

Joint Analysis of Two Breed Cross Populations for Genes Affecting Growth and Meat Quality in Pigs

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Summary and Implications

A joint analysis of two F₂ crosses between commercially relevant breeds, Berkshire x Yorkshire, and Berkshire x Duroc, was conducted to identify chromosomal regions (quantitative trait loci or QTL) associated with growth, composition, and meat quality traits for four chromosomes. Joint analysis led to greater power to detect QTL, greater QTL mapping precision and better characterization of QTL. This enables proper definition of QTL in terms of inheritance mode of gene action and of segregation of alleles within the parental breeds, which provides valuable information for subsequent QTL analyses and marker-assisted breeding schemes. Because the populations studied were derived from commercially relevant breeds, the QTL identified have important economic effects for pork production.

Introduction

Over the past decades, several resource populations have been developed from breed crosses to detect chromosomal regions associated with traits of economic importance, i.e. QTL. Although these studies have led to the identification of many QTL regions, their power has been limited by size of the individual mapping populations. Objectives of this work were to overcome the limited power of individual studies is by combining data from different QTL mapping populations.

Materials and Methods

Data on growth, carcass composition and meat quality traits from F₂ crosses between commercially relevant pig breeds were used: a Berkshire x Yorkshire cross with 525 F₂ progeny at Iowa State University (ISU), and a Berkshire x Duroc cross with 825 progeny at the University of Illinois (UOI). Twenty-six traits that were common to both populations were included in the joint analysis. These included traits related to preweaning growth (birth weight, weaning weight (at day 16 and 21 in the ISU and UOI populations, respectively), and average daily gain from birth

to weaning), post-weaning growth (average daily gain from weaning to slaughter and live weight at slaughter), body composition (carcass weight, carcass length, loin eye area, and backfat at the tenth, lumbar, last rib, and average backfat), fat content (lipid % in the loin and marbling score), glycogen (glycogen content, lactate content, glycolytic potential), color (color score, 24-hr Hunter reflectance in the loin), 24-hr loin pH, sensory measures (juiciness and tenderness score), and other taste-related measures (firmness, percent cooking loss, average star probe force, and average drip loss). All animals were genotyped for a total of 39 (ISU) and 32 (UOI) markers on chromosomes 2, 6, 13 and 18. Marker linkage maps derived from the individual and joint data were similar with regard to order and relative position, but some differences in absolute distances existed. Maps from the joint data were used in all analyses. The individual and joint data sets were analyzed using several least squares interval mapping models: line-cross (LC) models with Mendelian and parent-of-origin effects, halfsib models (HS), and combined models (CB) that include LC and HS effects. Lack of fit tests between the models were used to characterize QTL for mode of expression and to identify segregation of QTL within parental breeds.

Results and Discussion

A total of 26 (8), 47 (18) and 53 (16) QTL were detected at the 5% chromosome (genome)-wise significance level in the ISU, UOI and joint data for the 26 analyzed traits. Of the 53 QTL detected in the joint analysis, only 6 were detected in both individual populations and for many QTL, allele effects differed between the two crosses. Despite the lack of overlap between the two populations, joint analysis resulted in an increase in significance for many QTL, including detection of nine QTL that did not reach significance in either population. Confidence intervals for location on the chromosome of the detected were also smaller for several QTL. In contrast, 24 QTL, most of which were detected at chromosome-wise significance levels in the ISU or UOI population, were not detected in the joint analysis. Presence of a QTL that is only expressed when inherited through the sire, near the IGF2 region of chromosome 2, was confirmed. This QTL has major effects on backfat and loin-eye area. Paternally expressed QTL were also detected for carcass composition in the distal arm of chromosome 6.