KSN 2019
Seoul, Korea · May 23 - 26

Abstract Type : Poster
Abstract Submission No. : PO-1618

Clinical significance of CD8+ T cell subset analysis for the prediction of acute allograft rejection in kidney transplant recipients

Kyoung-Woon Kim[1], Jung-Woo Seo[3], Eun Jeong Ko[1], Bo-Mi Kim[1], Jang-Hee Cho[2], Chan-Duck Kim[2], Chul Woo Yang[1], Sang-Ho Lee[3], Byung Ha Chung[1]
[1]Department of Internal Medicine-Nephrology, The Catholic University of Korea, Seoul St. Mary's Hospital, Korea, Republic of
[2]Department of Internal Medicine-Nephrology, Kyungpook National University Hospital, Korea, Republic of
[3]Department of Internal Medicine-Nephrology, Kyung Hee University Hospital at Gangdong, Korea, Republic of

Objectives: In this study, we performed multi-color flowcytometry to analyze the CD8+T cell subsets in KTRs with acute rejection in comparison with KTRs with different clinical status.

Methods: At first, we included 121 KTRs from three transplant centers and we isolated PBMC at the time of allograft biopsy. They were divided into 3 groups according to the pathologic diagnosis; Normal biopsy control (NC) (n=32), Acute rejection (AR) (n=50), long term graft survival (LTGS) (n=39). **W**e performed multi-color flowcytometry analysis using following platform. We also did microarray analysis to investigate the significant changes in gene expression associated with cell types using SAM analysis.

Results: The percentage of CCR7^{+}CD8^{+} T cells showed significant decrease in the AR group compared to NC group or LTGS group ($P<0.05$ for each). In contrast, the percentage of CD28^{null}CD57^{+} T cell and CCR7^{-}CD45RA^{+}/CD8^{+} T cells and showed increase in AR group in comparison with other groups. Both effector CD8^{+} T cells showed significant negative correlation to CCR7^{+}CD8^{+} T cells in an ex vivo and also in an vitro conditions. In microarray analysis from blood of KTRs, we identified significant genes associated with CCR7^{-}CD45RA^{+}/CD8^{+} T and CD28^{null}CD57^{+}/CD8^{+} T cells by SAM analysis. Moreover, some of significant genes associated with CCR7^{-}CD45RA^{+}/CD8^{+} T cells and CD28^{null}CD57^{+}/CD8^{+} T cells showed negative correlation to expressed genes in CCR7^{+}CD8^{+} T cells. ROC analysis showed that the ratio between CCR7^{+}CD8^{+} T cells and CD28^{null}CD57^{+} CD8^{+} T cells showed best prediction for AR in the whole clinical cohort (AUC=0.800, $P<0.01$).

Conclusions: This study suggests that combined monitoring of the ratio between CCR7^{+} and CD28^{null}CD57^{+} T in CD8^{+} T gaiting may be useful for the prediction of AR. Validation of this result in the prospective cohort may be required.