# TOWARD PERSONALIZED LYMPHOMA IMMUNOTHERAPY: IDENTIFICATION OF COMMON DRIVER MUTATIONS RECOGNIZED BY PATIENT CD8 ${ }^{+}$T CELLS 

Julie S. Nielsen ${ }^{1}$, Colin G. Sedgwick ${ }^{1}$, Aniqa Shahid ${ }^{2}$, Zusheng Zong ${ }^{3}$, Zabrina L. Brumme ${ }^{2}$, Stephen Yu ${ }^{3}$, Lewis Y. Liu ${ }^{1}$, Joseph M. Connors ${ }^{4}$, Randy D. Gascoyne ${ }^{4}$, Brian R. Berry ${ }^{5}$, Marco A. Marra ${ }^{6}$, Ryan D. Morin ${ }^{3,6}$, Nicol Macpherson ${ }^{7}$, Brad H. Nelson ${ }^{1}$

${ }^{1}$ Trev and Joyce Deeley Research Centre and ${ }^{7}$ Department of Medical Oncology, BC Cancer Agency, Victoria, BC; ${ }^{2}$ Faculty of Health Sciences and ${ }^{3}$ Department of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, BC; ${ }^{4}$ Centre for Lymphoid Cancer and ${ }^{6}$ Canada’s Michael Smith Genome Sciences Centre, BC Cancer Agency, Vancouver, BC; ${ }^{5}$ Department of Pathology and Laboratory Medicine, University of British Columbia, Vancouver, BC

Background: A fundamental challenge in the era of next-generation sequencing (NGS) is to design effective, personalized treatments based on the mutational profiles of tumours. Many newly discovered cancer mutations are difficult to target pharmacologically; however, T cell-based therapies may provide a valuable alternative owing to the exquisite sensitivity and specificity of antigen recognition. Methods and Results: We assessed the immunogenicity of common driver mutations in follicular lymphoma (FL), an immunologically sensitive yet currently incurable disease. By applying NGS to 10 frequently mutated genes, we identified mutations in 43/53 samples. CD8 ${ }^{+}$T cells specific for bona fide mutant epitopes were identified in $23 \%$ of patients. Responding T cells were present at low precursor frequencies, suggesting that therapeutic intervention would be required to achieve clinically effective T cell responses against these mutations. Conclusions: Our results support the concept of using NGS to design individualized immunotherapies targeting common driver mutations in FL and other malignancies. Funding: This research was supported by the Canadian Cancer Society and the BC Cancer Foundation.

