PSXV-2 Genome-Wide Association and Gene Network Analysis of Fatty Acid Composition in Beef from Brangus Cattle.

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Abstract: Beef is high in key nutrients; however, it is often perceived as unhealthy because of its high fat content, particularly its saturated fat. The fat content of beef is controlled by multiple genetic factors and impacts meat quality traits. The objectives of this study were to 1) characterize the natural variation in fatty acid (FA) composition of Bos taurus indicus influenced beef cattle, 2) estimate phenotypic and genetic correlations of FA composition with carcass and meat quality traits, 3) use genome-wide association (GWAS) to identify genes with the greatest effect on FA composition, and 4) use gene network analysis to identify genes with small effects on FA content. The following traits were recorded on 1,066 Brangus steer: carcass weight (kg; 373 ± 36.3); marbling (436 ± 84.2); quality grade; back fat (cm; 1.6 ± 0.6); ribeye area (cm^2; 83.3 ± 9.5); yield grade (3.2 ± 0.9); Warner-Bratzler shear force (kg; 5.1 ± 1.0); and 27 FA [saturated (%; 47.6 ± 3.1), monounsaturated (%; 46.3 ± 3.5), and polyunsaturated (%; 6.1 ± 2.0)]. Carcass traits had weak beneficial correlations to FA composition suggesting the possibility to manage or select for beef with less saturated fat without negatively impacting meat quality. GWAS identified four QTL and gene network analysis identified 177 genes related to lipid storage, transportation, and modification.

Keywords: Brahman, gene-network, fatty-acid

PSXV-21 Transcriptome Analysis of Chicken Reveals the Impact of Herpesvirus of Turkeys on Bursa RNA Expression in Marek's Disease Virus Infections.

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Marek's disease virus (MDV) is an oncogenic herpesvirus that causes various clinical syndromes in chicken. MDV early infection induces a transient immunosuppression and harbored in B cells of the bursa during the cytolysis phase of its replication cycle. One of the most commonly used commercial vaccines is Herpesvirus of Turkeys (HVT), which is a nonpathogenic virus of domestic turkey and may influence the expression of RNA. The aim of this study is to characterize the regulation of bursa gene in MDV infections and the impact of HVT vaccination on RNA expression in MDV-infected chickens. We used RNA-seq on the bursa samples to compare the transcriptome differences among MDV-infected chickens, HVT-infected chickens, co-infected chickens and uninfected control groups at 4, 7, 14 and 21 days post infection. Meanwhile, we also compared the expression at three different time points to examine alterations in the expression pattern. The result of differential gene expression showed that 14 days post infection might be the point in time when HVT worked. At false discovery (FDR) < 0.05 and fold change (FC) ≥2, we found 745, 218 and 76 genes in MDV-infected chickens, HVT-infected chickens and co-infected chickens respectively as differentially expressed compared with control group and 713 genes between MDV-infected chickens and co-infected chickens at 14 dpi. KEGG and GO enrichment analysis showed that these genes were highly enriched for Lysosome, immune response, inflammatory response, plasma membrane and so on. Overall, these findings help to better understand host-pathogen interaction in the bursa and elucidate the mechanism how HVT contribute to resist MDV. Further investigation of the roles of these candidate genes and signaling pathways in the regulation of MDV-HVT interaction may lead new directions for the development of drugs or cultivation of highly MDV resistant chickens.

Keywords: chicken RNA-seq MDV