Genomic Analysis of Juvenile Serum IGF-I Concentration in Yorkshire Pigs Selected for Residual Feed Intake

A.S. Leaflet R2648

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Summary and Implications

Feed efficiency and related production traits continue to be of high interest in the swine industry as feed prices continue to rise. Two lines of Yorkshire pigs have been developed at Iowa State University to study the causes and effects of increased feed efficiency. The goal of this project was to use these lines to evaluate the genetic basis of juvenile serum IGF-I concentration, which has been shownto be an early indicator of genetic potential for feed efficiency later in life.

Introduction

Residual feed intake (RFI) is a measure of feed efficiency which is defined as the difference between observed feed intake and feed intake predicted from average requirements for growth and maintenance. Insulin-like growth factor-I (IGF-I) is a naturally occurring proteinthat circulates in the blood and can be measured early in life. Juvenile serum IGF-I concentration, measured around 35 to 42 d of age (juvenile IGF-I), has been shown to be associated with feed efficiency and other related production traits.

In the ISU selection experiment for improved RFI in Yorkshire pigs, selection for decreased RFIhas also significantly reduced juvenile IGF-I (Bunter et al., 2010, J. Anim. Sci.). The heritability of juvenile IGF-I was 0.28 in this population and juvenile IGF-I had significant positive genetic correlations with feed conversion ratio (0.78) and RFI (0.63). These results suggest that juvenile IGF-I could be a useful indirect selection criterion for increased efficiency later in life, reducing the need to measure feed intake. Genetic correlations of juvenile IGF-I with average daily feed intake, average daily gain, backfat, and loin muscle area were 0.26, 0.06, 0.52, and -0.35, respectively. An understanding of the genetic basis of differences in IGF-I is needed to understand the potential impact of using juvenile IGF-I as an indicator trait for feed efficiency. Thus, the objective of this project was to discover the genetic basis of juvenile IGF-I by identifying genomic regions associated with juvenile IGF-I.

Materials and Methods

Using purebred Yorkshire pigs, a selection line for decreased RFI and a randomly selected control line were started in 2001. In early generations, only pigs from the select line were evaluated for feed intake. In generations 2-5, juvenile IGF-I was measured on blood samples taken between 35 and 42 d of age.

A subset of animals from generations 4 and 5 (N=307),which were measured for juvenile IGF-I and had phenotypic records for RFI and performance traits,was genotyped for over 60,000 genetic markers across the genome. After quality control, 53,315 genetic markers were available for analysis. Using these animals (149 select and 158 control pigs) a whole-genome association analysis was performed to find genomic regions that were associated with juvenile IGF-I. The model for juvenile IGF-I accounted for the effects of date of bleeding, assay batch code, age at bleeding, and the interval between weaning and bleeding, The statistical program GenSel, which was developed by Drs. Dorian Garrick and Rohan Fernando at Iowa State University for use in genomic selection, was used for the association analysis.

Results and Discussion

Multiple genomic regions were found to be associated with juvenile IGF-I, including an unmapped marker that also had a strong association with backfat in this population. Markers near *BCL11B* on chromosome 7, near *NADSYN1* on chromosome 2, and near *GBX2* on chromosome 15 also showed strong associations. The gene *BCL11B* produces a protein associated with B-cells, which are involved in immune response. The gene *NADSYN1* is involved in the biosynthesis of NAD, which is involved in metabolic redox reactions and is a precursor for several cell signaling molecules. The gene *GBX2* plays a role in cell pluripotency and differentiation in the embryo.

The overlap of the unmapped marker between backfat and juvenile IGF-I supports the high genetic correlation (0.52) between these traits in this population. However, *MC4R*, which has been shown to be highly associated with growth and feed intake, did not show up as a genomic region significantly associated with juvenile IGF-I. Markers near *MC4R* were among the top markers for both average daily gain and average daily feed intake in this population, which could partially explain the lack of high genetic correlations between these traits and juvenile IGF-I. None of the top markers for RFI were among the top markers for juvenile IGF-I. However, the top markers for RFI were found to be involved in fatty acid metabolism and energy usage by cells, so they sharecommon pathways with the top markers for juvenile IGF-I. Further work is needed to investigate these relationships. Whole-genome association

studies for feed conversion ratio and loin muscle area have yet to be completed in this population.

Acknowledgments

This work was funded by the National Pork Board and the USDA-NIFA National Needs grant no. 2007-38420-17767. Development of the ISU RFI lines was supported by Hatch and State of Iowa funds through the ISU Center for Integrated Animal Genomics and made possible by the farm staff at the Lauren Christian Swine Breeding Research Center and the ISU Bilsland Memorial Swine Breeding Farm. IGF-I testing was funded by Primegro Ltd. and AGBU, University of New England, Australia.