



The 65th ASH Annual Meeting Abstracts

ONLINE PUBLICATION ONLY**605. MOLECULAR PHARMACOLOGY AND DRUG RESISTANCE: LYMPHOID NEOPLASMS****The KIR-HLA-CD16a Immunogenetic Profile Influences NK Cell-Mediated ADCC and Response to Rituximab Therapy in B-Cell Lymphomas**Rutvij A. Khanolkar, MD¹, Ariz Akhter, PhD¹, Jan Storek, MD PhD², Faisal Khan, PhD³¹Cumming School of Medicine, University of Calgary, Calgary, Canada²The University of Calgary Department of Medicine, Calgary, Canada³Department of Pathology and Laboratory Medicine, Cumming School of Medicine, University of Calgary, Calgary, CAN

Rituximab-based chemoimmunotherapy (R-CHOP) is the standard of care in most B-cell lymphomas, however there is marked interpatient heterogeneity in treatment response. An important mechanism of Rituximab (anti-CD20) action is through natural killer (NK) cell-mediated antibody-dependent cellular cytotoxicity (ADCC), but the factors influencing this are poorly understood. Here, we present findings from a preclinical study investigating the role of NK cell receptor polymorphisms and HLA allelic variation on ADCC against aggressive B-cell lymphoma cell lines. Genotyping was conducted using Luminex-based SSO and Sanger sequencing. Multicolor flow cytometry was used to assess the response of activated NK cells from healthy donors against 8 lymphoma cell lines. Individuals carrying the GG or GT allele in CD16a were found to have a 3-8 fold greater NK cell response compared to individuals with a TT allele and rituximab-mediated ADCC was significantly greater in individuals with a KIR-3DL1 allele when tested against B-cell lymphomas lacking the HLA-Bw4 allele. An additive effect was observed when considering both CD16a and KIR-HLA together. As expected, CD20 expression was a strong correlate of NK cell response. In summary, NK cell-mediated ADCC in response to ADCC appears to be influenced by the KIR-HLA-CD16a genotype. These findings suggest a potential role for immunogenotyping in B-cell lymphomas treated with Rituximab. Additionally, the presence of the shared Fc receptor domain opens the possibility of applying this framework towards predicting NK cell responses to antibody therapies in other diseases.

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