

DETECTION OF ACUTE REJECTION IN RENAL TRANSPLANT RECIPIENTS BY PROTEOMIC ANALYSIS OF URINE SAMPLES WITH ESI-TOF MASS SPECTROMETRY

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Reliable diagnosis of acute rejection after renal transplantation is still confined to allograft biopsy. This study evaluates proteomic analysis of urinary samples as a non-invasive method to detect acute rejection.

A novel high throughput method, capillary electrophoresis online coupled to mass spectrometry (CE-MS) was used to examine 19 patients with different grades of subclinical or clinical acute rejection (BANFF Ia to IIb), 10 patients with urinary tract infection, and 29 patients without rejection or infection.

Using support vector machines, a specific polypeptide pattern was identified that allowed correct classification of tubulointerstitial rejection in 16 of 17 cases. The two samples with vascular rejection could not be classified with this pattern. For urinary tract infection several polypeptides were found, permitting correct diagnosis in samples with infection and differentiation between infection and rejection in all cases. Potentially confounding variables like acute tubular lesions, tubular atrophy, tubulointerstitial fibrosis, and calcineurin inhibitor toxicity did not affect correct diagnosis making. Likewise, degree of proteinuria, hematuria, allograft function, and different immunosuppressive regimens did not interfere.

Detection of acute rejection by CE-MS is a promising tool for the post-transplantation surveillance of renal allograft recipients. Further efforts are necessary to establish separate patterns for vascular rejection and to explore whether changes in the urinary proteome occur before the onset of histologically discernible rejection.

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