Early maturation (EM) is of increasing concern in rainbow trout (*Oncorhynchus mykiss*) aquaculture as it may result in the production of smaller individuals with decreased flesh quality. This represents a significant economic loss to the industry. Maturation timing is a complex trait with a partial genetic component that could be modified via a marker assisted selection (MAS) programme. To identify quantitative trait loci (QTL) influencing maturation timing, we performed a genome scan using approximately 90 microsatellite loci in six inter-strain families. The six paternal half-sib families used in this study were created by crossing each of three full-sib sires to two dams, where the sires are hybrids derived from a normal maturing strain and one that is prone to EM, and the two dams are from EM and hybrid strains, respectively. Overall, QTL with significant effects on early maturation across multiple parents was detected on RT-7, RT-8, RT-9, RT-24 and RT-6 and 30. Interestingly some of these linkage groups contain candidate genes for maturation and growth traits. In addition, sex-specific interval mapping will be used to identify QTL for body weight (BW) and condition factor (*K*) as both of these traits have been associated with EM in previous studies.

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Detecting natural selection on MHC loci in farmed rainbow trout

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We will use the pattern of genetic variation at three loci, together encoding the entire peptide binding domains of the major histocompatibility complex molecules in rainbow trout, to test that balancing selection is operating on these loci. The MHC molecules are key components of the adaptive immune system, displaying pathogen-derived peptides on cell surfaces, where they initiate an immune response. Across a broad range of taxa, an extraordinary degree of polymorphism is concentrated at positions that determine which foreign peptides are bound by the MHC molecules, therefore the link between genetic and functional variability seems straightforward. In spite of this expectation, few studies demonstrate unequivocally a connection between MHC variation and disease resistance. The exact mechanisms maintaining the unprecedented genetic variation at MHC loci are strongly debated, and proposed mechanisms include disassortative mating, maternal–fetal interaction and pathogen driven selection. Farmed rainbow trout provide an ideal model for addressing these questions for two reasons: A) in contrast to the complicated architecture in mammals, the MHC of salmonid fishes consists of one major locus for MHCI and two closely coupled loci for MHCII, providing the simplest possible model of an MHC system with classical function. B) During the last 120 years, farmed trout in Denmark have been propagated by gathering and mixing eggs and milt, thus effectively eliminating prezygotic sexual selection. This allows us to separate effects of pathogen driven selection from sexual selection, and provides a tool in the search for selection markers enabling us to breed for pathogen resistant trout.

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A genetic linkage map of amago salmon (*Oncorhynchus masou ishikawae*) and mapping of quantitative trait loci associated with smoltification

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Amago salmon (*Oncorhynchus masou ishikawae*) is a Japanese native species in salmonids. We constructed a genetic linkage map using over one hundred microsatellite markers, and identified significant quantitative trait loci (QTL) associated with smoltification in Amago salmon. We searched for linkage among 110 microsatellite markers used to construct the male genetic linkage map in backcross family (F_1; sire) of amago salmon, produced by crossing high-smoltification (C3) and low-smoltification (G4) strains and alleles in the sire. QTL markers on linkage group AM-3 and on linkage group AM-21 were mapped by detecting an association between smoltification. Among three QTL markers on linkage group AM-3, no recombination was observed. Recombination rates

in male salmonids are repressed relative to females in centromeric regions of the chromosome. Block segregation of large chromosomal regions is thus common in male salmonids for most of the intertelomeric regions of a linkage group. Therefore in other backcross family (F1; dam), we searched for linkage among QTL markers on linkage group AM-3 to analyzed marker–trait associations in detail. We found closely linked QTL associated with smoltification on linkage group AM-3, which is corresponding to RT-19 linkage group in rainbow trout.

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Potential trade-offs in resistance of chinook salmon (*Oncorhynchus tshawytscha*) to two bacterial pathogens resulting from selection of broodstock based on antigen level

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We evaluate genetic variation in the ability of chinook salmon to resist two bacterial pathogens: *Renibacterium salmoninarum*, the agent of bacterial kidney disease (BKD), and *Listonella anguillarum*, an agent of vibriosis. After measuring levels of *R. salmoninarum* antigen in 415 male and 84 female adults, we mated each of 12 males with high and 12 males with low antigen levels to two females with low to moderate antigen levels. We then exposed their progeny to each pathogen in independent challenges. Family variation in mortality indicated the potential for rapid evolution of resistance to BKD but not vibriosis. A negative genetic correlation between resistances to the two pathogens indicated that broodstock selection based on antigen levels could alter susceptibilities to both pathogens. The relationship between survival in the BKD challenge and antigen loads in survivors was weak, providing no evidence that antigen load is linked to resistance. The results underscore the complexity of resistance of salmonids to bacterial pathogens and cast some doubt over the efficacy of culling hatchery broodstock, based on adult antigen levels, to reduce the likelihood of disease. The results also raise concern about the long-term consequences of such practices for resistance to different pathogens.

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Mapping heterosis QTL in the Pacific oyster *Crassostrea gigas*

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Aquacultural production of the Pacific oyster (*Crassostrea gigas*) was 4.4 mmt in 2003, worth just over US $3.7B. This bivalve mollusc shows remarkable heterosis (hybrid vigour) for yield, which underlies most crop improvement. Efforts to utilize heterosis to improve yield of farmed oysters through crossbreeding are underway on the U.S. west coast, but we are also interested in determining the underlying mechanisms of the phenomenon. We report QTL-mapping results on the number, location, and mode of action of genes affecting yield in an F2 family derived from a naturalized *C. gigas* population in Dabob Bay (WA). We reared 500 tagged individuals at low density and measured live weight monthly from June to October 2003. The phenotypic data were thus monthly live weight, absolute growth and higher order parameters of the logistic growth curve. We typed 188 individuals for 59 microsatellite DNA markers which mapped to 11 linkage groups. We detected five QTL peaks ($p<0.05$) on four chromosomes for weight, three of which appeared dominant/partially dominant (IV-1, VIII-1) and two of which were highly overdominant (IV-2). We could not confirm dominance or additivity of two other peaks because identity-by-descent was uncertain (IX-1, VII-1), although one appeared dominant and the other overdominant. Absolute dominant/additive (d/a) QTL effect ratios indicated dominance for initial weight (mean $d/a=0.98\pm0.0084$) but became strongly overdominant at final weight (mean $d/a=2.10\pm1.09$), suggesting an ontogenetic mixture of over and underdominance underlying heterotic effects. A QTL for the growth curve inflection point was coincident with one for