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

Rahim, L.M.¹, Talib, N.A.², Muhammad, N.², Hussain, F.A.², Zainuddin, N.² ³
¹Department of Biomedical Science, Kulliyyah of Allied Health Sciences, International Islamic University Malaysia, Kuantan, Pahang, Malaysia; ²Department of Pathology and Laboratory Medicine, Kulliyyah of Medicine, International Islamic University Malaysia, Kuantan, Pahang, Malaysia; ³Department of Pathology, School of Medical Sciences, University Sains Malaysia, Kubang Kerian, Kelantan, Malaysia

Abstract

Introduction: p16 gene plays an important role in the normal cell cycle regulation. Inactivation of p16 has been reported to be one of the genetic events contributing to the pathogenesis of diffuse large B cell lymphoma (DLBCL) which occurs 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 were collected from two hospitals located in the East Coast of Malaysia, namely Hospital Tengku Ampuan Jemaah (HTAJA), Pahang and Hospital Universiti Sains Malaysia (HUSM). All samples were obtained from the pathology department and were stored in the pathology laboratory. DNA extraction was performed from the formalin-fixed paraffin-embedded sections using the QIAamp DNA mini kit (Qiagen, Germany). The methylation status of p16 was determined using the MSP method. The association between p16 methylation status and patient's age (age ≥ 56 years old) was evaluated.

Conclusion: Our study demonstrated that methylation of p16 tumor suppressor gene in our DLBCL cases is common and significantly increased among patients aged 56 years and above. Aging is known to be an important risk factor for the development of cancer 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 correlates with findings with clinical-pathological parameters.

Author keywords

DNA methylation, diffuse large B cell lymphoma, p16 methylation

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