

라파마이신과 사이크로스포린 투여에 따른 생쥐 족세포에서의 단백질 변화 비교분석

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Comparative Proteomic Analysis of Rapamycin Versus Cyclosporine Combination Treatment in Mouse Podocyte

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Background: The mechanism of proteinuria observed with rapamycin (RPM) use remains unclear. The conversion from calcineurin inhibitors (CNIs) to RPM in kidney transplant recipients has been associated with a higher incidence of proteinuria. In this study, we performed proteomic analysis to investigate the alteration of protein expression in mouse podocyte treated with RPM in comparison with RPM/CNI combination.

Methods: Immortalized mouse podocytes were treated with 20 nM RPM or 20 nM RPM+1 µg/ml cyclosporine. Podocyte proteins were separated by two dimensional-polyacrylamide gel electrophoresis (PAGE) and identified by matrix-assisted laser desorption time-of-flight (MALDI-TOF) mass spectrometry and peptide fingerprinting. Selected proteins were analyzed by western blot assay.

Results: We identified 36 differentially expressed proteins after isolated RPM or RPM/CNI combination treatment in cultured mouse podocytes. There are three distinct patterns of protein expression: 1. Potentiated down-regulation of proteins by RPM/CNI treatment compared with isolated RPM treatment (n=4); 2. Partial offset of down-regulation by RPM/CNI in comparison with RPM (n=25); 3. No difference in down-regulation between RPM and RPM/CNI (n=7)

Conclusion: We found a significant interplay between RPM and CNI on the proteins expression in mouse podocyte. This might explain the higher incidence of proteinuria by RPM/CNI combination in clinical settings. Further study is required to elucidate the target protein associated with RPM induced proteinuria.

Key Words: 족세포, 라파마이신, 타크로리무스
Podocyte, Rapamycin, Cyclosporine