Analisis Varian Gen Alpha-Glucosidase (GAA) Ekson 10-20 pada Pasien Penyakit Pompe di Indonesia = Analysis of Exon 10-20 Alpha-Glucosidase (GAA) Gene Variants in Pompe Disease Patients in Indonesia

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Abstrak

Penyakit Pompe (Pompe disease (OMIM 232300)) merupakan suatu penyakit genetik autosomal resesif. Penyakit Pompe terjadi karena adanya varian patogenik pada gen alpha-glucosidase (GAA) yang terletak pada lokus 17q25.3 dan menyebabkan minimnya enzim GAA fungsional yang diproduksi serta mengakibatkan akumulasi glikogen secara masif pada lisosom yang berujung pada kerusakan sel dan disfungsi organ seperti kardiomegali, hepatomegali, dan kelemahan otot. Penelitian mengenai analisis varian gen GAA pada pasien penyakit Pompe telah dilakukan di berbagai negara, namun belum di Indonesia. Penelitian ini dilakukan untuk mendeteksi dan menganalisis mutasi gen GAA ekson 10—20 pada pasien penyakit Pompe di Indonesia. Penelitian dilakukan dengan menggunakan isolat DNA dari satu pasien penyakit Pompe dan 20 individu normal yang berasal dari sampel darah. Sebanyak enam pasang primer telah berhasil mengamplifikasi ekson 10—20 dan mendapatkan sekuens pada masingmasing sampel melalui automated Sanger sequencing. Berdasarkan analisis data sekuensing yang dihasilkan, didapatkan delapan temuan yaitu c.1581G>A (p.Arg527=) pada ekson 11, c.1726G>A (p.Gly576Ser) pada ekson 12, c.1942G>A (p.Gly648Ser) pada ekson 14, c.2065G>A (p.Glu689Lys) pada ekson 15, c.2133A>G (p.Thr711=) pada ekson 15, c.2338G>A (p.Val780Ile) pada ekson 17, c.2446G>A (p.Val816Ile) pada ekson 17, dan c.2553G>A (p.Gly851=) pada ekson 18. Hasil analisis varian dalam penelitian ini mendapatkan varian-varian yang reported pada beberapa populasi di dunia seperti populasi India dan Thailand.
.....Pompe disease (OMIM 232300) is an autosomal recessive genetic disease. Pompe disease occurs due to a pathogenic variant of the alpha-glucosidase (GAA) gene located at locus 17q25.3. It causes a lack of functional GAA enzymes produced and results in massive glycogen accumulation in lysosomes, leading to cell damage and organ dysfunction such as cardiomegaly, hepatomegaly, and muscle weakness. Research on the analysis of GAA gene variants in patients with Pompe disease has been carried out in various countries but not in Indonesia. This study was conducted to detect and analyze exon 10-20 GAA gene mutations in Pompe disease patients in Indonesia. The study was conducted using DNA isolates from one patient with Pompe disease and 20 normal individuals from blood samples. Six pairs of primers have successfully amplified exons 10—20 and obtained sequences for each sample through automated Sanger sequencing. Based on the analysis of the resulting sequencing data, eight findings were obtained, namely c.1581G>A (p.Arg527=) in exon 11, c.1726G>A (p.Gly576Ser) in exon 12, c.1942G>A (p.Gly648Ser) at exon 14, c.2065G>A (p.Glu689Lys) at exon 15, c.2133A>G (p.Thr711=) at exon 15, c.2338G>A (p.Val780Ile) at exon 17, c.2446G >A (p.Val816Ile) at exon 17, and c.2553G>A (p.Gly851=) at exon 18. The results of the analysis of variance in this study obtained the variances reported in several populations in the world, such as the population of India and Thailand.