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p16 tumor suppressor gene methylation in diffuse large B cell lymphoma: A study of 88 cases at two hospitals in the East Coast of Malaysia (Article)

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Abstract

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Introduction: p16 gene plays an important role in the normal cell cycle regulation. Methylation of p16 has been reported to be one of the epigenetic events contributing to the pathogenesis of diffuse large B-cell lymphoma (DLBCL) which occurring at varying frequency. DLBCL is an aggressive and high-grade malignancy which accounts for approximately 30% of all non-Hodgkin lymphoma cases. However, little is known regarding the epigenetic alterations of p16 gene in DLBCL cases in Malaysia. Therefore, the objective of this study was to examine the status of p16 methylation in DLBCL. Methods: A total of 88 formalin-fixed paraffin-embedded DLBCL tissues retrieved from two hospitals located in the east coast of Malaysia, namely Hospital Tengku Ampuan Afzan (HTAA) Pahang and Hospital Universiti Sains Malaysia (HUSM) Kelantan, were chosen for this study. DNA specimens were isolated and subsequently subjected to bisulfite treatment prior to methylation specific-PCR. Two pairs of primers were used to amplify methylated and unmethylated regions of p16 gene. The PCR products were then separated using agarose gel electrophoresis and visualised under UV illumination. SPSS version 12.0 was utilised to perform all statistical analysis. Result: p16 methylation was detected in 65 of 88 (74%) samples. There was a significant association between p16 methylation status and patients aged > 50 years old (p=0.04). Conclusion: Our study demonstrated that methylation of p16 tumor suppressor gene in our DLBCL cases is common and significantly increased among patients aged 50 years and above. Aging is known to be an important risk factor in the development of cancers and we speculate that this might be due to the increased transformation of malignant cells in aging cell population. However, this has yet to be confirmed with further research and correlate the findings with clinicopathological parameters.

Author keywords

Diffuse large B cell lymphoma | DNA methylation | Methylation specific PCR | P16

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