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 IGF1-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.

<table>
<thead>
<tr>
<th></th>
<th>No. of observations</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>SNP1</th>
<th>SNP2</th>
<th>SNP1.SNP2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adjusted_WBST</td>
<td>366</td>
<td>4.758</td>
<td>0.385</td>
<td>0.909</td>
<td>0.820</td>
<td>0.410</td>
</tr>
<tr>
<td>Adjusted_WBLD</td>
<td>366</td>
<td>4.228</td>
<td>0.676</td>
<td>0.987</td>
<td>0.487</td>
<td>0.369</td>
</tr>
<tr>
<td>ST weight</td>
<td>349</td>
<td>2.49</td>
<td>0.837</td>
<td>0.679</td>
<td>0.356</td>
<td>0.060†</td>
</tr>
<tr>
<td>LD weight</td>
<td>347</td>
<td>6.28</td>
<td>1.507</td>
<td>0.112</td>
<td>0.299</td>
<td>0.445</td>
</tr>
<tr>
<td>ST fibre diameter</td>
<td>276</td>
<td>66.04</td>
<td>12.84</td>
<td>0.412</td>
<td>0.505</td>
<td>0.175</td>
</tr>
<tr>
<td>meat %</td>
<td>330</td>
<td>68.62</td>
<td>2.99</td>
<td>0.306</td>
<td>0.686</td>
<td>0.111</td>
</tr>
<tr>
<td>Total meat weight</td>
<td>329</td>
<td>230.3</td>
<td>48.5</td>
<td>0.032*</td>
<td>0.284</td>
<td>0.406</td>
</tr>
<tr>
<td>carcass weight</td>
<td>356</td>
<td>334.7</td>
<td>61.7</td>
<td>0.013*</td>
<td>0.082†</td>
<td>0.192</td>
</tr>
</tbody>
</table>

* ($P<0.05$) † $P<0.10$

* Adjusted_WBST means Warner-Bratzler (WB) shear force (adjusted by mixed model) on $M. semitendinosus$ muscle (ST)
† Adjusted_WBLD means Warner-Bratzler (WB) shear force (adjusted by mixed model) on $M. longissimus dorsi$ muscle (LD)
* ST weight means the weight of $M. semitendinosus$ muscle (ST)
† LD weight means the weight of $M. longissimus dorsi$ muscle (LD)
* ST fibre diameter measured with $M. semitendinosus$ muscle (ST)
* meat % refers to meat percentage
* 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 $7.08 \pm 3.09$kg on meat weight and $11.76 \pm 4.05$kg 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.

<table>
<thead>
<tr>
<th>Trait</th>
<th>IGF1_SNP1 additive</th>
<th>IGF1_SNP1 dominance</th>
<th>IGF1_SNP2 additive</th>
<th>IGF1_SNP2 dominance</th>
</tr>
</thead>
<tbody>
<tr>
<td>meat weight</td>
<td>-4.24 (2.73)</td>
<td>7.08 (3.09)*</td>
<td>4.94 (4.33)</td>
<td>7.57 (4.76)</td>
</tr>
<tr>
<td>carcass weight</td>
<td>-4.51 (3.56)</td>
<td>11.76 (4.05)**</td>
<td>10.13 (5.27)†</td>
<td>12.89 (5.93) *</td>
</tr>
</tbody>
</table>

† (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.
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 affect growth overall. Hot standard carcass weight increased because the animals with the "C" allele of the *IGF1*-SNP2 and the "T" allele of the *IGF1*-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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**REFERENCES**


