# *IGF1* GENOTYPES AFFECT GROWTH NOT TENDERNESS IN CATTLE

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## SUMMARY

368 backcross progeny from crosses between two *Bos taurus* breeds (Limousin and Jersey) used to study the effects of IGF1 genotypes on meat weight, tenderness and muscle hypertrophy. The results revealed that single nucleotide polymorphisms (SNPs) in the *IGF1* gene were associated with carcass weight and meat weight but not tenderness as measured by shear force. Interestingly, the *IGF1* SNPs were not associated with meat percentage or fibre diameter, suggesting the gene affects growth in general rather than muscle hypertrophy specifically.

## INTRODUCTION

Insulin-like growth factor I (*IGF1*) is known to play an important role in various aspects of muscle growth and development (Bunter *et al*. 2005; Davis and Simmen 2006). Due to the effect of *IGF1* on the hypertrophy of muscle cells, muscle fibre diameter can be affected by *IGF1* (Musaro *et al.* 2001). Since increasing muscle fibre diameter may decrease tenderness (Herring *et al.* 2009), it can be postulated that *IGF1* may also affect tenderness by increasing the size of the muscle fibres (Koohmaraie *et al.* 1995). The aim of this study was to investigate relationship between DNA polymorphisms in the *IGF1* gene and tenderness and muscle development.

## MATERIALS AND METHODS

The experimental herd design, phenotypes and genotypes were used from JS Davies Gene Mapping Cattle Project (Esmailizadeh *et al*. 2008). The Australian mapping herd (with 368 backcross progeny) was derived from crosses between two extreme *Bos taurus* breeds (Limousin and Jersey). Two single nucleotide polymorphisms (SNPs) in the *IGF1* gene were genotyped using the Illumina system and high resolution melt, namely SNP1 (C/T) 313 bp before exon 1 in the 5' flanking region and SNP2 (C/T) 7 bp from the exon 4 of splice junction. Tenderness was quantified as a measure of Warner-Bratzler (WB) shear force on two muscles: *M. longissimus dorsi* muscle (LD) and *M. semitendinosus muscles* (ST). To improve the accuracy of the tenderness phenotype, the shear force values from four time points (that is, 4 different days of ageing) were adjusted for using a mixed model. The fixed effects fitted in the mixed model were cohort (combination of sex and year), breed, sire, *myostatin* F94L genotype (AA, AC, CC), ageing time (1, 5, 12 and 26 days), muscle (*M. longissimus dorsi* muscle, LD and *M. semitendinosus muscles*, ST) and their interactions. Random effects fitted in the mixed model included animal, animal.muscle and animal.ageing time. The BLUPs for animal.muscle were used as the 'adjusted' values for tenderness.

The phenotypes for the same animals of LD weight, ST weight, meat percentage, total meat weight, HSCW (carcass weight) and fibre diameter (from the ST muscles) were also used in the study. The effect of *IGF1* on tenderness was analysed with genotypes for *IGF1*-SNP1 and SNP2 and the interaction between these two SNPs of *IGF1* as fixed factors in the analysis model. For analysing the effect of the *IGF1* gene on the other traits, cohort (combination of sex and year), breed, sire, *myostatin* F94L genotype, genotypes for *IGF*1-SNP1 and SNP2 and the interaction between these two SNPs of *IGF1* were fitted as fixed factors in the model. The *myostatin* F94L had a large effect on body composition (Esmailizadeh *et al*. 2008) and therefore, was included in the model. The "C" allele frequency of the *IGF1*-SNP1 was 41% and for SNP2 was 80%. These

alleles were in Hardy-Weinberg equilibrium. All analyses were conducted with Genstat 8.1 (Lawes Agricultural Trust 2005). Significance was defined as P<0.05.

**RESULTS AND DISCUSSION**

The *IGF1* gene (SNP1, SNP2 or the interaction between the two SNPs) did not show any effect on tenderness as measured by shear force for either the LD or ST muscles (Table 1.). In addition, fibre diameter was not affected by *IGF1* in the ST muscle. Likewise, the weights of the LD and ST muscles were not affected by SNP1 and/or SNP2 of the *IGF1* gene. This suggests that the *IGF1* gene may not cause muscle hypertrophy in either the LD or ST muscles. This is not consistent with the previous research results that have shown a relationship between the level of IGF1 and hypertrophy of muscles (Musaro et al., 2001). However, the effect of the interaction between SNP1 and SNP2 of *IGF1* gene on ST muscle weight is nearly significant (P=0.06).

**Table 1. Test of significant of *IGF1* SNP genotypes on carcass traits.**

| | No. of observations | Mean | Standard Deviation | *SNP1* | *SNP2* | *SNP1.SNP2* |
|---|---|---|---|---|---|---|
| Adjusted_$WB_{ST}$ [a] | 366 | 4.758 | 0.385 | 0.909 | 0.820 | 0.410 |
| Adjusted_$WB_{LD}$ [b] | 366 | 4.228 | 0.676 | 0.987 | 0.487 | 0.369 |
| ST weight [c] | 349 | 2.49 | 0.837 | 0.679 | 0.356 | 0.060† |
| LD weight [d] | 347 | 6.28 | 1.507 | 0.112 | 0.299 | 0.445 |
| ST fibre diameter [e] | 276 | 66.04 | 12.84 | 0.412 | 0.505 | 0.175 |
| meat % [f] | 330 | 68.62 | 2.99 | 0.306 | 0.686 | 0.111 |
| Total meat weight | 329 | 230.3 | 48.5 | 0.032* | 0.284 | 0.406 |
| carcass weight [g] | 356 | 334.7 | 61.7 | 0.013* | 0.082† | 0.192 |

* (P<0.05) † P<0.10

[a] Adjusted_$WB_{ST}$ means Warner-Bratzler (WB) shear force (adjusted by mixed model) on *M. semitendinosus muscles* (ST)

[b] Adjusted_$WB_{LD}$ means Warner-Bratzler (WB) shear force (adjusted by mixed model) on *M. longissimus dorsi* muscle (LD)

[c] ST weight means the weight of *M. semitendinosus* muscle (ST)

[d] LD weight means the weight of *M. longissimus dorsi* muscle (LD)

[e] ST fibre diameter measured with *M. semitendinosus* muscle (ST)

[f] meat % refers to meat percentage

[g] carcass weight refers to hot standard carcass weight

On the other hand, the *IGF1*-SNP1 was associated with total meat weight (P=0.032) and hot standard carcass weight (HSCW) (P=0.013). Cattle with the TT and CT genotypes for *IGF1*-SNP1 had more meat than the cattle with CC genotype (Figures 1 and 2). The *IGF1*-SNP1 showed a significant dominance effect on meat weight and carcass weight (Table 2). The estimated allelic substitution effect was 7.08 ± 3.09kg on meat weight and 11.76 ± 4.05kg on hot standard carcass weight (Table 2).

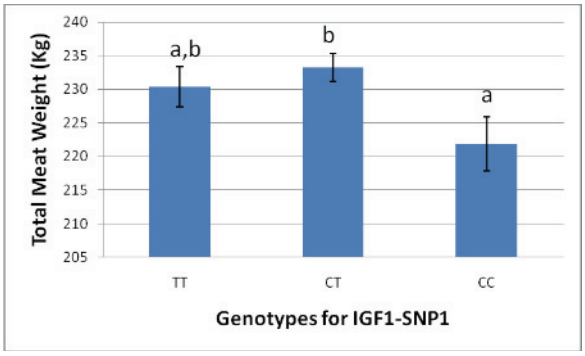


**Figure 1. Effect of *IGF1*-SNP1 on meat weight. Different letters indicate significant differences between groups.**

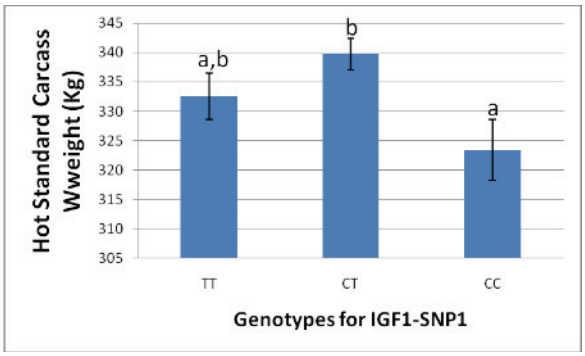


**Figure 2. Effect of *IGF1*-SNP1 on carcass weight. Different letters indicate significant differences between groups.**

**Table 2. Additive and dominance effects (+ standard errors) of *IGF1* SNPs on significant carcass traits.**

| | *IGF1*_SNP1 additive | *IGF1*_SNP1 dominance | *IGF1*_SNP2 additive | *IGF1*_SNP2 dominance |
|---|---|---|---|---|
| meat weight | -4.24 (2.73) | 7.08 (3.09)* | 4.94 (4.33) | 7.57 (4.76) |
| carcass weight | -4.51 (3.56) | 11.76 (4.05) ** | 10.13 (5.27) † | 12.89 (5.93) * |

†( P<0.10); * (P<0.05), * * (P<0.01), *** (P<0.001)

The *IGF1*-SNP2 did not show a significant effect on hot standard carcass weight (P=0.082). However, the cattle with the TT genotype for the *IGF1*-SNP2 had significantly lower carcass weights than the cattle with the CC and CT genotypes (Figure 3). The dominance effect was found and its estimated allelic substitution effect was 12.89 ± 5.93 (Table 2). These results support the observations of Davis and Simmen (2006), who found that serum IGF1 levels were moderately to highly heritable and were correlated to pre- and post-weaning weight gain in cattle.

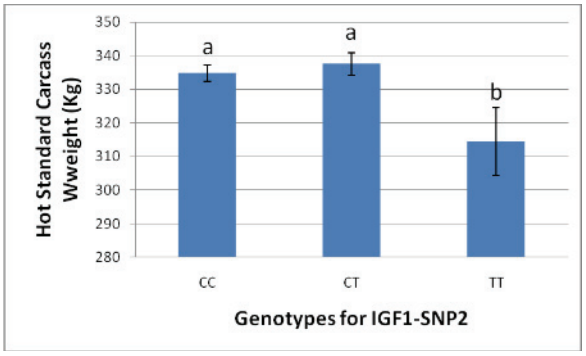


**Figure 3. Effect of *IGF1*-SNP2 on carcass weight. Different letters indicate significant differences between groups.**

Interestingly, meat percentage was not influenced by the *IGF1* gene. The results taken together suggest that the *IGF1* gene does not appear to specifically increase the size of the muscle fibres, but does affects growth overall. Hot standard carcass weight increased because the animals with the "C" allele of the *IGF*1-SNP2 and the "T" allele of the *IGF*1-SNP1 were larger overall, not because the animals had more muscle as a proportion of the carcass. Hence, the polymorphisms in the *IGF1* gene were only associated with growth but not with the size or weight of specific muscles. Given that DNA variants in the *IGF1* gene do not appear to be associated with muscle hypertrophy, it is not surprising the polymorphisms in the *IGF1* gene were also not associated with tenderness as measured by shear force. On the other hand, *IGF1* has been shown to change the proportions of muscle types, which may affect tenderness (Lynch *et al.* 2001 and Klont *et al.* 1998). Hence, the relationship between the *IGF1* gene, muscle fibre types and tenderness needs to be further investigated.

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