

Genetic and physical mapping of the Atlantic salmon (*Salmo salar*) genome with emphasis on MHC genes and microsatellites.

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INTRODUCTION

As a part of our program: "Gene mapping in Farm Animals and Fish", we have isolated and characterized Mhc class I and class II genes together with DNA microsatellite markers. Considerable polymorphism has been revealed in both systems and this will be utilized in our genome mapping effort. The material consisted of fish derived from the major Norwegian breeding pool, together with haploid offspring generated by haploid gynogenesis (Lie et al. 1994). The haploid material is very suitable for a variety of purposes, e.g. linkage analysis, defining alleles/haplotypes, developmental studies, identification of potential lethal genes etc. Physical mapping techniques (e.g. PFGE) are also in progress.

TEXT

We have isolated MHC class I and class II cDNAs from Atlantic salmon (Grimholt et al. 1993, Hordvik et al. 1993). Studies on variation in a material consisting of ten individuals revealed a considerable number of both MHC-Sasa class I $\alpha 2$ and MHC-Sasa class II $\beta 1$ domain exon variants. The number of variants per individual ranged from 1-5 for class I and 1-4 for class II. The polymorphic patterns were similar to those of higher vertebrates in respect of location of polymorphic residues and degree of replacement mutations (Grimholt et al. 1994). An investigation of the MHC class I $\alpha 2$ domain exon in two haploid and one diploid pedigrees indicated intra-exon recombination as a possible mechanism by which Atlantic salmon generates new alleles in the offspring at considerable frequencies. This would enable the use of already approved variable segments in a variety of combinations.

By screening a size selected genomic salmon library enriched for microsatellites, we have isolated and sequenced more than 70 (GT)_n containing clones (Slettan et al. 1993). The distribution of number of repeat units in these GT-microsatellites differ significantly from that of higher vertebrates. Atlantic salmon displayed a higher frequency of long and short repeat stretches (more than 21 and less than 12 repeats respectively), in addition to showing a lower frequency of intermediate length repeats, compared with those in man, swine and mouse. Flanking PCR primers have been designed for a selected array of the microsatellites. The number of alleles and the degree of heterozygosity have been revealed in a panel of unrelated fish. All the markers displayed a high polymorphic information content. Linkage studies are in progress using haploid offspring generated by haploid gynogenesis on a set of unrelated dams and tentative linkage groups have been established. The salmonide anc-

estor underwent a likely genome duplication event between 25 and 100 million years ago. The salmonid genomes are still under diploidization, and are thus partly tetraploid with still a restricted number of loci displaying tetrasomic inheritance. Our haploid fish material and microsatellites may in addition to speed up the genetic map development, facilitate the identification of different alleles/haplotypes and contribute to new insight into the genome evolution of vertebrates.

Physical mapping is so far concentrated to the region of MHC. Preliminary results from restriction fragment mapping and PFGE indicate 5 MHC class I loci, spanning a region of approximately 1 Mb. A cosmid library is under construction. Genes known to be linked to the MHC region in higher vertebrates, for instance the TNF, TAP and MHC class II alpha genes, are currently being isolated from Atlantic salmon.

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