# Methods of Treating Diffuse Large B Cell Lymphoma Based on Particular Genetic Subtype (LymphGen) - A Genetic Classifier to Aid in the Molecular Diagnosis and Treatment of Diffuse Large B-cell Lymphoma

## Summary

The National Cancer Institute (NCI) seeks research co-development or licensees for a precision medicine approach that classifies patients' DLBCL into genetic subtypes that are predictive of treatment response.

## NIH Reference Number

E-137-2019

## Product Type

- Diagnostics

## Keywords

- DLBCL, Diffuse Large B Cell Lymphoma, LymphGen, Predictive, Precision Medicine, Staudt

## Collaboration Opportunity

This invention is available for licensing and co-development.

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## Description of Technology

The development of precision medicine approaches for DLBCL (Diffuse Large B Cell Lymphoma) is complicated by its genetic, phenotypic and clinical heterogeneity. Current classification methods do not fully explain the observed differences in clinical outcomes to current chemotherapy and targeted therapy. Therefore, better analytical methods to classify and predict DLBCL patients' treatment response are needed.

Investigators at the NCI have developed LymphGen; a statistical algorithm that classifies a patient's DLBCL as belonging to one or more types of genetic subtypes. The algorithm uses a Bayesian model to quantify the probability that a patient's biopsy belongs to one of six DLBCL subtypes. In this way, LymphGen surpasses current clustering-based algorithms which are unsuitable for patient classification due to their sensitivity to other cohort samples. This classification provides biological insight into the oncogenic

mechanisms driving each lymphoma subtype. Investigations showed that LymphGen genetic subtypes were prognostic of patients' treatment responses to current options – such as R-CHOP chemotherapy, and targeted therapy – such as the BTK inhibitor ibrutinib. Patient samples can be derived from numerous sources, including fresh frozen tissue, formalin-fixed paraffin-embedded tissue (FFPE), or data from a subset of human genes present in a targeted sequencing platform.

In summary, NCI investigators developed a statistical framework that surpasses current algorithms in classifying DLBCL into genetic subtypes to better predict treatment response. The investigators are seeking licensing and/or collaborative research partners for further clinical development.

## Potential Commercial Applications
- Companion diagnostic to guide treatment decisions
- Targeted sequencing platform
- Add-on to existing sequencing platforms

## Competitive Advantages
- LymphGen algorithm provides the necessary statistical certainty to classify a patient's DLBCL tumor to one of six genetic subtypes
- LymphGen algorithm is successful in its predictions using any combination of mutation, copy number and translocation data
- LymphGen can be applied to data from a variety of patient samples like fresh frozen tissue, formalin-fixed paraffin-embedded tissue (FFPE), or data from a subset of human genes present in a targeted sequencing platform

## Inventor(s)

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## Development Stage
- Prototype

## Publications

Wright GW, et al. A Probabilistic Classification Tool for Genetic Subtypes of Diffuse Large B Cell Lymphoma with Therapeutic Implications.  [PMID 32289277]

## Patent Status
- **U.S. Provisional:** U.S. Provisional Patent Application Number 62/981,382, Filed 25 Feb 2020
- **PCT:** PCT Application Number PCT/US201/19605, Filed 25 Feb 2021

## Related Technologies

- E-172-2017 - Molecular Classification of Primary Mediastinal Large B Cell Lymphoma Using Formalin-Fixed, Paraffin-Embedded Tissue Specimens
- E-750-2013
- E-131-2016 - Clinical Outcome Predictors for Mantle Cell Lymphoma
- E-256-2008

## Therapeutic Area

- Cancer/Neoplasm

## Updated

Sunday, September 11, 2022

**Source URL:** https://techtransfer.cancer.gov/availabletechnologies/e-137-2019