

Differential protein expression in avian liver in response to invasion by *Salmonella gallinarum*

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Abstract

Salmonella gallinarum is a pathogen that is capable of causing disease in Korean native chicken. Although *Salmonella gallinarum* is important world-wide pathogens of poultry, little is understood of the mechanisms of pathogenesis of *Salmonella gallinarum* in the chicken.

This study was to investigate chicken liver proteins affected by infection of *Salmonella gallinarum* in Korean native chicken. The differentially expressed proteins of chicken livers were identified by using 2-dimensional electro-phoresis (2D-E) and mass spectrometry (MS).

We detected more than 300 protein spots on silver stained 2D gels using pH 3~10 gradients. Three differentially expressed protein spots were analyzed by MALDI-TOF MS and MS/MS. The obtained MS and MS/MS data were searched against a protein database using the Mascot search engine.

Further researches on the identified proteins can give valuable information of mechanism of pathogenesis in chicken.

Key words : Chicken, pathogenesis, MALDI-TOF MS, 2DE, *Salmonella gallinarum*

Introduction

Fowl typhoid caused by *Salmonella gallinarum* is an economic disease of worldwide significance. It has largely been eradicated from Korea which has an intensive poultry industry but the disease is still an important infectious disease resulting in severe economic distress due to high morbidity and mortality.

Although *Salmonella gallinarum* is important world-wide pathogens of poultry, little is understood of the mechanisms of pathogenesis of *Salmonella gallinarum* in the chicken.

This study was to investigate chicken liver proteins affected by infection of *Salmonella gallinarum* in Korean native chicken by using proteomic analysis methods.

Materials and Methods

Livers from normal and infected by *Salmonella gallinarum* chicken were immediately removed just after slaughter and quenched in liquid nitrogen for subsequent 2-DE gel analysis. Obtained 2DE gels were stained with silver and analysed with ImageMaster2D Elite Software (Amersham, USA). The differentially expressed proteins were analysed with MALDI-TOF Mass spectrometry for detailed

verification of the proteins.

Results

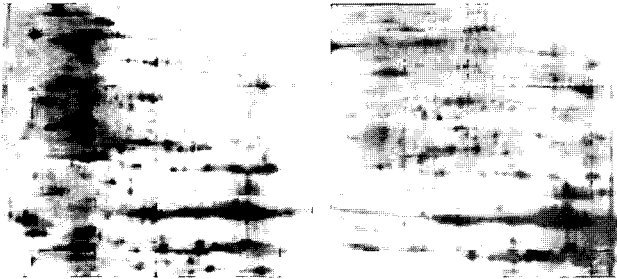


Figure 1. Comparative analysis of five identified protein affecting *Samonella gallinarum*.

All five protein spots identified are up-regulated when infected by *S. gallinarum* were increased. Spot volumes and areas are indicated on the right. five differentially expressed protein spots will be analyze by MALDI-TOF MS and MS/MS. The obtained MS and MS/MS data were searched against a protein database using the Mascot search engine. Further researches on the identified proteins can give valuable information of mechanism of pathogenesis in chicken.

적 요

본 연구는 proteomics의 방법을 이용하여 가금의 질병과 관련된 단백질을 찾고자 수행하였다. 가금 티푸스에 감염된 재래계와 대조구와의 비교에서 질병과 관련된 후보 단백질이 이 연구를 통하여 찾아졌다.

이 단백질들은 질병을 조절하고 모니터링하는 가금의 질병 단백질 마커로 중요하게 이용이 될 수 있을 것으로 추정된다.

References

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