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Homocysteine as a potential predictor of cardiovascular risk in patients with COVID-19

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Since the beginning of the novel coronavirus pandemic, the scientific community is in urgent need for reliable biomarkers related to disease progression, in order to early identify high risk patients. In fact, the rapid disease spread makes it necessary to divide patients in risk categories immediately after diagnosis, to ensure an optimal resource allocation. The identification of new biomarkers is strictly related to the understanding of viral pathogenetic mechanisms, as well as cellular and organ damage. Trustworthy biomarkers would be helpful for screening, clinical management and prevention of serious complications.

Preliminary studies described vasculitic processes underlying organ damage in seriously ill patients, induced by the activation of inflammatory cascades, complement activation and pro-inflammatory cytokines (i.e. IL-6) [1,2]. Vasculitic damage is not only relevant in the lung, where it causes oedema and acute respiratory distress syndrome, but plays a significant role in the cardiovascular damages (ischemia, deep venous thrombosis, pulmonary thromboembolism) and cerebral injuries (ischemia, hemorragy); its severity is unfortunately not easily predictable through currently used laboratory biomarkers such as D-Dimer or PT/aPTT [3,4].

The leading role of cardiovascular damage in SARS-CoV-2 patients is clearly pointed at by epidemiological observations, which recorded ischemic heart disease and hypertension as among the most frequent pre-existing comorbidities in deceased SARS-CoV-2 patients [5].

To date, current clinical practice, suggests determining IL-6, D-Dimer, LDH and transaminases in addition to routine laboratory tests, in order to identify high risk patients and those who might potentially benefit of anti-IL6 immunotherapies with Tolicizumab [6]. Beyond D-Dimer and fibrin degradation products [1], there are no specific predictive parameters of severe ischemic and thrombo-embolic disease. For this reason, it is not easy to cluster patients in risk categories for an appropriate early anticoagulant or fibrinolytic therapy.

Concerning new predictive parameters of specific cardiovascular risk, it is known that a high plasma level of homocysteine significantly increases the incidence of vascular damage in both small and large vessels [7,8]. In fact, homocysteine concentrations above the 90th percentile are associated with increased risk of degenerative and atherosclerotic processes [9] in the coronary, cerebral and peripheral circulatory system. In this regard, determining homocysteine together with other cardiovascular risk markers (Apo B, Lp(a), LDL, fibrinogen, PAI-1) now belongs to the clinical practice [10]; moreover, recent evidence suggests the role of homocysteine as a risk factor for thromboembolism, given its influence on platelet reactivity [11–13].

Following our preliminary clinical observations in a cohort of 40 patients, we suggest the routine determination of plasma homocysteine as a potential marker for severe disease in SARS-CoV-2 patients. This single time laboratory test can be easily performed on blood EDTA samples at diagnosis or at the time of hospitalization. Very recent data witnessed a predictive value of homocysteine (together with age, monocyte-lymphocyte ratio, and period from disease onset to hospital admission) for severe pneumonia on chest CT at first week from COVID-19 patients, but did not report on additional organ involvement [14]; A prospective study on 500 patients was started in our department in order to assess the predictive value of homocysteine as a specific marker for cardiovascular risk in SARS-CoV-2 patients, clustered into "ordinary", "sub-intensive" and "intensive" settings. Sharing preliminary observations on potential biomarkers for severe disease during a pandemic can lead to rapid improvement of current knowledge and significant benefit for patients.

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The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.mehy.2020.109859.

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