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## Gene expression profiling of natural resistance to coccidiosis in chicken lines

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## SNP BASED ASSOCIATION MAPPING OF DISEASE RESISTANCE TO VHS VIRUS IN RAINBOW TROUT

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We combine SNP-based association mapping with a genomic scan of differences in gene expression on rainbow trout challenged with highly pathogenic VHS virus. With this dual approach we aim to identify QTLs involved in the ability to survive virus challenge, and key immunological processing underlying this ability. Association mapping offers many advantages over traditional QTL-methods by sampling more of the standing genetic variation in the population, and improving the chance of finding QTLs relevant outside the specific experimental lines used in traditional mapping. However, this approach depends of the availability of existing map data for the markers, since the data are not suitable for recombination mapping. Working with a species for which a published genome map is not yet available, the first challenge of the project has been to assemble a sufficient panel of SNPs with map data across the genome.

## GENE EXPRESSION PROFILING OF NATURAL RESISTANCE TO COCCIDIOSIS IN CHICKEN LINES

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Coccidiosis is a parasitic disease with major economic impact, whose main causative agent is *Eimeria tenella*. Chicken breeds display variable natural resistance to this disease. Unraveling the genetic bases of such variations could provide new clues for protection strategies. Transcriptomic experiments were conducted on chicken 20K oligo microarrays, comparing resistant (Fayoumi) and susceptible (Leghorn) lines. Caecum (infection site) and caecal tonsils (lymphoid organ associated to caecum) were analysed. For each tissue, an «infected» (resp. control) Fayoumi v/s Leghorn comparison series was performed on 5 pairs of infected (resp. uninfected) individuals at d 6 post-infection. In caecal tonsils, the «infected» (resp. control) comparison displayed 61 differentially expressed genes (resp. 113), including 17 overlapping genes, whereas in the caecum, 1473 differentially expressed genes (resp. 174) were found, including 42 overlapping genes. Thus these tissues exhibit strikingly different responses. Forty (resp. 20) genes were common (resp. specific) to both tissue «infected» comparisons. Among the specific genes, 9 belonged to the 100 more differentially expressed genes of the «infected» caecum comparison. Four of these were found in a significant gene expression network (20% local FDR). Some of them belong to signaling and leucocyte migration pathways, and noteworthily, one is located in a coccidiosis-associated lesion QTL region. Two other genes from the 40 above mentioned but present in a control experiment, were found in an even more stringent gene network (10% local FDR). These first transcriptomic insights of genetic resistance to *E. tenella* in Chicken advocates genetic improvement as a protection strategy.