Genetical genomics for technological meat quality in chicken: targeted approach on a QTL affecting breast meat pH

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Background:

- Meat pH is one of the most important indicators of chicken meat technological quality whose variations can lead to changes in meat colour and meat drip loss (Figure 1).

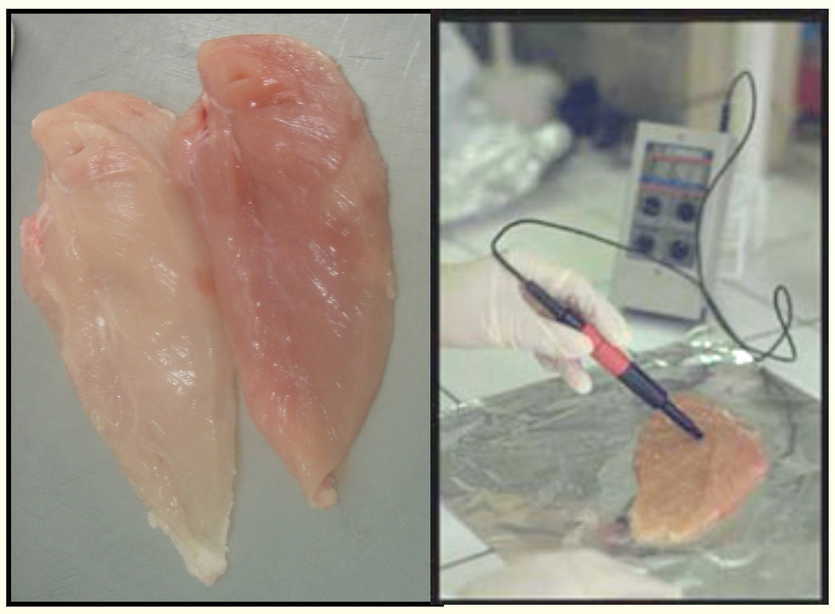

Figure 1. Two breast fillets differing in pH

- Low initial pH in early post-mortem, when the muscle temperature is still high, can lead to a higher drip loss in meat and the occurrence of a condition similar to PSE meat in pigs.
- The biological mechanisms and genes involved in the problem in chicken and its similarities and differences with the problem in pigs is one of the most controversial issues in literature.
- First QTL controlling the trait in chicken were identified in 2007.

  Here the aim is to better characterise the region and to identify the genes and pathways underlying one of the identified QTL, using targeted genetical genomics approach.

Approaches, Results and Perspectives:

- The QTL identified in an F2 population from a cross between 2 divergent lines for body weight (chicks pictured on the top of the poster) was chosen for this study.
- The QTL is located on chromosome 1; 11 new microsatellite markers (a total of 28 markers on the chromosome) were developed and animals (n=698) were genotyped for the new markers.
- The QTL was qualified as genome-wide significant (Figure 2a) and it was found that the effect of QTL was more important in females than in males (about a two-fold difference).
- Breast muscle samples of 32 female birds (16 from each genotype with a contrast of about 1.4 phenotypic SD) were selected for a microarray experiment (Figure 2b).
- Gene expression of the two genotypes (2*16) were compared on 16 Agilent arrays (60-mer oligonucleotide 44K microarray) in a dye-balanced design.
- The microarray experiment was recentlycompleted and the data are being analysed to find the genes and pathways involved (Figures 2e and 2d).

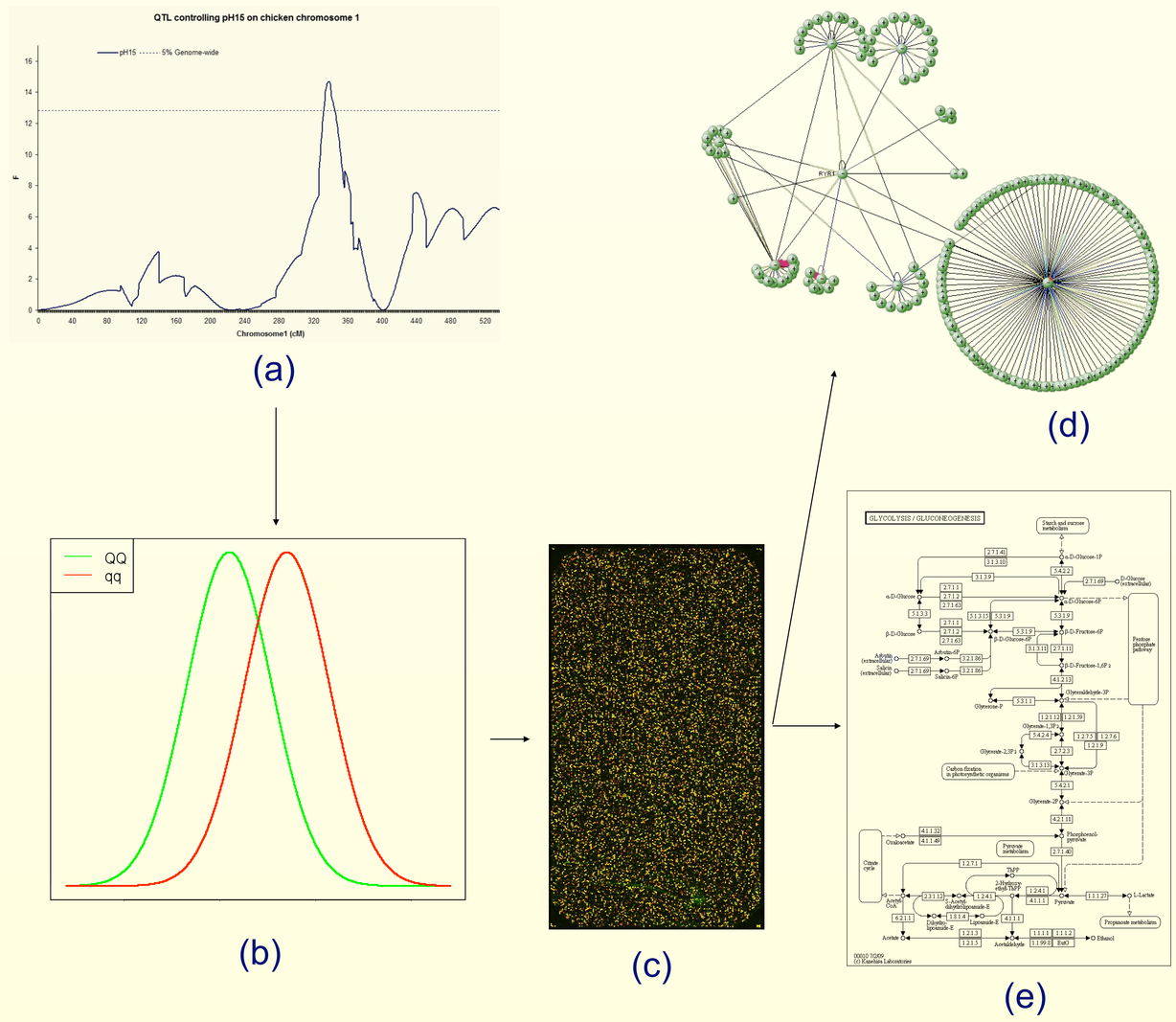

Figure 2. It represents different steps (sub-figures a to e) carried out in the present study:
a) Identification of the QTL;
b) selection of the 2 groups of F2 chickens (QQ or qq) differing in the phenotype;
c) Hybridization of RNA muscle samples;
The two next sub-figures are just examples of pathways, and gene by gene interactions potentially involved in the problem:
d) interaction of RYR1 gene; e) Glycolysis pathway

Acknowledgments

This work was conducted as part of the SABRETRAIN Project, funded by the Marie Curie Host Fellowships for Early Stage Research Training, as part of the 6th Framework Programme of the European Commission. This Publication represents the views of the authors, not the European Commission.