LETTER TO EDITOR

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# Heme Oxygenase-1 (HMOX1) Gene Polymorphisms as Predictive Markers of Increased Risk of Thrombosis among Patients with COVID-19

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**Dear Editor**,

The novel human severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a highly contagious virus and the coagulopathies are now known major causes of mortality. SARS-CoV-2 could be a highly prothrombotic virus that produces unidentified modifications in the coagulation cascade, leading to a progressive increase in D-dimer as the severity and extent of micro thrombosis increases [1] and widespread microvascular or macrovascular thrombosis could explain several disparate phenomena observed in COVID-19 [2].

Unfortunately, COVID-19 mortality rates in predominantly black COVID-19 patients are 6-folds higher than that in predominantly white patients [3] and the data regarding confirmed COVID-19 cases by race are largely incomplete despite the higher infection rates in African Americans was reported [4], and the impact of race on the susceptibility of ethnic minorities has not been discussed in detail worldwide [5].

Therefore, it is the potential that genetic polymorphisms are an underlying genetic susceptibility to SARS-CoV-2 infection that may be influencing the disparity of COVID-19 mortality rates in black communities. Furthermore, the evidence of the biological predisposition for high-risk comorbid conditions may be relevant to the ability to understand the address health disparities of COVID-19 deaths in blacks [3,6].

The inducible heme oxygenase-1 (HMOX1) gene encodes a key cytoprotective enzyme with anticoagulant activity acting in the vascular system and acting a key role in protecting patients at increased risk for thrombosis [7].

Heme oxygenase1 (HO-1) products have antithrombotic characteristics, and HO-1 activity deficiency may contribute to thrombus development [8]. Among the reported polymorphisms in the HMOX1promoter regions, two polymorphisms have been identified as functional: a (GT) n repeat dinucleotide length polymorphism (rs3074372) and A (-413) T single nucleotide polymorphism (SNP; rs2071746). Both have been shown to affect the transcriptional activity of HMOX1 under several conditions [9].

Many studies reported that the transcriptional activity of long GT-repeat alleles in the HMOX1 gene is lower as compared with short alleles. Long alleles are also related to a reduction in HO-1 anticoagulant activity and, as a result, an increased risk of thrombosis.

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There are further unique peaks of roughly (GT) 39 repetitions in the African population, notably in malaria-endemic areas, according to several published studies [9].

Another study reported that African Americans have a different HO-1 (GT) n allele distribution with more long alleles than European Americans and the higher prevalence of long HO-1 (GT)n alleles in African Americans, may contribute to a higher risk for inflammation, oxidative stress [10] and therefore increased risk of thrombosis.

Therefore, the long GT-repeat alleles in HO-1 among blacks may lead to decreased HO-1 anticoagulant activity and a low level of HO-1 as a result of a higher prevalence of comorbid disease which can increase the risk of thrombosis.

So, the determination of the association between HO-1 promoter polymorphisms and disease severity and increased risk of thrombosis among COVID19 Black patients might be helpful in identifying patients at high risk and HO-1 pathway activation and could be a therapeutic strategy against COVID-19 complications. **[GMJ.2022;11:e2398]**

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**Conflict of Interests**

The authors have declared that no conflict of interests.

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