Prediction of COVID-19 Severity by Hematological Parameters

Attapon Cheepsattayakorn^{1,2*}, Ruangrong Cheepsattayakorn³ and Porntep Siriwanarangsun¹

¹Faculty of Medicine, Western University, Pathumtani Province, Thailand ²10th Zonal Tuberculosis and Chest Disease Center, Chiang Mai, Thailand

*Corresponding Author: Attapon Cheepsattayakorn, 10th Zonal Tuberculosis and Chest Disease Center, Chiang Mai, Thailand.

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ORF3a, nucleocapsid phosphoprotein (N), and envelop protein (E) of SARS-CoV-2 (COVID-19) have been demonstrated by conserved domain analysis that they had heme-associated sites [1]. Ile304 of N, Cys44 of E, and Arg134 of ORF3a were the heme-ironlinked sites, whereas ORF3a possessed the conserved domains of bacterial EFeB protein and human cytochrome C reductase and could dissociate the iron of heme to form porphyrin [1]. ORF3a was specific and did not attack peroxide, normal cytochrome C, and blue blood protein and it would increasingly cause less hemoglobin levels, so developing manifestations of coagulation reaction, respiratory distress, and finally damaging many tissues and organs [1]. ORF3a, ORF10, and orf1ab could attack the 1-beta chain of hemoglobin, whereas some non-structural and structural viral proteins could bind porphyrin [1]. Heme-linked sites of N protein and E protein may be associated with virus replication and high virus infectivity, respectively [1]. Total lymphocyte counts, neutrophil/ lymphocyte count ratios (NLR), lymphocyte counts, neutrophil counts, and hemoglobin levels in association with COVID-19 severity are significantly differed, whereas the proper hemoglobin cut-off level for COVID-19 severity prediction was 11.6 g/dL [2]. A previous study in Iran demonstrated that anemic COVID-19 patients had higher frequency of respiratory ventilator requirement (anemic: 35.93% vs. nonanemic: 20.63%), ICU admission (anemic: 27.8% vs. nonanemic: 14.71%), and death (anemic: 23.9% vs. nonanemic: 13.8%) [3]. Statistically negative association between hemoglobin levels and age, creatinine levels, and D-dimer levels was demonstrated [2].

In conclusion, both hemoglobin levels and NLR are significant COVID-19 prognostic factors, whereas hospitalized anemic-CO-VID-19 patients were highly associated with poor COVID-19 outcomes

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³Department of Pathology, Faculty of Medicine, Chiang Mai University, Chiang Mai, Thailand