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

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PROBLEM: Boar taint is an unpleasant odour and off-flavour produced mainly in meat and fat tissues from intact male pigs. The two main compounds responsible for this defect are androstenone and skatole. 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. Alternative solutions , however, are of interest.

POTENTIAL SOLUTION: A genetic solution to the problem, through marker assisted selection, would be one way to reduce the risk of boar taint in intact males. This would allow for the selection against alleles responsible for increased levels of androstenone and skatole, the two main compounds responsible for boar taint, in swine populations.

OBJECTIVE: Researchers at the University of Guelph have developed a panel containing such genetic markers and it was used to investigate the feasibility of predicting the androstenone and skatole levels 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 had a fat sample collected at slaughter or *via* biopsy (Baes *et al.* 2013). Collected samples were then sent for DNA extraction and genotyped for 97 SNPs located in 40 candidate genes. Androstenone and skatole levels were also measured from these samples. SNPs with minor allele frequencies (MAF) less than 0.05 within breed were excluded. Animals weighing less than 90 kg, boars heavier than 150 kg or older than 300 days were excluded from further analyses.

BOAR TAINT MEASUREMENTS: Fat androstenone and skatole levels were measured using the methods described in 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, age and weight of the boar at time of sampling. Residuals of the GLM procedure were then used in gebv software (Sargolzaei *et al.* 2009) to predict genetic values for androstenone and skatole of boars (VanRaden, 2009). The oldest 80% of boars in each breed were assigned to a training group and the youngest 20% to a validation group (Table 1). Correlations between direct genomic values (DGVs) and adjusted androstenone and skatole values in the validation group were computed to validate the predictive ability of marker assisted genetic values for predicting boar taint compounds.

Table 1. Number of boars in training and validation groups

	Androstenone		Skatole	
Breed	Training	Validation	Training	Validation
Duroc	471	115	451	155
Landrace	574	143	544	130
Yorkshire	581	160	554	137

MARKER FREQUENCY: Sixty-one (61), 80 and 83 SNPs with a MAF>0.05 were segregating in Duroc, Landrace and Yorkshire breeds, respectively.

BOAR TAINT LEVELS: Across all three breeds, about 4% of boars were above consumer acceptance levels for both measured compounds, 28% were too high for androstenone but were acceptable for skatole, 6% were too high for skatole but were acceptable for androstenone and 62% were acceptable for both compounds (table below). Consumer acceptance levels of 1000 ng/g for androstenone and 200 ng/g for skatole were considered.

Table 2. Descriptive statistics on androstenone and skatole levels in Canadian boars

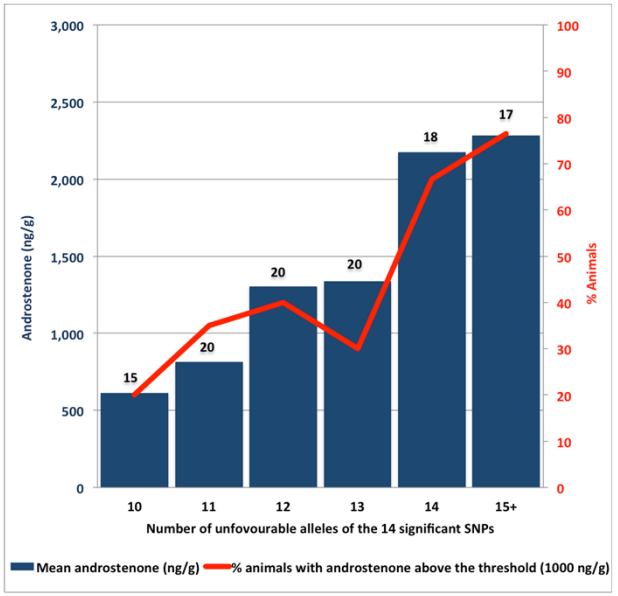
	Breed		
Boar taint compound	Duroc	Landrace	Yorkshire
Androstenone (ng/g)			
Number of animals	588	723	741
Mean	1,467	931	841
Standard deviation	1,567	1,116	875
Range	35 - 10,419	65 - 13,748	75 - 7,747
% Unacceptable	47	28	25
Skatole (ng/g)			
Number of animals	568	680	691
Mean	71	127	94
Standard deviation	129	216	170
Range	0 - 1,986	0 - 3,062	0 - 3,503
% Unacceptable	5	14	10

MARKER FREQUENCY AND LEVELS OF BOAR TAINT: Following the first step of the analysis, the number of unfavourable SNP alleles associated with androstenone in the Duroc breed was counted on each boar in the validation group. The number of unfavourable alleles were significantly correlated (r= 0.33, p<0.001) with fat androstenone levels (Figure 1).

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.

BENEFITS TO THE SWINE INDUSTRY: The percentage of animals with androstenone levels above the threshold were 20% and 76% for groups of animals with 10 and 15 or more unfavourable SNP alleles, respectively. These results show 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.

Figure 1. Relationship between number of unfavorable alleles of SNPs and levels of androstenone in Duroc pigs



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