IDENTIFICATION OF GENOMIC REGIONS ASSOCIATED WITH FATTY ACID METABOLISM ACROSS FOUR TISSUES IN PIGS

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Fatty acids (FAs) are components of lipids and have important roles such as structural components of cell membranes, cellular fuel sources, and precursors of signaling mediators. This study aims at identifying potential genomic regions associated with FA profiles in several tissues and explores their role on whole body metabolism in pigs. A total of 432 commercial Duroc pigs were employed in the present work. Samples of blood were collected at 60 ± 8 d of age to extract the plasma. In addition, samples of adipose tissue (backfat), liver, and *gluteus medius* muscle were collected after slaughter (180-200 d of age). All animals were genotyped with the *GGP Porcine HD Array* (*Illumina*). Genotypes were imputed from the whole-genome sequences of 100 animals and SNPs with MAF < 5% or missing genotypes > 10% were removed. GWAS was performed between the 9,751,141 resulting SNPs and FA composition traits by the *fastGWA* tool of *GCTA v1.94.0*. The genomic regions containing at least three significant consecutive SNPs with distances < 1 Mb were selected for gene annotation. The GWAS results showed a common interval at SSC2: 7.56-14.92 Mb associated with the Desaturase 5 activity in liver, backfat and muscle. Another interval located at SSC14: 103.81-115.64 Mb was identified for backfat and muscle FA composition, including UFA, SFA, C18:0, C18:1n7, C16:1n7/C16:0, and C18:1n9/C18:0. In addition, backfat-specific intervals were identified at SSC6: 146.07-148.36 Mb for MUFA, SFA, UFA, C18:1n9, and C18:1n9/C18:0 and at SSC4: 2.53-14.55 Mb for C14:0, C20:1n9, C20:2n6, C20:3n3, and C16:0/C14:0. In SSC15, a region at 86.99-101.29 Mb was associated with liver C18:4n3/C18:3n3. Finally, for plasma, the specific region SSC14: 118.92-124.75 Mb was associated with C18:0/C16:0. The current results increase our knowledge of the genetic architecture of FA-metabolism traits and will be useful in selection programs to improve health and energy metabolism in pigs.

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