IDENTIFICATION OF POTENTIAL PORCINE COAT COLOUR GENE MARKERS

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Abstract: Coat colour gene variants, such as *MC1R* and *KIT* alleles, are successfully used to characterize livestock breeds and populations. Moreover they constitute informative markers to determine genetic origin in traceability analysis. In pigs, several chromosomal regions with effects on coat colour patterns have been reported, however the identification of actual causal mutations is limited to *MC1R* and *KIT* polymorphisms. The aim of the current study was to analyse new positional and functional candidate genes for the previously identified QTLs in F2 pigs of a Black Iberian x Landrace experimental population. The previous QTL scan allowed us to detect the known QTLs on SSC6 (*MC1R* effect) and SSC8 (*KIT* effect), but also other QTLs on SSC1, SSC7, SSC9, SSC12, SSC13 and SSC17, for which polymorphisms in candidate genes have been investigated in the current study. The *SLC24A5, DTNBP1, KRT23, KRT24, XPC, AGOUTI*, and *ATRN* genes were selected as powerful positional and functional candidates. Genetic variants within these genes were identified from a previous RNA-Seq assay on an experimental F1 (Iberian x Landrace) x Landrace backcross. Polymorphisms for all seven genes were identified, however only the *SLC24A5, DTNBP1, KRT23, AGOUTI* and *ATRN* polymorphisms were validated and appeared segregating (MAF: 0.23, 0.27, 0.16, 0.27 and 0.48, respectively) in the F2 Iberian x Landrace pigs with colour records. The association analysis did not reveal causal effects of the tested variants.
Although the analyzed polymorphisms did not show relevant effects, their usefulness for pig population characterization and traceability analysis should be further investigated.

Keywords: coat colour pattern, QTLs, porcine, coat colour genes.

PO - 1359