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Identification of pathways associated with thermal stress in Romanian Brown breed

Daniela Elena ILIE^{1*}, Alexandru Eugeniu MIZERANSCHI^{1,2,3}, Ciprian Valentin MIHALI^{1,4},
Radu Ionel NEAMȚ¹, Andreea Ștefania ANTON¹, Ludovic Toma CZISZTER^{1,2}

¹Research and Development Station for Bovine, Arad, Romania

²University of Life Sciences 'King Mihai I' from Timișoara, Romania

³Institute for Advanced Environmental Research, West University of Timisoara, Romania

⁴Vasile Goldis Western University of Arad, Romania

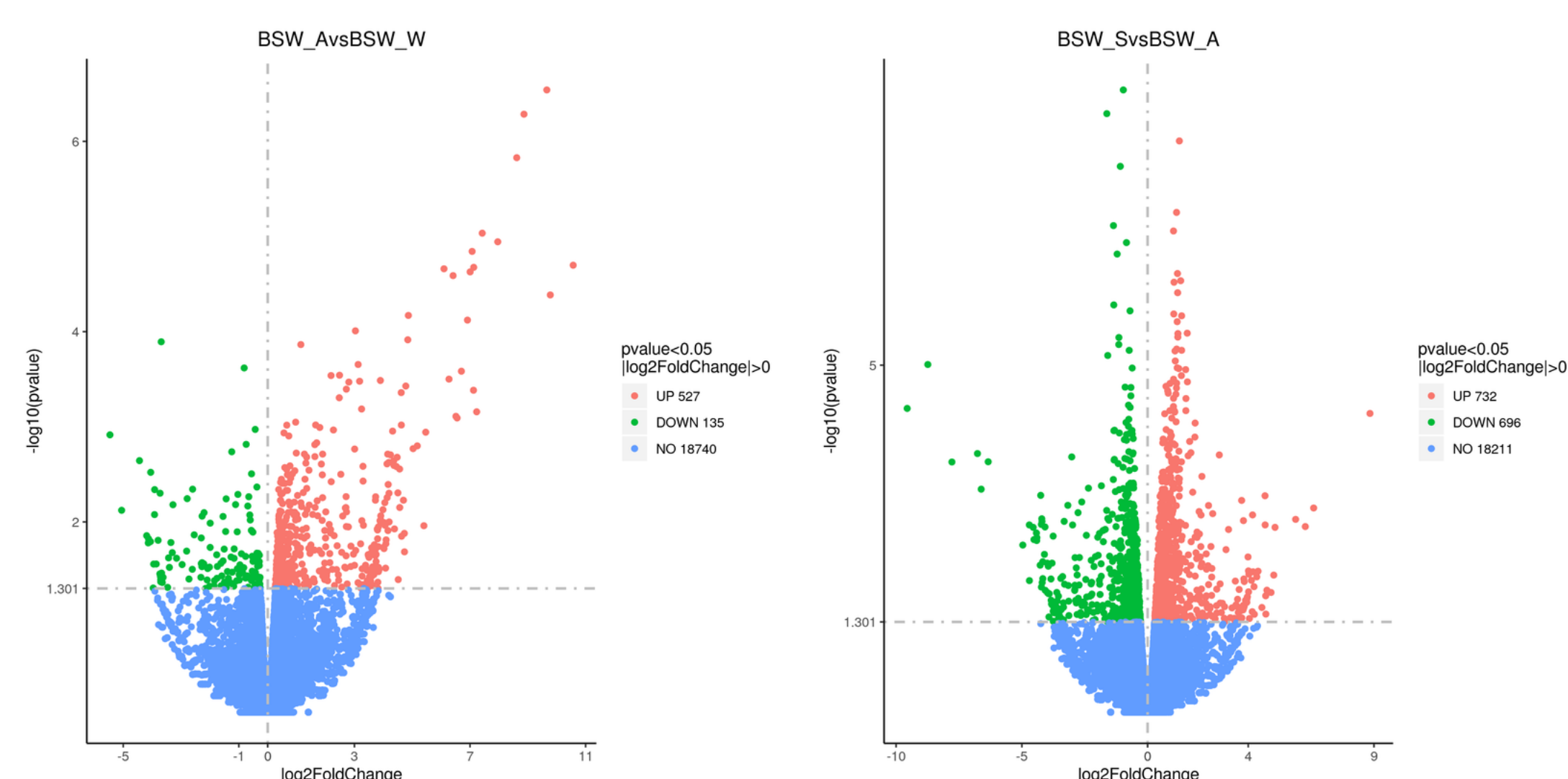
Introduction

- Thermal stress, during exposure to both heat (HS) and cold (CS) challenges, impacts productivity, reproductive efficiency, health and welfare in cattle.

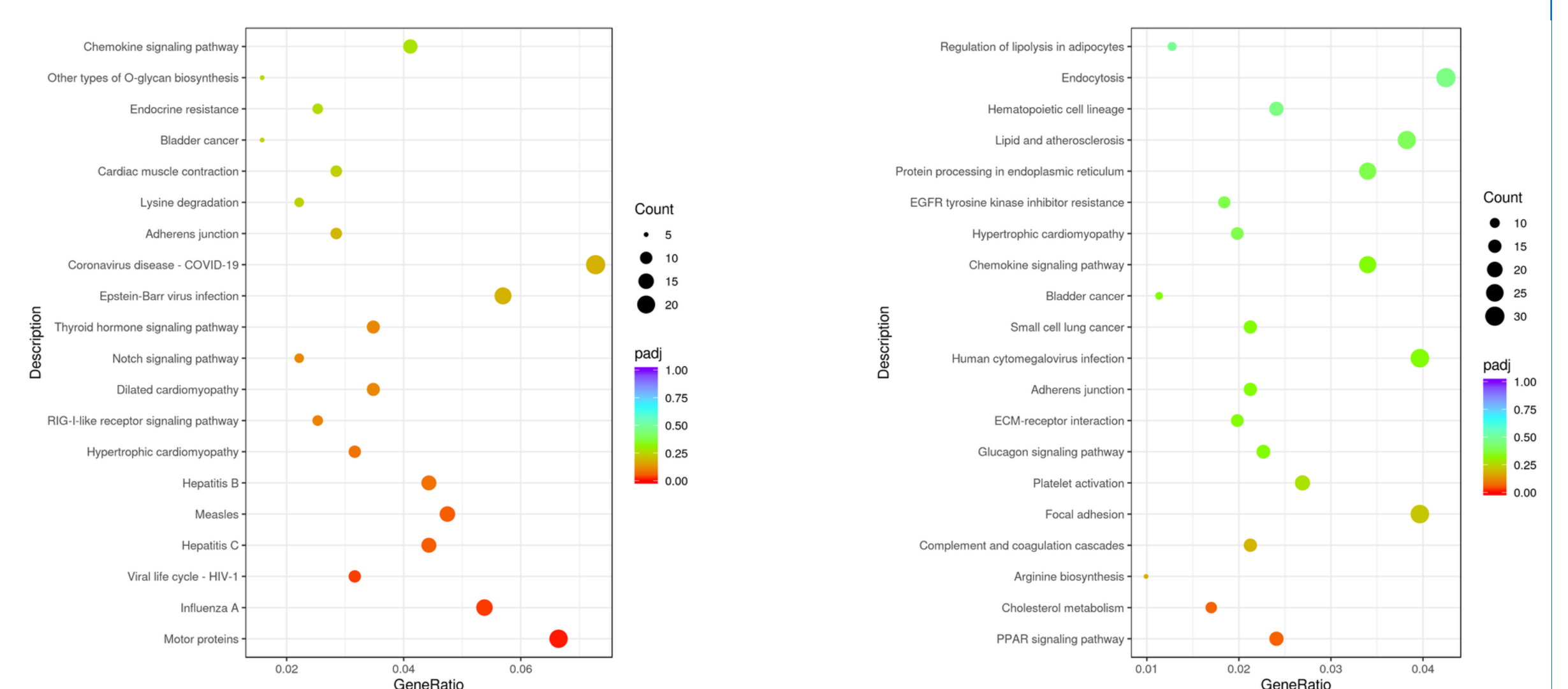
Material and methods

- A transcriptome analysis was employed on 7 Romanian Brown multiparous lactating cows under thermoneutral conditions (TN, 13°C), heat stress (36°C) and cold stress (-7°C) exposure.
- The gene expression profile in the blood samples of the cows under investigation was determined using RNA-seq.
- The differential expression analysis was carried out using the R package edgeR.
- The ClusterProfiler package was used for KEGG pathway enrichment.

Results



Differential Gene Volcano plot (CS/HS)



KEGG enrichment scatter plot (CS/HS)

- RNA-seq data analysis pointed out 1428 (732 up-regulated and 696 down-regulated) and 662 (527 up-regulated and 135 down-regulated) significantly differentially expressed genes ($p \leq 0.05$) in HS and CS, respectively, compared to TN.
- KEGG pathways for cows exposed to HS vs. TN highlighted the biological processes and pathways involved in cholesterol metabolism.
- The results for enrichment analysis of the differentially expressed genes (DEGs) of cows exposed to CS compared to TN were related to motor proteins, Influenza A, Viral life cycle - HIV-1, RIG-I-like receptor signaling pathway and Notch signaling pathway.

Conclusions

- These findings provide new insights related to molecular mechanisms involved in thermal response of Romanian Brown cows.

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