

**Single Nucleotide Polymorphisms in selected candidate genes  
and their association with body weight in *Gallus Gallus*  
*Domesticus* ecotypes**

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**ABSTRACT**

Indigenous chickens (IC) are known for their variability in body weight. Genetic studies have shown that body weight is polygenic. A total of 234 IC belonging to six ecotypes were used to evaluate the effect of ecotype on bodyweight (BW) and to determine the association between BW and single nucleotide polymorphism (SNPs) involved in growth. Neuropeptide Y (*NPY*), Dopamine receptor D2 (*DRD2*), Bone morphogenetic protein receptor 1B (*BMPR1B*) and Melanocortin 1 receptor (*Mel1C*) genes from a diverse population of IC ecotypes were genotyped and the association between the generated SNP profiles and BW was investigated. . Body weights were recorded once, DNA was extracted from blood samples, GWAS performed using Mixed Linear Model. The results showed that average BW ranged from 0.6 to 2.60 kg. There were significance differences in BW between sexes ( $p < 0.01$ ) and ecotypes ( $p < 0.05$ ). The average BW was  $1.38 \pm 0.32$ kg and  $1.20 \pm 0.29$ kg for male and female chickens, respectively. The average BW was highest in SNNPR ( $1.39 \pm 0.07$  kg) and Tigray ( $1.36 \pm 0.05$ kg) ecotypes. Different ecotypes had varied average BW of  $1.26 \pm 0.03$ kg (Amhara),  $1.13 \pm 0.01$ kg (Afar),  $1.18 \pm 0.06$ kg (Gumuz) and  $1.06 \pm 0.04$ kg (Oromia). Nine SNPs (*NPY*-3; SNP rs794226974,  $p$ -value=1.924; rs15938915,  $p$ -value=1.972 and rs738097857,  $p$ -value =1.685); *Mel1C*-3 (SNP rs734475748,  $p$ -value=3.219, SNP rs317836677,  $p$ -value=2.92 and SNP rs315819466,  $p$ -value=2.92), *DRD2*-2 (SNP rs313898728,  $p$ -value=2.28 and SNP rs732873238,  $p$ -value=2.166) and *BMPR1B*-1 (rs13524270) were associated with BW. The results indicate that SNPs on *BMPR1B*, *NPY*, *DRD2* and *Mel1C* genes are associated with the BW trait and are potential markers for use in molecular marker-assisted selection programs.

**Keywords:** Candidate genes, genomic selection, GWAS, QTLs