

Development of a Resource Family to Identify Genes for Meat Quality Traits in the Pig

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Summary and Implications

A three-generation resource family was initiated from a cross of Berkshire grand sires and Yorkshire grand dams. This family has now progressed to breeding F1 animals to produce 500 F2 animals. This family will be eventually used for a genome wide scan to study meat quality traits. It is hoped that genes influencing meat and muscle quality will be identified for use in future breeding programs.

Introduction

The techniques of molecular biology and molecular genetics are rapidly progressing. These methods, coupled with advances in human genetics, have opened new vistas for those investigators wishing to identify quantitative genes (quantitative trait loci or QTL) which control traits. Also over the past two years a great deal of progress has been made in development of genetic maps in the pig. Already a large international mapping effort (Archibald et al., 1994), a USDA/ARS effort (Rohrer et al., 1994), and a U.S. coordinated effort (Rothschild, 1994) have produced several genetic linkage maps for the pig. In total, approximately 1,600 genes (as of September, 1996) have now been mapped in the pig with a majority of these being anonymous molecular markers called microsatellites. These efforts to place genes and markers on chromosomes are already paying dividends in the search for molecular genetic markers for traits such as growth, backfat (Andersson et al., 1994; Rothschild et al., 1995), meat quality (Milan, et al., 1995), and reproduction (Rothschild et al., 1996).

Recent results from the NPPC Genetic Evaluation Program (Goodwin, 1995) have revealed that considerable differences in meat quality exist between the breeds and that the Berkshire breed, in particular, has very positive meat quality traits. The general use of genes and genetic markers makes it possible to localize the QTL responsible for meat quality traits. However, useful resource families (those which can be used to discover the genes and markers for the traits of interest) do not exist. Three generation resource families need to be developed with the Berkshire breed in order to determine the genes responsible for, and the markers associated with, meat quality traits. Thus, enormous opportunities exist to fully extend the previous research to pinpoint the location of genetic markers associated with meat quality in the pig if resource families can be developed. Our research will lay the framework for the study of the genetics of meat quality in pigs. We plan to produce a large, three generation family which will

produce crosses that can be studied for meat quality traits. At present, such families for meat quality traits are limited and none include the Berkshire breed.

Objectives

The overall goal of this research is to develop a three generation resource family for muscle quality traits and to eventually identify and pinpoint specific molecular genetic markers which control quantitative trait loci (QTL) which affect these traits in the pig.

Results to Date

Procedures to develop a resource family include breeding diverse breeds of animals. The Berkshire breed and the Yorkshire breeds have been chosen for the F0 generation. A total of approximately 2 Berkshire boars (chosen with NPPC guidance) and 14 Yorkshire females were used to produce 14 useful F1 litters. Semen from boar studs was used and sows mated at the ISU Swine Breeding Farm. The two boars used were Casino and Count. From the F1 litters, 6 boars and 23 females were chosen to produce 500 F2 animals for genetic and meat trait analysis. Breedings for the F2 generation have been completed and litters are due in January.

Blood samples are being collected from all animals. DNA samples from all resource family members will be collected as needed for future molecular analysis. We expect to start collecting growth, carcass, and meat and muscle quality data beginning in June 1997. A plan (Figure 1) is being devised to genotype all 500 F2 and their parent and grandparents for 75 well spaced genetic markers. These genetic markers will be about four per chromosome (see Figure 2 for an example for chromosome 4) and this genome scan will then be used to identify regions of the genome that are associated with meat and muscle quality. This research is a truly multidisciplinary effort and combines the fields of gene mapping and molecular genetics with quantitative swine genetics. Funding for this three year project is about \$210,000. NPPC and several breeding companies, Babcock, Danbred, Dekalb, PIC, and Newshams have agreed to participate in the funding of the project. Additional companies or organizations may also participate.

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Figure 1. Meat quality genome scan project plan.

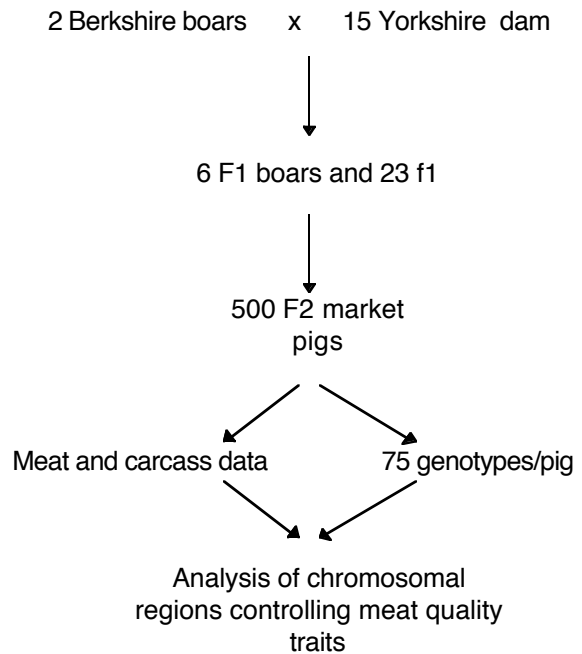


Figure 2. Example of anonymous genetic markers to scan chromosome 4 for meat quality traits.

