MLL1 inhibition reduces IgM levels in Waldenström macroglobulinemia Mona Karbalivand¹, Luciana Almada, PhD², Stephen M Ansell, MD/PhD², Martin Fernandez-Zapico, MD² and, Sherine F. Elsawa, PhD¹

¹Department of Molecular, Cellular and Biomedical Sciences, University of New Hampshire, Durham, NH 03824 ²Mayo Clinic, Rochester, MN 55905

Abstract

Waldenström macroglobulinemia (WM) is a B cell lymphoma characterized by the overproduction of a monoclonal IgM antibody, a leading pathogenic feature of the disease. Current therapies are based on our knowledge at the signaling and genetic scale, but recent research has identified epigenetic dysregulation, one of the important dynamics in the biology of this disease. In this study, we found that Mixed-lineage leukemia 1 (MLL1) histone methyltransferase and its chromatin tethering partner Menin are upregulated in WM patients. KMT2A knockdown using short hairpin RNA (shRNA) and inhibition of MLL1 function using the menin-MLL1 inhibitor (MI-2) in WM cells resulted in a significant reduction in IgM levels without significantly impacting WM cell growth and survival. Further analysis identified MLL1 binding at multiple sites in the 5' Em enhancer of the immunoglobulin heavy (IGH) chain. We found increased histone 3 lysine 4 trimethylation (H3K4me3) enrichment at multiple MLL1 binding sites upon LPS stimulation, a known inducer of IgM. Finally, we found that disruption of Menin-MLL1 complex using the MI-2 inhibitor in tumor-bearing mice significantly reduced human IgM levels in mice sera. Taken together, these results identify MLL1 as a regulator of IgM and define MLL1 as a new therapeutic target for WM.



MLL1 histone methyltransferase (HMT) complex.







Figure 4: H3K4me3 deposition near IGH E μ enhancer and Im region. A) Schematic of IGH region. Variable region (VDJ) and constant region (Cm) are shown in gray. Blue triangles represent five candidate MLL1 binding sites. The $E\mu$ enhancer (green), Iµ region (blue) and switch (Sm) region are indicated. Black brackets indicate primers used for ChIP-qPCR to detect binding to MLL1 binding sites (BS1, BS2, BS3 and BS4). B) BCWM.1 cells (10 x 10⁶) were fixed and lysed as indicated in materials and methods. Lysates were used in ChIP assay followed by qPCR to determine basal MLL1 or it's mark H3K4me3 deposition in the IGH region in WM cells. C) CD19+ cells were purified from PBMCs followed by stimulation with LPS for 3 hr to activate B cells. Cells were then used in ChIPqPCR to determine H3K4me3 deposition in the IGH region. D) BCWM.1 cells were treated with 5 mM MI-2 or DMSO control and cells were used to determine H3K4me3 deposition in IGH region by ChIP-qPCR. These experiments were performed at least 3 times.





Figure 1: KMT2A and Menin are overexpressed in WM patients and cell lines. Expression of A) KMT2A and B) *MEN1* in WM cells lines (BCWM.1, MWCL-1 and RPCI-WM1), CD19⁺ CD138⁺ cells from WM patients (P14, P15 and P17), normal CD19⁺ cells from PBMCs were compared to expression in THP-1 cells. Right panels represent the average expression of KMT2A and *MEN1*. Bars represent \triangle Ct relative to THP-1 +/- SEM.



Figure 2: MLL1 depletion and disruption of menin-MLL1 complex reduce Cµ expression and secretion in WM. A) WM cells (4 x 10⁶) were transfected with shMLL1 or scrambled control (shScr) for 48 hr followed by quantification of IgM levels in the culture supernatant by ELISA. An additional set of cells were transfected and lysed in RPIA buffer followed by western blot to confirm MLL1 knockdown (blots shown above each graph). B) WM cells were transfected with shMLL1 or shScr for 48 hr. Cells were harvested and RNA was purified and used to determine Cµ expression by qRT-PCR. C) WM cells (2 x 10⁶) were treated with 5 mM MLL1 inhibitor MI-2 or DMSO control for 72 hr followed by ELISA to quantify IgM levels or D) qRT-PCR to determine Cµ expression. These experiments were repeated at least 3 times with similar results and the bars represent the average of 3 independent experiments performed in triplicate +/- SEM. E) Immunoprecipitation assay was performed to assess inhibition of Menin-MLL1 interaction following treatment with 5 mM MI-2. BCWM.1 cells were lysed and MLL1 protein was immunoprecipitated using aMLL1 antibody. IgG pull-down was used as negative control. Menin protein was detected by western blot using a Menin antibody.



Day

tumors

Results



Figure 5: MLL1 inhibition reduces IgM secretion in tumor-bearing mice. A) Hariless SCID mice were implanted with 10 x 10⁶ BCWM.1 cells. Groups of mice were treated with either 5 mM MI-2 or vehicle control. B) Human IgM levels were quantified in mice sera at experiment end-point using ELISA. C) Tumor volume in MI-2 and Vehicle treated mice. D) Mice weight was determined in MI-2 and vehicle treated mice.

Acknowledgement









Figure 3: MLL1 inhibition does not affect WM cell viability. A) WM cells (2 x 10⁶) were transfected with shMLL1 or shScr. Cells were resuspended in 0.6 ml and 100 ml were plated/well in 96-well plates. After 3 days of culture, cell proliferation was assessed using XTT assay. B) WM cells (25 x 10³ cells/well) were plated in 96-well plates and treated with either 5 mM MI-2 or DMSO control. After 3 days, cell proliferation was assessed using XTT. C) WM cells (0.25 x 106 cells/ml) were cultured in triplicated wells in 24-well plates and treated with 5 mM MI-2 or DMSO control. Cell viability was assessed daily using trypan blue exclusion. D) WM cells (4 x 10⁶) were transfected with shMLL1 or shScr for 72 hr followed by examination of cell viability by trypan blue exclusion. Bars represent the average of at least 3 independent experiments performed in triplicate +/- SEM.

Summary

- KMT2A and MEN1 expression are elevated in WM patients and WM cell lines and promotes disease biology.
- Inhibition of menin-MLL1 reduces IgM expression and secretion *in vitro* and *in vivo*.

CIBBR

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