

35th International Society for Animal Genetics Conference

P4067 Comparing genetic diversity of pig populations on the US mainland, Pacific Islands and China: Y chromosome evaluation. D. A. Faria (National Animal Germplasm Program, Fort Collins, CO), S. R. Paiva (Embrapa-Labex US-Secretariat International Affairs, Brasilia, Brazil), C. Wilson (National Animal Germplasm Program ARS-USDA, Fort Collins, CO), and H. Blackburn (National Animal Germplasm Program ARS-USDA, Fort Collins, CO)

Genetic diversity unpins a country's ability to adapt its livestock populations to varying environmental, production and consumer changes. Conservation of genetic resources in gene banks supports national conservation efforts. Previous work with ruminants suggests US populations held in the national gene bank are genetically diverse. Here we evaluate the genetic variability captured in the US gene bank focusing on differences among Y chromosomes for different pig populations. Pigs provide an interesting model for such a study in that mitochondrial analyses suggested pigs and wild boars have a worldwide distribution with multiple domestication centers. This study analyzed 485 boars belonging to 16 breeds (7 commercial: Berkshire, Duroc, Hampshire, Landrace, Yorkshire, Chester White, Spotted; 6 rare: Guinea Hog, Hereford, Large Black, Mangalista, Ossabaw Island, Tamworth; 3 from China: Fengjing, Meishan, Minzhu) and 3 feral populations (Pacific islands of Guam, Kauai and Hawaii) by 14 SNP markers on the Y chromosome in a commercial 70K chip. After quality control (SNP call rate, heterozygosity and absence of polymorphism), 6 of the 14 markers remained in the analysis. Five different haplotypes were found among the animals sampled. The H3 was present in 278 samples (57%). Except for Large Black and Mangalista, this haplotype was observed in all breeds that came to the US via the Atlantic. H3 was also the only haplotype observed in Duroc, Yorkshire, Tamworth, Hampshire and Guinea Hog breeds. The haplotypes H1 and H2 were present in pigs from the Hawaiian Islands, China, and the US mainland. If this represents admixture between Asian and European populations it would seem to have taken place a relatively long ago. The H4 haplotype was exclusive to animals from China and the Pacific islands. Pigs from Guam and Kauai islands were the only populations exhibiting the H5 haplotype. Median joining network analysis has shown that haplotypes H4 and H5 (China and Pacific islands) are closer than the remaining three haplotypes. However, there seems to have been no human migration between Guam and Kauai Islands but there may have been exchange between Guam and Polynesia. We find it interesting that 10 of the populations sampled only exhibited one haplotype and this lack of variation was inclusive of both rare, commercially important, and Chinese breeds.

Key Words: animal genetics resources, molecular markers, conservation genetics, gene banks, phylogeography