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Transcriptome responses to different forage allowance in the hypothalamus of grazing beef cows

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Abstract Text:

Hypothalamus plays a major role in the response to changes in dietary nutrients supply. The aim of this study was to evaluate the effect of long-term nutrition at two different forages allowances (FA) of native pastures on the hypothalamic transcriptome of beef cows. Thirty-two multiparous cows (Angus, Hereford and F1 crossbred) were used, from May 2007 to May 2010, in a complete randomized block design with two FA throughout the year (4 vs. 2.5 kgDM/100kgBW/d; HI vs. LO). At the end of the third experimental year and at 190 ± 10 d postpartum (45 d after calf weaning), cows were slaughtered and the hypothalamus were collected. A subsample of 10 hypothalamus (n= 5 per treatment) from F1 crossbreed cows was used. Total RNA extraction, amplification, library preparation and sequencing were performed following the Illumina mRNA-Seq. Reads were mapped to the bovine reference genome using Tophat, and the resulting alignments were used to reconstruct transcript models using Cufflinks. Differential gene expression was evaluated using Cuffdiff. Additionally, gene set enrichment analysis was performed using goseq and meshr R packages. Overall, 217 genes were found to be differentially expressed at $FDR < 0.05$ and fold change ≥ 2 between HI vs LO. Most differentially expressed genes were related to defense response and immune system, brain and neuronal development, neuronal regeneration and synaptic plasticity, neuronal communication, receptor and intracellular signaling, and metabolic hormone activity. The enrichment analysis using Gene Ontology (GO) and Medical Subject Headings (MeSH) databases revealed that GO biological process and MeSH terms related to defense response and immune system, negative regulation of proteolysis, chemotaxis and regulation of JAK-STAT cascade, were up-regulated in HI cows compared to LO cows. Meanwhile, GO biological processes and MeSH terms related to brain and neuronal development, synaptic plasticity and neuronal communication, were up-regulated in LO cows compared to HI cows. These transcriptional changes in the hypothalamus would indicate a differential adaptation of grazing crossbreed cows to different nutritional environments. [This study was supported by CSIC Research Funds, UdelaR, Uruguay]

Keywords: grazing, transcriptome, RNA-sequencing

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