

Identifying metabolic processes shared among genome-wide association studies for reproductive phenotypes in bovine

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The expressive improvement obtained in the production traits for bovines was followed by an increase in the frequency of reproductive disorders. Male reproductive traits have high heritability and a higher potential to segregate in the population, once male, generally, have largest offspring than females. Some association studies successfully identified genomic regions/genes associated with male reproductive phenotypes. Therefore, each one of these studies identified different candidate regions/genes, which difficult the interpretation of the biological meaning of the results, when evaluated together. An alternative to make this interpretation easier is the analysis of metabolic pathways in which each candidate genomic region/gene is involved, grouping them in larger biological units. The aim of the present study was to identify the metabolic pathways shared among studies that identified genomic regions associated with testicular size (3 studies) and noncompensatory fertility (2 studies) in bovines. In order to reach this aim, the genes mapped in those regions and the metabolic pathways, which each genes are related, were identified using the R packages biomaRt and reactome.db, respectively. From this analysis, 30 metabolic processes were found as shared among the three studies which identified genomic regions associated with testicular size. Moreover, 20 metabolic processes were shared between the two studies which identified genomic regions associated with noncompensatory fertility. The metabolic processes shared among the regions associated with testicular size in the three studies are related with cellular cycle control, regulation of translation and transcription, signal transduction, neuronal system and metabolism of lipids and proteins. These metabolic processes point to important components involved in the regulation of cell proliferation and metabolism of protein and lipids, contributing to the control of testicular morphology. Furthermore, supporting that the same processes, which regulate the increasing of milk production, could also regulate the development of reproductive traits. The 20 metabolic processes shared between the two studies, which evaluated the noncompensatory fertility phenotype, are related with the control of ionic channels, cellular interaction and activation of GABA receptors, metabolic processes directly related with the fecundation. The identification of these shared metabolic processes can help in the development of functional studies, leading to a better understanding of the biological basis of reproductive phenotypes in bovines. Moreover, once identified the most important pathways and biological markers, the development of breeding strategies aiming at the reduction of reproductive disorders frequency in the herds will be possible, consequently, reducing the economic losses caused by these phenotypes.