

## 쥐 신장 피질의 막층에서 알도스테론 의존적으로 발현된 단백질들의 동정을 위한 단백질체적 접근법

경북대학교 의과대학 분자의학교실<sup>1</sup>, 경북대학교 의과대학 생화학세포생물학교실<sup>2</sup>  
전홍배<sup>1</sup> · 송미나<sup>1</sup> · 김혜정<sup>1</sup> · 이정은<sup>1</sup> · 최효정<sup>2</sup> · 권태환<sup>2</sup> · 백문창<sup>1</sup>

### Proteomic Approach to Identify the Aldosterone Dependently Expressed Proteins in Membrane Fraction from Rat Kidney Cortex

Hong Bae Jeon<sup>1</sup>, Mi Na Song<sup>1</sup>, Hye Jeong Kim<sup>1</sup>, Jeong Eun Lee<sup>1</sup>  
Hyo Jeong Choi<sup>2</sup>, Tae-Hwan Kwon<sup>2</sup> and Moon-Chang Baek<sup>1</sup>

Kyungpook National University School of Medicine Department of Molecular Medicine<sup>1</sup>  
Kyungpook National University School of Medicine Department of Biochemistry and Cell Biology<sup>2</sup>

Aldosterone from adrenal cortex is the most important mineralocorticoid for the sodium reabsorption, potassium excretion, and water retention in the distal region of the nephron. This action led to regulation of blood pressure and balance of fluids and electrolytes in blood. In addition, high level of aldosterone induces fibrosis of heart tissue. In molecular mechanism of aldosterone action, aldosterone- mineralocorticoid receptor (MR) complex acts as a transcription factor in nucleus, which transactivates or represses the transcription of target genes related to physiological consequences for salt and water homeostasis. However, many of them have not been identified and analyzed yet.

In this study, targeted proteomic strategy and advanced proteomic technologies with aldosterone rat model were applied to analyze and identify the aldosterone dependently expressed proteins in rat kidney cortex. To address this, we conducted comparative analysis between normal and aldosterone- treated proteome from membrane fractions using two- dimensional differential gel electrophoresis (2D- DIGE) and label free quantification with UPLC- Q- TOF mass spectrometry. The changed proteins by aldosterone were quantified by DeCyder and PLGS software and subjected to identification with LC- MS/MS.

As a result, modulated proteins were identified, which could produce the clues for the understanding of aldosterone action on kidney.

In conclusion, the combination of gel and non- gel based proteomic approach is high- throughput and effective method for global analysis of aldosterone dependent proteins.

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Aldosterone, proteomics, 2D- DIGE