

Mapping of quantitative trait loci associated with leg weakness-related traits in pigs

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Introduction

Leg weakness problems are of special interest in pigs breeding as well as in regard to animal welfare. The affected pig shows leg weakness may have no access to feed and water which will lead to the performance losses. Therefore the problem of leg weakness in pigs required a comprehensive study. It has been previously suggested that leg weakness and its related traits are under genetic control (Serenius *et al.* 2001; Jørgensen & Nielsen 2005; Kadarmideen & Jans 2005). However, knowledge about the genetic basis of leg weakness related traits including leg and feet score, osteochondrosis (OC) and bone mineral-related traits is limited in commercial pig breed. The aim of this study was to identify the quantitative trait loci affecting leg weakness and its related traits in a Duroc x Pietrain cross bred.

Material and methods

Animals and phenotypes. A total of 310 F2 pigs were used for leg weakness related traits measurements and verification of QTL regions. Animals were based on well-established model of Duroc × Pietrain resource population as described earlier (Liu *et al.* 2007). Leg and feet were scored following a set of attributes in live animals. OC was histologically scored at the head and condylus medialis of the left femur and humerus. A GE Lunar DPX-IQ scanner combined with the appendicular software mode were used for measuring bone mineral density (BMD), bone mineral content (BMC) and bone mineral area (BMA) in the whole third and fourth metacarpal bones.

Genotyping and statistical analyses. A total of 82 genetics markers were used to genotyping animals in this study. Data were analyzed using SAS (v.9.2) for descriptive statistics and to analyze correlation with other performance traits. QTL were analyzed using QTL Express.

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Results and discussion

A total of 15 chromosomal regions including three imprinting QTL were identified on nine porcine autosomes in this study. Most of the QTL were found on porcine chromosome 2, 3, 5, 6 and 9. All QTL reached the 5% chromosome-wide significance level. Two and three QTL were detected for each of leg score and feet score, respectively. OC scores were found to be influenced by six chromosomal regions in this study. Three imprinting QTL were paternally expressed or maternally imprinted, two of which were identified on SSC5 and one on SSC9. This study is the first linkage screen for genes underlying leg weakness and its related traits in a fast growing cross bred pig between Duroc and Pietrain. Though a number of factors are known to influence the development of leg weakness; especially body weight, growth rate, body and leg structure and mechanical stress are important. Our results showed novel linkage regions and also support some of the previously reported (Andersson-Eklund *et al.* 2000; Lee *et al.* 2003; Christensen *et al.* 2009; Guo *et al.* 2009).

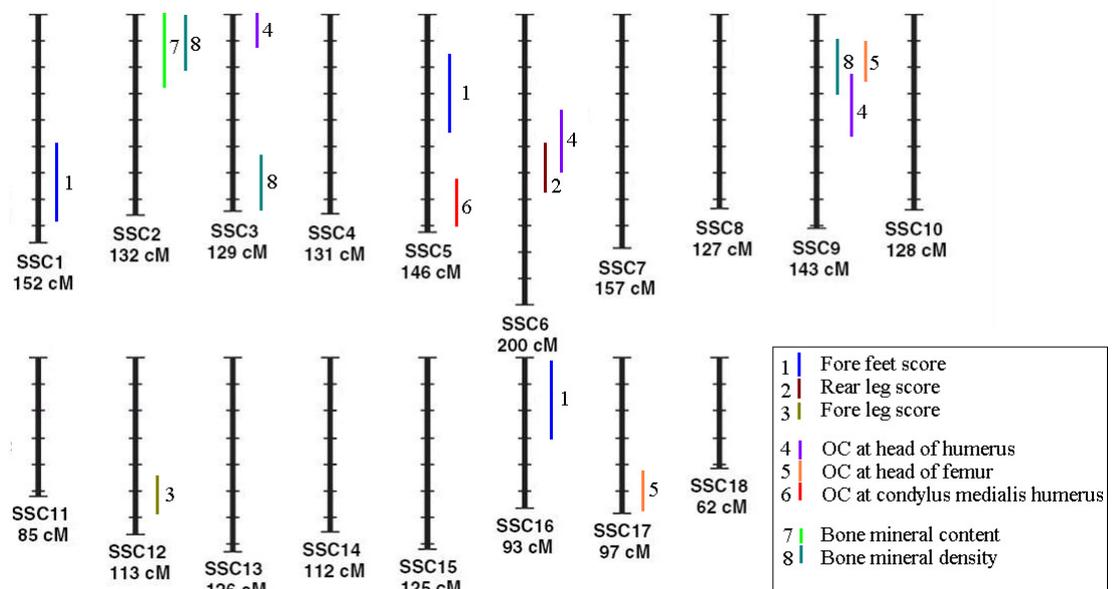


Figure 1: QTL for leg score, feet score, OC score and DXA traits. FLS= fore leg score; RLS= rear leg score; FFS = fore feet score; HH= OC at head of humerus; CMH= OC at condylus medialis humeri; HF= OC at head of femur; BMD = bone mineral density; BMC = bone mineral contents.

Conclusion

This study provides information on new QTL for leg weakness related traits in pigs. Some of our results confirmed previous studies on the related traits. Identification of QTL directly associated with leg weakness could help to more accurately select those animals in early life for the robust to fracture and less prone to suffer from the leg weakness. Furthermore, these findings will be helpful to identify genes or markers within the chromosomal regions, and their utilization in marker-assisted selection to improve the leg problems and increase the performance of pigs.

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