

Transcriptomic analysis on susceptibility of different inbred chicken lines towards very virulent infectious bursal disease virus infection

ABSTRACT

Infectious bursal disease virus (IBDV) is an economically important virus which affects the poultry industry worldwide. The virus is a causative agent for Gumboro disease which can cause high mortality rate in young chickens by infecting and destroying actively dividing IgM-bearing B lymphocytes in the bursa of Fabricius leading to immunosuppression. Previous studies have identified differential expression of immune-mediated genes related to inflammatory response in chickens with different genetic susceptibility to IBDV infections. However, the mechanisms of genetic resistance against IBD are not known. RNA sequencing through next-generation sequencing (NGS) technologies provide an excellent platform to study differentially expressed genes of known or unknown function to better define effective mechanism of host resistance. Therefore, this study is aimed at investigating susceptibility of different inbred chicken lines toward very virulent IBDV through transcriptomic analysis. This analysis allows for quantification of gene expression and identification of possible single nucleotide polymorphisms (SNPs), indels, and novel protein-coding sequence. RNA isolated from bursa of day 3 IBDV-infected and control chickens were used for Illumina sequencing. Bioinformatics analysis of this data will allow function annotation of differentially expressed genes, indicating possible roles in the response to infection. Gene of interest, virus detection and copy number variation between different lines will be validated using qPCR. Genes of interest that exhibit novel SNP and/or indels will be validated using siRNA experiments. This study is expected to provide information that able to decipher the genetic resistance of chickens towards IBDV infection.

Keyword: Infectious bursal disease virus; Next-generation sequencing; Transcriptome