

Title: Using Behavioral and Genomic Tools to Identify Pigs Suited for Group Living,
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Scientific Abstract:

A welfare concern for group-housed pigs is aggression, particularly in the first 24 h following re-grouping with new individuals. This study characterized social behaviors of pigs in group-housing environments, related behavioral responses to health and productivity and identified genetic components associated with key behaviors for application in breeding programs. Data were collected from 1,092 purebred Yorkshire pigs. Pigs were strategically mixed into new groups at 3 ages: weaning (~27 d of age), move to finisher pens (~72 d of age), and at approximately 100 kg (~150 d of age, gilts only). Total number of fresh lesions (< 24 h old, bright red marks on skin) were counted prior to mixing (baseline), 24 h post mixing, and 3 wk post mixing. Video recordings made immediately and 3 wk after mixing were decoded to characterize behavior. Pigs were genotyped using a 70k SNP chip (Neogen Corporation – GeneSeek Operations). Phenotypically, pigs show different levels and types of aggression. Further, aggression as measured using lesion scores, is heritable, (0.17 - 0.46); thus selection against undesirable aggressive phenotypes is possible. Pigs housed with each other in the nursery prior to moving to a new group in the finishing stage displayed 2.62 times less fighting compared to unfamiliar animals ($P < 0.01$). Fights and one-sided attacks follow body-pressing events between two pigs in 75% of observations ($P < 0.01$); thus, pressing can be used to predict damaging aggression. Fear tests on a subset of barrows ($n = 257$) found no relationship between measures of fear (i.e., latency to approach or touch a novel object) and lesion scores ($P > 0.15$). Fear and inter-pig social aggression may be regulated by different processes, enabling selection against aggression without affecting fear response. Analysis of a subset of gilts ($n = 270$) suggested no relationship between lesions and backfat ($P = 0.584$) or between backfat and interactions with humans ($P = 0.607$). There was also no relationship between lesions and total interactions with humans ($P = 0.509$) or with total number of bites ($P = 0.196$). Thus, for this group of Yorkshire gilts, leaner pigs were not necessarily more aggressive than pigs with more fat, and pig-pig aggression was not related to the how pigs interacted with humans. In addition to generating data related to phenotypic expression and underlying genetic components of aggression, several statistical programs and packages have been developed for genetic analysis of behavioral data. These facilitate fitting of models, perform genome-wide association studies, and summarize and graphically present behavioral data from decoded videos. We are combining our data with existing data from 2 additional groups of pigs in a meta-analysis. We will also complete genome-wide association studies to identify regions within the genome responsible for the observed variation. In summary, aggression is variable among pigs and heritable, but does not appear to be directly related to fearfulness, response to humans, or to leanness, suggesting that selection against aggression should not negatively impact these traits. However, our results and previously published findings indicate that it is not as simple as selecting against all aggression, but that selection must be targeted in ways that does not affect long-term group stability

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