Association of *leptin* genotypes with beef cattle characteristics


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**Summary**

A single nucleotide polymorphism (C/T) in bovine *leptin*, resulting in an arginine to cysteine amino acid substitution (p.Arg25Cys), has previously been shown to have an impact on carcass characteristics. Given the significant energetic relationship between fat and animal efficiency, further evaluation of this SNP across larger animal populations is warranted. Of the total number of 136,286 genotyped cattle in this study, 92,112 and 53,189 were analysed for backfat and body weight measurements, respectively. Results showed a significant positive relationship ($P<0.0001$) between the T allele frequency and animal backfat, with TT, CT and CC animals having estimates of $6.79 \pm 0.02$, $6.49 \pm 0.01$ and $6.28 \pm 0.01$ mm, respectively. Calculations using rate of backfat accretion showed that animals with CC genotypes would require more days to reach 12 mm of backfat (45 days) than animals with CT (42 days) and TT (38 days) genotypes. Animal weight was also shown to be positively associated ($P<0.0001$) with genotype, as animals of the TT, CT and CC genotypes weighed $484.2 \pm 0.7$, $488.0 \pm 0.5$ and $487.3 \pm 0.6$ kg, respectively, further underscoring the effects of this SNP on key market cattle characteristics.

**Keywords** body weight, leptin genotype, ultrasound backfat.

Variation in body composition of market beef cattle is a fundamental problem in beef production because it represents an inefficient allocation of resources in overfed, larger, fatter animals, and missed opportunity in underfed, smaller, thinner animals. Previously, a SNP was discovered in the *LEP* gene coding for *leptin*, a hormone known to regulate feed intake and energy balance in mammals (Houseknecht *et al.* 1998). Exploration of the influence of this SNP in the body composition of feedlot cattle reveals a powerful application for genomics in beef feedlot production.

Using a small subset of animals ($n=1577$), it was established that a SNP in the *LEP* gene (Leptin p.Arg25Cys), which results in an arginine to cysteine amino acid substitution, is associated with carcass characteristics of finishing cattle (Kononoff *et al.* 2005). While these results are congruent with previous findings linking animal fatness to this SNP (see Buchanan *et al.* 2002), other researchers (see Barendse *et al.* 2005) found no significant association between this base substitution and any level of animal fatness. The objective of the following study was to test for an association between this SNP and live animal backfat thickness and body weight in Western Canadian feedlot cattle.

The cattle sampled in the following study were of mixed breed and were crossbred steers and heifers that arrived as calves or yearlings that originated from 63 provincially inspected Western Canadian feedlots between 2007 and 2010. Upon arrival at the feedlot, cattle were implanted and fed standard finishing rations (approximately 70% grain) for a minimum of 45 days. Cattle ear tissue samples were used for genotyping ($n=136,286$) by qPCR using primer sets and conditions outlined in Kononoff *et al.* (2005). Ultrasound measurements of the 12th rib ($n=92,112$), obtained using an Aloka Company Limited SSD-500V diagnostic ultrasound unit equipped with a 20.0-cm, 3.5-MHz linear array transducer (Aloka Company Limited, Tokyo, Japan), and weight measurements ($n=53,189$) were taken either at arrival (yearlings) or re-implant time (calves), such that the animals were at...
similar points in their growth curve. Backfat measurements were collected following the procedure described by Perkins et al. (1992). Briefly, the Beef Imaging Analysis (Designer Genes, Harrison, AR, USA) software program was used to capture and measure the level of backfat thickness for each image. Estimations for number of days to reach 12 mm of backfat thickness were extrapolated using the following equation:

\[ y = \left( \ln(10) - \ln(x) \right)/k \]

where \( y \) is the adjustment from the initial day on feed, \( x \) is the backfat measure at the beginning of the experimental period, and \( k \) (0.0103) is the estimated rate of increase for projecting animals with 12 mm (Brethour 2000).

The effect of leptin genotype on live weight and backfat thickness was tested using the MIXED procedure of SAS (version 8.2; SAS Institute, Cary, NC, USA). All significant effects were declared at \( P < 0.0001 \). All means presented were generated using the LSMEAN statement. A fixed-effects model was used to test the effect of leptin genotype as follows: \( y_{ij} = \mu + \tau_i + e_{ij} \), where \( y_{ij} \) is the value of either backfat or body weight for subject \( j \) of the genotype \( i \). \( \mu \) is the overall mean, \( \tau_i \) is the effect of genotype \( i \) on the dependent variable, and \( e_{ij} \) is the effect of the \( j \)th animal of the genotype \( i \).

Animals homozygous for the C allele had the lowest backfat thickness, while the frequency of the T allele (CT and TT, respectively) was associated with progressive increases in backfat thickness (Table 1), similar to previous observations in both mature beef bulls (Buchanan et al. 2004) and feeder cattle (Nkrumah et al. 2004). Utilizing a previous observation that the T allele frequency increases the rate of backfat deposition, we extrapolated, based on an exponential equation outlined by Brethour (2000), the number of feeding days for finishing cattle to reach 12 mm (Brethour et al. 2005) that linked this SNP to cattle fatness. Discrepancies between the results of the current study and conclusions of Barendse et al. (2005) are explainable in that the latter study sampled fewer animals with larger variations in weight, days on feed, diet and backfat thickness measures at the 12th rib. In addition, some breeds in the Barendse study were not present in the current study. Future research should further explore the impact of this SNP while also evaluating its interaction with other functional SNPs.

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### References


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**Table 1** Association between leptin genotype and live cattle characteristics.

<table>
<thead>
<tr>
<th>Leptin genotype</th>
<th>CC</th>
<th>CT</th>
<th>TT</th>
</tr>
</thead>
<tbody>
<tr>
<td>( n )</td>
<td>27,412</td>
<td>43,710</td>
<td>20,783</td>
</tr>
<tr>
<td>Backfat (mm)</td>
<td>6.28±0.01</td>
<td>6.49±0.01</td>
<td>6.79±0.02</td>
</tr>
<tr>
<td>( n )</td>
<td>16,441</td>
<td>25,395</td>
<td>11,342</td>
</tr>
<tr>
<td>Body weight (kg)</td>
<td>487.3±0.56</td>
<td>488.0±0.45</td>
<td>484.2±0.70</td>
</tr>
</tbody>
</table>

The number of animals that were measured for either backfat thickness or body weight in each genotypic group is shown. Mean values ± SEM are shown. Genotype means with different letters are significantly different from each other (\( P < 0.0001 \)).
