

Metabolic pathways involved in bovine temperament

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Bovine behavior is defined as the actions and reactions of the animal when in contact with humans and it is composed of many phenotypes. Among these, the most studied is temperament, which involves alertness, reactivity, physical movement, aggression, emotions, and even curiosity. This trait is very important because it reflects the fear felt by the animal in human presence, directly impacting on the animal-creator relationship and on the animal welfare. When compared to calm animals, the ones with bad temperament exhibit lower weight gain, lower reproductive efficiency and lower milk production. Besides that, these animals produce meat of lower quality, are more susceptible to diseases and are usually involved in work accidents. This way, animals with a bad temperament usually increase the costs of herd maintenance. As a complex trait, temperament is difficult to measure and, to date, only few studies on the genetics of temperament returned the same candidate regions, genes or QTLs. Many regions in different chromosomes have been identified as associated with temperament. A recent review of the literature on the genetics of temperament, reported 22 QTLs associated with temperament. These QTLs were obtained from 4 articles. All those results, difficult the interpretation of the biological causes for bad temperament, when analyzed together. In this context, the present study aims to identify the main biological pathways recovered by the four studies. A pathway was considered as shared, when it presented at least one gene from the same pathway in all the 4 articles. Additionally, an enrichment analysis was performed aiming at identifying the most enriched pathways recovered by the 4 studies. In order to reach these aims, the genes mapped in the candidate regions associated with temperament in these studies and the metabolic pathways, to which each gene is related, were identified using the R packages biomaRt and reactome.db, respectively. The enrichment analysis was performed using an Exact Fisher test in R. As a result, 14 pathways were shared among the 4 studies. Among these, we highlight Signal transduction, immune system, cell cycle and axon guidance. After Bonferroni correction, one shared pathway was still significantly enriched: the signal transduction. This pathway contains important genes that regulate the transmission of a molecular signal inside the cell, inducing cell modifications, recruitment of protein complexes, culminating on changes of expression patterns. Signal transduction pathway is essential to the functioning of synapses, being though a strong candidate pathway for behavioral traits.