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### Title

Expression of ROR1 and ROR2 in Hairy Cell Leukemia Cells Enhances Constitutive Activation of ERK1/2 and Cancer Stemness

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### Authors

Widhopf, George F

Ghia, Emanuela M

Cring, Matthew R

et al.

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## The 66th ASH Annual Meeting Abstracts

## ORAL ABSTRACTS

## 621.LYMPHOMAS: TRANSLATIONAL - MOLECULAR AND GENETIC

**Expression of ROR1 and ROR2 in Hairy Cell Leukemia Cells Enhances Constitutive Activation of ERK1/2 and Cancer Stemness**George F. Widhopf II, PhD<sup>1,2,3</sup>, Emanuela M. Ghia, PhD<sup>1,2,3</sup>, Matthew R. Cring, PhD<sup>1,2</sup>, Thomas J. Kipps, MD<sup>1,2,3</sup><sup>1</sup>Center for Novel Therapeutics, University of California, San Diego, La Jolla, CA<sup>2</sup>Division of Hematology Oncology, Department of Medicine, University of California, San Diego, La Jolla, CA<sup>3</sup>Moore's Cancer Center, University of California, San Diego, La Jolla, CA

Hairy cell leukemia (HCL) is a malignancy of B-cells that co-express CD19, CD20, CD11c, CD25, CD103, CD123, and CD200 (but not CD5, CD10, CD21, or CD23) and that harbor a V600E BRAF mutation, which promotes constitutive activation of ERK1/2. HCL variant (HCL-V) is a rare subtype of HCL that does not express CD25 and typically lacks BRAF V600E. We examined both types of HCL for expression of ROR1 and ROR2, which are developmentally-restricted receptors for Wnt5a. We generated monoclonal antibodies (mAbs) that each are highly specific for human ROR1 (zilovetamab) or ROR2 (6E6) and that respectively can block Wnt5a-induced ROR1- or ROR2-dependent signaling. We examined HCL cells from 17 pts (13 male, 4 female). Fifteen had classic HCL (cHCL) and 2 pts had HCL-V. We found that the HCL cells of all pts expressed ROR1 and ROR2; a finding validated by analysis of anti-ROR1 or anti-ROR2 immune precipitates of HCL-cell lysates by iTRAQ mass spectrometry. We assessed the numbers of ROR1 or ROR2 on HCL cells by measuring the molecules of equivalent soluble fluorochrome (MESF) using fluorochrome-labeled microbeads. The numbers of ROR1 (median =  $3.7 \times 10^3$  molecules per cell,  $n=17$ , range  $1.4-4.8 \times 10^3$ ) or ROR2 (median =  $3.1 \times 10^3$  molecules per cell,  $n=17$ , range  $0.6-11.1 \times 10^3$ ) on cHCL or HCL-V were less than the median ROR1 levels on chronic lymphocytic leukemia (CLL) cells, for which  $5.8 \times 10^3$  ROR1 molecules per cell was the threshold that defined high-level expression of ROR1 that was associated with adverse prognosis (*Cancer Stem Cell* 22:951, 2018). Nonetheless, the median combined number of ROR1 and ROR2 molecules per HCL cell among pts with HCL was  $6.8 \times 10^3$  ( $n=17$ , range 3.6-12.5). 13 of the 17 patient samples had combined numbers of ROR1 and ROR2 that exceeded the threshold for defining high-expression ROR1, which associated with a significantly shorter median time from diagnosis until initial therapy and overall survival in pts with CLL (*Blood* 128:2931, 2016). To evaluate for ROR1- and ROR2-signaling in cHCL we performed transcriptome analyses of negatively-selected leukemia cells before and after culture without or with Wnt5a, zilovetamab, and/or 6E6. Gene-set enrichment analyses (GSEA) comparing the cHCL cells of two pts before and after 36-hour culture in serum-free media without exogenous Wnt5a demonstrated significant time-dependent attenuation in the expression of stemness genes, which included gene targets of the Yamanaka factors Oct4, Sox2, and c-Myc, along with genes induced by activation of ERK1/2, despite each case harboring the activating BRAF V600E mutation (FDR  $q$  value  $<0.001$ ). Addition of exogenous Wnt5a upon initiation of culture significantly enhanced expression of such genes. However, treatment of HCL cells with either zilovetamab or 6E6 significantly inhibited Wnt5a-induced expression of target genes induced by Oct4, Sox2, and c-Myc, along with genes induced by activation of ERK1/2 (FDR  $q$  value  $<0.001$ ). Co-treatment with zilovetamab and 6E6 also repressed expression of such gene sets (FDR  $q$  value  $<0.001$ ). Our studies demonstrate that ROR1 and ROR2 are expressed in cHCL and HCL-V. In cHCL cells that harbor BRAF V600E, we found that Wnt5a ROR1/2-dependent signaling can enhance ERK1/2 activation significantly above that induced by the BRAF V600E mutation alone. In addition, we found Wnt5a can induce ROR1/2-dependent activation of targets of Oct4, Sox2, and c-Myc and cancer stemness genes signatures found expressed by embryonic stem cells. We speculate that strategies that target ROR1 and/or ROR2, or that block ROR1/2-dependent signaling, may reverse HCL cancer stemness *in vivo* and mitigate the risk of tumor dormancy and disease-relapse that may be seen years after apparent successful therapy.

**Disclosures Kipps:** Abbvie/Janssen/Pharmacyclics/Genentech: Consultancy, Honoraria, Membership on an entity's Board of Directors or advisory committees; Oncternal Therapeutics: Current equity holder in private company; Lymphoma and Leukemia Society: Research Funding.

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