Title: Association of genetic markers with structural soundness and its relationship to gilt development and sow longevity – NPB #06-019

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Abstract

Identification and culling of replacement gilts with poor skeletal conformation and foot and leg unsoundness is a measure used to reduce replacement and mortality rates in breeding stock. Previous culling rates have been estimated to range from 10 to 40% because of unsoundness in young breeding stock. Due to low to moderate heritability of soundness traits, it may be preferable to improve them using marker assisted selection (MAS). In this study, genes related to published QTL regions, skeletal development pathways and the diseases of human bone and joints were chosen for discovery of SNPs relevant to body conformation and leg and foot soundness scores in pigs. Commercial females (n = 2,066) were scored for 17 traits describing body conformation and foot and leg structure and were used for association analyses. The ISU Berkshire × Yorkshire resource family (ISU B×Y) was utilized for linkage mapping. Large-scale genotyping was implemented using Sequenom’s MassARRAY system. A total of 66 genes were mapped to the expected chromosomes based on comparative mapping between pig and human. Utilizing the association results from single trait and PCA, it was found that APOE, CALCR, COLIA2, COL9A1, DKFZ and VDBP were very highly significantly (P < 0.001) associated with body conformation traits; ALOX5, BMP8, CALCR, COLIA2, OPG, OXTR and WNT16 were very highly significantly (P < 0.001) associated with feet and leg structures, and APOE, CALCR, COLIA2, GNRHR, IHH, MTHFR and WNT16 were highly significantly (P < 0.01) associated with overall leg action.