Regulation of gene expression of SARS-CoV2 Receptors

Pandemic severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) causes coronavirus 19 disease (COVID-19). The disease manifests with a large spectrum of features and with fatal outcomes in vulnerable people.
Knowledge of the entry receptor is a critical point to understand SARS-CoV-2 tropism, transmission and pathogenesis. Early evidence demonstrated angiotensin-converting enzyme 2 (ACE2) as most important player in SARS-CoV-2 infection, and as the main receptor for virus entry (Hoffmann et al,2020).
We focused our analyses on ACE2 (OMIM 300335) gene locus, evaluating several aspects related to genetic variability and expression regulation, through different in silico and experimental approaches.
We characterized allelic variants within its promoter region, that might be involved in inter-individual variability of ACE2 expression, and thus in vulnerability to SARS-CoV-2.
To test the effects of specific allelic variants in a regulatory region of ACE2 on transcription levels we performed a luciferase assay, by cloning the selected region in place of luciferase promoter.
We demonstrated that combinations of different allelic variants in the selected region determines consistent luciferase activity changes, thus suggesting their relevance in ACE2 expression.

References:
Hoffmann M., Kleine-Weber H., Schroeder S., Krüger N., Herrler T., Erichsen S., Schiergens T.S., Herrler G., Wu N.-H., Nitsche A. SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor. Cell. 2020;181:271–280.

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Contacts: Chiara Parisi chiara.parisi@cnr.it
Website(s): http://www.ibbc.cnr.it/researchers/chiara-parisi/
Collaborations: Prof. Viviana Caputo, Sapienza University of Rome