Gene landscape and correlation between B cell infiltration and PD-L1 expression by analyses of TCGA lung adenocarcinoma patients

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Background: Tumor infiltrating lymphocytes are related to positive clinical prognoses in numerous kinds of cancer. Programmed death ligand 1 (PD-L1), a mediator of the PD-1 receptor, exhibits an inhibitory role in cancer immune responses. Several studies identified that upregulation of PD-L1 impeded infiltrating T cell functions in lung adenocarcinoma (LUAD), a subtype of lung cancer. However, associations between PD-L1 levels and infiltrating B cells, another important immune regulator, remain unknown. Hence, we aimed to investigate the role of infiltrating B cells in LUAD progression and its relation with PD-L1 expression.

Methods and results: The Cancer Genome Atlas (TCGA) LUAD dataset was utilized to explore associations among B cell infiltration, PD-L1, and LUAD patients' clinical outcomes. We found that high B cell infiltration was correlated with better prognoses, but PD-L1 might interfere with the survival advantage in patients with high B cell infiltration. In addition, the gene landscape with distinct PD-L1 levels of high infiltrating B cell populations was also comprehensively characterized. Using a gene set enrichment analysis, five upregulated signaling pathways were obtained: apoptosis, tumor necrosis factor (TNF)- α signaling via nuclear factor (NF)- κ B, the apical surface, the interferon- α response, and KRAS signaling. Furthermore, four candidate genes and their related target drugs were provided by a drug enrichment analysis: *interleukin-2 β receptor (IL2RB)*, *IL-2 γ receptor (IL2RG)*, *toll-like receptor 8 (TLR8)*, and *TNF*.

Conclusions: These findings suggest that tumor infiltrating B cells could act as a clinical factor for considering anti-PD-L1 immunotherapy in LUAD.