Signatures of Selection for Intramuscular Fat in Duroc Pigs

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Eui-Soo Kim, Research Associate;
Roger Ros-Freixedes, Graduate Student, Univeristy of
Lleida, Spain; Joan Estany, Professor, University of Lleida,
Spain;
Tom Baas, Professor, Department of Animal Science;
Max Rothschild, Professor, Department of Animal Science

Summary and Implications

Intramuscular fat (IMF) content is an important trait affecting the quality of pork. Two Duroc populations (Iowa and Spain) selected for IMF were used to identify signatures of selection associated with IMF. The effects of selection were analyzed between two groups representing essentially select and control animals within each population using a discriminant analysis of principal components and Wright's fixation index (F_{ST}) using 60k SNPs. Moreover, extended haplotype homozygosity-based approaches were used to examine the changes in haplotype frequency due to recent selection. New genomic regions have been identified by use of selection signatures and should provide useful information identification of genes involved in IMF and future selection.

Introduction

IMF affects both the organoleptic quality and nutritional value of pork. Selection experiments for high levels of IMF have been performed in Duroc pigs. Genome-wide association studies (GWAS) enable researchers to determine regions affecting variation in a trait. Previous studies have reported quantitative genetic parameters and GWAS of IMF. However, GWAS can generate some false positive associations. This remains an obstacle, although sophisticated statistical tests have been proposed to reduce false positives. To tackle this problem, a complementary approach has been suggested called identification of signatures of selection to reveal genomic regions associated with recent selection for a trait.

Materials and Methods

A total of 144 Duroc pigs were sampled from the 6th generation of a selection experiment for IMF at Iowa State University, Ames Iowa USA (Population A). In Population A, half of the animals (n=73) were obtained from the line selected for increased IMF without restrictions (High IMF line; with 4.46% IMF in loin, SD 1.80%), while the remaining 71 animals were randomly sampled from the control line that maintained average levels of IMF (Low IMF line; with 2.71%, SD 0.98%). A population of 138 Duroc barrows from a Spanish Duroc line were also sampled (Population B). Because IMF content was considered near the optimum in Population B (3.58%, SD 1.21%), selection during the period from 2002 to 2009 was aimed at maintaining IMF. All Duroc pigs were genotyped using the PorcineSNP60 (Illumina, CA). F_{ST} is calculated as a measure of population differentiation between two genetically divergent groups. Moreover, we used methods to detect a decay of the extended haplotype homozygosity (EHH) in regions that have been subject to variation influencing fitness. EHH was performed within each line (iHS) or the comparison of lines (Rsb) in a population.

Results and Discussion

Each statistical method identified 10-20 selection signatures, which may reveal those regions under different footprints of selection. Out of these candidate regions, less than 10 selection signatures were confirmed by more than two different statistical methods (Table 1). A few haplotype-based signatures of selection agreed with limited GWAS, while F_{ST} measures showed better agreement with GWAS results. Agreement of marker-trait associations and signatures of selection was limited and further examination will be necessary to understand the effect of selection on this trait and why some regions identified by GWAS did not appear to respond to the selection practiced. Identifying the regions involved in selection for IMF will be useful to find potential candidate genes underlying genetic improvement.

Table 1. Genome-wide signatures of selection and associations[*]

SSC	Region (Mb)	F_{ST} (Mb)	GWAS (Mb)	EHH
1	281.2-285.5	0.55 (283.5)	3.57 (284.3)	EHH (Rsb)
4	4.54-7.74	0.73 (50.1)	3.68 (50.1)	EHH (Rsb)
9	31.1-38.1	0.61 (32.1)	3.47 (32.0)	EHH(iHS)-Low line
	106.5-108.4	0.46 (107.8)	3.38(108.4)	-
11	0.3-4.4	0.45 (1.0)	4.01 (1.1)	-
	21.1-22.8	-	3.25 (21.3)	EHH(iHS)-High line
13	17.9-21.5	0.54 (19.9)	3.06 (19.9)	-
15	28.4-35.6	0.36 (31.6)	3.55 (31.4)	-

[*]significance level; 0.4 for FST; -log10 > 2.7 for GWAS; |iHS|>3; |Rsb|>3.