

Application of genetic capture-mark-recapture methods for invasive wild pigs

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Abstract

Wild pigs (*Sus scrofa*) are a highly destructive invasive species across the globe, making them subject to intensive management including lethal control. Robust estimates of population abundance are needed to assess and optimize the effectiveness of control efforts. Genetic capture mark-recapture (GCMR) offers considerable promise for monitoring invasive wild pigs. However, obtaining robust estimates from GCMR can be difficult due to low quality DNA, particularly in moist, hot environments that promote fast DNA degradation. To examine if GCMR is feasible for estimating wild pig abundance, we collected pig fecal samples in three sites (bottomland hardwoods, mixed forest, and upland pine) at the Savannah River Site, South Carolina, USA. Amplification success across nine microsatellite loci varied across habitats with bottomland hardwoods having the lowest success (18%) compared to the mixed forest (56%) and upland pine (65%). Resultant abundance and density estimates were relatively similar between field-based methods and GCMR in the bottomland hardwoods and upland habitats, but estimates for the bottomland hardwoods had larger confidence intervals. Tests with additional extraction methods in the bottomland hardwoods found low amplification, with a combination of Nucleospin soil kits and Zymo clean-up kits performing the best. While our study found reasonable estimates of density across three habitats, environmental conditions have a powerful influence on amplification success and the corresponding number of recaptures in wild pig GCMR, particularly in the bottomland hardwoods where flooding was frequent during sampling. Successful GCMR studies should, therefore, consider both sampling intensity and laboratory costs when designing studies because dryer habitats have higher amplification success but lower pig densities.

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