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Signatures of Selection in Two Independent Populations of Pigs Divergently Selected for Feed Efficiency

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Signatures of Selection in Two Independent Populations of Pigs Divergently Selected for Feed Efficiency

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Summary and Implications

In two independent populations of pigs, divergent selection for increased and decreased feed efficiency, measured as residual feed intake (RFI), was performed over ten generations in purebred Yorkshire pigs at Iowa State University (ISU) and eight generations in French Large White pigs at the French National Institute for Agricultural Research (INRA). Over time and generations, favorable alleles for improved feed efficiency were expected to increase in frequency in the more feed efficient (Low RFI) lines, while unfavorable alleles decrease, and vice versa in the less feed efficient (High RFI) lines. When changes in allele frequency over time are more extreme than what could be caused by genetic drift, this indicates a selection signature. Genes that are important in both populations were expected to have overlapping selection signatures. In this study, two such selection signatures were identified for RFI, on chromosomes 2 and 13, with candidate genes related to protein turnover rate and mitochondrial function. These selection signatures give insight into the genetic basis of feed efficiency in pigs and markers in these regions can be used to select for more feed efficient pigs.

Introduction

In the U.S. swine industry, over 50% of production costs are attributed to feed. Genetic selection for more feed efficient pigs is desirable both from an economic stand-point and for environmental sustainability. With the objective of better understanding the genetic, physiological, and biological basis of feed efficiency (measured as residual feed intake [RFI]) in pigs, two independent populations of pigs were selected for increased and decreased feed efficiency at Iowa State University (ISU) and the French National Institute for Agricultural Research (INRA). Both selection experiments used commercial Large White pigs (commonly referred to as Yorkshire pigs in the U.S.) from their respective countries and performed divergent selection for 8 generations at INRA and 10 generations at ISU. Using genomic data on pigs from the more and less feed efficient lines (RFI lines) of these populations, genomic regions that appear to be under selection, so-called selection signatures, were identified in both populations.

Materials and Methods

Using genotype data on 3,065 pigs from the ISU RFI lines and 859 pigs from the INRA RFI lines, quality control of genotype data was performed, and 30,676 single nucleotide polymorphisms (SNP) were retained and used for further analysis. A statistic called hapFLK, that accounts for population structure and linkage disequilibrium, was used to assess changes in allele frequencies in genomic regions beyond what could be expected from genetic drift, to identify signatures of selection. False discovery rate (FDR) was used to determine a confidence threshold and only selection signatures regions with FDR less than or equal to 0.2 were considered signatures of selection.

Results and Discussion

Two genomic regions, on *Sus scrofa* chromosomes (SSC) 2 and 13, were identified as signatures of selection for feed efficiency (i.e. RFI) when the ISU and INRA populations were jointly analyzed. This indicated that these 2 genomic regions were under selection in both the ISU and INRA populations.

Further investigation of the genomic region on SSC 2, from 103 to 106 mega bases (Mb), yielded a biologically relevant candidate gene, CAST or calpastatin. Calpastatin is known to inhibit the calpain system, which breaks down proteins. Protein turnover rate has been previously shown to contribute to differences in feed efficiency in beef cattle and in the ISU RFI lines; calpastatin activity in the longissimus muscle was found to be greater in the more feed efficient line of pigs at ISU. The role of calpastatin and the calpain system in the INRA RFI lines is less clear because no significant differences in calpain activity were observed in previous studies.

The signature of selection on SSC 13, from 189 to 191 Mb, was also investigated further and the GA binding protein transcription factor alpha subunit (GABPA) gene, which is likely involved in mitochondrial function, was identified as a biological candidate. Mitochondrial activity and efficiency have been shown to contribute to differences observed in feed efficiency in both populations (ISU and INRA).

In conclusion, signatures of selection were identified in two independent populations of pigs selected for increased and decreased feed efficiency. These regions contain candidate genes related to protein turnover rate and mitochondrial efficiency, suggesting that these biological processes underlie differences in feed efficiency in pigs.