

INTISARI

Ketergantungan obat dan penyalahgunaannya menjadi sebuah permasalahan negara yang harus ditangani bersama. Angka prevalensi penyalahgunaan obat mencapai lebih dari 4 juta orang pada tahun 2016 dan diyakini akan terus meningkat. Telah dilaporkan bahwa polimorfisme gen Dopamine Receptor D2 (*DRD2*) *Taq1A* memiliki hubungan dengan risiko ketergantungan obat. Penelitian ini bertujuan untuk mengetahui prevalensi polimorfisme gen *DRD2 Taq1A* pada populasi orang Indonesia serta membandingkan frekuensi genotip di kedua grup, baik pada pasien dengan ketergantungan obat maupun subjek sehat, kemudian menganalisis pengaruhnya terhadap ketergantungan obat.

Penelitian *cross-sectional* dilakukan terhadap 91 pasien ketergantungan obat di Balai Besar Rehabilitasi Badan Narkotika Nasional, Lido, Bogor, dan 91 subjek sehat dari Yogyakarta. Identifikasi polimorfisme gen *DRD2 Taq1A* dilakukan menggunakan metode alel-spesifik *Polymerase Chain Reaction* (PCR) yang dimodifikasi. Analisis prevalensi polimorfisme gen *DRD2 Taq1A* dilakukan menggunakan teori *Hardy-Weinberg Equilibrium* (HWE) dan analisis perbandingan frekuensi genotip dan alel antara kedua kelompok dilakukan menggunakan *chi square test*. Untuk mengetahui asosiasi polimorfisme gen *DRD2 Taq1A* yang dianggap sebagai faktor risiko pada pasien ketergantungan obat dilakukan perhitungan *odds ratio*.

Hasil menunjukkan perbedaan signifikan antara kelompok control dengan kelompok kecanduan obat (T/T 0%; C/T 3,3%; C/C 96,7%) dan (T/T 6,6%; C/T 63,7%; C/C 29,6%). Maka dari itu gen *DRD2 Taq1A* berhubungan dengan perkembangan dalam kecanduan obat.

Kata kunci: Ketergantungan obat, reseptor dopamin, DRD2, polimorfisme gen *Taq1A*

ABSTRACT

Drug addiction and abuse become a state problem that must be handled together. The prevalence of drug abused reached more than 4 million people in 2016, and keep increasing. It has been reported that *DRD2 Taq1A* gene polymorphism has an association with drug addiction. This study aims to determine the prevalence of the *DRD2 Taq1A* gene polymorphism in Indonesian population and compares the genotype frequency of both group, in drug addicted patients and non-addicted control subjects, then evaluate it association to drug addiction.

A cross-sectional study is conducted on 91 drug addicted patients in Rehabilitation Center of National Narcotics Agency, Lido, Bogor, and 91 non-addicted control subjects from Yogyakarta. Genetic screening of *DRD2 Taq1A* polymorphism is carried out by modified allele-specific polymerase chain reaction (PCR) method. Prevalence analysis of *DRD2 Taq1A* gene polymorphism is conducted using *Hardy-Weinberg Equilibrium* (HWE) theory and comparison analysis of allele and genotype frequency between the two groups is conducted using *chi square test*. The association of *DRD2 Taq1A* gene polymorphism which is thought to be a risk factor for drug addiction is analyzed by *odds ratio* calculation.

The frequency of the T/T and C/T was significantly higher in the addicted than control subjects. They are 6.6% and 63.7% compared to 0% and 3.3%. The frequency of the T allele between the addicted and control subjects shows a significantly different (*p-value* < 0.0001; 95% CI), with the addicted being at a higher risk of having the T allele (OR = 37.3; 95% CI [11.46-121.29]). Thus, there is an association the *DRD2 Taq1A* gene polymorphism with the development of drug addiction.

Keywords. Drug addiction, dopamine receptor, *DRD2*, *Taq1A*, gene polymorphism