

**DETEKSI VARIAN rs17151919 (c.280G>C) DAN
rs10487505 (g.128220110G>C) GEN *LEPTIN*
PADA PASIEN KELEBIHAN BERAT BADAN**

Enjang Sekaryati Prasetyaningrum

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Dosen Pembimbing

Prof. Dr. Niken Satuti Nur Handayani, M.Sc.

INTISARI

Kelebihan berat badan dan obesitas adalah penyakit kronis multifaktorial yang terjadi ketika Indeks Massa Tubuh (IMT) melebihi batas normal. Menurut World Health Organization (WHO), pada tahun 2022 sekitar 1 dari 8 orang di dunia mengalami obesitas. Di Indonesia, angka obesitas meningkat lebih dari dua kali lipat antara tahun 2007 hingga 2018, dengan prevalensi di perkotaan naik dari 23,0% menjadi 50,1%. Sekitar 28,7% orang dewasa diklasifikasikan sebagai obesitas, dengan 15,4% di antaranya termasuk obesitas berat ($IMT \geq 27$). Beberapa varian gen *LEP* dapat meningkatkan risiko obesitas, di antaranya varian rs17151919 dan rs10487505. Penelitian ini bertujuan menentukan frekuensi alel rs17151919 dan rs10487505 pada gen *LEP* pasien obesitas di Rumah Sakit Panti Rapih Yogyakarta. Deteksi varian dilakukan dengan metode Sanger sekuensing. DNA diperoleh dari ekstraksi sampel saliva pasien dan kontrol, kemudian diamplifikasi menggunakan metode *Polymerase Chain Reaction* (PCR) sebelum dilakukan sekuensing. Analisis data hasil sekuensing dilakukan dengan metode pensejajaran terhadap sekuens referensi NM_000230.3. Hasil penelitian menunjukkan bahwa varian rs17151919 (c.280G>C) tidak terdeteksi pada subjek, sedangkan varian rs10487505 (g.128220110G>C) terdeteksi pada subjek. Selain itu, varian lain, yaitu rs17151914 (g.128254354C>T), ditemukan pada satu subjek laki-laki kontrol normal. Prevalensi varian c.280G>C adalah 0%, sedangkan prevalensi varian g.128220110G>C adalah 100%.

Kata kunci: gen *LEP*, obesitas, rs10487505, rs17151919

**DETECTION OF rs17151919 (c.280G>C) AND rs10487505
(g.128220110G>C) LEPTIN GENE VARIANTS IN
OVERWEIGHT PATIENTS**

Enjang Sekaryati Prasetyaningrum

21/483268/BI/10904

Supervisor

Prof. Dr. Niken Satuti Nur Handayani, M.Sc.

ABSTRACT

Overweight and obesity is a chronic and multifactorial disease that occurs when the Body Mass Index (BMI) exceeds the normal threshold. According to the World Health Organization (WHO), in 2022, approximately 1 in 8 people worldwide were affected by obesity. In Indonesia, the prevalence of obesity more than doubled between 2007 and 2018, with urban obesity rates increasing from 23.0% to 50.1%. About 28.7% of adults are classified as obese, with 15.4% categorized as severe obesity (BMI \geq 27). Several variants of the *LEP* gene have been associated with an increased risk of obesity, including rs17151919 and rs10487505. This study aimed to determine the allele frequencies of rs17151919 and rs10487505 in the *LEP* gene among obese patients at Panti Rapih Hospital, Yogyakarta. Variant detection was performed using the Sanger Sequencing method. DNA was extracted from saliva samples of patients and controls, amplified using the Polymerase Chain Reaction (PCR) method, and subsequently sequenced. Data analysis was conducted through alignment with the reference sequence NM_000230.3. The results of the study showed that the rs17151919 variant (c.280G>C) was not detected in the subjects, while the rs10487505 (g.128220110G>C) variant was detected. In addition, another variant, rs17151914 (g.128254354C>T), was found in a normal male control. The prevalence of the c.280G>C variant is 0%, while the prevalence of the g.128220110G>C variant is 100%.

Keywords: *LEP* gene, obesity, rs10487505, rs17151919