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Molecular pathways in diffuse large B-cell lymphoma and their implication in the development of novel therapeutic agents

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Diffuse large B cell lymphoma (DLBCL) is the most common aggressive lymphoma, accounting for 30-40% of the non-Hodgkin lymphoma. DLBCL has been demonstrated to be biologically heterogeneous. Gene expression profiling has identified two main subgroups of DLBCL, germinal center B cell like (GCB-like) and activated B cell like (ABC-like) DLBCL. Current standard therapy includes cyclophosphamide, doxorubicin/epirubicin, vincristine, prednisone and rituximab (R-CHOP). With this regime, ABC-like DLBCL has significantly inferior outcome compared with the GCB subtype. The advance in technology has enabled identification of several unique molecular pathways in different subtypes of DLBCL. Mutations in EZH2, a gene encoding a histone methyltransferase, have been identified only in GCB DLBCL. Mutations in genes involved in B-cell receptor/NF-κB pathway have been predominantly found in the ABC DLBCL. The findings have resulted in the development of novel agents targeting different molecular pathways. These novel agents are promising in improving patient outcomes. This talk will review different molecular pathways identified in the ABC and GCB subtypes as well as novel therapeutic agents under development.

Biography

Jiong Yan is an Assistant Professor in the Department of Pathology and Laboratory Medicine at University of Saskatchewan. She obtained her doctoral degree in Medicine in China and her PhD degree in molecular Genetics at Baylor College of Medicine. She then completed her Pathology residency and Hematopathology fellowship trainings at New York-Presbyterian Hospital/Weill Cornell Medical Center. She has published about 20 peer-reviewed papers in reputed journals.

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