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☆ Extranodal natural killer T-cell lymphoma (Lin, 2019)

Guo-Wang Lin, et al.
The Lancet Oncology

Cancer Nose Infection Blood

STUDY SUMMARY

Identification of 2 novel genetic variants associated with lymphoma found in the nose.

STUDY DESCRIPTION



Extranodal natural killer T-cell lymphoma (NKTCL) is an aggressive blood cancer that grows outside of the lymphatic system, usually in the nose. While NKTCL is rare in European populations, it is common in individuals of Asian and South American ancestry. Infection with Epstein-Barr virus, has been previously linked to the development of NKTCL. Other evidence suggests that genetic variants within a gene responsible for immune system regulation also contribute to the development of NKTCL. Researchers that conducted this study sought to identify novel genetic variants associated with NKTCL. Using genomic data from ~8,500 individuals of Han Chinese ancestry, the researchers identified 2 novel genetic regions associated with increased risk of developing NKTCL. These genetic regions play a role in inflammation and immune system regulation. The results of the study were also replicated in cohorts from other parts of East Asia, including Hong Kong, Taiwan, Singapore, and South Korea.

DID YOU KNOW?

Natural killer (NK) cells are a type of white blood cell that play an important role in the body's innate immune response, specifically providing rapid responses to kill infected cells. Interestingly, unlike other cells that are part of the innate immune system, NK cells can remember old "enemies".

YOUR DETAILED RESULTS

The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to NKTCL. The variants highlighted in blue have **negative effects sizes** and decrease your genetic predisposition to NKTCL. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to NKTCL. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our [Nebula Library tutorial](#).

VARIANT [ⓘ]	YOUR GENOTYPE [ⓘ]	EFFECT SIZE [ⓘ]	VARIANT FREQUENCY [ⓘ]	SIGNIFICANCE [ⓘ]
rs9271688_C 	T / C	0.43 (↑)	42%	9.35×10^{-28}
rs13016714_G 	T / T	0.33 (-)	44%	2.83×10^{-16}