

Using genomics to identify wild boar in Alberta

Dr. Julie Colpitts, julie.colpitts@usask.ca
Hannah McKenzie, Agriculture and Irrigation, hannah.mckenzie@gov.ab.ca

WHY IDENTIFICATION MATTERS

- Alberta designates wild boar, including wild boar hybrids, as **agricultural pests**.
- Hybrids can resemble domestic pigs, so genetic testing provides additional evidence to support identification of hybrids when appearance is inconclusive.

Alberta’s 25% wild boar ancestry policy

Under Alberta policy, an animal with wild boar ancestry of 25% or greater is considered a wild boar for regulatory purposes.

WHY VALIDATION WAS NEEDED

- Wild boar ancestry (Smyser *et al.*, 2020) and Delta Likelihood (Smyser *et al.*, 2024) methods were developed using the Porcine 80K array, which has been replaced by the newer Porcine 50K array.
- We tested whether the 50K array produced comparable results.

HOW ALBERTA USES GENETIC EVIDENCE

- Inspectors consider physical characteristics and genetic evidence against Alberta’s 25% wild boar ancestry policy threshold.
- Under Alberta policy, strong genetic evidence requires both the **ancestry estimate and its entire 95% confidence interval** to exceed the threshold.
- Final decisions are at the discretion of the Inspector who considers all available evidence.

MAKING GENOMICS MORE ACCESSIBLE

- We developed a prototype Shiny app and analysis pipeline to deliver ancestry and Delta Likelihood results from genotype data through a web portal.
- Testing of the Shiny app is ongoing but will require hosting and ongoing support.
- In the future, the portal could allow producers to receive genetic analyses while requiring only the collection of a genetic sample (e.g. by ear tagging).
- Testing cost is approximately \$50 CAD per sample.

References:

Smyser, T. J., et al. (2020). Mixed ancestry from wild and domestic lineages contributes to the rapid expansion of invasive feral swine. *Molecular Ecology*, 29, 1103–1119. <https://doi.org/10.1111/mec.15392>

Smyser, T. J., et al. (2024). Probabilistic genetic identification of wild boar hybridization to support control of invasive wild pigs (*Sus scrofa*). *Ecosphere*, 15, e4774. <https://doi:10.1002/ecs2.4774>

The new Porcine 50K SNP array reliably estimates wild boar ancestry

- Paired analysis of samples from 94 Canadian and 120 U.S. wild pigs found no statistically significant difference between the newer Porcine 50K and retired Porcine 80K arrays for wild boar ancestry or Delta Likelihood results
- Validated genetic tools are supporting evidence-based identification of wild boar hybrids in Alberta



Two juvenile pigs displayed a mix of wild boar and domestic pig characteristics



Genetic testing found strong genetic evidence that wild boar ancestry exceeded the 25% policy threshold

- ▶ 37% (95% CI: 28-45%)
- ▶ 37% (95% CI: 30-45%)



These animals were determined to be wild boar for the purposes of the *Alberta Agricultural Pests Act*.

Acknowledgements:

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Learn more:

[Alberta.ca/wildboar](https://alberta.ca/wildboar)



VALIDATION DETAILS

Sample selection

We compared paired genotypes produced with both the Porcine 80K and 50K arrays for 214 wild pigs samples [94 collected from Alberta, Saskatchewan, and Manitoba; 120 sampled across the invaded range in the U.S.].

Reference set

We retained the reference populations used by (Smyser *et al.*, 2020) and (Smyser *et al.*, 2024).

Marker selection

The existing marker-selection method prioritizes SNPs that distinguish wild boar from domestic pigs while reducing redundancy through linkage-disequilibrium pruning. The 50K array did not disproportionately lose highly informative markers, supporting continued use of the original marker-selection approach.

Results

- The report found **no statistically significant differences** in wild boar ancestry estimates (Figure 1) or Delta Likelihood results (Figure 2) between the arrays.

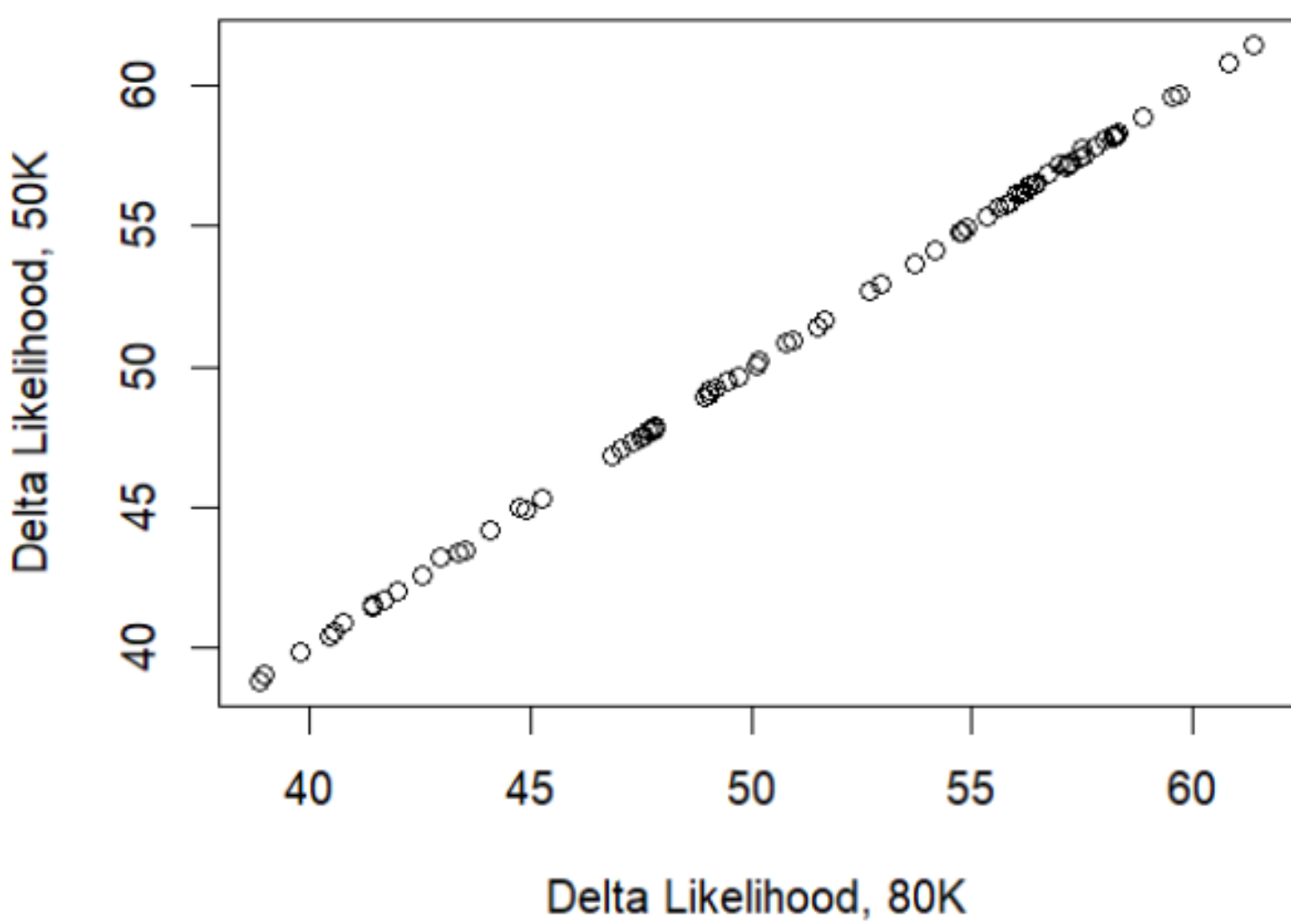


Figure 1. Correlation of Delta Likelihood statistic (as per Smyser *et al.*, 2024) calculated for 79 Canadian genotypes obtained directly from the Porcine 80K SNP chip (x axis) and the Porcine 50K SNP chip (y axis).

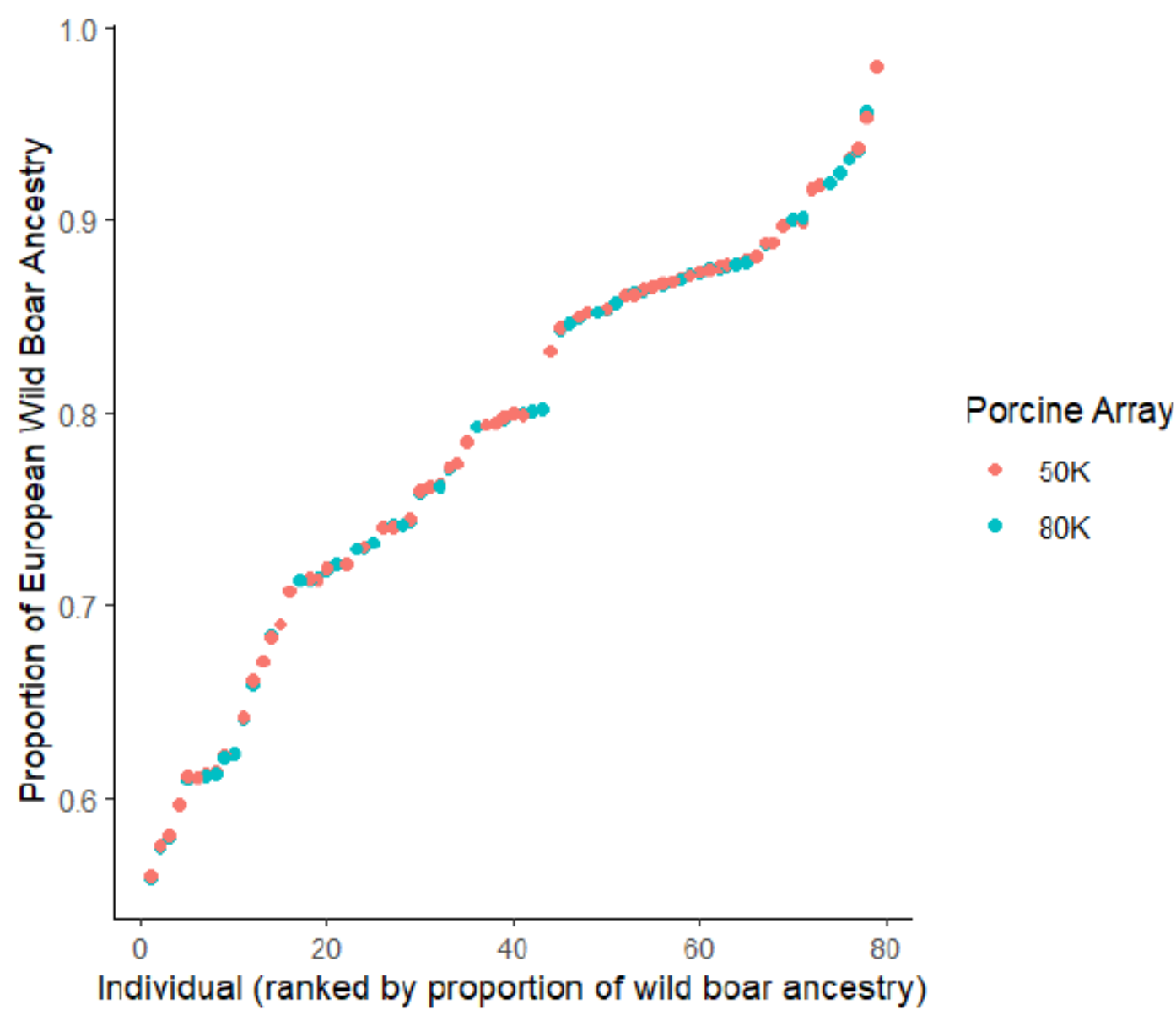


Figure 2. Individual-based comparison of European Wild Boar ancestry (as per Smyser *et al.*, 2020) for 79 Canadian genotypes obtained directly from the Porcine 80K SNP chip (blue dots) and the Porcine 50K SNP chip (red dots).

Genotyping error rates

- Genotyping error rates, measured by per-locus and per-individual discrepancies between the 50K and 80K arrays for all the SNPs they had in common, were <1% most of the time.
- Slightly higher discrepancies were seen in Canadian samples. This may reflect separate DNA extractions and testing on the 80K and 50K arrays years apart in the case of the Canadian samples, compared with U.S. samples which were tested together using a single extraction.