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Mapping QTL for white striping in relation to breast muscle yield and meat quality traits in broiler chicken

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Background

White striping (WS) is an emerging muscular defect occurring on breast and thigh muscles of broiler chickens and characterized by the presence of white striations parallel to the muscle fibers. This defect has significant consequences on meat quality, altering both its appearance, nutritional values and technological properties. The etiology of WS remains unknown but previous studies demonstrated that the prevalence of this defect is directly related to broiler growth and muscle yield. Moreover, recent studies showed moderate to high heritability values of WS, which emphasized the role of genetics in its determinism.



The aim of this study was to specify the genetic and molecular mechanisms involved in the appearance of WS by identifying the first QTLs for WS as well as breast muscle yield and meat quality traits

Materials

- © Chicken divergent lines selected for meat quality through Pectoralis major ultimate pH (pHu) and concerned by WS defect
- 558 birds of the 6th generation of selection (278 pHu + and 280 pHu -)
- Phenotyping: WS, breast yield, color parameters of meat (L*, a*, b*), drip and cooking loss, intramuscular fat, TBARS...
- Francisco Genotyping: Illumina chicken SNP 57K Beadchip

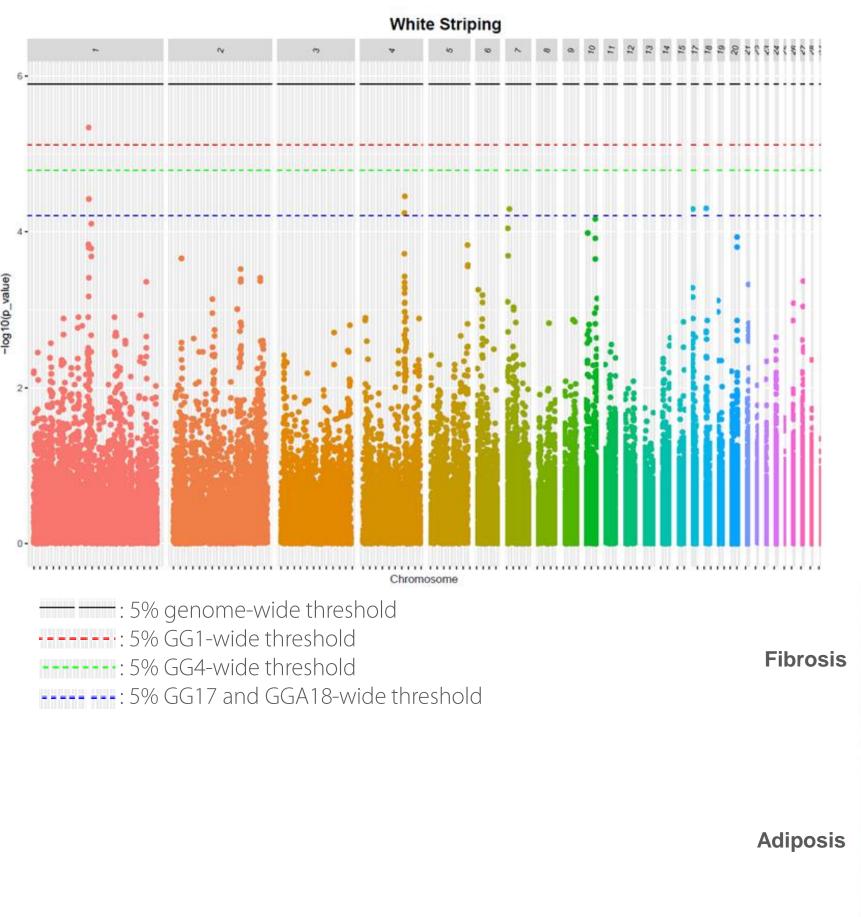
Methods Figure 1: Phenotypic evolution of pHu Genome wide association study Univariate linear mixed model (GEMMA software) **Quantification of gene** QTL detection **Genes environment GWAS** expression Identification of regions of **Identification of** eQTL (281/558 birds) candidate genes detection interest RT-qPCR (Fluidigm) **Identification of candidate** genes and gene networks

NORM: normal, MOD: moderate WS, SEV: severe WS

Results & Discussion

20 QTLs identified including 5 associated with **WS** on GGA 1, 4, 7, 17 and 18

Figure 3: Manhattan plot showing the association between SNPs and WS



16 candidate genes identified including 13 for WS mostly involved in:

Figure 2: Incidence of WS is higher in the pHu + line

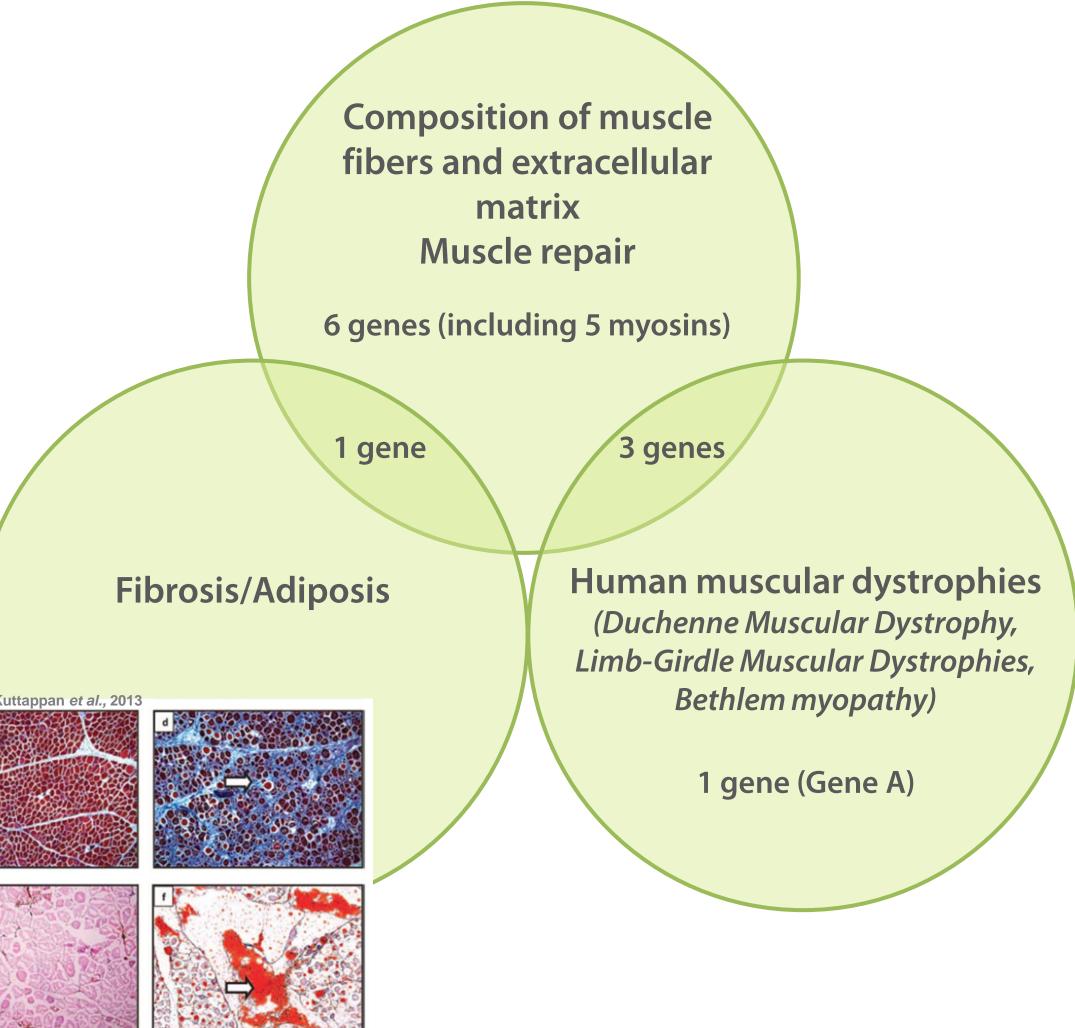


Figure 4: Transversal cross section, normal fillet vs WS fillet

Normal fillet

19 eQTLs identified including 2 cis-eQTLs

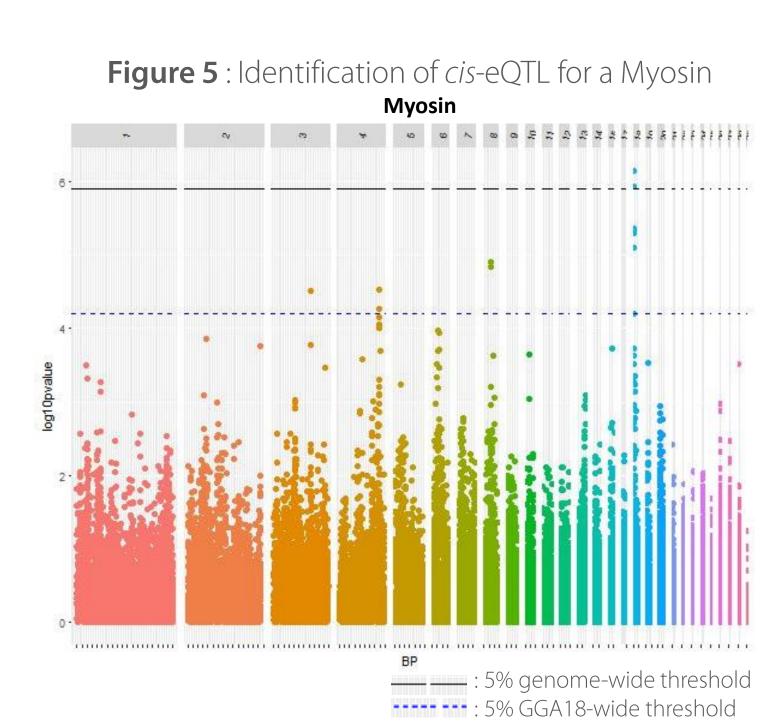


Figure 6 : Identification of *cis-*eQTL for Gene A : 5% genome-wide threshold : 5% GGA17-wide threshold

- Several co-localizations between QTLs and eQTLs:
 - © On **GGA17** between WS-QTL and Gene A *cis*-eQTL
 - © On **GGA4** between a pleiotropic region associated with 4 meat quality traits and *trans*-eQTL for 4 different genes

Fillet with WS

© On **GGA18** between WS-QTL and myosin gene

POLYGENIC DETERMINISM OF WS AND MEAT QUALITY TRAITS

CANDIDATE GENES INVOLVED IN COMPOSITION OF MUSCLE FIBERS, MUSCLE REPAIR, FIBROSIS, ADIPOSIS AND MUSCULAR DYSTROPHIES SEVERAL CO-LOCALIZATIONS QTLs/eQTLs WHICH SUGGEST CAUSATIVE GENES AND GENE NETWORKS INVOLVED IN THE VARIABILITY OF MEAT **QUALITY TRAITS AND BREAST MEAT YIELD**

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