Feral Swine Genetic Archive

Last Modified:

APHIS established the Feral Swine Genetic Archive in 2014 to guide and support the control of invasive feral swine through the use of genomic tools. APHIS works collaboratively with other Federal and State agencies and academic partners to address feral swine damage and disease issues.

Samples

The Feral Swine Genetic Archive includes more than 40,000 samples (i.e., hair, blood, tissue, etc.) collected from feral swine across their invaded range within the United States. Researchers have analyzed more than 24,000 of these samples with a high-density SNP (single nucleotide polymorphism) array—providing a robust database for evaluating a diversity of management questions.

Research Questions

Research questions are driven by the changing needs of feral swine control and management. Examples of recent topics include the following:

- Mapping the illegal movement of feral swine from release points back to the original source populations.
- Using genetics to distinguish between feral swine and domestic pigs. This supports State efforts to enforce laws prohibiting the possession and/or transport of feral swine.
- Identifying the evolutionary processes that are contributing to make feral swine so profoundly invasive.

Contact Us

To learn more about the Feral Swine Genetic Archive, how it is used to further USDA’s mission, or to explore opportunities for collaboration, email us at WSFeralSwineGeneticArchive@usda.gov.

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