

## Summary

In beef cattle, body weight is an important trait and optimizing size at various ages is of key economic interest. In our previous study, we identified some large-effect pleiotropic QTLs located on BTA5, 6, 7, 14, 20 and 24 associated with body weights in several beef breeds. Some 96 new functional variants of candidate genes within these QTL regions were selected from the dbSNP and assayed into the new versions of GeneSeek Genomic Profilers (GGP-LD, GGP-UHD and GGP-50K). Some 5,964 Simmental, 2,982 Gelbvieh and 2,871 Red Angus animals were genotyped with one of these assays and recorded for birth, weaning and yearling weights. We performed an association study using linear mixed model in GEMMA software. Some functional variants including rs385670251 encoding p.Ala64Pro in HMGA2, rs109570900 encoding p.Ile442Met in NCAPG, rs109901274 encoding p.Tyr182Cys in ARRDC3, rs136369910 encoding g.25019900A>G in PLAG1 and rs43350563 encoding c.322G>A in ERGIC1 were among significantly associated markers with remarkable consistent impact on body weights. The animals with GG compare to TT genotypes for rs109570900 on BTA6 at 38777311 bp were on average 2.0 kg heavier at birth, 7.6 kg heavier at weaning and 16.2 kg heavier at yearling. The phenotypic variance explained by these 96 markers were significant and remarkable for most traits in these breeds (e.g. 15% for birth weight in Simmental). These new functional variants will be included into the future genetic evaluations of the International Genetic Solutions (IGS), which is a home for international genetic evaluations of 12 breed associations across the world.

*Keywords: functional variant, genomic, major genes, beef cattle, IGS*