

Genetic variation and functional diversity in Chinese and European pig breeds

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Protection of genetic diversity requires effective methods of germ-plasm conservation and analysis. The EC PigBioDiv2 project (www.pigbiodiv2.com) uses molecular approaches to characterize pig genomic diversity and introduces new methods of analysis for improved assessment of genetic resources, in particular the identification of genomic regions contributing to functional differences among breeds. An understanding of genetic diversity, along with phenotypic characterization, of breeds will assist the agricultural industry in its ability to respond to market changes and to manage genetic resources in a sustainable manner. PigBioDiv2 is also a unique project in the global effort to maintain animal genetic diversity. China is a major international reserve of pig genetic diversity and PigBioDiv2 is a co-operation between Chinese and European partners to characterize this immense resource.

The European pig industry currently relies on a limited number of breeds but in spite of the dominance of these breeds there remain a large number of traditional breeds in Europe (33% of the UN Food and Agriculture Organization inventory). A similar situation exists in China, a country which also has a very large number of traditional breeds (34% of the FAO inventory) which are unique to the region. These traditional breeds provide potential sources of novel genetic variants which may be valuable to producers, supplying the diversity which will allow exploitation of future market opportunities and the creation of sustainable agricultural systems in the 21st century.

The PigBioDiv2 project uses the methods, markers and database resources established by the first EC pig biodiversity project, PigBioDiv1. In addition, inclusion of mtDNA and Y chromosome markers, the first time the Y chromosome has been studied in the pig, has enhanced the characterization of diversity. The study of trait candidate genes and genomic regions containing known quantitative trait loci (QTL) also gives insight into the origin and distribution of functional mutations in the pig. Analysis of thirty candidate genes implicated in growth, meat quality, fertility, disease resistance and coat colour shows 50 European and Chinese breeds dividing into two major groups. A few breeds show intermediate characteristics suggestive of mixed ancestry. Breed groupings, based on loci affecting different traits, follow the patterns predicted by known phenotype.

Key words: Chinese, European, genetic, diversity