عنوان مقاله:

A Computational Method to Identifying TFGene Modules in Immune System

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خلاصه مقاله:

Immune system is one of the most important biological systems that effects on health and reproduction of livestock. Stress is one of the known factors with the negative impact on the immune system. Here, to enhance the understanding of the regulatory genenetwork involved in stress-related immune system, we proposed a method to integrate bovine leukocyte RNA-seq gene expression data with sequence based predictions of transcription factors (TFs) toconstruct an integrated regulatory network. We applied module inference to construct modules of co-expressed genes. Then TFs were assigned to these modules using Lemon-Tree algorithms. Additionally,assigned TFs to each module were confirmed by promoter analysis. At the first 191 co-expressed modules were identified. They were mainly enriched for immune response or related immune response terms. Then Lemon-Tree assigned one to seven potential TFs to each module. Nine of assigned TFs with high probability score (> 100) were selectedfor sequence based predictions verification. Interestingly, most of TFs' targets were confirmed by promoter analysis. Combining module network inference with sequence based predictions allowed us topredict nine candidate TFs for stress-related immune system which most of their targets were functionally enriched for immune response terms. This included TFs that previously known to be involved inimmune response (GATA2, CEBPE and MYBL2), and TFs (MYBL2,SPI1, CEBPZ, HBP1, STAT2, MZF1 and HMGA1) that had not been recognized previously and were identified for the first time in this study as novel regulatory candidates in immune response. Our integrated regulatory network provides valuable insights into the regulatory programs involved in stress-related immune system.

کلمات کلیدی:

Module network, RNA-seq, Promoter analysis, integrated network