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Polymorphisms and Severity of COVID-19

To the Editor:

We would like to share ideas on the publication "A *MUC5B* gene polymorphism, rs35705950-T, confers protective effects against COVID-19 hospitalization but not severe disease or mortality" (1). Verma and colleagues conducted the current investigation to determine whether the Million Veteran Program participants' rs35705950-T genotype confers differential risk for clinical outcomes related to coronavirus disease (COVID-19) infection (1). According to this study, the rs35705950-T allele was associated with fewer COVID-19 hospitalizations (1). The MUC5B variant rs35705950-T, according to Verma and colleagues, may provide protection in COVID-19 hospitalizations (1).

We are all in agreement that the genetic mutation under examination has a strong therapeutic potential. It should be mentioned that the presence of particular diseases might be influenced by a range of factors. Because the current study is expected to diminish or eliminate environmental influences, confounding genetic variants should be addressed. Angiotensinogen, angiotensin-converting enzyme, angiotensin-II receptor 1, PNPLA3, TLL-1, HADHA, and DRC1 polymorphisms may also be linked to the occurrence of COVID-19 in children (2, 3). The likelihood of COVID-19 infection was reduced by the II genotype of ACE rs4646994 and the I allele (2). PNPLA3 and TLL-1 polymorphisms are proven potential predictors of disease severity in patients with COVID-19 (3). Genetic variations in HADHA and DRC1 have been linked to severe COVID-19 results (4). As a result, many unstudied genetic variations may be related to how severe COVID-19 is. Multiple genetic variations may have an impact; however, Verma and colleagues' current study (1) does not investigate this possibility. As a result, more research into the potential repercussions of newly discovered genetic variations would be beneficial. ■

Author disclosures are available with the text of this article at www.atsjournals.org.

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