

Genetic Pathways to Environmentally Friendly Pigs

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Summary and Implication

The Environmental Protection Agency (EPA) has enacted regulations that will restrict the amount of phosphorus (P) that can be applied to land. With the vast majority of swine production sites operating at high stocking densities and having less available land on which to apply animal effluent, increased P levels in manure could substantially increase production costs.

Introduction

The costs associated with P supplementation, as well as public concerns and the new regulatory milieu (Federal Register, 2003), have driven research towards finding ways to reduce the need for inorganic P supplementation to animal diets as well as reducing the excretion of P by these animals. In order to reduce P excretion while maintaining animal performance, researchers have examined improving the bioavailability of P from plant sources, as well as the P requirements for different genotypes and management conditions (reviewed by Jongbloed and Lenis, 1998). Despite the amount of work conducted in this area, little, if any, research has examined the underlying genetic mechanisms behind P utilization and how this may impact commercial pig production. Some research has begun to look at the effects of P nutrition on gene expression (Masuyama et al., 2000; Yoshida et al., 2001; Azam et al., 2003; Sugiura et al., 2003), but this work has only been conducted in non-agriculturally relevant species and has examined only a few specific genes. To date, no one has examined large-scale gene expression related to P metabolism and its impact on bone strength and growth of commercial pigs.

Results and Discussion

We have examined the effect of P nutrition on large-scale gene expression in pigs from two different sire lines. Exciting phenotypic differences between piglets sired by a line selected for meat quality versus those sired by a line selected for growth rate, suggesting that these pigs differed significantly in their homeorhetic control of P metabolism. Significant sire, treatment, and sire \times treatment effects were seen in gene expression in both liver and muscle tissue using microarray analysis. Several of these differentially expressed genes have been validated by real-time RT-PCR. Sire \times treatment effects were also seen in the expression, in

bone marrow, of genes known to effect osteoblast and osteoclast differentiation. Additionally, after only two

weeks on experimental diets significant sire effects on bone strength and percent ash were seen. Sire \times treatment effects were also seen for ADG and F:G, two important economic traits in US pig production. However, traditional plasma indicators of phosphorus status, inorganic P concentration and alkaline phosphatase activity, did not show any sire or sire \times treatment effects.

Our future work will look to identify new gene targets for better P utilization, as well as markers for genotype specific P requirements. This will enable genetic selection of pigs that will require less P, and therefore excrete less P as well as allow for the recommendation of specific genetic lines for producers with different waste management strategies. Improving our understanding of the genetic regulation of P homeostasis may also lead to genetic markers or new intervention strategies to improve bone integrity issues related to sow and boar longevity. Additionally, due to the physiological similarities between pigs and humans, this information could lead to genetic tests for predisposition to osteoporosis in humans.

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