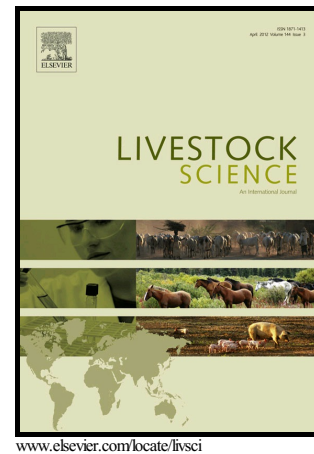


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Identification of new loci for body weight traits in F2 chicken population using genome-wide association study

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ABSTRACT

Understanding the genetic control of growth traits is one of the most important breeding goals in poultry industry. In order to find genes and genomic regions affecting growth traits, we performed a genome-wide association study (GWAS) using Illumina 60K chicken SNP Beadchip in a chicken F2 resource population derived from the reciprocal cross between Arian fast-growing line and Orumieh indigenous slow-growing chicken. A total of 312 F2 birds in eight half sib families from five hatches were produced. Growth traits including body weight (BW) from birth to 12 weeks of age and average daily gain (ADG) were measured for all of the F2 chickens. The GWAS analysis for growth traits was performed using the generalized linear model (GLM) and compressed mixed linear model (cMLM). The results indicated that nine SNPs reached to 5% Bonferroni genome-wide significance ($P < 2.43E-6$) and 12 were suggestively passed genome-wide significance ($P < 4.8E-6$) for BW and ADG traits. These nine SNPs were located nearby or in 10 candidate genes, including *DIS3*, *BORA*, *UBE2H*, *CNOT10*, *SGOL1*, *ADGRB3*, *DTNB*, *SETD3*, *EFNA5* and *SPINZ*. Cell division, skeletal myogenesis, regulation of actin and microtubule cytoskeleton organization and

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