

عنوان مقاله:

Transcriptomic analysis of host immune response in the chickens infected by avian leukosis virus J using RNA-Seq

محل انتشار:

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خلاصه مقاله:

The poultry's immune system is regulated by various genes involved in both innate and acquired immune responses. Understanding the changes in gene expression post-infection is essential for developing effective intervention strategies and improving disease management in the poultry industry. This study aimed to employ RNA-Seq to investigate the differential gene expression profiles and to identify the essential genes and pathways involved in the host response of poultry infected with the avian leukosis virus. For this purpose, RNA-Seq data of healthy and avian leukosis virus-infected birds on days ۲۴ (n=۶) and ۴۰ (n=۶) post-infection were used. After quality control and preprocessing, we aligned the reads to the chicken reference genome using STAR software and quantified gene expression using HTSeq-Count. Differential gene expression analysis was performed using the edgeR package in R. The results of this study showed that the uniquely mapped read percentage ranged from ۷۸.۰۷% to ۸۷.۷۴%, and the mismatch rate per base was found to vary between ۰.۷۷% and ۱.۴۵%. A total of ۲,۲۱۳ and ۱۱۶۵ genes exhibited significant differential expression compared to the control group on day ۲۴ and ۴۰ post-infection, respectively ($p < ۰.۰۵$). The gene ontology enrichment and pathway analysis revealed that six candidate genes, AvBD۱, AvBD۶, CATH۱, CATH۲, CATH۳, and DEFBA, are associated with the immune response on days ۲۴ and ۴۰. Additionally, on day ۲۴, two more candidate genes, AvBD۵ and LYG۲, were found to be involved in the immune response. The poultry's immune system is regulated by various genes involved in both innate and acquired immune responses. Understanding the changes in gene expression post-infection is essential for developing effective intervention strategies and improving disease management in the poultry industry. This study aimed to employ RNA-Seq to investigate the differential gene expression profiles and to identify the essential genes and pathways involved in the host response of poultry infected with the avian leukosis virus. For this purpose, RNA-Seq data of healthy and avian leukosis virus-infected birds on days ۲۴ (n=۶) and ۴۰ (n=۶) post-infection were used. After quality control and preprocessing, we aligned the reads to the chicken reference genome using STAR software and quantified gene expression using HTSeq-Count. Differential gene expression analysis was performed using the edgeR package in R. The results of this study showed that the uniquely mapped read percentage ranged from ۷۸.۰۷% to ۸۷.۷۴%, ... and the mismatch rate per base was found to vary

کلمات کلیدی:

Differential gene expression analysis, Immune system, Gallus Gallus, Avian leukosis viruses, RNA-seq

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