Genetics and Molecular Research

A genome-wide association study of growth trait-related single nucleotide polymorphisms in Chinese Yancheng chickens

C.F. Jin, Y.J. Chen, Z.Q. Yang, K. Shi and C.K. Chen

Institute of Agricultural Sciences of Yanchen and Coastal Area of Jiangsu Province, Yancheng, China

Corresponding author: Y.J. Chen
E-mail: ycaasjin@163.com

Genet. Mol. Res. 14 (4): 15783-15792 (2015)
Received August 19, 2015
Accepted October 23, 2015
Published December 1, 2015
DOI http://dx.doi.org/10.4238/2015.December.1.30

ABSTRACT. Chicken (*Gallus gallus*) growth traits are important economic traits, and many studies have been conducted on genetic selection for body weight. However, most of these studies have detected functional chromosome mutations or regions by conventional molecular markers or gene chips. In this study, we performed a new genome-wide association study using specific-locus amplified fragment sequencing (SLAF-seq) technology in purebred Yancheng chickens. Single nucleotide polymorphisms (SNPs) that were significantly associated with phenotypic traits were identified by GAPIT-compressed mixed linear models. Eighteen SNP markers reached 5% Bonferroni genome-wide significance. A region spanning 72.3 to 82.1 Mb on *GGA4* had a strong influence on growth traits. Four genes (*FAM184B*, *KCNIP4*, *MIR15A*, and *GLI3*) were closely associated with body weight. Some SNPs were coincident with previously reported quantitative trait locus regions. Our results would promote the researches of Chinese chickens and accelerate the utilization of Chinese chicken, specially Yancheng chicken.

Key words: Yancheng chicken; SLAF-seq; Genome-wide association study; GWAS