Identifikasi Metilasi Tumor Suppressor Genes (TSGs) pada Kanker Tiroid dengan Metode Methylation-Specific Multiplex Ligation-Dependent Probe Amplification (MS-MLPA) = Identification of Tumor Suppressor Genes (TSGs) Methylation in Thyroid Cancer using Methylation-Specific Multiplex Ligation-Dependent Probe Amplification (MS-MLPA)

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Abstrak

Metilasi DNA merupakan perubahan epigenetik yang umum terjadi sebagai penyebab inaktivasi gen pada tumor suppressor genes (TSGs). Metilasi pada promoter TSG memiliki asosiasi dengan pembentukan kanker tiroid. Metode methylation-specific multiplex ligation dependent-probe amplification (MS-MLPA) merupakan salah satu metode berbasis PCR yang dapat melakukan identifikasi metilasi pada beberapa gen dan analisis copy number variant secara simultan. Tujuan dari penelitian ini adalah untuk mengoptimasi metode MS-MLPA dan mengidentifikasi metilasi TSG pada kanker tiroid dengan metode MS-MLPA. Sebanyak 40 sampel fine needle aspiration biopsy (FNAB) dikumpulkan secara retrospektif di Rumah Sakit Kanker Dharmais. Sampel FNAB berasal dari pasien yang memiliki kelainan nodul tiroid. Metilasi TSG dianalisis dengan metode MS-MLPA menggunakan probemix Tumour Suppressor Mix 1 ME001-C2 (MRC-Holland). Sampel FNAB dibandingkan dengan reference sample berupa sampel darah yang berasal dari individu sehat. Penelitian ini berhasil mengoptimasi metode MS-MLPA dan mendeteksi metilasi pada 4 jenis tumor suppressor genes, yaitu gen RASSF1A, gen CASP8, gen FHIT, dan gen CHFR. Hasil identifikasi menunjukkan bahwa terdapat 20 sampel tumor ganas dan 2 sampel tumor jinak mengalami metilasi.

.....DNA methylation is a common epigenetic change that causes gene inactivation in tumor suppressor genes (TSGs). TSGpromoter methylation has an association with the formation of thyroid cancer. Methylation-specific multiplex ligation-dependent probe amplification (MS-MLPA) is a PCR-based method that can identify methylation in several genes and copy number variant simultaneously. The aim of this study is to optimize methylation-specific multiplex ligation-dependent probe amplification (MS-MLPA) and to identify tumor suppressor genes methylation of thyroid cancer using MS-MLPA. Retrospectively 40 Fine Needle Aspiration Biopsy samples were collected in Dharmais Cancer Hospital. FNAB samples were collected from patients with thyroid nodules abnormalities. Tumor suppressor genes methylation were analyzed using Tumour Suppressor Mix 1 ME001-C2 probemix (MRC-Holland) as MS-MLPA reagents. FNAB samples were compared with reference sample from blood that were collected from healthy people. This study has successfully optimizing MS-MLPA method and detecting 4 methylated tumor suppressor genes, RASSF1A, CAPS8, FHIT and CHFR. Methylation identification shows 20 malignant histopathology samples and 2 benign histopathology samples were methylated. <i/>