한국가금학회 제20차 정기총회 및 학술발표회

Proteomics for monitoring of chicken responses to immune system in Korean Native Chickens

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Abstract

Specific biomarkers to detect significant immunological or physiological responses would be extremely valuable on the development of feeding technique. Proteomics, the study of proteins within a cell or biological samples, may offer a novel approach to immunological or physiological monitoring of chicken responses to immune system. By studying the protein content of cells responding to a vaccine or growth factor, it may be possible to develop a metric for quantitating the magnitude of immunological or physiological responses. Proteomics could also provide a tool for obtaining valuable information regarding the underlying regulatory mechanisms and pathways in Korean Native Chicken by comparing with subspecies of KNC and other species, like Cornish and White Leghorns.

Materials and Methods

(1) Materials - Birds

5 strains of Korean Native Chicken, Cornish, and White Leghorns Samples were collected from each strains

(2) Methods - 2-D PAGE

Following excision, chicken tissue was immediately frozen at 80 °C. Separation of proteins in two dimensional system. Protein Identification: For protein identification by mass spectrometry, 2-D gels were stained using a modified silver staining method, and excised proteins were digested. A peptide mass profile was obtained using a MALDI-TOF.

Results and Discussion

Lymphocytes of spleen samples from chickens, including five strains of Korean Native Chicken, Cornish, and White Leghorns, were collected. They are used to develop a metric for quantitating the magnitude of immunological or physiological responses in Korean Native Chicken using proteomics approaches by comparing different strains. The proteomic approach for the identification of specific biomakers that elicit physiological responses such as immunity, which we have applied to various samples from subspecies of KNC and other species, like Cornish and White Leghorns. Following

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two-dimensional electrophoresis of samples, matrix-assisted laser desorption ionization time-of-flight and liquid chromatography-tandem mass spectrometry were used for protein identification. This concept and the identification of multiple novel immune-recognized components should assist future vaccine development strategies or the development of feeding technique.

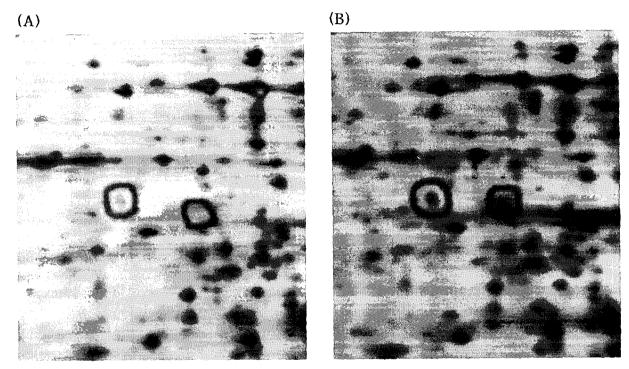


Fig 1. 2D gel images for the ConA treated Korean Native Chicken Lymphocyte(B) compared with control(A). The differentially expressed proteins are indicated as circles.

적 요

본 연구는 proteomics의 방법을 이용하여 가금의 면역시스템에 관련된 단백질을 찾고자 수행하였다. 면역활성 물질을 처리한 후 면역활성화시 발현되는 단백질을 찾아보았다. 이 결과는 가금의 면역과 관 련된 단백질 마커의 이용뿐 아니라 현재까지 밝혀지지 않은 가금의 2D map을 만드는데 역시 중요하게 이용이 될 것이다.

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