

Hierarchical clustering of Banff scores in renal allograft biopsies: Evidence questioning whether current “v” scoring in Banff detects T-Cell Mediated Rejection

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To visualize the relationship between Banff lesions, we performed unsupervised hierarchical cluster analyses using Banff scores, C4d staining, and peritubular capillary basement membrane multilayering (PTCBMML) values (the highest number of BM layers) in 135 renal allograft biopsies with deterioration of renal function. Of these, 27 (20%) were diagnosed as T-cell mediated rejection (TCMR), 20 (15%) borderline, 13 (10%) antibody-mediated rejection (ABMR), 11 (7%) transplant glomerulopathy (TG), 17 (13%) glomerulonephritis (GN), and 47 (35%) miscellaneous. Hierarchical clustering with Banff scores did not show a clear separation among different diagnoses, but TCMR cases were clustered closer in comparison to the other diagnoses. With addition of C4d and PTCBMML values, ABMR cases were clustered together. Cluster analysis also pointed out that PTCBMML is not only associated with chronic ABMR, but also associated with other disease states i.e. TCMR, TG (without C4d and alloantibody), and GN. We observed a significant correlation between PTCBMML and C4d, glomerular double contours (cg), and increase in mesangial matrix (mm) (Table 1). Thus PTCBMML is strongly associated with features of late antibody mediated rejection. Tubulitis (t) and interstitial inflammation (i) correlated each other. However, intimal arteritis (v) scores failed to correlate with inflammation or tubulitis. Thus the reliability of v score for detection of TCMR seems low, and the scoring criteria of v should be revisited.

Table 1. Spearman correlation coefficients between Banff scores, C4d staining, and peritubular capillary basement membrane multilayering (PTCBMML).

	PTCBMML	C4d	cg	mm	i	t	v
PTCBMML		.378*	.388*	.445*	NS	NS	NS
C4d			.266*	.284*	NS	NS	.196*
cg				.614*	NS	NS	NS
mm					.186*	NS	NS
i						.561*	NS
t							NS
cv	.224*	NS	.331*	.325*	.181*	NS	NS

* p<0.05