The Application of Pharmacoinformatic Methods for the Prioritization of Drug Targets and Therapeutics for Multisystem Inflammatory Syndrome in Children (MIS-C)

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Abstract

Post COVID-19 multisystem inflammatory syndrome in children (MIS-C) is a rare but severe condition characterized by multiorgan damage. Herein, we aim to study MIS-C's network biology to guide drug discovery efforts. Pharmacoinformatics approaches were leveraged to reveal underlying disease mechanisms using a query biomarker signature consisting of 243 diagnostic and prognostic MIS-C biomarkers. Our results highlighted the NF-κB and the JAK-STAT pathways as key players in the disease pathogenesis. Nineteen drug targets were prioritized for treating MIS-C, including top scoring proteins chemokine (C-C motif) ligand 2 (CCL2) and interleukin 6 (IL-6). Furthermore, seven drugs targeting CCL2 and four drugs targeting IL-6 were prioritized as MIS-C disease-modifying treatments or preventive drugs including the small molecule drugs luminol, naringenin and trabectedin. This approach can be applied to study the network biology of other diseases to prioritize drug targets and drugs.

Keywords: Bioinformatics, COVID-19, multisystem inflammatory syndrome in children (MIS-C).