Landscape genetics of feral pigs in Australia: Phase 1 pilot study

Prepared by: Peter Durr, CSIRO Australian Animal Health Laboratory

Date: 24-Jan-2019

_____

Summary

This pilot project will explore using DNA samples to delineate sub-populations of feral pigs in mainland Australia, with sub-populations defined as those between which there is limited movement. Being able to map sub-populations is an essential step for effective planning for population control as well as for surveillance of exotic diseases such as African swine fever (ASF). The pilot will sample 200 pigs from northern and southern populations and compare the performance of tissue, blood and hair samples for the genetic testing. At the end of the project in September 2020, we will know the feasibility of up-scaling the activity nationwide.

Objectives

1. Compare three methods of sampling and transport on the quality of the extracted DNA and the SNP results for 200 pigs collected from two regions (NSW and northern Australia)

2. Confirm that the SNP genotyping can inform the landscape genetics of feral pigs populations in both of these populations, despite their presumed difference in the percentage of Asian vs. European ancestry (Gongora *et al*., 2004)

3. Inform the possibility of developing a BeadChip with a reduced number of SNPs which will be as - or almost - as useful as that of Illumina's 60K BeadChip.

4. Develop SOPs for field sampling and specimen handling and dispatch, including photos, text and possibly videos.

5. Conditional on the findings of the pilot study, develop recommendations for upscaling the landscape genetics work to a national project.

Workplan

- Working closely with NAQS (Darwin / Cairns) and the NSW DPI (Orange), develop a sampling plan to obtain 100 samples from each region, ideally collecting them from two presumed genetically distinct populations, whilst avoiding sampling from within family groups.

- From each killed or captured feral pig, collect three samples - as well as sample collection data (age class, sex, sample date and location etc.)

    1 - Ear cartilage using the Allflex sampling kit – which will be the gold standard method:

    https://www.allflex.global/au/product/tsu-set

    2 - Blood samples collected using GenoTube Livestock Swabs:

https://www.thermofisher.com/order/catalog/product/9062010#/9062010

3 - Hair follicles placed in a sealed plastic bag with desiccant

- Dispatch the samples to the lab at AgriBio (Bundoora) where DNA extract will occur and quality scores assigned, followed by genotyping using the PorcineSNP60 v2 Genotyping BeadChip

    https://jp.illumina.com/content/dam/illumina-marketing/documents/products/datasheets/datasheet_porcinesnp60.pdf

- Analyse the data, determining (1) the relative sensitivity of blood and hair follicles in comparison with ear cartilage to assign lineage; and (2) the relative (theoretical) performance of using less SNPs in the BeadChip.

- Report the results back to the Department of Agriculture, including recommendations for sampling and potential of a smaller sized BeadChip for the Phase 2 project. In addition, provide detailed planning for how this Phase 2 project might be undertaken.

- Depending on the results, produce a short communication comparable to McClure *et al* (2009) and commission a smaller sized BeadChip.

Timelines

- The work is intended to be completed and reported by September 2020 - in time to assess whether to continue to a follow-on national Phase 2 project.

- Sampling in NSW can potentially start shortly after the project is approved, but sampling in NT/QLD will be delayed until April due to the pigs dispersing during the wet season

- The SNP testing will occur in late May, during one of the batch runs undertaken by AgriBio. The analysed results will be reported back to CSIRO-AAHL by mid July 2020

- The project report – including recommendations for a follow-on project – will be delivered at the end of September 2020

References

Gongora J, Fleming P, Spencer PBS, et al. (2004) Phylogenetic relationships of Australian and New Zealand feral pigs assessed by mitochondrial control region sequence and nuclear GPIP genotype. Molecular Phylogenetics and Evolution 33:339-348.

McClure MC, McKay SD, Schnabel RD, et al. (2009) Assessment of DNA extracted from FTA cards for use on the Illumina iSelect BeadChip. BMC research notes 2:107.