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P4066 Genetic diversity of pig populations from the US mainland, Pacific islands and China:

Autosomal SNP evaluation. H. Blackburn (National Animal Germplasm Program ARS-USDA, Fort Collins, CO), D. A. Faria (National Animal Germplasm Program, Fort Collins, CO), C. Wilson (National Animal Germplasm Program ARS-USDA, Fort Collins, CO), and S. R. Paiva (EMBRAPA- LABEX US-Secretariat International Affairs, Brasilia, Brazil)

Genetic diversity for 19 pig populations ($n = 500$) that had entered the US gene bank were evaluated using a commercially available 70K SNP chip for pigs. Berkshire, Duroc, Hampshire, Landrace, Yorkshire, Chester White, and Spotted represented commercially vibrant breeds; Fengjing, Guinea Hog, Hereford, Large Black, Mangalista, Meishan, Minzhu, Ossabaw Island, and Tamworth were among the minor breeds; and feral hogs from the Pacific islands of Guam, Kauai (Hawaii, HI), and Hawaii (HI) were included in the study. All breeds, with the exception of Mangalista, have been well established in the US for one century or longer, or they were developed in the US. After basic quality control procedures a total of 8765 SNPs were used for analysis. Observed heterozygosity ranged from 0.29 (Meishan) to 0.62 (Mangalista). A Bayesian genetic structure analysis suggested 7 main clusters: 1.) Chester White–Landrace; 2.) Meishan–Fengjing–Minzhu; 3.) Guam–Kauai–Hawaii; 4.) Tamworth–Duroc–Hereford; 5.) Berkshire; 6.) Hampshire; and 7.) Yorkshire. All breeds evaluated were aligned on four vectors in a three dimensional principal components (PC) analysis. The first principal component (PC) indicated a distinct separation among breeds derived from Asia and the US, with the Pacific island populations being intermediate. The second and third PCs placed Hampshire, Duroc and Yorkshire at extreme positions corroborating their unique genetic variability. Also aligned on those three vectors were breeds that tended to be red, black or white in color. The Landrace and Chester White were closely placed and distinctly separated from Yorkshire. The rare breeds Guinea Hog, Large Black, and Mangalista were found to be at or near the origin of the three PCs. To better understand the genetic structure of Pacific islands populations and rare breeds a new Bayesian analysis was performed with nine populations. Two Chinese breeds and seven of the more widely sampled US breeds were discarded. With 5 clusters identified the Pacific islands populations were unique and showed little admixture with the other populations evaluated. The data suggested populations from Kauai and Hawaii are different from each other. In addition, pigs sampled on Guam were different from those from the Hawaiian Islands and China (Minzhu). This assessment suggests US pig populations have substantial genetic variability for future use and further exploration of genetic diversity among feral island populations in the Pacific is warranted.

Key Words: genetic diversity, pigs, feral populations