EDITORIAL

HTLV-1: Neglected Virus in Southeast Asia for Decades

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There are more than 100 types of human pathogenic viruses, with seven currently known oncogenic viruses (Hulo et al., 2011). Hepatitis B (HBV)/C (HCV) viruses (Mohamed et al., 2023) and human papillomavirus (Wee et al., 2024) are pathogens of public health concern not only in Malaysia but also in many other countries, while Burkitt's lymphoma (Epstein-Barr virus) and Kaposi's sarcoma (Kaposi's sarcoma-associated herpesvirus) pose serious complications for AIDS patients (Carbone et al., 2022).

Then, what about Human T-cell leukemia virus type 1 (HTLV-1)?

Like human immunodeficiency virus (HIV), HTLV-1 is a retrovirus, once the infection is established, the individual becomes a carrier for life. Similar to HBV, HTLV-1 is transmitted through sexual contact or from mother to child. However, unlike other oncogenic viruses, this virus has the characteristic of transmission through breastfeeding. Given the crucial role of breastfeeding in both nutritional and emotional aspects between mother and infant, it becomes an important source of infection (Nakahata et al., 2023).

Epidemiological studies on HTLV-1 infection have been conducted in many countries, but unfortunately, reliable surveys have been scarce in Southeast Asian countries. However, what has become evident in the past decade is the high prevalence in coastal

regions of China and Taiwan, as well as the discovery of extremely high infection rates in Australian aborigines (Legrand et al., 2022).

HTLV-1 is a virus originating from primates, with infections of its prototype confirmed in African and Asian non-human primates (Gessain et al., 2023). What does it mean to a high prevalence of HTLV-1 in a continent like Australia, where primates are not native?

During the ice age (Zeberg et al., 2024), when sea levels were several hundred meters lower than they are today, it is likely that humans infected with HTLV-1 were moving repeatedly in the region that formed the continent (Sundaland), eventually reaching Australia (Tao et al., 2023). This is evidenced by the presence of the virus among local tribes in Papua New Guinea.

I have been collaborating with the research team at Universiti Malaysia Sabah (UMS) since 2015 to investigate the presence of HTLV-1 infection in Sabah, Malaysian Borneo. If HTLV-1 is found in Sabah, it would pose the following new challenges for us to address in the future:

- How prevalent is HTLV-1 infection in Sabah, and subsequently in Malaysia?
- What proportion of patients previously diagnosed with conventional leukemia or lymphoma actually developed adult T-cell leukemia/lymphoma (ATL) due to HTLV-1 infection?
- What is the origin of HTLV-1 in Southeast Asia? Was it transmitted from humans or was it of simian origin?

We are determined to face these new challenges and to find strategies to elucidate the reality of HTLV-1 infection in Sabah, Malaysia, and Southeast Asia as a whole, and to eradicate HTLV-1.

REFERENCES

- Carbone, A., Vaccher, E., & Gloghini, A. (2022). Hematologic cancers in individuals infected by HIV. Blood, 139(7), 995–1012. https://doi.org/10.1182/blood.2020005469
- Gessain, A., Ramassamy, J.-L., Afonso, P. V., & Cassar, O. (2023). Geographic Distribution, clinical epidemiology and genetic diversity of the human oncogenic retrovirus HTLV-1 in Africa, the world's largest endemic area. Frontiers in Immunology, 14. https://doi.org/10.3389/fimmu.2023.1043600
- Hulo, C., de Castro, E., Masson, P., Bougueleret, L., Bairoch, A., Xenarios, I., & Le Mercier, P. (2011). ViralZone: a knowledge resource to understand virus diversity. Nucleic Acids Research, 39(Database issue), D576-582. https://doi.org/10.1093/nar/gkq901
- Legrand, N., McGregor, S., Bull, R., Bajis, S., Valencia, B. M., Ronnachit, A., Einsiedel, L., Gessain, A., Kaldor, J., & Martinello, M. (2022). Clinical and public health implications of human T-lymphotropic virus type 1 infection. Clinical Microbiology Reviews, 35(2). https://doi.org/10.1128/cmr.00078-21
- Mohamed, R., Yip, C., & Singh, S. (2023). Understanding the knowledge, awareness, and attitudes of the public towards liver diseases in Malaysia. European Journal of Gastroenterology & Tepatology, 35(7), 742–752. https://doi.org/10.1097/meg.000000000000002548
- Nakahata, S., Enriquez-Vera, D., Jahan, M. I., Sugata, K., & Satou, Y. (2023). Understanding the immunopathology of HTLV-1-associated adult T-cell leukemia/lymphoma: A comprehensive review. Biomolecules, 13(10), 1543. https://doi.org/10.3390/biom13101543
- Tao, Y., Wei, Y., Ge, J., Pan, Y., Wang, W., Bi, Q., Sheng, P., Fu, C., Pan, W., Jin, L., Zheng, H.-X., & Zhang, M. (2023). Phylogenetic evidence reveals early Kra-Dai divergence and dispersal in the late holocene. Nature Communications, 14(1). https://doi.org/10.1038/s41467-023-42761-x
- Wee, H.-L., Canfell, K., Chiu, H.-M., Choi, K. S., Cox, B., Bhoo-Pathy, N., Simms, K. T., Hamashima, C., Shen, Q., Chua, B., Siwaporn, N., & Toes-Zoutendijk, E. (2024). Cancer screening programs in south-East Asia and Western Pacific. BMC Health Services Research, 24(1). https://doi.org/10.1186/s12913-023-10327-8

Zeberg, H., Jakobsson, M., & Pääbo, S. (2024). The genetic changes that shaped neandertals, Denisovans, and modern humans. Cell, 187(5), 1047–1058. https://doi.org/10.1016/j.cell.2023.12.029