Prediction of Boar Taint in Major Breeds of Canadian Pigs Using Genetic Markers

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PROBLEM: Boar taint is an unpleasant odour produced by the accumulation of androstenone and skatole in fat tissues of intact male pigs. Meat produced from intact males containing too much taint can affect the eating quality of pork. Castration is a common practice for preventing boar taint. However, alternative solutions are of interest due mainly to animal welfare concerns. Moreover, in comparison to castrates, raising entire males is also more profitable due to better feed efficiency and leaner carcasses (Babol and Squires, 1995).

POTENTIAL SOLUTION: Genetic selection is a potential solution for decreasing boar taint levels in meat from intact males. Technologies are available to scan animals for candidate genes associated with boar taint, which would allow for selection against alleles responsible for increased levels of androstenone or skatole.

OBJECTIVE: To investigate the feasibility of predicting the amount of androstenone and skatole in fat tissues of intact males using SNP markers in candidate genes.

SAMPLING: A total of 3,474 purebred Canadian Duroc, Landrace and Yorkshire boars were sampled and genotyped for 97 SNPs located in 40 candidate genes. SNPs with minor allele frequencies (MAF) less than 0.05 were excluded and animals < 90 kg, weighing less than 90 kg were excluded because they may not have reached sexual maturity. Animals heavier than 150 kg were also excluded due to potential changes in levels of boar taint compounds over time in older animals. A fat sample was collected from market weight boars at slaughter plants or via biopsies (Baes et al, 2013) for DNA extraction and to measure levels of boar taint compounds.

BOAR TAINt MEASUREMENTS: Fat samples were processed to measure androstenone and skatole levels following to Squires and Lundström (1997) and Lanthier et al. (2007), respectively. The natural logarithms of androstenone and skatole were calculated and used as phenotypes.

VALIDATION: The SAS GLM procedure was used to adjust phenotypes for season, as well as for boar’s age and weight at time of sampling. Residuals of the GLM procedure were then used in gembv software (Sargolzaei et al., 2009) to predict the genetic value (VanRaden, 2009) of the boars for androstenone and skatole. The oldest 80% of boars were assigned to a training group and the youngest 20% of boars to a validation group. The correlations of direct genomic values (DGVs) with the adjusted values of androstenone and skatole in the validation group were calculated to validate the predictive ability of marker assisted genetic values for the prediction of boar taint compounds.

Marker Assisted Genetic Values Accuracy: Correlations of the marker assisted genetic values with the adjusted values of androstenone and skatole levels in the validation groups were 0.35 and 0.05 in Duroc, 0.26 and 0.26 in Landrace and 0.40 and -0.05 in Yorkshire, respectively. The low correlations observed for skatole may be a consequence of the lower incidence of skatole values above consumer acceptance thresholds. These results show, however, the potential of the markers as a tool to select breeding animals against high levels of androstenone, the compound most responsible for unacceptable levels of taint in this study.

Marker Frequency and Levels of Boar Taint: Following the first step of the analysis, the number of unfavorable SNP alleles associated with androstenone in Duroc was counted on each boar in the validation group. The number of unfavorable alleles were significantly correlated (r = 0.33, p<0.001) with androstenone levels in fat (chart below).

Relationship between number of unfavorable alleles of SNPs and levels of androstenone in Duroc pigs

Acknowledgements: Financial support provided by the Canadian Agricultural Adaptation Program (CAAP), regional swine improvement centres across Canada and participating Canadian breeders.