

THE GENETIC ARCHITECTURE OF THE CHICKEN GENOME

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ABSTRACT

Quantitative traits are controlled by several genes and the environment. Most of the genes that underlie these traits are not known thus it is important to identify quantitative trait loci (QTL) and the genes underlying them. The objectives of this study were to detect QTL regions for growth, skeletal traits and body composition on the chicken genome, to identify candidate genes in QTL regions on chicken chromosome Z (GGAZ) by comparative mapping and to detect candidate genes in a major QTL region on GGA4 through the detection of CpG islands and comparative mapping.

QTL for age-related body weight (BW), shank length (SL), shank diameter (SD), breast meat yield and abdominal fat were localized in 695 individuals in an F₂ population. A pleiotropic QTL on GGA4 explained 7-11% of the variance and affected BW at 5 to 9 weeks, SL and SD at 9 weeks, and carcass traits. Through comparative mapping of the chicken, mouse and human genomes 197 potential candidate genes were detected in QTL regions on GGAZ. The annexin A1 gene, follistatin and the nicotinic acetylcholine receptor (*nAChR*) gene were some of the putative candidate genes identified for egg production and abdominal fat. The *nAChR* is located in the QTL region for abdominal fat and could be used as a therapeutic agent for controlling feed intake and obesity. A major QTL region on GGA4 was characterized. Six putative novel genes were identified through CpG island detection and comparative mapping with 23 other species. One of the novel genes is an analog of the rhotekin 2 gene which has *nAChR* associated protein activity.