Scientists identify genetic drivers of common lymphoma

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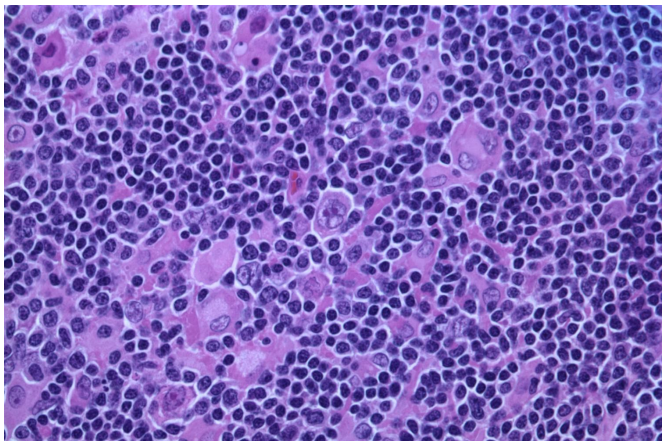

Hodgkin lymphoma, nodular lymphocyte predominant (high-power view) Credit: Gabriel Caponetti, MD./Wikipedia/CC BY-SA 3.0

An international team of scientists has pinpointed the genetic drivers of diffuse large B-cell lymphoma—the most common type of blood cancer—and determined the genes' clinical significance. The study, published in the journal *Cell*, provides important insights for the development of future therapies.

Leo I. Gordon, MD, the Abby and John Friend Professor of Cancer Research, was a co-author of the study.

Diffuse large B-cell lymphoma (DLBCL), an aggressive form of non-Hodgkin lymphoma, affects roughly 7 out of 100,000 people in the U.S. each year.

Previous research into the genetic origins of DLBCL has been impeded by the significant heterogeneity of the disease, and the small sample size of past studies. Further, while some genetic mutations had already been implicated in the disease, their association with functional and clinical outcomes had remained unclear.

In the current study, the scientists performed a technique called whole exome sequencing in samples from more than 1,000 patients. They identified 150 genetic drivers of DLBCL, many of which were newly implicated.

The team further characterized the functional impact of each of the genes, by using the gene-editing tool CRISPR to screen for those essential to cancer cell survival. They also linked the genetic findings to clinical outcomes in patients, developing a new genetic risk model that outperformed established methods.

Overall, the study provides a comprehensive understanding of the genetic drivers of DLBCL and their role in the disease—findings which, according to the authors, will be essential for improving outcomes in patients.

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