EXPRESSION ANALYSIS OF HEPCIDIN GENE IN SHEEP

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Introduction: Hepcidin is part of the innate immune system, and it plays a central role in the regulation of iron homeostasis. The hepcidin up-regulation limits the iron bioavailability for microorganisms.

Objectives: The aim of this study was to perform hepcidin expression analysis in different tissues collected from four healthy sheep.

Methods: Total RNA was extracted, treated with DNase and cDNA was prepared. Ovine hepcidin (GQ901053) qPCR was performed in triplicate (SYBR Green). βactin (NM_001009784) was used as endogenous control and relative data processing was used. The mean basal expression of liver hepcidin received the relative value of 1.0 and other tissues were normalized proportionately. Statistical analysis using ANOVA and the Tukey post-test were performed. The procedures were approved by local Ethical Committee.

Results: The relative concentration of mRNA compared to liver was 7.2 x 10⁻³ (abomasum), 2.1 x 10⁻³ (duodenum), 1.8 x 10⁻³ (lung), 2.9 x 10⁻⁴ (heart), 2.3 x 10⁻⁴ (bladder), 7.7 x 10⁻⁵ (lymph node), 5.7 x 10⁻⁵ (kidney), 4.4 x 10⁻⁵ (muscle), 3.9 x 10⁻⁵ (spleen) and 2.0 x 10⁻⁵ (cerebellum).

Discussion and conclusions: Ovine hepcidin expression was highest in the liver. Although the expression in other tissues was low, hepcidin expression in abomasum, duodenum and lung were significantly higher (p< 0.001) than other tissues. The high abomasum hepcidin expression may indicate the possible role of this peptide for local innate immunity. These results of hepcidin expression in ovine tissues will be helpful for additional studies on hepcidin, inflammation and iron metabolism. This research was supported by CNPq.