

DETECTION OF ACUTE REJECTION BY PROTEOMIC ANALYSIS OF URINARY SAMPLES IN RENAL TRANSPLANT RECIPIENTS

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Diagnosis of acute rejection after renal transplantation is still confined to allograft biopsy upon functional graft impairment. This study evaluates proteomic analysis of urinary samples as a non-invasive method to detect acute rejection in patients.

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

Using support vector machines, a specific polypeptide pattern was identified by CE-MS that segregated patients with acute rejection from patients without. This pattern was present in each acute tubulointerstitial rejection, but not in two samples with vascular rejection. Among the samples with tubulointerstitial rejection (n=17), one sample could not be classified correctly. With regard to urinary tract infection, several polypeptides were found enabling correct diagnosis in all samples with infection as well as differentiation between infection and rejection. Potentially confounding variables like acute tubular lesions, tubular atrophy, tubulointerstitial fibrosis, and calcineurin inhibitor toxicity did not affect correct diagnosis. Likewise, degree of proteinuria, hematuria, allograft function, and different immunosuppressive regimens did not interfere. Prospective studies are currently underway, the data on these will be presented as well.

Detection of acute rejection by CE-MS is a promising non-invasive 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 acute rejection can be diagnosed when urinary tract infection is simultaneously present.

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