RESEARCH ABSTRACT
ANIMAL SCIENCE

Title: Genome-wide association meta-analysis of experimental populations to identify QTL for pork quality and validation in commercial populations – **NPB #11-042** **r**evised

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Scientific Abstract

In the current era of livestock genomic evaluation it is common practice to derive a genome-wide association analysis (GWA) from a genomic evaluation model of a single population. Analysis of multiple populations, however, is more difficult. An alternative to joint analysis could be the meta-analysis of several GWA from independent genomic evaluations. Meta-analysis of GWA allows combining results from individual studies, accounting for population substructure. The objectives of this research were: (a) to derive GWA from genomic evaluations for pork quality traits in three populations; and (b) to implement a Meta-analysis (MA) to find significant associations across populations. Data from two populations (MARC_Com and MARC_Res) were provided by Meat Animal Research Center and one population was provided by Michigan State University (MSUPRP). Population-specific GWA were derived from genomic evaluation models fit to each population for ultimate pH (n=1857 MARC_Com; n=530 MARC_Res; n=904 MSUPRP) and shear force (SF; n=1234 MARC_Com; n=1892 MARC_Res; n=911 MSUPRP). A MA was implemented by combining z-scores derived for each SNP in each population using two different weighting schemes: a) sample size (*N*) and b) estimated variance of SNP effects. For pH, one peak was identified for MSU and commercial populations on SSC15, (135Mb, p-value<1.21e-11 for MSUPRP and 134MB, p-value<9.26e-11 for MARC_Com). In the N-weighted MA, a peak was detected on SSC15 at position 134Mb (p-value < 2.13e-13). A virtually identical result was obtained using variance-weighted MA: a peak on SSC15, at 135Mb, p-value<5.18e-11. For shear force, GWA for MSUPRP showed one peak on SSC15 (135Mb, p-value<1.48e-8) and another peak on SSC2 (2.9Mb, p-value< 2.88e-8). For MARC_Com and MARC_Res, peaks on SSC2 were identified at positions 109Mb and 5.5Mb (p-value<1.83e-7 and 1.64e-7 respectively). The variance-weighted MA detected one peak on SSC2 (6.3Mb, p-value<7.82e-11) and another on SSC15 (135Mb, p-value<2.14e-7). In contrast, N-weighted MA, yielded two peaks on SSC2, at 5.9Mb and at 105Mb (p-value<6.73e-12 and 1.23e-6 respectively). According to our results, selecting a weighting scheme for MA-GWA is very important because it may influence the results. Regardless of the approach used to implement it, MA-GWA focused on peaks that were present in at least two populations. Thus, the presented MA-GWA methodology is an attractive alternative to synthesize results from multiple GWA derived from genomic evaluations and it can be used to elucidate the genetic architecture of economically relevant traits, when several populations are available.