706	0.87	0.732	0.837	0.709
Pr39 A/ Ar	10	9.206	10	8	6	5.696	8	7.722	7	6.677	5	4.998	7	6.53
Over all incl Pr39	0.405	0.424	0.431	0.427	0.419	0.424	0.483	0.433	0.484	0.43	0.436	0.411	0.485	0.427
St. err. over all incl Pr39	0.0339	0.0279	0.0331	0.0317	0.0384	0.0277	0.0353	0.0319	0.0439	0.0319	0.0523	0.0369	0.0499	0.0357

Table 4.4. (continued)

	F6_S1		F6_S2		F6_C		F6_L		F6_L2	
	Ho	Hs	Ho	Hs	Ho	Hs	Ho	Hs	Ho	Hs
M9_403	0.449	0.393	0.469	0.492	0.48	0.485	0.28	0.243	0.26	0.258
M1046_Dreyer	0.531	0.443	0.58	0.494	0.44	0.466	0.408	0.429	0.48	0.407
M1046_2	0.42	0.357	0.3	0.285	0.18	0.229	0.327	0.303	0.3	0.285
M30_Dreyer	0.51	0.502	0.327	0.395	0.42	0.398	0.49	0.412	0.5	0.431
GH1	0.42	0.398	0.5	0.505	0.596	0.499	0.49	0.457	0.48	0.453
GH2_60	0.531	0.5	0.34	0.472	0.551	0.491	0.56	0.484	0.52	0.476
GH2_74	0.38	0.358	0.34	0.335	0.271	0.295	0.32	0.271	0.28	0.243
GH2_165	0.5	0.483	0.52	0.453	0.5	0.48	0.62	0.458	0.42	0.481
GH2_211	0.354	0.345	0.49	0.495	0.5	0.415	0.391	0.343	0.44	0.424
Myostatin	0.204	0.375	0.367	0.43	0.3	0.336	0.327	0.374	0.4	0.407
Prolactin_1	0.24	0.409	0.28	0.426	0.469	0.505	0.5	0.471	0.48	0.502
Prolactin_2	0.4	0.503	0.449	0.5	0.468	0.494	0.4	0.454	0.367	0.489
TBC_1	0.56	0.504	0.4	0.505	0.347	0.422	0.5	0.489	0.48	0.453
SF1	0.417	0.332	0.12	0.114	0.24	0.213	0.38	0.358	0.22	0.229
M987	0.46	0.412	0.78	0.645	0.5	0.443	0.68	0.547	0.96	0.565
M9	0.28	0.243	0.06	0.059	0.24	0.213	0.04	0.04	0.16	0.149
Over all	0.416	0.41	0.395	0.413	0.406	0.399	0.42	0.383	0.422	0.391
St. err. through jackknifing over all loci	0.0263	0.0189	0.0432	0.0377	0.0315	0.0268	0.0379	0.0312	0.0453	0.0299
Pr39	0.72	0.751	0.66	0.535	0.7	0.7	0.98	0.71	0.88	0.696
Pr39 A/ Ar	7	6.635	8	6.981	8	7.518	6	5.638	8	7.448
Over all incl Pr39	0.434	0.43	0.411	0.42	0.424	0.417	0.452	0.402	0.449	0.409
St. err. over all incl Pr39	0.0305	0.0268	0.0435	0.0361	0.0342	0.0308	0.0485	0.0351	0.0504	0.0333

4.3.3 Hardy-Weinberg disequilibrium and G_{IS}

Hardy-Weinberg equilibrium

22 out of 204 tests showed significant deviations from HW-equilibrium, only six of which were significant after B-H corrections for multiple tests: myostatin in the F2, M987 in L2_F5 and F6, and Pr39 in F5 L2 and F6 L1 and L2. Closer investigation revealed that the significant deviation of myostatin was the result of a heterozygote deficiency and deviations of M987 in the L2 line were the result of an excess of heterozygotes of “307” (the allele without an insert present) and the most common allele with an insert: “317”. Significant deviations in L-lines for locus Pr39 are the result of a deficiency in homozygotes for allele “174” and a large excess in heterozygotes of this allele with either allele “178” or “180”.

G_{IS}

To ensure no significant genetic patterning was ignored, e.g. by inflating the type II error rate due to stringent corrections for multiple testing, results from HW-equilibrium tests and G_{IS} estimates were compared directly to reveal whether deviations in one or the other underlie interesting genetic patterns that may be the result of different selection regimes.

Table 4.5 shows significant G_{IS} estimates ($p < 0.05$) with different degrees of statistical support. 49 out of 204 G_{IS} estimates were significant (Table 4.5). The expected number of significant estimates (based on a 5% type I error rate) equals ten but out of the initial 49 significant estimates, only 22 did not stand up to corrections for multiple testing, nor were supported by significant HW probability tests. Fourteen tests had significant G_{IS} values and deviations of HW-equilibrium but not after correcting for multiple testing. However, four of these tests showed putative interesting patterns between treatments, which justifies closer investigation. Prolactin1 revealed significant G_{IS} values and a heterozygote excess in F6_S1 and F6_S2 only, indicating a potential effect of selection for small size on heterozygosity. However, this pattern was not present in the F5. Weak support for significant G_{IS} values was furthermore observed for Pr39 in F5_L1 and M987 in F6_S2 and F6_L1. As, like in other populations, the heterozygote excess was caused by a deficiency in “174” homozygotes at locus Pr39 in F5_L1, and a heterozygote excesses for M987, these deficiencies are still of interest, despite weak support.

Significance after B-H correction in one of the two tests remained for a “174” homozygote deficiency in Pr39 in F5_L2 and a small heterozygote deficiency for prolactin2 in F5_S1 and for myostatin in F6_S1. HW deviations and non-zero G_{IS} values remained significant after B-H corrections in both tests at myostatin in the F2, Pr39 in F6_L1 and F6_L2, and at M987 in F5_L2 and F6_L2.

Table.4.5. G_{IS} estimates for 17 candidate loci in pre-selection populations F0 and F2 and selected lines and control line in the F5 and F6 generations. G_{IS} significance was assessed using 9999 permutations. Colour scales indicate the significance of the estimate based on G_{IS} permutation tests using GenoDive and/ or HW probability tests in GenePop and B-H corrections for multiple tests on both.

	MB_403	M1046_ Dreyer	M1046_ 2	M30_Dr	GH1	GH2_ 165	GH2_ 211	Myostatin	Proactin1	Proactin2	TBC_1	SF1	Pt39	MB987	MB9
F0	0.317	-0.365			0.154			0.193			0.207	0.109			
F2								0.259						0.108	
F5_S1	0.367			0.255	-0.296			0.333		**0.444		0.199			
F5_S2				-0.299											
F5_C			0.183	-0.335										-0.294	
F5_L1	0.188	0.234	0.382	-0.296	0.09	0.216					-0.37		-0.188	**0.363	
F5_L2				-0.303		-0.287							*0.18	-0.478	-0.043
F6_S1								**0.456	0.413						
F6_S2						0.28			0.342				-0.234	-0.209	
F6_C						0.081									
F6_L1						-0.354							-0.381	-0.243	-0.01
F6_L2									0.249				-0.265	-0.699	-0.077

Legend:

significant G_{IS} , no support from H-W probability test

significant G_{IS} , supported by H-W probability test, but not significant after B-H correction

***significant G_{IS} but not after B-H corrections , supported by H-W test significant after B-H correction**

****significant G_{IS} after B-H corrections , supported by H-W probability test**

significant G_{IS} , supported by H-W probability test, after B-H corrections for both

significant G_{IS} after B-H correction for multiple tests, no support from H-W probability test

Four tests retained significant G_{IS} estimates after B-H corrections but these results were not supported by HW probability tests (Table 4.5). However, these were most likely the result of discrepancies between the different ways of calculating deviations in both tests, as G_{IS} permutation tests appear sensitive to small deviations from expectations at loci with few alleles, i.e. SNPs. This is exemplified by M9_403 and myostatin in the F0, both of which had only very small heterozygote deficiencies (five and two individuals out of 42 respectively). For M987, the negative G_{IS} in F6_S2 stems from a heterozygote excess of only four individuals out of 50, and the positive G_{IS} in M987 from an excess of eleven heterozygotes in 192 individuals.

In summary, heterozygosity levels of prolactin1, M987 and Pr39 deviate from random expectations in a pattern corresponding to the selection treatments and show signatures of selection.

4.3.4 Genotypic differentiation

Out of 340 within-generation pairwise tests for genotypic differentiation, 118 revealed significant differentiation at candidate loci between population pairs, 83 of which were significant after B-H corrections. These included population pairs for all candidate loci except GH2_74, M1046_Dreyer, M1046_2 and myostatin, for which no significant genotypic differentiation was observed between any population pairs.

Table 4.6 shows p -values for loci for which significant differentiation was observed between at least some population pairs. Full tables can be found in Appendix VI. The majority of loci differ either consistently over both generations or show a stronger signal in the F6 compared to the F5. The two L-lines are remarkably similar and do not differ significantly for any candidate loci. The two S-lines however differ from each other at several loci, in particular in the F6. The table further shows that S2 differs from L-lines and/ or the control as well at these loci, and more differences exist between L-lines and S2 than between L-lines and S1. In particular, S2 differs at locus M30_Dreyer from all other lines, while the remaining lines are all similar at this locus. No differences between S-lines are observed for prolactin1, but differences between S- and L-lines are observed for this locus. Differentiation at prolactin2 is

observed only in the F6 between S2 and L1, and has weak statistical support ($p = 0.0320$). This locus is therefore not considered a suitable candidate. M9_403 is significantly different between both L-lines and S2 and the control. The difference between L-lines and S1 at this locus was significant before B-H correction only ($p = 0.0156-0.0453$). Marker Pr39 and M987 are differentiated between most comparisons and, with M9_403, seem the most likely candidates for selection based on this analysis.

Table 4.6 is based on genotypic differentiation. The allele frequencies underlying these genotypes are summarised in Fig. 4.1, which shows minor allele frequencies

Table 4.6. Significant values for pairwise tests of genotypic differentiation, as obtained from a log-likelihood based exact test. Shown are B-H corrected p -values for each possible population pair within each generation for the different putative candidate loci. Tests between S- and L-lines are shown in grey, within-treatment and between treatments and Control line in white. A significant value for prolactin2 is shown in *Italic*, to highlight the weak support for genotypic differentiation at this locus, which justifies it not being discussed in detail in the text.

	F5		F6			F5		F6				
	Locus	p	Locus	p		Locus	p	Locus	p			
L-L												
S-S			GH1	0.0126	C-S1	TBC_1	0.0084	GH1	0.0321			
			GH2_165	0.0018				Prolactin1	0.0147			
			GH2_211	0.0134				TBC_1	0.0225			
	M30_Dreyer	0.0413	SF1	0.0076				M30_Dreyer	0.0321			
	M987	0.0016	M30_Dreyer	0.0022				Pr39	0.0010			
Pr39	0.0083	M987	0.0000									
S1-L1	Prolactin1	0.0126	Prolactin1	0.0001	C-S2	SF1	0.0175	Prolactin1	0.0276			
	M987	0.0001	M9_indel	0.0109				M30_Dreyer	0.0000			
	Pr39	0.0000	M987	0.0000				M987	0.0000			
S1-L2	Prolactin1	0.0280	Pr39	0.0000	C-L1	M9_403	0.0492	GH2_60	0.0413			
	M987	0.0000	M987	0.0000				TBC_1	0.0009			
	Pr39	0.0002	Pr39	0.0000				M9_indel	0.0326			
S2-L1	GH2_60	0.0206	GH2_60	0.0147	C-L2	M987	0.0083	M9_403	0.0007			
	GH2_165	0.0484	GH2_165	0.0000				TBC_1	0.0000			
			GH2_211	0.0109				M9_403	0.0015			
			Prolactin1	0.0004				M987	0.0015			
	SF1	0.0042	<i>Prolactin2</i>	<i>0.0320</i>				Pr39	0.0035			
	M9_403	0.0001	SF1	0.0058								
	M30_Dreyer	0.0000	M9_403	0.0002								
M987	0.0022	M30_Dreyer	0.0000									
Pr39	0.0000	M987	0.0000									
S2-L2			Pr39	0.0000								
			GH2_60	0.0083								
	M9_indel	0.0145	GH2_165	0.0022								
	M9_403	0.0010										
	M30_Dreyer	0.0000										
	M987	0.0058										
Pr39	0.0019											

for all bi-allelic loci, frequencies of the allele without an insert for M987 and of allele “174” for Pr39. The figure supports and clarifies the findings in Table 4.6. The control line shows increasing divergence from selected lines at TBC1 over generations, which differs very little between selected lines. Allele frequencies for S2 differ markedly at GH2_165 and GH2_211, M30_dreyer and SF1 suggesting these markers may be under selection in S2. At GH1 and GH2_60 however, the differences observed between the S2 and other lines are less consistent and drift seems a more likely explanation for changes in allele frequencies. S1 and S2 are similar for prolactin1 and different from other lines, but the magnitude of this difference does not fall outside the range of frequencies of the control line over generations.

The frequency of the insert in M9_indel was significant only between S1 and L1 in the F6 (corrected $p = 0.0109$) and between S2 and L2 in the F4 and F5 (corr. $p < 0.0146$). The insert frequency of S2 in the F6 is however the same as for L-lines ($p = 0.1997 - 1.000$).

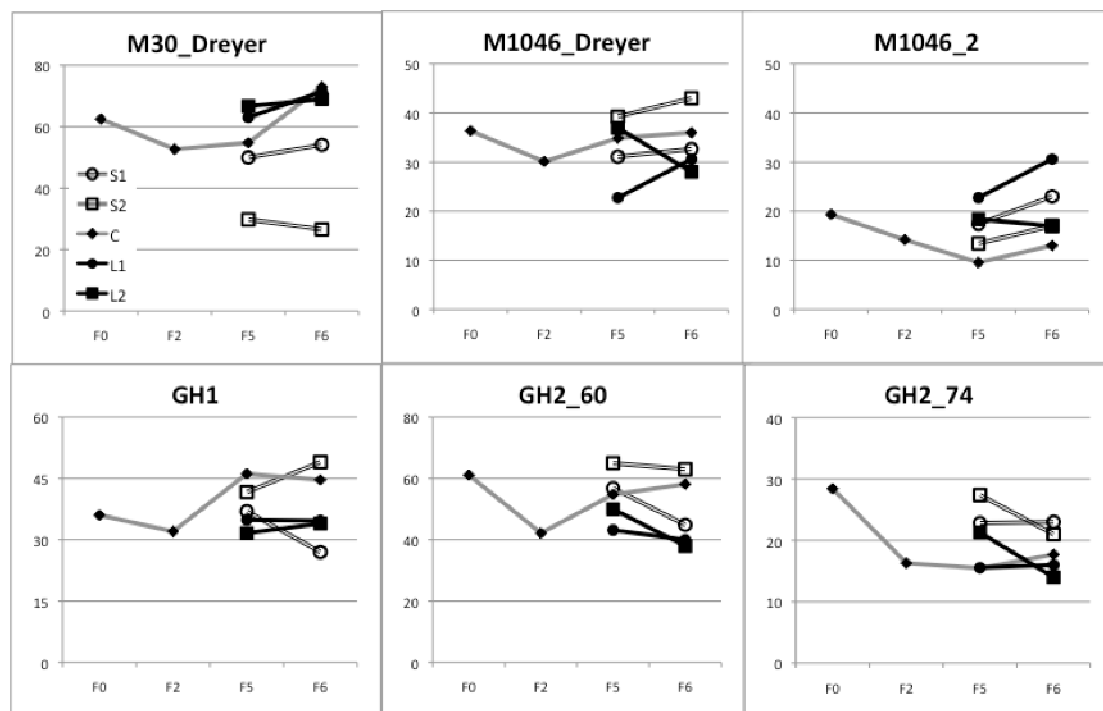


Fig. 4.1. Allele frequencies of minor alleles of candidate SNP markers in generations F0, F2, F5 and F6, and insert frequencies of M9_indel in generations F0, F2, F4-F6, no insert frequencies for M987 in F0, F2-F6 and allele 174 frequencies for Pr39 in F0-F6. The y-axis show relative allele frequencies on a scale of 0-100. L-lines are depicted by closed squares (L1) and circles (L2), S-lines by open circles (S1) and squares (S2) and the Control by a grey line and closed diamonds.

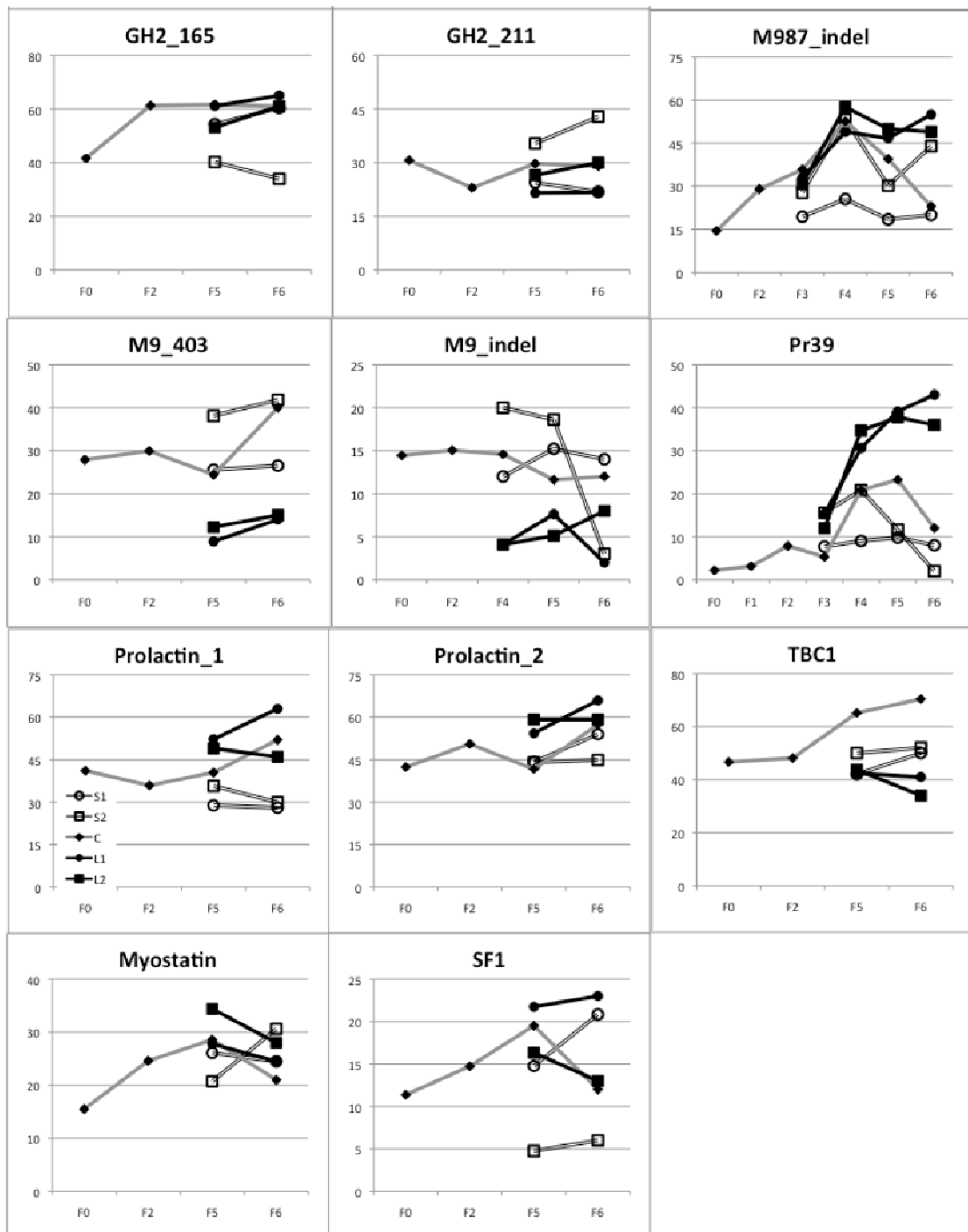


Fig. 4.1. (continued)

Whilst differentiation is observed between all lines at locus M987, when simplifying this locus to the presence/ absence of an insert (rather than incorporating all three different insert sizes as for the analysis of Table 4.6), it is only S1 that appears different from other lines, having a markedly lower frequency of the short allele compared to other lines ($p = 0.000-0.0016$) except compared to the control in the F6

($p = 0.9299$). Fig. 4.1 further clarifies that the consistent low frequency in the S1 is not outside the range of frequencies observed in the control line over generations.

No support for significant differentiation was observed for GH2_74, myostatin, M1046_Dreyer and M1046_2. However, from Fig. 4.1 it appears that for GH2_74, both S-lines have higher minor allele frequencies than other lines. Despite this pattern not being significant this is a noteworthy observation.

For locus Pr39, a strikingly similar increase in frequency of allele 174 is observed for L-lines. Most notably, this increase in frequency is not associated with an increase in homozygotes for this allele (Fig. 4.2). The latter is in particular indicative of selection, because drift is not expected to result in deviations from Hardy-Weinberg equilibrium. This is supported by the microsatellite data in Chapter 3, which revealed no deviations from HW-equilibrium despite drift between lines.

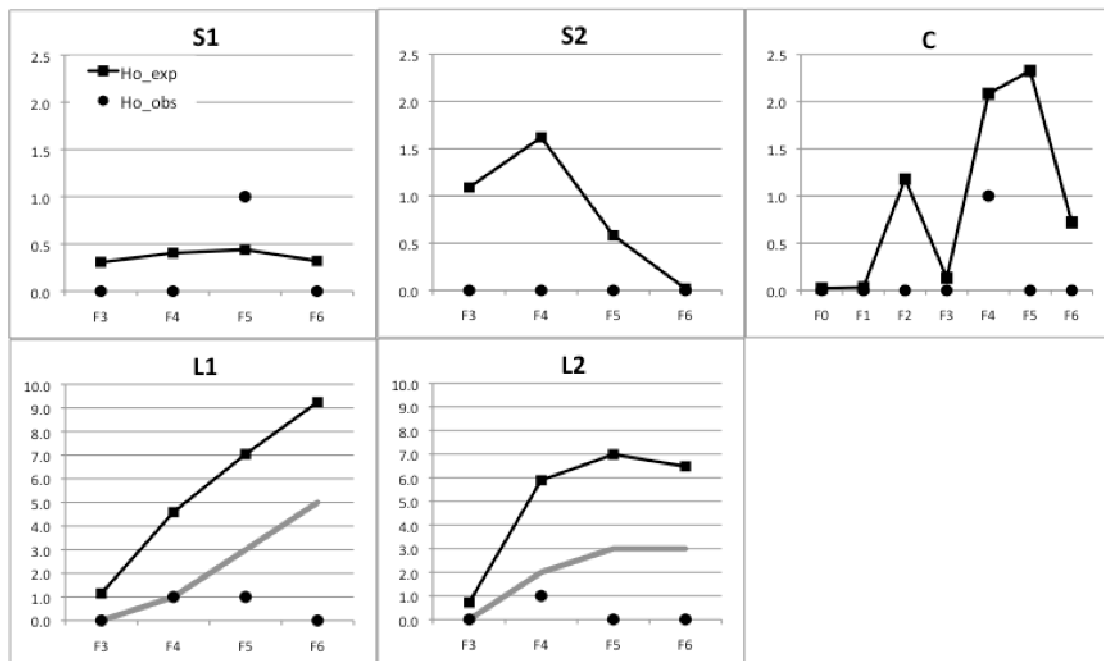


Fig. 4.2. Expected (squares) and observed (circles) number of homozygotes for allele 174 for S-lines (S1, S2) Control (C) and L-lines (L1, L2) in generations F3-F6, showing increasing homozygote deficiencies for L-lines but not for S-lines or the Control. The solid grey line in the L1 and L2 graphs represent the cumulative binomial distribution of homozygosity probability for allele 174, based on the allele frequency. Any value of observed homozygosity below the line has a probability less than 0.05. Note the difference in scale on the y-axes between L-lines and the other treatments.

Based on analysis of allele frequencies between lines and treatments, M30_Dreyer, GH2_60 and GH2_165 may be under selection in the S2, M987 in the S1 and TBC1 in the control line. Consistent patterns between treatments are observed for prolactin1, M9_403 and Pr39, suggesting divergent selection between treatments may be taking place at these loci.

4.3.5 AMOVA

Analysis of molecular variance (AMOVA) in the F5 and F6 revealed that a significant component of the variation observed in candidate markers was a result of variation between treatments, in contrast to what was observed for microsatellite loci (Fig. 4.3), indicating an effect of the direction of selection on allele frequency distributions at candidate loci. Although the among-treatments component of variation was significant in both generations and identical in size ($F_{CT} = 0.024$), it was less strongly supported in the F6 generation ($p = 0.0005$ and 0.036 respectively). A greater proportion of variation at the within-treatments, among-lines level in the F6 may explain this pattern.

Since not all candidate loci are likely to respond to selection, it is important to reveal which loci are responsible for the observed elevated level of variation between treatments compared to microsatellite loci. However, looking at individual loci, no significant values for F_{CT} were observed in each generation independently, although F_{CT} for TBC1 was nearly significant ($F_{CT} = 0.027$ and 0.0685 , and $p = 0.068$ and 0.065 in the F5 and F6 respectively). When statistical power was increased by examining the partitioning of variance in both generations combined, the overall pattern did not differ dramatically (Fig. 4.3) but several loci provide independent statistically significant contributions to the variance observed (Table 4.7). Most notably, the variance components for GH2_74, prolactin1, prolactin2 and TBC1 are significant at the among-treatments level, but not at the among-lines, within-treatments level. Complete AMOVA tables with variance components and accompanying F statistics for each locus are provided in Appendix III.

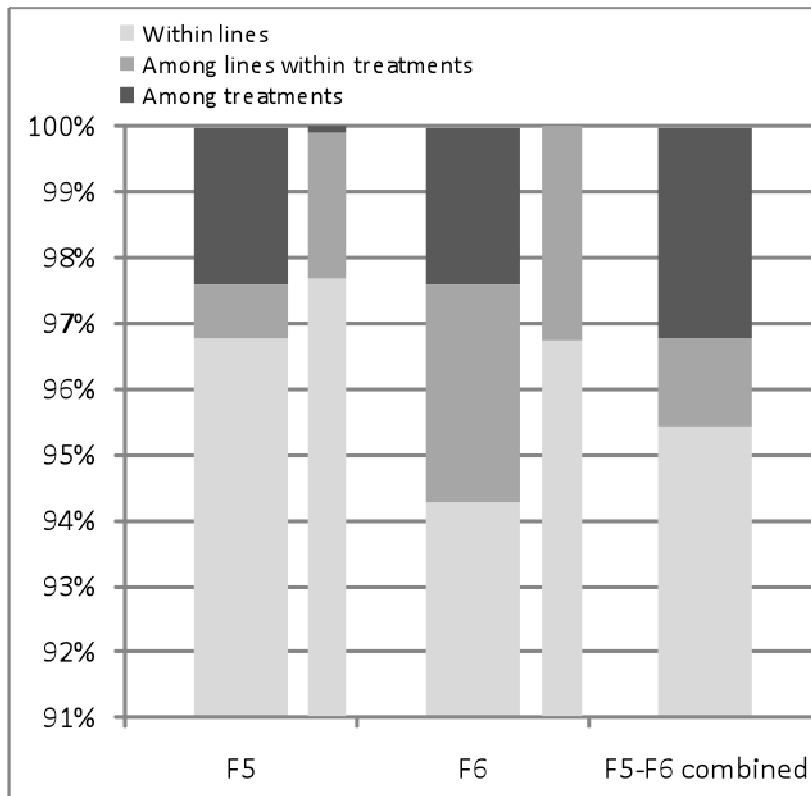


Fig.4.3. AMOVA of candidate loci in generations F5 and F6, partitioning variance among treatments (black bars) among lines within treatments (dark grey bars) and within lines (light grey bars). Partitioning of variance in microsatellite loci is depicted in the thin bars for comparison.

In summary, AMOVA suggests that selection may operate at GH2_74, M30_Dreyer, TBC1, prolactin1, prolactin2, M9_403 and Pr39, as for these loci significant differentiation between treatments was observed.

4.3.6 Outlier analyses: multiple-marker-based neutrality tests

Pairwise differentiation

Fig. 4.4 shows pairwise levels of differentiation over all microsatellite and candidate loci between all pairs of population in the F5 and F6 generations. Comparing both graphs, showing F_{ST} (a) and G''_{ST} (b) respectively, two observations are immediately obvious: firstly, candidate loci show a strong increase in levels of differentiation from within-treatment to comparisons with the control line and between-treatments

comparisons, which is not observed for neutral microsatellite loci. Secondly, standardisation removes the majority of the difference between microsatellite- and candidate loci, although the gradient over treatments is still only observed for candidates.

Pairwise G''_{ST} per locus is provided in Fig. 4.5 and reveals that high G''_{ST} is observed in particular for M30_Dreyer between populations S2 and C, L1 and L2 in the F6. No other loci are suggested to be under selection by this analysis. Full tables of both pairwise F_{ST} and G''_{ST} are provided in Appendix IV.

Table 4.7. Values of F_{CT} , F_{SC} , and F_{ST} values accompanying Fig. 4.7 with significance levels as ns (not significant), * ($p < 0.05$), ** ($p < 0.01$) and *** ($p < 0.001$). Shown are values over all loci for the F5, F6 and both generations combined and values per locus for the joint analysis over both generations only. Full AMOVA tables per locus for all three analyses are provided in Appendix III.

	Among treatments (Fct)	Among lines within treatm. (Fsc)	Within lines (Fst)		Among treatments (Fct)	Among lines within treatm. (Fsc)	Within lines (Fst)
F5	0.02412 ***	0.00823 **	0.03216 ***	F6	0.02405 *	0.03389 ***	0.05713 ***
F5 & F6	0.03217 ***	0.01404 *	0.04576 ***				
Per locus for the F5 and F6 combined:							
M9_403	0.07371 *	0.01712 *	0.08957 ***	Myostatin	-0.00059 ns	-0.00125 ns	-0.00184 ns
M1046_Dreye	0.00343 ns	0.00201 ns	0.00543 ns	Pro lactin_1	0.05934 **	0.00597 ns	0.06496 ***
M1046_2	0.00466 ns	-0.00391 ns	0.00076 ns	Pro lactin_2	0.01726 *	0.00448 ns	0.02166 *
M30_Dreyer	0.08899 *	0.03798 ***	0.12359 ***	TBC_1	0.06024 **	-0.00299 ns	0.05743 ***
GH1	0.00634 ns	0.00634 ns	0.01265 *	SF1	0.00197 ns	0.01915 **	0.02108 **
GH2_60	0.02455 ns	0.00903 *	0.03336 ***	Pr39	0.05519 **	0.02617 ***	0.07991 ***
GH2_74	0.00937 *	-0.00576 ns	0.00367 ns	M987	0.04379 ns	0.04881 *	0.09047 ***
GH2_165	0.01661 ns	0.02061 **	0.03688 ***	M9_Indel	0.01074 ns	0.01653 **	0.02709 ***
GH2_211	-0.00181 ns	0.01352 *	0.01173 *	Over all loci	0.03217 ***	0.01404 *	0.04576 ***

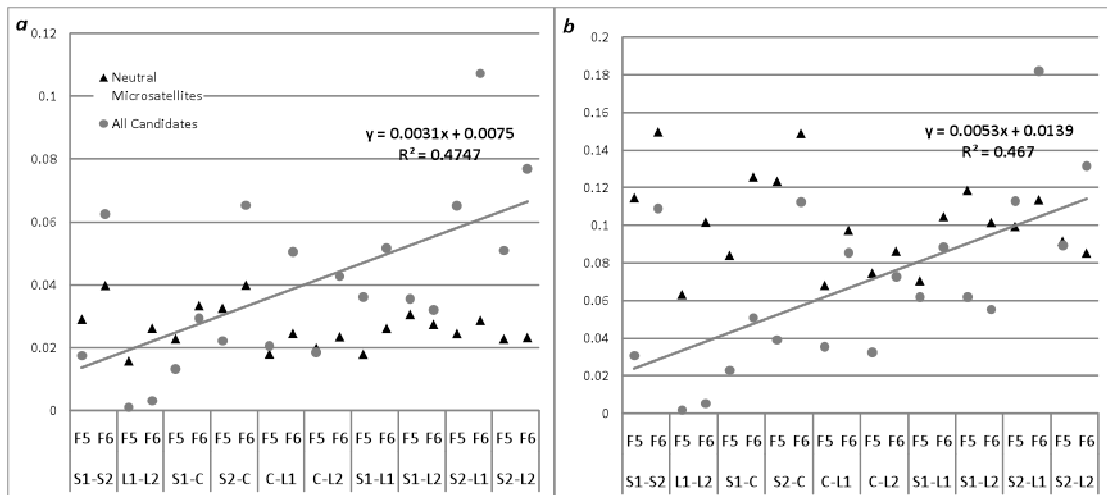


Fig 4.4. Pairwise F_{ST} (a) and G''_{ST} (b) over all microsatellite loci (black triangles) and over all putative candidate markers for selection (grey circles) between all pairs of populations in generations F5 and F6. The grey solid line shows a linear relationship between differentiation and treatment for candidate loci; from within-treatment comparisons (left) to comparisons with the Control line (middle) and between treatments (right). For microsatellites, such relationship is not visible.

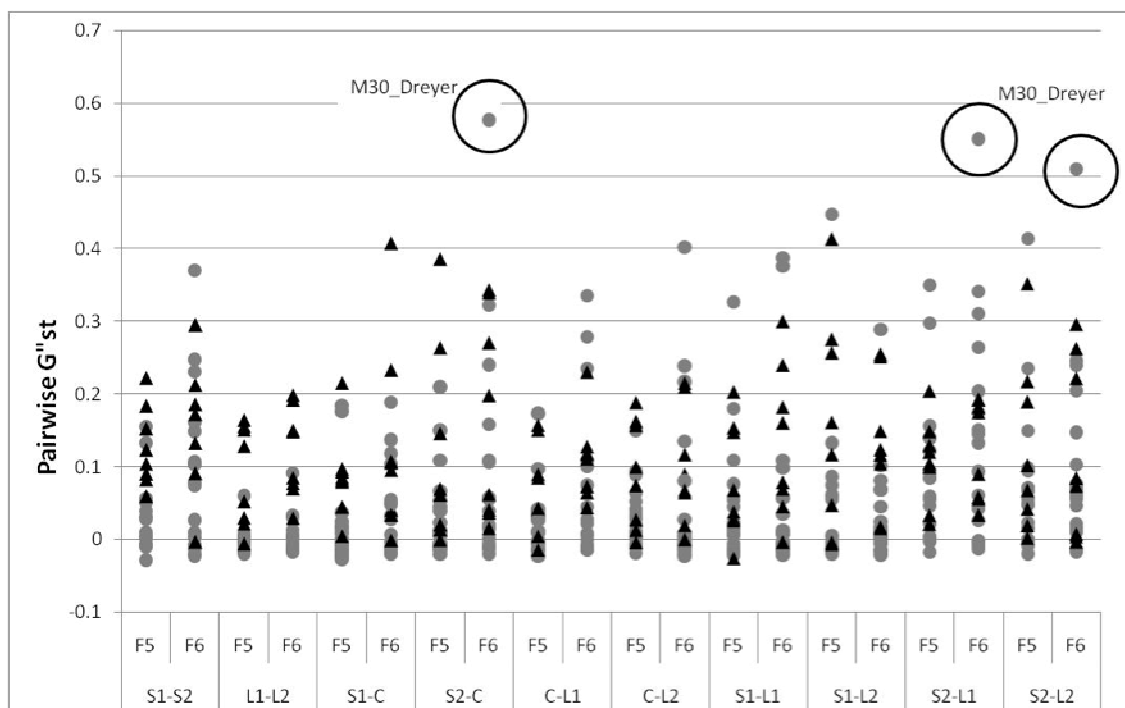


Fig 4.5. Pairwise G''_{ST} values for individual microsatellite loci (black triangles) and putative candidates for selection (grey circles) between all pairs of populations in generations F5 and F6. Putative outliers for locus M30_Dreyer between S2 and C, L1 and L2 in generation F6 are encircled.

Fdist

Lositan Selection Workbench was used to detect outlier loci following the fdist method (Beaumont and Nichols 1996). Depending on which combination of populations was compared, different loci emerged as putative outliers and candidates for divergent selection, although considerable overlap in outlying loci was identified.

In the F5, only locus M987 and microsatellite locus G82 were identified as potential candidates for selection in population pairs S1-L2 and C-S2 respectively (Table 4.8). There was no evidence of selection on these loci in the F6. However, when both generations were combined, evidence of selection on both loci was supported.

Table 4.8. Summary of significant outliers detected by the fdist method using LOSITAN. The table shows expected heterozygosity, F_{ST} and p value for all significant loci in the different analyses, with rows showing different pairwise comparisons (between individual populations, treatments and over all) and divided over columns according to generation (F5, F6 or F5 and F6 combined). Grey rows show L-S comparisons. P values are given as: 1 – the chance that simulated $F_{ST} <$ sample F_{ST} . Output figures from all analyses are provided in Appendix VII.

	F5				F6				F5 & F6			
	Locus	He_exp	Fst	p	Locus	He_exp	Fst	p	Locus	He_exp	Fst	p
L-L												
S-S												
S1-L1									Prolactin1	0.5054	0.1105	0.0188
									M987	0.7867	0.0711	0.0234
S1-L2									Pr39	0.5501	0.1316	0.0058
	M987	0.6335	0.2259	0.0065					M987	0.5651	0.1316	0.0203
S2-L1					M30_Dreyer	0.6006	0.3288	0.0217	M30_Dreyer	0.5251	0.1904	0.0120
									Pr39	0.7417	0.1173	0.0164
S2-L2					M30_Dreyer	0.5892	0.2990	0.0149	M30_Dreyer	0.5256	0.1922	0.0011
C-S1									Pr92	0.7581	0.0603	0.0041
C-S2					M30_Dreyer	0.6080	0.3486	0.0107	M30_Dreyer	0.5210	0.1762	0.0087
	G82	0.6099	0.1962	0.0093					G82	0.5806	0.1257	0.0138
C-L1												
C-L2					TBC1	0.5653	0.2267	0.0082	M9_403	0.3611	0.0772	0.0074
									TBC1	0.5127	0.1071	0.0000
									G82	0.5560	0.0613	0.0239
									M987	0.5846	0.0608	0.0101
C-L					TBC1	0.5244	0.1336	0.0181	TBC1	0.5071	0.0752	0.0037
									M9_403	0.3133	0.0745	0.0073
C-S					M30_Dreyer	0.5361	0.1956	0.0201	M30_Dreyer	0.5093	0.1085	0.0064
L-S					M30_Dreyer	0.5157	0.1565	0.0209	M30_Dreyer	0.5047	0.1111	0.0016
					Pr39	0.7587	0.1113	0.0183	Pr39	0.7455	0.0772	0.0030
									M987	0.5946	0.0841	0.0073
All					M30_Dreyer	0.4998	0.1443	0.0077	M30_Dreyer	0.4987	0.0999	0.0027
									Pr39	0.7382	0.0638	0.0095
									M987	0.5808	0.0771	0.0043

In the F6 generation, evidence for selection at locus M30_Dreyer was obtained for comparisons between S2 and control- and L-lines, but not between S1 and the other populations. Over both S-lines however, a signal for selection at this locus was still identified between S and both control- and L-lines. Support for selection at locus TBC1 and Pr39 was obtained between the control- and L-lines and at locus Pr39 furthermore between S- and L-lines combined. Over all five lines, only locus M30_Dreyer was identified as a candidate for selection.

In analyses where both generations were combined, the same loci were identified as candidates for divergent selection as in both generations separately. Additionally, the analyses indicated selection at M987 and prolactin1 for S1 and L1 and at Pr39 between several S- and L-line combinations (Table 4.8). Additionally, evidence for selection was identified at microsatellite locus Pr92 between the control line and S1, and at M9_403 between control line and L2 and both L-lines combined. Between the control and L2, M987 and microsatellite locus G82 were identified as candidates for selection besides TBC1 and M9_403.

Using the fdist method, M30_Dreyer thus was detected as an outlier locus comparing S2 to the other lines, and TBC1 only when comparing C and L2. M987 and Pr39 were identified as outlier loci in most F6 and F5 + F6 comparisons. No evidence for selection at any loci was supported for within-treatment comparisons (L-L and S-S comparisons).

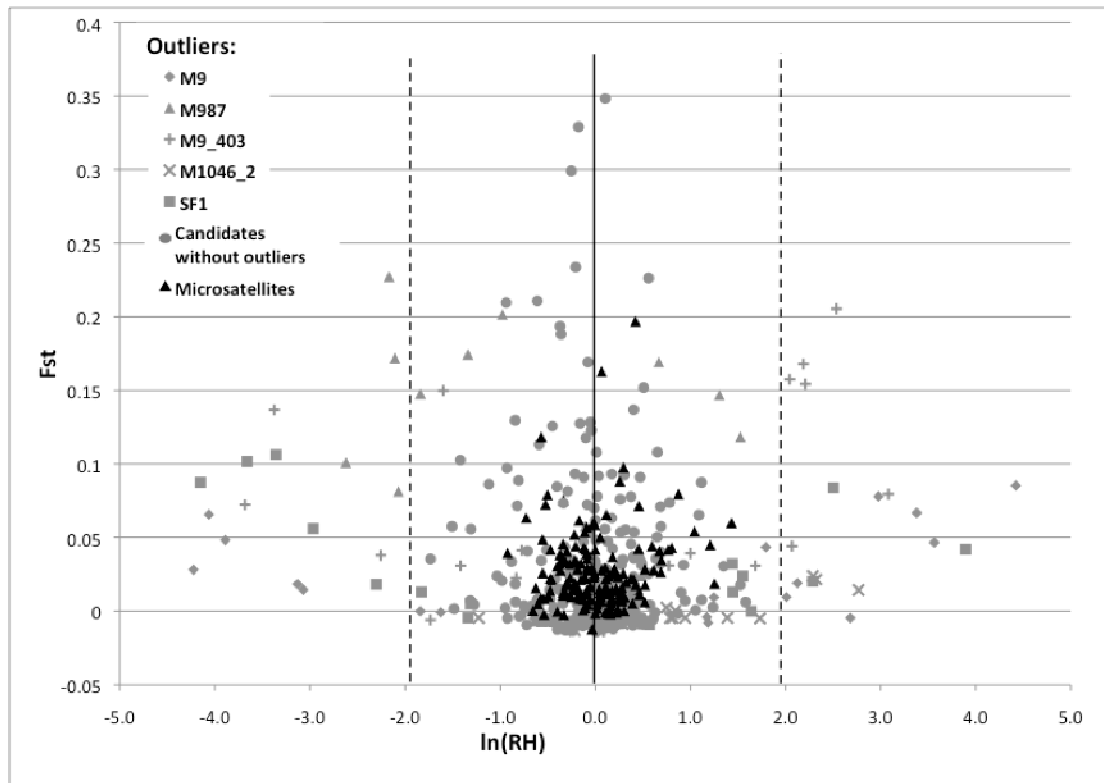


Fig. 4.6. Plot of $\ln(RH)$ and F_{ST} of microsatellite loci (black triangles) and putative candidate genes (grey symbols), showing outliers outside the 95% confidence limits (-1.96 – 1.96, black dotted lines). $\ln(RH)$ was calculated as the natural logarithm of (He_{pop1}/He_{pop2}) and normalised over all 25 loci per pairwise comparison to mean = 0 and st. deviation = 1.

Schlötterer’s method

Schlötterer’s method identified several loci as significant outliers. Fig. 4.6 depicts the distribution of $\ln(RH)$ for all loci between all population pairs and shows the outliers from the distributions, which are summarised in the legend and Table 4.9. It is clear from Fig. 4.6 that microsatellite loci have a much narrower distribution of $\ln(RH)$ values than candidate loci. Furthermore, the sign of the $\ln(RH)$ value indicates which population of the pair has the reduced heterozygosity; a negative sign implying greater He for the population in the right side of the table, and a positive sign greater He for the population on the left (e.g. a negative $\ln(RH)$ for pair S1-L1 indicates reduced heterozygosity in S1 compared to L1 for the specific locus).

Table 4.9 shows that the five loci which show outlying values do so in a range of population pairs, not all in concordance with expected differences between selection regimes. For example, locus M9_indel demonstrates higher than expected $\ln(RH)$

values between- and within treatments, and no pattern is visible that indicates selection at this locus is the result of different selection regimes in different lines. Similarly, for locus M1046_2, there is some support for reduced heterozygosity in the control compared to selection lines, but this is only observed between the control and S1 and F5_L2, therefore providing only little support for selection at this locus. For locus M987, the analysis indicates that S1 has reduced diversity compared to all other lines, but in the F5 only. In the F6, this difference is no longer visible. For locus SF1, the analysis indicates reduced heterozygosity in the S2 when compared to S1, as well as to both L-lines, and the control in the F5. In the F6, S1 has greater diversity than the control line at this locus. For M9_403 some indication of an effect of treatment on diversity is observed: no support for selection is obtained for within-treatment comparisons or comparisons between the control and S-lines, but L-lines are less heterozygous than both control and S-lines, with exception of S1 in the F6. This is the only locus for which this analysis suggests differentiation to be a result of the selection regime. Full tables of all (normalised) $\ln(RH)$ values are provided in Appendix VIII.

Table 4.9. Summary of loci having $\ln(RH)$ values falling outside the 95% confidence limits. $\ln(RH)$ was calculated as the natural logarithm of He_{pop1}/He_{pop2} , pop1 being the population on the left of the pair, and pop2 the population on the right, and normalised per pairwise comparison to mean = 0 and standard deviation = 1 over all 25 loci. The table shows negative outliers in light grey (indicative of a selective sweep in the population on the left of the pair) and positive outliers in dark grey (selective sweep in the population on the right of the pair). Full tables of (normalised) $\ln(RH)$ values of all microsatellite and candidate loci are provided in Appendix VIII.

		M9_indel	M987	M9_403	M1046_2	SF1
F5	S1-S2	-0.6462	-2.0699	-0.8335	0.7871	3.8949
F6	S1-S2	3.3790	-1.3399	-0.7738	0.3653	2.5015
F5	L1-L2	2.6813	-0.1820	-1.7344	-1.2260	1.6398
F6	L1-L2	-4.2258	-0.0215	-0.1117	0.2853	1.5491
F5	S1-C	1.1725	-2.6220	0.0889	2.7675	-1.3387
F6	S1-C	0.5197	-0.6372	-1.4174	2.2878	2.2868
F5	S2-C	1.2467	0.2505	0.7727	0.9438	-4.1524
F6	S2-C	-3.8904	1.3043	0.1731	0.8131	-1.8285
F5	L1-C	-1.6258	0.4157	-3.6832	1.7310	0.5000
F6	L1-C	-4.0632	0.6671	-1.5984	0.8407	1.4416
F5	L2-C	-3.1313	0.4887	-2.2562	2.3248	-0.5637
F6	L2-C	-1.8409	1.5254	-3.3758	1.3882	0.5680
F5	S1-L1	2.1235	-2.1078	3.0808	0.4452	-1.3122
F6	S1-L1	4.4216	-0.9780	0.9985	0.1793	-0.4399
F5	S1-L2	3.5638	-2.1697	2.0678	-0.2393	-0.3837
F6	S1-L2	2.0097	-1.8398	1.6833	0.7478	1.4468
F5	S2-L1	1.7933	-0.0346	2.5347	-0.2180	-3.3583
F6	S2-L1	1.1856	0.4777	2.1872	-0.2371	-3.6620
F5	S2-L2	2.9764	-0.1085	2.0441	-0.7142	-2.9660
F6	S2-L2	-3.0703	0.4852	2.2082	0.0405	-2.3017

4.3.7 Association analysis

Using SNPstats, several associations between male standard length and candidate alleles were found, and for several loci, multiple inheritance models (e.g. co-dominant, recessive) remained significant after corrections for multiple testing. Here, I focus on those models with best support in the whole dataset and the control line and only the most likely models (lowest p -value and AIC, support in most analyses) are discussed. Complete analysis tables can be found in Appendix IX.

Fig. 4.7 shows the most likely inheritance models for those SNPs and analyses for which a significant association was observed. Strongest support was observed for an association between M987 and standard length and individuals with an insert were significantly smaller than individuals without an insert (corrected $p < 0.0007$). This observation held over all populations (F0, F2, all F5 and all F6), in the F5 and F6 separately, as well as in the control line, indicating that the association is not only a result of divergence in allele frequencies in selection lines, but is also present within (random breeding) populations.

A similarly strong association was found for allele 174 and standard length over all populations, in the F5 and F6 (corr. $p < 0.00016$), 174 being associated with large size. Although this association was not significant for the control line, data for the control is shown here nevertheless (black bars) as it shows the same pattern despite being non-significant ($p = 0.069$ before B-H correction). As only two homozygotes for allele 174 were observed in the entire dataset, a distinction between dominance or co-dominance of the allele could not be resolved. The latter was also the case for M9_indel, for which only two homozygotes were present in the data as well, and for which a significant association between the insert and small size was observed overall and in the F5 (corr. $p = 0.0196$ and 0.0012 respectively).

For locus TBC1, no consistent support for a specific mode of inheritance was observed for the association between standard length and SNP genotype. In the F6, only dominance ($GG > GT$ or TT , $p = 0.0088$) was significantly supported after B-H correction. In the control, overdominance of the heterozygote ($p = 0.0316$). Over all

populations, only support for a recessive model (TT smaller than GT and GG) was obtained ($p = 0.0305$).

A log-additive³ association between M9_403 and standard length was observed overall ($p = 0.0036$) and in the F5 but in the F5 equal support for dominance of G was observed ($p = 0.0006$ and AIC = 913.3 and 913.4 respectively). A log-additive model was also supported overall and in the F5 for prolactin1, also with equal support for dominance of one allele in the F5 ($p = 0.0007$ overall, $p = 0.0025$ and AIC = 916.7 for both models in the F5).

For M30_Dreyer, SF1 and GH2_60, all suggested to be under selection in the S2 in analyses elsewhere (see above), an association was observed over all data and in the F5 for M30_Dreyer (C recessive overall, $p = 0.0008$, co-dominance in the F5, $p = 0.0001$) and overall only for SF1 (overdominance, $p = 0.0339$). For GH2_60, a significant association was observed over all data and in the control (log-additive, $p = 0.0007$ and 0.0390). Equal support for dominance of G was observed in the control ($p = 0.0390$ and AIC = 1093 and 193.3 respectively). In the F5 dominance of G was also the mode of inheritance with strongest statistical support, ($p = 0.0320$). In the F6, this association was significant but not after B-H corrections ($p = 0.0430$ before corrections). GH2_60 may be under selection in the S2 only, as indicated by previous analyses (see 4.3.4), but the significance of an association in the control line independently, suggests that the association of this marker with standard length is more universal and not explained by allelic differentiation between S2 and other lines alone.

³ Log-additive model: additive effects of each copy of an allele on standard length, showing a logarithmic relationship between copy number and increase/ decrease in trait value.

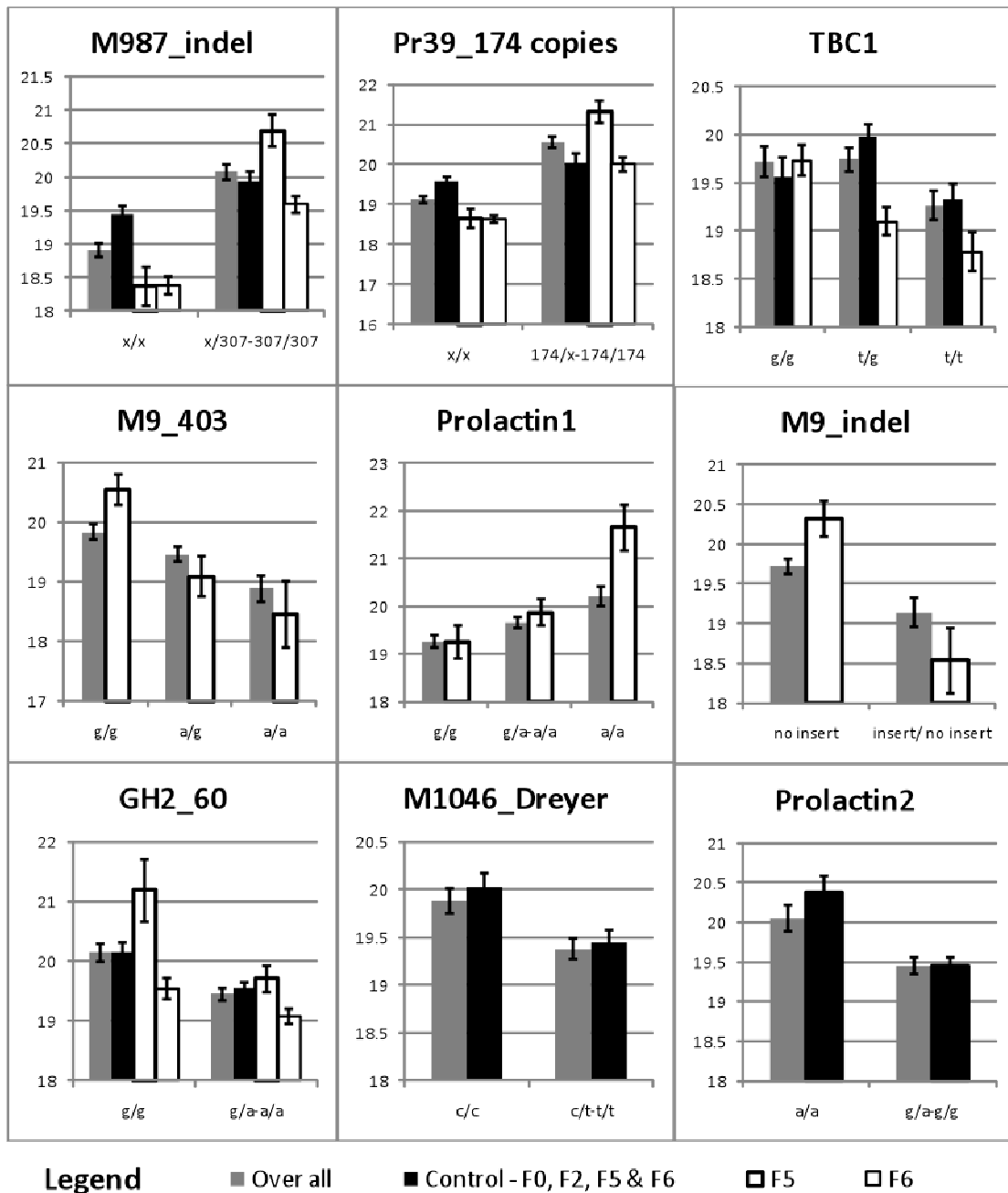


Fig. 4.7. Summary of inheritance models of candidate loci with the strongest statistical support, showing genotype (x-axis) associations with standard length in mm (y-axis) over all data in generations F0, F2, F5 and F6 (grey bars), within the Control line only over generations F0, F2, F5 and F6 (black bars), the F5 (white bars, thick black outline) and the F6 (white bars, thin white outline). Error bars present standard errors of the means. With exception of the Control line for locus Pr39 and the F6 for GH2_60, only significant associations are shown. All graphs with three bars represent co-dominance of alleles, most graphs with two bars imply dominance/recessivity of one allele, except for locus SF1, which shows overdominance. For locus Pr39 and M9_indel, too few homozygotes were observed for one allele, which made it impossible to decide on the most likely inheritance model. For locus TBC1, standard length associations are shown for each allele but no conclusion on a most likely inheritance model could be obtained from the analyses. Further details on the graphs can be found in the text. Full association tables are provided in Appendix VIII.

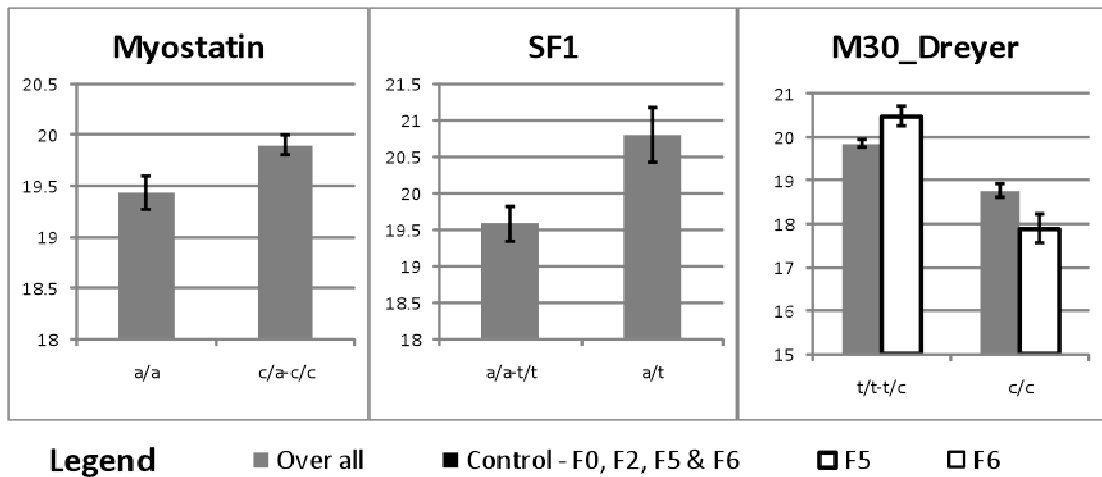


Fig. 4.7. (continued).

For M1046_Dreyer, prolactin2 and myostatin, no convincing support for selection between treatments was observed in any of the other analyses in this chapter, but a significant association between standard length and genotype was nevertheless observed through dominance of one allele for all four loci. For M1046_Dreyer and prolactin2, the association was observed over all data ($p = 0.0081$ and 0.0231 respectively) and in the control line ($p = 0.0030$ and 0.0004 respectively), suggesting these loci are good candidates for selection but have not been selected for in our lines. For myostatin, weak support was found only over all populations (corrected $p = 0.015$).

4.4 CONCLUSIONS & DISCUSSION

4.4.1 Evidence for selection at candidate loci

In this chapter, I tried to resolve whether selection over few generations can leave detectable signatures of selection at individual loci. Genetic variation has successfully been characterised at 17 putative candidate markers and detectable rapid evolution over just three generations of selection was revealed in laboratory breeding populations. Several complementary analyses have been used, providing strong support for selection at some markers and ambiguous support for selection at others. Here, the results are briefly summarised.

Table 4.10 summarises the support for selection at different loci for the different analyses in this chapter. From this table, two main observations can be made: first, no unambiguous conclusion on selection for a specific candidate gene can be reached from the analyses, and secondly, there seems to be more variation at candidate loci within the small selected lines than within the large selected lines.

Table. 4.10. Summary of analyses for selection detection at putative candidate loci in Chapter 4, showing the magnitude of support for selection at each locus and for each analysis. An “X” indicates strong indications for selection for the particular analysis at that specific locus. Less convincing support, i.e. high *p*-value, no consistent differences between treatments, is indicated by “(x)”. If selection is found for one specific line or population pair only, this is indicated in the Table. Details of all findings and analyses can be found in the text.

	HW diseq/ Gis	Genotypic differentiation	Allele frequency patterning	AMOVA	Pairwise differentiation	Lositan (fdist)	Schlotterer's method (ln(RH))	SNPstats association analysis
Myostatin								
GH1								
GH2_60		X - S2	(x - S2)					X - (S2)
GH2_74				X				
GH2_165		X - S2	X - S2					
GH2_211		(x - S2)	X - S2					
SF1		(x - S2)	X - S2				X - S2	(x - S2)
M30_Dreyer		X - S2	X - S2	X	X - S2	X - S2		(x - S2)
TBC_1		(x - C)	X - C	X		X - C-L2		(x)
M1046_2							(x - C)	
M1046_Dreyer								xx
Prolactin_1	X	X	X	X				(x)
Prolactin_2			(x)	X				xx
M9_indel		(x)	X				(x)	
M9_403		X	X	X			X	(x)
M987	X	X	X			X		X
Pr39	X	X	X	X		X		X
G82							(x)	
Pr92							(x)	

No signatures of selection were observed at myostatin, GH1 and M1046_Dreyer. Some suggestive evidence was observed for selection at M1046_2, prolactin2 and GH2_74. However, this was not observed throughout different analyses and the differences observed at these loci are most likely the result of stochastic change in allelic frequencies between lines and over generations. Visual inspection of the allelic frequencies in Fig. 4.1 clearly shows that the range of allelic differences between treatments at these loci is well within the range observed for the control line over generations. This suggests that drift, rather than selection is responsible for genetic differences between lines at these loci. For TBC1, an obvious pattern for differentiation between the control and selection lines was observed looking at allele frequencies directly in Fig. 4.1. However, statistical support for differentiation at this locus was weak (only in the AMOVA and between L2 and C in LOSITAN) and no conclusive inheritance pattern could be resolved for this locus. Therefore, selection at this locus resulting in differentiation between control and selection lines is not regarded more likely than drift causing the observed pattern of differentiation.

Ambiguous support for selection

Only few analysis suggested selection at M9_indel but the allele frequencies at this locus are stable over generations for the control line and, with exception of S2 and the L-lines in the F6, differ between S- and L-lines. The strong decrease in insert frequency in the F6 of S2, may indicate that the magnitude of drift over generations is greater than suspected based on temporal analyses of genetic diversity in 3.3.3 and 4.3.2. However, the stability of frequencies in the four other lines makes this an unlikely explanation. Otherwise, the sudden change in S2 frequencies may reflect that selection for the insert in S-lines has not been sufficient to lead to (near) fixation of the insert in the S2. This rationale stems from the fact that the F5 represent the 10% extreme males from the population, whereas the F6 is a random sample of all male offspring of that generation. Differences between allele frequencies in the F5 and the F6 may thus reflect the different portion of the population being sampled. A third possibility is that divergence between S-lines at this locus represents increased divergence between S-lines and the genetic basis of small size, compared to the genetic basis of large size in L-lines.

At several other loci the observation of increased differentiation between S-lines compared to L-lines is supported. Deviant allele frequencies in the S2 were observed for SF1, M30_Dreyer, GH2_165 and GH2_211 and several analyses identify these loci, in particular M30_Dreyer, as candidates for selection (Table 4.10). Again, it could be argued that drift has caused divergence of the S2 gene frequencies from other lines. However, except between both GH markers, the analysis did not reveal Linkage Disequilibrium (LD) between any of the markers suggested to be under selection in the S2, which makes drift at all loci causing similar deviations less likely. Furthermore, an association between M30_Dreyer and standard length has already been demonstrated elsewhere (Tripathi et al. 2009a), making this SNP a highly likely candidate for selection here. Combined, these findings make differential selection between S1 and S2 rather than drift a likely cause for the observed genetic differences at these candidate loci, in particular at M30_Dreyer.

Polymorphism of haplotypes within the growth hormone

For the five SNPs in Growth Hormone (GH), a minimum of nine different haplotypes was observed in the F0 generation, which were not in Hardy-Weinberg equilibrium (Appendix V). This is an exceptionally high number of alleles for a coding gene sequence and raises the question whether the sequence as posted on GenBank may contain an intronic fragment, despite it not being classified as such. This indeed proved to be the case (Venkatesh, pers. comm.). Intronic variation can also explain why difficulties were encountered in successful amplification and sequencing of the two additional primer pairs designed for this locus (GH3 and GH4). The presence of an intron is therefore the most likely explanation for the observed variation within the GH sequence, although it cannot be excluded that incomplete replication of fragments during PCR resulted in chimeric products. Polymerase may use such incomplete fragments as templates in subsequent PCR cycles, which can create apparent recombinant alleles (Bradley and Hillis 1997).

Strong candidates for selection

Out of 17 putative candidate markers, consistent differences between treatments were observed for M987, Pr39, M9_403 and prolactin1, which were supported by a

majority of the analyses. For prolactin1, the differences are small, and the association between SNP genotype and standard length at this locus is weak (not supported in the F6 or control line). However, the differences are nevertheless consistent and suggest a role of selection in allelic differences between S-lines and the other treatments.

For locus M9_403, a significant association between genotype and standard length was only found over all data and within the F5, but work by Dreyer and colleagues (Tripathi et al. 2009a) has previously suggested an association between M9 and standard length, which makes this marker a more likely candidate here. Similarly as at prolactin1, genotypic differences between lines are small but consistent, and visual inspection of allele frequencies clearly revealed similarly divergent frequencies for L-lines compared to S-lines and the control, which were statistically supported.

Locus M987 was identified as a likely locus under selection by the majority of analyses and had significantly higher insert frequencies in S1. HW-deviations in other lines (heterozygote excesses in the S2 and both L-lines) furthermore revealed that the allelic diversity at this locus does not conform to random expectations in other lines. Although Fig. 4.1 reveals that insert frequencies vary substantially over generations within the control line, and drift at this locus thus likely is of considerable magnitude, a strong association between standard length and the absence/ presence of an insert was observed in all association analyses, including the control line independently. This suggests that, despite high stochasticity, this locus, or a tightly linked locus, may be involved in the genetic basis of standard length and selection is likely at least partially responsible for the allelic divergence between S1 and other lines. Furthermore, Tripathi et al. (2009a) also found an association between a SNP in M987 and standard length, providing further support for the relevance of the association found here. The observation of S1 and S2 differing in genotype frequencies at this locus, adds further support to the hypothesis of a different genetic basis to small size in the S1 compared to the S2.

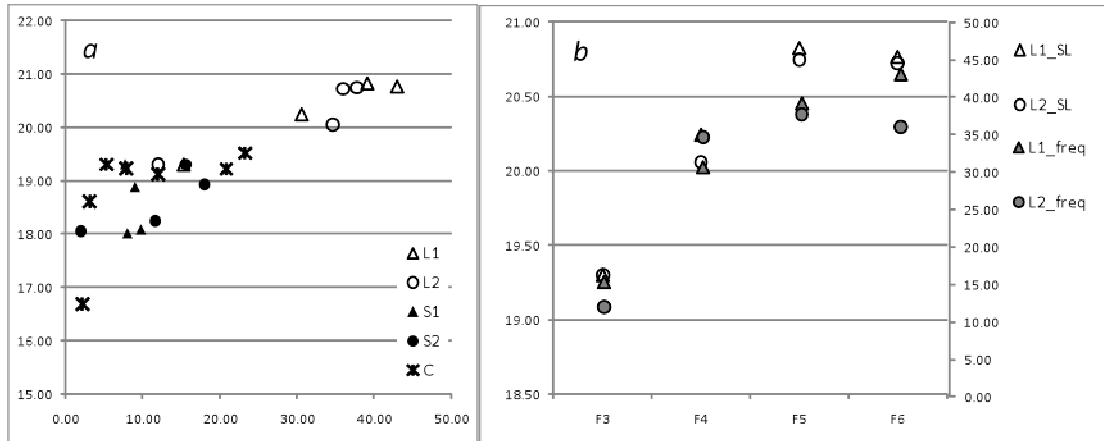


Fig. 4.8a. Relationship between 174 allele frequency of locus Pr39 (x-axis) and mean male standard length in mm (y-axis) for L-lines (open symbols), S-lines (closed symbols) and the Control (black asterices), including generations F0-F6.

b: Correlation between mean male standard length in mm (left y-axis, open circle and triangle) and allele 174 frequency of Pr39 (right y-axis, closed circle and triangle) in L1 (triangles) and L2 (circles) over generations F3-F6 ($r = 0.953$; $p < 0.001$).

The most convincing support for allele frequencies at individual loci responding to selection on standard length was found for microsatellite locus Pr39. A strong association of the presence of allele “174” with standard length was found, and the frequency of this allele increased in parallel with standard length in L-lines (Fig. 4.8).

Finally, although no evidence for selection at this locus was observed in the analyses, the association between M1046_Dreyer and male standard length, as observed by Tripathi et al. (2009a), has been confirmed.

4.4.2 Congruence and discrepancies between analyses

The majority of analyses suggested the same loci as most likely candidates for selection: M987, Pr39, M30_Dreyer and, although the divergence between lines is less pronounced, M9_403 and prolactin1. However, in contrast to the other analyses performed, tests for pairwise differentiation and Schlötterer’s method did not put most of these loci forward as likely candidates for selection and only few outlier loci were suggested from these analyses (only M30_Dreyer by pairwise tests of differentiation and SF1 and M9_403 by Schlötterer’s method). In fact, not one locus was identified as an outlier by all three outlier methods and only M30_Dreyer by more than one. What could explain these discrepancies between analyses?

The major difference between the different outlier detection methods is the statistics used to determine outliers. *Fdist* uses a simulated distribution of F_{ST} values to determine a neutral distribution of F_{ST} , from which outliers can be identified. For the pairwise tests of differentiation, the neutral distribution is obtained from a comparison between neutral microsatellites and putative candidate genes directly. Thereby, greater stochasticity in defining “neutral” differentiation levels between population pairs is introduced, which can reduce the power to detect outlier loci. The use of G''_{ST} rather than F_{ST} as a measure of differentiation, furthermore increased differentiation for microsatellite loci disproportionately compared to SNPs, thereby reducing differences between neutral and putative candidate loci. G''_{ST} differs from F_{ST} , in that it corrects for variable levels of heterozygosity affecting maximum differentiation (Meirmans and Hedrick 2011). Using F_{ST} , SNP markers are expected to have higher levels of differentiation than microsatellites, as a result of lower average heterozygosity levels than found on average at microsatellite loci. G''_{ST} corrects for this bias by normalising loci over the maximum attainable differentiation level, based on heterozygosity, and is therefore more suitable for comparing differentiation between different classes of loci (i.e. microsatellites and SNPs).

LOSITAN is based on F_{ST} and does not correct for a potential bias in differentiation due to variable levels of heterozygosity and to my knowledge, G''_{ST} -based outlier methods following the *fdist* method do not yet exist. A second potential factor biasing outlier detection in LOSITAN is caused by the different mutation models likely to underlie microsatellites and SNP markers. An infinite alleles model (IAM) was used for our analyses, but a (partial) stepwise mutation model (SMM) may be more appropriate for microsatellite loci. This can lead to underestimation of differentiation levels at microsatellite loci (Excoffier et al. 2009) and thereby may have inflated differences between putative candidates and microsatellites. However, despite these limitations, microsatellite locus Pr39 was identified as a candidate locus by *fdist*, suggesting that the use of F_{ST} rather than G''_{ST} and an IAM have not majorly biased differentiation measurements between microsatellites and SNP candidate markers and not seriously limited the potential of the *fdist* method to detect outlier loci among the diverse set of markers here used.

Schlötterer's method is based on the expected normal distribution of the natural logarithm of differences in heterozygosity between two populations. Thereby, it differs from the other outlier methods in that it does not use F-statistics to detect differentiation between populations, but is only sensitive to reductions in heterozygosity in one population compared to another (Schlötterer 2002). In particular for Pr39, for which only a single allele is likely to be under selection and reveals an association with standard length, heterozygosity did not differ between populations. Consequentially, selection for this allele remains easily undetected by an analysis based on selective sweeps. When the analysis is done with Pr39 as a bi-allelic locus (so looking at the presence/ absence of allele 174 only), this locus is identified as an outlier in pairwise comparisons between all treatments (Fig. d in Appendix VIII).

Such discrepancies between analyses have been reported elsewhere too. Beaumont & Nichols (1996) and Vitalis et al. (2001) used the same set of data to illustrate the use of different outlier methods (fdist and DetSel respectively) and identified different outlier loci. Vitalis et al. (2001) ascribed this to differences in sensitivity to the inclusion of isolated populations and variation in population size, to which fdist appeared to be more sensitive. However, as populations here are all of the same size and isolated from each other, this is not a concern in our dataset. Martínez et al. (2011) also observed discrepancies between candidate loci retrieved by fdist and $\ln(RH)$ and attributed these differences to the non-linear relationship between variation in allele frequencies and heterozygosity. The authors furthermore emphasised that, although congruence between different methods provides greater support for true outliers and minimises the likelihood of false positives, due to the different underlying statistics, true outliers can be obtained despite contrasting results in different analyses.

Variation between generations

An interesting observation when comparing results between analyses, is that not all analyses identified the same loci as most likely loci under selection in the same generations. Tests for pairwise differentiation, LOSITAN, HW-equilibrium and,

although the difference is less pronounced, tests for genotypic differentiation all identified higher numbers of loci as putatively under selection in the F6 than in the F5. Using Schlötterer's, the difference between generations was not pronounced but in SNPstats, most significant associations were found in the F5 rather than the F6.

Greater differentiation between the F6 populations compared to the F5 may be expected, since another generation of breeding separates the lines. However, the F6 samples are a random subset of each population, whereas the F5 represent the smallest/ largest 10% of males in the selected lines. The fact that still a greater signal for selection is observed in the F6 may be regarded as an indication of the efficacy of the selection regime in causing genetic change at candidate loci throughout the population, and not just in the extreme percentiles.

In contrast to the other analyses performed, SNPstats identified most significant associations between genotype and standard length in the F5 rather than in the F6. However, patterns between genotypes and standard length were the same in the F6 as in other generations despite being non-significant. The observation of such a dilution of the association in the random samples of the F6 generation, compared to the extreme samples of the F5, most likely stems from the fact that the phenotypes and genotypes in the F5 represent the 10% extremes from each selection line, whilst both are a random sample of populations in the F6. Consequentially, phenotypic distributions are less extreme in the F6 than in the F5 and associations will be weaker.

In the AMOVA, more variation between lines within treatments was observed in the F6 compared to the F5, which was a result of increasing variation between S1 and S2. Increasing genetic variation between S1 and S2, as opposed to L1 and L2, supports the phenotypic results obtained in 2.4.3, which revealed variation in maturation age and size between S-lines but not between L-lines.

The power to detect selection

For all three outlier methods used here, by definition 5% of loci are expected to be outliers if the desired significance level is $p = 0.05$. Pairwise differentiation resulted in only one obvious outlier (M30_Dreyer), which is below the 5% margin and therefore this locus may not be a true outlier but due to random chance. Schlötterer's method revealed five out of 25 loci (20%) to be candidates for selection in at least one population pair and LOSITAN provided eight out of 25 loci (32%), including two microsatellite loci, for which no other analysis suggested selection to be the cause of differentiation (G82 and Pr92). Although the proportion of outliers in both tests is higher than can be expected at random, the identification of the two microsatellites as outliers in a small fraction of the comparisons (C-S2 all for both and C-S2_F5 as well for G82) suggests that false positives are a real concern for the outlier analyses and emphasises the importance of complementary analyses in detecting selection: the lack of support for selection at G82 or Pr92 in any of the other analyses strengthens the conviction that these two markers represent false positives rather than loci under selection.

A complication with the analysis performed here is that, with exception of the AMOVA, none of the analyses allows for implementation of the nested design of replicate lines within treatments. Ignoring such a hierarchy may result in an inflated type II error rate. Several other aspects of our approach may have affected the power to detect selection in our experiments. First of all, considerable portions of the DNA sequences used to mine SNPs were unreadable, minimising the gene regions in which candidate SNPs could be identified. Secondly, the number of putative candidate markers (17) was greater than the number of putative neutral loci (8), which results in little confidence in determining neutral genetic distributions to compare candidates to. Numerous outlier studies have been previously conducted by others employing tens to hundreds of markers (Nielsen et al. 2009b; Martínez et al. 2011; Russello et al. 2011) consequentially having greater scope and power to detect outliers. Studies using numbers of loci comparable to our own often compensate for this with greater sample sizes (Larsson et al. 2007). Although the sample sizes of 50 individuals used here proved sufficient to prevent major drift and

inbreeding in our lines, it may well limit the power to detect small genetic change over few generations and at low levels of differentiation (Ryman et al. 2006; Excoffier et al. 2009). Furthermore, SNPs have lower power to detect population differentiation than multi-allelic (microsatellite) loci (Xiong and Jin 1999; Ryman et al. 2006). On the other hand, the use of candidate markers for which prior knowledge supports a role in growth and size (either from linkage mapping or known gene function), provides convincing support for associations found here (i.e. M30_Dreyer, M9_403, M987, prolactin1).

Selection or drift?

Prior information on the candidate loci used in this study also decreases the likelihood of drift explaining the patterning between selection lines as opposed to selection. However, it is difficult to exclude a role for drift in the observed changes. Comparing the change in allele frequencies of the control to those at selection lines (Fig. 4.1) reveals that, at least for M987 and prolactin1, the magnitude of drift may be considerable. For M30_Dreyer and Pr39 however, the magnitude of allelic change between treatments is far greater than that observed between generations in the control, supporting the conclusion of selection rather than drift inducing genetic change at these candidate genes.

Further support for a lack of drift affecting candidate gene distributions, is the lack of support for significant trends in heterozygosity over generations within lines or differences between control- and selected lines. This is also visualised by Schlötterer's method, which found little support for selective sweeps occurring, thereby indirectly supporting the conclusion that captive breeding and selection did not cause genetic erosion in breeding lines (Chapter 3).

Perhaps the most convincing support for the effect of selection on genetic variance at candidate loci comes from the AMOVA. Not only was there a significant value for F_{CT} (variation among treatments) at candidate loci, no significant F_{CT} was observed for neutral microsatellites (see 3.3.4), illustrating the different genetic processes, i.e. drift and selection, underlying differentiation at neutral and candidate loci. However,

F_{SC} (variation among lines within treatments) was also significant for candidate loci, including Pr39, M987, M30_Dreyer and M9_403, but not prolactin1, signifying that drift too is likely to play a considerable role in candidate gene differentiation between lines.

4.4.3 The genetic basis of male body size: differences between small and large size

The data presented here reveals that the two L-lines are strikingly genetically similar when compared to S-lines, between which differentiation is observed in the F6 in particular. This observation corresponds with the observed differences in size and age of maturation between S1 and S2 described in Chapter 2 (see 2.4.3), which indicated, although not statistically significant, that S2 individuals matured and grew to larger sizes than the S1.

As previously hypothesised in Chapter 2.5.3, greater diversity in the genetic basis of small body size compared to large body size can be expected due to effects of inbreeding and the broader genetic basis of small size compared to large size. Based on the phenotypic data from our experiments, I predicted greater heterozygosity underlying large body size and a higher frequency of recessive homozygotes under small fish.

Over all candidate genes (4.3.2) or at neutral microsatellites (3.3.3), no differences in levels of heterozygosity were observed either over all candidate genes (4.3.2) or at neutral microsatellites (3.3.3). However, looking at individual candidate loci and using the association analysis of putative candidate genes as performed in 4.3.7, some support for heterozygosity being associated with large size is observed. Out of nine associations where standard length was significantly different between homozygotes of one allele and both heterozygotes and homozygotes of the other allele (Fig. 4.7), five revealed an association of small body size with homozygosity (M987, Pr39, myostatin, SF1, M30_Dreyer) and four revealed homozygotes to be the larger genotypes (M9_indel, GH2_60, M1046_Dreyer, prolactin2). Although overall these findings do not support the hypothesis, the prediction does hold for the strongest candidates for selection; homozygotes for one allele were observed to be

smaller than heterozygotes and homozygotes of the other allele at Pr39, M987, and M30_Dreyer (Fig. 4.7). For prolactin1 and M9_403, the other two strong candidates for selection, small body size is associated with homozygotes, but a co-dominant model of inheritance obtained the strongest statistical support. Over these five loci, no significant differences in H_O or H_S were observed between S- and L-lines ($p > 0.181$). However, this is mainly an effect of M9_403. Over the three dominantly inheriting loci and prolactin1, a significant difference in observed heterozygosity (H_O) is found between S- and L-lines (independent sample t-test over the F5 and F6 combined; $T_{(2),30} = -2.554$ and $T_{(2),22} = 0.842$, $p = 0.016$ and 0.01 for tests with and without prolactin1 respectively). This indicates reduced heterozygosity at the most likely candidate loci for selection in S-lines compared to L-lines. No differences in expected heterozygosity (H_S) were observed ($p > 0.290$). These data thus indicate that part of the observed variation in standard length between treatments may be associated with differences in heterozygosity.

However, no differences in H_O or H_S were observed between S1 and S2 at these loci ($p > 0.316$). Conversely, at M30_Dreyer, GH2_60 and SF1; the loci for which support for selection at S2 only was observed (Table 4.10), a significant difference in H_O was found in the F6, indicating greater heterozygosity in the S1 – the smaller fish – than the S2 ($T_{(2),4} = 2.817$, $p = 0.048$). At the individual loci, homozygosity was associated with large size at GH2_60, but with small size at M30_Dreyer (Fig. 4.7). Large size at locus SF1 was associated with the heterozygous genotype over all data, further abating a role of this locus in explaining the differences between S1 and S2. In conclusion, these data suggest that, as can be expected for a quantitative trait, a considerable source of genetic variation underlying variation in standard length between selection lines is unaccounted for in our analyses.

4.4.4 The genetic basis to body size: Y-linkage of candidates

The phenotypic response to selection, as described in Chapter 2, indicated strong y-linkage of the genes involved in the selection response, as no response was observed in females and heritabilities were high. The genetic data here presented provide further support for this conclusion and suggest Y-linkage of candidate genes through two main observations.

Firstly, it was already known from the work by Tripathi et al. (2009a), that M9, M30 and M987, some of the strongest candidates for selection in our experiments, are located on the sex chromosome in guppies. In addition, significant LD between M1046 and M987 in our study further suggests that M1046, the melanocortin-4 receptor gene, may also be located on this chromosome. This is further supported by knowledge on the location of this gene on the sex chromosome of *Xiphophorus spp.* (Lampert et al. 2010).

Contrasting to sex chromosomes in mammals, those in many fish species, including the guppy, are in early stages of differentiation and can be regarded as pseudo-autosomes: sex-linkage of alleles at marker loci may be observed at loci closely linked to the sex determining locus (SDL) but recombination between the x- and y-chromosome is possible throughout the majority of the pseudo-autosome. Therefore, heterozygosity and Y-linkage – two incompatible terms for mammal species – can be observed in fish (Volff and Schartl 2001; Tripathi et al. 2009b). The guppy SDL specifically has been mapped to the far distal end of the y-chromosome (Tripathi et al. 2009a, 2009b). M9, M30 and M987 can be found at the top end of the chromosome, separated from the SDL by a large repeat-rich region. Tripathi et al. (2009a) observed sex-specific segregation of alleles at these markers, although no allele was exclusively associated with the Y-chromosome. This observation is supported by our findings. For M987, for which an association between standard length and the presence of an insert has been demonstrated here, heterozygotes and homozygotes for both the presence and absence of an insert were observed throughout the dataset. Contrastingly, homozygotes for the insert of M9_indel, which is located not far (0.9 cM) from M987, were observed in only 8 out of 960

genotypes, providing stronger support for sex linkage of a candidate gene for male standard length located in the near vicinity of these markers.

Y-linkage may also explain the results obtained for Pr39, for which an association with only one specific allele, “174” and standard length was observed, and for which L-lines, where the allele was most frequent, showed a strong heterozygote excess. Homozygotes for 174 were only observed in five individuals out of the entire dataset of 1236 male fish. This suggests that a closely linked gene affecting male size may have a genotype causing large size linked to the almost exclusively Y-linked 174 allele specifically. Although this rationale can explain the heterozygosity excess for 174 and the fact that only a single allele shows the association with standard length, it remains speculative as no female genetic samples are available and therefore Y-linkage of markers could not be tested. A literature search for usage of Pr39 in QTL mapping studies (e.g. Shen et al. 2007b; Tripathi et al. 2009a) or population genetic studies reporting on allele-specific deviations from HW-equilibrium (van Oosterhout et al. 2006a; Barson et al. 2009; Suk & Neff 2009) remained futile.

4.4.5 Putative gene function of major candidate genes

Out of the five major candidate genes for selection; prolactin, M9, M30, M987 and Pr39, three genes have been assigned a putative function. Besides microsatellite marker Pr39, no function could be assigned to M987, which did not yield any significant hits in a blast search. The presence of insertions of 9, 10 and 11 bp within the sequence of this marker strongly suggests this is a non-coding sequence. Prolactin consists out of an mRNA sequence highly similar to prolactin mRNA of *Tilapia nilotica* (blast E-value: $1e^{-52}$). Thirteen percent of the mRNA sequence M9 resembles rab interacting lysosomal-like protein-1 (RILPL1) in chimpanzee (*Pan troglodytes*, E-value: $9e^{-47}$). In humans, RILPL are neuroprotective proteins, inhibiting the apoptotic function of glyceraldehydes 3-phosphate dehydrogenase (GAPDH) and thereby affecting cell turnover rate (neXtprot database. Available at: <http://www.nextprot.org/db>). In rainbow trout (*O. mykiss*), RILPL is differentially expressed between starved and unstarved fish (Salem et al. 2007). M30 consists out of the mRNA sequence of fructose-1,6-bisphosphatase 1 (FBPase) and closely

resembles FBPAse in, amongst others *Salmo salar*, *Oreochromis niloticus* (E-value: 0.0) and *Danio rerio* (E-value: $3e^{-155}$). FBPAse is an enzyme involved in glucose synthesis and a variety of metabolic pathways affecting energy generation and development (e.g. Douglas et al. 2008). The open reading frames (ORFs) for these markers are unidentified and therefore it is unknown whether the SNPs investigated represent synonymous or non-synonymous mutations.

4.4.6 Overall conclusions

The data here presented provide evidence for rapid evolutionary change at specific candidate loci, induced by strong directional selection on male standard length. To our knowledge, this study represents one of the first cases where detectable selection at individual loci has been demonstrated in artificial selection system over few generations. I only know of one other example of an artificial selection study (Fidler et al. 2007) where selection at a candidate locus has been revealed over such a short timeframe. However, Fidler et al. (2007) did not use a control line in their selection experiments nor compared candidate gene frequencies with supposedly neutral, stochastic, genetic change between selection lines and generations. This emphasises the unique position of our work, in which the effects of selection have been quantified both at a phenotypic and a genetic level and have been compared to neutral variation.

Out of seventeen putative candidate loci, five revealed substantial support to be responding to selection on standard length in our experiments (Pr39, prolactin1, M9_403, M30_Dreyer and M987). For the latter three of these markers, an association with standard length was already established in previous work (Tripathi et al. 2009a) and at M30_Dreyer specifically, this association was established for the same polymorphism. A previously observed association between the M1046_Dreyer and standard length could also be confirmed with our data, but selection at this SNP did not occur.

The analyses performed in our study highlight the importance of using a variety of methods in the search for loci under selection: selection may act on heterozygosity,

allele frequencies, HW-equilibrium or a combination of these and our analyses have revealed that different methods are sensitive to different levels of change in these parameters. Especially under the low levels of change that can be expected after only few generations of selection, discriminating between drift and selection can be challenging and is aided by using complementary analyses, replicate populations for different treatments and careful selection of candidate loci, as the present study testifies.

5. GENERAL DISCUSSION

5.1 SUMMARY OF MAIN RESULTS AND NOVELTIES OF THE RESEARCH

The present study represents the first case of size-selective harvesting on selection lines established from wild-caught fish, in which the phenotypic response is compared directly to genetic change at both neutral genetic markers and genes under selection. Our findings revealed that size-selective harvesting can cause significant genetic change and phenotypic shifts in life history traits of captive populations of Trinidadian guppies. Over only three generations of selection, standard length changed by -6.5% and 7.5% in lines selected for small and large body size respectively (Chapter 2). Allele frequencies at the major candidate locus changed by as much as 41% over generations (Pr39, from 0.022 to 0.43 in L-lines) whilst the range of allele frequencies in the random breeding control was only 0.022-0.21 (Chapter 4).

We revealed considerable additive genetic variation for male standard length, and confirmed the Y-linkage of this trait, as observed in other studies using guppies (Reynolds and Gross 1992; Reznick et al. 1997). Microsatellite analysis demonstrated that the selection regime did not affect neutral genetic diversity and to my knowledge, this work is the first study that has monitored molecular genetic variation over so few generations within selection lines. Although drift between lines was observed, no inbreeding or genetic erosion occurred over the generations bred in captivity, neither in selection lines, nor in the random breeding control (Chapter 3).

In contrast to the observation at neutral loci, we detected strong signatures of selection at individual candidate loci for male standard length, including three loci known to be in close linkage with a major QTL for male body length on the Y-chromosome (two of which have been assigned a putative function), the prolactin gene and an unmapped microsatellite marker. Both divergence in allele frequencies between treatments, as well as associations of standard length with body size were observed at these loci.

In addition, an association between standard length and two individual SNPs (M30_Dreyer, M1046_Dreyer) corroborated the results found elsewhere (Tripathi et al. 2009a). Tripathi et al. (2009a) used crosses between a high predation population from the Cumaná River in Venezuela and a low predation population from the Quare River from the Oropuche Drainage on Trinidad. Both these populations are from phylogenetic clades that are distinct to those used here (Willing et al. 2010). Hence, observing an association between common SNPs and standard length yields particularly strong support for their role in male standard length.

We present the first study demonstrating that fisheries-induced selection can be detected at individual loci over few generations of size-selective harvesting, revealing a quantifiable genetic basis to shifts in standard length (Fig. 4.7; 4.8). Other studies have identified QTLs for body size (e.g. Tripathi et al. 2009a), but have not analysed the adaptive evolutionary potential of this genetic variation in artificial selection experiments. Furthermore, due to the simplified nature of our experiment, other forms of selection affecting body size could be ruled out to induce patterns between the differentially harvested lines, (i.e. density-dependence, temperature). Thus, we have shown that rapid fisheries-induced evolution (FIE) can occur and that genetic change is detectable under experimental conditions.

The magnitude of the phenotypic response observed is comparable to the response observed in a similar experiment (Conover & Munch 2002) and less than five times as high as those estimated for human-harvested systems estimated by Darimont et al. (2009). What can these results say about the likelihood of genetic change by fisheries on exploited populations?

5.2 BROADER RELEVANCE OF THE OBTAINED RESULTS

5.2.1 Life history evolution of Trinidadian guppies

Here we have for the first time mimicked selection on body size (known to be a major driver of differentiation of wild guppy populations) under controlled conditions. In doing so, we elucidated the genetic basis of this important trait in guppy biology, and contribute to the understanding of genetic structuring among wild guppy populations exposed to contrasting predation regimes.

Assuming that the lines are representative of the wild Tacarigua population, these results suggest that both additive and non-additive genetic variation is present for standard length in an environment where this trait is under different selection pressures by predators and female mate choice. The data indicate that the genetic basis to male standard length consists prominently of Y-linked variation and furthermore that large size is associated with dominance variation and heterozygosity at underlying loci (Chapter 4).

It would be desirable and highly relevant to investigate the markers for which an association was found here in wild populations, to see whether our findings correspond with genetic variation between guppies in high- and low predation habitats. This could contribute significantly to our understanding of the role of the observed associations in determining male size in guppies, as well as of different genetic backgrounds, environmental variation and selection pressures on genetic variation in the wild at candidate genes for body size (Korsten et al. 2010). For example, no previous studies using microsatellite locus Pr39 in population genetic analyses, which exhibited strong signatures of selection in our study, have reported either significant deviations from Hardy-Weinberg equilibrium at this locus or an association between one specific allele and predation regime (e.g. van Oosterhout et al. 2006a; Suk & Neff 2009). Although these studies did not examine a relationship between Pr39 and standard length directly, a lack of evidence for selection at Pr39 in the wild may suggest that the association observed in the present study is not indicative of very close linkage of Pr39 to a major gene underlying male standard

length. Alternatively, differences in the demographic history of wild populations, together with potential gene flow (Crispo et al. 2006; Barson et al. 2009) and the polygenic basis of quantitative traits may obscure signals of divergence at single genes in the wild. Nevertheless, it might prove informative to explore the dynamics and patterns of divergence at Pr39, and closely linked loci, to investigate its relationship to variance in male standard length further.

5.2.2 Fisheries-induced evolution

Despite demonstrating a direct link between harvesting selection of known intensity and measurable responses at phenotypic and genetic levels, extension of such patterns to the wild requires careful consideration. What remains to be solved, is whether current harvesting selection on commercial species is of such magnitude that it likely provokes a genetic response associated with the observed phenotypic shifts. Such a genetic response needs to be quantified and better understood before any claims on its importance for management of harvested fish species can be made (Kuparinen and Merilä 2007; Law 2007; Morita et al. 2009).

Brown et al. (2008) used data from Conover and Munch (2002) to convert the intense selection over few generations there executed to more realistic harvesting pressures for natural populations. They inferred that, for realistic commercial fishing selection pressures, a similar magnitude of evolutionary change as observed in the selection experiments by Conover and Munch (2002) could be expected over 30 generations. Such a simulation study has not been performed on our own data but nevertheless allows for coarse extrapolation of our data to more realistic scenarios. Considering that the rates of evolutionary change observed by Conover and Munch (2002) were 2-3 times our own (95-156 compared to $50-55 \times 10^3$ d), and their selection intensity was 2.5 times as high ($i = 0.7$ compared to $i = 1.8$, Falconer and Mackay 1996), a direct comparison between these two experiments is possible. Taking the extrapolation further, based on the findings by Brown et al. (2008), the magnitude of our results could be realistic for commercially exploited species over twelve generations. However, similar to the experimental approach here and in Conover and Munch (2002), Brown et al. (2008) modelled selection on discrete

generations, which is not realistic for most wild fishery scenarios. Therefore, though any response critically depends on the rate and magnitude of selection (Law 2000), a response in the wild is likely to be considerably slower than observed here (Andersen and Brander 2009). Additionally, three separate arguments can be proposed to counter such a direct comparison between our experiments and other work.

Firstly, we may have observed a greater response to selection as a result of different heritabilities. We observed h^2 estimates ranging from 0.20-0.27 for selected lines and 0.52 for the control line, assuming full Y-linkage of the traits (thus a minimum h^2 estimate). Full Y-linkage of standard length may be unlikely but considering the lack of a response observed in females (Chapter 2.4.3) and the >1 estimate in the control line if no Y-linkage is taken into account (Chapter 3.3.5), the true h^2 for our selection lines is most likely closer to $h^2 = 0.20-0.27$ than to $h^2 = 0.40-0.54$ (which assumes autosomal inheritance). Estimates observed here are thus comparable to those observed for wild fish species ($h^2 = 0.2-0.5$, and depending on whether standard length is considered as a morphological or life history trait, Weigensberg and Roff 1996; Law 2000), or those obtained by Conover and Munch ($h^2 = 0.2$).

A second argument which may confound the observed strong response to selection may lie in the considerable differences in population size used here, by Conover and Munch (2002), and those realistic for wild populations. Firstly, greater population size will yield greater power for statistical tests to detect signals of selection and population differentiation (Ryman et al. 2006). Furthermore, larger populations, with larger effective population sizes and greater genetic variance, may be expected to have higher additive genetic variance at quantitative traits for selection to act upon (Hanrahan et al. 1973). The reduction in Allelic Richness but not in heterozygosity observed in our lines when comparing the F0 and F1 to the lab-born generations (see 3.3.3) indicates that such a reduction in genetic variation compared to the wild may indeed be present in our selection lines.

Of greater concern for the generality of the present study is the apparent high proportion of Y-linked genetic variation observed for male body size in guppies, and the strong influence of drift that has affected genetic differentiation between lines. Whilst the phenotypic change observed here seems comparable to other scenarios, I question whether the genetic change observed is equally analogous to the genetic basis of FIE in the wild. Both Y-linkage (no response to selection was observed in females) and drift (AMOVA F_{SC} 0.033-0.034 in the F6 at microsatellites and candidate genes respectively) will have contributed to the rate of change observed in our genetic data and are unlikely to be of similar importance in larger populations, or in other species. In guppies, sexual dimorphism in morphology is particularly pronounced and male fish virtually stop growth after maturation. Such differences are less prominent or not present for Atlantic silverside (*Menidia menidia*) and many exploited species, where indeterminate growth is more common, although females often represent the larger sex as well. Consequentially, the genetic basis of body size could differ considerably across species and in other taxa, physical linkage between (sexually dimorphic) genes may be less pronounced than in guppies. In addition, other selection pressures and environmental factors in the wild may prevent or obscure efficient selection by fisheries, as has been elaborately discussed in the introduction (1.2.4 – 1.2.6).

However, the prolonged and unusually high fishing mortalities observed for commercially exploited species are unrivalled by natural selection events on adult fish (Jackson 2001; Darimont et al. 2009; Stenseth and Dunlop 2009). Large effective population sizes, which minimise effects of drift, in combination with microgeographic differentiation in some marine fish species (Conover et al. 2006; Hauser and Carvalho 2008) promote local adaptation to harvesting patterns and significant evolutionary rates by fishing. For example, Jakobsdóttir et al. (2011) observed an 80% decline in Pan I^B frequency in Icelandic cod, associated with late maturing fish, over a period of 60 years. Assuming a generation time for cod of 4.8 years (Árnason et al. 2009), this corresponds to roughly 12.5 generations. Thus, genetic change in the wild under realistic harvesting pressures is possible over

similar timescales as found for the present study, strengthening confidence in the wider significance of our data.

5.3 FUTURE DIRECTIONS

The findings from this study are, besides being of intrinsic value for evolutionary biology and understanding genetic dynamics on brief timescales, relevant for guppy biology, FIE and the aquaculture industry. Results on the magnitude of a selective response on both a phenotypic and a genetic level are valuable for understanding life history evolution of guppies in the wild and more broadly for evolutionary effects of fishing. Despite the simplicity of the design, the principles shown here hold in light of FIE and prove detectable genetic change can be induced at specific loci over few generations under intense directional size-specific selection. The results here obtained may be taken forward in several directions to obtain more valuable information.

5.3.1 Characterisation of genetic differences between selection lines

The complementary analyses performed in the present study have revealed genetic differentiation at candidate loci between selection lines. However, in order to fully implement the hierarchical structure of our data of replicate lines within treatments over multiple generations, more complex modelling of the data would be needed. Mixed modelling of standard length as a function of line nested within treatment and genotype as a mediator, furthermore implementing interaction effects between loci and the non-independence of data from different generations can be expected to increase the resolution of the data and provide a sounder statistical framework to distinguish between loci under selection and drift. Secondly, it is important to determine the open reading frames (ORFs) of the genes at which selection was observed. ORFs were not published with the sequences of most genes studied here. Moreover, ORFs could not be determined due to substantial unreadable portions within our own sequences, resulting from the direct sequencing of genomic fragments rather than cloned amplicons. Therefore, we have been unable to establish whether mutations observed were synonymous or non-synonymous and could not determine their function within the gene. Cloning of the desired gene

fragments to obtain whole-length readable sequences would allow for determining the most likely ORFs in our sequences.

Secondly, the number of candidate genes explored here is limited, especially considering the likely broad genetic basis of the quantitative traits examined (body size, size and age at maturation). It will therefore be extremely valuable to increase the number of markers compared between selection treatments to allow for association mapping of genes responding to the selection treatments more precisely on the guppy genome. Already, effort is being put in a follow-up project to this work, where crosses between differently selected lines will be made and segregating markers in the F2 identified using a combination of QTL linkage mapping and RAD tagging (Baird et al. 2008). Such efforts will explore more directly the role in size determination of the polymorphisms identified in the present work and will complement our findings with further candidate markers.

In addition, as already mentioned briefly, it would be very valuable to test whether signatures of selection observed in the selection lines used, are present at the same loci in the wild. Both confirming the role of these loci and the absence of an association in the wild source population or other populations, would provide valuable information on the genetic basis of standard length and generality of evolutionary pathways selecting on this important trait (Korsten et al. 2010; Rand et al. 2010).

5.3.2 Other putative traits under selection

Because only adult size was measured in the present study and, with exception of generation F2, not growth rate, it was not possible to infer whether the observed differences between selection lines were the result of differences in growth rate besides absolute growth. Obtaining a quantification of growth rate and differences herein between lines would be highly relevant, as a substantial part of the debate on FIE is centred around its effects on growth (e.g. Hilborn and Minte-Vera 2008; Kuparinen et al. 2008; Nusslé et al. 2009).

Secondly, there is considerable evidence suggesting correlations between life history traits and other traits, such as aspects of morphology and behaviour (Ruzzante and Doyle 1991; Walsh et al. 2006; Chiba et al. 2007; Biro and Stamps 2008; Uusi-Heikkilä et al. 2008). Quantifying a correlated response to selection on body size of life history traits (maturation, reproductive allotment, reproductive output), behaviour (mating preference, schooling, personality traits) and morphology (colour patterns, morphometrics) would be extremely interesting. Both the field of guppy biology and fisheries science would benefit from an improved understanding of relationships between such traits.

Finally, it would be interesting to investigate the response to relaxing and/ or reversing the selection intensity. Measuring the response to a change in the selection regime could yield insights into the different pathways the response to selection can take: Does sufficient additive genetic variance remain for selection in the opposite direction? Are rates of evolutionary change comparable between the initial response and the response to reverse selection? Does selection act upon the same genes when its direction is reversed or is previously untouched variation utilised? To be able to answer such questions would be highly relevant for understanding effects of FIE and how these are best incorporated into management strategies (Conover et al. 2009).

5.3.3 The significance of evolutionary principles for fisheries management

We confirm that genetic change by size selective harvesting can occur on contemporary time scales and these experimental results are indirectly comparable to the effects of commercial fishing in the wild. Thereby, this study provides support for the need to incorporate evolutionary principles into fisheries management (Stokes and Law 2000; Jorgensen et al. 2007; Dunlop et al. 2009). Although our results do not provide insights into the likely reversibility of a genetic response to size selective harvesting, it has been shown experimentally that selective harvesting over few generations can be reversed (Conover et al. 2009). However, modelling studies suggest this can be expected to be a slow process in the wild (Enberg et al. 2009) and a precautionary principle towards fisheries-induced genetic change seems

justified (Law 2007; Dunlop et al. 2009). “Fish less and fish more carefully, protecting the larger individuals of the stocks”, is a message heard increasingly (Stokes and Law 2000; Law 2007; Hilborn and Minto-Vera 2008; Dunlop et al. 2009). However, considering the first advice of this kind was proposed at the beginning of the last century (Rutter 1902) current managers seem to lack either the insight or the power to enforce such changes in management strategies. While debate on the importance of FIE for sustaining fisheries yield and high quality stocks has placed the topic higher on the political and commercial agenda (Browman et al. 2000; Jorgensen et al. 2007; Dunlop et al. 2009), ambiguity within the scientific community has not facilitated change in management strategies. I hope the present study will contribute to a better understanding of the genetic effects of selective fishing and provides a constructive element for the development of sustainable fisheries.

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APPENDICES

APPENDIX I – Primers and sequences

- a. Microsatellite primer pairs showing marker name, annealing temperature used (AT), forward (F) and reverse (R) primer sequence, including a universal tail on each forward primer, complementary to a fluorescently labelled universal primer. The colour of the tail is shown under F tail, and its sequence shown at the bottom of the table, as well as in small letters included in each respective forward primer.
- b. Candidate primer sequences obtained from C. Dreyer, which were used in QTL mapping by Tripathi et al. (2009a) and found to be in close linkage with a major QTL for of standard length. In addition, two newly designed primer pairs for genotyping of M9 and M987 in a microsatellite multiplex panel are shown (M9_indel and M987_indel).

a.

Marker	AT	Primer sequence	F tail	Reference
Pret32	58	F tgtaaaacgacggccagtGACCCCGACCCACAGAGAC R CACACGGCATAACGCACAT	Fam	Watanabe et al.2003
Pret69	53	F gccgctctagaactagtgGGTTGCTGCATGTGGTC R CTAGCGTTCCTGCATTCTG	Vic	""
Pret77	53	F tgtaaaacgacggccagtCTGCCACTGACCCCTTTATTC R TTTGTTGCCAGCATTAC	Fam	""
Hull70-2	53	F gcaggaaacagctatgacTCAGGGAAGTGGTAATGATAATG R GGGTAACGACAAGTCTATCTTCAA	Pet	van Oosterhout et al. 2006
G82	58	F gcaggaaacagctatgacATCACAGGGCGTCATAGA R GATAAGGTTAGGGTTAGGAA	Pet	Shen et al. 2007
G102	53	F tgtaaaacgacggccagtGCTGGCTTCAATCAACTG R GATAGAGGTGGGGAGC	Fam	""
G289	58	F gccgctctagaactagtgATTGGGATTGATGAGGTG R GTGTTCCAGCAGGTCACT	Vic	""
Pr92	58	F gcaggaaacagctatgacACCTGTGCAGCAAGAC R TGGGCTGCTTTGTGAAGT	Pet	Becher et al. 2002
Pr39	53	F tagaaggcacagtcgaggGGTAAGGACTGATGAATAGCTTG R TTAGGGCCGTGCTTTTTG	Ned	""
FAM tail	50	TGTA AACGACGGCCAGT		Tysklind 2009
VIC tail	50	GCCGCTCTAGA ACTAGTG		
PET tail	50	GCAGGAAACAGCTATGAC		
NED tail	50	TAGAAGGCACAGTCGAGG		

b.

Marker	AT	Primer sequence	F tail	Reference
M987_indel	58	F tgtaaaacgacggccagtAGCGGTCATGCACTAACAAAG R ACATCTGCTCTGCCACAAA	Fam	This study
M9_indel	58	F gccgctctagaactagtgAATCGTTTTCCACAGGAGGTG R AGTCGCTAAATGCTGGTGGT	Vic	
M9	56	F CTCATTCTGTGCTTCAACCTG R GAAATGGCCTCCAGTATCTCC	---	Dreyer et al. 2007
M30	56	F TTGGTAGACCGAGACGTGAAG R TCAGCCTTGACATGAGTTACG	---	""
M61	56	F CAGTGGTCAGCGTGAAACTC R TGGAGAAGGTACAGGTCAACG	---	""
M155	56	F GACGAGTTTCTTCCGTTTCG R CAATGTTCTTAACCAAATGTCCG	---	""
M380	56	F CATGATTAAGTCTATTACGCTGCAC R AGATGTGAGTGGCAACATGG	---	Tripathi et al. 2009
M987	56	F AGCGGTCATGCACTAACAAAG R CTGCCAACGAACATAAATGC	---	""
M1064	56	F GCTGGAGAACATCCTKGTG R GGAACATGTGGACGTAGAG	---	Hoffmann & Dreyer 2009, direct submission

- c. Primer pairs designed for sequencing of candidate genes in the present study, including redesigned primer pairs for marker M1078, initially obtained from C. Dreyer.
- d. SNP genotypes and flanking regions for polymorphisms genotyped in all male

C.

Marker	AT	Primer sequence
M1078/ IGF-1 new primers	53	F AAACCAGCTTTCACCTTTACACG R TGGAAAGTGAAGTGAAGGAA
GH-1	53	F TTTTGACCCAGGAGCATTGT R GGAGGTTTGAGGCGTCAGTA
GH-2	56	F CTGCAGAAATACGCCACTCA R ACAATGCTCCTGGGTCAAAA
GH-3	failed	F TTCTTTTGGCAGATTATTTCA R TTAGCACTGAGAAGGCAGAG
GH-4	53	F GGAAGTGAAGACGGGAATCA R CATGCGTCATGAGGAACAAG
TBC-1	53	F TGC GGCTGTATTGATAAAAT R CAACGAAAAGT GAGCTAGGA
TBC-2	54	F CGGCTAAAGACAGAGTGGACA R TACAGTCCTTTGCACCTTGC
IGF2	54	F AGATCCGGACACCACTCAC R AACTTTTTGGCCCTCAGGAT
HSP-1	failed	F CGTCTTCGAGGACTTCTCTG R GACGTCACCTTCTCGATGTT
HSP-2	53	F TGGCCAAGAAGTAGGAAGAA R TCGGTTGCTTTCTAATCCAG
Myostatin-1	56	F TAAAAGCCTGGACAGACCAA R ACTCACATCTCGGGTTCCT
Myostatin-2	failed	F AGTTTGCACTACGGACACC R CAAGCTACAGACTTTATTTGTTGA
Pit54-1	56	F TGCAGTGAAGGGAGTCTAC R CTACAGTTCCATTGCCCTGA
Pit54-2	56	F CAGCAAATGGCTTTAGAAGG R GTGCGTAAGTGC GACTTCTT
Prolactin	53	F TCATCACAGTGGTGTACCTG R AGCGAAGGACTTTCAAGAAG
JunB	53	F CTCCACAAGATGAACCAGAT R GTGCGTTAGGACCTTCTGTT

d.

SNP ID	Single nucleotide polymorphism and flanking regions
M9_403	CTGCRAGKGAATAATTTGGCACCGTTTAGTTTTACGGTATTTTAAAGTTTTCCAGGCAC[G/A]TTGGTCCYGACATGTGATCACACCAGCAATTTAGCGACTTCTGAGCGACTCTACGGATCA
M1046_Dreyer	ACATCACCATCTCTACGCCCTGGGTACCAACAACATGTACCATTCCAGGGGG[G/T]/C]TGTGGTCAATYRCCGGGATCWGGACGTGCTGCACCGTCTCCGGCATCCTCTTCATCATCTA
M1046_2	GACTCCATGATNGCAGMTCTGTCTCGCCTCCATCTGCAGCTTGTCCCATGGCC[A/G]TTCAGCCGCTACATCACCATCTTCTAGCCTTGCCTGACCAACATCTGCACCATCCAGCG
M30_Dreyer	CTGGTGTAGGGGGGATCTTCTTATACCCTGCCAACGTCAAGAGTCCAAAGGGCAAGGTAG[G/C]/T]AAGCAGAGAYTCTGAAGCAAAAACAATCTTCTTCCAGGTAATCCTTGTAAATCTATT
GH1	ATGTTAATACTGTTAATACTCTGCATCTTTAAGATTGTCAGATGAAAAATTRGCATAAAAAATCTT[G/T]CATCAATCACTACTCTCCCTGTGAACCTGTACCTGAGAAAACGTACCCTGAGCTTGCAAGGCCAA
GH2_60	TTCCTCTGCCTTCTCAGTGTAACTGCAGAAAATACGCCACTCAITTCGAAATAACCAATCA[A/G]AACCAAGGAGGAGGSTCTTAAcGCTGTCAATCAAGCGHATGTAAACACTCTCAACCCCTCCCCYtGTCTCTCAACT
GH2_74	CTGCCTTCTCAGTCTAACTGCAGAAAATACGCCACTCAITTCGAAATAACCAATCARAACCAAGGAGG[G/C]/G]TCTTAAcGCTGTCAATCAAGCGHATGTAAACACTCTCAACCCCTCCCCYtGTCTCTCAACT
GH2_165	TAAACACTCCTCAACCCCTCCCCYtGTCTCAACTAYGTNACAGCTAGCACAGCCCTGTCAAGAA[G/T]GCTAATGTAGTAGCATGACGRCAGATAAATAGTTTTCTGTAAMTGTAAGT
GH2_211	AGCTAGCACAGCCTGTCATGAAGCTAATGCTAGTTAGCATGACGRCAGATAAATAGTTTTCTGTAA[A/C]TGTAAAGTTGTTCTCTRCCAATTAGCAGTGNKAGATGAGCATAAATTTGCTAGCACTAAGACCC
Myostatin	CgITTTGGAGACCCGTTGGAGTCAAGTTTCAACCCAGCTGAGCCGCCAAMAWTGAAGCTCCAGAA[A/C]AGTAACAGACCCGCTGGTTAGCAGCATYCCCCCKTTAGTcGACTAATAATTCAGCTAAACTCTC
Prolactin_1	GTGCCATGTGCAGAGCCGTGCCCTTCTCCTAGGACTCTACTTTCCTTACGGTAGGATGCA[A/G]CGCTCCGACAAAATGCACCTCTGAGCACGCTGCCACCCAGGAGATGGTAAGACCTTMTGCTACCTGATT
Prolactin_2	CATTGTGATGATCACCCCTTCTCCTAGGACTCTACTTTCCTTACGGTAGGATGCA[A/G]ATGCCTCCTGCGGACTGCCACACCTCCGCTCTACAGAGCCCAATGACAAAAGACAAGCTC
TBC1	AACTACTTATTTACCTGGAAGGGCTTCGGGAATATTCCTTACGGATTTTGGACTAGAGTAAGT[G/T]AATGTTAAGGGAGRCAGCGAGAGCAGCTCCCGTCCCGACTCCCAACATGGA
SF1	AGACAAAGTGTCCGGATACCACTACGGTCTCACCTGCGAAAAGCTCAAGGTGGTCAAGCTCTATAGCTC[A/T]CATTTNAGCCCGCACCGTCCCGCATAGWTTCTGGGTCTAAATGGTCTTCAGATT

APPENDIX II – Microsatellite loci allele frequencies, H_s and H_o

Pret69	F0	F1	F2	F3_S1	F3_S2	F3_C	F3_L1	F3_L2	F4_S1	F4_S2	F4_C	F4_L1	F4_L2	F5_S1	F5_S2	F5_C	F5_L1	F5_L2	F6_S1	F6_S2	F6_C	F6_L1	F6_L2
126	22.83	18.75	21.47	18.27	21.11	11.96	18.37	20.00	25.00	12.00	14.58	13.27	27.55	15.22	13.95	17.44	15.22	29.59	21.00	18.00	14.00	23.00	24.00
128	1.09	3.13	4.71	18.27	7.78	8.70	4.08	4.00	16.00	6.00	8.33	8.16	3.06	14.13	6.98	11.63	6.52	6.12	12.00	1.00	9.00	4.00	3.00
132	3.26	29.69	23.30	20.19	18.89	22.83	23.47	21.00	19.00	18.00	17.71	26.53	22.45	17.39	31.40	19.77	20.65	14.29	15.00	37.00	12.00	25.00	17.00
134	25.00	9.38	15.45	8.65	14.44	21.74	14.29	20.00	16.00	17.00	18.75	22.45	15.31	15.22	5.81	13.95	16.30	16.33	20.00	8.00	25.00	6.00	26.00
136	16.30	9.38	4.19	5.77	2.22	5.43	4.08	5.00	6.00	6.00	6.25	5.10	2.04	11.63	4.65	2.17	2.04	2.04	2.00	1.00	1.00	7.00	3.00
138	6.52	9.38	14.66	20.19	15.56	9.78	16.33	10.00	23.00	26.00	16.67	9.18	7.14	34.78	18.60	16.28	15.22	3.06	28.00	24.00	25.00	16.00	10.00
146	11.96	1.56	0.79	2.88	1.11	6.52	6.12	6.00	2.00	2.00	4.17	7.14	15.31	1.09	2.33	8.14	7.61	12.24	2.00	3.00	8.00	8.00	6.00
148	1.09	1.56	4.19	2.88	2.22	1.09	3.06	5.00	1.00	1.00	1.04	1.02	3.06	1.16	1.16	4.65	7.14	7.14	2.00	3.00	4.00	1.00	7.00
152	2.17	9.38	2.88	1.92	3.33	3.26	5.10	3.00	2.00	2.00	3.13	1.02	1.02	1.16	1.16	1.16	9.78	3.06	3.00	3.00	5.00	3.00	3.00
164	1.09	3.14	2.36	0.96	8.89	1.09	1.02	1.00	6.00	6.00	1.04	1.02	1.02	3.49	3.49	1.16	2.17	1.02	2.00	2.00	3.00	3.00	3.00
168	1.09	4.69	2.36	2.88	1.11	4.35	1.02	4.00	1.00	3.00	1.04	5.10	2.04	1.09	2.33	2.33	4.35	5.10	2.00	3.00	2.00	1.00	1.00
172	4.35	1.56	0.79	2.88	2.22	1.09	1.02	1.00	1.00	3.00	1.04	1.02	1.02	1.09	3.49	2.33	4.35	5.10	2.00	3.00	2.00	1.00	1.00
196	1.09	1.56	0.79	2.88	2.22	1.09	1.02	1.00	1.00	3.00	1.04	1.02	1.02	1.09	3.49	2.33	4.35	5.10	2.00	3.00	2.00	1.00	1.00
220	1.09	1.56	0.79	2.88	2.22	1.09	1.02	1.00	1.00	3.00	1.04	1.02	1.02	1.09	3.49	2.33	4.35	5.10	2.00	3.00	2.00	1.00	1.00
224	1.09	1.56	0.79	2.88	2.22	1.09	1.02	1.00	1.00	3.00	1.04	1.02	1.02	1.09	3.49	2.33	4.35	5.10	2.00	3.00	2.00	1.00	1.00
232	1.09	1.56	0.79	2.88	2.22	1.09	1.02	1.00	1.00	3.00	1.04	1.02	1.02	1.09	3.49	2.33	4.35	5.10	2.00	3.00	2.00	1.00	1.00

Pret77	F0	F1	F2	F3_S1	F3_S2	F3_C	F3_L1	F3_L2	F4_S1	F4_S2	F4_C	F4_L1	F4_L2	F5_S1	F5_S2	F5_C	F5_L1	F5_L2	F6_S1	F6_S2	F6_C	F6_L1	F6_L2
173	5.43	6.25	5.76	8.65	12.22	11.70	6.12	7.00	3.00	10.00	5.21	8.16	5.10	3.26	9.30	3.49	5.43	3.06	3.00	6.00	4.00	7.00	1.00
177	15.22	14.06	11.26	12.50	10.00	8.51	8.16	5.00	14.00	6.00	7.29	6.12	7.14	22.83	5.81	5.81	4.35	14.29	15.00	12.00	2.00	5.00	8.00
179	57.61	51.56	55.50	50.00	55.56	48.94	64.29	68.00	50.00	55.00	57.29	54.08	61.22	44.57	53.49	58.14	61.96	57.14	53.00	61.00	58.00	53.00	64.00
181	3.13	3.13	3.13	12.50	13.33	14.89	7.14	9.00	16.00	11.00	19.79	4.08	11.22	22.83	12.79	19.77	5.43	13.27	14.00	11.00	25.00	5.00	13.00
183	5.43	4.69	12.57	2.88	2.62	6.38	2.04	1.00	7.00	2.00	2.00	2.04	3.06	1.09	4.65	4.65	1.09	3.06	2.00	1.00	4.00	5.00	5.00
185	3.26	3.13	0.79	0.96	1.11	1.11	1.02	2.00	3.00	3.00	1.04	3.06	6.12	2.17	2.33	2.33	5.43	1.02	4.00	7.00	7.00	3.00	3.00
191	1.09	1.56	1.83	5.77	2.22	5.32	3.06	3.00	3.00	1.00	1.04	8.16	4.08	3.26	5.81	3.49	3.26	2.04	3.00	1.00	2.00	8.00	4.00
195	9.78	4.69	1.31	0.96	1.11	1.11	1.02	2.00	3.00	1.00	1.04	1.02	1.02	1.16	1.16	1.16	1.02	1.02	1.00	1.00	1.00	15.00	2.00
197	1.09	1.56	1.83	5.77	2.22	5.32	3.06	3.00	3.00	1.00	1.04	1.02	1.02	1.16	1.16	1.16	1.02	1.02	1.00	1.00	1.00	15.00	2.00
199	1.09	1.56	1.83	5.77	2.22	5.32	3.06	3.00	3.00	1.00	1.04	1.02	1.02	1.16	1.16	1.16	1.02	1.02	1.00	1.00	1.00	15.00	2.00
201	1.09	1.56	1.83	5.77	2.22	5.32	3.06	3.00	3.00	1.00	1.04	1.02	1.02	1.16	1.16	1.16	1.02	1.02	1.00	1.00	1.00	15.00	2.00
203	1.09	1.56	1.83	5.77	2.22	5.32	3.06	3.00	3.00	1.00	1.04	1.02	1.02	1.16	1.16	1.16	1.02	1.02	1.00	1.00	1.00	15.00	2.00
207	1.09	6.25	4.19	4.81	4.44	4.26	6.12	1.00	4.00	8.00	7.29	10.20	1.02	4.65	4.65	4.65	13.04	5.10	1.00	1.00	1.00	15.00	2.00

G102	F0	F1	F2	F3_S1	F3_S2	F3_C	F3_L1	F3_L2	F4_S1	F4_S2	F4_C	F4_L1	F4_L2	F5_S1	F5_S2	F5_C	F5_L1	F5_L2	F6_S1	F6_S2	F6_C	F6_L1	F6_L2
248	11.96	3.13	3.66	4.81	5.56	3.19	1.02	3.00	3.00	10.00	3.13	3.06	2.04	6.52	13.95	4.65	2.17	1.02	6.00	13.00	3.00	2.00	1.00
250	5.43	0.26	0.26	0.96	2.22	4.26	1.02	1.00	1.00	1.00	3.13	1.02	1.02	1.09	1.16	1.16	2.17	1.02	3.00	3.00	3.00	3.00	3.00
252	1.09	6.25	2.88	0.96	2.22	4.26	1.02	1.00	1.00	1.00	3.13	1.02	1.02	1.09	1.16	1.16	2.17	1.02	3.00	3.00	3.00	3.00	3.00
254	41.30	54.69	56.81	60.58	47.78	55.32	59.18	49.00	50.00	59.00	58.33	50.00	65.31	51.09	60.47	61.63	39.13	56.12	44.00	62.00	63.00	41.00	66.00
256	18.48	10.94	8.12	4.81	6.67	9.57	10.20	11.00	8.00	2.00	5.21	8.16	5.10	2.17	8.14	8.14	10.87	7.14	1.00	2.00	3.00	16.00	1.00
258	13.04	21.88	21.20	25.96	23.33	22.34	23.47	32.00	32.00	21.00	25.00	30.61	24.49	32.61	16.28	19.77	36.96	29.59	37.00	13.00	22.00	29.00	30.00
260	1.56	0.52	0.52	0.96	2.22	4.26	1.02	1.00	2.00	7.00	5.21	1.02	2.04	1.09	1.16	1.16	1.09	5.10	1.00	7.00	6.00	1.00	8.00
262	2.17	1.56	0.52	0.96	2.22	4.26	1.02	1.00	2.00	7.00	5.21	1.02	2.04	1.09	1.16	1.16	1.09	5.10	1.00	7.00	6.00	1.00	8.00
264	6.52	6.02	6.02	1.92	10.00	5.32	4.08	3.00	5.00	7.00	5.21	6.12	2.04	5.43	6.98	6.98	7.61	5.10	11.00	7.00	6.00	8.00	2.00

Hull170-2	F0	F1	F2	F3_S1	F3_S2	F3_C	F3_L1	F3_L2	F4_S1	F4_S2	F4_C	F4_L1	F4_L2	F5_S1	F5_S2	F5_C	F5_L1	F5_L2	F6_S1	F6_S2	F6_C	F6_L1	F6_L2
210	5.43	1.56	6.54	1.92	5.56	3.19	12.24	11.00	4.00	9.00	6.25	10.20	20.41		13.95	9.30	15.22	19.39		15.00	5.00	15.00	14.00
218	1.09		0.26																				
222	6.52	7.81	5.50	4.81	1.11	1.06	8.16	10.00	1.00	1.00		7.14	5.10	7.61			11.96	5.10	7.00	1.00		8.00	2.00
228	6.52	9.38	13.35	14.42	11.11	17.02	12.24	22.00	22.00	13.00	16.67	16.33	21.43	21.74	12.79	11.63	9.78	16.33	29.00	23.00	14.00	9.00	22.00
232	22.83	17.19	20.94	25.96	30.00	25.53	20.41	23.00	30.00	25.00	29.17	19.39	19.39	27.17	22.09	34.88	20.65	29.59	22.00	16.00	25.00	21.00	26.00
236	6.52	7.81	10.47	12.50	14.44	10.64	13.27	4.00	6.00	10.00	16.67	16.33	2.04	8.70	6.98	11.63	13.04	4.08	5.00	4.00	19.00	11.00	13.00
240	10.87	7.81	7.07	0.96	8.89	9.57	5.10	3.00	4.00	4.00	2.08	6.12	2.04	2.17	2.33	4.65	5.43	1.02	1.00	6.00	1.00	7.00	3.00
244	2.17	6.25	3.14	3.85	2.22	7.45	1.02	1.00	1.00	7.00	7.29	3.06	4.08	1.09	1.16	5.81	1.09	3.06		1.00	8.00	11.00	3.00
248	7.61	6.25	2.36	3.85	2.22	2.13	5.10	1.00	4.00	5.00	1.04	1.02	1.02	3.26	3.49	1.16			3.00	1.00	1.00		
252	3.26	6.25	3.40		3.33	5.32	5.10	2.00	4.00	1.00	3.13	1.02	1.02	2.17	1.16	2.33	1.09	3.06	3.00	3.00	1.00	3.00	3.00
256	1.09																						
260		3.13	0.52			1.06							1.02		1.16								
264	2.17	3.13	4.19	1.92	3.33	3.19	2.04	2.00	1.00	4.00	3.13	5.10	2.04	5.43	12.79	6.98		1.02	4.00	12.00	10.00	2.00	3.00
266	1.09		2.62	1.92	1.11			1.00	1.00	1.00	1.04		2.04	1.09	2.33	2.33		5.10	2.00		1.00		
270	2.17	1.56	1.57		2.22	2.13	1.02	1.00	1.00	5.00	1.04				2.33	3.49	1.09		1.00	5.00	7.00	1.00	
274	1.09	1.56	1.31	0.96		1.06	1.02	1.00		3.00	1.04				1.16	1.16				3.00	2.00		
278	8.70	7.81	7.07	10.58	12.22	5.32	4.08	4.00	9.00	6.00	2.08	4.08	4.08	8.70	9.30	1.16	9.78	1.02	9.00	7.00	4.00	4.00	6.00
282	3.26	1.56	3.93	7.69		1.06	5.10	5.00	5.00	5.00	2.08	4.08	9.18	3.26	2.33		1.09	8.16	4.00	3.00	3.00		
286	4.35	3.13	2.36	0.96		2.13	4.08	6.00	2.00	3.00	8.33	3.06	2.04	4.35	3.49	2.33	5.43	1.02	3.00		3.00	4.00	2.00
290			0.26		1.11	1.06				1.00					1.16	1.16							
292	2.17	6.25	2.88	7.69	1.11	1.06	2.04	4.00	5.00	2.00		3.06		3.26			3.26		5.00		3.00	3.00	1.00
296	1.09	1.56	0.26				3.06	1.00	4.00				3.06		1.16		1.09	2.04	2.00		1.00	1.00	2.00

Pret32	F0	F1	F2	F3_S1	F3_S2	F3_C	F3_L1	F3_L2	F4_S1	F4_S2	F4_C	F4_L1	F4_L2	F5_S1	F5_S2	F5_C	F5_L1	F5_L2	F6_S1	F6_S2	F6_C	F6_L1	F6_L2
123	1.11		1.31	0.96					3.00														
127	1.11																						
135	26.67	21.88	17.80	24.04	16.67	15.96	17.35	16.00	20.00	20.00	25.00	10.42	17.35	27.17	17.44	25.00	20.65	8.16	26.00	17.00	16.33	17.00	8.00
137	2.22		2.36	3.85	1.11	3.19		1.00	1.00	3.00				2.17	3.49				1.00	1.00			
139	7.78	3.13	4.97	5.77	8.89	9.57	3.06		1.00	6.00	6.25	2.08	2.04	1.09	10.47	5.95	1.09	1.02		8.00	9.18	1.00	
141	3.33	4.69	3.40	3.85	5.56	4.26	6.12	5.00	1.00	3.00	3.13	6.25	2.04	1.09	4.65	1.19		1.02	1.00		4.08	2.00	
145	5.56	1.56	2.62	1.92	3.33	2.13	6.12	7.00	3.00	5.00		3.13	1.02	11.96	4.65	2.38	5.43	5.10	6.00	14.00	9.18	7.00	9.00
147	11.11	10.94	12.83	10.58	10.00	19.15	15.31	14.00	12.00	11.00	17.71	12.50	13.27	13.04	8.14	21.43	17.39	13.27	20.00	7.00	15.31	11.00	14.00
149	5.56	4.69	3.93	3.85	6.67	7.45	4.08	4.00	4.00	7.00	12.50	7.29	4.08	3.26	9.30	3.57	6.52	2.04	3.00	13.00	7.14	8.00	
151	2.22	1.56	3.14	5.77	2.22	2.13	4.08	7.00	2.00		1.04	4.17	4.08	2.17	1.16		1.09	2.04	1.00	1.00	2.04	2.00	2.00
153	1.11																						
155	14.44	23.44	19.63	12.50	23.33	17.02	25.51	25.00	23.00	17.00	19.79	31.25	24.49	15.22	12.79	26.19	27.17	25.51	24.00	14.00	20.41	26.00	23.00
157	4.44	7.81	9.69	12.50	7.78	8.51	9.18	8.00	14.00	9.00	4.17	8.33	8.16	13.04	8.14	2.38	13.04	5.10	6.00	9.00	4.08	17.00	6.00
159	11.11	15.63	6.81	5.77	5.56	3.19	8.16	7.00	3.00	5.00	4.17	5.21	12.24	3.26	9.30	3.57	4.35	16.33	10.00	10.00	1.02	5.00	22.00
171	1.11																						
173		3.13	9.42	5.77	5.56	7.45	1.02	5.00	13.00	10.00	6.25	9.38	10.20	5.43	6.98	8.33	3.26	16.33	10.00	6.00	10.20	4.00	14.00
175	1.11		1.83	2.88	3.33			1.00	3.00					1.09	2.33				2.00		1.02		
177		1.56	0.26						1.00				1.02		1.16		4.08						2.00

G82	F0	F1	F2	F3_S1	F3_S2	F3_C	F3_L1	F3_L2	F4_S1	F4_S2	F4_C	F4_L1	F4_L2	F5_S1	F5_S2	F5_C	F5_L1	F5_L2	F6_S1	F6_S2	F6_C	F6_L1	F6_L2
184	48.91	54.69	49.74	47.12	47.78	56.38	65.31	49.00	51.00	45.00	68.75	56.12	50.00	58.70	39.53	70.93	59.78	51.02	57.00	40.00	64.00	64.00	47.00
186	43.48	29.69	42.67	46.15	43.33	35.11	30.61	43.00	38.00	51.00	18.75	39.80	45.92	36.96	56.98	18.60	38.04	42.86	40.00	57.00	20.00	35.00	49.00
188	7.61	10.94	7.07	6.73	7.78	8.51	4.08	8.00	10.00	2.00	12.50	4.08	4.08	4.35	3.49	10.47	2.17	6.12	3.00	1.00	16.00	1.00	4.00
190		4.69	0.52		1.11				1.00	2.00										2.00			

P192	F0	F1	F2	F3_S1	F3_S2	F3_C	F3_L1	F3_L2	F4_S1	F4_S2	F4_C	F4_L1	F4_L2	F5_S1	F5_S2	F5_C	F5_L1	F5_L2	F6_S1	F6_S2	F6_C	F6_L1	F6_L2
172	26.09	35.94	30.37	28.85	41.11	30.85	33.67	42.00	32.00	39.00	41.67	27.55	35.71	23.91	32.56	43.02	30.43	37.76	22.00	32.00	36.00	26.00	28.00
174	13.04	20.31	21.47	23.08	15.56	20.21	20.41	21.00	11.00	12.00	23.96	28.57	14.29	20.65	11.63	17.44	21.74	10.20	9.00	20.00	32.00	27.00	15.00
176	42.39	25.00	28.53	31.73	31.11	30.85	19.39	19.00	38.00	28.00	17.71	29.59	27.55	43.48	24.42	18.60	28.26	28.57	49.00	17.00	14.00	26.00	27.00
178	14.13	14.06	14.14	11.54	7.78	11.70	22.45	13.00	15.00	19.00	15.63	11.22	15.31	9.78	25.58	19.77	13.04	14.29	12.00	24.00	15.00	14.00	22.00
182	2.17	3.13	3.66	2.88	3.33	6.38	4.08	5.00	1.00	1.00	1.04	2.04	6.12	2.33	1.16		3.26	9.18		2.00	3.00	2.00	7.00
186	1.09	1.56	1.83	1.92	1.11				3.00	1.00		1.02	1.02	2.17	3.49		3.26		8.00	5.00		5.00	1.00
188																							

G289	F0	F1	F2	F3_S1	F3_S2	F3_C	F3_L1	F3_L2	F4_S1	F4_S2	F4_C	F4_L1	F4_L2	F5_S1	F5_S2	F5_C	F5_L1	F5_L2	F6_S1	F6_S2	F6_C	F6_L1	F6_L2
301	2.17		0.26	3.85	1.11	2.13	1.02	1.00	4.00		2.08	11.22	12.24	4.35				2.04	2.00				3.00
305	1.09		2.36	3.85	10.00	3.19	9.18	9.00	2.00	1.00	10.42	20.41	27.55	31.52	16.28	32.56	28.26	16.33	19.00	15.00	14.00	9.00	19.00
307	7.61	10.94	10.21	26.92	18.89	19.15	27.55	16.00	24.00	22.00	18.75	13.27	8.16	2.17	3.49	5.81	14.13	7.14	4.00	3.00	25.00	28.00	16.00
309	23.91	15.63	17.54	1.92	1.11	3.19	4.08	4.00	1.00		3.13	13.27	8.16	2.17	1.16	3.49	14.13	7.14	4.00	3.00	2.00	10.00	3.00
311	3.26	4.69	2.09	1.92	1.11	3.19	4.08	4.00	1.00		3.13	13.27	8.16	2.17	1.16	3.49	14.13	7.14	4.00	3.00	2.00	10.00	3.00
313	6.52	4.69	1.57	0.96	2.22	4.26		1.00		1.00	1.04		1.02		1.16	1.16				5.00	3.00		
315	8.70	6.25	10.73	12.50	8.89	12.77	8.16	12.00	7.00	21.00	10.42	14.29	5.10	17.39	22.09	12.79	11.96	6.12	12.00	25.00	10.00	15.00	7.00
317	9.78	18.75	18.32	7.69	20.00	13.83	17.35	22.00	9.00	15.00	11.46	13.27	20.41	3.26	22.09	2.33	11.96	16.33	4.00	24.00	3.00	12.00	15.00
319	14.13	6.25	9.69	7.69	4.44	6.38	5.10	8.00	14.00	8.00	3.13	6.12	5.10	13.04	11.63	4.65	13.04	5.10	11.00	4.00	6.00	12.00	3.00
321	1.09	3.13	2.36	1.92	1.11	2.13	3.06	4.00	3.00		3.13	3.06	3.06	1.09	2.33	2.33	3.06	3.06	5.00	5.00	6.00	3.00	3.00
323	1.09	20.31	11.26	15.38	16.67	18.09	9.18	7.00	11.00	13.00	17.71	10.20	6.12	11.96	6.98	13.95	8.70	11.22	14.00	5.00	16.00	6.00	16.00
325	9.78	3.13	9.69	13.46	12.22	11.70	10.20	10.00	20.00	9.00	11.46	2.04	4.08	9.78	1.16	9.30	2.17	13.27	22.00	10.00	12.00	2.00	10.00
327	1.09	1.56	0.26					3.00															
329	9.78	3.13	3.66	3.85	3.33	3.19	4.08	3.00	5.00	10.00	7.29	9.18	5.10	5.43	13.95	11.63	6.52	6.12	5.00	8.00	9.00	6.00	5.00
347																							

Expected heterozygosity per locus and population

	F0	F1	F2	F3_S1	F3_S2	F3_C	F3_L1	F3_L2	F4_S1	F4_S2	F4_C	F4_L1	F4_L2
Pret69	0.8452	0.8507	0.8481	0.8469	0.8674	0.8677	0.8616	0.8616	0.8053	0.8525	0.8743	0.8445	0.8273
Pret77	0.6350	0.7103	0.6583	0.7114	0.6532	0.7163	0.5716	0.5248	0.7026	0.6701	0.6254	0.6829	0.6045
Hull70-2	0.9104	0.9320	0.9039	0.8749	0.8562	0.8794	0.9001	0.8723	0.8461	0.8921	0.8485	0.8900	0.8660
G102	0.7645	0.6458	0.6215	0.5659	0.7061	0.6360	0.5883	0.6499	0.6438	0.5984	0.5961	0.6514	0.5153
Pret32	0.8762	0.8611	0.8848	0.8893	0.8871	0.8861	0.8632	0.8731	0.8598	0.8935	0.8478	0.8539	0.8647
G82	0.5721	0.6081	0.5670	0.5659	0.5843	0.5575	0.4831	0.5743	0.5913	0.5420	0.4816	0.5304	0.5430
Pr92	0.7224	0.7579	0.7606	0.7556	0.7106	0.7591	0.7631	0.7313	0.7248	0.7261	0.7206	0.7494	0.7566
G289	0.8841	0.8854	0.8814	0.8613	0.8694	0.8810	0.8618	0.8859	0.8608	0.8519	0.8860	0.8761	0.8548

	F5_S1	F5_S2	F5_C	F5_L1	F5_L2	F6_S1	F6_S2	F6_C	F6_L1	F6_L2
Pret69	0.7907	0.8320	0.8695	0.8715	0.8452	0.8079	0.7711	0.8327	0.8471	0.8329
Pret77	0.7021	0.6862	0.6200	0.5936	0.6369	0.6774	0.5986	0.6014	0.6822	0.5673
Hull70-2	0.8581	0.8908	0.8386	0.8858	0.8405	0.8511	0.8778	0.8640	0.8931	0.8475
G102	0.6316	0.5902	0.5767	0.6992	0.5956	0.6602	0.5814	0.5539	0.7216	0.4786
Pret32	0.8576	0.9111	0.8184	0.8349	0.8582	0.8242	0.8907	0.8809	0.8547	0.8491
G82	0.5227	0.5239	0.4566	0.5029	0.5580	0.5194	0.5198	0.5301	0.4725	0.5428
Pr92	0.7088	0.7625	0.7190	0.7695	0.7442	0.6895	0.7760	0.7323	0.7772	0.7806
G289	0.8321	0.8462	0.8378	0.8505	0.8914	0.8691	0.8418	0.8626	0.8531	0.8780

Observed heterozygosity per locus and population

	F0	F1	F2	F3_S1	F3_S2	F3_C	F3_L1	F3_L2	F4_S1	F4_S2	F4_C	F4_L1	F4_L2
Pret69	0.8913	0.8438	0.8586	0.8846	0.8889	0.8478	0.8367	0.8200	0.8000	0.8200	0.8958	0.8980	0.8367
Pret77	0.5870	0.6250	0.6126	0.7115	0.6667	0.7447	0.6735	0.5800	0.6800	0.6600	0.6667	0.6735	0.5918
Hull70-2	0.9348	0.8438	0.8534	0.8654	0.8889	0.8298	0.8163	0.9200	0.8000	0.8400	0.8125	0.8571	0.8980
G102	0.6739	0.5938	0.6126	0.5769	0.6000	0.6383	0.5510	0.5200	0.7400	0.5600	0.5833	0.6939	0.5918
Pret32	0.8222	0.7188	0.8743	0.8077	0.8444	0.8085	0.7959	0.8600	0.7800	0.8000	0.8750	0.9167	0.8571
G82	0.6304	0.4375	0.4869	0.5962	0.6222	0.5319	0.4490	0.6000	0.5600	0.5400	0.3750	0.6735	0.6735
Pr92	0.8043	0.7188	0.7644	0.7692	0.6889	0.6596	0.6939	0.7000	0.6800	0.6800	0.7292	0.7347	0.8163
G289	0.7826	1.0000	0.8848	0.8462	0.8000	0.8085	0.8980	0.8600	0.8800	0.8200	0.8750	0.8163	0.7755

	F5_S1	F5_S2	F5_C	F5_L1	F5_L2	F6_S1	F6_S2	F6_C	F6_L1	F6_L2
Pret69	0.8043	0.8837	0.8140	0.8696	0.9388	0.8000	0.7600	0.9000	0.8600	0.8200
Pret77	0.7391	0.6977	0.6512	0.6087	0.6122	0.6600	0.6000	0.4600	0.7800	0.5600
Hull70-2	0.8696	0.8605	0.8140	0.9783	0.8776	0.8000	0.8400	0.9000	0.8000	0.8600
G102	0.6304	0.6977	0.5349	0.7174	0.6735	0.7800	0.6400	0.5800	0.6400	0.4600
Pret32	0.8043	0.8372	0.7143	0.7826	0.7959	0.8600	0.8600	0.8571	0.8400	0.8800
G82	0.5217	0.5814	0.4884	0.3261	0.4694	0.5600	0.4600	0.3800	0.5000	0.6400
Pr92	0.7391	0.8140	0.6744	0.8478	0.7347	0.7200	0.7800	0.8600	0.8600	0.7400
G289	0.8261	0.7907	0.9070	0.9348	0.9184	0.9000	0.9000	0.8200	0.7800	0.9800

APPENDIX III – Full AMOVA Tables

- Summary of AMOVA statistics, showing the value of the different variance component among treatments (V_A) among lines within treatments (V_B) and within lines (V_C) and the % of variation they explain for over all neutral microsatellite loci and in each of the generations F3-F6, as well as for a temporal hierarchy over these generations.
- Per-locus AMOVA tables showing sum of squares of the deviations (SSD), degrees of freedom (d.f.) the different variance components among treatments (V_A) among lines within treatments (V_B) and within lines (V_C) and the % of variation they explain for each neutral microsatellite locus and in each of the generations F3-F6, as well as for a temporal hierarchy over these generations.
- Fixation indices among treatments (F_{CT}) among lines within treatments (F_{SC}) and within lines (F_{ST}) and p -values for the analyses for each neutral microsatellite locus and over all loci for each of the generations F3-F6, as well as for a temporal analysis over these generations. Significant p -values are shown in bold.

a.

F3				F4			
Source of variation	Sum of squares	Variance component	Percentage of variation	Source of variation	Sum of squares	Variance component	Percentage of variation
Among treatments (Va, Fct)	10.614	0.01061	0.35	Among treatments (Va, Fct)	16.351	0.01747	0.58
Among lines within treatments (Vb, Fsc)	7.348	0.00665	0.22	Among lines within treatments (Vb, Fsc)	10.93	0.02504	0.83
Within lines (Vc, Fst)	1453.8	3.02417	99.43	Within lines (Vc, Fst)	1453.2	2.98568	98.60
Total	1471.7	3.04143		Total	1480.4	3.02819	

F5				F6			
Source of variation	Sum of squares	Variance component	Percentage of variation	Source of variation	Sum of squares	Variance component	Percentage of variation
Among treatments (Va, Fct)	19.107	0.00345	0.11	Among treatments (Va, Fct)	21.352	-0.01444	-0.48
Among lines within treatments (Vb, Fsc)	18.44	0.06804	2.24	Among lines within treatments (Vb, Fsc)	25.985	0.10043	3.31
Within lines (Vc, Fst)	1331.3	2.96701	97.65	Within lines (Vc, Fst)	1459	2.9492	97.17
Total	1368.9	3.0385		Total	1506.3	3.03519	

Temporal hierarchy F3-F6			
Source of variation	Sum of squares	Variance component	Percentage of variation
Among treatments (Va, Fct)	81.566	0.04271	1.41
Among lines within treatments (Vb, Fsc)	58.44	0.00948	0.31
Within lines (Vc, Fst)	5697.3	2.98153	98.28
Total	5837.3	3.03372	

b.

LOCUS	AMONG TREATMENTS				AMONG LINES WITHIN TREATMENT				WITHIN LINES				
	SSD	d.f.	Va	% variation	SSD	d.f.	Vb	% variation	SSD	d.f.	Vc	% variation	
F3	Pret69	1.6157	2	0.0024	0.5442	0.8913	2	0.0002	0.0363	206.1294	479	0.4303	99.4195
	Pret-77	1.8855	2	0.0050	1.5671	0.3241	2	-0.0016	-0.4956	152.7143	481	0.3175	98.9285
	Hull 70-2	1.9380	2	0.0025	0.5696	1.1611	2	0.0015	0.3287	210.8844	481	0.4384	99.1017
	G102	0.3571	2	-0.0022	-0.7127	1.0545	2	0.0022	0.6970	150.8415	481	0.3136	100.0156
	Pret-32	1.4047	2	0.0023	0.5255	0.6843	2	-0.0010	-0.2266	211.5653	481	0.4398	99.7011
	G82	0.9762	2	-0.0004	-0.1375	1.1016	2	0.0028	1.0073	132.9283	481	0.2764	99.1302
	Pr92	1.3943	2	0.0015	0.4001	0.9323	2	0.0010	0.2565	179.0438	481	0.3722	99.3435
	G289	1.0421	2	-0.0005	-0.1126	1.1985	2	0.0017	0.3824	209.6587	481	0.4359	99.7302

F4	Pret69	2.6915	2	0.0025	0.5762	1.9303	2	0.0055	1.2852	204.6729	487	0.4203	98.1386
	Pret-77	0.9726	2	-0.0007	-0.2093	1.1965	2	0.0027	0.8231	160.0971	487	0.3287	99.3862
	Hull 70-2	2.0060	2	0.0009	0.2145	1.7204	2	0.0043	0.9787	211.5054	487	0.4343	98.8067
	G102	0.2347	2	-0.0039	-1.3008	1.4747	2	0.0044	1.4653	146.3841	487	0.3006	99.8355
	Pret-32	1.7462	2	0.0031	0.7014	0.7917	2	-0.0004	-0.0846	209.5621	485	0.4321	99.3832
	G82	4.0746	2	0.0103	3.6513	0.8587	2	0.0016	0.5762	131.0362	487	0.2691	95.7725
	Pr92	1.9332	2	0.0024	0.6489	1.1801	2	0.0023	0.6030	179.0900	487	0.3677	98.7481
	G289	2.6922	2	0.0030	0.6693	1.7781	2	0.0046	1.0462	210.8123	487	0.4329	98.2846

F5	Pret69	3.0138	2	0.0002	0.0466	3.0102	2	0.0118	2.7262	188.9342	449	0.4208	97.2272
	Pret-77	1.6309	2	-0.0007	-0.2260	1.8767	2	0.0067	2.0285	145.3559	449	0.3237	98.1974
	Hull 70-2	2.1130	2	0.0002	0.0333	2.1021	2	0.0067	1.5395	193.6131	449	0.4312	98.4272
	G102	2.1261	2	0.0012	0.3804	1.8079	2	0.0065	2.0378	139.0351	449	0.3097	97.5817
	Pret-32	2.4200	2	0.0007	0.1687	2.2571	2	0.0076	1.7468	191.3185	447	0.4280	98.0845
	G82	3.8170	2	0.0065	2.3902	1.9825	2	0.0080	2.9428	115.3987	449	0.2570	94.6670
	Pr92	1.6773	2	-0.0020	-0.5191	2.2802	2	0.0084	2.2225	166.3178	449	0.3704	98.2966
	G289	2.3088	2	-0.0026	-0.6022	3.1231	2	0.0124	2.8341	191.3588	449	0.4262	97.7682

F6	Pret69	2.9210	2	-0.0016	-0.3893	3.4450	2	0.0131	3.1220	202.5400	495	0.4092	97.2673
	Pret-77	1.8920	2	0.0014	0.4439	1.4400	2	0.0041	1.2802	154.7800	495	0.3127	98.2759
	Hull 70-2	3.2130	2	0.0032	0.7178	2.1950	2	0.0066	1.4986	214.5100	495	0.4334	97.7836
	G102	1.2930	2	-0.0106	-3.4259	4.6850	2	0.0204	6.6028	148.2900	495	0.2996	96.8232
	Pret-32	1.8557	2	-0.0051	-1.1544	3.4850	2	0.0131	2.9968	211.9545	493	0.4299	98.1576
	G82	4.3460	2	0.0051	1.8737	2.7000	2	0.0109	3.9761	127.9400	495	0.2585	94.1502
	Pr92	2.8000	2	-0.0042	-1.0784	4.1400	2	0.0169	4.3636	185.9000	495	0.3756	96.7148
	G289	3.0310	2	-0.0027	-0.6096	3.8950	2	0.0152	3.4250	213.0800	495	0.4305	97.1846

Locus	AMONG LINES				AMONG LINES WITHIN GENERATIONS				WITHIN LINES				
	SSD	d.f.	Va	% variation	SSD	d.f.	Vb	% variation	SSD	d.f.	Vc	% variation	
Temporal hierarchy F3-F6	Pret69	11.5850	4	0.0059	1.3843	9.1422	15	0.0020	0.4591	802.2764	1910	0.4200	98.1566
	Pret-77	7.1866	4	0.0038	1.1601	5.1291	15	0.0002	0.0682	612.9473	1912	0.3206	98.7718
	Hull 70-2	10.2423	4	0.0052	1.1885	8.0538	15	0.0011	0.2411	830.5129	1912	0.4344	98.5705
	G102	6.9595	4	0.0034	1.0862	6.5498	15	0.0014	0.4369	584.5508	1912	0.3057	98.4769
	Pret-32	8.7678	4	0.0044	1.0011	7.5654	15	0.0008	0.1706	824.4005	1906	0.4325	98.8284
	G82	15.9286	4	0.0096	3.4883	4.1341	15	0.0001	0.0387	507.3033	1912	0.2653	96.4730
	Pr92	9.1944	4	0.0045	1.1793	8.6311	15	0.0021	0.5586	710.3516	1912	0.3715	98.2621
	G289	11.7023	4	0.0060	1.3607	9.2342	15	0.0019	0.4343	824.9098	1912	0.4314	98.2051

C.

		Fixation indices:					
		FSC	<i>p</i> -value	FST	<i>p</i> -value	FCT	<i>p</i> -value
F3	Pret69	0.00036	0.406	0.00580	0.064	0.00544	0.135
	Pret-77	-0.00504	0.832	0.01071	0.022	0.01567	0.137
	Hull 70-2	0.00331	0.165	0.00898	0.007	0.00570	0.134
	G102	0.00692	0.165	-0.00016	0.386	-0.00713	1.000
	Pret-32	-0.00228	0.766	0.00299	0.301	0.00526	0.132
	G82	0.01006	0.107	0.00870	0.079	-0.00137	0.461
	Pr92	0.00258	0.287	0.00657	0.121	0.00400	0.268
	G289	0.00382	0.164	0.00270	0.166	-0.00113	0.675
	All loci	0.00219	0.124	0.00567	0.001	0.00349	0.077

F4	Pret69	0.01293	0.009	0.01861	0.000	0.00576	0.273
	Pret-77	0.00821	0.074	0.00614	0.060	-0.00209	0.659
	Hull 70-2	0.00981	0.019	0.01193	0.001	0.00215	0.394
	G102	0.01446	0.025	0.00164	0.127	-0.01301	1.000
	Pret-32	-0.00085	0.568	0.00617	0.067	0.00701	0.064
	G82	0.00598	0.154	0.04227	0.000	0.03651	0.132
	Pr92	0.00607	0.144	0.01252	0.013	0.00649	0.329
	G289	0.01053	0.022	0.01715	0.000	0.00669	0.204
	All loci	0.00832	0.000	0.01404	0.000	0.00577	0.047

F5	Pret69	0.02727	0.000	0.02773	0.000	0.00047	0.596
	Pret-77	0.02024	0.008	0.01803	0.001	-0.00226	0.732
	Hull 70-2	0.01540	0.002	0.01573	0.000	0.00033	0.531
	G102	0.02046	0.009	0.02418	0.001	0.00380	0.533
	Pret-32	0.01750	0.003	0.01915	0.000	0.00169	0.461
	G82	0.03015	0.031	0.05333	0.000	0.02390	0.400
	Pr92	0.02211	0.004	0.01703	0.001	-0.00519	0.664
	G289	0.02817	0.000	0.02232	0.000	-0.00602	0.728
	All loci	0.02242	0.000	0.02353	0.000	0.00114	0.432

F6	Pret69	0.03110	0.000	0.02733	0.000	-0.00389	0.599
	Pret-77	0.01286	0.024	0.01724	0.002	0.00444	0.328
	Hull 70-2	0.01509	0.002	0.02216	0.000	0.00718	0.204
	G102	0.06384	0.000	0.03177	0.000	-0.03426	1.000
	Pret-32	0.02963	0.000	0.01842	0.000	-0.01154	0.930
	G82	0.04052	0.003	0.05850	0.000	0.01874	0.400
	Pr92	0.04317	0.000	0.03285	0.000	-0.01078	0.668
	G289	0.03404	0.000	0.02815	0.000	-0.00610	0.732
	All loci	0.03293	0.000	0.02833	0.000	-0.00476	0.777

Temporal hierarchy F3-F6	Pret69	0.00466	0.004	0.01843	0.000	0.01384	0.000
	Pret-77	0.00069	0.308	0.01228	0.000	0.01160	0.000
	Hull 70-2	0.00244	0.059	0.01430	0.000	0.01188	0.000
	G102	0.00442	0.040	0.01523	0.000	0.01086	0.002
	Pret-32	0.00172	0.186	0.01172	0.000	0.01001	0.000
	G82	0.00040	0.410	0.03527	0.000	0.03488	0.000
	Pr92	0.00565	0.010	0.01738	0.000	0.01179	0.000
	G289	0.00440	0.004	0.01795	0.000	0.01361	0.000
	All loci	0.00317	0.000	0.01720	0.000	0.01408	0.000

- d. Summary of AMOVA statistics, showing the value of the different variance component among treatments (V_A) among lines within treatments (V_B) and within lines (V_C) and the % of variation they explain for over all putative candidate loci in generations F5-F6, as well as for an analysis over these two generations combined.
- e. Per-locus AMOVA tables showing sum of squares of the deviations (SSD), degrees of freedom (d.f.) the different variance components among treatments (V_A) among lines within treatments (V_B) and within lines (V_C) and the % of variation they explain for each putative candidate locus in generations F5-F6, as well as for an analysis over these two generations combined
- f. Fixation indices among treatments among treatments (F_{CT}) among lines within treatments (F_{SC}) and within lines (F_{ST}) and p -values for the analyses for each candidate locus and over all loci for generations F5-F6, as well as for an analysis over these two generations combined. Significant p -values are shown in bold.

d.

F5				F6			
Source of variation	Sum of squares	Variance component	Percentage of variation	Source of variation	Sum of squares	Variance component	Percentage of variation
Among treatments (Va, Fct)	38.215	0.09014	2.41	Among treatments (Va, Fct)	60.38	0.09014	2.41
Among lines within treatments (Vb, Fsc)	12.695	0.03002	0.80	Among lines within treatments (Vb, Fsc)	31.656	0.12393	3.31
Within lines (Vc, Fst)	1591.8	3.61627	96.78	Within lines (Vc, Fst)	1733.5	3.53319	97.29
Total	16.42.662	3.73643		Total	1825.5	3.74726	

F5 & F6			
Source of variation	Sum of squares	Variance component	Percentage of variation
Among treatments (Va, Fct)	89.278	0.12043	3.22
Among lines within treatments (Vb, Fsc)	58.685	0.05088	1.36
Within lines (Vc, Fst)	3325.2	3.57254	95.42
Total	3425.8	3.64225	

e.

LOCUS	AMONG TREATMENTS				AMONG LINES WITHIN TREATMENT				WITHIN LINES			
	SSD	d.f.	Va	% variation	SSD	d.f.	Vb	% variation	SSD	d.f.	Vc	% variation
M9_403	4.0692	2	0.0117	6.7578	0.7360	2	0.0023	1.3309	70.6233	443	0.1594	91.9114
M1046_Dreyer	0.2661	2	-0.0033	-1.4937	1.2010	2	0.0043	1.9456	95.7488	435	0.2201	99.5481
M1046_2	0.2862	2	0.0005	0.3624	0.1538	2	-0.0005	-0.4299	55.8368	443	0.1260	100.0675
M30_Dreyer	5.5171	2	0.0131	5.1327	1.8412	2	0.0076	2.9650	103.6372	441	0.2350	91.9023
GH1	0.9761	2	0.0030	1.2460	0.1458	2	-0.0018	-0.7658	101.9648	433	0.2355	99.5199
GH2_60	1.7270	2	0.0045	1.7817	0.4918	2	0.0000	-0.0021	105.6913	429	0.2464	98.2204
GH2_74	0.6436	2	0.0014	0.8658	0.2416	2	-0.0005	-0.2853	71.4639	439	0.1628	99.4195
GH2_165	1.3539	2	0.0007	0.2894	1.1587	2	0.0037	1.4894	108.1780	441	0.2453	98.2212
GH2_211	0.3252	2	-0.0011	-0.5271	0.6249	2	0.0013	0.6387	86.9254	437	0.1989	99.8884
Myostatin	0.5298	2	0.0007	0.3556	0.3265	2	-0.0004	-0.2070	88.0694	439	0.2006	99.8515
Prolactin_1	3.0380	2	0.0099	3.9988	0.2519	2	-0.0013	-0.5053	104.4578	439	0.2379	96.5065
Prolactin_2	2.0250	2	0.0068	2.6757	0.1111	2	-0.0021	-0.8470	108.8279	439	0.2479	98.1713
TBC_1	3.0419	2	0.0098	3.8522	0.2773	2	-0.0012	-0.4692	107.5705	439	0.2450	96.6170
SF1	0.9003	2	0.0012	0.9210	0.5697	2	0.0017	1.2990	56.8071	439	0.1294	97.7800
Pr39	6.0115	2	0.0137	3.6626	2.1050	2	0.0076	2.0431	157.9892	449	0.3519	94.2943
M987	6.4829	2	0.0144	4.8242	2.3783	2	0.0100	3.3379	123.0177	449	0.2740	91.8379
M9_Indel	1.0209	2	0.0033	3.1640	0.0808	2	-0.0007	-0.6324	44.9423	449	0.1001	97.4684

LOCUS	AMONG TREATMENTS				AMONG LINES WITHIN TREATMENT				WITHIN LINES			
	SSD	d.f.	Va	% variation	SSD	d.f.	Vb	% variation	SSD	d.f.	Vc	% variation
M9_403	5.8177	2	0.0147	7.1411	1.1530	2	0.0039	1.9157	91.7390	491	0.1868	90.9432
M1046_Dreyer	0.7763	2	0.0007	0.2962	0.5637	2	0.0006	0.2583	110.0774	491	0.2242	99.4455
M1046_2	0.3267	2	0.0004	0.2960	0.1893	2	-0.0005	-0.3535	71.9339	493	0.1459	100.0575
M30_Dreyer	11.2936	2	0.0238	9.3413	3.7486	2	0.0169	6.6268	104.5388	489	0.2138	84.0319
GH1	0.6824	2	-0.0054	-2.2999	2.4224	2	0.0099	4.1809	112.5781	487	0.2312	98.1190
GH2_60	3.3237	2	0.0053	2.1024	1.6419	2	0.0058	2.2949	118.9618	491	0.2423	95.6027
GH2_74	0.4949	2	0.0014	0.9480	0.0400	2	-0.0013	-0.8662	73.7696	491	0.1502	99.9181
GH2_165	2.8362	2	-0.0021	-0.8535	3.4980	2	0.0153	6.1435	115.7283	491	0.2357	94.7100
GH2_211	0.3999	2	-0.0067	-3.2427	2.4620	2	0.0107	5.1519	97.6484	481	0.2030	98.0908
Myostatin	0.2943	2	0.0002	0.0834	0.2447	2	-0.0007	-0.3689	93.8112	489	0.1918	100.2855
Prolactin_1	7.3361	2	0.0185	7.2693	1.4650	2	0.0050	1.9732	113.7692	493	0.2308	90.7575
Prolactin_2	1.7217	2	0.0035	1.4026	0.6400	2	0.0008	0.3111	118.1771	485	0.2437	98.2863
TBC_1	7.2086	2	0.0218	8.4554	0.2650	2	-0.0011	-0.4062	117.0084	493	0.2373	91.9507
SF1	0.3287	2	-0.0040	-3.1068	1.5777	2	0.0067	5.2817	61.0533	491	0.1243	97.8251
Pr39	10.1460	2	0.0163	4.3122	4.9400	2	0.0213	5.6467	168.1500	495	0.3397	90.0411
M987	7.0500	2	0.0032	1.0995	6.0200	2	0.0275	9.3871	129.7100	495	0.2620	89.5134
M9_Indel	0.3430	2	-0.0014	-1.9130	0.7850	2	0.0032	4.4615	34.8300	495	0.0704	97.4515

LOCUS	AMONG TREATMENTS				AMONG LINES WITHIN TREATMENT				WITHIN LINES			
	SSD	d.f.	Va	% variation	SSD	d.f.	Vb	% variation	SSD	d.f.	Vc	% variation
M9_403	9.4036	2	0.0141	7.3706	3.2171	7	0.0030	1.5863	162.3623	934	0.1738	91.0432
M1046_Dreyer	0.9874	2	0.0008	0.3430	1.8489	7	0.0005	0.2003	205.8262	926	0.2223	99.4567
M1046_2	0.5565	2	0.0006	0.4659	0.6031	7	-0.0005	-0.3896	127.7707	936	0.1365	99.9237
M30_Dreyer	15.7407	2	0.0227	8.8989	7.3801	7	0.0088	3.4599	208.1759	930	0.2239	87.6413
GH1	1.6224	2	0.0015	0.6343	2.6046	7	0.0015	0.6304	214.5430	920	0.2332	98.7353
GH2_60	4.5830	2	0.0062	2.4555	3.1563	7	0.0022	0.8805	224.6532	920	0.2442	96.6640
GH2_74	1.0241	2	0.0015	0.9370	0.5041	7	-0.0009	-0.5703	145.2335	930	0.1562	99.6333
GH2_165	3.9277	2	0.0041	1.6614	5.0121	7	0.0051	2.0266	223.9063	932	0.2402	96.3120
GH2_211	0.6961	2	-0.0004	-0.1813	3.1945	7	0.0028	1.3542	184.5738	918	0.2011	98.8271
Myostatin	0.2766	2	-0.0001	-0.0594	1.2116	7	-0.0002	-0.1249	181.8806	928	0.1960	100.1843
Prolactin_1	9.6514	2	0.0149	5.9344	2.5675	7	0.0014	0.5619	218.2270	932	0.2342	93.5037
Prolactin_2	3.2699	2	0.0043	1.7258	2.4446	7	0.0011	0.4406	227.0050	924	0.2457	97.8336
TBC_1	9.6015	2	0.0154	6.0242	1.2135	7	-0.0007	-0.2808	224.5788	932	0.2410	94.2566
SF1	0.8702	2	0.0003	0.1973	2.5152	7	0.0025	1.9110	117.8604	930	0.1267	97.8917
Pr39	15.0672	2	0.0207	5.5186	8.6197	7	0.0093	2.4723	326.1392	944	0.3455	92.0091
M987	10.9931	2	0.0129	4.3789	11.0518	7	0.0137	4.6677	252.7277	944	0.2677	90.9535
M9_Indel	1.0068	2	0.0009	1.0736	1.5406	7	0.0014	1.6357	79.7723	944	0.0845	97.2907

f.

		Fixation indices:					
		FSC	<i>p-value</i>	FST	<i>p-value</i>	FCT	<i>p-value</i>
F5	M9_403	0.0143	0.126	0.0809	0.000	0.0676	0.136
	M1046_Dreyer	0.0192	0.083	0.0045	0.174	-0.0149	0.794
	M1046_2	-0.0043	0.557	-0.0007	0.485	0.0036	0.393
	M30_Dreyer	0.0313	0.015	0.0810	0.000	0.0513	0.263
	GH1	-0.0078	0.702	0.0048	0.241	0.0125	0.202
	GH2_60	0.0000	0.290	0.0178	0.024	0.0178	0.199
	GH2_74	-0.0029	0.469	0.0058	0.201	0.0087	0.329
	GH2_165	0.0149	0.089	0.0178	0.031	0.0029	0.532
	GH2_211	0.0064	0.163	0.0011	0.246	-0.0053	0.671
	Myostatin	-0.0021	0.511	0.0015	0.437	0.0036	0.533
	Prolactin_1	-0.0053	0.561	0.0349	0.006	0.0400	0.135
	Prolactin_2	-0.0087	0.813	0.0183	0.094	0.0268	0.068
	TBC_1	-0.0049	0.558	0.0338	0.005	0.0385	0.203
	SF1	0.0131	0.091	0.0222	0.023	0.0092	0.402
	Pr39	0.0212	0.003	0.0571	0.000	0.0366	0.203
	M987	0.0351	0.001	0.0816	0.000	0.0482	0.137
	M9_Indel	-0.0065	0.578	0.0253	0.013	0.0316	0.066
All loci	0.0082	0.001	0.0322	0.000	0.0241	0.001	

F6	M9_403	0.0206	0.041	0.0906	0.000	0.0714	0.336
	M1046_Dreyer	0.0026	0.244	0.0055	0.162	0.0030	0.459
	M1046_2	-0.0036	0.506	-0.0006	0.455	0.0030	0.527
	M30_Dreyer	0.0731	0.000	0.1597	0.000	0.0934	0.329
	GH1	0.0409	0.005	0.0188	0.006	-0.0230	0.734
	GH2_60	0.0234	0.035	0.0440	0.001	0.0210	0.349
	GH2_74	-0.0087	0.885	0.0008	0.443	0.0095	0.135
	GH2_165	0.0609	0.000	0.0529	0.000	-0.0085	0.399
	GH2_211	0.0499	0.002	0.0191	0.006	-0.0324	1.000
	Myostatin	-0.0037	0.591	-0.0029	0.662	0.0008	0.604
	Prolactin_1	0.0213	0.061	0.0924	0.000	0.0727	0.202
	Prolactin_2	0.0032	0.329	0.0171	0.081	0.0140	0.267
	TBC_1	-0.0044	0.582	0.0805	0.000	0.0846	0.065
	SF1	0.0512	0.002	0.0218	0.003	-0.0311	0.801
	Pr39	0.0590	0.000	0.0996	0.000	0.0431	0.201
	M987	0.0949	0.000	0.1049	0.000	0.0110	0.463
	M9_Indel	0.0438	0.001	0.0255	0.002	-0.0191	0.738
All loci	0.0339	0.000	0.0571	0.000	0.0241	0.036	

F5 & F6	M9_403	0.0171	0.017	0.0896	0.000	0.0737	0.016
	M1046_Dreyer	0.0020	0.279	0.0054	0.162	0.0034	0.232
	M1046_2	-0.0039	0.721	0.0008	0.470	0.0047	0.088
	M30_Dreyer	0.0380	0.000	0.1236	0.000	0.0890	0.031
	GH1	0.0063	0.090	0.0127	0.018	0.0063	0.204
	GH2_60	0.0090	0.042	0.0334	0.000	0.0246	0.053
	GH2_74	-0.0058	0.833	0.0037	0.312	0.0094	0.027
	GH2_165	0.0206	0.002	0.0369	0.000	0.0166	0.118
	GH2_211	0.0135	0.015	0.0117	0.011	-0.0018	0.497
	Myostatin	-0.0013	0.613	-0.0018	0.676	-0.0006	0.482
	Prolactin_1	0.0060	0.158	0.0650	0.000	0.0593	0.005
	Prolactin_2	0.0045	0.262	0.0217	0.014	0.0173	0.044
	TBC_1	-0.0030	0.631	0.0574	0.000	0.0602	0.002
	SF1	0.0192	0.004	0.0211	0.001	0.0020	0.367
	Pr39	0.0262	0.000	0.0799	0.000	0.0552	0.004
	M987	0.0488	0.000	0.0905	0.000	0.0438	0.092
	M9_Indel	0.0165	0.004	0.0271	0.000	0.0107	0.177
All loci	0.0140	0.000	0.0458	0.000	0.0322	0.000	

APPENDIX IV – Pairwise F_{ST} and G''_{ST} estimates per locus

All Microsatellites		Pret69		Pret77		Hull70-2		G102		Pret-32		G82		Pr92		G289			
		Fst	G''st	Fst	G''st	Fst	G''st	Fst	G''st	Fst	G''st	Fst	G''st	Fst	G''st	Fst	G''st		
F3	S1-S2	0.0027	0.0111	0.0054	0.0373	-0.0050	-0.0156	0.0043	0.0325	0.0085	0.0228	0.0023	0.0207	-0.0089	-0.0209	0.0047	0.0177	0.0062	0.0459
	L1-L2	0.0015	0.0058	-0.0045	-0.0327	-0.0031	-0.0070	0.0022	0.0197	0.0034	0.0089	-0.0081	-0.0616	0.0300	0.0637	-0.0001	-0.0004	0.0012	0.0094
	S1-C	0.0016	0.0068	0.0165	0.1155	-0.0066	-0.0232	0.0051	0.0415	-0.0026	-0.0065	0.0022	0.0196	0.0087	0.0197	-0.0088	-0.0366	-0.0034	-0.0264
	S2-C	-0.0012	-0.0052	0.0063	0.0479	-0.0031	-0.0099	-0.0016	-0.0118	-0.0037	-0.0113	-0.0030	-0.0265	0.0018	0.0042	-0.0014	-0.0052	-0.0049	-0.0395
	C-L1	0.0035	0.0141	-0.0003	-0.0023	0.0182	0.0507	0.0051	0.0466	-0.0080	-0.0206	0.0026	0.0204	0.0005	0.0009	0.0055	-0.0229	0.0035	-0.0269
	C-L2	0.0062	0.0257	-0.0043	-0.0314	0.0293	0.0767	0.0110	0.0887	0.0004	0.0013	0.0044	0.0364	0.0000	0.0001	0.0068	0.0266	0.0043	0.0369
	S1-L1	0.0097	0.0387	0.0077	0.0527	0.0117	0.0328	0.0078	0.0695	-0.0053	-0.0125	0.0081	0.0662	0.0432	0.0911	0.0098	0.0409	0.0025	0.0184
	S1-L2	0.0121	0.0491	0.0188	0.1292	0.0247	0.0649	0.0116	0.0915	0.0069	0.0175	0.0083	0.0699	-0.0081	-0.0187	0.0134	0.0523	0.0164	0.1302
	S2-L1	0.0062	0.0249	-0.0026	-0.0193	0.0040	0.0101	0.0082	0.0678	0.0041	0.0115	-0.0041	-0.0329	0.0337	0.0720	0.0177	0.0676	-0.0012	-0.0089
	S2-L2	0.0033	0.0137	0.0005	0.0042	0.0116	0.0279	0.0224	0.1649	-0.0007	-0.0022	-0.0024	-0.0200	-0.0098	-0.0233	0.0035	0.0125	-0.0014	-0.0118
	S1-S2	0.0080	0.0326	0.0117	0.0685	0.0078	0.0248	0.0055	0.0422	0.0141	0.0372	-0.0028	-0.0229	0.0133	0.0308	0.0011	0.0039	0.0159	0.1110
	L1-L2	0.0085	0.0331	0.0148	0.0898	0.0078	0.0220	0.0133	0.1092	0.0163	0.0391	0.0004	0.0027	-0.0006	-0.0012	0.0105	0.0423	0.0043	0.0324
S1-C	0.0154	0.0605	0.0099	0.0619	0.0044	0.0131	0.0101	0.0664	0.0018	0.0047	0.0090	0.0620	0.0502	0.1087	0.0354	0.1279	0.0107	0.0847	
S2-C	0.0149	0.0584	0.0008	0.0057	-0.0007	-0.0019	-0.0003	-0.0021	-0.0038	-0.0095	0.0004	0.0030	0.1351	0.2773	0.0080	0.0290	0.0071	0.0546	
C-L1	0.0129	0.0511	0.0043	0.0308	0.0161	0.0467	0.0038	0.0289	-0.0008	-0.0020	0.0176	0.1179	0.0536	0.1084	0.0155	0.0584	0.0061	0.0514	
C-L2	0.0198	0.0739	0.0189	0.1266	0.0052	0.0134	0.0288	0.2017	-0.0039	-0.0088	0.0072	0.0499	0.0935	0.1918	0.0072	0.0277	0.0126	0.0979	
S1-L1	0.0133	0.0549	0.0256	0.1462	0.0145	0.0473	0.0129	0.0983	-0.0087	-0.0246	0.0051	0.0356	-0.0033	-0.0074	0.0176	0.0668	0.0317	0.2409	
S1-L2	0.0137	0.0530	0.0312	0.1700	0.0076	0.0221	0.0192	0.1335	0.0182	0.0432	-0.0014	-0.0100	-0.0004	-0.0009	0.0011	0.0041	0.0275	0.1935	
S2-L1	0.0108	0.0445	0.0174	0.1150	-0.0006	-0.0018	0.0015	0.0142	0.0107	0.0286	0.0103	0.0819	0.0150	0.0324	0.0209	0.0796	0.0119	0.0879	
S2-L2	0.0116	0.0449	0.0400	0.2499	0.0023	0.0064	0.0170	0.1409	0.0036	0.0083	0.0005	0.0043	-0.0035	-0.0075	-0.0063	-0.0242	0.0251	0.1717	
S1-S2	0.0291	0.1146	0.0347	0.1834	0.0278	0.0909	0.0132	0.1051	0.0233	0.0599	0.0095	0.0828	0.0591	0.1240	0.0405	0.1528	0.0357	0.2224	
L1-L2	0.0159	0.0631	0.0222	0.1556	0.0118	0.0307	0.0178	0.1295	0.0187	0.0527	0.0231	0.1513	-0.0023	-0.0050	0.0054	0.0221	0.0213	0.1644	
S1-C	0.0229	0.0840	0.0158	0.0930	0.0280	0.0827	0.0149	0.0981	0.0178	0.0450	0.0138	0.0856	0.0408	0.0801	0.0617	0.2154	0.0008	0.0047	
S2-C	0.0326	0.1234	0.0103	0.0692	0.0001	0.0004	0.0084	0.0623	0.0087	0.0208	0.0196	0.1463	0.1970	0.3861	0.0036	0.0137	0.0417	0.2640	
C-L1	0.0181	0.0680	-0.0019	-0.0145	0.0168	0.0427	0.0218	0.1581	0.0543	0.1506	0.0009	0.0049	0.0442	0.0854	0.0111	0.0433	0.0141	0.0899	
C-L2	0.0200	0.0745	0.0143	0.0997	-0.0012	-0.0031	0.0122	0.0755	0.0055	0.0133	0.0252	0.1573	0.0797	0.1631	0.0073	0.0273	0.0255	0.1885	
S1-L1	0.0180	0.0704	0.0259	0.1533	0.0715	0.0228	0.0191	0.1486	0.0089	0.0266	0.0045	0.0292	-0.0122	-0.0251	0.0100	0.0382	0.0109	0.0684	
S1-L2	0.0306	0.1186	0.0754	0.4132	0.0159	0.0482	0.0245	0.1621	-0.0014	-0.0036	0.0390	0.2760	-0.0025	-0.0054	0.0320	0.1172	0.0355	0.2570	
S2-L1	0.0245	0.0994	0.0155	0.1045	0.0080	0.0220	0.0113	0.1010	0.0725	0.2043	0.0164	0.1298	0.0586	0.1208	0.0079	0.0338	0.0226	0.1489	
S2-L2	0.0228	0.0915	0.0570	0.3517	0.0011	0.0033	0.0139	0.1031	0.0278	0.0682	0.0218	0.1899	0.0195	0.0428	0.0048	0.0196	0.0285	0.2177	
S1-S2	0.0397	0.1497	0.0391	0.1857	-0.0007	-0.0020	0.0181	0.1336	0.0656	0.1725	0.0304	0.2130	0.0442	0.0919	0.0791	0.2959	0.0429	0.2957	
L1-L2	0.0262	0.1017	0.0237	0.1482	0.0265	0.0706	0.0111	0.0860	0.0601	0.1504	0.0295	0.1989	0.0384	0.0779	0.0065	0.0296	0.0259	0.1923	
S1-C	0.0334	0.1257	-0.0002	-0.0014	0.0149	0.0415	0.0333	0.2340	0.0417	0.1059	0.0051	0.0342	0.0456	0.0960	0.1183	0.4082	0.0144	0.1077	
S2-C	0.0399	0.1489	0.0537	0.2706	0.0165	0.0414	0.0257	0.1992	0.0069	0.0160	0.0071	0.0625	0.1629	0.3437	0.0091	0.0370	0.0502	0.3397	
C-L1	0.0246	0.0973	0.0370	0.2302	0.0423	0.1182	0.0156	0.1287	0.0431	0.1191	0.0097	0.0735	0.0325	0.0653	0.0109	0.0444	0.0157	0.1112	
C-L2	0.0235	0.0862	0.0150	0.0894	0.0085	0.0204	0.0099	0.0688	0.0003	0.0007	0.0291	0.2157	0.0976	0.2107	0.0286	0.1173	0.0084	0.0649	
S1-L1	0.0262	0.1046	0.0277	0.1604	0.0226	0.0705	0.0383	0.3011	0.0141	0.0456	0.0127	0.0792	-0.0014	-0.0029	0.0487	0.1824	0.0333	0.2402	
S1-L2	0.0275	0.1015	0.0222	0.1234	0.0063	0.0167	0.0177	0.1176	0.0450	0.1044	0.0418	0.2553	0.0084	0.0179	0.0396	0.1494	0.0320	0.2516	
S2-L1	0.0287	0.1136	0.0107	0.0558	0.0213	0.0590	0.0220	0.1936	0.0635	0.1822	0.0115	0.0904	0.0883	0.1753	0.0076	0.0341	0.0294	0.1927	
S2-L2	0.0233	0.0853	0.0520	0.2626	-0.0010	-0.0023	0.0117	0.0855	0.0348	0.0740	0.0289	0.2222	0.0022	0.0047	0.0017	0.0077	0.0417	0.2962	

Fst	M9_indel	M987	M9_403	M1046_Dreyer	M1046_2	M30_Dreyer	GH1	GH2_60	GH2_74	GH2_165	GH2_211	Myostatin	Prolactin1	Prolactin2	TBC_1	SF1	Pr39	All SNPs	All Candidates
F5	Average Ho	0.194	0.334	0.456	0.276	0.503	0.518	0.551	0.337	0.520	0.442	0.337	0.459	0.438	0.501	0.270	0.790	0.425	0.448
	Average He	0.172	0.349	0.444	0.271	0.448	0.467	0.488	0.313	0.480	0.402	0.392	0.469	0.492	0.482	0.253	0.690	0.411	0.420
	S1-S2	-0.005	0.023	0.002	-0.005	0.071	-0.004	0.006	-0.005	-0.005	0.029	0.018	-0.006	0.002	0.002	0.042	0.031	0.011	0.018
	L1-L2	-0.005	-0.006	0.035	-0.005	-0.005	-0.008	0.000	0.002	0.002	0.003	-0.003	-0.001	-0.009	-0.006	0.000	0.015	-0.001	0.001
F6	C-S1	-0.004	0.101	-0.009	0.014	-0.007	0.008	-0.007	0.006	0.000	-0.004	-0.012	0.021	-0.013	0.093	-0.005	0.013	0.006	0.013
	C-S2	0.009	0.003	-0.007	-0.005	0.113	-0.006	0.012	0.031	0.078	-0.003	0.004	-0.004	-0.010	0.035	0.087	0.015	0.025	0.022
	C-L1	-0.001	0.013	0.024	-0.005	0.006	0.014	0.016	-0.011	-0.012	0.006	-0.012	0.017	0.021	0.091	-0.009	0.055	0.017	0.021
	C-L2	0.018	0.037	-0.010	0.022	0.022	0.034	-0.004	0.001	0.006	-0.007	-0.007	-0.004	0.004	0.078	-0.007	0.014	0.017	0.018
F5	S1-L1	0.019	0.172	0.004	-0.009	0.023	-0.009	0.028	0.007	-0.003	-0.009	-0.013	0.097	0.008	-0.008	0.005	0.093	0.015	0.036
	S1-L2	0.047	0.227	-0.004	-0.009	0.046	-0.002	0.002	-0.009	-0.009	-0.008	0.004	0.072	0.030	-0.010	-0.011	0.062	0.011	0.036
	S2-L1	0.043	0.038	0.050	-0.013	0.194	-0.001	0.081	0.031	0.072	0.036	0.001	0.044	0.011	0.002	0.106	0.126	0.061	0.065
	S2-L2	0.078	0.058	-0.010	0.000	0.234	0.013	0.037	0.000	0.024	0.010	0.034	0.025	0.034	-0.004	0.056	0.073	0.047	0.051
F6	S1-S2	0.067	0.174	0.014	0.002	0.137	0.089	0.053	-0.009	0.123	0.086	-0.004	-0.013	0.005	-0.010	0.084	0.108	0.046	0.063
	L1-L2	0.028	0.002	-0.008	-0.009	-0.007	-0.009	-0.008	-0.007	-0.006	0.008	-0.008	0.047	-0.002	0.001	0.024	0.014	0.001	0.003
	C-S1	-0.007	-0.007	-0.007	0.024	0.065	0.058	0.026	-0.002	-0.010	0.004	-0.010	0.103	-0.009	0.074	0.020	0.063	0.029	0.029
	C-S2	0.048	0.147	0.001	-0.005	0.348	-0.006	-0.006	-0.007	0.128	0.032	0.013	0.085	0.020	0.058	0.013	0.041	0.060	0.065
F6	C-L1	0.066	0.169	-0.004	0.000	-0.008	0.012	0.056	-0.009	-0.005	0.005	-0.008	0.014	0.004	0.152	0.032	0.093	0.032	0.050
	C-L2	0.000	0.118	0.005	-0.005	-0.005	0.015	0.070	-0.005	-0.011	-0.009	0.003	-0.003	-0.012	0.226	-0.009	0.047	0.036	0.043
	S1-L1	0.085	0.202	-0.009	-0.002	0.054	0.004	-0.004	0.007	-0.004	-0.010	-0.013	0.211	0.018	0.007	-0.007	0.118	0.026	0.052
	S1-L2	0.010	0.148	-0.003	0.002	0.037	0.002	0.000	0.018	-0.011	0.007	-0.009	0.056	-0.007	0.042	0.013	0.092	0.013	0.032
F6	S2-L1	-0.008	0.038	0.023	-0.009	0.329	0.032	0.091	-0.001	0.169	0.087	-0.002	0.188	0.076	0.013	0.102	0.210	0.102	0.107
	S2-L2	0.015	0.024	0.040	-0.010	0.299	0.036	0.108	0.008	0.128	0.025	-0.009	0.042	0.028	0.054	0.018	0.130	0.077	0.077

G"st	M9_indel	M987	M9_403	M1046_Dreyer	M1046_2	M30_Dreyer	GH1	GH2_60	GH2_74	GH2_165	GH2_211	Myostatin	Prolactin1	Prolactin2	TBC_1	SF1	Pr39	All SNPs	All Candidates
Average Ho	0.194	0.682	0.334	0.456	0.276	0.503	0.518	0.337	0.520	0.442	0.337	0.459	0.438	0.501	0.270	0.790	0.425	0.448	
Average He	0.172	0.534	0.349	0.444	0.271	0.448	0.467	0.488	0.313	0.480	0.402	0.392	0.469	0.492	0.253	0.690	0.411	0.420	
S1-S2	-0.007	0.156	0.040	0.004	-0.006	0.133	-0.007	0.011	-0.008	0.057	0.031	-0.009	0.003	-0.028	0.004	0.029	0.020	0.031	
L1-L2	-0.005	0.008	-0.007	0.061	-0.006	-0.009	-0.015	0.000	0.002	0.005	-0.004	-0.002	-0.019	-0.012	-0.017	0.001	-0.001	0.002	
S1-C	-0.005	0.185	-0.022	-0.016	0.019	-0.013	0.015	-0.014	0.009	0.001	-0.006	-0.021	0.037	-0.026	0.176	0.025	0.011	0.023	
S2-C	0.013	0.007	0.054	-0.013	-0.006	0.210	-0.012	0.023	0.046	0.151	-0.006	0.006	-0.008	-0.020	0.067	0.109	0.039	0.044	
C-L1	-0.001	0.030	0.098	0.040	-0.006	0.012	0.027	0.033	-0.015	-0.023	0.010	-0.021	0.034	0.042	0.174	-0.013	0.039	0.029	
C-L2	0.021	0.090	0.053	-0.018	0.029	0.042	0.064	-0.007	0.001	0.012	-0.012	-0.007	0.009	0.095	0.149	-0.010	0.035	0.029	
S1-L1	0.024	0.326	0.110	0.007	-0.012	0.046	-0.017	0.055	0.010	-0.005	-0.013	-0.021	0.180	0.015	-0.016	0.076	0.026	0.062	
S1-L2	0.056	0.447	0.062	-0.008	-0.013	0.087	-0.003	0.004	-0.014	-0.017	-0.013	0.006	0.133	0.060	-0.020	0.075	0.019	0.062	
S2-L1	0.055	0.094	0.298	0.086	-0.017	0.350	-0.003	0.156	0.047	0.140	0.059	0.002	0.085	0.022	0.004	0.139	0.103	0.113	
S2-L2	0.094	0.150	0.235	-0.019	0.000	0.414	0.024	0.071	0.000	0.048	0.017	0.056	0.049	0.067	-0.008	0.072	0.098	0.089	
S1-S2	0.079	0.370	0.074	0.027	0.004	0.248	0.162	0.104	-0.013	0.231	0.149	-0.006	-0.022	0.010	-0.020	0.107	0.105	0.109	
L1-L2	0.031	0.006	-0.012	-0.014	-0.013	-0.012	-0.017	-0.015	-0.009	-0.010	0.013	-0.013	0.092	-0.004	0.002	0.034	0.006	0.002	
S1-C	-0.009	-0.012	0.055	-0.013	0.034	0.119	0.104	0.051	-0.002	-0.019	0.007	-0.015	0.189	-0.019	0.137	0.028	0.048	0.049	
S2-C	0.056	0.322	-0.019	0.002	-0.006	0.577	-0.011	-0.012	-0.010	0.241	0.059	0.020	0.158	0.040	0.107	0.015	0.109	0.102	
C-L1	0.075	0.335	0.236	-0.008	0.000	-0.014	0.022	0.109	-0.012	-0.009	0.008	-0.012	0.028	0.008	0.279	0.045	0.101	0.054	
C-L2	0.000	0.239	0.217	0.009	-0.006	-0.009	0.028	0.135	-0.007	-0.020	-0.015	0.004	-0.007	-0.023	0.402	-0.012	0.081	0.060	
S1-L1	0.099	0.387	0.057	-0.015	-0.003	0.099	0.008	-0.008	0.010	-0.007	-0.015	-0.021	0.376	0.035	0.014	-0.011	0.109	0.044	
S1-L2	0.012	0.289	0.045	-0.005	0.004	0.069	0.004	0.001	0.025	-0.021	0.012	-0.015	0.102	-0.014	0.081	0.018	0.069	0.022	
S2-L1	-0.008	0.094	0.265	0.043	-0.013	0.551	0.061	0.174	-0.001	0.311	0.151	-0.004	0.341	0.145	0.026	0.133	0.204	0.173	
S2-L2	0.016	0.061	0.246	0.073	-0.013	0.509	0.069	0.205	0.011	0.239	0.047	-0.016	0.078	0.056	0.103	0.022	0.148	0.131	

APPENDIX V – Haplotypes for five Growth Hormone SNPs

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(1...1050)GAAAAAATAGTTTTCTCTGCCTTCTCAGTGCTAACTGCAGAAATACGCCACT
CATTCTGAAATAACCAATCA[A/G]AACCAGGAGGAGG[C/G]TCTTAAcGCTGTCAATCA
AGCGtATGTAAACACTCCTCAACCCTCCCCYtGTCTCTCAACTAYGTNACAGCTAGCACAG
CCTGTCATGAA[G/T]GCTAATGCTAGTTAGCATGACGRCAGATAAATAGTTTTCTGTAA
[A/C]TGTAAGTTGTTTTCTTRCCATTAGCAGTGNKKAGATGAGCATAATTGCTAGCACTA
AGACCCGCCTCCTGGCCCTGATTGGTTGTTTTGACCCAGGAGCATTGTATTTGTGCAGA
TCGCTAAAATAGCTCAGTGAAGAGGTAGAGGAGCGCGAGTTTTTTCAGATTTTCTGCCTC
ATAGCATTCTGTCACAACAGAGATTTTCAAATAAATGTTAATACTGTTAATACTCTGCA
TCTTTAAGATTGTCAGATGAAAATTRGCATAAAAATCTT[G/T]CATCAATCATCACTATCT
CCCTGTGAACCTGTTACCTGAGAACTGACCACCTGAGCTTGCAGGCCAATCAGGACGT
ACCAGAGATCTTTACTGACGCCTCAAACCTCCAGTTGGCACCTTACGGAAATTATTATCA
GAGTCTGGAAGCTGACGAGTCGCTGCGGAGAACCTACGAACTGCTGGCGTGCTTCAA
AAGGACATGAA
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Poecilia reticulata Growth Hormone sequence showing the location of five SNPs in grey as they appear in the sequence: GH2_60, GH2_74, GH2_165, GH2_174, GH2_211, GH1.

Haplotype frequencies of nine different haplotypes as they are present in generation F0, showing the five SNP genotypes as a single haplotype, its frequency and the minimal number of recombinations required to obtain the haplotype from one of the most frequent combination of two haplotypes (GGTCT and ACGAG). The location of recombination indicates between which two SNPs recombination must have occurred; 12 indicating between GH2_60 and GH2_74, 23 between GH2_74 and GH2_165, 34, between GH2_165 and GH2_211 and 45 between GH2_211 and GH1. Most recombination events surround GH2_74. Genotype frequencies within the F0 were not in Hardy-Weinberg equilibrium (Hardy-Weinberg probability exact test, 10.000 batches and 10.000 iterations per batch. F_{IS} : 0.0891, p -value: 0.000).

Haplotype	F0 frequency	Number of recombinations	Location of recombination
GGTCT	27.63	0	---
ACGAG	11.84	0	---
AGGAG	19.74	2	12-23
ACGCT	17.11	1	34
GGTCG	7.89	1	45
AGTCG	7.89	2	12-45
AGGCT	5.26	3	12-23-34
AGGAT	1.32	3	12-23-45
GGGCG	1.32	3	23-34-45

APPENDIX VI – Full tables for genotypic differentiation

The table shows test *p*-values, significant Benjamini-Hochberg corrected *p*-values and standard errors for each locus and each population pair within generations F5 and F6 for tests of pairwise genotypic differentiation. An exact G-test was used in GenePop with the following Markov chain parameters: dememorisation number 1000, 10.000 batches and 10.000 iterations per batch. Within-treatment comparisons are shown in light grey, comparisons between selected lines and the Control in white and between selection lines in dark grey.

Locus	Population pair	P-Value	B-H corr. sign. p-values	St. error
TBC_1	F5_L2 & F5_L1	0.8748		0.00005
TBC_1	F5_S2 & F5_S1	0.3359		0.00014
TBC_1	F6_L2 & F6_L1	0.3722		0.00016
TBC_1	F6_S2 & F6_S1	0.8904		0.00005
TBC_1	F5_C & F5_S1	0.0014	0.0084	0.00001
TBC_1	F5_C & F5_S2	0.0551		0.00007
TBC_1	F5_C & F5_L1	0.0007	0.0048	0.00001
TBC_1	F5_C & F5_L2	0.0051	0.0245	0.00002
TBC_1	F6_C & F6_S1	0.0046	0.0225	0.00002
TBC_1	F6_C & F6_S2	0.0176		0.00005
TBC_1	F6_C & F6_L1	0.0001	0.0009	0.00000
TBC_1	F6_C & F6_L2	0.0000	0.0000	0.00000
TBC_1	F5_L1 & F5_S1	1.0000		0.00000
TBC_1	F5_L1 & F5_S2	0.3097		0.00013
TBC_1	F5_L2 & F5_S1	0.8801		0.00005
TBC_1	F5_L2 & F5_S2	0.4617		0.00014
TBC_1	F6_L1 & F6_S1	0.2413		0.00014
TBC_1	F6_L1 & F6_S2	0.1774		0.00014
TBC_1	F6_L2 & F6_S1	0.0258		0.00005
TBC_1	F6_L2 & F6_S2	0.0205		0.00005

GH1	F5_L2 & F5_L1	0.7487		0.00009
GH1	F5_S2 & F5_S1	0.4793		0.00013
GH1	F6_L2 & F6_L1	1.0000		0.00000
GH1	F6_S2 & F6_S1	0.0023	0.0126	0.00001
GH1	F5_C & F5_S1	0.2193		0.00012
GH1	F5_C & F5_S2	0.6037		0.00011
GH1	F5_C & F5_L1	0.1534		0.00012
GH1	F5_C & F5_L2	0.0443		0.00007
GH1	F6_C & F6_S1	0.0073	0.0321	0.00003
GH1	F6_C & F6_S2	0.5504		0.00013
GH1	F6_C & F6_L1	0.1560		0.00012
GH1	F6_C & F6_L2	0.1186		0.00011
GH1	F5_L1 & F5_S1	0.8686		0.00005
GH1	F5_L1 & F5_S2	0.4162		0.00014
GH1	F5_L2 & F5_S1	0.3889		0.00015
GH1	F5_L2 & F5_S2	0.1277		0.00011
GH1	F6_L1 & F6_S1	0.2679		0.00015
GH1	F6_L1 & F6_S2	0.0435		0.00007
GH1	F6_L2 & F6_S1	0.3439		0.00016
GH1	F6_L2 & F6_S2	0.0435		0.00007
GH2_60	F5_L2 & F5_L1	0.3344		0.00014
GH2_60	F5_S2 & F5_S1	0.2598		0.00013
GH2_60	F6_L2 & F6_L1	0.8770		0.00005
GH2_60	F6_S2 & F6_S1	0.0222		0.00005
GH2_60	F5_C & F5_S1	0.8537		0.00005
GH2_60	F5_C & F5_S2	0.1536		0.00011
GH2_60	F5_C & F5_L1	0.1455		0.00011
GH2_60	F5_C & F5_L2	0.4847		0.00012
GH2_60	F6_C & F6_S1	0.0736		0.00009
GH2_60	F6_C & F6_S2	0.5766		0.00014
GH2_60	F6_C & F6_L1	0.0098	0.0413	0.00003
GH2_60	F6_C & F6_L2	0.0046	0.0225	0.00002
GH2_60	F5_L1 & F5_S1	0.0668		0.00008
GH2_60	F5_L1 & F5_S2	0.0041	0.0206	0.00002
GH2_60	F5_L2 & F5_S1	0.2775		0.00012
GH2_60	F5_L2 & F5_S2	0.0337		0.00005
GH2_60	F6_L1 & F6_S1	0.5432		0.00013
GH2_60	F6_L1 & F6_S2	0.0028	0.0147	0.00002
GH2_60	F6_L2 & F6_S1	0.3691		0.00015
GH2_60	F6_L2 & F6_S2	0.0013	0.0083	0.00001

GH2_74	F5_L2 & F5_L1	0.3087		0.00019
GH2_74	F5_S2 & F5_S1	0.5862		0.00014
GH2_74	F6_L2 & F6_L1	0.8275		0.00006
GH2_74	F6_S2 & F6_S1	0.8621		0.00006
GH2_74	F5_C & F5_S1	0.2518		0.00016
GH2_74	F5_C & F5_S2	0.0808		0.00010
GH2_74	F5_C & F5_L1	1.0000		0.00000
GH2_74	F5_C & F5_L2	0.3240		0.00018
GH2_74	F6_C & F6_S1	0.3823		0.00017
GH2_74	F6_C & F6_S2	0.5979		0.00014
GH2_74	F6_C & F6_L1	0.8456		0.00007
GH2_74	F6_C & F6_L2	0.5539		0.00016
GH2_74	F5_L1 & F5_S1	0.2381		0.00017
GH2_74	F5_L1 & F5_S2	0.0480		0.00009
GH2_74	F5_L2 & F5_S1	0.8544		0.00006
GH2_74	F5_L2 & F5_S2	0.3509		0.00017
GH2_74	F6_L1 & F6_S1	0.2567		0.00018
GH2_74	F6_L1 & F6_S2	0.4463		0.00018
GH2_74	F6_L2 & F6_S1	0.1263		0.00014
GH2_74	F6_L2 & F6_S2	0.2478		0.00018
GH2_165	F5_L2 & F5_L1	0.2907		0.00015
GH2_165	F5_S2 & F5_S1	0.0588		0.00008
GH2_165	F6_L2 & F6_L1	0.6425		0.00012
GH2_165	F6_S2 & F6_S1	0.0002	0.0018	0.00000
GH2_165	F5_C & F5_S1	0.3459		0.00014
GH2_165	F5_C & F5_S2	0.0054	0.0253	0.00002
GH2_165	F5_C & F5_L1	1.0000		0.00000
GH2_165	F5_C & F5_L2	0.2400		0.00013
GH2_165	F6_C & F6_S1	1.0000		0.00000
GH2_165	F6_C & F6_S2	0.0002	0.0014	0.00000
GH2_165	F6_C & F6_L1	0.6254		0.00012
GH2_165	F6_C & F6_L2	1.0000		0.00000
GH2_165	F5_L1 & F5_S1	0.3920		0.00016
GH2_165	F5_L1 & F5_S2	0.0117	0.0484	0.00003
GH2_165	F5_L2 & F5_S1	0.8740		0.00005
GH2_165	F5_L2 & F5_S2	0.0625		0.00007
GH2_165	F6_L1 & F6_S1	0.5124		0.00014
GH2_165	F6_L1 & F6_S2	0.0000	0.0000	0.00000
GH2_165	F6_L2 & F6_S1	1.0000		0.00000
GH2_165	F6_L2 & F6_S2	0.0003	0.0022	0.00000

GH2_211	F5_L2 & F5_L1	0.4624		0.00017
GH2_211	F5_S2 & F5_S1	0.1068		0.00011
GH2_211	F6_L2 & F6_L1	0.2311		0.00015
GH2_211	F6_S2 & F6_S1	0.0024	0.0134	0.00001
GH2_211	F5_C & F5_S1	0.4803		0.00015
GH2_211	F5_C & F5_S2	0.4754		0.00014
GH2_211	F5_C & F5_L1	0.2210		0.00015
GH2_211	F5_C & F5_L2	0.7178		0.00011
GH2_211	F6_C & F6_S1	0.2943		0.00017
GH2_211	F6_C & F6_S2	0.0450		0.00007
GH2_211	F6_C & F6_L1	0.2741		0.00017
GH2_211	F6_C & F6_L2	1.0000		0.00000
GH2_211	F5_L1 & F5_S1	0.7187		0.00010
GH2_211	F5_L1 & F5_S2	0.0475		0.00007
GH2_211	F5_L2 & F5_S1	0.8547		0.00007
GH2_211	F5_L2 & F5_S2	0.1960		0.00014
GH2_211	F6_L1 & F6_S1	1.0000		0.00000
GH2_211	F6_L1 & F6_S2	0.0019	0.0109	0.00001
GH2_211	F6_L2 & F6_S1	0.2483		0.00016
GH2_211	F6_L2 & F6_S2	0.0761		0.00009
M1046_Dreyer	F5_L2 & F5_L1	0.0631		0.00009
M1046_Dreyer	F5_S2 & F5_S1	0.2883		0.00015
M1046_Dreyer	F6_L2 & F6_L1	0.7479		0.00010
M1046_Dreyer	F6_S2 & F6_S1	0.1086		0.00011
M1046_Dreyer	F5_C & F5_S1	0.6387		0.00012
M1046_Dreyer	F5_C & F5_S2	0.6216		0.00012
M1046_Dreyer	F5_C & F5_L1	0.1028		0.00010
M1046_Dreyer	F5_C & F5_L2	0.8720		0.00005
M1046_Dreyer	F6_C & F6_S1	0.6447		0.00012
M1046_Dreyer	F6_C & F6_S2	0.3716		0.00015
M1046_Dreyer	F6_C & F6_L1	0.4658		0.00015
M1046_Dreyer	F6_C & F6_L2	0.2768		0.00015
M1046_Dreyer	F5_L1 & F5_S1	0.2854		0.00015
M1046_Dreyer	F5_L1 & F5_S2	0.0283		0.00006
M1046_Dreyer	F5_L2 & F5_S2	0.7560		0.00009
M1046_Dreyer	F5_L2 & F5_S1	0.4553		0.00015
M1046_Dreyer	F6_L1 & F6_S1	0.8733		0.00005
M1046_Dreyer	F6_L1 & F6_S2	0.0696		0.00009
M1046_Dreyer	F6_L2 & F6_S1	0.4937		0.00016
M1046_Dreyer	F6_L2 & F6_S2	0.0238		0.00005

M1046_2	F5_L2 & F5_L1	0.4521		0.00016
M1046_2	F5_S2 & F5_S1	0.5140		0.00017
M1046_2	F6_L2 & F6_L1	0.8485		0.00007
M1046_2	F6_S2 & F6_S1	0.3462		0.00019
M1046_2	F5_C & F5_S1	0.1968		0.00014
M1046_2	F5_C & F5_S2	0.4739		0.00015
M1046_2	F5_C & F5_L1	0.4297		0.00013
M1046_2	F5_C & F5_L2	0.0831		0.00012
M1046_2	F6_C & F6_S1	0.0950		0.00011
M1046_2	F6_C & F6_S2	0.5672		0.00014
M1046_2	F6_C & F6_L1	0.3458		0.00016
M1046_2	F6_C & F6_L2	0.5673		0.00014
M1046_2	F5_L1 & F5_S1	0.7081		0.00010
M1046_2	F5_L1 & F5_S2	1.0000		0.00000
M1046_2	F5_L2 & F5_S1	1.0000		0.00000
M1046_2	F5_L2 & F5_S2	0.3697		0.00014
M1046_2	F6_L1 & F6_S1	0.4535		0.00018
M1046_2	F6_L1 & F6_S2	0.8485		0.00007
M1046_2	F6_L2 & F6_S1	0.3463		0.00019
M1046_2	F6_L2 & F6_S2	1.0000		0.00000
M30_Dreyer	F5_L2 & F5_L1	0.5861		0.00013
M30_Dreyer	F5_S2 & F5_S1	0.0098	0.0413	0.00003
M30_Dreyer	F6_L2 & F6_L1	0.7338		0.00010
M30_Dreyer	F6_S2 & F6_S1	0.0003	0.0022	0.00000
M30_Dreyer	F5_C & F5_S1	0.5425		0.00013
M30_Dreyer	F5_C & F5_S2	0.0002	0.0018	0.00000
M30_Dreyer	F5_C & F5_L1	0.1996		0.00012
M30_Dreyer	F5_C & F5_L2	0.0655		0.00008
M30_Dreyer	F6_C & F6_S1	0.0074	0.0321	0.00003
M30_Dreyer	F6_C & F6_S2	0.0000	0.0000	0.00000
M30_Dreyer	F6_C & F6_L1	0.8659		0.00006
M30_Dreyer	F6_C & F6_L2	0.6209		0.00013
M30_Dreyer	F5_L1 & F5_S1	0.0999		0.00010
M30_Dreyer	F5_L1 & F5_S2	0.0000	0.0000	0.00000
M30_Dreyer	F5_L2 & F5_S1	0.0258		0.00005
M30_Dreyer	F5_L2 & F5_S2	0.0000	0.0000	0.00000
M30_Dreyer	F6_L1 & F6_S1	0.0138		0.00004
M30_Dreyer	F6_L1 & F6_S2	0.0000	0.0000	0.00000
M30_Dreyer	F6_L2 & F6_S1	0.0339		0.00006
M30_Dreyer	F6_L2 & F6_S2	0.0000	0.0000	0.00000

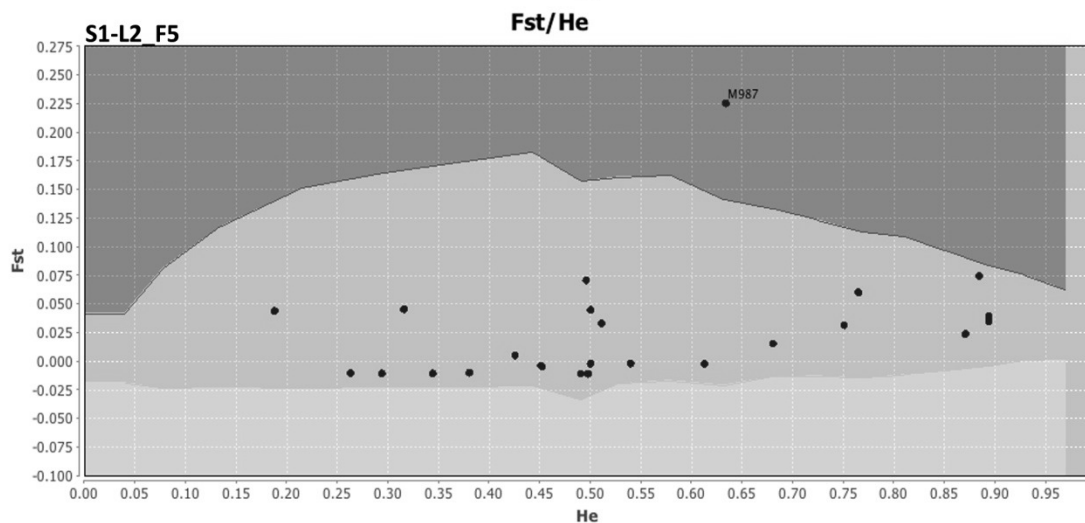
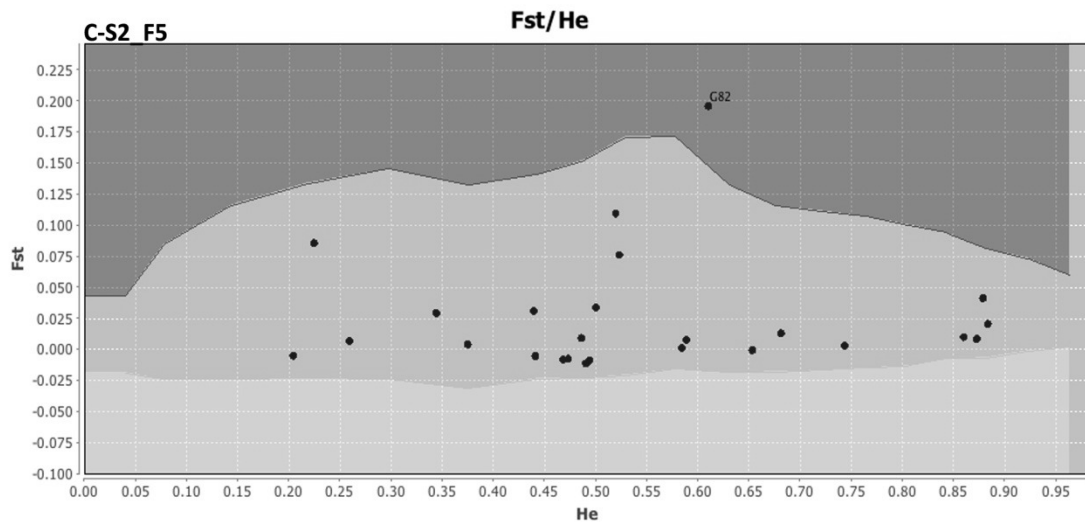
M9_inde1	F5_L1 & F5_S1	0.1351		0.00010
M9_inde1	F5_L1 & F5_S2	0.0281		0.00005
M9_inde1	F5_L2 & F5_S1	0.0201		0.00004
M9_inde1	F5_L2 & F5_S2	0.0027	0.0145	0.00001
M9_inde1	F6_L1 & F6_S1	0.0019	0.0109	0.00001
M9_inde1	F6_L1 & F6_S2	1.0000		0.00000
M9_inde1	F6_L2 & F6_S1	0.2269		0.00012
M9_inde1	F6_L2 & F6_S2	0.1997		0.00009
M9_inde1	F5_C & F5_S1	0.4825		0.00013
M9_inde1	F5_C & F5_S2	0.2403		0.00012
M9_inde1	F5_C & F5_L1	0.4220		0.00012
M9_inde1	F5_C & F5_L2	0.1557		0.00009
M9_inde1	F6_C & F6_S1	0.8200		0.00006
M9_inde1	F6_C & F6_S2	0.0226		0.00004
M9_inde1	F6_C & F6_L1	0.0076	0.0326	0.00002
M9_inde1	F6_C & F6_L2	0.4540		0.00012
M9_inde1	F5_L2 & F5_L1	0.5450		0.00009
M9_inde1	F5_S2 & F5_S1	0.5116		0.00013
M9_inde1	F6_L2 & F6_L1	0.0917		0.00006
M9_inde1	F6_S2 & F6_S1	0.0064	0.0291	0.00002
M9_403	F5_L2 & F5_L1	0.5128		0.00014
M9_403	F5_S2 & F5_S1	0.1338		0.00012
M9_403	F6_L2 & F6_L1	1.0000		0.00000
M9_403	F6_S2 & F6_S1	0.0328		0.00006
M9_403	F5_C & F5_S1	0.8771		0.00005
M9_403	F5_C & F5_S2	0.0751		0.00009
M9_403	F5_C & F5_L1	0.0120	0.0492	0.00003
M9_403	F5_C & F5_L2	0.0431		0.00007
M9_403	F6_C & F6_S1	0.0458		0.00007
M9_403	F6_C & F6_S2	0.8869		0.00005
M9_403	F6_C & F6_L1	0.0001	0.0007	0.00000
M9_403	F6_C & F6_L2	0.0002	0.0015	0.00000
M9_403	F5_L1 & F5_S1	0.0156		0.00004
M9_403	F5_L1 & F5_S2	0.0000	0.0001	0.00000
M9_403	F5_L2 & F5_S1	0.0453		0.00007
M9_403	F5_L2 & F5_S2	0.0001	0.0010	0.00000
M9_403	F6_L1 & F6_S1	0.0230		0.00006
M9_403	F6_L1 & F6_S2	0.0000	0.0002	0.00000
M9_403	F6_L2 & F6_S1	0.0451		0.00008
M9_403	F6_L2 & F6_S2	0.0001	0.0007	0.00000

M987	F5_L2 & F5_L1	0.2068		0.00019
M987	F5_S2 & F5_S1	0.0002	0.0016	0.00000
M987	F6_L2 & F6_L1	0.1223		0.00012
M987	F6_S2 & F6_S1	0.0000	0.0000	0.00000
M987	F5_C & F5_S1	0.0001	0.0009	0.00000
M987	F5_C & F5_S2	0.1390		0.00016
M987	F5_C & F5_L1	0.0042	0.0210	0.00002
M987	F5_C & F5_L2	0.0014	0.0083	0.00001
M987	F6_C & F6_S1	0.9299		0.00006
M987	F6_C & F6_S2	0.0000	0.0000	0.00000
M987	F6_C & F6_L1	0.0000	0.0000	0.00000
M987	F6_C & F6_L2	0.0002	0.0015	0.00000
M987	F5_L1 & F5_S1	0.0000	0.0001	0.00000
M987	F5_L1 & F5_S2	0.0003	0.0022	0.00001
M987	F5_L2 & F5_S1	0.0000	0.0000	0.00000
M987	F5_L2 & F5_S2	0.0009	0.0058	0.00001
M987	F6_L1 & F6_S1	0.0000	0.0000	0.00000
M987	F6_L1 & F6_S2	0.0000	0.0000	0.00000
M987	F6_L2 & F6_S1	0.0000	0.0000	0.00000
M987	F6_L2 & F6_S2	0.0004	0.0030	0.00001
Myostatin	F5_L2 & F5_L1	0.3606		0.00016
Myostatin	F5_S2 & F5_S1	0.5186		0.00014
Myostatin	F6_L2 & F6_L1	0.6419		0.00012
Myostatin	F6_S2 & F6_S1	0.4836		0.00016
Myostatin	F5_C & F5_S1	0.7604		0.00009
Myostatin	F5_C & F5_S2	0.2995		0.00015
Myostatin	F5_C & F5_L1	1.0000		0.00000
Myostatin	F5_C & F5_L2	0.4401		0.00015
Myostatin	F6_C & F6_S1	0.6571		0.00012
Myostatin	F6_C & F6_S2	0.1710		0.00013
Myostatin	F6_C & F6_L1	0.6330		0.00012
Myostatin	F6_C & F6_L2	0.3392		0.00016
Myostatin	F5_L1 & F5_S1	0.8797		0.00005
Myostatin	F5_L1 & F5_S2	0.3091		0.00015
Myostatin	F5_L2 & F5_S1	0.3072		0.00016
Myostatin	F5_L2 & F5_S2	0.0530		0.00008
Myostatin	F6_L1 & F6_S1	1.0000		0.00000
Myostatin	F6_L1 & F6_S2	0.4552		0.00016
Myostatin	F6_L2 & F6_S1	0.6641		0.00012
Myostatin	F6_L2 & F6_S2	0.7651		0.00009

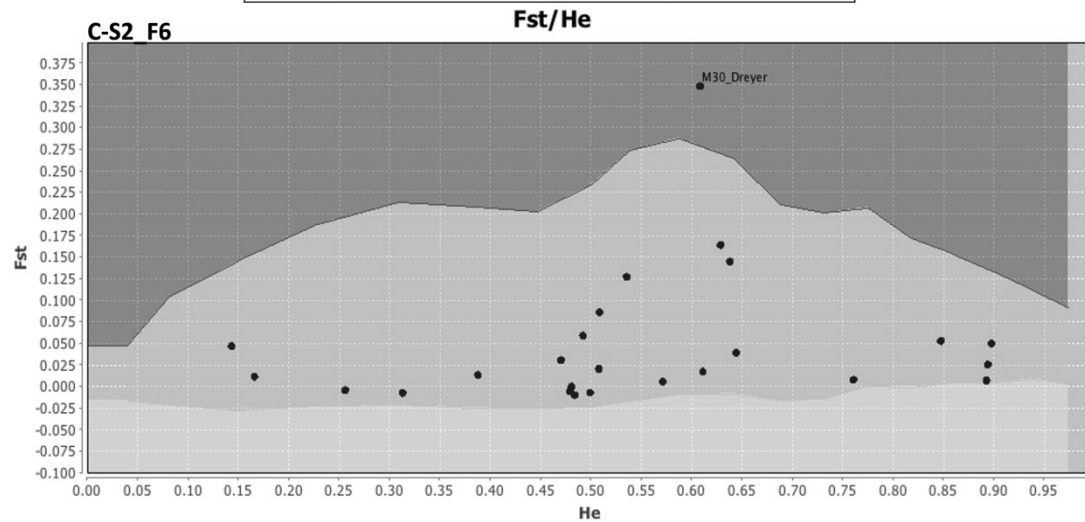
Pr39	F5_L2 & F5_L1	0.0262		0.00008
Pr39	F5_S2 & F5_S1	0.0014	0.0083	0.00001
Pr39	F6_L2 & F6_L1	0.0237		0.00008
Pr39	F6_S2 & F6_S1	0.0000	0.0000	0.00000
Pr39	F5_C & F5_S1	0.0575		0.00012
Pr39	F5_C & F5_S2	0.1685		0.00021
Pr39	F5_C & F5_L1	0.0003	0.0021	0.00001
Pr39	F5_C & F5_L2	0.2493		0.00023
Pr39	F6_C & F6_S1	0.0001	0.0010	0.00000
Pr39	F6_C & F6_S2	0.0000	0.0002	0.00000
Pr39	F6_C & F6_L1	0.0000	0.0000	0.00000
Pr39	F6_C & F6_L2	0.0005	0.0035	0.00001
Pr39	F5_L1 & F5_S1	0.0000	0.0000	0.00000
Pr39	F5_L1 & F5_S2	0.0000	0.0000	0.00000
Pr39	F5_L2 & F5_S1	0.0000	0.0002	0.00000
Pr39	F5_L2 & F5_S2	0.0002	0.0019	0.00001
Pr39	F6_L1 & F6_S1	0.0000	0.0000	0.00000
Pr39	F6_L1 & F6_S2	0.0000	0.0000	0.00000
Pr39	F6_L2 & F6_S1	0.0000	0.0000	0.00000
Pr39	F6_L2 & F6_S2	0.0000	0.0000	0.00000
SF1	F5_L2 & F5_L1	0.3387		0.00019
SF1	F5_S2 & F5_S1	0.0554		0.00007
SF1	F6_L2 & F6_L1	0.0948		0.00012
SF1	F6_S2 & F6_S1	0.0012	0.0076	0.00001
SF1	F5_C & F5_S1	0.4365		0.00015
SF1	F5_C & F5_S2	0.0034	0.0175	0.00002
SF1	F5_C & F5_L1	0.8426		0.00007
SF1	F5_C & F5_L2	0.6879		0.00012
SF1	F6_C & F6_S1	0.0850		0.00009
SF1	F6_C & F6_S2	0.1921		0.00011
SF1	F6_C & F6_L1	0.0523		0.00009
SF1	F6_C & F6_L2	1.0000		0.00000
SF1	F5_L1 & F5_S1	0.2544		0.00016
SF1	F5_L1 & F5_S2	0.0006	0.0042	0.00001
SF1	F5_L2 & F5_S1	0.8468		0.00006
SF1	F5_L2 & F5_S2	0.0156		0.00004
SF1	F6_L1 & F6_S1	0.7113		0.00013
SF1	F6_L1 & F6_S2	0.0009	0.0058	0.00001
SF1	F6_L2 & F6_S1	0.1532		0.00016
SF1	F6_L2 & F6_S2	0.1503		0.00013

APPENDIX VII – Fdist figures

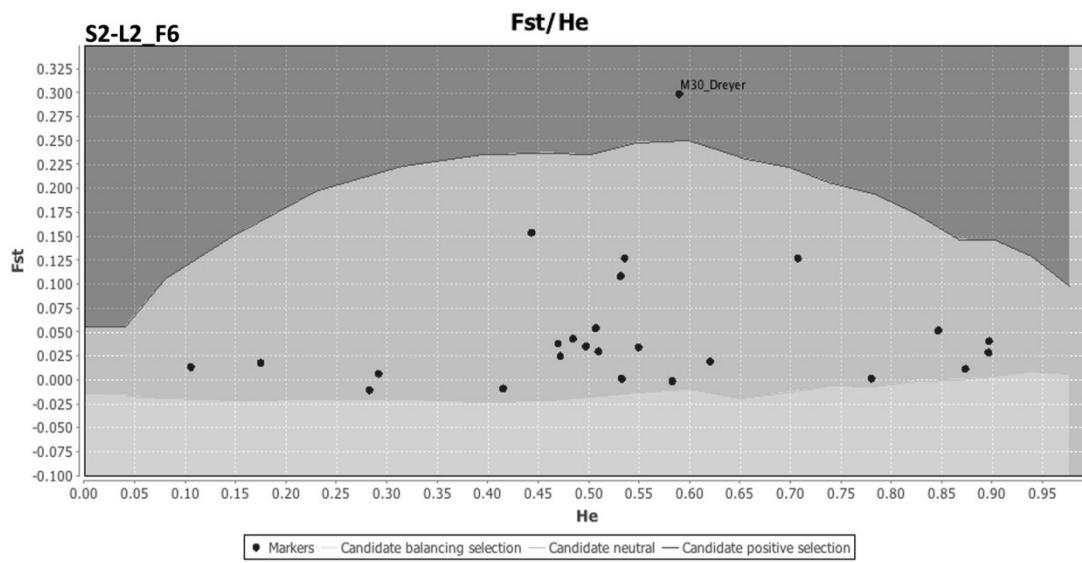
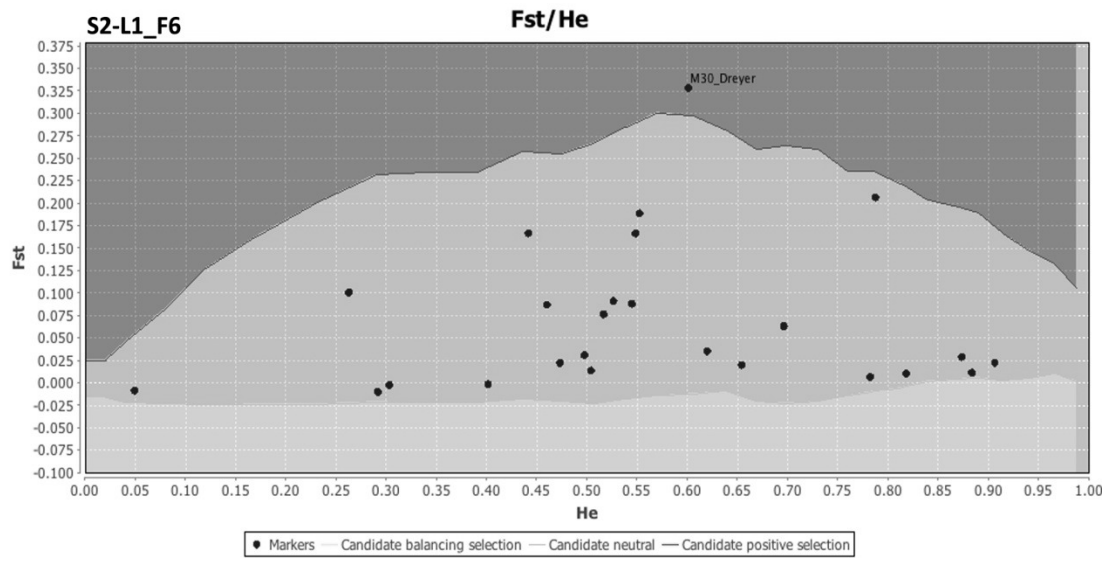
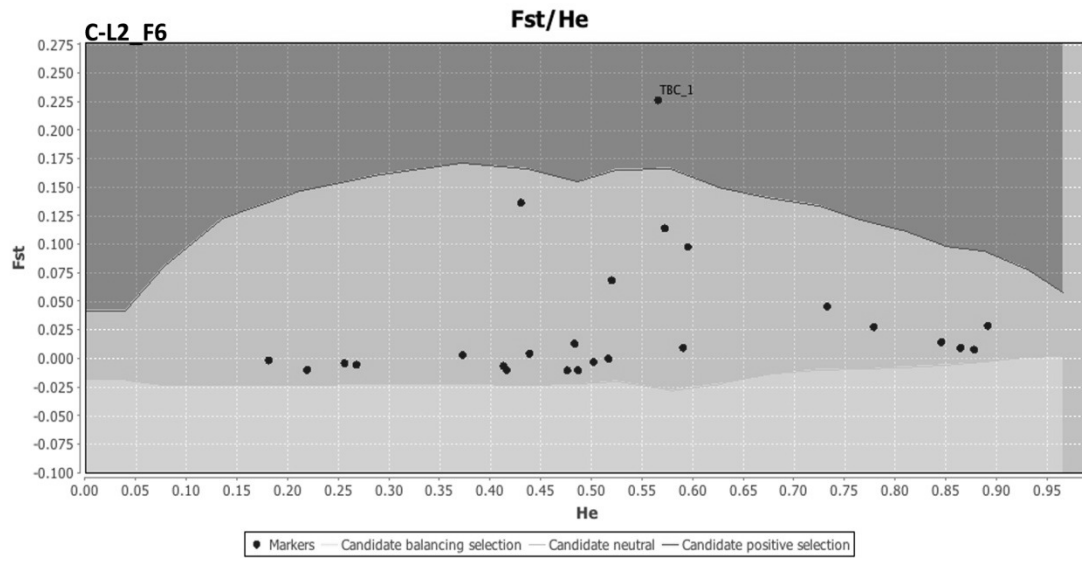
The figures show the results for pairwise comparisons in LOSITAN in which significant outlier loci were detected. Each graph plots F_{ST} as a function of marker heterozygosity. Candidates for divergent selection lie in the dark grey area above the simulated neutral distribution (light grey). Marker names are shown for outlier loci only.

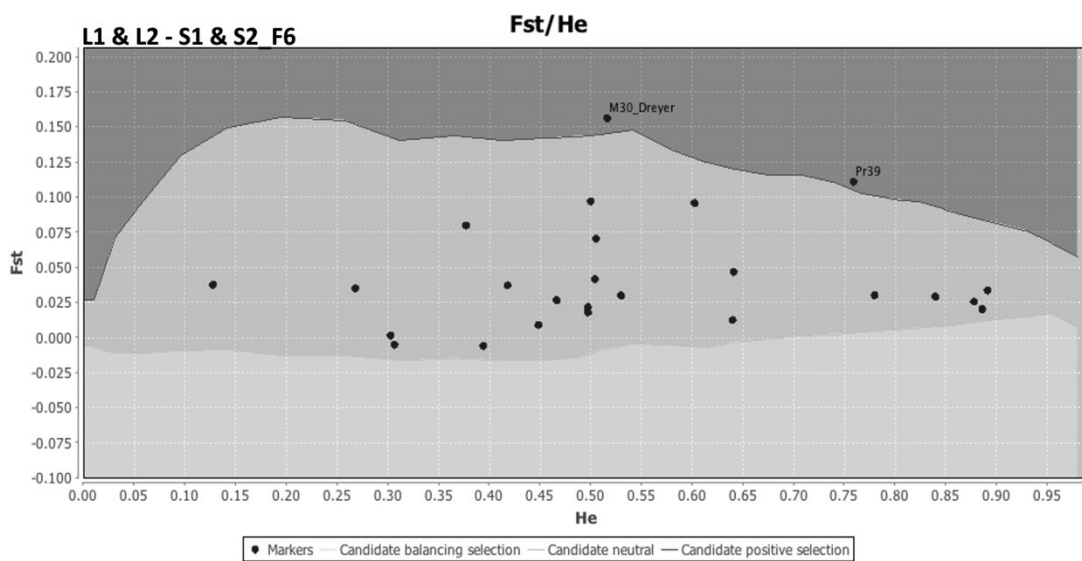
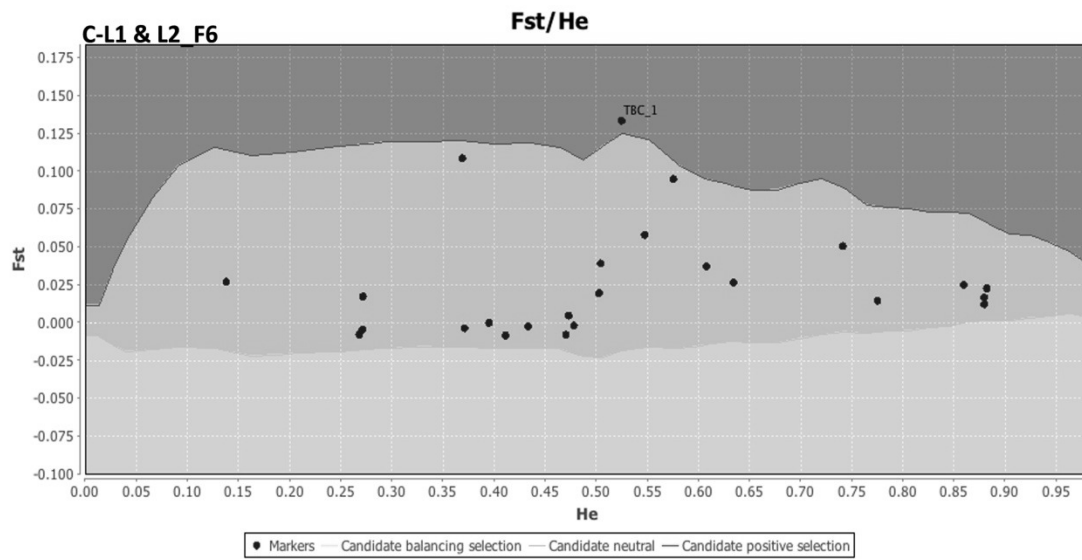
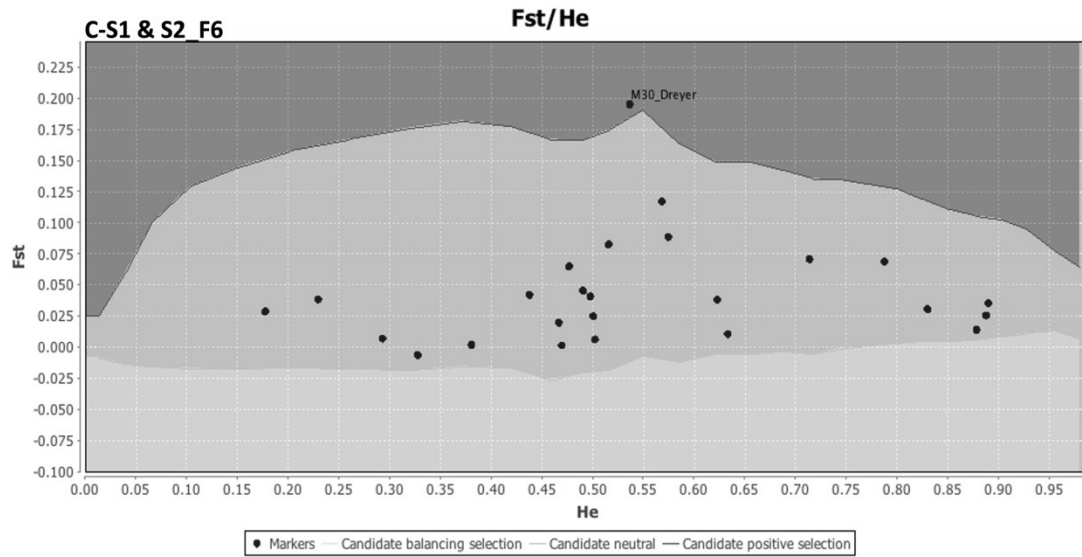


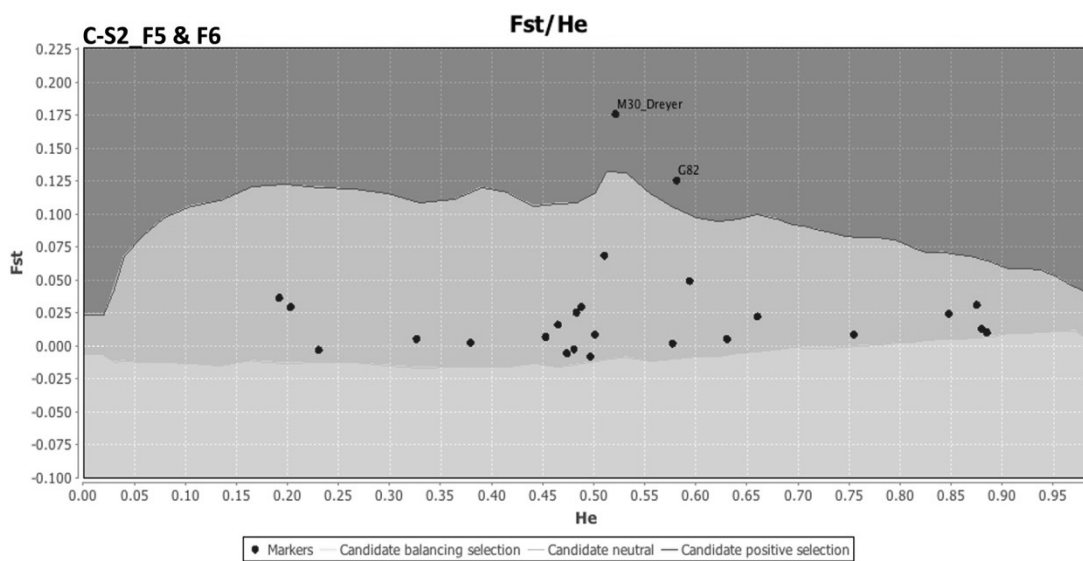
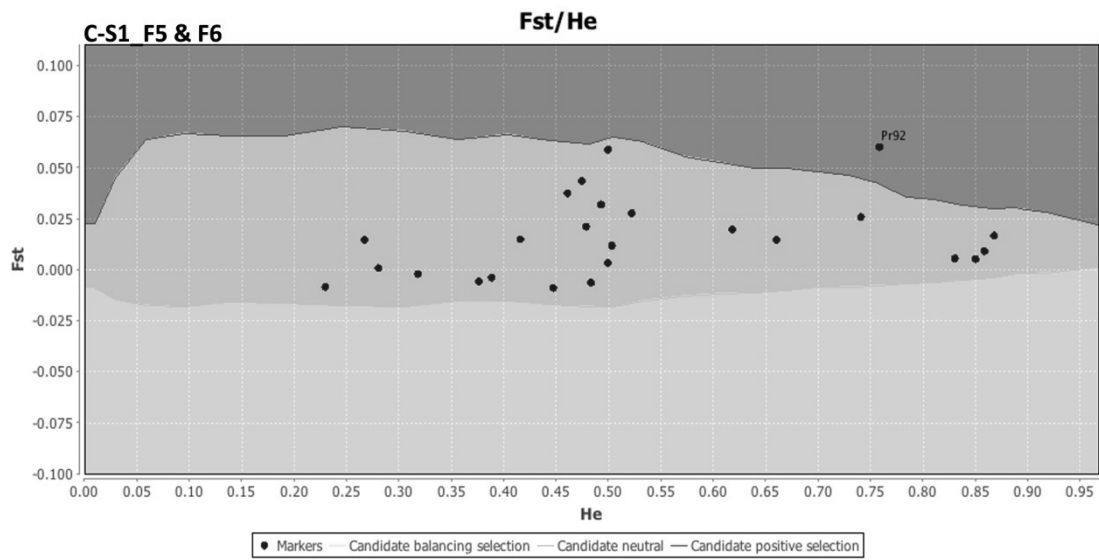
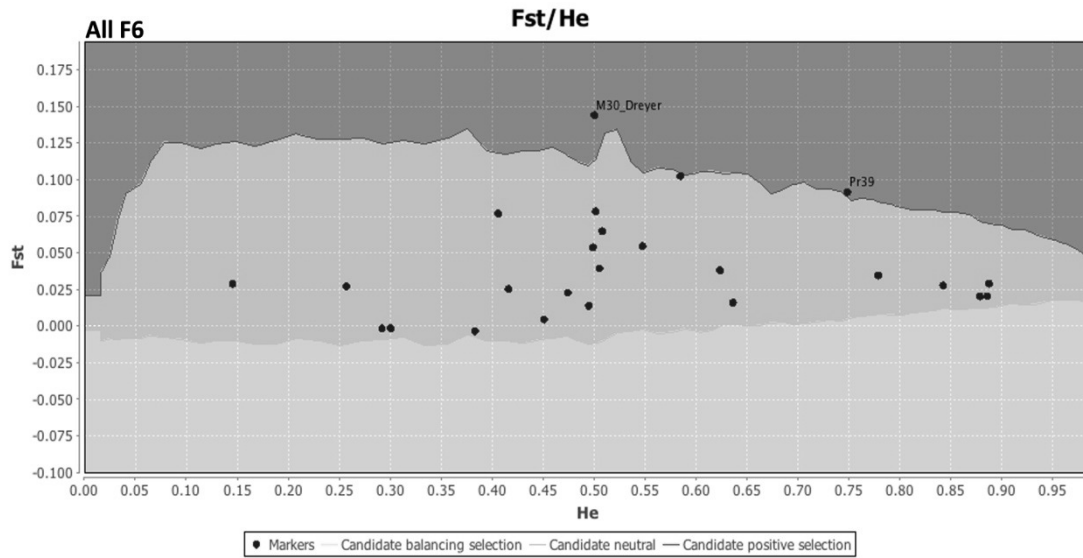
● Markers — Candidate balancing selection — Candidate neutral — Candidate positive selection

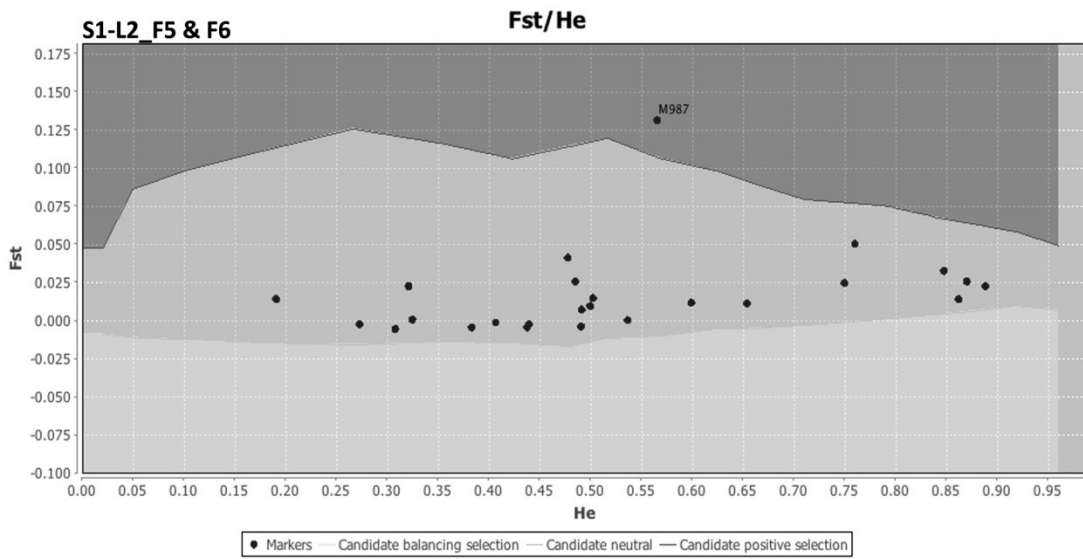
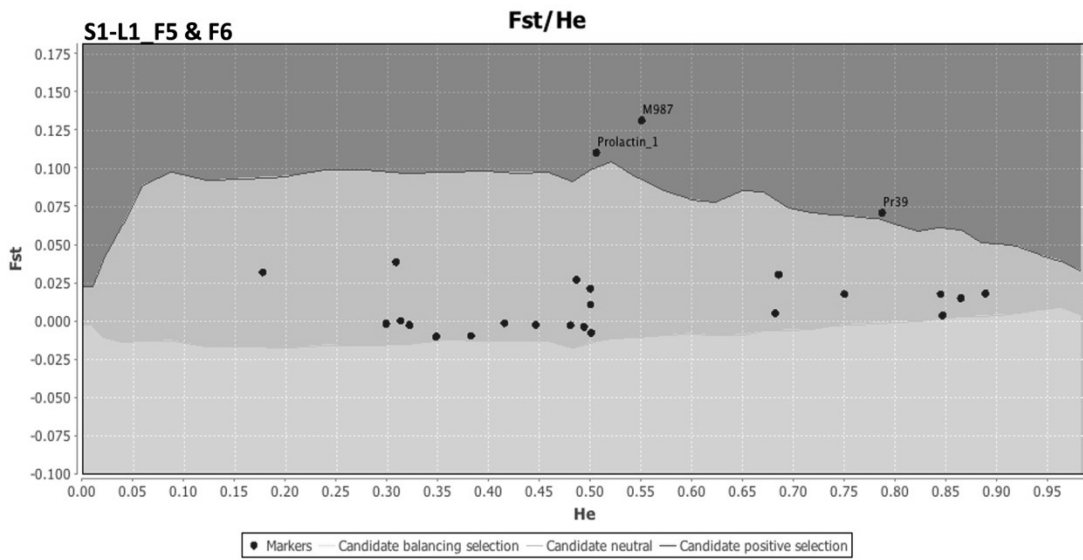
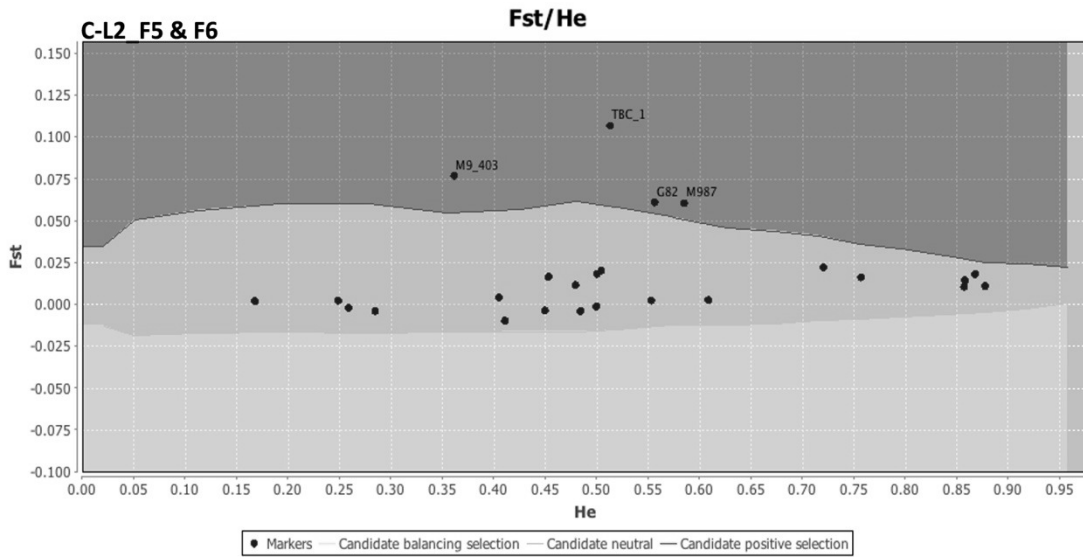


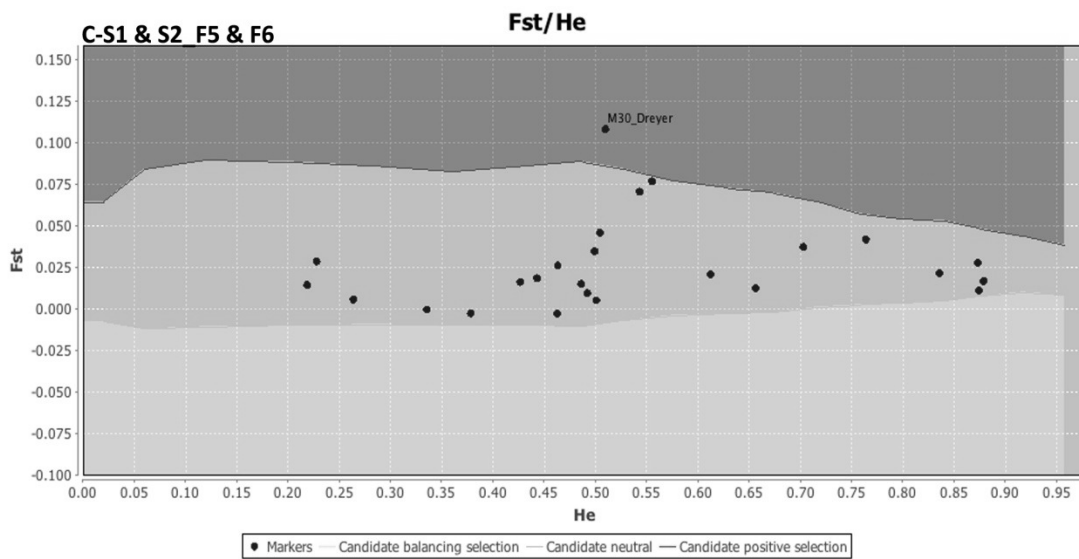
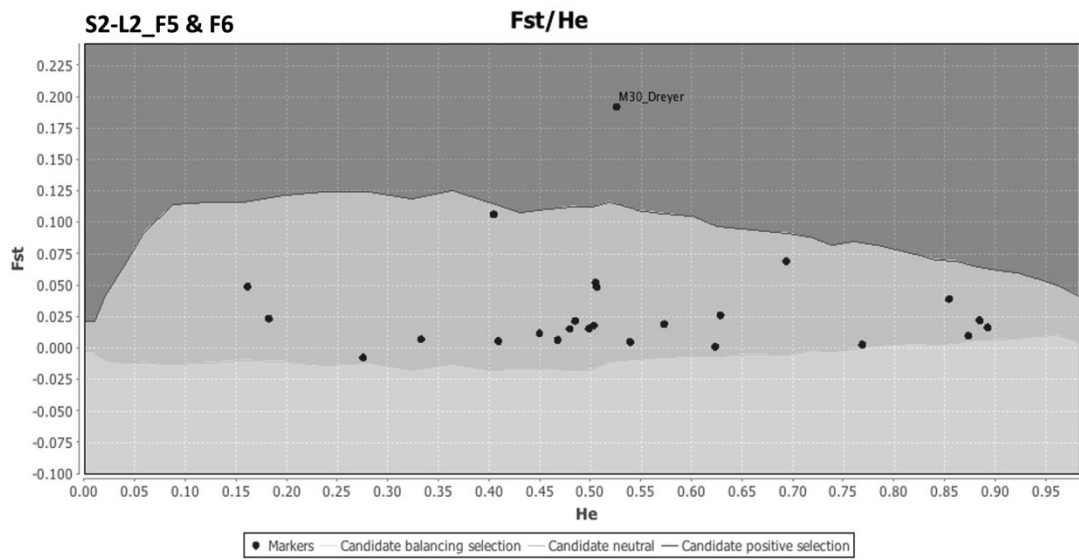
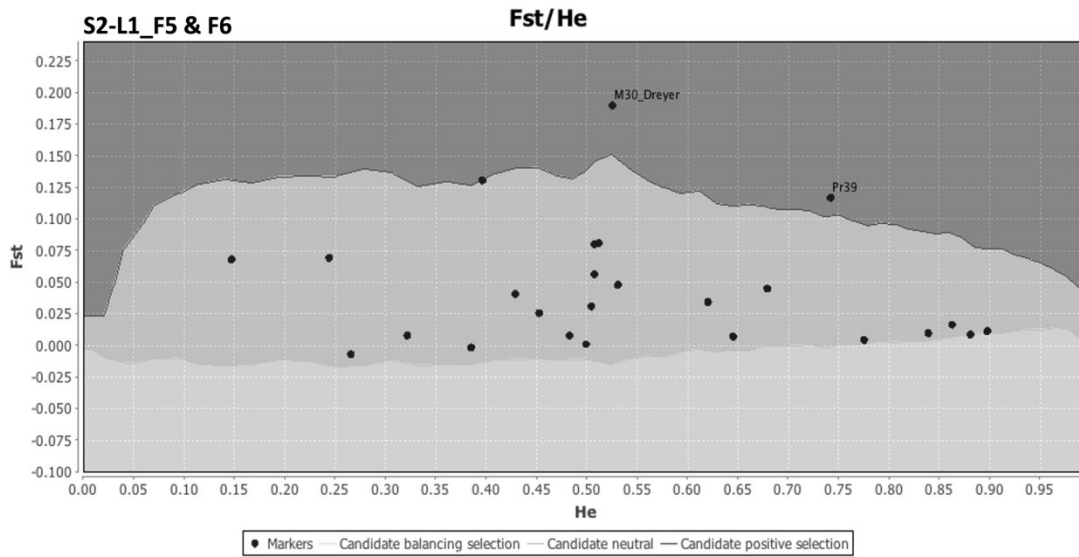
● Markers — Candidate balancing selection — Candidate neutral — Candidate positive selection

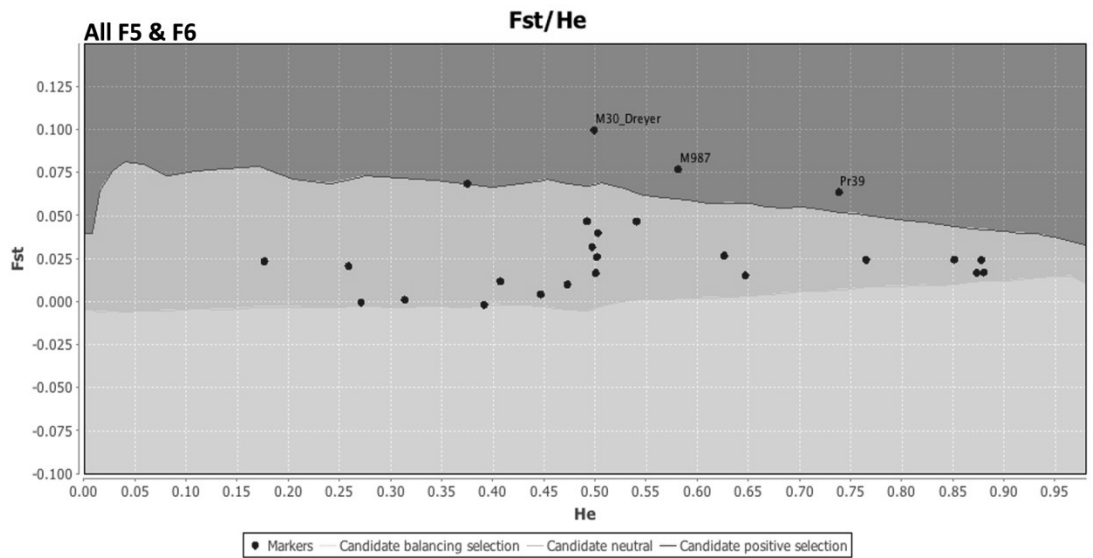
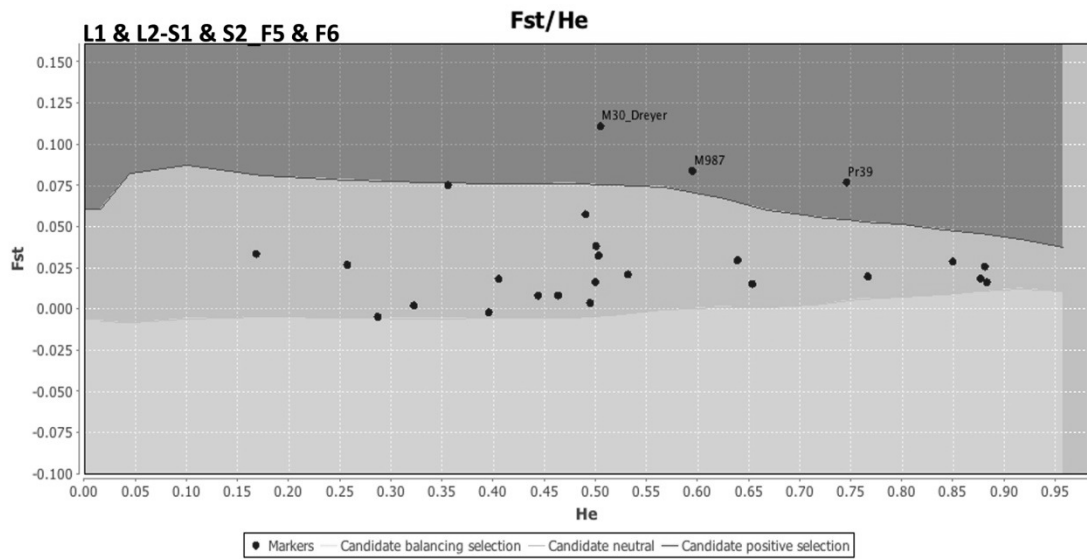
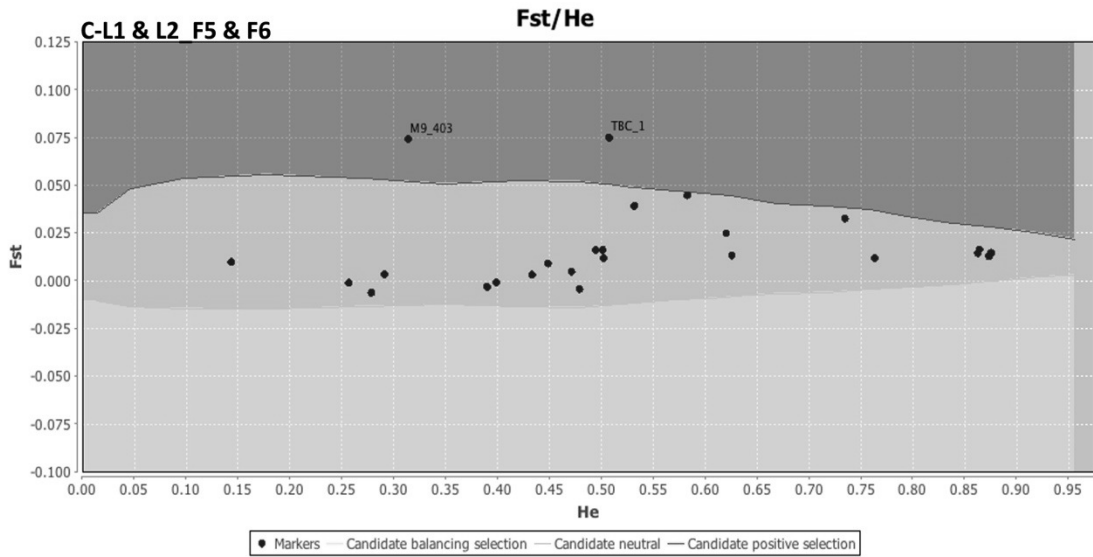












APPENDIX VIII – Raw- and normalised ln(RH) data

- Expected heterozygosity at all microsatellite- and candidate loci for each line in generations F5 and F6. S-lines are shown in light grey, the Control in white and L-lines in dark grey.
- Raw ln(RH) values for each pairwise comparison within each generation. ln(RH) is calculated as the natural logarithm of the ratio of heterozygosity of the population on the left of the pair over the population on the right of the pair: $\ln(H_{e_{\text{left}}} / H_{e_{\text{right}}})$.
- Normalised ln(RH) values so that, per population pair, the mean over all loci is 0 and the standard deviation equals 1.

a.		Pret69	Pret-77	Hull 70-2	G102	Pret-32	G82	Pr92	G289	Pr39	M9_indel	M987
F5	S1	0.791	0.702	0.858	0.632	0.858	0.523	0.709	0.832	0.726	0.260	0.356
	S2	0.832	0.686	0.891	0.590	0.911	0.524	0.763	0.846	0.636	0.306	0.607
	C	0.869	0.620	0.839	0.577	0.818	0.457	0.719	0.838	0.706	0.208	0.557
	L1	0.871	0.594	0.886	0.699	0.835	0.503	0.769	0.850	0.732	0.142	0.590
F6	L2	0.845	0.637	0.841	0.596	0.858	0.558	0.744	0.891	0.709	0.098	0.621
	S1	0.808	0.677	0.851	0.660	0.824	0.519	0.689	0.869	0.751	0.243	0.412
	S2	0.771	0.599	0.878	0.581	0.891	0.520	0.776	0.842	0.535	0.059	0.645
	C	0.833	0.601	0.864	0.554	0.881	0.530	0.732	0.863	0.700	0.213	0.443
F6	L1	0.847	0.682	0.893	0.722	0.855	0.473	0.777	0.853	0.710	0.040	0.547
	L2	0.833	0.567	0.847	0.479	0.849	0.543	0.781	0.878	0.696	0.149	0.565

b.		Pret69	Pret-77	Hull 70-2	G102	Pret-32	G82	Pr92	G289	Pr39	M9_indel	M987
F5	S1-S2	-0.051	0.023	-0.037	0.068	-0.060	-0.002	-0.073	-0.017	0.132	-0.163	-0.534
	L1-L2	0.031	-0.070	0.052	0.160	-0.027	-0.104	0.033	-0.047	0.032	0.371	-0.051
	S1-C	-0.095	0.124	0.023	0.091	0.047	0.135	-0.014	-0.007	0.028	0.223	-0.448
	S2-C	-0.044	0.101	0.060	0.023	0.107	0.137	0.059	0.010	-0.104	0.386	0.086
	L1-C	0.002	-0.043	0.055	0.193	0.020	0.096	0.068	0.015	0.036	-0.382	0.058
	L2-C	-0.028	0.027	0.002	0.032	0.047	0.200	0.034	0.062	0.004	-0.753	0.109
	S1-L1	-0.097	0.168	-0.032	-0.102	0.027	0.039	-0.082	-0.022	-0.008	0.605	-0.505
	S1-L2	-0.067	0.098	0.021	0.059	-0.001	-0.065	-0.049	-0.069	0.024	0.976	-0.556
F6	S2-L1	-0.046	0.145	0.006	-0.170	0.087	0.041	-0.009	-0.005	-0.141	0.768	0.028
	S2-L2	-0.016	0.075	0.058	-0.009	0.060	-0.063	0.024	-0.052	-0.109	1.139	-0.023
	S1-S2	0.047	0.124	-0.031	0.127	-0.078	-0.001	-0.118	0.032	0.339	1.416	-0.448
	L1-L2	0.017	0.185	0.052	0.411	0.007	-0.139	-0.004	-0.029	0.020	-1.315	-0.032
	S1-C	-0.030	0.119	-0.015	0.175	-0.066	-0.020	-0.060	0.007	0.070	0.132	-0.073
	S2-C	-0.077	-0.005	0.016	0.048	0.011	-0.020	0.058	-0.024	-0.269	-1.284	0.376
	L1-C	0.017	0.126	0.033	0.264	-0.030	-0.115	0.059	-0.011	0.014	-1.672	0.211
	L2-C	0.000	-0.058	-0.019	-0.146	-0.037	0.024	0.064	0.018	-0.006	-0.357	0.243
F6	S1-L1	-0.047	-0.007	-0.048	-0.089	-0.036	0.095	-0.120	0.019	0.056	1.804	-0.283
	S1-L2	-0.031	0.177	0.004	0.322	-0.030	-0.044	-0.124	-0.010	0.076	0.489	-0.316
	S2-L1	-0.094	-0.131	-0.017	-0.216	0.041	0.095	-0.002	-0.013	-0.283	0.389	0.165
	S2-L2	-0.077	0.054	0.035	0.195	0.048	-0.043	-0.006	-0.042	-0.263	-0.926	0.132

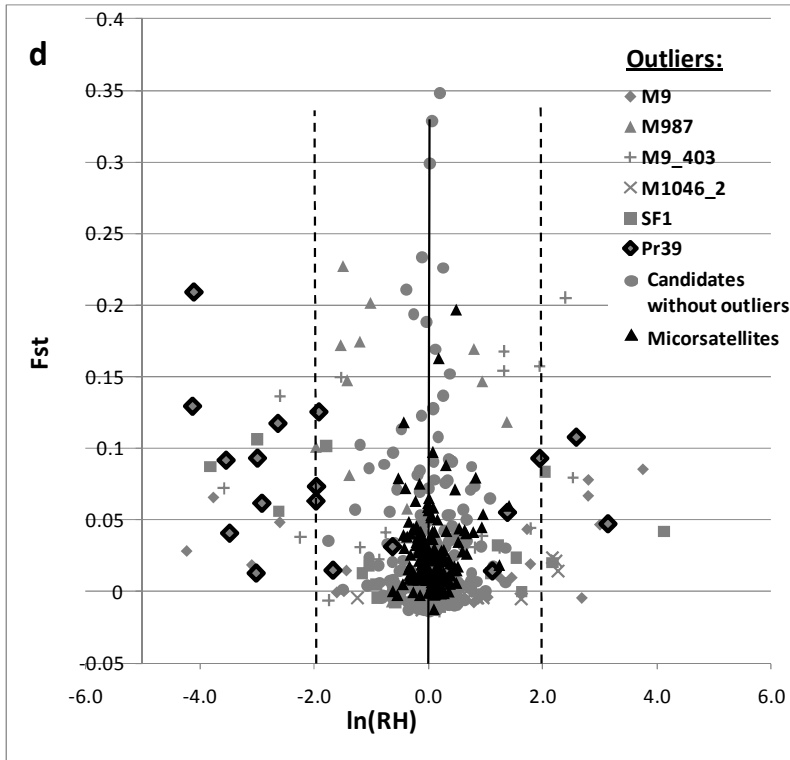
c.		Pret69	Pret-77	Hull 70-2	G102	Pret-32	G82	Pr92	G289	Pr39	M9_indel	M987
F5	S1-S2	-0.216	0.068	-0.164	0.240	-0.253	-0.030	-0.301	-0.085	0.488	-0.646	-2.070
	L1-L2	0.373	-0.311	0.521	1.253	-0.021	-0.540	0.392	-0.154	0.382	2.681	-0.182
	S1-C	-0.627	0.614	0.040	0.424	0.175	0.675	-0.171	-0.128	0.068	1.173	-2.622
	S2-C	-0.181	0.302	0.166	0.041	0.321	0.422	0.160	-0.001	-0.382	1.247	0.250
	L1-C	0.159	-0.053	0.403	1.043	0.241	0.596	0.463	0.218	0.316	-1.626	0.416
	L2-C	-0.088	0.145	0.041	0.167	0.231	0.874	0.176	0.293	0.049	-3.131	0.489
	S1-L1	-0.553	0.458	-0.303	-0.570	-0.080	-0.035	-0.495	-0.265	-0.213	2.124	-2.108
	S1-L2	-0.337	0.277	-0.010	0.132	-0.090	-0.332	-0.270	-0.345	0.001	3.564	-2.170
F6	S2-L1	-0.219	0.253	-0.091	-0.524	0.111	-0.003	-0.127	-0.117	-0.452	1.793	-0.035
	S2-L2	-0.090	0.150	0.107	-0.072	0.111	-0.215	0.017	-0.186	-0.337	2.976	-0.108
	S1-S2	-0.087	0.108	-0.283	0.117	-0.401	-0.207	-0.504	-0.124	0.654	3.379	-1.340
	L1-L2	0.140	0.689	0.257	1.431	0.106	-0.370	0.070	-0.010	0.150	-4.226	-0.022
	S1-C	-0.398	0.447	-0.312	0.767	-0.603	-0.342	-0.568	-0.184	0.172	0.520	-0.637
	S2-C	-0.112	0.114	0.178	0.280	0.163	0.067	0.309	0.052	-0.713	-3.890	1.304
	L1-C	0.180	0.454	0.221	0.802	0.062	-0.151	0.287	0.110	0.173	-4.063	0.667
	L2-C	0.163	-0.166	0.053	-0.658	-0.044	0.295	0.520	0.261	0.130	-1.841	1.525
F6	S1-L1	-0.367	-0.263	-0.370	-0.475	-0.339	0.000	-0.555	-0.197	-0.100	4.422	-0.978
	S1-L2	-0.475	0.519	-0.309	1.209	-0.471	-0.541	-0.923	-0.378	0.034	2.010	-1.840
	S2-L1	-0.341	-0.457	-0.098	-0.727	0.087	0.258	-0.048	-0.086	-0.938	1.186	0.478
	S2-L2	-0.218	0.221	0.159	0.694	0.201	-0.105	0.020	-0.101	-0.843	-3.070	0.485

a. (continued)		M9_403	M1046_Dreyer	M1046_2	M30_Dreyer	GH1	GH2_60	GH2_74	GH2_165	GH2_211	Myostatin	Prolactin1	Prolactin2	TBC_1	SF1
F5	S1	0.386	0.434	0.29	0.507	0.47	0.494	0.356	0.501	0.373	0.391	0.415	0.502	0.492	0.255
	S2	0.477	0.483	0.235	0.422	0.491	0.46	0.402	0.486	0.462	0.333	0.463	0.498	0.506	0.092
	C	0.374	0.459	0.175	0.499	0.503	0.5	0.265	0.478	0.423	0.413	0.486	0.492	0.459	0.318
	L1	0.164	0.356	0.246	0.47	0.46	0.496	0.265	0.482	0.342	0.406	0.505	0.501	0.492	0.343
F6	L2	0.217	0.471	0.302	0.448	0.436	0.504	0.338	0.502	0.393	0.456	0.505	0.489	0.498	0.276
	S1	0.393	0.443	0.357	0.502	0.398	0.5	0.358	0.483	0.345	0.375	0.409	0.503	0.504	0.332
	S2	0.492	0.494	0.285	0.395	0.505	0.472	0.335	0.453	0.495	0.43	0.426	0.5	0.505	0.114
	C	0.485	0.466	0.229	0.398	0.499	0.491	0.295	0.48	0.415	0.336	0.505	0.494	0.422	0.213
L1		0.243	0.429	0.303	0.412	0.457	0.484	0.271	0.458	0.343	0.374	0.471	0.454	0.489	0.358
	L2	0.258	0.407	0.285	0.431	0.453	0.476	0.243	0.481	0.424	0.407	0.502	0.489	0.453	0.229

b. (continued)		M9_403	M1046_Dreyer	M1046_2	M30_Dreyer	GH1	GH2_60	GH2_74	GH2_165	GH2_211	Myostatin	Prolactin1	Prolactin2	TBC_1	SF1
F5	S1-S2	-0.212	-0.107	0.210	0.184	-0.044	0.071	-0.122	0.030	-0.214	0.161	-0.109	0.008	-0.028	1.019
	L1-L2	-0.280	-0.280	-0.205	0.048	0.054	-0.016	-0.243	-0.041	-0.139	-0.116	0.000	0.024	-0.012	0.217
	S1-C	0.032	-0.056	0.505	0.016	-0.068	-0.012	0.295	0.047	-0.126	-0.055	-0.158	0.020	0.069	-0.221
	S2-C	0.243	0.051	0.295	-0.168	-0.024	-0.083	0.417	0.017	0.088	-0.215	-0.048	0.012	0.097	-1.240
	L1-C	-0.824	-0.254	0.341	-0.060	-0.089	-0.008	0.000	0.008	-0.213	-0.017	0.038	0.018	0.069	0.076
	L2-C	-0.544	0.026	0.546	-0.108	-0.143	0.008	0.243	0.049	-0.074	0.099	0.038	-0.006	0.082	-0.142
	S1-L1	0.856	0.198	0.165	0.076	0.022	-0.004	0.295	0.039	0.087	-0.038	-0.196	0.002	0.000	-0.296
	S1-L2	0.576	-0.082	-0.041	0.124	0.075	-0.020	0.052	-0.002	-0.052	-0.154	-0.196	0.026	-0.012	-0.079
F6	S2-L1	1.068	0.305	-0.046	-0.108	0.065	-0.075	0.417	0.008	0.301	-0.198	-0.087	-0.006	0.028	-1.316
	S2-L2	0.788	0.025	-0.251	-0.060	0.119	-0.091	0.173	-0.032	0.162	-0.314	-0.087	0.018	0.016	-1.099
	S1-S2	-0.225	-0.109	0.225	0.240	-0.238	0.058	0.066	0.064	-0.361	-0.137	-0.041	0.006	-0.002	1.069
	L1-L2	-0.060	0.053	0.061	-0.045	0.009	0.017	0.109	-0.049	-0.212	-0.085	-0.064	-0.074	0.076	0.447
	S1-C	-0.210	-0.051	0.444	0.232	-0.226	0.018	0.194	0.006	-0.185	0.110	-0.211	0.018	0.178	0.444
	S2-C	0.014	0.058	0.219	-0.008	0.012	-0.039	0.127	-0.058	0.176	0.247	-0.170	0.012	0.180	-0.625
	L1-C	-0.691	-0.083	0.280	0.035	-0.088	-0.014	-0.085	-0.047	-0.191	0.107	-0.070	-0.084	0.147	0.519
	L2-C	-0.631	-0.135	0.219	0.080	-0.097	-0.031	-0.194	0.002	0.021	0.192	-0.006	-0.010	0.071	0.072
S1-L1		0.481	0.032	0.164	0.198	-0.138	0.033	0.278	0.053	0.006	0.003	-0.141	0.102	0.030	-0.075
	S1-L2	0.421	0.085	0.225	0.152	-0.129	0.049	0.387	0.004	-0.206	-0.082	-0.205	0.028	0.107	0.371
	S2-L1	0.705	0.141	-0.061	-0.042	0.100	-0.025	0.212	-0.011	0.367	0.140	-0.100	0.097	0.032	-1.144
	S2-L2	0.646	0.194	0.000	-0.087	0.109	-0.008	0.321	-0.060	0.155	0.055	-0.164	0.022	0.109	-0.698

c. (continued)		M9_403	M1046_Dreyer	M1046_2	M30_Dreyer	GH1	GH2_60	GH2_74	GH2_165	GH2_211	Myostatin	Prolactin1	Prolactin2	TBC_1	SF1
F5	S1-S2	-0.834	-0.431	0.787	0.684	-0.188	0.253	-0.487	0.096	-0.842	0.596	-0.441	0.010	-0.128	3.895
	L1-L2	-1.734	-1.734	-1.226	0.491	0.529	0.057	-1.485	-0.110	-0.778	-0.623	0.165	0.330	0.083	1.640
	S1-C	0.089	-0.407	2.768	0.000	-0.474	-0.158	1.580	0.176	-0.801	-0.399	-0.983	0.024	0.303	-1.339
	S2-C	0.773	0.134	0.944	-0.591	-0.115	-0.312	1.349	0.020	0.258	-0.750	-0.196	0.005	0.289	-4.152
	L1-C	-3.683	-1.033	1.731	-0.130	-0.267	0.111	0.148	0.187	-0.840	0.069	0.326	0.232	0.471	0.500
	L2-C	-2.256	0.140	2.325	-0.422	-0.569	0.065	1.054	0.237	-0.278	0.448	0.193	0.006	0.374	-0.564
	S1-L1	3.081	0.573	0.445	0.107	-0.100	-0.197	0.943	-0.035	0.149	-0.326	-0.930	-0.174	-0.182	-1.312
	S1-L2	2.068	-0.394	-0.239	0.375	0.193	-0.163	0.107	-0.095	-0.283	-0.663	-0.822	0.011	-0.133	-0.384
F6	S2-L1	2.535	0.649	-0.218	-0.371	0.056	-0.291	0.925	-0.084	0.639	-0.595	-0.320	-0.120	-0.035	-3.358
	S2-L2	2.044	0.019	-0.714	-0.207	0.268	-0.291	0.413	-0.134	0.382	-0.883	-0.279	0.001	-0.006	-2.966
	S1-S2	-0.774	-0.481	0.365	0.402	-0.808	-0.059	-0.037	-0.043	-1.119	-0.552	-0.308	-0.190	-0.210	2.501
	L1-L2	-0.112	0.257	0.285	-0.063	0.113	0.139	0.442	-0.076	-0.610	-0.193	-0.124	-0.159	0.335	1.549
	S1-C	-1.417	-0.513	2.288	1.088	-1.507	-0.124	0.870	-0.191	-1.272	0.395	-1.420	-0.124	0.779	2.287
	S2-C	0.173	0.311	0.813	0.105	0.166	0.005	0.526	-0.053	0.680	0.900	-0.404	0.166	0.690	-1.829
	L1-C	-1.598	-0.070	0.841	0.224	-0.083	0.101	-0.076	0.020	-0.341	0.407	-0.038	-0.075	0.508	1.442
	L2-C	-3.376	-0.597	1.388	0.608	-0.380	-0.012	-0.925	0.174	0.282	1.236	0.129	0.105	0.559	0.568
S1-L1		0.999	-0.162	0.179	0.266	-0.602	-0.161	0.475	-0.107	-0.230	-0.238	-0.610	0.020	-0.167	-0.440
	S1-L2	1.683	0.076	0.748	0.400	-0.948	-0.094	1.524	-0.310	-1.316	-0.721	-1.309	-0.194	0.181	1.447
	S2-L1	2.187	0.403	-0.237	-0.177	0.272	-0.123	0.627	-0.078	1.117	0.398	-0.361	0.262	0.058	-3.662
	S2-L2	2.208	0.691	0.041	-0.252	0.405	0.012	1.119	-0.161	0.560	0.225	-0.511	0.115	0.405	-2.302

- d. Plot of normalised $\ln(RH)$ values with Pr39 and M987 included as bi-allelic loci. The plot shows that, when only the presence/ absence of allele 174 at Pr39 is considered, the analysis does identify this locus as an outlier.



Pr39		
F5	S1-S2	-0.6266
F6	S1-S2	2.5919
F5	L1-L2	0.2535
F6	L1-L2	0.2785
F5	S1-C	-3.0141
F6	S1-C	-1.9677
F5	S2-C	-1.6694
F6	S2-C	-3.4803
F5	L1-C	1.3859
F6	L1-C	1.9510
F5	L2-C	1.1207
F6	L2-C	3.1453
F5	S1-L1	-2.9910
F6	S1-L1	-2.6341
F5	S1-L2	-2.9145
F6	S1-L2	-3.5415
F5	S2-L1	-1.9167
F6	S2-L1	-4.1038
F5	S2-L2	-1.9578
F6	S2-L2	-4.1268

APPENDIX IX – Association analyses models of inheritance

Models of inheritance for all candidate markers showing a significant association between standard length and genotype in at least one of the four test groups: 1) over the F0, F2, all populations in the F5 and the F6 combined, 2), within the F5, 3) within the F6 and 4) over all of the Control line populations (F0, F2, F5_C and F6_C). Shown are sample size (n), mean response associated with the respective genotype (R), standard error of the mean and the difference between the genotypes in mm. For significant associations, furthermore are shown the 95% confidence intervals of the difference and the *p*-values associated with the test. The test value is shown in bold and the *p*-value after Benjamini-Hochberg correction is shown below each *p*-value. AIC in the final column stands for the Akaike Information Criterion. The AIC is useful to decide on the most likely model of inheritance, which should be supported by the lowest AIC. The most likely model of inheritance for each test is shown in grey.

F0, F2, All F5, All F6

<u>M9_indel</u>	Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	no insert	498	19.72	0.09	0.00			
	insert/ no insert	133	19.11	0.18	-0.62	(-1.01 - -0.23)	0.0071	2720.4
	2 copies							
	insert	4	20.3	0.56	0.57		0.0196	

All F5

<u>M9_indel</u>	Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	no insert	146	20.32	0.23	0.00			
	insert/ no insert	44	18.54	0.41	-1.78	(-2.69 - -0.86)	0.0002	923.8
	2 copies							
	insert	---					0.0012	

All F6

<u>M9_indel</u>	Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	no insert	207	19.21	0.11	0.00			
	insert/ no insert	37	19.05	0.25	-0.16		n.s.	
	2 copies							
	insert	---						

Control only

<u>M9_indel</u>	Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	no insert	213	19.72	0.11	0.00			
	insert/ no insert	73	19.51	0.19	-0.21		n.s.	
	2 copies							
	insert	4	20.3	0.56	0.58			

F0, F2, All F5, All F6

<u>SF1</u>	Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Overdominant	a/a-t/t	466	19.52	0.1	0.00		n.s.	
	a/t	168	19.86	0.16	0.34			

All F5

<u>SF1</u>	Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Overdominant	a/a-t/t	137	19.58	0.24	0.00		0.0092	918.1
	a/t	50	20.79	0.37	1.21	(0.31 - 2.12)	0.0339	

All F6

<u>SF1</u>	Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Overdominant	a/a-t/t	178	19.21	0.11	0.00		n.s.	
	a/t	64	19.17	0.22	-0.04			

Control only

<u>SF1</u>	Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Overdominant	a/a-t/t	214	19.67	0.11	0.00		n.s.	
	a/t	78	19.71	0.17	0.04			

F0, F2, All F5, All F6

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	334	19.83	0.12	0.00	(-0.71 - -0.03)	0.0032	2677.1
	241	19.46	0.13	-0.04	(-1.55 - -0.34)	0.0109	
	51	18.89	0.22	-0.94			
Dominant	334	19.83	0.12	0.00	(-0.79 - -0.15)	0.0042	2678.4
	292	19.36	0.11	-0.47		0.0132	
Recessive	575	19.68	0.09	0.00	(-1.37 - -0.20)	0.0088	2679.8
	51	18.89	0.22	-0.79		0.0213	
Overdominant	385	19.71	0.11			n.s.	
	241	19.46	0.13				
Log additive	---	---	---	-0.43	(-0.68 - -0.18)	0.0008	2675.4
	---	---	---			0.0036	

All F5

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	117	20.54	0.26	0.00	(-2.31 - -0.58)	0.0006	914.7
	56	19.09	0.34	-1.45	(-3.55 - -0.63)	0.0029	
	15	18.45	0.55	-2.09			
Dominant	117	20.54	0.26	0.00	(-2.38 - -0.78)	0.0001	913.4
	71	18.95	0.29	-1.58		0.0006	
Recessive	173	20.07	0.22	0.00	(-3.09 - -0.15)	0.0320	923.3
	15	18.45	0.55	-1.62		n.s.	
Overdominant	132	20.3	0.25	0.00	(-2.08 - -0.35)	0.0067	920.5
	56	19.09	0.34	-1.21		0.0271	
Log additive	---	---	---	-1.20	(-1.81 - -0.60)	0.0001	913.3
	---	---	---			0.0006	

Control only

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	126	19.39	0.14	0.00		n.s.	
	96	19.01	0.16	-0.38			
	20	18.91	0.21	-0.48			
Dominant	126	19.39	0.14	0.00		n.s.	
	116	18.99	0.14	-0.39			
Recessive	222	19.22	0.11	0.00		n.s.	
	20	18.91	0.21	-0.32			
Overdominant	146	19.32	0.13	0.00		n.s.	
	96	19.01	0.16	-0.31			
Log additive	---	---	---	-0.30		n.s.	

All F6

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	130	19.57	0.13	0.00			
	128	19.89	0.14	0.32		0.032	
	27	19.08	0.27	-0.49	(-1.14 - 0.16)	n.s.	
Dominant	130	19.57	0.13	0.00		n.s.	
	155	19.75	0.13	0.18			
Recessive	258	19.73	0.1	0.00	(-1.27 - -0.03)	0.041	1069.4
	27	19.08	0.27	-0.65		n.s.	
Overdominant	157	19.49	0.12	0.00	(0.04 - 0.77)	0.031	1068.8
	128	19.89	0.14	0.41		n.s.	
Log additive	---	---	---	-0.03		n.s.	

FO, F2, All F5, All F6

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	c/c	271	19.88	0.13	0.00		
	c/t	299	19.37	0.11	-0.52	(-0.85 - -0.18)	0.0094
	t/t	56	19.44	0.3	-0.45		0.0216
Dominant	c/c	271	19.88	0.13	0.00		2675.3
	c/c-t/t	355	19.38	0.11	-0.50	(-0.83 - -0.18)	0.0023
Overdominant	c/c-t/t	327	19.81	0.12	0.00		2677.5
	c/t	299	19.37	0.11	-0.44	(-0.76 - -0.12)	0.0076
Log additive	---	---	---	-0.34	(-0.59 - -0.09)	0.0080	2677.6

All F5

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	c/c	82	20.15	0.32	0.00		
	c/t	83	19.6	0.29	-0.55		n.s.
	t/t	19	19.86	0.72	-0.29		
Dominant	c/c	82	20.15	0.32	0.00		n.s.
	c/c-t/t	102	19.65	0.27	-0.50		
Overdominant	c/c-t/t	101	20.1	0.29	0.00		n.s.
	c/t	83	19.6	0.29	-0.50		
Log additive	---	---	---	-0.29		n.s.	

All F6

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	c/c	100	19.3	0.15	0.00		
	c/t	118	118	0.15	-0.13		n.s
	t/t	24	24	0.34	-0.54		
Dominant	c/c	100	100	0.15	0.00		n.s
	c/c-t/t	142	142	0.14	-0.20		
Overdominant	c/c-t/t	124	124	0.14	0.00		n.s
	c/t	118	118	0.15	-0.03		
Log additive	---	---	---	-0.22		n.s	

Control only

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	c/c	126	20.03	0.14	0.00		
	c/t	141	19.41	0.14	-0.62	(-1.00 - -0.24)	0.0065
	t/t	22	19.64	0.29	-0.38		0.03934
Dominant	c/c	126	20.03	0.14	0.00		1086.9
	c/c-t/t	163	19.44	0.13	-0.59	(-0.95 - -0.22)	0.02314
Overdominant	c/c-t/t	148	19.97	0.12	0.00		1087.6
	c/t	141	19.41	0.14	-0.56	(-0.92 - -0.20)	0.0243
Log additive	---	---	---	-0.39	(-0.68 - -0.09)	0.0110	1090

F0, F2, All F5, All F6

GH2_60

Model	n		R	St. err.	Difference	95% CI	p-value	AIC
	n	R						
Codominant	g/g	151	20.14	0.15	0.00			
	g/a	333	19.54	0.11	-0.60	(-0.99 - -0.21)	0.0004	2669.1
	a/a	142	19.22	0.17	-0.92	(-1.39 - -0.46)	0.0021	
Dominant	g/g	151	20.14	0.15	0.00		0.0003	2669.7
	g/a-a/a	475	19.45	0.1	-0.70	(-1.07 - -0.32)	0.0017	
Recessive	g/g-g/a	484	19.73	0.09	0.00		0.0090	2676.1
	a/a	142	19.22	0.17	-0.51	(-0.89 - -0.13)	0.0213	
Log additive	---	---	---	---	-0.46	(-0.70 - -0.23)	0.0001	2667.8
							0.0007	

All F5

GH2_60

Model	n		R	St. err.	Difference	95% CI	p-value	AIC
	n	R						
Codominant	g/g	29	21.19	0.52	0.00			
	g/a	110	19.75	0.26	-1.44		0.0290	895.5
	a/a	44	19.58	0.41	-1.61	(-2.90 - -0.32)	n.s.	
Dominant	g/g	29	21.19	0.52	0.00		0.0083	893.7
	g/a-a/a	154	19.7	0.22	-1.49	(-2.58 - -0.39)	0.0320	
Recessive	g/g-g/a	139	20.05	0.24	0.00		n.s.	
	a/a	44	19.58	0.41	-0.47		0.0280	895.8
Log additive	---	---	---	---	-0.73	(0.09 - 1.37)	n.s.	

All F6

GH2_60

Model	n		R	St. err.	Difference	95% CI	p-value	AIC
	n	R						
Codominant	g/g	64	19.54	0.18	0.00			
	g/a	119	19.11	0.15	-0.43		n.s.	
	a/a	59	19	0.21	-0.54			
Dominant	g/g	64	19.54	0.18	0.00		0.043	906.7
	g/a-a/a	178	19.07	0.12	-0.46	(-0.91 - -0.02)	n.s.	
Recessive	g/g-g/a	183	19.26	0.11	0.00		n.s.	
	a/a	59	19	0.21	-0.26			
Log additive	---	---	---	---	-0.27		n.s.	

Control only

GH2_60

Model	n		R	St. err.	Difference	95% CI	p-value	AIC
	n	R						
Codominant	g/g	71	20.14	0.18	0.00			
	g/a	155	19.61	0.12	-0.53	(-0.98 - -0.09)	0.015	1094.3
	a/a	63	19.38	0.23	-0.76	(-1.30 - -0.22)	n.s.	
Dominant	g/g	71	20.14	0.18	0.00		0.0062	1093.3
	g/a-a/a	218	19.54	0.11	-0.60	(-1.03 - -0.17)	0.03934	
Recessive	g/g-g/a	226	19.77	0.1	0.00		n.s.	
	a/a	63	19.38	0.23	-0.40			
Log additive	---	---	---	---	-0.39	(-0.66 - -0.12)	0.0053	1093
							0.0390	

F0, F2, All F5, All F6

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
t/t	192	19.88	0.15	0.00			
Codominant t/c	309	19.81	0.12	-0.07		<0.0001	2681.6
c/c	129	18.76	0.15	-1.12	(-1.58 - -0.67)	0.0008	
t/t	192	19.88	0.15	0.00		0.0340	2704
Dominant t/c-c/c	438	19.5	0.1	-0.37	(-0.73 - -0.03)	n.s.	
t/t-t/c	501	19.84	0.09	0.00		<0.0001	2679.8
c/c	129	18.76	0.15	-1.08	(-1.47 - -0.69)	0.0008	
Overdominant t/t-c/c	321	19.43	0.11	0.00		0.0200	2703.1
t/c	309	19.81	0.12	0.38	(0.06 - 0.71)	0.0405	
Log additive ---	---	---	---	-0.51	(-0.74 - -0.29)	<0.0001	2688.8
						0.0008	

All F5

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
t/t	48	20.95	0.41	0.00			
Codominant t/c	100	20.24	0.27	-0.72		<0.0001	894.4
c/c	39	17.89	0.33	-3.07	(-4.17 - -1.96)	0.0001	
t/t	48	20.95	0.41	0.00		0.0033	914.1
Dominant t/c-c/c	139	19.58	0.23	-1.38	(-2.28 - -0.47)	0.0141	
t/t-t/c	148	20.47	0.23	0.00		<0.0001	894.8
c/c	39	17.89	0.33	-2.58	(-3.51 - -1.66)	0.0001	
Overdominant t/t-c/c	87	19.58	0.31	0.00		n.s.	
t/c	100	20.24	0.27	0.66		<0.0001	896.9
Log additive ---	---	---	---	-1.49	(-2.04 - -0.93)	0.0001	

All F6

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
t/t	86	19.28	0.17	0.00			
Codominant t/c	109	19.35	0.17	0.07		0.028	902.9
c/c	46	18.64	0.16	-0.65	(-1.20 - -0.09)	n.s.	
t/t	86	19.28	0.17	0.00		n.s.	
Dominant t/c-c/c	155	19.14	0.13	-0.14			
t/t-t/c	195	19.32	0.12	0.00		0.0079	901
c/c	46	18.64	0.16	-0.68	(-1.18 - -0.18)	n.s.	
Overdominant t/t-c/c	132	19.06	0.13	0.00		n.s.	
t/c	109	19.35	0.17	0.29			
Log additive ---	---	---	---	-0.27		n.s.	

Control only

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
t/t	93	19.57	0.17	0.00			
Codominant t/c	146	19.83	0.14	0.26		n.s.	
c/c	52	19.55	0.18	-0.02			
t/t	93	19.57	0.17	0.00		n.s.	
Dominant t/c-c/c	198	19.75	0.11	0.18			
t/t-t/c	239	19.73	0.11	0.00		n.s.	
c/c	52	19.55	0.18	-0.18			
Overdominant t/t-c/c	145	19.56	0.13	0.00		n.s.	
t/c	146	19.83	0.14	0.26			
Log additive ---	---	---	---	0.03		n.s.	

FO, F2, All F5, All F6

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
a/a	367	19.43	0.11	0.00			
Codominant	195	19.86	0.15	0.43	(0.07 - 0.79)	0.0170	2683.6
c/c	64	20.02	0.24	0.59	(0.05 - 1.14)	0.0361	
Dominant	367	19.43	0.11	0.00		0.0049	2681.9
c/a-c/c	259	19.9	0.13	0.17	(0.14 - 0.80)	0.0149	
Log additive	---	---	---	0.34	(0.10 - 0.58)	0.0053	2682.1
						0.0155	

All F5

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
a/a	102	19.56	0.27	0.00			
Codominant	67	20.24	0.36	0.68		n.s.	
c/c	19	20.85	0.63	1.30			
Dominant	102	19.56	0.27	0.00		0.0470	924.8
c/a-c/c	86	20.38	0.31	0.82	(0.02 - 1.62)	n.s.	
Log additive	---	---	---	0.66	(0.06 - 1.26)	0.0310	924
						n.s.	

Myostatin

All F6

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
a/a	140	19.04	0.14	0.00			
Codominant	77	19.45	0.18	0.41		n.s.	
c/c	24	19.29	0.27	0.25			
Dominant	140	19.04	0.14	0.00		n.s.	
c/a-c/c	101	19.41	0.15	0.37			
Log additive	---	---	---	0.22		n.s.	

Control only

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
a/a	178	19.63	0.12	0.00			
Codominant	80	19.77	0.17	0.14		n.s.	
c/c	28	20.04	0.25	0.42			
Dominant	178	19.63	0.12	0.00		n.s.	
c/a-c/c	108	19.84	0.14	0.21			
Log additive	---	---	---	0.19		n.s.	

Myostatin

FO, F2, All F5, All F6

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
g/g	229	19.26	0.13	0.00			
codominant	296	19.66	0.12	0.40	(0.05 - 0.76)	0.0003	2711.8
a/a	109	20.22	0.2	0.96	(0.50 - 1.43)	0.0017	
Dominant	229	19.26	0.13	0.00		0.0012	2715.8
g/a-a/a	405	19.81	0.1	0.55	(0.22 - 0.89)	0.0049	
g/g-g/a	525	19.48	0.09	0.00		0.0007	2714.8
a/a	109	20.22	0.2	0.74	(0.31 - 1.16)	0.0033	
Log additive	---	---	---	0.47	(0.24 - 0.69)	0.0001	2710
						0.0007	

All F5

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
g/g	61	19.25	0.34	0.00			
codominant	100	19.87	0.28	0.61		0.0009	916.7
a/a	27	21.65	0.48	2.40	(1.16 - 3.64)	0.0041	
Dominant	61	19.25	0.34	0.00		0.0240	923.7
g/a-a/a	127	20.25	0.25	0.99	(0.14 - 1.85)	n.s.	
g/g-g/a	161	19.64	0.22	0.00		0.0005	916.7
a/a	27	21.65	0.48	2.01	(0.90 - 3.13)	0.0025	
Log additive	---	---	---	1.07	(0.48 - 1.66)	0.0005	916.7
						0.0025	

Prolactin1

All F6

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
g/g	90	18.93	0.17	0.00			
codominant	97	19.3	0.15	0.37		n.s.	
a/a	56	19.41	0.21	0.47			
Dominant	90	18.93	0.17	0.00		0.048	9111.1
g/a-a/a	153	19.34	0.12	0.41	(0.01 - 0.82)	n.s.	
g/g-g/a	187	19.12	0.11	0.00		n.s.	
a/a	56	19.41	0.21	0.29			
Log additive	---	---	---	0.25		n.s.	

Control only

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
g/g	101	19.68	0.16	0.00			
codominant	146	19.63	0.13	-0.06		n.s.	
a/a	43	19.88	0.26	0.20			
Dominant	101	19.68	0.16	0.00		n.s.	
g/a-a/a	189	19.69	0.12	0.00			
g/g-g/a	247	19.65	0.1	0.00		n.s.	
a/a	43	19.88	0.26	0.23			
Log additive	---	---	---	0.07		n.s.	

Prolactin1

F0, F2, All F5, All F6
Prolactin2

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	185	20.05	0.16	0.00	(-0.89 - -0.13)	0.0021	2687.6
	280	19.54	0.12	-0.51	(-1.18 - -0.32)	0.0078	
Dominant	185	20.05	0.16	0.00	(-0.95 - -0.24)	0.0010	2687
	442	19.45	0.1	-0.60		0.0043	2692.4
Recessive	465	19.74	0.1	0.00	(-0.81 - -0.08)	0.0190	
	162	19.3	0.16	-0.44		0.0394	
Overdominant	347	19.7	0.11	0.00		n.s.	
	280	19.54	0.12	-0.16		0.0006	2686.2
Log additive	---	---	---	-0.38	(-0.60 - -0.16)	0.0030	

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	48	20.37	0.43	0.00		n.s.	
	85	20.08	0.31	-0.29			
Dominant	52	19.4	0.37	-0.97		n.s.	
	48	20.37	0.43	0.00			
Recessive	137	19.82	0.24	-0.55			
	133	20.18	0.25	0.00		n.s.	
Overdominant	52	19.4	0.37	-0.78			
	100	19.87	0.28	0.00		n.s.	
Log additive	85	20.08	0.31	0.21		n.s.	
	---	---	---	-0.49			

Control only
Prolactin2

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	84	19.36	0.17	0.00		n.s.	
	99	19.18	0.15	-0.19			
Dominant	56	18.97	0.24	-0.40		n.s.	
	84	19.36	0.17	0.00			
Recessive	155	19.1	0.13	-0.26		n.s.	
	183	19.26	0.11	0.00			
Overdominant	56	18.97	0.24	-0.30		n.s.	
	140	19.2	0.14	0.00			
Log additive	99	19.18	0.15	-0.03		n.s.	
	---	---	---	-0.20			

All F6
Prolactin2

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	75	19.55	0.18	0.00		< 0.0001	1077.5
	137	19.39	0.12	-0.17	(0.33 - 1.33)	0.00041	
Dominant	76	20.38	0.2	0.83		< 0.0001	1076
	76	20.38	0.2	0.00	(-1.35 - -0.53)	0.00041	
Recessive	212	19.45	0.1	-0.94		n.s.	
	213	19.74	0.11	0.00			
Overdominant	75	19.55	0.18	-0.19		0.002	1086.1
	151	19.97	0.14	0.00	(-0.95 - -0.22)	0.02314	
Log additive	137	19.39	0.12	-0.58	(-0.67 - -0.16)	0.0013	1085.4
	---	---	---	-0.42		0.0231	

F0, F2, All F5, All F6
IBC.1

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	g/g	165	19.72	0.16	0.00		
	t/g	317	19.74	0.12	0.02	0.0480	2714.9
	t/t	151	19.26	0.15	-0.46	(-0.91 - -0.01)	n.s.
Dominant	g/g	165	19.72	0.16	0.00	n.s.	
	t/g-t/t	468	19.58	0.1	-0.13		
Recessive	g/g-t/g	482	19.73	0.1	0.00	0.0140	2712.9
	t/t	151	19.26	0.15	-0.47	(-0.85 - -0.10)	0.0305
Overdominant	g/g-t/t	316	19.5	0.11	0.00	n.s.	
	t/g	317	19.74	0.12	0.24		
Log additive	---	---	---	---	-0.22	n.s.	

All F6
IBC.1

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	g/g	67	19.73	0.16	0.00		
	t/g	110	19.1	0.15	-0.63	(-1.10 - -0.16)	0.0016
	t/t	66	18.78	0.2	-0.94	(-1.47 - -0.42)	0.0154
Dominant	g/g	67	19.73	0.16	0.00	0.0008	903.6
	t/g-t/t	176	18.98	0.12	-0.75	(-1.18 - -0.32)	0.0088
Recessive	g/g-t/g	177	19.34	0.12	0.00	0.015	908.9
	t/t	66	18.78	0.2	-0.55	(-0.99 - -0.11)	n.s.
Overdominant	g/g-t/t	133	19.26	0.13	0.00	n.s.	
	t/g	110	19.1	0.15	-0.16		
Log additive	---	---	---	---	-0.47	0.0005	902.6
					(-0.73 - -0.21)	0.0064	

All F5
IBC.1

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	g/g	45	19.83	0.46	0.00		
	t/g	102	20.18	0.28	0.35	n.s.	
	t/t	40	19.53	0.38	-0.31		
Dominant	g/g	45	19.83	0.46	0.00	n.s.	
	t/g-t/t	142	20	0.23	0.17		
Recessive	g/g-t/g	147	20.08	0.23	0.00	n.s.	
	t/t	40	19.53	0.38	-0.55		
Overdominant	g/g-t/t	85	19.69	0.3	0.00	n.s.	
	t/g	102	20.18	0.28	0.50		
Log additive	---	---	---	---	-0.14	n.s.	

Control only
IBC.1

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	t/t	87	19.33	0.16	0.00		
	t/g	141	19.97	0.14	0.64	(0.21 - 1.06)	0.011
	g/g	63	19.56	0.2	0.23	n.s.	1099.5
Dominant	g/g	63	19.56	0.2	0.00	n.s.	
	t/g-t/t	228	19.72	0.11	0.17		
Recessive	g/g-t/g	204	19.84	0.11	0.00	0.013	1100.4
	t/t	87	19.33	0.16	-0.51	(-0.91 - -0.11)	n.s.
Overdominant	g/g-t/t	150	19.42	0.12	0.00	0.0039	1098.2
	t/g	141	19.97	0.14	0.54	(0.18 - 0.91)	0.03159
Log additive	---	---	---	---	-0.15	n.s.	

F0, F2, All F5, All F6

Pr39

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
x/x	422	19.12	0.09	0.00			
Codominant	215	20.56	0.1	1.44	(1.12 - 1.76)	<0.0001	2673.7
174/174	2	19.27	3.13	0.15		0.0001	
Dominant	422	19.12	0.09	0.00		<0.0001	
174/x-	217	20.55	0.15	1.43	(1.11 - 1.75)	0.0001	2672.5
174/174						<0.0001	2675.4
Log additive	---	---	---	1.38	(1.06 - 1.70)	0.0001	

All F5

Pr39

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
x/x	100	18.64	0.24	0.00			
Codominant	88	21.36	0.27	2.72	(2.01 - 3.43)	<0.0001	889.9
174/174	2	19.27	3.13	0.63		0.0001	
Dominant	100	18.64	0.24	0.00		<0.0001	889.3
174/x-	90	21.31	0.27	2.67	(1.96 - 3.38)	0.0001	
174/174						<0.0001	894.6
Log additive	---	---	---	2.43	(1.75 - 3.12)	0.0001	

All F6

Pr39

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
x/x	146	18.63	0.1	0.00			
Codominant	98	20.01	0.17	1.39	(1.02 - 1.75)	<0.0001	867
174/174	---					0.000154	
Dominant							
Log additive	---						

Control only

Pr39

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
x/x	236	19.6	0.1	0.00			
Codominant	58	20.03	0.24	0.43		0.069	1113.2
174/174	---					n.s.	
Dominant							
Log additive	---						

F0, F2, All F5, All F6
M98Z

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	258 317	18.91 20.04	0.11 0.12	0.00 1.13	(0.80 - 1.45) (0.82 - 1.94)	<0.0001 0.0001	2677.5
Dominant	258 376	18.91 20.08	0.11 0.11	0.00 1.17	(0.85 - 1.48)	<0.0001 0.0001	2676.3
Recessive	575 59	19.53 20.29	0.09 0.25	0.00 0.76	(0.21 - 1.31)	0.0074 0.0196	2719.7
Overdominant	317 317	19.17 20.04	0.11 0.12	0.00 0.87	(0.55 - 1.19) (0.61 - 1.11)	<0.0001 0.0001	2698.2 2681.3
Log additive	---	---	---	0.86		0.0001	

All F5
M98Z

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	64 112	18.38 20.67	0.29 0.26	0.00 2.29	(1.49 - 3.10) (0.89 - 3.91)	<0.0001 0.0001	908.8
Dominant	64 126	18.38 20.69	0.29 0.24	0.00 2.31	(1.52 - 3.09)	<0.0001 0.0001	906.8
Recessive	176 14	19.84 20.78	0.21 0.69	0.00 0.94		n.s.	
Overdominant	78 112	18.81 20.67	0.28 0.26	0.00 1.86	(1.09 - 2.63) (1.06 - 2.34)	<0.0001 0.0001	916.5 912.5
Log additive	---	---	---	1.70		0.0001	

All F6
M98Z

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	81 140	18.38 19.6	0.14 0.13	0.00 1.23	(0.82 - 1.63) (0.43 - 1.79)	<0.0001 0.000154	885.2
Dominant	81 163	18.38 19.59	0.14 0.12	0.00 1.21	(0.82 - 1.60)	<0.0001 0.000154	883.3
Recessive	221 23	19.15 19.49	0.1 0.35	0.00 0.33		n.s.	
Overdominant	104 140	18.62 19.6	0.14 0.13	0.00 0.98	(0.50 - 1.36) (0.49 - 1.11)	<0.0001 0.000154	893.3 893
Log additive	---	---	---	0.80		0.0002	

Control only
M98Z

Model	n	R	St. err.	Difference	95% CI	p-value	AIC
Codominant	153 109	19.44 19.8	0.12 0.16	0.00 0.36		0.0019 0.02314	1088.9
Dominant	153 136	19.44 19.95	0.12 0.14	0.00 0.51	(0.14 - 0.88)	0.0068 0.03934	1092.1
Recessive	262 27	19.59 20.57	0.1 0.29	0.00 0.99	(0.36 - 1.61)	0.0023 0.02329	1090.1
Overdominant	180 109	19.61 19.8	0.12 0.16	0.00 0.19		n.s.	
Log additive	---	---	---	0.49	(0.21 - 0.76)	0.0006 0.0162	1087.8