Association Between Aggressive Behavior And Candidate Gene Polymorphisms:

Study Of The Brain Serotonergic System In Pigs

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Introduction

It has long been clear that there are no genes controlling behavior directly, but that there are behavior regulators in the brain. Numerous neurophysiological, neurochemical and neuropharmacological studies have demonstrated a pivotal role of brain neurotransmitters in the regulation of emotionality and behavior while current knowledge indicates that behavior-affecting genes might act via brain neurotransmitters. The problem of searching for the genetic and neurochemical determinants of aggressive behavior is complicated by their apparent heterogeneity. In fact, aggressive behavior is a complex trait, regulated by multiple factors, both environmental and genetic, as well as by a set of neurotransmitters. At the same time, it is evident that, for effective regulation, the number of genes and neurotransmitters must be limited and, therefore, the contribution of different candidate genes must be different; some genes and neurotransmitters being predominant for most kinds of behaviors (Popova, 2006).

Aggression between pigs occurs when unfamiliar pigs are mixed (on farms; in trucks carrying animals to the slaughterhouse, and during lairage). Aggression affects pig welfare (social stress, biting leading to skin lesions), production efficiency, and product quality (carcass yield because of skin lesions, meat quality). The present project is related to the European SABRE projects (WP8, “genomics and animal well-being”) and WELFARE QUALITY (WP3.2, “genetic solutions to welfare problems”). The aim is (a) to better understand the relationship between aggression, stress and meat quality at the phenotypic level and by studying gene expression in tissues relating to stress (adrenal gland) and meat quality (loin muscle), (b) to investigate the effect of aggressiveness on aggression, stress and meat quality.

A genetic component to individual aggressiveness has been described in pigs, mice and other species (e.g. Turner et al., 2006; Maxson, 1999). It is therefore possible to consider genetic selection against excessive aggressive tendencies but direct phenotypic selection is difficult in the context of commercial facilities. An alternative strategy is to search for molecular genetic polymorphisms associated with aggressive tendencies and use these for marker-

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assisted selection. We sought polymorphisms in genes known from the literature to be associated with aggressive behavior, or that will be validated as candidate genes in experimental animals. Our primary interest is the components of the brain serotonergic system that has been identified as a primary neurochemical system involved in the regulation of aggressive behavior in pigs.

Material and methods

Individual aggressive tendencies (aggressiveness) were measured after weaning at five weeks of age following a standardized mix as described and validated by Turner et al. (2006). Phenotypic information, DNA and pedigree are available for 500 animals.

Candidate genes were selected from the literature about the genetics of aggressive behaviors. They are involved in the regulation of the serotonergic system (5-HTR1A, 5-HTR1B, 5-HTR2A, 5-HTT, COMT, MAOA MAOB), the dopaminergic system (DRD1) and vasopressin (AVP, AVPR1A).

The sequences of candidate genes were obtained from the most recent databases (http://www.ensembl.org/Sus_scrofa/Info/Index) and primers for sequencing were designed with adapted software (Primer Express et Primer 3). When possible, all exons of candidate genes were sequenced in 12 animals with extreme phenotypes to detect polymorphisms. The softwares CodonCode Aligner and BioEdit were used for sequence assembly and polymorphism detection.

All animals were genotyped for these SNPs by the best available technique, such as sequencing or high-resolution melting (HRM). This technique was recently introduced to genotype single-nucleotide polymorphisms (SNPs) within small amplicons. It is based on the study of thermal denaturation of a double-stranded DNA and has advantages over other genotyping technologies (low cost, simple, fast and powerful thus able to accurately genotype many samples rapidly)

Results and discussion

Numerous new polymorphisms have been detected in these candidate genes and association studies are in progress.

Conclusion

These studies open the way towards efficient marker-assisted selection in farm animal species.

References

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