MACROH2A1 was identified as a biomarker associated with refractory COVID-19

Accurate predictors of refractory cases in COVID-19 have not yet been established. To identify potential serum biomarkers and examine the proteins associated with the pathogenesis of refractory COVID-19, Takahiro Kawasaki (Immunopathology, IFReC), Yoshito Takeda (Graduate School of Medicine, Osaka University), and the research group conducted high-coverage proteomics on serum extracellular vesicles collected from 12 patients with COVID-19 at different disease severity levels and 4 healthy controls. Furthermore, single-cell RNA sequencing of peripheral blood mononuclear cells collected from 10 patients with COVID-19 and 5 healthy controls was performed. Among the 3046 extracellular vesicle proteins that were identified, expression of MACROH2A1 was significantly elevated in refractory cases compared to non-refractory cases; moreover, its expression was increased according to disease severity. In single-cell RNA sequencing of peripheral blood mononuclear cells, the expression of MACROH2A1 was localized to monocytes and elevated in critical cases. Consistently, single-nucleus RNA sequencing of lung tissues revealed that MACROH2A1 was highly expressed in monocytes and macrophages and was significantly elevated in fatal COVID-19. Their findings highlight that MACROH2A1 in extracellular vesicles.

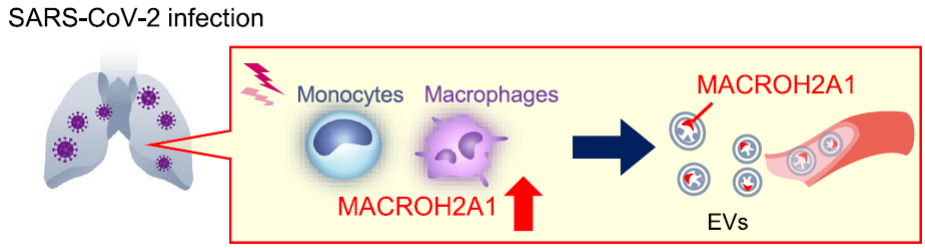

Figure: In response to SARS-CoV-2 infection, immune response including TLR signaling and cytokine secretion such as INF-gamma enhances expression of MACROH2A1 in monocytes. Subsequently, MACROH2A1 is secreted in circulating exosomes, which are more abundant in severely ill patients with COVID-19 than in those who are not.

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