**DIFFERENTIAL EXPRESSION OF MITOGEN-ACTIVATED PROTEIN KINASE SIGNALING PATHWAY GENES IN THE INTESTINAL MUCOSAL LAYER OF NECROTIC ENTERITIS-AFFLICTED CHICKEN LINES**

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**Background**

Mitogen-activated protein kinase (MAPK) signaling pathways play a key role in innate immunity, inflammation, cell proliferation, cell differentiation, and cell death. The main objective of this study was to investigate the expression level of candidate MAPK pathway genes in the intestinal mucosal layer of two genetically disparate chicken lines (Marek’s disease-resistant line 6.3 and Marek’s disease-susceptible line 7.2) induced with necrotic enteritis (NE).

**Materials and methods**

Chickens were randomly selected and infected with *E. maxima* strain 41A (1.0 × 104 oocysts/chicken) by oral gavage on day 14 post-hatch, followed by oral gavage with *C. perfringens* strain Del-1 (1.0 × 109 CFU/chicken) on day 18 post-hatch. Total RNA was extracted from samples on day 20 post-hatch and used for RNA-Seq, qRT-PCR and data analyses.

**Results and discussion**

Using RNA-seq, we investigated 178 MAPK signaling pathway related genes that were significantly and differentially expressed between the intestinal mucosal layers of the NE-afflicted and control chickens. In total, 15 MAPK pathway genes were further measured by quantitative real-time PCR (qRT-PCR) and the results were consistent with the RNA-sequencing data. All 178 identified genes were annotated through Gene Ontology and mapped onto the KEGG chicken MAPK signaling pathway. Several key genes of the MAPK pathway, ERK1/2, JNK1–3, p38 MAPK, MAP2K1–4, NF-κB1/2, c-Fos, AP-1, Jun-D, and Jun, were differentially expressed in the two chicken lines.

**Conclusion**

We believe that RNA sequencing and qRT-PCR analysis provide resourceful information for future studies on MAPK signaling of genetically disparate chicken lines in response to pathogens.

*Key words:* Chicken, DEG, MAPK pathway, RNA-seq, qRT-PCR