

第50回日本免疫学会学術集会 Technical Seminar T2

第1日目 2021年12月8日 (水) 11:45-12:45

テクニカルセミナー T2 Room C会場 (会議室3+4)

《Nara Kasugano International Forum - I RA KA -》

演題 : TCR repertoire analysis reveals spatiotemporal responses of tumor-reactive T cell clones

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要旨 : Understanding how tumor-specific T cells are induced and maintained in a tumor-bearing host is essential for optimizing cancer immunotherapy with immune checkpoint inhibitors (ICIs). TCR repertoire analysis is a powerful tool to track tumor-reactive T cell induction and maintenance using TCR sequences as molecular barcodes. We have previously reported the results of treatment of tumor-bearing mice with an anti-CD4 depleting antibody, which acts as an ICI by removing CD4+ and Foxp3+ regulatory T cells, promoting proliferation of tumor-specific CD8+ T cells in tumor-draining lymph nodes (dLN), and inhibiting tumor growth by increasing tumor-infiltrating CD8+ T cells. TCR repertoire analysis of the dLN and tumors in individual mice revealed that each dLN and corresponding tumor share a significant proportion of CD8+ T cell clones. The number and total frequency of these overlapping clones increase significantly with ICI treatments such as anti-CD4, anti-PD-L1, and anti-CD4/PD-L1. Surprisingly, ICI treatments did not affect expansion of the top10 overlapping clones, but increased the total frequency of less prevalent overlapping clones, the degree of which correlated with the antitumor efficacy of the ICIs. These results suggest that mobilization and expansion of diverse tumor-reactive clones contribute to the anti-tumor effect of ICIs. I will here introduce the potential of TCR repertoire analysis for investigating spatiotemporal responses of tumor-reactive T cell clones in clinical and pre-clinical studies.

共催 : 日本免疫学会・トミーデジタルバイオロジー株式会社