Functional prediction of de novo uni-genes from chicken transcriptomic data following infectious bursal disease virus at 3-days post-infection

ABSTRACT

Background: Infectious bursal disease (IBD) is an economically very important issue to the poultry industry and it is one of the major threats to the nation's food security. The pathogen, a highly pathogenic strain of a very virulent IBD virus causes high mortality and immunosuppression in chickens. The importance of understanding the underlying genes that could combat this disease is now of global interest in order to control future outbreaks. We had looked at identified novel genes that could elucidate the pathogenicity of the virus following infection and at possible disease resistance genes present in chickens. Results: A set of sequences retrieved from IBD virus-infected chickens that did not map to the chicken reference genome were de novo assembled, clustered and analysed. From six inbred chicken lines, we managed to assemble 10,828 uni-transcripts and screened 618 uni-transcripts which were the most significant sequences to known genes, as determined by BLASTX searches. Based on the differentially expressed genes (DEGs) analysis, 12 commonly upregulated and 18 downregulated uni-genes present in all six inbred lines were identified with false discovery rate of q-value < 0.05. Yet, only 9 upregulated and 13 downregulated uni-genes had BLAST hits against the Non-redundant and Swiss-Prot databases. The genome ontology enrichment keywords of these DEGs were associated with immune response, cell signalling and apoptosis. Consequently, the Weighted Gene Correlation Network Analysis R tool was used to predict the functional annotation of the remaining unknown uni-genes with no significant BLAST hits. Interestingly, the functions of the three upregulated uni-genes were predicted to be related to innate immune response, while the five downregulated uni-genes were predicted to be related to cell surface functions. These results further elucidated and supported the current molecular knowledge regarding the pathophysiology of chicken's bursal infected with IBDV. Conclusion: Our data revealed the commonly up- and downregulated novel uni-genes identified to be immune- and extracellular binding-related, respectively. Besides, these novel findings are valuable contributions in improving the current existing integrative chicken transcriptomics annotation and may pave a path towards the control of viral particles especially towards the suppression of IBD and other infectious diseases in chickens.

Keyword: Gallus gallus; RNA-sequencing; Transcriptomics; Infectious bursal disease virus; De novo; Bursa; Immune; Upregulated; Downregulated; Chickens