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Transcriptome Analysis Reveals Distinct Immune Responses to Newcastle Disease Virus in Spleen Between Resistant and Susceptible Chicken Lines

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Introduction

- As a major infectious disease in poultry, Newcastle disease has caused:
  I. Considerable economic loss in poultry industry worldwide
  II. Serious problem in some rural areas where chickens are a significant source of income and nutrition
- Vaccination is an important strategy to prevent the disease but is not always executable or effective due to:
  I. Lack of cold chain and proper management in rural communities in African and Asia
  II. Evolution and diversity of Newcastle disease virus (NDV)
- Selection and breeding provides a promising approach to enhance resistance to the disease so that
  I. Global poultry industry productivity will be increased
  II. Poverty and food insecurity in developing countries will be alleviated
- Two objectives of this study:
  I. Identify genes and pathways regulating host response to NDV
  II. Identify genes and pathways related to distinct genetic resistance between the two inbred chicken lines

Methods

- Hatch
- Leghorn
- Susceptible model
- Phosphate-buffered saline
- (N=3-4/group)
- Lentogenic
- 23 d
- 2 dpi
- 6 dpi
- RNA isolation
- RNase
- RNAseq library construction
- RNA sequencing in Illumina HiSeq 2500
- Quality control (Fast QC)
- Mapping to galGal4 reference genome (TopHat2)
- Sequence counting (HTseq)
- Differential expression analysis (edgeR)
- Co-expression analysis (WGCNA)
- Validation with Fluidigm Biomark FCM
- Gene ontology enrichment analysis
- Ingenuity pathway analysis (IPA)

Results

- Figure 1. Samples separated well between Fayoumi (FA) and Leghorn (LH), 2 and 6 dpi, and NDV challenged and non-challenged (CT) chickens (except FA 6dpi) in PCA plot.
- Figure 2. Number of differentially expressed genes (DEGs) with false discovery rate (FDR) <0.05 for NDV vs. CT contrast in two chicken lines at two time points.
- Table 1. Four unique DEGs in Fayoumi at 2dpi
- Table 2. Four shared DEGs in all groups
- Table 3. Gene annotation enrichment analysis
- Table 4. Gene ontology enrichment analysis

Conclusion

- Response of gene expression to NDV challenge decreases with time in both chicken lines, but Leghorn has more dynamic response to NDV challenge than Fayoumi at both time points.
- IFN, Mx, CMPK2, and USP18 are commonly upregulated in NDV challenged birds, indicating their universal role in regulating immune response to NDV in chicken spleen.
- PLA2R1, GLUL, GPT2 and CFHR2 are uniquely upregulated in NDV challenged Fayoumi chickens at 2dpi. They may play a key role in enhancing genetic resistance to NDV and therefore be potential targets for breeding of NDV resistant chickens.
- WGCNA co-expression analysis revealed a module positively related to NDV challenge. Gene annotation enrichment analysis with this module suggested enhanced innate immune response against viral infection in chicken spleen in response to NDV.
- IPA predicted increased glutamine synthesis in NDV challenged Fayoumi but increase cell apoptosis in NDV challenged Leghorn chickens at 2dpi, providing a clue for distinct resistance to NDV in the two inbred lines.

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References


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