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中華民國90年5月24日

核發單位：中華民國大法官最高法院法官

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Cytogenetic and molecular genetic analyses of EBV-associated T/NK cell lymphoma in Taiwan (1/2)

Abstract

Nasal T/NK cell lymphoma is a special subtype of malignant lymphoma that is more prevalent in Asia than in America and Europe. This type of tumor in Asia tends to affect the nasal and paranasal regions and pursues a highly aggressive clinical course. The exact cellular origin and detailed tumorogenesis are not yet understood. Previous studies have identified a common region of deletion at 6q21-22 in several CDS6+ putative NK lymphoma-associated regions.

Preceding events that were relevant to the study included a past history of Epstein-Barr virus (EBV) infections in patients with nasopharyngeal carcinoma (NPC). EBV has been well documented to be associated with NPC.

Microsatellite instability (MIN) in nasopharyngeal carcinoma.

Loss of heterozygosity (LOH) and microsatellite instability in NPC.

The study aimed to investigate the molecular genetic alterations in EBV-associated T/NK cell lymphoma in Taiwan.

Keywords: EBV, T/NK cell lymphoma, Microsatellite instability, Loss of heterozygosity.
**Keywords:** Epstein-Barr virus, T/NK-cell lymphoma, LOH analysis

**Investigation:** Chromosome 9q22 region reveals further polymorphic data within large genome-wide scan. We have used this data to perform a comprehensive analysis of 10 MS markers. Although the current sample size is too small to reach any significant conclusion, our study suggests that the region within the major histocompatibility complex (MHC) on chromosome 9q22 may be associated with MS. Further studies with a larger sample size are needed to confirm these findings.

Upon completion of the study, we plan to conduct additional experiments to further support the hypothesis that the 9q22 region is involved in the pathogenesis of MS.

**Summary:** The investigation suggests a potential role for the 9q22 region in MS pathogenesis. Further studies are needed to confirm these findings and to better understand the molecular mechanisms involved.
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LOH > 0.4
LOH close to 0.6
Heterozygote: O
Homozygote: H
LOH > 0.6 OR < 1.7
LOH < 0.6

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