

Clonal architecture of CXCR4 WHIM-like mutations in Waldenström Macroglobulinaemia

Xu L¹, Hunter ZR^{1,2}, Tsakmaklis N¹, Cao Y^{1,2}, Yang G^{1,2}, Chen J¹, Liu X^{1,2}, Kanan S¹, Castillo JJ^{1,2}, Tai YT^{2,3}, Zehnder JL⁴, Brown JR^{2,5}, Carrasco RD^{2,5}, Advani R⁶, Sabile JM⁶, Argyropoulos K⁷, Lia Palomba M⁷, Morra E⁸, Trojani A⁸, Greco A⁸, Tedeschi A⁸, Varettoni M^{9,10}, Arcaini L^{9,10}, Munshi NM^{2,3}, Anderson KC^{2,3}, Treon SP^{1,2}.

¹Bing Center for Waldenström's Macroglobulinemia, Dana Farber Cancer Institute, Boston, MA, USA, ²Department of Medicine, Harvard Medical School, Boston, MA, USA, ³Lipper Center for Multiple Myeloma, Dana Farber Cancer Institute, Boston, MA, USA, ⁴Department of Pathology, Stanford University Medical Center, Stanford, CA, USA. ⁵Department of Medical Oncology, Dana Farber Cancer Institute, Boston, MA, USA, ⁶Department of Medical Oncology, Stanford University Medical Center, Stanford, CA, USA, ⁷Department of Medical Oncology, Memorial Sloan Kettering Cancer Center, New York, NY, USA, ⁸Haematology Unit, Niguarda Hospital, Milan, Italy, ⁹Department of Molecular Medicine, University of Pavia, Pavia, Italy, ¹⁰Department of Haematology Oncology, Fondazione IRCCS Policlinico San Matteo, Pavia, Italy.

CXCR4^{WHIM} somatic mutations are distinctive to Waldenström Macroglobulinaemia (WM), and impact disease presentation and treatment outcome. The clonal architecture of CXCR4^{WHIM} mutations remains to be delineated. We developed highly sensitive allele-specific polymerase chain reaction (AS-PCR) assays for detecting the most common CXCR4^{WHIM} mutations (CXCR4 (S338X C>A and C>G)) in WM. The AS-PCR assays detected CXCR4 (S338X) mutations in WM and IgM monoclonal gammopathy of unknown significance (MGUS) patients not revealed by Sanger sequencing. By combined AS-PCR and Sanger sequencing, CXCR4^{WHIM} mutations were identified in 44/102 (43%), 21/62 (34%), 2/12 (17%) and 1/20 (5%) untreated WM, previously treated WM, IgM MGUS and marginal zone lymphoma patients, respectively, but no chronic lymphocytic leukemia, multiple myeloma, non-IgM MGUS patients or healthy donors. Cancer cell fraction analysis in WM and IgM MGUS patients showed CXCR4 (S338X) mutations were primarily subclonal, with highly variable clonal distribution (median 35.1%, range 1.2-97.5%). Combined AS-PCR and Sanger sequencing revealed multiple CXCR4^{WHIM} mutations in many individual WM patients, including homozygous and compound heterozygous mutations validated by cloning/sequencing and deep RNA sequencing analysis. The findings show that CXCR4^{WHIM} mutations are

more common in WM than previously revealed, and are primarily subclonal, supporting their acquisition after MYD88^{L265P} in WM oncogenesis. The presence of multiple CXCR4^{WHIM} mutations within individual WM patients may be indicative of targeted CXCR4 genomic instability. Recent studies identified BTK Cys481 mutations in WM patients with relapsed diseases after ibrutinib treatment. Interestingly, the patients positive for CXCR4^{WHIM} were also positive for the Cys481 mutations in the study cohort. The strong correlation between CXCR4^{WHIM} and the Cys481 mutations may suggest a contribution of CXCR4^{WHIM} to the risk of ibrutinib resistance.