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Integrating QTL controlling fatness, lipid metabolites and gene expressions to genetically dissect the adiposity complex trait in a meat chicken cross

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Background: Many studies have been performed to identify QTL affecting fat deposition in chicken. Most of them used a single QTL model. We propose in this study focused on abdominal fatness (AF) trait in a meat chicken cross to use multiple QTL models. In addition, we will analyze the co-localization between the QTL controlling AF, the mQTL controlling different hepatic lipid components and the eQTL controlling gene expressions to better functionally characterize the AF QTL regions through these elementary phenotypes that they control.

Methods: A total of 177 offspring in 4 sire families originating from crosses between two lines divergently selected for AF were analyzed for AF, hepatic lipid composition (about 30 variables) and hepatic gene expression (28743 probes).

Results: Using single-QTL and multi-QTL models, 4 and 2 QTL for AF were detected on five chromosomes. For each QTL region, co-localized eQTL were identified with a hotspot on GGA2 (339 genes, including 1 cis-eQTL, $P < 0.01$). We analyze this hotspot gene list using functional GO, KEGG and IPA terms information and constructing a gene network. Functional terms related to lipid metabolism have been identified. The mapping of mQTL controlling hepatic lipid profiles is currently performed and should also be used to characterize the QTL region.

Conclusion: This large-scale information at different levels of observation can bring precious information about the "function" of a QTL region of interest and then about the causative genes. As far as we know, it is the first time in a study on livestock species that metabolite measurements and gene expressions are included in a QTL analysis.