

Feral Swine Genetic Attributes of Arizona



Valerie Burton, Timothy J. Smyser, Chris Tiffany, Toni Piaggio, Richard Meyers,
Brenda Zaun and David Bergman

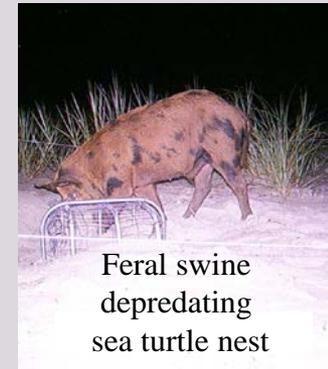
USDA – APHIS – WS - Arizona Program

USDA – APHIS – WS - National Wildlife Research Center - Fort Collins, CO

USFWS – Havasu NWR

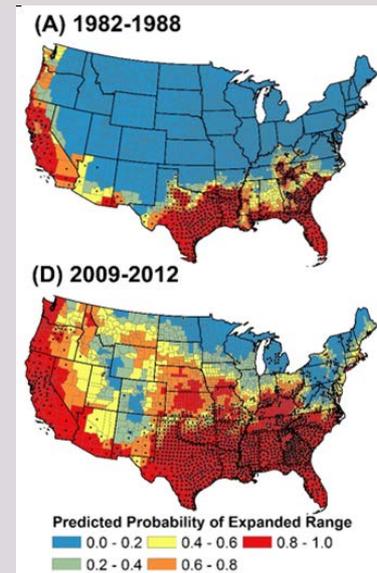
What are feral swine?

- Feral swine = Invasive Wild Pigs:
 - Free-ranging *Sus scrofa* of domestic and/or wild origins
- Most ecologically destructive invasive species in the world
 - Habitat destruction swine
 - Competition, predation/depredation:
 - Threatened and endangered species
 - Game species
- Economically costly:
 - >\$1.5 billion/year for US economy
 - Crop/property damage, disease reservoir



History of Feral Swine in the US

- 1539 - introduced to continental US
 - Spanish exploration/colonization
- 1600s through mid-1900s - augmented from free-range livestock
- 1900s wild boar augmentation
 - Improve hunting characteristics
- Remained largely restricted to SE and California until 1980s
 - Rapidly expanding in abundance and distribution
 - 1988 – 17 states
 - 2011 – 38 states

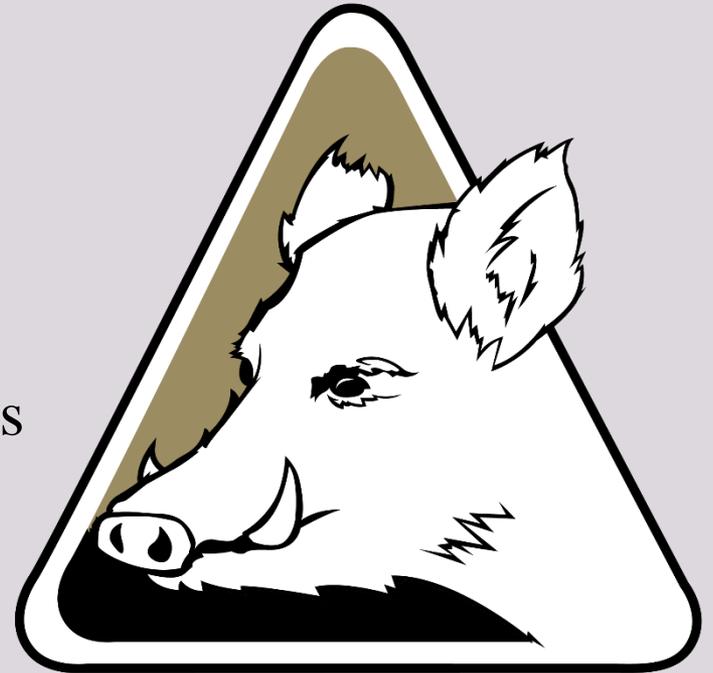


White 2011
*Environmental
History*

Snow et al. 2017 *Journal
of Applied Ecology*

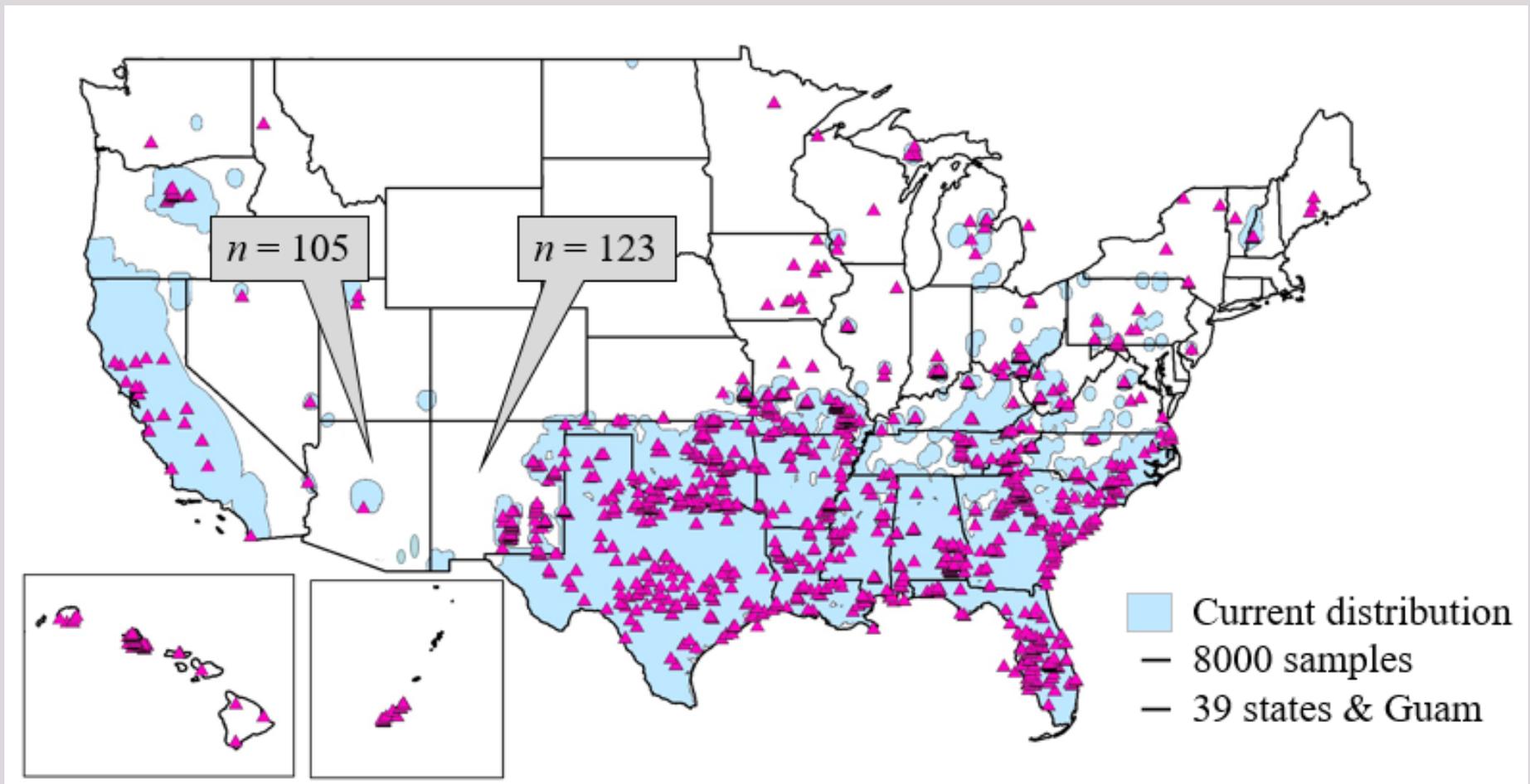
National Feral Swine Damage Management Program

- Established 2014
- National approach with local applications
 - Objectives:
 - Facilitate management efforts
 - Disease surveillance
 - Public outreach
 - Development of new management tools
 - Feral Swine Genetic Archive

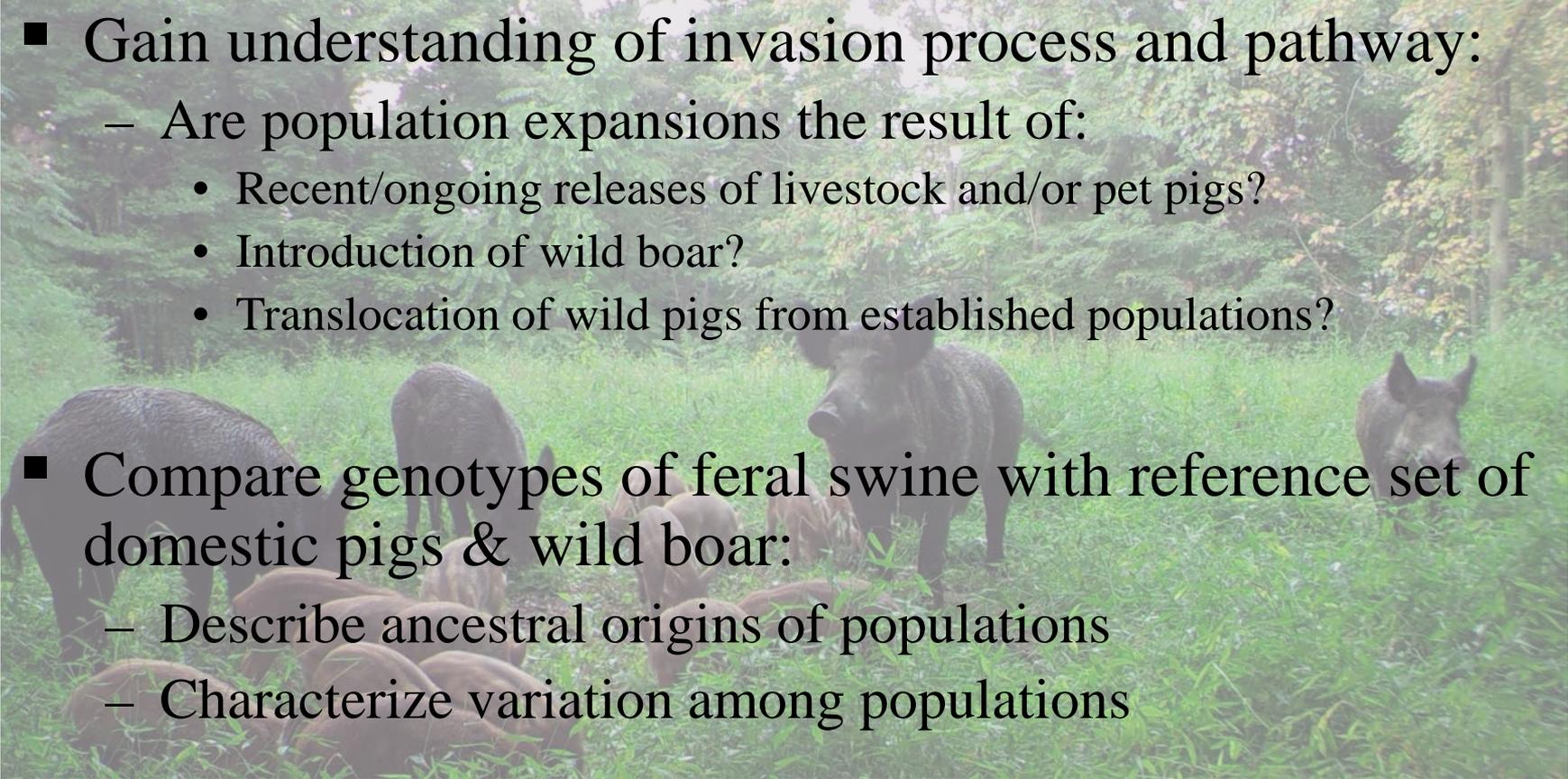


**Manage the Damage
Stop Feral Swine**

Feral Swine Genetic Archive

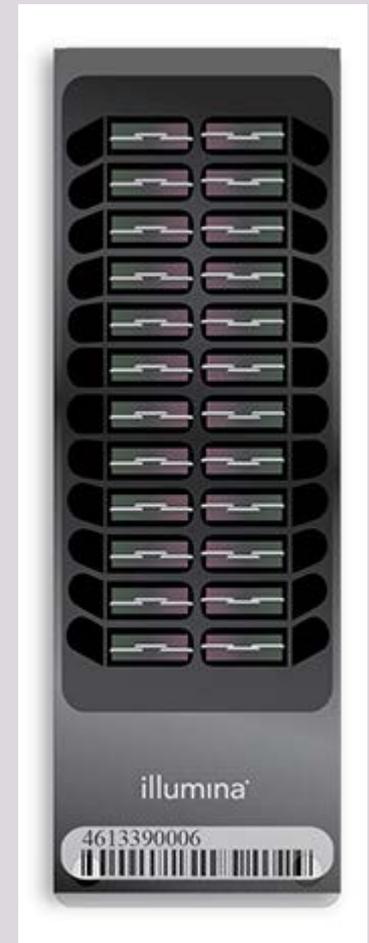


Objective

- 
- Gain understanding of invasion process and pathway:
 - Are population expansions the result of:
 - Recent/ongoing releases of livestock and/or pet pigs?
 - Introduction of wild boar?
 - Translocation of wild pigs from established populations?
 - Compare genotypes of feral swine with reference set of domestic pigs & wild boar:
 - Describe ancestral origins of populations
 - Characterize variation among populations

Genotyping Methods

- 2516 reference samples
 - 134 reference groups
 - US/European domestic breeds ($n = 1385$)
 - European wild boar ($n = 403$)
 - Asian domestic breeds ($n = 591$)
 - Asian wild boar ($n = 109$)
 - Sister taxa ($n = 28$)
- 7622 feral swine
 - Distributed throughout US (AZ = 105, NM = 123)
- Genotyped all samples at 29,375 loci
 - 2 allele Single Nucleotide Polymorphisms (SNPs)



Analysis Methods

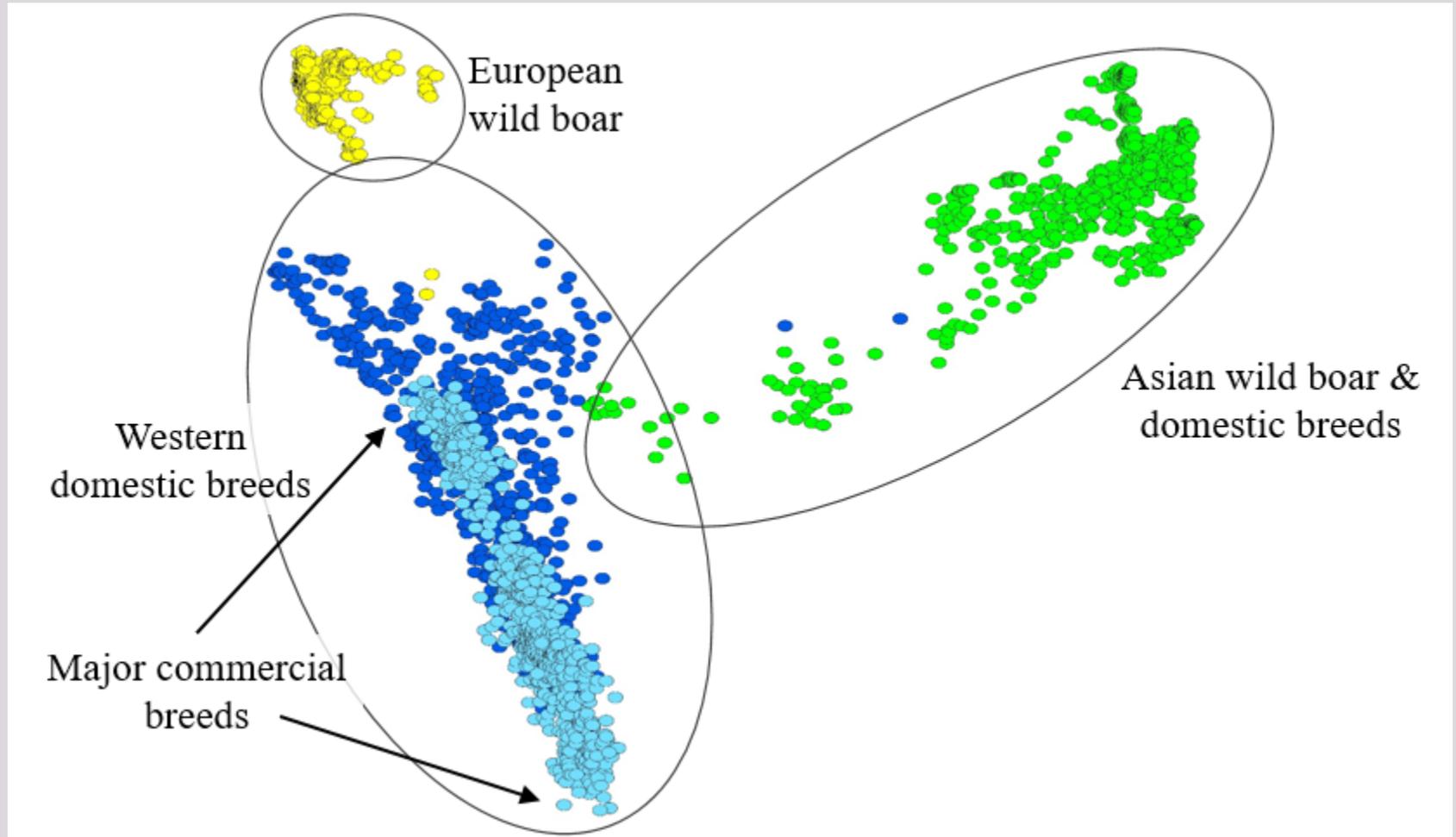
Qualitative Analysis:

- Principal Component Analysis
 - Visualize structure and pattern of data

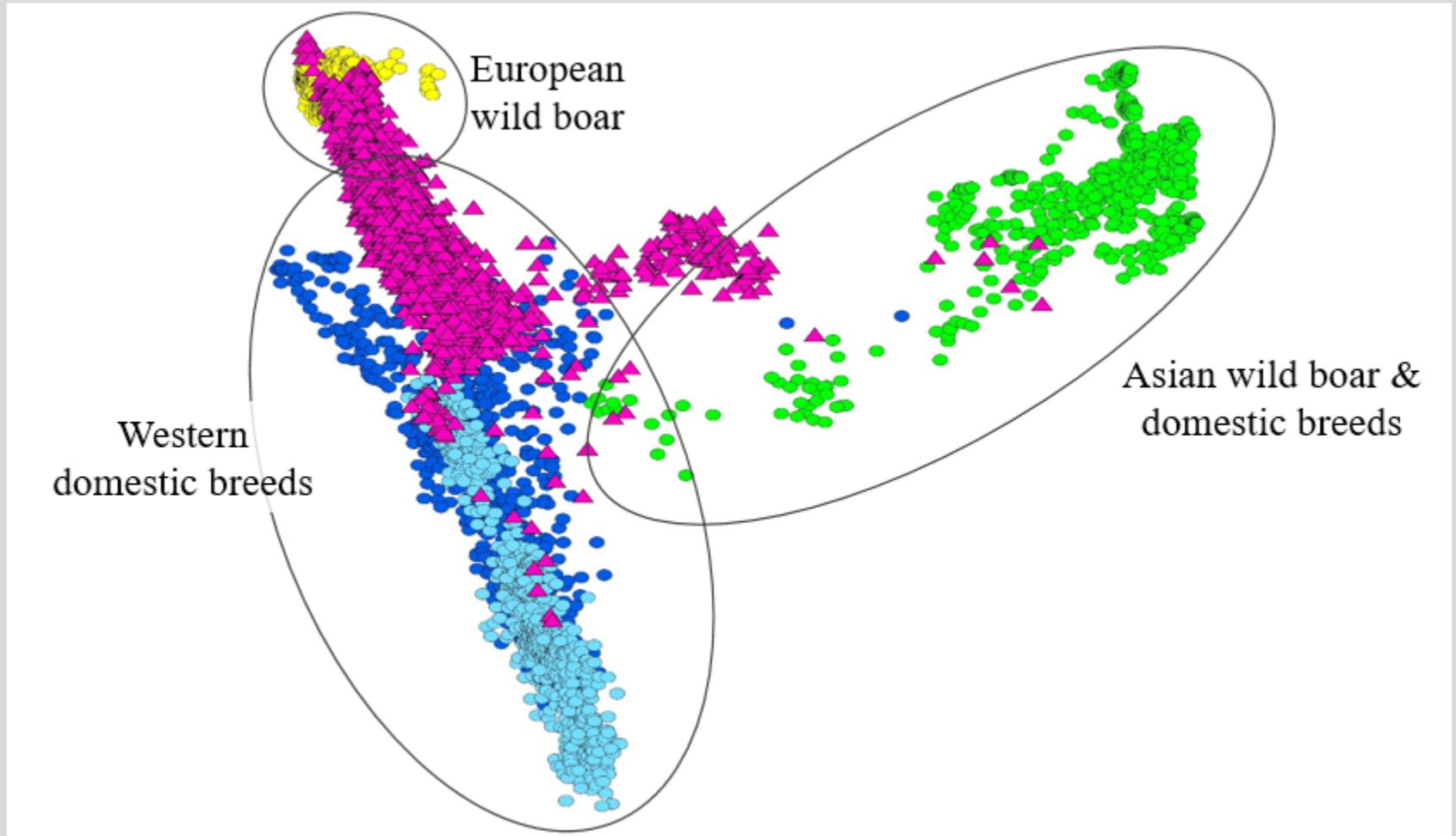
Quantitative Analysis:

- Consolidated 134 reference groups into 17 reference clusters
 - Genetically similar breeds (or populations of wild boar) combined into clusters
- Queried unknown feral swine against reference clusters
 - Allocate proportion of a feral swine genome among 17 reference clusters

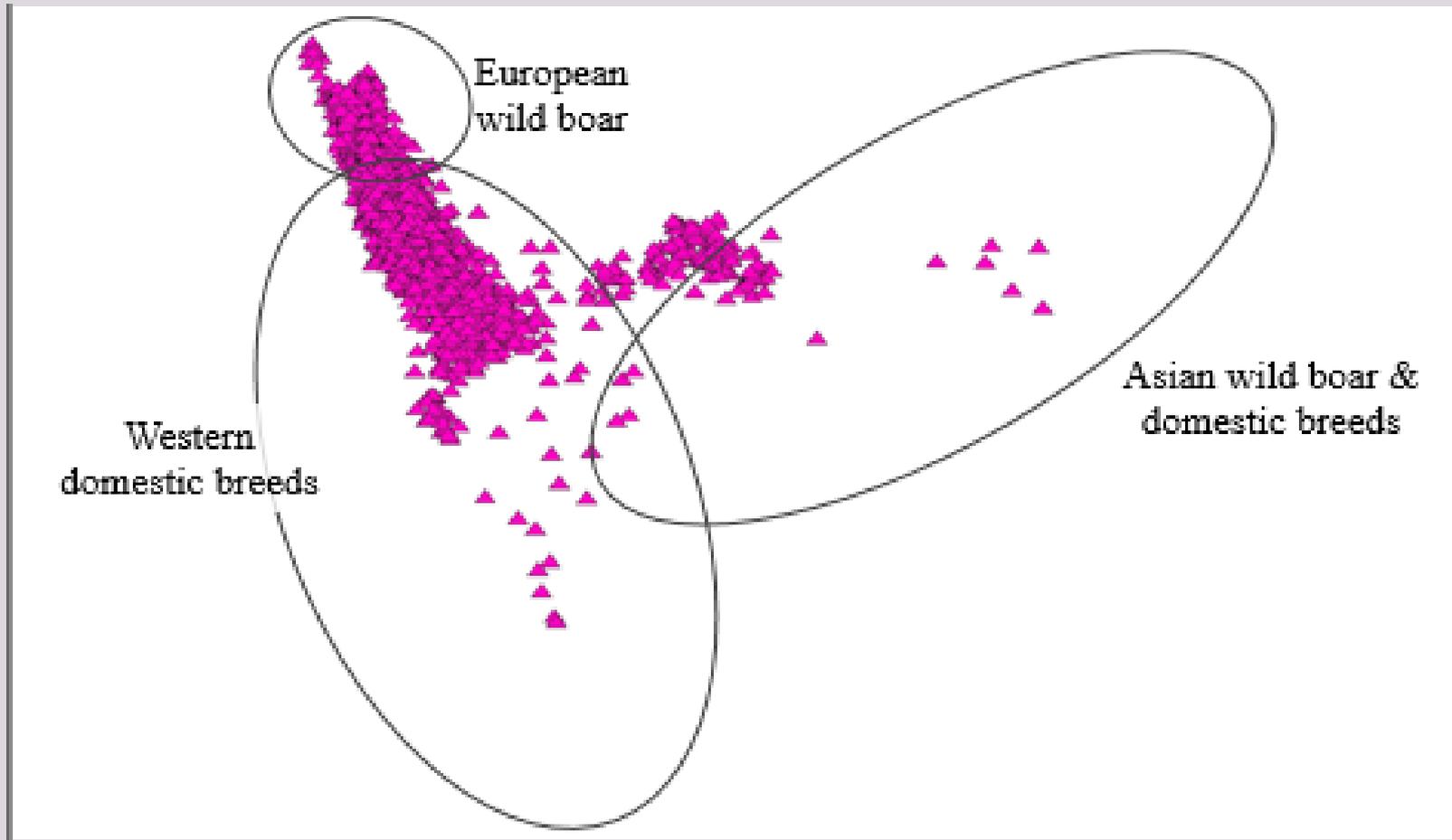
PCA Results



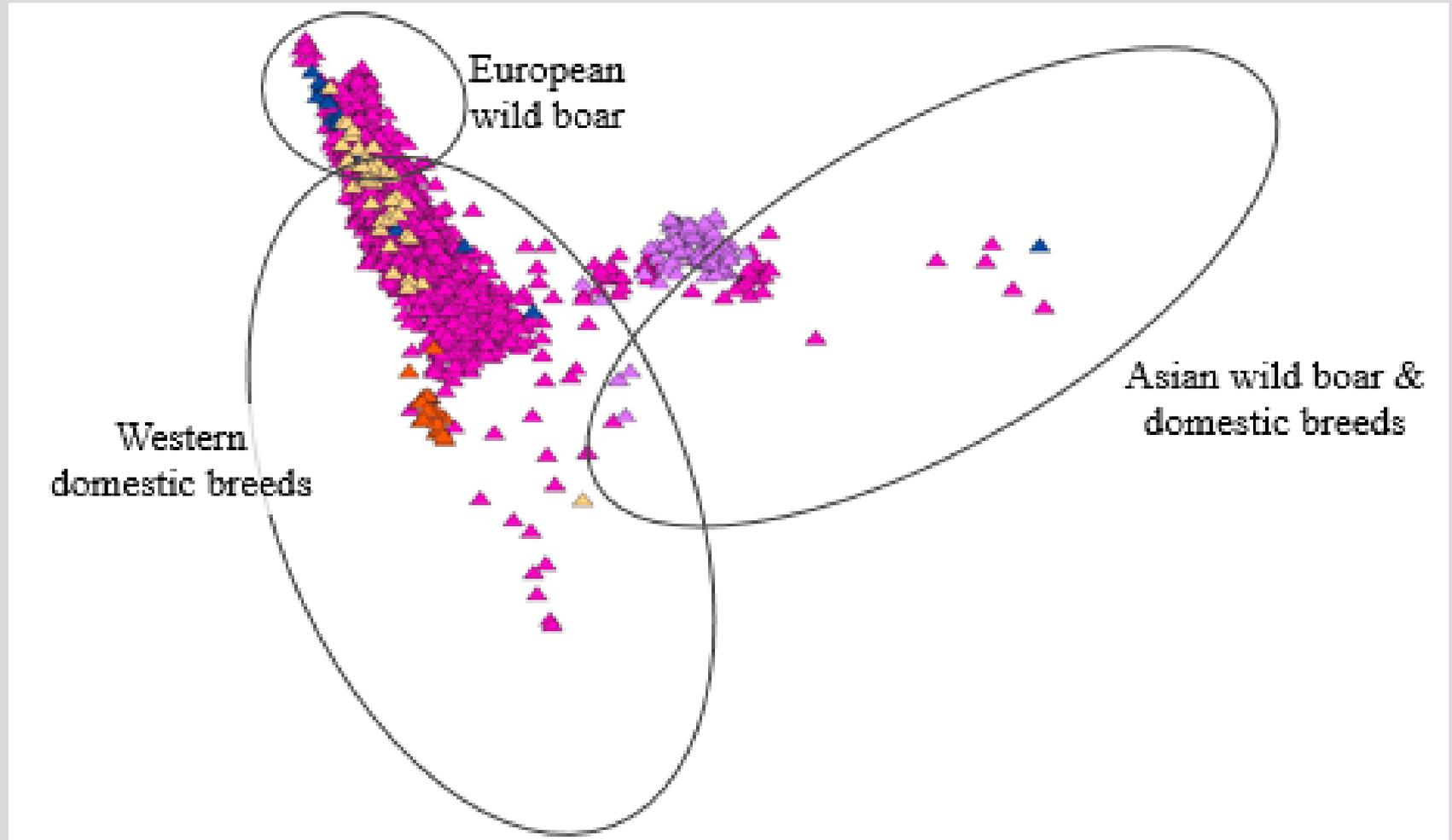
PCA Results



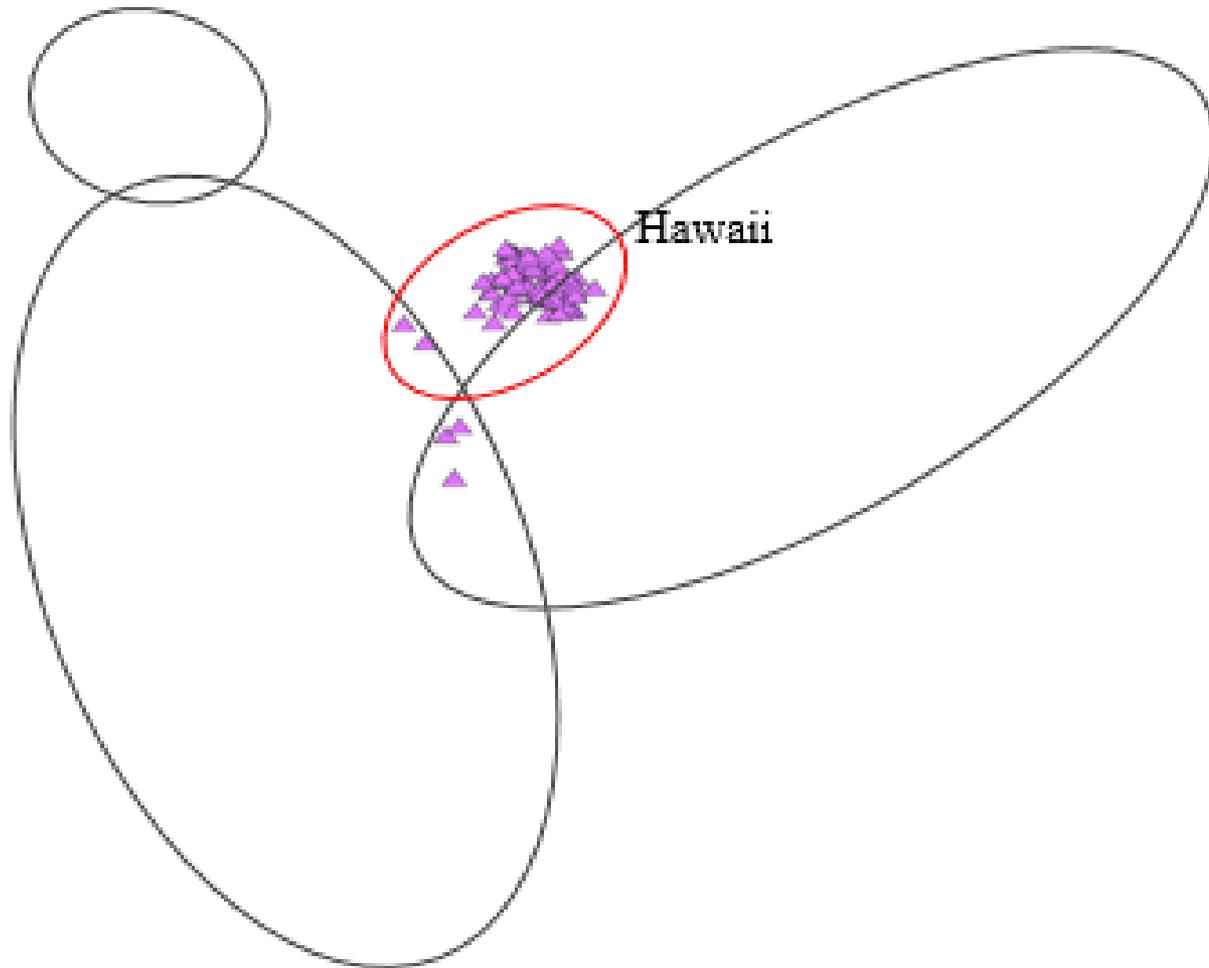
PCA Results



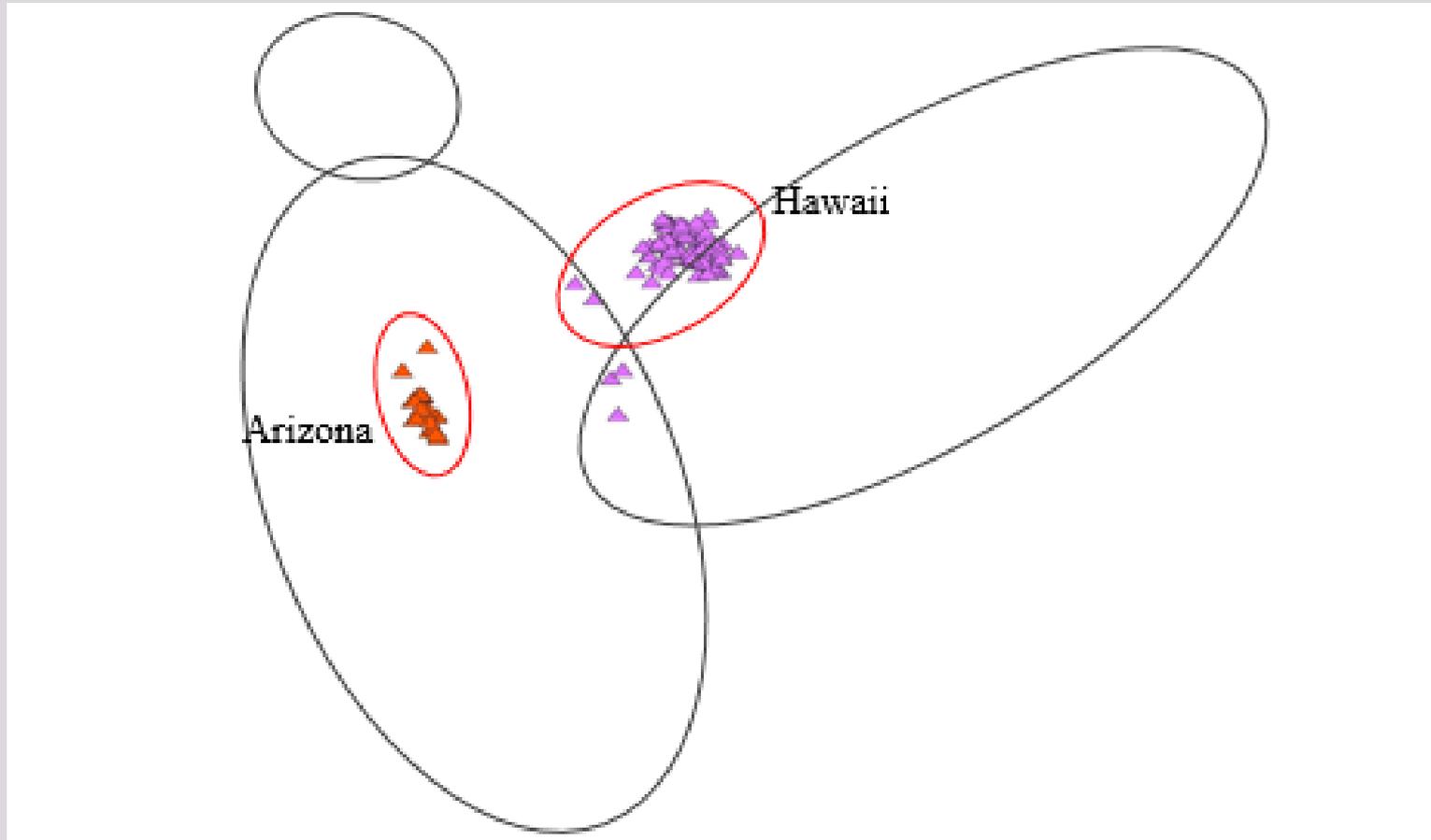
PCA Results



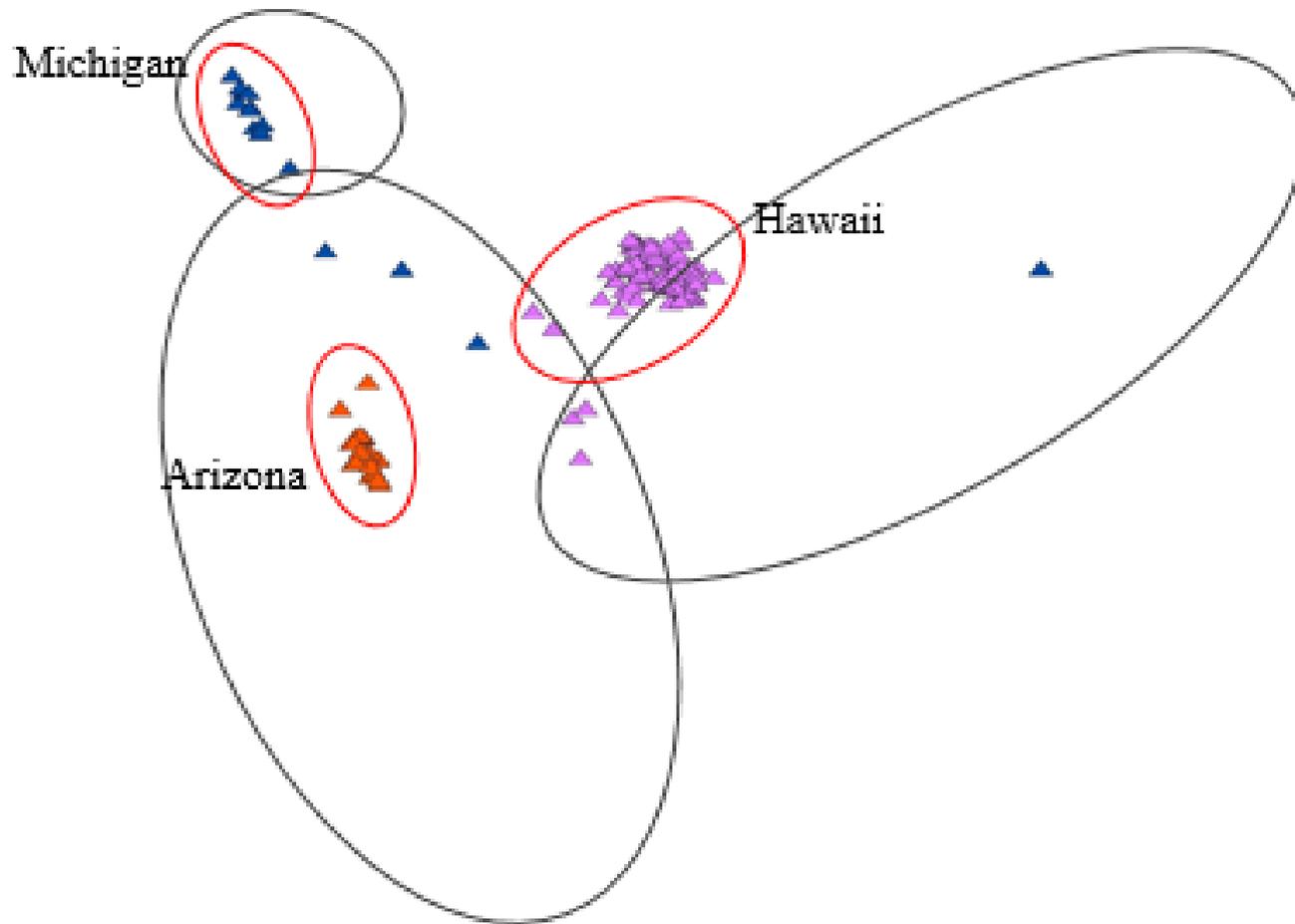
PCA Results



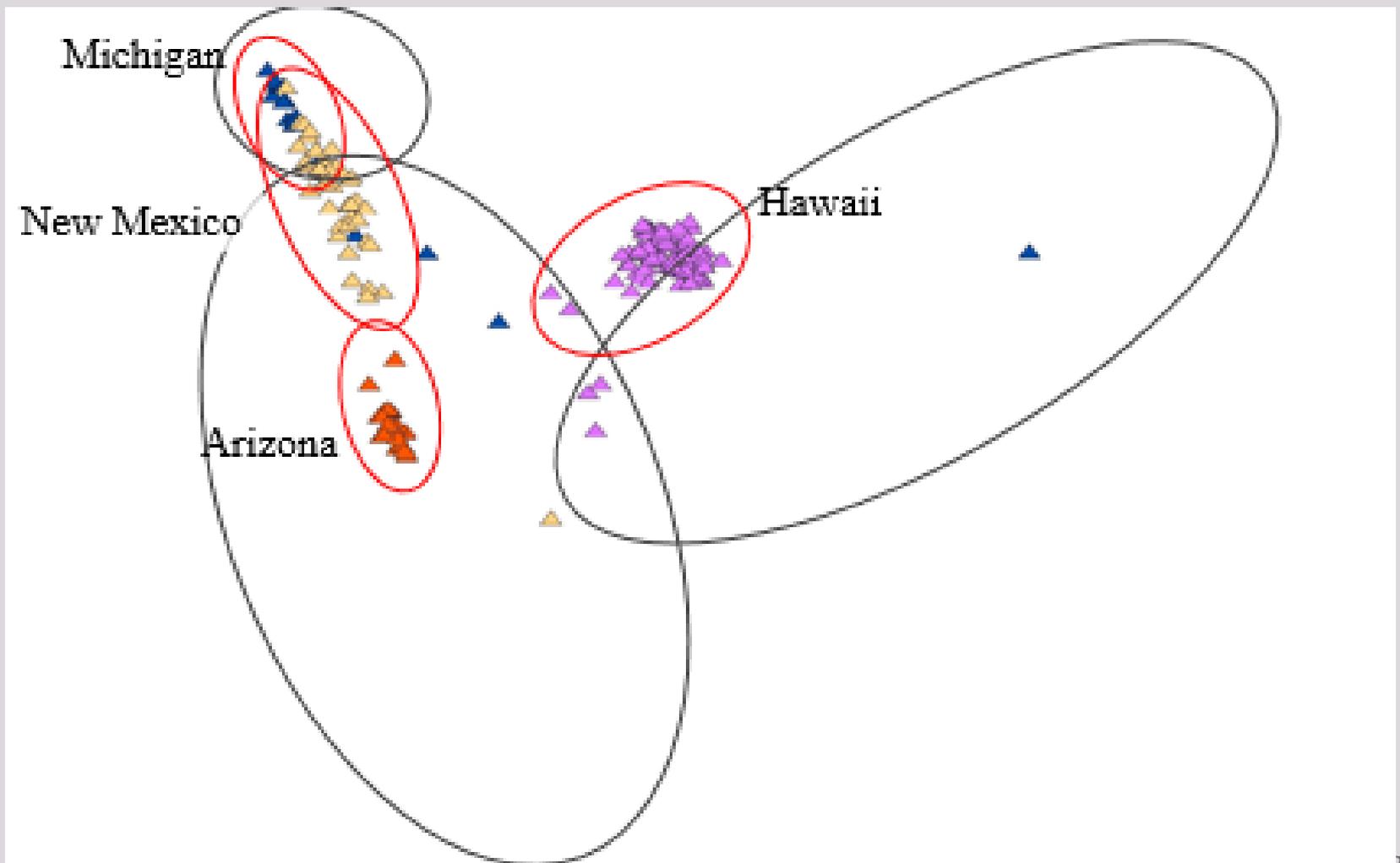
PCA Results



PCA Results



PCA Results



ADMIXTURE Results - *Continental Populations*

- Most closely associated with reference cluster composed of numerous heritage breeds
 - e.g., Guinea hog, Mulefoot, Large black, Iberian, Tamworth
 - Continental = 45%
 - Arizona = 50%
 - New Mexico = 40%
- Followed by European wild boar
 - Continental = 32%
 - Arizona = 5%
 - New Mexico = 40%
- Numerous other reference clusters make up balance

Conclusion

- Natural expansion and/or translocation most likely driver of increasing distribution
 - Recent releases from domestics or wild boar < 2% of population



Havasu NWR Feral Swine



Western Domestic Breed



European Wild Boar

Acknowledgments

- Support
 - Countless individuals from Wildlife Services Field Operations and local cooperators for collection of samples
 - Blake McCann, National Park Service
- Funding
 - National Feral Swine Damage Management Program
 - National Wildlife Disease Program
- Publically Available Data
 - Alexandri et al. 2016. Distinguishing migration events of different timing for wild boar in the Balkans. *Journal of Biogeography* 44:259-270.
 - Burgos-Paz et al. 2013. Porcine colonization of the Americas: a 60k SNP story. *Heredity* 110:321-330.
 - Goedbloed et al. 2013. Genome-wide single nucleotide polymorphism analysis reveals recent genetic introgression from domestic pigs into Northwest European wild boar populations. *Molecular Ecology* 22:856-866.

For more information

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

Thank you

