Amplification of mixed lineage leukemia gene perturbs hematopoiesis and cooperates with partial tandem duplication to induce acute myeloid leukemia

Genetic alternation of the mixed lineage leukemia (*MLL*) gene can be found in up to 10% of acute myeloid leukemia (AML).[1,2] Similar to *MLL* fusions and *MLL* partial tandem duplication (PTD), *MLL* amplification (*MLL*(n)) is reported in approximately 1% AML and myelodysplastic syndrome (MDS) associates with adverse treatment outcomes.[3,4] In spite of the success in modeling AML induced by *MLL* fusions,[1] there has been no *in vivo* disease model for *MLL*(n) leukemia. On the other hand, while previous studies have proposed a recessive gain-of-function by *MLL*-PTD in suppressing the expression of wild-type *MLL* in normal karyotype

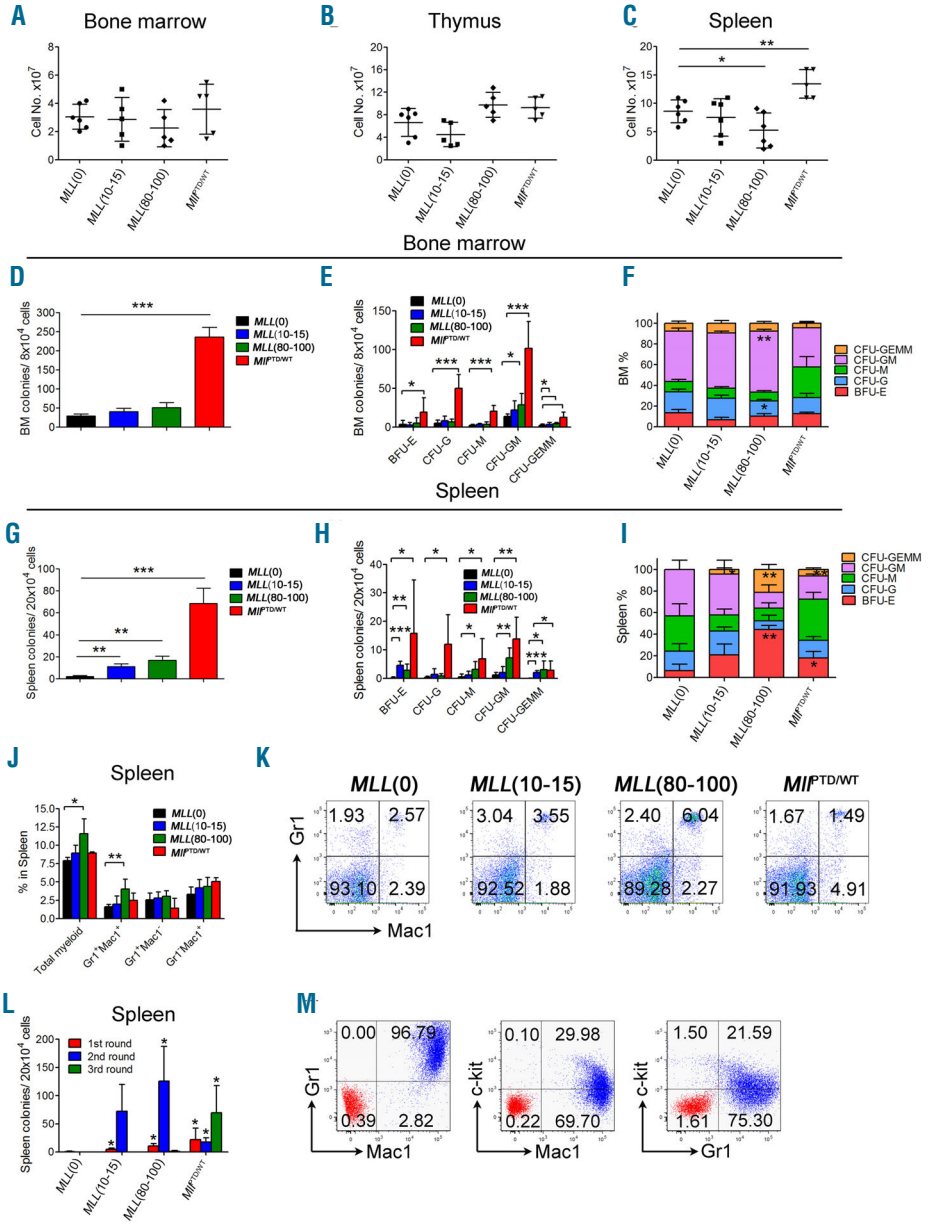

Figure 1. *MLL* amplification perturbs myeloid development in mouse models. Total cell counts in (A) bone marrow (2 femurs), (B) thymus and (C) spleen of the control *MLL*(0), *MLL*(10-15), *MLL*(80-100) and *Mll*$^{PTD/WT}$ mice. (D) Total colony numbers generated from bone marrow cells of *MLL*(n) and *Mll*$^{PTD/WT}$ mice. Bone marrow colonies were classified into burst forming unit-erythroid (BFU-E), colony forming unit-granulocyte (CFU-G), CFU-macrophage (CFU-M), CFU-granulocyte/macrophage (CFU-GM), and CFU-granulocyte/erythroid/macrophage/megakaryocyte (CFU-GEMM). (E) Absolute number and (F) relative proportion of each colony type from the bone marrow of indicated genotypes. (G) Total colony numbers formed from splenocytes of *MLL*(0) control, *MLL*(n) and *Mll*$^{PTD/WT}$ mice. (H) Absolute number and (I) relative proportion of each colony type from the spleen of indicated genotypes. (J) Percentages of myeloid cell populations (Total: Gr-1$^+$ or Mac-1$^+$, Gr-1$^+$Mac-1$^+$, Gr-1$^+$Mac-1- and Gr-1-Mac-1$^+$) in spleens of *MLL*(0) control, *MLL*(n) and *Mll*$^{PTD/WT}$ mice. (K) Representative flow cytometry plots showing percentages of Gr-1$^+$Mac-1$^+$ cell population in spleens of *MLL*(0) control, *MLL*(n) and *Mll*$^{PTD/WT}$ mice. (L) Splenocytes (20x10^4 cells) from different mice were seeded into methylcellulose for replating assays. Enumeration of colonies and replating of cells to the next round were performed after 6 days of culture. (M) Flow cytometry analysis of the third round of replating *Mll*$^{PTD/WT}$ splenic colonies. Red dots, unstained cells; blue dots, cells stained with indicated antibodies. Results in panel A to C were obtained from 5 independent experiments, panel D to I were obtained from 6 independent experiments, whereas panel J and L were obtained from 5 independent experiments. Bar graphs show mean+S.E.M. (*P<0.05, **P<0.01 and ***P<0.001, paired t-test).

AML,[5] both *Mll*$^{PTD/WT}$ and *Mll*$^{PTD/-}$ mice failed to develop leukemia, thus questioning the role of *MLL*-PTD in acute leukemogenesis and indicating a requirement of cooperating mutation(s) for full malignant transformation.[6,7] Intriguingly, *MLL*-PTD can be found to co-exist with *MLL*(n) in AML patients,[8,9] suggesting an alternative pathological relationship between these 2 *MLL* aberrations in myeloid leukemogenesis.

To gain insights into the role of *MLL*(n) and *MLL*-PTD in hematopoietic development, we generated an *in vivo* mouse model of *MLL* amplification where the full-length human *MLL* cDNA was expressed under the murine *Scl*-promoter/3'enhancer (*Online Supplementary Figure S1A*), which has been successfully used to drive oncogene expression in hematopoietic stem and progenitor

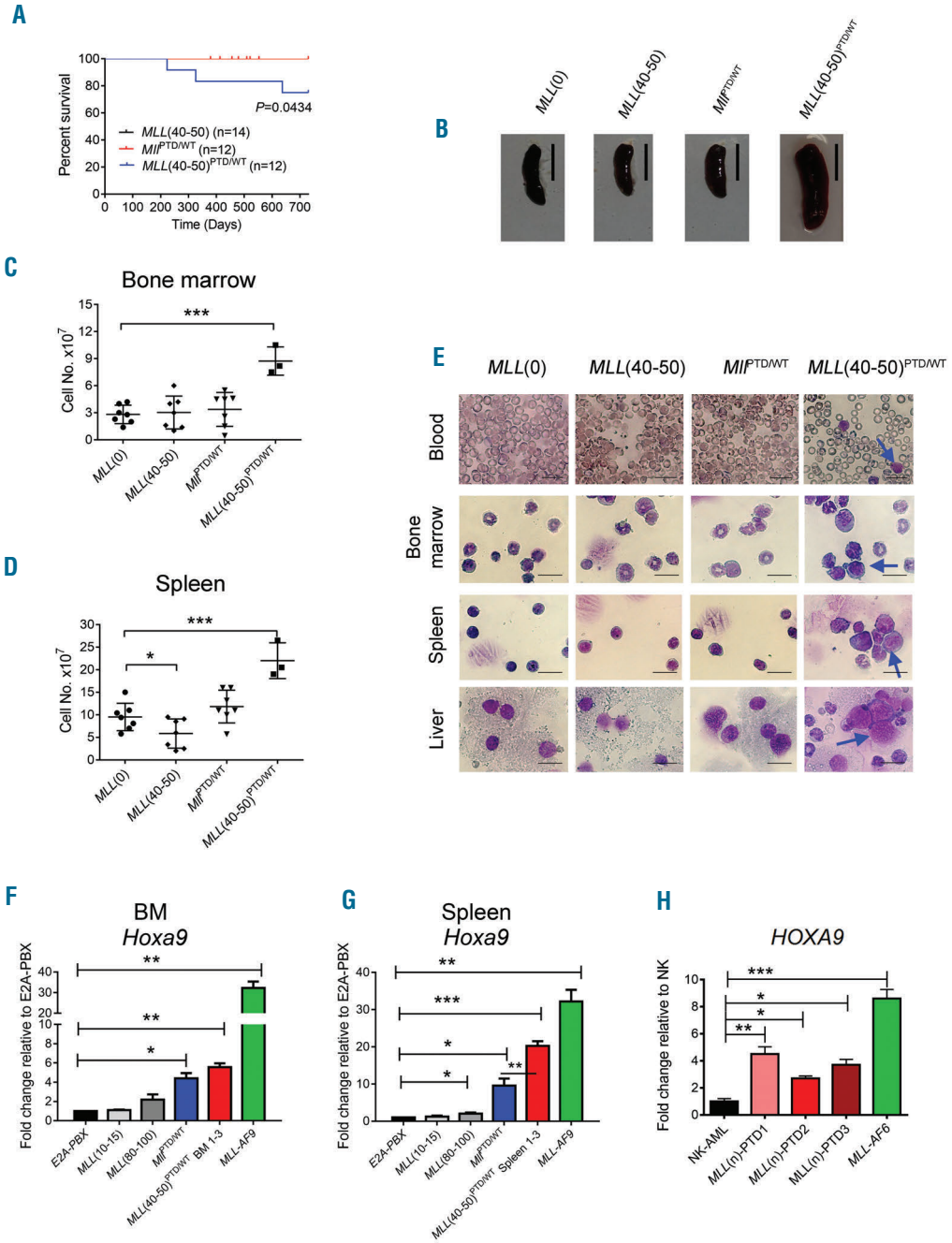

Figure 2. Potential cooperation between *MLL* amplification and *MLL*-PTD results in leukemic transformation in *MLL*(40-50)$^{PTD/WT}$ mice. (A) Survival curves of *MLL*(40-50) (n=14), *Mll*$^{PTD/WT}$ (n=12) and *MLL*(40-50)$^{PTD/WT}$ (n=12) mice. Three out of 12 *MLL*(40-50)$^{PTD/WT}$ mice developed AML but none of the control mice showed any sign of disease (*P<0.05). (B) Representative images of spleens from *MLL*(0), *MLL*(40-50), *Mll*$^{PTD/WT}$ and leukemic *MLL*(40-50)$^{PTD/WT}$ mice. All control mice were age-matched to leukemic mice. Scale bar, 1 cm. Total cell counts in (C) bone marrow (2 femurs) and (D) spleens of *MLL*(0), *MLL*(80-100), *Mll*$^{PTD/WT}$ and leukemic *MLL*(40-50)$^{PTD/WT}$ mice. (E) Peripheral blood smears and cytospins of the cells prepared from the bone marrow, spleen and liver of *MLL*(0), *MLL*(40-50), *Mll*$^{PTD/WT}$ and *MLL*(40-50)$^{PTD/WT}$ mice are shown. Leukemic blasts are indicated by blue arrows. Cells were stained with May-Grunwald-Giemsa. Scale bars represent 30 μm. (F) Relative expression levels of *Hoxa9* in *MLL*(n), *Mll*$^{PTD/WT}$, leukemic *MLL*(40-50)$^{PTD/WT}$ bone marrow and *MLL-AF9* leukemic cells compared to *E2A-PBX* leukemic cells by q-RT-PCR. (G) Relative expression levels of *Hoxa9* in *MLL*(n), *Mll*$^{PTD/WT}$, leukemic *MLL*(40-50)$^{PTD/WT}$ splenocytes and *MLL-AF9* leukemic cells compared to *E2A-PBX* leukemic cells by q-RT-PCR. (H) Relative expression of *HOXA9* in human *MLL*(n)-PTD bone marrow cells and in normal karyotype AML (NK-AML) and *MLL-AF6* expressing human bone marrow cells. Bar graphs show mean+S.E.M. (*P<0.05, **P<0.01 and ***P<0.001, paired *t*-test).

cells (HSPCs) resulting in AML.[10] Two different founders with 10-15 and 40-50 copies of concatemeric transgenes were selected for establishment of stable lines containing 10-15 (*MLL*(10-15)) or 80-100 copies (*MLL*(80-100)) of *MLL*, respectively (*Online Supplementary Methods* and *Online Supplementary Figure S1B,C*). Western blotting and quantitative reverse transcription polymerase chain reaction (RT-PCR) confirmed the transgene expression as being, approximately, a 3-5- and 6-10-fold increase in the bone marrow and spleen of *MLL*(10-15) and *MLL*(80-100) mice, respectively (*Online Supplementary Figure S2A,B*). These findings are consistent with previously reported *Scl*-enhancer's property[10] and in line with the expression level of *MLL* in human MDS/AML patients carrying 5-10 or more than 10 copies of *MLL* with, approximately, a 1.5- and 9-fold increase, respectively.[11]

To investigate the impacts of *MLL* amplification on normal hematopoiesis, *MLL*(n) mice at three months old were analyzed in parallel with $Mll^{PTD/WT}$ mice and non-transgenic control (*MLL*(0)). Although no significant difference in total cellularity was found in bone marrow and thymus, a significant increase in splenic cells was observed in $Mll^{PTD/WT}$ mice (Figure 1A-C). In contrast, a reduction in splenic cells was found in *MLL*(n) mice, especially in *MLL*(80-100) mice (Figure 1C), suggestive of a mild differentiation and/or proliferation defect. Consistently, the splenocytes of *MLL*(10-15) and *MLL*(80-100) mice displayed a trend towards a significant increase in the percentage of Annexin-V^+PI^- apoptotic cells compared to those of *MLL*(0) mice (*Online Supplementary Figure S2C*), providing a potential explanation for the lower cellularity observed in the spleen of *MLL*(n) mice. Functionally, $Mll^{PTD/WT}$ bone marrows produced approximately 4 times more colonies than those by *MLL*(n) and the control (Figure 1D,E). While the ratio between each colony type remained constant in $Mll^{PTD/WT}$, *MLL*(80-100) had a significant increase in the percentage of colony forming units-granulocyte/monocyte (CFU-GM) and a decrease in the percentage of colony forming unit-granulocyte (CFU-G; Figure 1F), consistent with a mild shift to immature myeloid. *MLL*(n) splenocytes showed a slightly but significantly higher colony forming ability (Figure 1G,H), where they consistently exhibited an increase in immature colony forming units-granulocyte/erythrocyte/macrophage/megakaryocyte (CFU-GEMM) and burst forming units-erythroid (BFU-E; Figure 1I). The degrees of expansion were even more notable in *MLL*(n) mice with a higher copy number of the *MLL* transgene (Figure 1G-I), suggesting an aberrant selection of proliferative myeloid clones. While there was no apparent difference in the proportions of B cells and T cells in these mice (*Online Supplementary Figure S3A*), an expansion of the Gr-1+Mac-1+ cell population was found in the *MLL*(80-100) spleen (Figure 1J,K). Consistently, a transient enhanced replating ability was observed in *MLL*(n) and $Mll^{PTD/WT}$ splenocytes (Figure 1L). Compared to non-transgenic controls, *MLL*(10-15) and *MLL*(80-100) splenocytes, the latter in particular, were able to form a substantial number of secondary colonies (Figure 1L). $Mll^{PTD/WT}$ splenocytes were able to generate compact myeloid colonies even in the third round of replating (Figure 1L,M). In contrast, there was no obvious difference in the replating ability of bone marrow cells (*Online Supplementary Figure S3B*), consistent with the observed phenotypes in these mice (Figure 1A-C).

Apart from a significant decrease in the percentage of common lymphoid progenitors (CLPs) in the bone marrow of $Mll^{PTD/WT}$ mice, further investigation into the effect of *MLL*(n) and PTD on early HSPC populations revealed no significant difference in hematopoietic stem cells (long-term (LT)-HSCs, short-term (ST)-HSCs), early myeloid/lymphoid progenitor (multipotent progenitors [MPPs], common myeloid progenitors [CMPs], granulocyte-monocyte progenitors [GMPs], megakaryocyte-erythroid progenitors [MEPs]), or lymphoid (B-[$B220^+$], T-[$CD4^+CD8^-$ and $CD4^-CD8^+$]) cell populations in their bone marrows (*Online Supplementary Figure S3C-E*). RT-qPCR confirmed the over-expression of *MLL* in c-kit^+ HSPC bone marrow cells, albeit to a lesser extent than in whole bone marrow cells in *MLL*(n) mice (*Online Supplementary Figure S3F,G*), suggesting that mild over-expression of *MLL* or *MLL*-PTD alone has a rather limited impact on HSPC compartments. Consistently, none of the animals developed leukemia during two years of observation (*Online Supplementary Figure S3H*), indicating that additional events are required for overt leukemia as observed in humans.

On the other hand, the recurrent reports of AML possessing both *MLL*(n) and *MLL*-PTD[8,9] raise the intriguing possibility that these 2 different *MLL* aberrations may collaborate in acute leukemogenesis.[1] To address this long outstanding question, we crossed *MLL*(80-100) with $Mll^{PTD/WT}$ mice to produce a novel double mutant *MLL*(40-50)$^{PTD/WT}$ mouse (*Online Supplementary Figure S1C* and *S4*). In contrast to *MLL*(40-50) and $Mll^{PTD/WT}$ controls, which did not develop any malignancy, 3 out of 12 *MLL*(40-50)$^{PTD/WT}$ mice succumbed to AML with immature myeloblasts and splenomegaly after 7 to 21 months (P=0.0434) (Figure 2A-D). Examination of peripheral blood revealed anemia and circulating myeloblasts (Figure 2E), which also infiltrated the spleen and liver and resulted in an alteration in their normal architecture (*Online Supplementary Figure S5* and *Online Supplementary Table S1*). Flow cytometric analysis further confirmed expansion of Gr-1^+Mac-1^+c-kitlow myeloblasts (*Online Supplementary Figure S6A*), which was in contrast to a drastic reduction of $B220^+$ cells (*Online Supplementary Figure S6B*). These results indicate that *MLL* amplification and *MLL*-PTD cooperate to block normal myeloid differentiation and to induce their aberrant expansion leading to overt AML.

To gain further molecular insights underlying these cooperating *MLL* aberrations, we assessed the transcriptional and epigenetic status of *Hoxa9*, a key downstream target for *MLL* leukemongenesis.[12,13] By comparison with *MLL*(40-50), $Mll^{PTD/WT}$ controls and *E2A-PBX* mouse leukemic cells, which expressed basal level of *Hoxa9*, *MLL*(40-50)$^{PTD/WT}$ leukemic cells, in particular those from the spleen, expressed significant levels of *Hoxa9*; almost 10-fold higher than *MLL*(40-50) and twice more than $Mll^{PTD/WT}$; showing the possibility of functional cooperation in *MLL* aberrations (Figure 2F-G). In addition to *Hoxa9*, a considerably higher level of *Meis1*,[1] another target for *MLL* leukemongenesis, was also detected in *MLL*(80-100) and *MLL*(40-50)$^{PTD/WT}$ bone marrow cells, which provides an explanation for the transformation in the double mutants (*Online Supplementary Figure S7A*). To further confirm this finding in the relevant human disease, we also examined the expression and epigenetic status of *HOXA9* in primary human AML blasts carrying both *MLL*(n) and *MLL*-PTD (*Online Supplementary Figure S7B*). *HOXA9* was significantly over-expressed in all 3 *MLL*(n)-PTD samples and *MLL*-AF6 leukemia as compared to normal karyotype AML (Figure 2H).

At the epigenetic level, similar to *MLL*-AF9 mouse leukemic cells, we observed an upregulation of the H3K4me3 and H3K79me2 activation marks and a reduction of H3K9me2 repressive mark in *MLL*(40-50)$^{PTD/WT}$ bone marrow cells, where higher levels of *MLL* expression were detected in comparison with non-transgenic controls or *Mll*-PTD (Figure 3A,B). Interestingly, Kühn *et al*. have observed profound enrichment of H3K79me2 marks at the highly expressed *HOXA* cluster locus in *MLL*-PTD positive leukemia cell lines.[14] They found that DOT1L inhibition abrogated H3K79me2 and led to downregulation of *MLL* targets in *MLL*-PTD leukemia cell lines,[14] suggesting that DOT1L is a potential therapeutic target for *MLL*-PTD leukemia. Consistent with the mouse model, we also observed similar histone modification patterns in human *MLL*(n)-PTD blasts (Figure 3C). While *MLL*(n)-PTD samples exhibited an increased H3K79me2 mark, it was significantly lower than that seen in *MLL* fusion leukemia. Conversely, H3K4me3 was invariably present at a high level in all *MLL*(n)-PTD samples (Figure 3C), which is in line with the detection of elevated expression of wild-type *MLL* in primary AML patients (Figure 3D), suggesting that H3K4me3 mediated by the *MLL/SET* family may also play a critical role for activation of downstream targets in these leukemias. To further test this hypothesis, pharmacological inhibition of MLL catalytic activity by a small molecule inhibitor WDR-010315 significantly reduced cell viability (Figure 3E), induced cell differentiation (Figure 3F) and repressed ribonucleic acid (RNA) expression of *Meis1* (Figure 3G) of

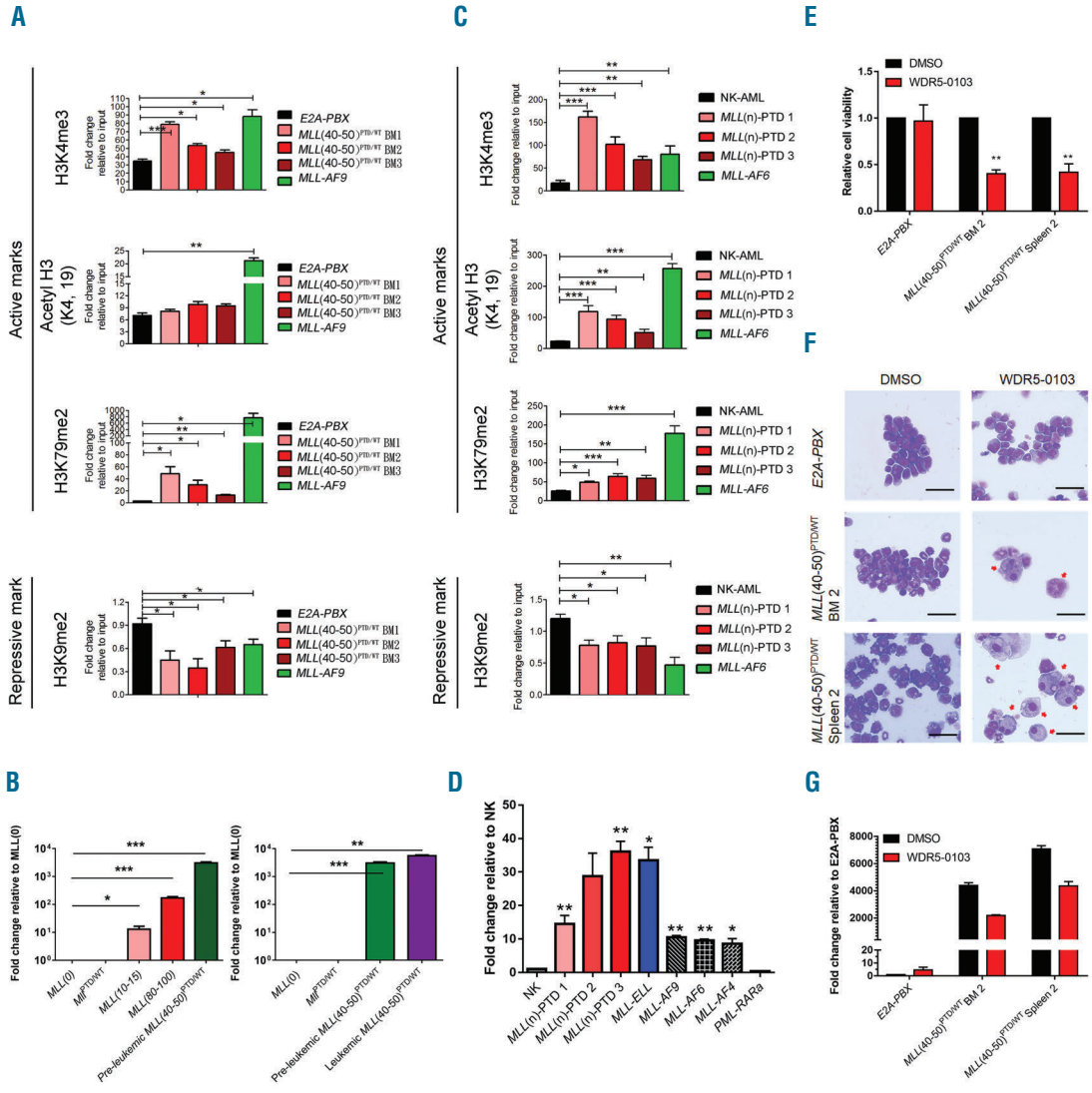

Figure 3. RNA expression and histone modifications of *HOXA9* in *MLL*(40-50)$^{PTD/WT}$ mice and *MLL*(n)-PTD patients. (A) Fold change of H3K4me3, acetyl H3, H3K79me2 and H3K9me2 histone marks within the *Hoxa9* locus are shown. Results were obtained from 4 independent experiments. (B) Relative expression levels of *MLL* in the bone marrow of *Mll*$^{PTD/WT}$, *MLL*(n), and pre-leukemic *MLL*(40-50)$^{PTD/WT}$ mice compared to age-matched wild-type *MLL*(0) mice (left panel), pre-leukemic and leukemic *MLL*(40-50)$^{PTD/WT}$ mice compared to age-matched wild-type *MLL*(0) mice (right panel). Results were obtained from 5 mice with the exception of *MLL*(40-50)$^{PTD/WT}$ where only 3 mice were available. (C) Fold change of H3K4me3, acetyl H3, H3K79me2 and H3K9me2 histone marks within the *HOXA9* locus using bone marrow cells from human *MLL*(n)-PTD, NK-AML, and *MLL*-AF6 samples. Results were obtained from 3 independent experiments. (D) Relative expression levels of *MLL* in human primary samples with *MLL*(n)-PTDs, *MLL* fusions and *PML-RARa* compared to NK-AML. Expression of *Gapdh* was used as an endogenous control to standardize the cDNAs. Results were obtained from 3 independent experiments. Bar graphs show mean+S.E.M. (*P<0.05, **P<0.01 and ***P<0.001, paired *t*-test). (E) Relative cell viability (n=3), (F) cytospins and (G) RNA levels of *Meis1* (n=2) of BM 2 and spleen 2 from *MLL*(40-50)$^{PTD/WT}$, *E2A-PBX* and *MLL-AF9* mouse cells treated with 40 μM WDR5-0103 for 5 days. Red arrows indicate differentiated cells. Scale bars represent 6.25 μm. Bar graphs show mean+S.D. (**P<0.01, paired *t*-test).

MLL(40-50)$^{PTD/WT}$ transformed cells, supporting the fact that the histone methyltransferase activity of *MLL* is crucial for transcriptional activation and downstream leukemogenesis.

In spite of their frequent association with poor prognostic AML, the lack of appropriate leukemia models has significantly hindered the progress in understanding the function of *MLL*-PTD and *MLL* amplification in leukemogenesis.[1,2] While the relatively long latency and partial penetrance of AML in *MLL*(40-50)$^{PTD/WT}$ mice indicate the requirement of additional events, such as genes co-amplified in the 11q23 amplicon[8,9] for the development of full-blown leukemia, the study herein provides the first experimental evidence and novel insights into a cooperative transformation mechanism mediated by *MLL*-PTD and *MLL* amplification to induce leukemia in part by epigenetic deregulation of *MLL* downstream targets. Intriguingly, both gain-of-function and loss-of-function *MLL* mutations have been reported in acute leukemia, indicating that the appropriate activity of *MLL* is required for normal development, and its deregulation in either direction can lead to leukemogenic transformation.[1] Instead of being a passive player in *MLL*-PTD leukemia, the study herein demonstrates the pathogenic functions and potential therapeutic value of targeting *MLL* amplification in acute leukemogenesis.

Bon Ham Yip,[1] Chiou Tsun Tsai,[1] Jayant K. Rane,[1] Winston Vetharoy,[1] Eduardo Anguita,[2] Shuo Dong,[3] Michael A. Caligiuri[4] and Chi Wai Eric So[1]

[1]Leukemia and Stem Cell Biology Group, Department of Haematological Medicine, Division of Cancer Studies, King's College London, UK; [2]Haematology Department, Hospital Clínico San Carlos, Madrid, Spain; [3]Sbarro Institute for Cancer Research, College of Science and Technology, Temple University, Philadelphia, PA, USA and [4]The Comprehensive Cancer Center, The James Cancer Hospital and Solove Research Institute, The Ohio State University, Columbus, OH, USA

Acknowledgements: we would like to thank Tony Green and Mel Greaves for Scl promoter/enhance element, Suming Huang for β-globin HS4 core insulator sequence, Bernd Zeisig, Tsz Kan Fung and Amanda Wilson for helpful discussions and technical support.

Funding: This work was funded by Bloodwise with additional support from Cancer Research UK (CRUK) to CWES, and in part by grants from the U.S. National Cancer Institute to MAC (CA89341 and CA140158).

Correspondence: eric.so@kcl.ac.uk
doi:10.3324/haematol.2016.161406

Information on authorship, contributions, and financial & other disclosures was provided by the authors and is available with the online version of this article at www.haematologica.org.

References

1. Yip BH, So CW. Mixed lineage leukemia protein in normal and leukemic stem cells. Exp Biol Med (Maywood). 2013;238(3):315-323.
2. Zeisig BB, Kulasekararaj AG, Mufti GJ, So CW. SnapShot: Acute myeloid leukemia. Cancer Cell. 2012;22(5):698-698 e691.
3. Maitta RW, Cannizzaro LA, Ramesh KH. Association of MLL amplification with poor outcome in acute myeloid leukemia. Cancer Genet Cytogenet. 2009;192(1):40-43.
4. Michaux L, Wlodarska I, Stul M, et al. MLL amplification in myeloid leukemias: A study of 14 cases with multiple copies of 11q23. Genes Chromosomes Cancer. 2000;29(1):40-47.
5. Whitman SP, Liu S, Vukosavljevic T, et al. The MLL partial tandem duplication: evidence for recessive gain-of-function in acute myeloid leukemia identifies a novel patient subgroup for molecular-targeted therapy. Blood. 2005;106(1):345-352.
6. Dorrance AM, Liu S, Yuan W, et al. Mll partial tandem duplication induces aberrant Hox expression in vivo via specific epigenetic alterations. J Clin Invest. 2006;116(10):2707-2716.
7. Bernot KM, Nemer JS, Santhanam R, et al. Eradicating acute myeloid leukemia in a Mll(PTD/wt):Flt3(ITD/wt) murine model: a path to novel therapeutic approaches for human disease. Blood. 2013; 122(23):3778-3783.
8. Ariyama Y, Fukuda Y, Okuno Y, et al. Amplification on double-minute chromosomes and partial-tandem duplication of the MLL gene in leukemic cells of a patient with acute myelogenous leukemia. Genes Chromosomes Cancer. 1998;23(3):267-272.
9. Pajuelo-Gamez JC, Cervera J, Garcia-Casado Z, et al. MLL amplification in acute myeloid leukemia. Cancer Genet Cytogenet. 2007; 174(2):127-131.
10. Eguchi M, Eguchi-Ishimae M, Green A, Enver T, Greaves M. Directing oncogenic fusion genes into stem cells via an SCL enhancer. Proc Natl Acad Sci USA. 2005;102(4):1133-1138.
11. Poppe B, Vandesompele J, Schoch C, et al. Expression analyses identify MLL as a prominent target of 11q23 amplification and support an etiologic role for MLL gain of function in myeloid malignancies. Blood. 2004;103(1):229-235.
12. Smith LL, Yeung J, Zeisig BB, et al. Functional crosstalk between Bmi1 and MLL/Hoxa9 axis in establishment of normal hematopoietic and leukemic stem cells. Cell Stem Cell. 2011;8(6):649-662.
13. Esposito MT, Zhao L, Fung TK, et al. Synthetic lethal targeting of oncogenic transcription factors in acute leukemia by PARP inhibitors. Nat Med. 2015;21(12):1481-1490.
14. Kuhn MW, Hadler MJ, Daigle SR, et al. MLL partial tandem duplication leukemia cells are sensitive to small molecule DOT1L inhibition. Haematologica. 2015;100(5):e190-193.
15. Senisterra G, Wu H, Allali-Hassani A, et al. Small-molecule inhibition of MLL activity by disruption of its interaction with WDR5. Biochem J. 2013;449(1):151-159.