# QTL detection and estimation of the epistasis extent for chicken production and resistance to disease traits

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**Recently, approaches targeting the whole genome (genome wide selection, GWS) have expanded. However, using an additive model without possible interaction (epistasis) between loci, in particular between the few QTLs which explain a large part of the genetic variance of the traits, would be likely to reduce the efficiency of this strategy. In chicken, coccidiosis susceptibility is an economically important trait which could make the most of GWS. Therefore, we proposed to search for QTLs affecting coccidiosis susceptibility, to test if the selection of this trait could have an impact on production traits and to estimate the extent of the epistasis for all these traits. Our final aim is to implement these results for GWS in commercial lines.**

## Materials and Methods

- **Biological material**

| | Coccidiosis and growth | | Growth, body composition and meat quality | |
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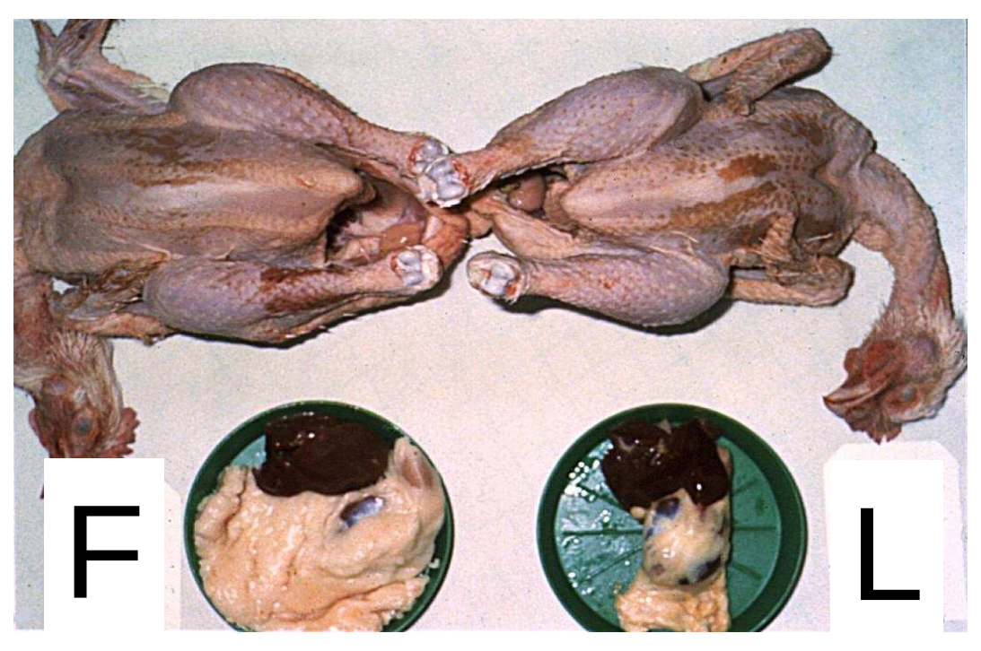
| • Experimental lines: | **6 F1 families**<br>**860 F2 animals** |  | **5 F1 + 5 backcross families**<br>**1200 animals** |  |
| • Commercial lines: | **20 sires**<br>**560 animals** |  | **10 sires**<br>**1000 animals** | |

- **Genotyping**

All experimental lines were previously genotyped for about 120 microsatellites. The experimental lines sires were genotyped using a first set of 9216 SNP covering all the available genome sequence to estimate the informativity of the markers. The 1536 SNP used to genotype the experimental lines animals were selected based on their genomic location and informativity using MarkerSet, a homemade software. Finally, the commercial lines will be genotyped by 384 SNP located in previously detected QTL regions.

- **QTL analyses**

• **Additive model**: For the QTL analyses under the additivity hypothesis we are using QTLMAP which offer the possibility to perform multi-QTL and multi-traits analyses. Another particularity of this software is the possibility to analyse discrete traits, such as lesions values in our dataset.

• **Epistasis model**: Detecting interacting QTL is challenging for two reasons: the computation time necessary for testing all the possible interactions and the genetic model used for the detection itself. Especially, one of the most challenging part of the project is to develop a model for outbreed crosses.

## Results and Outlooks

- **Genotyping**

The 1536 selected SNP were heterozygous for 50% of the sires. In the progeny, the heterozygozity is decreased to 35% probably as the dams were not genotyped to optimize the selection. The commercial lines still have to be genotyped.

- **QTL analyses**

• **Additive model**: The QTL analyses with SNP are undergoing but the results previously obtained with microsatellites revealed 11 QTL affecting body composition, 9 QTL affecting meat quality and 21 QTL affecting Coccidiosis susceptibility. For the SNP analyses, QTLMAP have been extended for computation of the parent haplotypes and transmission probabilities to be able to handle large set of markers.

• **Epistasis model**: The genetic model used in QTLMAP will be extended for epistasis analyses and will allow analyses of outbreed crosses. Reducing the computing time being a large part of the challenge, several algorithms will be tested and compared and eventually integrated in QTLMAP.

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