

Initial study on TMPRSS2 p.Val160Met genetic variant in COVID-19 patients

Delvac Oceandy

University of Manchester, Manchester, UK

Abstract

Coronavirus disease 2019 (COVID-19) may be a global ill health that causes many deaths worldwide. The clinical manifestation of COVID-19 widely varies from asymptomatic infection to severe pneumonia and systemic disease. It is thought that host genetic variability may affect the host's response to the viral infection and thus cause severity of the disease. The SARS-CoV-2 virus requires interaction with its receptor complex within the host cells before infection. The trans membrane protease serine 2 (TMPRSS2) has been identified together of the key molecules involved in SARS-CoV-2 virus receptor binding and cell invasion. Therefore, during this study, we investigated the correlation between a genetic variant within the human TMPRSS2 gene and COVID-19 severity and viral load.

Biography

Delvac Oceandy graduated from the School of Medicine, University of Airlangga, Indonesia in 1996. After a short stint working at the Eijkman Institute Indonesia under Prof Sangkot Marzuki, I went to the University of Queensland and completed my PhD in 2001 under Professors Brandon Wainwright and David Hume. I did a short post-doctoral study in the Institute of Molecular Bioscience, Queensland before joining the laboratory of Prof Ludwig Neyses in Manchester in 2002. I have been awarded the British Heart Foundation Intermediate Fellowship in 2009 and was appointed as Lecturer in Cardiovascular Medicine in 2009. Division of Cardiovascular Sciences, Faculty of Biology, Medicine and Health, Manchester Academic Health Science Centre, The University of Manchester, Manchester, UK