To: Sara Oyler-McCance

From: Chris Geremia

Re: Summary of genetic and population conditions in YELL bison

* We estimated genetic and population conditions for the YELL bison population following the methods in Natural Resource Report NPS/NRSS/BRD—2020/2097.
* One hundred and ninety individuals (n=190) were genotyped using 52 microsatellite loci for diversity and 15 microsatellite loci for cattle introgression. Sampled bison (n=190) were a subset of the population (N=5,000) that entered a brucellosis quarantine program during 2015-2020. Program eligible animals were captured after migrating out of the park, brucellosis negative at the time of capture, and less than 22 months of age. The sample is not assumed to represent overall population condition but indicate the genetic conditions of bison that can be transferred to other herds. State and federal regulations prohibit the live transfer of Yellowstone origin bison to other animals that fail to complete brucellosis quarantine.
* Cattle introgression was not detected.
* Observed heterozygosity was similar to expected heterozygosity based on Hardy-Weinberg genetics. HO= 0.628 (SD=0.14, Range 0.242-0.863) and HE= 0.631 (0.13, 0.234-0.824) averaged across loci. Classical Chi-Squared tests indicated that expected diversity was greater than observed diversity for 4 loci and was less than observed diversity for 1 locus. Mean allelic richness was AR= 4.90 (1.39). The Inbreeding Coefficient was FIS= 0.008(0.091)
* Principal component analysis and k-means clustering did not detect population structuring within the data.
* We used Program R and the adegenet, pegas, and hierfstat packages to evaluate the data.

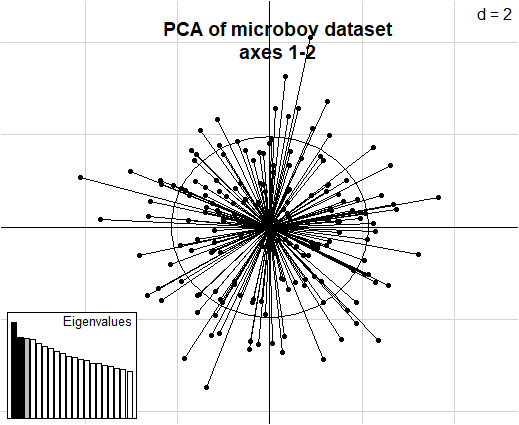


Figure 1. Principal component analysis of 52 microsatellite loci of 190 Yellowstone-origin bison