Association of melanocortin 4 receptor (MC4R) and high mobility group AT-hook 1 (HMGA1) polymorphisms with pig growth and fat deposition traits


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Summary

The aim of this study was to analyse the combined effect of melanocortin 4 receptor (MC4R) and high mobility group AT-hook 1 (HMGA1) polymorphisms on growth and fatness traits in Duroc pigs. No significant interaction was observed between MC4R and HMGA1 for back-fat traits. An additive mode of inheritance of both gene effects was found for average daily gain and lean meat content. Maximum mean differences from combined genotypic effects were over 2 mm for backfat, 70 g/day for average daily gain and 2% for lean meat content. Therefore, utilization of polymorphisms in both MC4R and HMGA1 for marker-assisted selection could result in an economic benefit to the pig industry.

Keywords economic traits, HMGA1, MC4R, pig breeding.

A porcine melanocortin 4 receptor (MC4R) variant (Asp298Asn) on pig chromosome 1 has been associated with feed intake, fatness and growth traits in several commercial populations (Kim et al. 2000; Houston et al. 2004; Meidtner et al. 2006). Functional studies of the MC4R gene polymorphism demonstrated that agonist-stimulating signalling was defective in a cell line expressing the Asn298 MC4R protein. Therefore, the porcine MC4R locus may exert a direct effect on phenotypic traits rather than being a marker for a linked gene (Kim et al. 2004a). However, the size of this MC4R genotypic effect differs among pig populations (Kim et al. 2000; Park et al. 2002; Stachowiak et al. 2006), which is probably due to differences in genetic background or in allelic frequency.

Several studies have demonstrated the existence of growth and fatness quantitative trait loci (QTL) on pig chromosome 7 (Rothschild 2004), and this QTL is still segregating in elite pig populations subjected to intensive selection to improve commercial performance (Nagamine et al. 2003). The high mobility group AT-hook 1 (HMGA1) gene has been mapped to the peak of the fat deposition QTL on pig chromosome 7, and HMGA1 polymorphisms are consistently associated with fat deposition traits across several pig populations, except for a pure Duroc population in which the distribution of a specific HMGA1 genotypic class was relatively small (Kim et al. 2004b). These results suggest that the observed HMGA1 polymorphism might be in strong linkage disequilibrium with causative mutation(s) for fatness in pigs.

Preliminary analyses of MC4R and HMGA1 genotypes revealed an additive mode of genetic effects on fat deposition in multiple pig breeds (Kim et al. 2004b). However, MC4R and HMGA1 interactions for other growth-related traits, such as average daily gain and lean muscle content, were not tested. The aims of the present study were to further investigate the phenotypic association of the HMGA1 polymorphism in a pure Duroc breed population and to determine the interaction of HMGA1 with MC4R for performance traits.

Phenotypic data and DNA samples were collected for 470 Duroc animals from the Korea Swine Association. Measurements for average daily gain (g/day), back-fat depth (mm) and lean meat content (%) at an off-test weight of 90 kg were also collected on each animal. Polymerase chain reactions were performed according to Kim et al. (2004b) for amplification of MC4R and HMGA1 fragments. Primers used for genotyping the MC4R variant (Asp298Asn) were 5’-TACCCTGACCATTTGATTG-3’ and 5’-ATAGCAAACAGATGCCTCTTGTG-3’; primers for genotyping the HMGA1 polymorphism were 5’-AGAAGGCCAGCAGGATG-3’ and 5’-ACAGTGCTACACCACAGGTC-3’. The MC4R missense substitution (G>A) at position 298 of the protein sequence was genotyped with TaqI, yielding a 220-bp fragment for the A allele (Asn298) and 150- and 70-bp fragments for the
Table 1  Combined frequencies of the melanocortin 4 receptor (MC4R) and high mobility group AT-hook 1 (HMGA1) polymorphisms in Duroc pigs (n = 470).

<table>
<thead>
<tr>
<th>HMGA1 genotype</th>
<th>MC4R genotype</th>
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<tr>
<td></td>
<td>AA</td>
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<tr>
<td>CC</td>
<td>0.22</td>
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<tr>
<td>TC</td>
<td>0.25</td>
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<td>TT</td>
<td>0.05</td>
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A single nucleotide polymorphism (SNP) was significantly associated with back-fat thickness ($P < 0.03$) but had no association with average daily gain ($P > 0.31$) or lean meat content ($P < 0.45$). In contrast, the MC4R SNP was not associated with back-fat thickness ($P < 0.13$), but it was significantly associated with average daily gain ($P < 0.01$) and lean meat content ($P < 0.04$). No significant interaction was observed between the MC4R and HMGA1 genotypes ($P < 0.07$). These results generally agree with those from Kim et al. (2004b).

Combined association analyses revealed that the HMGA1 SNP was associated with back-fat thickness in the AA MC4R genotype pigs ($P < 0.03$), but back-fat thickness was not different among the HMGA1 genotypes in pigs with the AG and GG MC4R genotypes. In pigs with the TC and CC HMGA1 genotypes, back-fat thickness was significantly different across the MC4R genotypes (Fig. 1a). The least squares mean difference of back-fat thickness between the [AA MC4R × CC HMGA1] and the [GG MC4R × TC HMGA1] pigs was over 2 mm (Fig. 1a). Pigs with the GG MC4R genotype had a significantly lower average daily gain than the AA and AG MC4R pigs (Fig. 1b). In addition, a significant HMGA1 effect on the average daily gain was
observed within the AA MC4R genotype (Fig. 1b). The least squares mean difference of average daily gain between the [AA MC4R × TT HMGA1] and the [GG MC4R × CC HMGA1] pigs was over 70 g/day (Fig. 1b). The GG MC4R genotype had the highest lean meat content among animals with the TC HMGA1 genotype (Fig. 1c). No significant HMGA1 effect on lean meat content was detected.

Previously, combined MC4R and HMGA1 effects on growth and lean mass traits have not been reported for commercial Duroc pigs. Results from this study indicated that the MC4R polymorphism affects lean growth in Duroc pigs without significant interaction with the HMGA1 polymorphism. Moreover, additive effects for both the MC4R and HMGA1 polymorphisms were found for growth, fatness and lean meat content. Utilization of both polymorphisms for marker-assisted selection could be useful for producing uniform commercial pigs with desirable performance in the future.

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References


