Bartosz Czech

Title of doctoral dissertation: The application of bioinformatics tools for the analysis of the genetic background of heat stress resistance in cattle

Scientific field: natural sciences

Scientific discipline: biological sciences

Abstract prepared: 12.09.2023

Keywords: heat stress; *Bos taurus*; multiomics; bioinformatics; microbiome; gene expression; GWAS

Abstract

Global warming and the associated rise in temperatures pose a significant threat to mammals, inducing heat stress and adversely impacting their health and biological functions. This issue is particularly pertinent in livestock farming, where animals bred for high production yields and increased metabolic loads are especially vulnerable to heat stress. In dairy cattle, heat stress leads to reduced milk production, compromised welfare, and stunted growth. This research addresses the pressing need to understand the long-term effects of heat stress susceptibility on organisms, focusing on the genomic, transcriptomic, and microbiota levels of Holstein cattle under heat stress conditions. Bioinformatics emerges as a pivotal tool in this research, aiding in the identification of genetic variants, candidate genes, and pathways associated with heat stress response. The integration of genomics, transcriptomics, and metagenomics data provides a holistic understanding of how these factors interplay in the face of heat stress. Three distinct studies are presented: the first identifies microbial markers indicative of heat stress in cattle; the second unravels gene expression regulation influenced by the microbiome; and the third identifies genetic markers associated with heat stress resilience. These findings collectively inform strategies to enhance animal welfare and productivity amidst climate-induced heat stress. In the face of climate change's global impact, this study emerges as a pivotal foundation, delving into the biological intricacies that underlie the effects of heat stress on cattle. By dissecting the interplay of microbiome, transcriptome, and genome, this research unveils the complex biological mechanisms shaping cattle's responses to environmental challenges. Moreover, this dissertation imparts invaluable biological insights that may refine livestock management and breeding strategies, ultimately strengthening agricultural sustainability and bolstering global food security.