

## Association of Vascular Endothelial Growth Factor Gene +405 C>G and -460 T>C Polymorphism with Type 2 Diabetic Foot Ulcer Patient in Cipto Mangunkusumo National Hospital Jakarta

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**Abstract :** Introduction: Vascular endothelial growth factor (VEGF) gene shows association with various angiogenesis conditions including Diabetic Foot Ulcer (DFU) disease. In this study, we performed this study to examine VEGF gene polymorphism associated with DFU. Methods: Case-control study of polymorphism of VEGF gene +405 C>G and -460 T>C, of diabetes mellitus (DM) type 2 with Diabetic Foot Ulcer (DFU) in Cipto Mangunkusumo National Hospital (RSCM) Jakarta from June to December 2016. Results: There were 203 patients, 102 patients with DFU and 101 patients without DFU. Forty-nine point 8 percent of total samples is male and 50,2% female with mean age 56,06 years. Distribution of the wild-type genotype VEGF +405 C>G wild type CC was found in 6,9% of respondents, the number of mutant heterozygote CG was 69,5% and mutant homozygote GG was 19,7%. Cumulatively, there were 6,9% wild-type and 85,2% mutant and 3,9% of total blood samples could not be detected on PCR-RFLP. Distribution of VEGF allele +405 C>G C alleles were 43% and G alleles were 57%. Distribution of genotype from VEGF gene -460 T>C is wild type TT 42,9%, mutant heterozygote TC 37,9% and mutant homozygote CC 13,3%. Cumulatively, there were 42,9% wild-type and 51% mutant type. Distribution of VEGF -460 T>C were 62% T allele and 38% C allele. Conclusion: In this study we found the distribution of alleles from VEGF +405 C>G is C 43% and G 57% and from VEGF -460 T>C; T 62% and C 38%. We propose that G allele in VEGF +405 C>G can act as a protective allele and on the other hands T allele in VEGF -460 T>C could be acted as a risk factor for DFU in diabetic patients.

**Keywords :** diabetic foot ulcer, diabetes mellitus, polymorphism, VEGF

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