Detection and Characterization of Genes for Meat Quality in Pigs using Combined Line-cross and Half-sib Analysis

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Summary and Implications

Data from an F2 cross between the Berkshire and Yorkshire breeds was used to detect and characterize chromosomal regions (quantitative trait loci, QTL) that affect growth, composition, and meat quality traits. A new method of analysis was used that combines the power of the line-cross model to detect QTL that differ between the breeds and the half-sib model to detect QTL that segregate within the breeds. The complementary information that is capitalized on in the combined models increased the number of QTL detected and allowed characterization of the detected QTL in terms of their segregation within the original breeds. This provides valuable information for subsequent QTL analyses and marker-assisted breeding schemes.

Introduction

Data from an F_2 cross between breeds of livestock is typically analyzed using a least squares line-cross (LC) or half-sib (HS) model to detect QTL that differ between breeds or that segregate within breeds, respectively. The LC and HS models can also be combined (CB model) to increase power to detect QTL. The purpose of this study was to develop and evaluate this method of analysis and to apply the developed methods to detect and characterize QTL for growth, carcass composition and meat quality in a cross between two commercial breeds of pigs.

Materials and Methods

Methods for analysis of data from a breed cross using the LC, HS, and CB models were developed. To evaluate the power of the CB model and to determine the ability to differentiate LC, HS, and CB QTL, phenotypic data, marker data and a biallelic QTL were simulated on 512 F_2 progeny with various differences in QTL allele frequencies between the grandparental breeds.

Methods were applied to data on 39 growth, body composition and carcass quality traits on 525 F2 pigs from a cross between the Berkshire and Yorkshire breeds were used. Pigs were genotyped for 183 genetic markers across the genome. The LC, HS, and CB models were applied to the data to detect QTL across the genome. Lack of fit tests were used to distinguish between QTL that are fixed for alternate alleles in the Berkshire and Yorkshire breeds (LC QTL), or that are segregating at similar (HS QTL) or different (CB QTL) frequencies between the two breeds. Significance tests were derived using data permutation.

Results and Discussion

Application of the three models to the simulated data resulted in an increase in the power to detect a range of QTL, depending on their frequency difference (FD) between the parental breeds. The LC model was most powerful to detect QTL that were fixed for alternate QTL alleles in the parental breeds (FD=1); the HS model most powerful for QTL that were segregating at similar frequencies in the breeds (FD=0), and the CB model was most powerful for QTL with FD around 0.5. The proportion of detected QTL that was declared as LC QTL was greatest for FD=1 and decreased with FD. The opposite was observed for HS QTL. The proportion of CB QTL was greatest for FD=0.5 and decreased as FD moved away from 0.5. The latter was more pronounced for the large than for the small QTL.

Application of the developed methods to the Berkshire x Yorkshire data resulted in the detection of a total of 160 QTL for the 39 growth, carcass composition and quality traits at a 5% chromosome-wise significance level. In many cases, QTL for several traits with similar characteristics were found in the same chromosomal region. These may represent QTL with pleiotropic effects. Of the 160 QTL, 72, 54 and 34 QTL were declared as LC, HS, and CB QTL, respectively. Fourteen QTL were detected only by the CB model. Forty QTL were highly significant (at the 5% genome-wise level). Of these, 16, 8, and 16 QTL were declared as LC, HS and CB QTL, respectively. The QTL at the 5% genome-wise level explained from 3.5% to 13.3% of phenotypic variance. These results confirm that application of the three models improves the ability to detect and characterize QTL by providing some information on the distribution of QTL alleles across the parental breeds. The latter is important information for follow-up QTL analyses and for their use in marker-assisted breeding schemes.