Analysis of Public Single Nucleotide Polymorphisms in Commercial Pig Populations

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Abstract

Farm animal breeders have started applying marker-assisted selection to improve the quality and performance of their livestock (1). However, so far, only relatively few genetic markers associated with economically important traits in pig have been identified. These markers include polymorphisms associated with commercially important variation in growth and fatness, litter size, disease resistance, meat quality and muscle growth (meat yield). Recently, the US Meat Animal Research Center (MARC) has identified and deposited in the public domain more than 5500 pig SNPs (2). In that project, Fahrenkrug and collaborators used for SNP discovery, a DNA panel made from animals representing Chinese and Western breeds. The value for linkage and association studies of these SNPs in commercial populations remained unknown, as they may only segregate in one or the other of the foundation breeds. Therefore, determination of the allele distribution and heterozygosity in populations important to pork production is critical for the commercial application of these polymorphisms.

To test the usefulness of these public SNPs, we analysed 109 pig SNPs in six commercial populations. A functional PCR assay was obtained for 103 SNPs and it was possible to validate ~59% by PCR-RFLP. Furthermore, polymorphisms were found using a relatively limited number of genomic DNA samples, indicating that these polymorphisms are segregating at a useful frequency in these populations.

The high percentage of validated markers in breeds important to commercial pork production demonstrates the utility of the pig SNPs deposited in the public domain. This resource will help pig breeding companies to identify loci responsible for economically important traits, such as disease resistance, meat quality or reproductive performance. In addition, this collection of public SNPs will allow the development of new tools for individual identification and parentage analysis (3-4).

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References

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