Studi Variasi Genetik Gen Angiotensin Converting Enzyme terhadap Tingkat Risiko Penyakit Hipertensi dan COVID-19 sebagai Rancangan Pendahuluan pada Terapi Presisi (Model: Populasi Palu-Sulawesi Tengah) = Study of Genetic Variations in the Angiotensin Converting Enzyme Gene on the Risk Level of Hypertension and COVID-19 as a Preliminary Design for Precision Therapy (Model: Palu-Central Sulawesi Population)

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Abstrak

Hipertensi merupakan penyakit penyerta yang paling umum ada pada penderita COVID-19. Faktor risiko seperti genetik, sosiodemografi, dan kondisi klinis awal diduga dapat memengaruhi kerentanan individu terhadap hipertensi dan COVID-19. Salah satu gen yang berhubungan dengan hipertensi adalah gen ACE. Penelitian ini bertujuan untuk mengkaji variasi genetik gen ACE dalam hubungannya dengan risiko kerentanan dan penanganan penyakit hipertensi dan COVID-19 menggunakan model populasi Palu-Sulawesi Tengah. Penelitian ini merupakan studi observasional dengan desain cross-sectional. Data faktor non-genetik diperoleh dari rekam medis dan kuesioner. Identifikasi variasi genetik dilakukan pada 4 lokasi pada gen ACE, yaitu rs1799752 (I/D) dengan metode PCR, dan rs4331 (A/G), rs4341 (G/C), dan rs4343 (G/A) dengan rhAmp SNP genotyping. Data faktor genetik dan non-genetik kemudian disusun menjadi model instrumen translasional. Studi melibatkan 136 subjek, dan analisis variasi genetik menunjukkan genotipe dominan untuk rs1799752 adalah II (50%), rs4331 adalah GG (51%), rs4341 adalah GG (100%), dan rs4343 adalah AA (65%). Varian alel D rs1799752, alel A rs4331, dan alel G rs4343 menunjukkan hubungan dengan kerentanan terhadap hipertensi, COVID-19, dan keparahan COVID-19. Analisis regresi menunjukkan bahwa jenis kelamin, usia, riwayat hipertensi, LDL, asam urat, glukosa darah, dan variasi genetik gen ACE adalah prediktor dalam menilai tingkat risiko hipertensi. Sementara itu, jenis kelamin, trigliserida, HDL, komorbiditas hipertensi, dan variasi genetik gen ACE adalah prediktor dalam menilai risiko terhadap kejadian COVID-19, sementara komorbiditas hipertensi, IMT, asam urat, dan variasi genetik gen ACE adalah prediktor dalam menilai risiko keparahan COVID-19. Asesmen prediksi instrumen translasional menunjukkan bahwa 31% dari kelompok hipertensi berisiko tinggi terhadap kejadian COVID-19 dan 46% memiliki berisiko sangat tinggi untuk mengalami keparahan yang lebih tinggi. Asesmen prediksi instrumen translasional hipertensi menunjukkan bahwa 22% subjek memiliki risiko sangat tinggi dan 23% diantaranya memerlukan penyesuaian pola terapi. Variasi gen ACE rs4331, rs1799752, dan rs4343, bersama dengan faktor risiko non-genetik, dapat digunakan sebagai prediktor untuk kejadian hipertensi, COVID-19, dan keparahan COVID-19. Variasi gen dan faktor non-genetik ini dapat dikembangkan menjadi model pengobatan presisi untuk mengevaluasi tingkat risiko dan penanganan individu terhadap hipertensi, COVID-19, dan keparahan COVID-19 di kalangan populasi Palu-Sulawesi Tengah secara translasional.
......Hypertension is the most common comorbidity in COVID-19 sufferers. Risk factors such as genetics, sociodemographics, and initial clinical conditions are thought to influence an individual's susceptibility to hypertension and COVID-19. One of the genes associated with hypertension is the ACE gene. This study examines the ACE gene's genetic variation in summary with the risk of developing hypertension and

COVID-19 using the Palu-Central Sulawesi population model. This research is an observational study with a cross-sectional design. Data on non-genetic factors were obtained from medical records and questionnaires. Identification of genetic variations was carried out at 4 locations in the ACE gene, namely rs1799752 (I/D) using the PCR method, rs4331 (A/G), rs4341 (G/C), and rs4343 (G/A) using rhAmp SNP genotyping. Data on genetic and non-genetic factors are then compiled into a translational instrument model. The study involved 136 subjects, and analysis of genetic variations showed that the dominant genotype for rs1799752 was II (50%), rs4331 was GG (51%), rs4341 was GG (100%), and rs4343 was AA (65%). The variant D allele rs1799753, A allele rs4331, and G allele rs4343 showed an association with susceptibility to hypertension, COVID-19, and severity of COVID-19. Regression analysis showed that gender, age, history of hypertension, LDL, uric acid, blood glucose, and genetic variations of the ACE gene were predictors in assessing the level of hypertension risk. Meanwhile, gender, triglycerides, HDL, comorbid hypertension, and genetic variations of the ACE gene are predictors in determining the risk of COVID-19. In contrast, comorbid hypertension, BMI, uric acid, and genetic variations of the ACE gene are predictors in assessing the risk of COVID-19 severity. -19. The translational instrument prediction assessment showed that 31% of the hypertension group were at high risk of experiencing COVID-19, and 46% were at very high risk of experiencing higher severity. The translational instrument prediction assessment for hypertension showed that 22% of subjects had a very high risk, and 23% of them required adjustment of therapy patterns. ACE gene variations rs4331, rs1799752, and rs4343, together with non-genetic risk factors, can be used as predictors for the incidence of hypertension, COVID-19, and severity of COVID-19. These gene variations and non-genetic factors can be developed into a precision medicine model to evaluate the risk level and individual treatment of hypertension, COVID-19, and the severity of COVID-19 among the Palu-Central Sulawesi population in a translational.