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ACE2 AND SARS-COV-2 INFECTION RISK: INSIGHTS FROM PATIENTS WITH TWO RARE GENETIC TUBULOPATHIES, GITELMAN'S AND BARTTER'S SYNDROMES

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BACKGROUND AND AIMS: COVID-19 is spreading globally with Angiotensin Converting Enzyme (ACE)-2 serving as the entry point of SARS-CoV-2 virus. This raised concerns how ACE2 and Renin-Angiotensin (Ang)-System (RAS) are to be dealt with given their involvement in COVID-19's morbidity and mortality. Specifically, increased ACE2 expression in response to treatment with ACE inhibitors (ACEi) and Ang II receptor blockers (ARBs) might theoretically increase COVID-19 risk by increasing SARS-CoV-2 binding sites. However, ACE2 is part of the protective counter-regulatory ACE2-AngI-7-MasR axis, which opposes the classical ACE-AngII-AT1R regulatory axis. We used Gitelman's and Bartter's syndromes (GS/BS) patients, rare genetic tubulopathies, who have endogenously increased levels of ACE2, to provide more insight on these issues.

METHOD: 128 genetically confirmed GS/BS patients, living in Lombardia, Emilia Romagna and Veneto, the Northern Italy hot spots for COVID-19, were surveyed via telephone survey regarding COVID-19.

RESULTS: The survey found no COVID-19 infection and absence of COVID-19 symptoms in any patient. Comparison analysis with the prevalence of COVID-19 in those Regions [8.96% (95% CI 8.96-8.99% vs 0.00% (95% IC 0.00-3.62%)] showed statistical significance ($p < 0.01$).

CONCLUSION: The results of the study contribute to suggest that increased ACE2 does not increase risk of COVID-19 and that ACEi and ARBs by blocking excessive AT1R-mediated Ang II activation, might favour the increase of ACE2-derived Ang 1-7. The GS/BS patients' increased ACE2 and Ang 1-7 levels and their characteristic chronic metabolic alkalosis might suggest for SARS-COV-2 a mechanism similar to that of chloroquine/hydroxychloroquine effect altering ACE2 glycosylation which resulted, in previous studies, in SARS-COV binding inhibition and block/inhibition of viral entry. Studies from our laboratory are ongoing to explore in GS/BS ACE2 glycosylation.