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Differential gene expression analysis in pure and crossbreeds of Sistani and Montbeliarde cattle populations using RNA-seq data

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Abstract

Transcriptome study of the desired crossbreed and comparing it with pure parental population is one of the methods for evaluating and selecting cross with appropriate productivity, and yet disease resistant, high tolerance to environmental stresses and adapted to the climate of the breeding tract. The aim of this study was to investigate the gene expression profiles and identify genes with significantly different expression between pure and crossbreed Sistani and montbeliarde using RNA-Seq data. For this purpose, blood samples were collected from pure and crossbreed Sistani and Montbeliarde breeds (two pure and two its crossbreed) under the same environmental, nutritional and management conditions located in the Sistani Cattle Breeding Center in Zabol. After RNA extraction and assurance of the quantity and quality of RNAs, the samples were sent to BGI China for cDNA library sequencing and sequencing. After data collection, all the preparation and quality control and bioinformatics analysis were performed in Linux environment. In the first step of data analysis, Quality control of reads was performed with FastQC and Based on the quality control results, low quality readings were edited using Trimmomatic software. Bioinformatics analysis was then performed to investigation gene expression profile and identify genes with significantly different expression. Tophat2 software was used to map reads on the reference genome and to generate transcripts. The percentage of total map for forward and reverse readings in the pure Sistani breed and its crossbreed with Montbeliarde were 72.9% and 78.1%, respectively. In the next step, Bowtie2 was used to align transcripts and cuffmerge was used to merge transcripts and finally, cuffdiff was used to differential expression analysis. In total, 45 significantly differentially expressed genes were detected between purebred Sistani and Sistani × Montbeliard crossbreed. Factors such as single nucleotide mutations, environment, and epigenetic alterations can be reasoned for the difference expression of these genes in the pure and crossbreed of Sistani × Montbeliarde. Gene Ontology enrichment and pathway analysis revealed that these differentially expressed genes were highly enriched in Inflammation mediated by chemokine and cytokine signaling pathways. These genes are reported to have role in immune response, calving, fertility, resistance to mastitis and also may have a role in different levels of heat

tolerance and disease resistance. These pathways may, at different levels, contribute to tolerating adverse environmental and heat conditions and disease resistance in the Sistani and Monolithic crossbreed. Therefore, Sistani × Montbeliard crossbred could be suitable for the climatic conditions of the Sistan region in Iran.

Key words: Sistani cow, differentially expressed genes, Crossbred, RNA sequencing