T-CELL IMMUNOPHENOTYPIC PROFILES ASSOCIATED WITH CLINICAL SEVERITY OF COVID-19

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Background: T-cell response is essential for antiviral immunity. Despite a similarity to SARS and MERS, the infection caused by SARS-CoV-2 presents distinct characteristics, and lymphopenia was proposed to predict disease severity. Whether an extreme activation or rather T-cell deficiency underlies COVID-19 pathology remains an open question.

Aim: Extensive immunophenotypic analysis of circulating T cells in COVID-19 patients was performed in order to identify profiles associated with infection severity.

Materials and methods: Peripheral blood samples were obtained from hospitalized SARS-CoV-2 PCR+ patients (n=83). Lymphocyte absolute counts (LyAC) and proportions of T, B and NK cells were determined in TRUCount standard tubes. Proportions of Th1 (CD196+CD183-), Th2 (CD183-CD196), Th17 (CD183-CD196+), Treg (CD39+/CD25^{hi}CD127^{lo}), naïve (CD27+CD45RA+), memory (CD27-CD45RA-), effector (CD27-RA+), apoptotic (CD28-CD57+), activated (CD38+/HLA-DR+) T cells and antibody-secreting B cells (CD19loCD27+CD38hi) were determined by 8-color flowcytometry. The number of CD38 molecules (CD38ABC) was calculated using Quantibrite kit (FACSCAnto II, FACSDiva 6.1.2, BD Biosciences).

Results: Three subgroups were defined: A, w/o lymphopenia (LyAC >1100,n=31); B, mild lymphopenia (650<LyAC<1100,n=31); C, severe lymphopenia (LyAC<650,n=22). Mild lymphopenia was associated with decreased proportion of Th1 (B,22% vs.A,40%), and increased activation markers: CD38/CD8ABC (B,4965 vs. A,2164); CD38+HLA-DR+CD4 (29% vs. 23%), $p<0.01$ for all comparisons. The most significant aberration in severe lymphopenia was the increased share of Treg (C,9.3% vs. A,5.2%; $p<0.01$). Analysis by clinical severity, revealed a significantly increased share of induced CD39+Treg among the moderate 0cases as compared to the mild ones (24% vs. 14%, $p<0.05$).

Conclusions: The induction of Treg might underlie a deficient antiviral response and development of late complications due to co-infections, thus contributing to unfavorable prognosis in COVID-19 patients.

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