

ABSTRACT

Estimation of inbreeding and effective population size of full-blood Wagyu cattle registered with the American Wagyu Cattle Association

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The objective of this research was to examine the population structure of full-blood (100%) Wagyu cattle registered in the United States with the American Wagyu Association, with the aim of estimating and comparing the levels of inbreeding from both pedigree and genotypic data. A total of 4132 full-blood Wagyu cattle pedigrees were assessed and used to compute the inbreeding coefficients (FIT and FST) and the effective population size (N_e) from pedigree data for the period 1994 to 2011. In addition to pedigree analysis, 47 full-blood Wagyu cattle representing eight prominent sire lines in the American Wagyu cattle population were genotyped using the Illumina BovineSNP50 BeadChip. Genotypic data were then used to estimate genomic inbreeding coefficients (FROH) by calculating runs of homozygosity. The mean inbreeding coefficient based on the pedigree data was estimated at 4.80%. The effective population size averaged 17 between the years 1994 and 2011 with an increase of 42.9 in 2000 and a drop of 1.8 in 2011. Examination of the runs of homozygosity revealed that the 47 Wagyu cattle from the eight prominent sire lines had a mean genomic inbreeding coefficient (FROH) estimated at 9.08% compared to a mean inbreeding coefficient based on pedigree data of 4.8%. These data suggest that the mean genotype inbreeding coefficient of full-blood Wagyu cattle exceeds the inbreeding coefficient identified by pedigree. Inbreeding has increased slowly at a rate of 0.03% per year over the past 17 years. Wagyu breeders should continue to utilize many sires from divergent lines and consider outcrossing to other breeds to enhance genetic diversity and minimize the adverse effects of inbreeding in Wagyu.