

Determination of Genes Associated with Leg and Body Conformation Traits in Pigs

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Suneel K. Onteru, post doctoral research associate;
Bin Fan, post doctoral research associate;
Benny Mote, graduate student;
Timo Serenius, visiting scientist;
Marja Nikkiläe, graduate student;
Kenneth J. Stalder, associate professor;
Max F. Rothschild, distinguished professor

Abstract

Sow reproductive life is greatly influenced by lameness issues. It has been reported that up to 44 percent of sows have locomotive problems. Hence, the present study examined 134 porcine genes affecting skeletal development, mineral metabolism and other candidate genes in 2000 commercial pigs for genetic variants called single nucleotide polymorphisms (SNPs). The association analyses of the first 22 genes revealed that nine genes such as *CALCR*, *HDBP*, *CALCA*, *MTHFR*, *OXTR*, *IHH*, *ANKH*, *LRCH1* and *OPN* were significantly associated with leg and body conformation traits, which affect the health and productivity of pigs.

Introduction

Feet and leg abnormalities can eventually lead to lameness, which is associated with longevity, health and well-being in pigs. Lameness is one of the main causes for culling of sows. It has been estimated that culling rates range from 10% to 40% due to soundness problems in breeding stock in USA. Unexpected high sow culling rates will reduce the litters per sow per year and increase the cost for replacement gilts, and thereby creating significant loss to farmers. Feet and leg problems can occur at any time. But often they begin in first parity and second parity animals before the sows reach the most productive period of their life. It is beneficial to identify animals with a predisposition to feet and leg problems and cull them as early as possible. Feet and leg as well as body conformation traits have been shown to be lowly to moderately heritable and the heritability ranges from 0.10 to 0.40. Marker assisted selection (MAS) is one method used to improve these lowly to moderately heritable traits. Hence the present study was conducted to find genetic variants called single nucleotide polymorphisms (SNPs) for genes affecting skeletal pattern development (e.g., *IHH*, Indian hedgehog), bone cell differentiation (e.g., *HDBP*, Vitamin D binding protein), bone matrix biosynthesis (e.g., *OPN*, Osteopontin) and phosphorus metabolism (e.g., *Cacitonin*). The objectives of

this study are to discover (SNPs) associated with feet, leg and other body conformation unsoundness and further employ these SNPs in MAS practices.

Materials and Methods

Two populations, a commercial population of gilts from a National Pork Board (NPB) funded project (n=2066) and the ISU Berkshire × Yorkshire (BY) resource family (n=572) were genotyped for leg and body conformation traits and gene mapping, respectively. The phenotypes were determined by scoring a total of 17 leg and body conformation traits based on the standards of NSIF (National Swine Improvement Federation) scoring standards and modified Finnish scoring systems. The DNA was isolated from ear tissue and genetic variants examined in pooled DNA samples. Genotyping was done in a large multigenotyping system. The genotyping data was used to map the genes in the BY population and association analyses were done in the NPB population using a standard statistical software package.

Results and Discussion

There were 370 SNPs found in 134 genes. To date, 22 genes have been analyzed and nine of them such as *CALCR*, *HDBP*, *CALCA*, *MTHFR*, *OXTR*, *IHH*, *ANKH*, *LRCH1* and *OPN* were found to be significantly related to leg and body conformation traits. The genotype effects of these significant genes are shown in Fig 1. In addition, the genes were mapped to the corresponding chromosomes as follows, *CALCA* (2), *MTHFR* (6), *HDBP* (8), *OPN* (8), *CALCR* (9), *LRCH1* (11), *OXTR* (13), *IHH* (15), *ANKH* (16), *IL6* (9), *Matrillin3* (3), *ADAM12* (14), *COL9A2* (6), *GNAS* (17), *TNF1* (7), *NPP1* (1), *HSP90* (7), *TRAF6* (2) and *NRP2* (15). These chromosomes were found to be anchoring quantitative trait loci (QTL) for leg and foot scores, conformation measurements and osteochondrosis traits. This is the first attempt using molecular markers for leg and body conformation traits in pigs. The SNPs in the present study could be in linkage disequilibrium with causative mutations. Hence these candidate genes should be strongly considered for marker assisted selection to improve leg and body conformation traits in commercial sow population.

Acknowledgements

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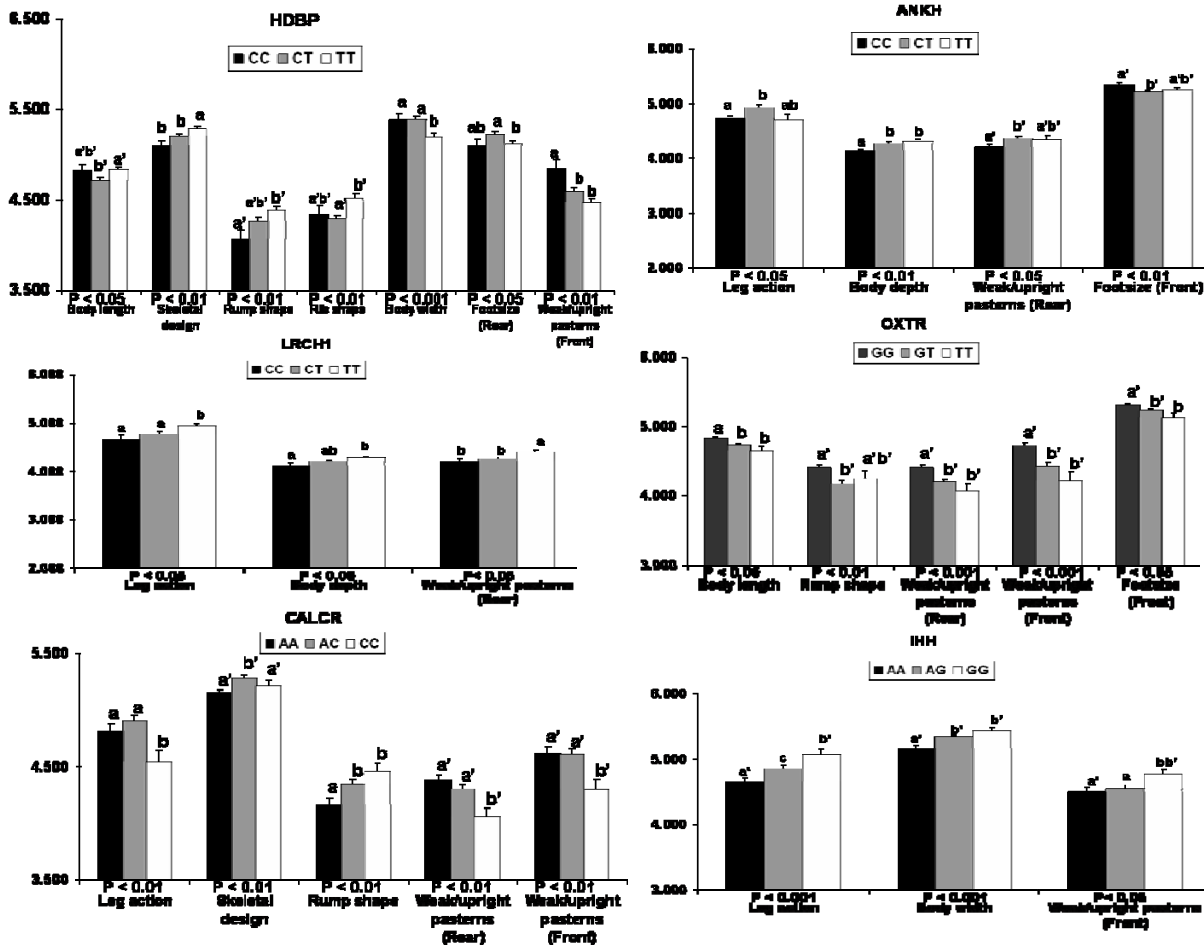


Fig.1. Genotype effects of candidate genes on leg and body conformation traits. The X axis has leg and body conformation traits and the Y axis indicates phenotype scores. The values with different letters a b and c differ significantly ($p < 0.05$). The values with different letters a', b', and c' differ significantly