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Pleiotropic effects of a QTL region for androstenone level on pig chromosome 6

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Androstenone is one of the main compounds causing boar taint in boars. A 1.94 Mbp region on pig chromosome 6 (SSC6) was found to affect androstenone level. Within this region, two major haplotypes (high- and low-androstenone) can be distinguished. Analysis of sequence data showed that the low-androstenone haplotype originated from Asian breeds and was found at different frequencies in European commercial breeds. Because androstenone levels were not taken into account in typical breeding programs, we hypothesize that this haplotype accumulated indirectly by selection for another correlated trait. In this study, three pig lines were used for the estimation of pleiotropic effect of the 1.94 Mbp region on SSC6: sow line 1 (~1,450 animals); sow line 2 (~1,300 animals); and a boar line (~900 animals). Phenotypes were available for eight traits: birth weight, backfat thickness, growth rate, total number born, litter birth weight, teat number, sperm motility, and number of spermatozoa per ejaculation. Association between phenotypes and haplotypes were tested using ASReml v3.0. For both sow lines, a favorable effect for teat number (+0.11) was detected of the low-androstenone haplotype (P=0.058; P=0.013 respectively). In sow line 2, a favorable effect of the low-androstenone haplotype on number of spermatozoa per ejaculation was detected (P=0.023). No effects were identified on production and female reproduction traits. These results show that pleiotropic effects for androstenone level on SSC6 are favorable and have low magnitude. The absence of unfavorable pleiotropic effects suggests that selection for low-androstenone levels at this location is possible without negative effects on other traits.

Using NGS data to characterize genetics of meat-type and egg-type chicken lines

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New sequencing technologies called 'NGS' allow the analysis of full genomes. In this new context, our study aims at characterizing at the genome scale polymorphisms within INRA broilers and layers experimental lines divergent for abdominal fatness (G/M) and feed efficiency (R+/R-), respectively. Genomes of about 15 animals per line were sequenced either in pools (R+/R-) or individually (G/M), using a HiSeq 2000 and with a depth of 19X. On those 4 lines, we identified 11 million SNPs. In addition, 386,177 SNPs discriminating R+ from R- and 510,577 SNPs discriminating G from M were identified. About 1.5% of these SNP are localized in genes, possibly with a functional modification, which is currently analyzed. A fine study of genes functions leads to new hypotheses on how the divergence between lines occurred. Finally, these approaches allowed us to identify one mutation that might be functional in a candidate gene for a QTL affecting abdominal fatness.