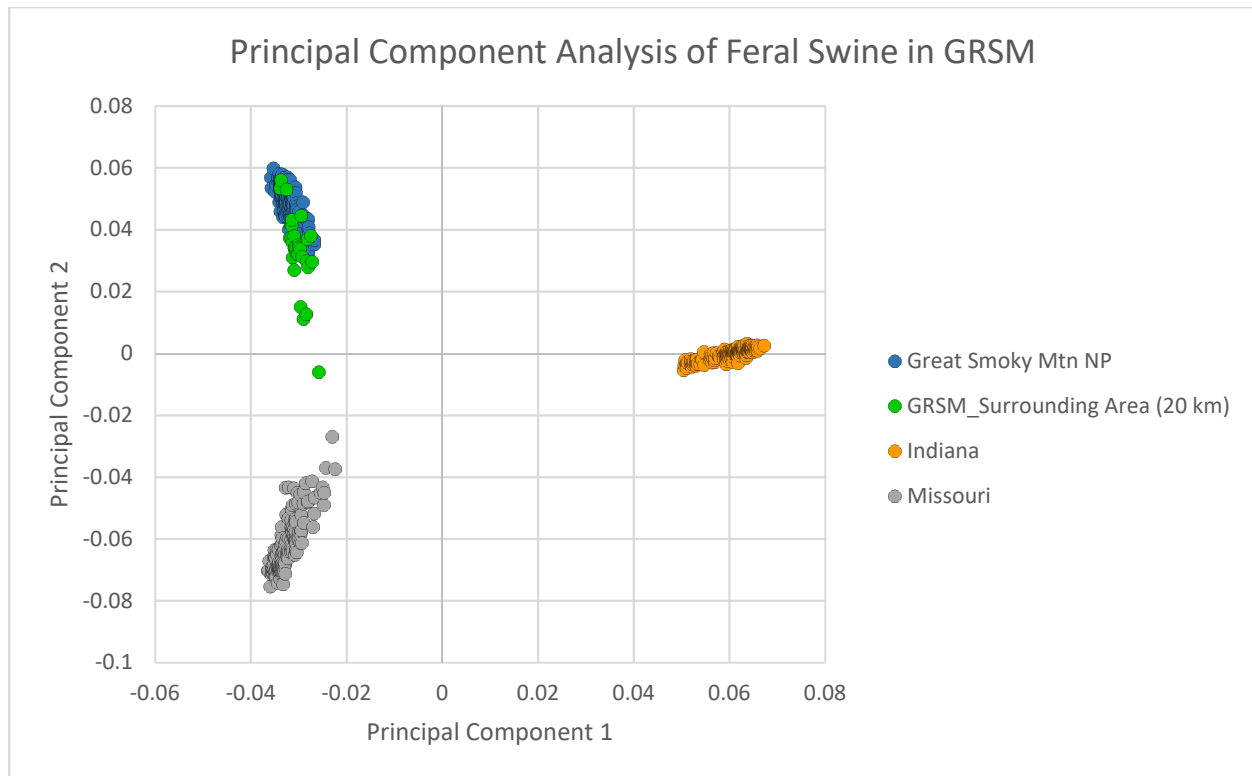


Genetic Analysis of Feral Swine in Great Smoky Mountain National Park

We have successfully genotyped 161 feral swine samples collected in Great Smoky Mountain National Park that were submitted to the USDA-National Feral Swine Genetic Archive by NPS personnel. Preliminary analyses have not demonstrated immigration of feral swine into GRSM. Specifically, all GRSM samples form a genetically cohesive group that could be considered a single biological population. Below we have presented results of a Principal Component Analysis in which we have compared GRSM samples with samples collected by Wildlife Services personnel within the vicinity of park boundaries (20 km). We have also included 2 additional feral swine populations as outgroups –Indiana and eastern Missouri. The plot below illustrates that some samples collected outside GRSM (green) have a genetic association with samples collected inside the park (blue). These samples could be interpreted as having emigrated from GRSM or their direct ancestors emigrated from the park. However, we do not have evidence of samples collected inside GRSM that appear to have originated outside of the park. One limitation of this analysis is, at this time, we do not know how far the biological population of feral swine that occupies GRSM extends outside of park boundaries. Using the analyses methods described, we cannot identify patterns of immigration/emigration within a biological (genetically cohesive) population. Thus, there may be movement across Park boundaries but that appears to be consistent with natural patterns of feral swine dispersal as opposed to anthropogenic translocation, which is frequently described for this invasive species.



Genetic ancestry has been evaluated for a subset of GRSM samples with results presented below. In sum, GRSM samples have a genetic association with European wild boar similar to that found among samples from Indiana and eastern Missouri. Indiana and eastern Missouri were deliberately selected as outgroups for this analysis due to their high wild boar association. Along with Indiana and eastern Missouri, GRSM is among the feral swine populations in the US with the highest wild boar association. However, this analysis unequivocally demonstrates that GRSM animals are of hybrid origin in contrast to small, localized populations of genetically pure wild boar found elsewhere in the US. Further, GRSM feral swine have higher wild boar associations than other feral swine found in the vicinity of the park.

Population	Sample Size	Berkshire	Hampshire	Sister Taxa	WB Sardinia	Brit Saddleback	Pietrain	Chester White_Other Breeds	Duroc_Other Breeds	Landrace	Minisibs	Minzhu_Leanhua	Sutai_Lichahei	Yorkshires	Japanese Wild Boar	Meishan_Other Asian breeds	Western Heritage Breeds	European Wild Boar
Great Smoky Mtn NP	11	5%	2%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	35%	58%
GRSM_Surrounding Area (20 km)	19	2%	2%	0%	0%	0%	0%	0%	1%	0%	0%	0%	0%	0%	0%	0%	42%	51%
Eastern Missouri	82	3%	4%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	36%	57%
Indiana	178	2%	1%	0%	0%	1%	0%	0%	0%	0%	0%	0%	0%	0%	0%	0%	38%	58%

Timothy J. Smyser, PhD
 Biologist, Wildlife Genetics
 National Wildlife Research Center
 4101 LaPorte Ave.
 Fort Collins, CO 80521
 (970) 266-6365 (office)
 (765) 586-5890 (cell)
Timothy.J.Smyser@aphis.usda.gov