Application of genomics to selective breeding for disease resistance (Houston, R).

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Host resistance to infectious diseases in aquaculture species has a genetic and an environmental component. The genetic component (heritability) can be exploited in long-term breeding programmes to produce more resistant and resilient stock. This has been partially achieved for a number of diseases via family-based selection; typically involving data collected from large-scale disease challenges or field outbreaks on the relatives of the selection candidates. However, the study and application of disease resistance in Atlantic salmon has been transformed by genomics tools. Genome-wide genetic marker data can now be rapidly generated in the candidates and their disease-challenged relatives. These data can enable genetic-marker-based selective breeding methods, including marker-assisted selection (MAS) for resistant alleles at specific loci, or genomic selection (GS) utilising all loci simultaneously. Marker-based selective breeding has the twin advantages of capturing within-family genetic variation and enabling identification of the more resistant selection candidates even in the absence of disease challenge data. To generate the large-scale marker data for studying disease resistance in salmon, we have applied genotyping by sequencing techniques (e.g. RAD Sequencing) and developed a high density Atlantic salmon single-nucleotide polymorphism (SNP) array. When combined with the amenable family structure in commercial salmon populations (typically hundreds of large full and half-sibling families), this high marker density enables powerful studies of the genetic basis of simple and complex disease traits. While we find that host resistance is consistently and often highly heritable, the underlying genetic architecture of this resistance varies substantially. Some examples will be presented, including the nearly-monogenic inheritance of Infectious Pancreatic Necrosis (IPN) virus resistance, the polygenic inheritance of sea lice (*Lepeophtheirus salmonis*) resistance, and the intermediate nature of resistance to Salmonid Alphavirus (the causative agent for Pancreas Disease). This genetic architecture impacts on the strategy for application of results within breeding programs, i.e. use of MAS or GS. In summary, genetic improvement in resistance to a range of pathogens and parasites can now be readily achieved via the application of genetic markers in salmon breeding programmes.