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Serum miRNA disregulation during transport-related stress in turkey (*Meleagris gallopavo*).

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ABSTRACT

MicroRNAs (miRNAs) are small 21-25 nucleotide regulatory non-coding RNAs that modulate gene expression in eukaryotic organisms. miRNAs are complementary to the 3'-untranslated regions of mRNA and act as post-transcriptional regulators of gene expression, exhibiting remarkable stability in extracellular fluids such as blood. Turkey (*Meleagris gallopavo*) farming is a species economically relevant but the lack of efficient protocols for the evaluation of commercial turkeys prevents to measure the impact of industry practices on birds productivity and welfare. In order to identify potential molecular biomarkers for monitoring stress in turkey's handling, we investigated by TaqMan qPCR the abundance of five circulating miRNA, namely miR-22, miR-155, miR-181a, miR-204 and miR-365, previously demonstrated to be involved in stress in chicken due to feed deprivation. Road transportation related procedures were selected as stressful model for this study. The serum of twenty healthy animals was collected before and after 2h transportation. Our results demonstrated that miR-22, miR-155 and miR-365 are statistically more expressed after road transportation. Receiver-operator characteristics (ROC) analysis was used to estimate the diagnostic value of these miRNAs to evaluate the stress in animals. The serum level of miR-22, miR-155 and miR-365 can discriminate stressed from non-stressed animals with an AUC=0.763, 0.710 and 0.704, respectively, and the average expression of their combination has the same specificity (AUC=0.745). miR-22, miR-155 and miR-365 are stress-specific markers and can be considered as suitable biomarkers to identify turkeys stressed by road transportation.

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