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Comparison of lines or strains differentially susceptible to diseases is a powerful tool to identify the genetic elements that regulate resistance to a disease and the key defence mechanisms and pathways. In fish, the production of individuals with extreme phenotypes may be accelerated using chromosome manipulation techniques. Doubled-haploid homozygous clones which present many interesting features for genetic and immunological studies can be produced after two successive generations of gynogenesis. We used nine of those clones and the control (original population) in a study of the resistance to two rhabdoviruses, VHSV (Viral Haemorrhagic Scepticemia Virus) and IHNV (Infectious Hematopoietic Necrosis Virus). Water route infection and intraperitoneal injection were tested. For VHSV, survival after waterborne challenge was 17% in control and ranged from 0 to almost 100% among clones. Resistant clones remained resistant when challenged in cohabitation with susceptible ones, an encouraging result in view of 'on field' applications. For IHNV (five clones only and control tested), survival after waterborne challenge increased with age/weight and significantly depended on clones. Correlation between resistance to both diseases was borderline significant (Spearman coefficient 0.77, $P=0.07$). For both viruses, injection provoked complete mortality whatever the group. Implications of the results in terms of mechanisms of resistance will be discussed. Extreme clones will provide key support for further genetic (search for QTL and candidate genes) and immunopathological (specific candidate molecules or gene expression profiling) studies aiming at the identification of the immune pathways and genetic factors regulating susceptibility to the viruses.

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Effect of selection for muscle lipid content on body shape, fat deposition and dressing yields in rainbow trout

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A two-way selection for muscle lipid content was performed on pan-size fish using a non-destructive measure of muscle lipid content in live fish (Distell Fish Fatmeter®). The present study aimed at characterising direct and indirect responses after three generations of selection at the size where selection was applied as well as in larger individuals. Six experimental progeny were produced. Breeders of each selected line (lean, L and fat, F) were mated according to a factorial design to produce 4 diploid groups: lean (LL2), fat (FF2) and two reciprocal hybrids (LF2 and FL2). Triploids (LL3 and FF3) were also produced to obtain large sterile fish. Each group was reared in 3 replicated tanks, examined at 12 months (pan-size; all groups) and 19 months old (2 kg, triploids only). Main results demonstrated that there was no indirect effect of selection on growth performance, irrespective of the age. Body shape however was modified, FF fish being more rotund with a smaller relative head length. Muscle lipid content varied in a wide range according to the line, hybrids exhibiting intermediate values ($LL<(FL=LF)<FF$). There was no effect of triploidy on this trait. Increase in muscle lipid content was associated with an increase of subcutaneous fat deposition but a decrease in visceral fat content. Values of the majority of traits were intermediate in hybrids. In large fish, carcass and fillet yields were better in FF fish. Effects of muscle lipid content on flesh quality traits are presented in a separate abstract (Lefevre et al.).

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Genetic characterization of natural populations of the European anchovy (*Engraulis encrasicolus*) through RFLPs of mtDNA

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The European anchovy *Engraulis encrasicolus* is a species distributed in the Mediterranean and Eastern Atlantic coasts, from Norway to Angola. It is a target population of commercial fishing and for that reason it has been put under on fishing. In spite of the social and economic importance of this species few studies of genetic characterization exist of the same one, mainly of the south Mediterranean and north Atlantic zone. The study of the variation of the mitocondrial DNA (mtDNA) for this species was made with samples of 6 natural populations: Punta Umbira, Barbate and Almeria (Spain) and Larache, Tangier and Nador (Morocco). The polymorphisms in the length of fragments of restriction (RFLPs) of the NADH dehydrogenase (gene ND) complex were analyzed by using the polymerase chain reaction (PCR) with universal primers. The obtained product of PCR has a size of 2.5 kb coding for genes ND5 and ND6. The restriction enzymes used (*Cfo*I, *Hin*fI, *Sau*96I and *Taq*I) revealed until 30 composite haplotypes in only 100 fish, whereas other authors found 53 composite haplotypes using 6 endonucleasas for 140 fish of the Mediterranean whole number. The geographic location of the studied populations and the hydrology of the Straits of Gibraltar influencing the distribution of larvae of the species could explain the high obtained genetic variability.

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A genetic linkage map for Atlantic halibut (*Hippoglossus hippoglossus*)

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We report the construction of a moderate density genetic linkage map for Atlantic halibut (*Hippoglossus hippoglossus*) that was generated using two maternal half-sib families ($n=90$). To date, more than 250 microsatellite loci have been placed on the map. These markers have been derived from several sources: ~125 were from an Atlantic halibut genomic library enriched for (GT)n sequences, ~75 were derived from microsatellites in Genbank sequences from other pleuronectid species and >50 were identified in halibut EST sequences. The latter group has allowed us to begin to locate specific genes on the map. In addition, more than 350 AFLP markers, generated from 64 combinations of primers, have been mapped. The map consists of 23 linkage groups, in close agreement with the 24 chromosomes in this species. As expected, the rate of recombination is slightly higher (1.2:1) in the heterogametic females. Approximate centromere locations are currently being estimated for each linkage group by genotyping selected microsatellites in gynogenetic offspring and determining their recombination frequency. Morphometric data were collected for each experimental family to potentially identify quantitative trait loci (QTL) associated with pigmentation, body size (length, width, weight) and metamorphosis (eye migration, myotome height). Our plans for QTL discovery will also be presented. A genetic map and the identification of markers associated with traits of economic importance will allow the Atlantic halibut industry to make significant production gains through marker assisted selection and broodstock enhancement.

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Design and evaluation of the use of MAS with selective breeding of abalone

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A computer simulation model has been used to optimise the use of marker assisted selection (MAS) in a selective breeding program for the Australian abalone industry. The simulation model utilised genetic data collected from industry brood stock regarding marker-QTL linkage phase, size of QTL effect and estimated QTL-marker positions for several marker loci known to have an effect on growth rate (refer to Baranski et al., this symposium). Simulations accounted for the possibility of early induction of reproductive condition and generation of families, and reduced recombination rates with the production of male gametes. Preliminary simulations suggested that MAS could improve rates