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## Transcriptome profiling reveals interaction between two QTL for fatness in chicken

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In the "genetical genomics" field, different approaches are proposed to improve characterization of QTL regions for various traits combining QTL detection and transcriptome profiling. The most common approach is to identify genes whose eQTL colocalize with QTL of interest, providing new functional hypothesis about the QTL causative mutation. A second approach used only by Schadt et al (2003) and our laboratory (Le Mignon et al (2009)) consists in performing linkage analysis for the trait using only some of the animal subgroups of a F2 population generated on the basis of their transcriptome profiles. Such an approach can refine some QTL and detect new ones.

This approach was applied to hepatic transcriptome profiles for 45 offspring of a chicken known to be heterozygous for a QTL for abdominal fatness (AF) on GGA5 at 168cM. 688 gene expressions significantly correlated to the AF trait were obtained using a recent method taking into account the hidden dependence structure independent of the trait of interest as the population structure or microarray expression artefacts (Friguet *et al*, 2009, Blum *et al*, 2010). A hierarchical clustering analysis using these 688 genes distinguished five subtypes for fatness among the 45 birds. After removing a subtype of 7 lean birds, linkage analysis revealed another QTL on the GGA5 at ~102cM. Interestingly, these 7 animals presented the same paternal haplotypes for the QTL at 168cM, suggesting that the two QTL are in interaction. We showed by different approaches (ANOVA, linkage analysis) a significant interaction between the two QTL. These results illustrate the power of the approach: transcriptome data allows separating a population into genetically homogenous phenotype subgroups, revealing the complexity of the genetic regulation of a complex trait.