

Understanding Feed Efficiency and Growth in Swine through Genetic Marker Studies

A.S. Leaflet R2645

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Summary and Implications

Swine feed efficiency has become a concern of producers in recent years as feed prices have risen. Over the last decade, Iowa State University has been developing lines of pigs to research the causes and effects of genetic differences in feed efficiency. Over 700 of these animals were recently genotyped for over 60,000 markers across the genome to determine which regions of the genome play the biggest roles in impacting feed intake, growth, backfat, and efficiency. The goals of the project were to gain a better understanding of the biology behind these traits in order to suggest improved management practices and genetic selection techniques. Several significant genomic regions were identified for each trait.

Introduction

As grain prices have increased in recent years, pork producers have become more concerned with feed efficiency. Much of the feed consumed is converted into weight gain, but other processes such as heat production and digestibility can increase feed costs without similarly increasing profits. Residual feed intake (RFI) is a measure of feed efficiency that quantifies how much feed an animal consumes compared to how much it is expected to consume based on maintenance and growth requirements. This linear measure allows us to assess which animals are more profitable for the same feed input costs.

Materials and Methods

Iowa State University (ISU) has developed two lines of Yorkshire pigs from a single base population. One line has been selected for decreased RFI (more efficient) over six generations. The other line was initially randomly selected for five generations to serve as a control, but has been selected for increased RFI in the most recent generations to increase the divergence between the two lines. Each generation, growing pigs have been measured for average daily feed intake (ADFI) using electronic FIRE feeders, for 10th rib backfat (BF) using ultrasound at approximately 115 kg, and for average daily gain (ADG) between approximately 90 and 210 days of age. A whole-genome association analysis was completed using 716 pigs with

complete phenotypic data from these lines (387 from the select line, 329 from the control line). Animals were genotyped for 64,232 genetic markers spread across the genome. A statistical program called GenSel, which was written by Drs. Dorian Garrick and Rohan Fernando at Iowa State University, was used to determine which genetic markers were most likely associated with RFI, ADFI, ADG, and BF.

Results and Discussion

For each trait, RFI, ADFI, ADG, and BF, a total of 33%, 48%, 43%, and 69%, respectively, of the variation in phenotypes between pigs was explained by sets of about 300 markers. Based on build 9 of the porcine genome, genes within the regions encompassed by the top markers were examined for functional relevance to the corresponding trait. For RFI, two candidate pathways were identified: fatty acid metabolism and production and use of energy by cells. For ADFI, the *MC4R* gene, which has been shown in several studies to impact both feed intake and growth, was confirmed to be located in a highly significant region, as well as two genes which are necessary for discriminating odors. For ADG, *MC4R* was again found to be in a significant chromosomal region. Furthermore, protein digestion was implicated in ADG differences by the genome positions of two serpins that act during digestion to block protein breakdown, as well as other genes. Finally, for BF, a very highly significant marker was in an unknown location in the genome. The *DOPEY2* gene was found near other significant markers for BF. This gene has been implicated in marbling and fat deposition in beef cattle. Overall, several previously identified and several new genes were predicted to be associated with swine feed intake and growth in this study. These gene pathways can be useful for improving our understanding of feed efficiency, which could lead to improved herd management and genetic selection.

Acknowledgements

Authors would like to thank the farm staff at the Lauren Christian Swine Research Center. Funding was provided by the Iowa Agricultural Home Economics Experiment Stations through the Center for Integrated Animal Genomics, State of Iowa and Hatch funding, the Iowa Pork Producers Association, and the National Pork Board. Support for D.M. Gorbach was provided by USDA National Needs Graduate Fellowship Competitive Grant No. 2007-38420-17767 from the National Institute of Food and Agriculture. FIRE feeders were provided by PIC and Newsham Choice Genetics.