

Distinguishing between Eurasian Wild boar Hybrids and Feral Swine Using Molecular Analyses

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ABSTRACT: Wild hogs (*Sus scrofa*) are a serious threat that impact natural areas, farmland, and even urban landscapes. They destroy personal property, predate on wildlife, displace native species, and destroy the diversity of native wetlands. Previous research has shown that examining the differences in the gene MC1R using molecular methods and the examination of the hair coat of wild hogs has the potential to identify wild hogs and hybrids from domestic species; however, this technique has also not been evaluated in such a manner that would make it useful for conservation officers and prosecutors in a court of law. Therefore, we propose to evaluate both the morphological and genetic methods as a tool for identifying wild hogs using the model of disease testing where the morphological methods are applied by field personnel as a screening test and the genetic methods are used in a confirmatory manner. The objective is to determine the accuracy and precision of each of these methods for identifying wild hogs in the US. We will compare the MC1R gene between samples of DNA from known Eurasian wild boar, domestic hogs, wild hogs exhibiting the white-tipped guard hair phenotype, and feral swine that do not exhibit the white-tipped guard hair. We will use gel electrophoresis will be used to differentiate between the various wild and domestic hogs breeds. We will also enlist biologists, students, and other wildlife professionals assess photos and patches of hair from each type of hog to determine the accuracy of morphological assessment for identifying wild hybrids and recently released feral hogs. We believe these methods will be instrumental for law enforcement to identify and prosecute individuals involved in the anthropogenic spread of wild hogs in Kentucky and throughout the US.

Key Words: DNA, Eurasian wild boar, feral swine, genetics, molecular, wild hogs

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