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**PSVI-5 Optimizing Limited Deep Phenotyping
Capacity for Genetic Studies and Routine
Genetic Evaluations: Application to Boar**

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Abstract: In the context of genetic research, but even more for routine genetic evaluations, a recurrent problem is the difficulty to obtain measurements for certain required phenotypes. This can be caused by limited facilities, difficulties in sampling, expensive analyses, limited staff relative to number of animals, and many other reasons. It may therefore be necessary to select which animals to phenotype while maintaining the phenotyping quality and avoiding bias or omitting some animals of interest. This implies developing strategies to do the phenotyping in a non-biased way using a priori available minimum knowledge. An example could be predicting post weaning growth of cattle based on earlier information as birth weight and weaning weight to optimize the use of feed intake or methane measurement facilities. In pigs, similar situations might occur for growth or emissions. However, another important example is boar taint (BT) which shows that not only sequential weighing, but also partial measurements of BT may require attention. BT is defined as urinary and fecal and associated with 2 major compounds, androstenone (AND) and skatole (SKA). The classical method of odor discrimination, “Human Nose Score” (HNS), is notoriously unreliable. Even if odor is known to be complex, adding AND and SKA to HNS would help reveal better the boar taint condition (i.e., phenotype). However, the measurements of AND and SKA or other compounds in fat are expensive. Therefore, it would be important to optimize these measurements by selecting relevant fat samples taken at slaughterhouses. We tested the following optimization strategy. The objective was to obtain a good distribution of a posteriori measured AND and SKA in the selected samples given initial asymmetric populations with positive HNS (3 to 10% declared positives). In a first step, the strategy pooled 2 available HNS for 997 across 22 contemporary groups (CG) and added limited chemical measurements (218/997) available for older samples. The data were obtained from a boar progeny testing scheme; therefore, CG were linked through connecting sires from artificial insemination having sons in different CG. A multi-trait BLUP model was used adjusting for metabolic weight using a 4-generation pedigree. A total of 15% of the animals in the last

6 contemporary groups were selected using first positive HNS (17/300), then keeping the highest and lowest predictions and maintaining diversity by not repeating boars from the same sire-family (i.e., when a family was already present, the next animal was taken). A posteriori chemical analyses were performed on selected samples to compare predicted and observed classifications in tainted and untainted. Research showed an accuracy of 0.73 (Table 1), leading to 58% tainted and 42% untainted compared with the expected ratio. Improvements of this strategy are currently in development, including using genomics.

Table 1: Confusion matrix between predicted and *a posteriori* observed actual distribution of tainted and untainted samples showing an accuracy (i.e., true positive and true negative relative to the total number of samples) of 0.73.

Actual	Predicted	
	Tainted	Untainted
Tainted	18	8
Untainted	4	15

Keywords: breeding, pigs, sampling

