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ANP32A dysregulation contributes to abnormal megakaryopoiesis in acute megakaryoblastic leukemia

Xueqin Sun¹, Bin Lu¹, Cuijuan Han¹, Wanlin Qiu¹, Qi Jin¹, Dengju Li², Qiubai Li³, Qiong Yang⁴, Qiang Wen⁴, Puneet Opal⁴, Ameet R. Kini⁵, John D. Crispino⁴ and Zan Huang¹

Acute megakaryoblastic leukemia (AMKL) is a rare type of leukemia characterized by indefinite proliferation of megakaryocytes¹. The prognosis of AMKL is dismal and no target therapy is available that urges for development of novel therapy². Recent research proposed that forcing AMKL cells to undergo polyploidization and differentiation was a good therapeutic strategy for AMKL³. Thus, regulators controlling megakaryopoiesis could be potential targets for AMKL therapy. *ANP32A* gene was implied to be a potential regulator of hematopoiesis and megakaryopoiesis⁴. However, its role in blood remains unclear.

In this study, we observed a potential correlation between *ANP32A* downregulation and megakaryocyte differentiation. Hematopoietic stem cells (HSCs) (CD133⁺CD34^{dim}) and megakaryocyte-erythrocyte progenitor expressed a higher level of *ANP32A* than colony-forming unit-megakaryocyte (CFU-Mk) and mature megakaryocytes (Fig. 1a)⁵, and significant upregulation of *ANP32A* was verified in primary AMKL cells (Fig. 1b). However, *ANP32A* was downregulated in leukemic cells undergoing megakaryocytic differentiation (Supplementary Fig. 1A, B). Interestingly, complete blood count of *Anp32A*^{-/-} mice were apparently normal (data not shown). Both *Anp32A*^{-/-} and *ANP32*-overexpressing megakaryocyte cultures showed comparable CD41 and CD42 expression compared with wild-type (WT) cells. *ANP32A*-deficient megakaryocytes only exhibited mild increased of polyploidy in CD42⁺ megakaryocytes and

slight decrease of CFU-Mk, whereas *ANP32A* overexpression had an opposite but marginal effect (Supplementary Fig. 2A–F). These observations suggest a dispensable role of *ANP32A* on normal megakaryopoiesis. This may be due to the compensatory effect of *ANP32B* and *ANP32E* as proposed previously⁶. In sharp contrast, *ANP32A* knockdown (sh*ANP32A*#1) in 6133/MPL W515L cells induced spontaneous megakaryocytic differentiation in the absence of phorbol 12-myristate 13-acetate (PMA) with increased CD41 and CD42 expression (Fig. 1c), which was confirmed in multiple AMKL cell lines (Supplementary Fig. 3A–F). Although *ANP32A* overexpression failed to promote K562 cell proliferation, it did impair PMA-induced megakaryocytic differentiation (Supplementary Fig. 4A–C). Furthermore, *ANP32A* knockdown significantly reduced colony-forming ability of these cells in soft agar (Fig. 1d). Notably, *ANP32A* downregulation significantly impaired the ability of 6133/MPL W515L cells to induce AMKL in mice⁷ and improved the survival rate (Fig. 1e). These observations indicate that *ANP32A* may be critical for AMKL cell to maintain hyper-proliferative and undifferentiated status and contribute to the pathogenesis of AMKL.

Mechanistically, ectopic expression of *ANP32A* dampened the induction of RUNX1 and FLI1 and inhibited extracellular-signal-regulated kinase (ERK) activation by phorbol myristate acetate (PMA) (Fig. 2a). In contrast, *ANP32A* downregulation caused an opposite phenotype (Fig. 2b). These findings were consistent to previous reports showing that PMA induces activation of mitogen-activated protein kinase/ERK and stress-activated protein kinase/c-Jun NH(2)-terminal kinase pathways and subsequently regulate the expression of RUNX1 and FLI1 to promote megakaryopoiesis^{8, 9}. Noticeably, further

Correspondence: Zan Huang (z-huang@whu.edu.cn)

¹College of Life Sciences, Hubei Key Laboratory of Cell Homeostasis, Wuhan University, Wuhan, China

²Department of Hematology, Tongji Hospital of Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

Full list of author information is available at the end of the article

Xueqin Sun, Bin Lu, and Cuijuan Han contributed equally to this work.

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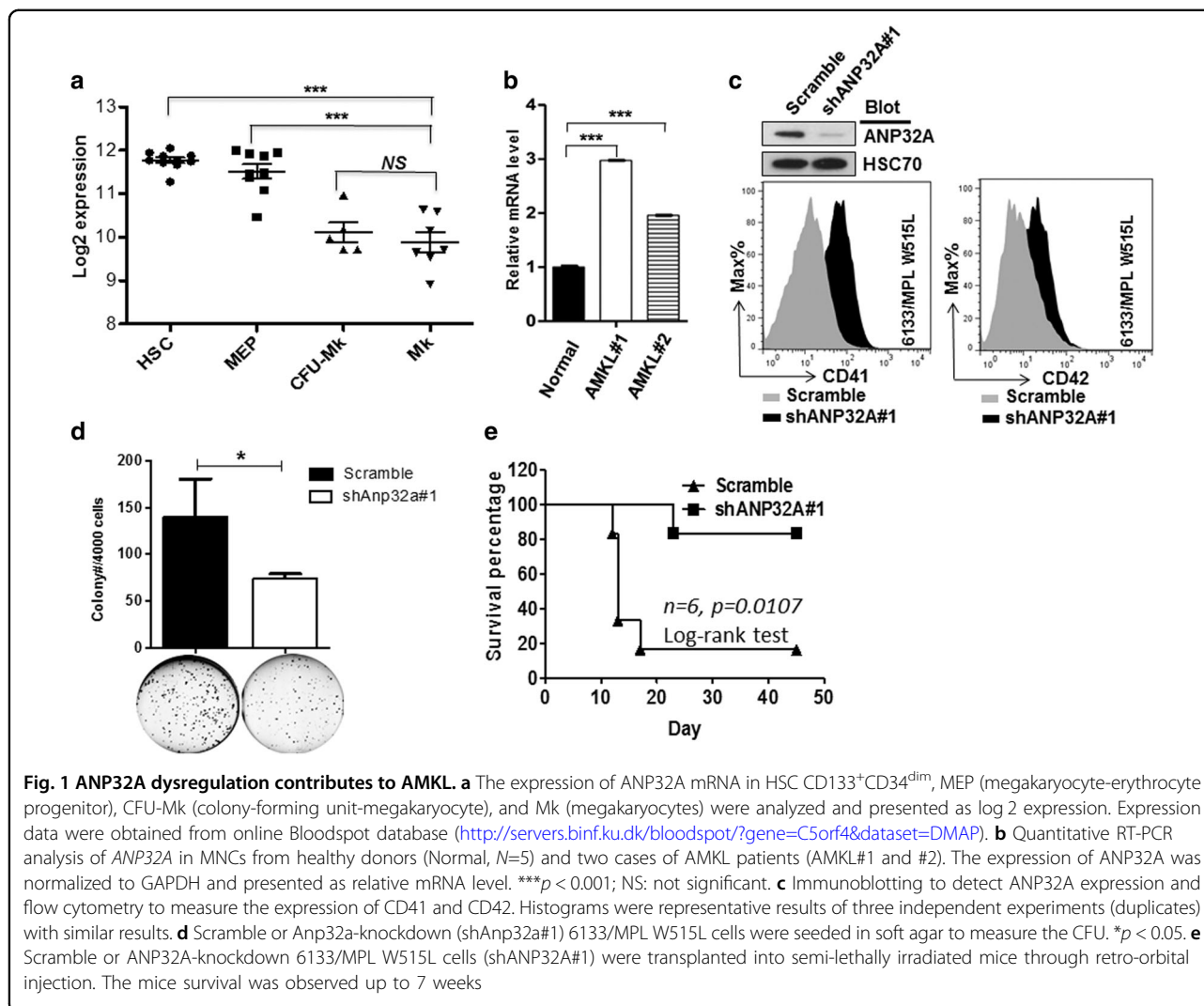
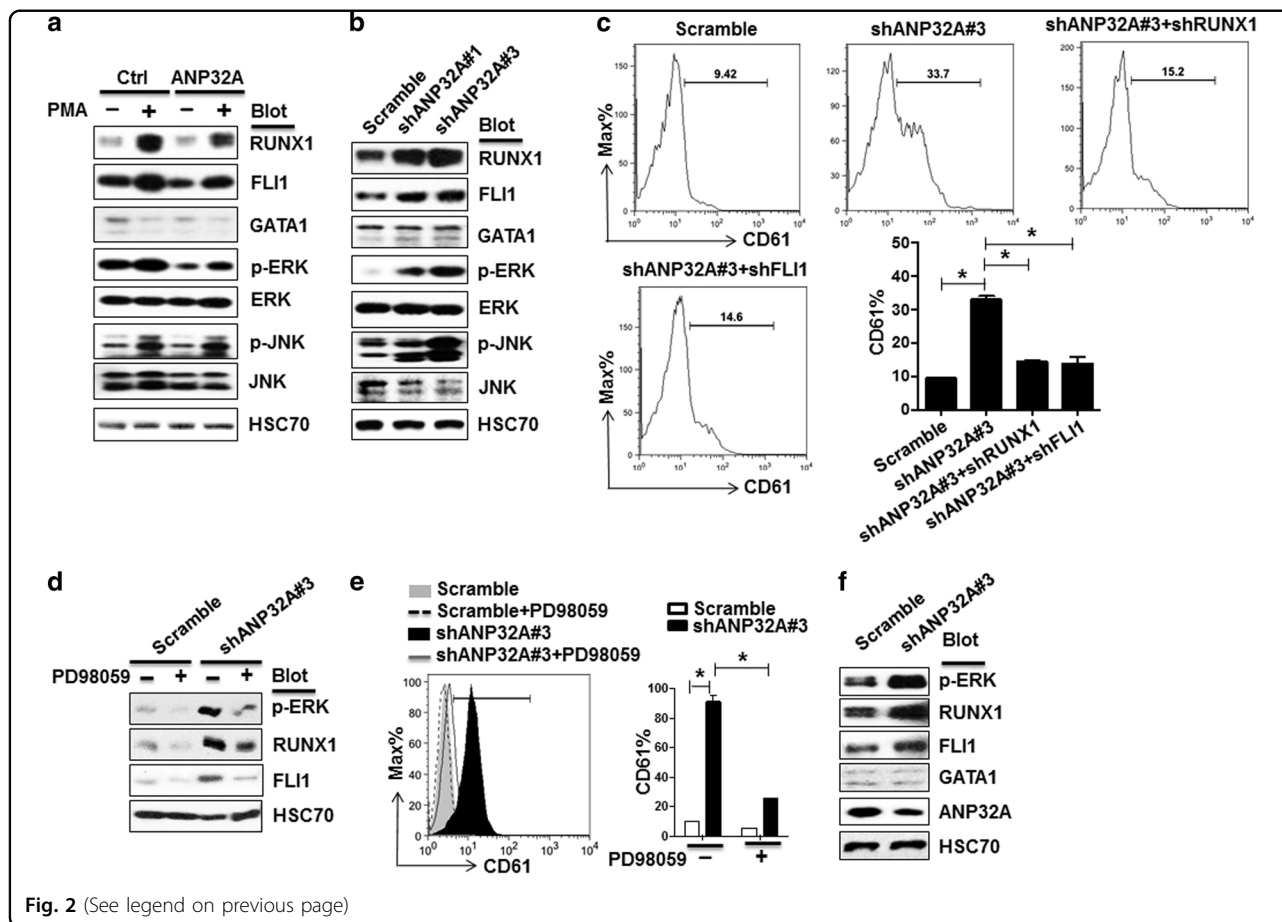


Fig. 2 ANP32A impairs megakaryocyte differentiation by repressing ERK signaling and subsequent RUNX and FLI1 expression. **a** Immunoblotting to detect protein expression and phosphorylation in control and ANP32A-expressing K562 cells treated with (+) or without (–) PMA for 2 days. HSC70 served as a loading control. **b** Immunoblotting to detect protein expression and phosphorylation in Scramble or ANP32A-knockdown K562 cells (shANP32A#1, shANP32A#3). HSC70 served as a loading control. **c** RUNX1 or FLI1 was further knocked down in ANP32A-knockdown K562 cells. CD61 expression in the resultant cells was measured by flow cytometry. Histograms were representative results of three independent experiments (duplicates) with similar results. **p* < 0.05. **d** Immunoblotting to detect RUNX1, FLI1 expression, and ERK phosphorylation in Scramble or ANP32A-knockdown (shANP32A#3) K562 cells treated with or without PD98059. HSC70 served as a loading control. **e** Flow cytometry to measure CD61 expression in the resultant cells in **d**. Histogram was representative data from three independent experiments (duplicates) with similar results. **p* < 0.05. **d** Immunoblotting to detect protein expression and phosphorylation in Scramble or ANP32A-knockdown primary AML cells (shANP32A#3). HSC70 served as a loading control

RUNX1 knockdown (shANP32A#3+shRUNX1) or FLI1 knockdown (shANP32A#3+shFLI1) efficiently abrogated shANP32A#3-induced megakaryocytic differentiation (Fig. 2c, Supplementary Fig. 5). Moreover, ERK inhibitor PD98059 significantly suppressed the induction of RUNX1 and FLI1 expression and abolished shANP32A#3-induced megakaryocytic differentiation

(Fig. 2d, e). Interestingly, ANP32A knockdown in primary AML cells increased the expression of RUNX1 and FLI1 and enhanced ERK phosphorylation while GATA1 was intact (Fig. 2f). Our findings suggest that ANP32A may inhibit ERK and subsequently repress RUNX1 and FLI1 to promote megakaryocyte differentiation.



In summary, our study reveals that ANP32A dysregulation may be a critical factor contributing to AMKL and ANP32A may be a good target for AMKL therapy. Previous studies showed that ANP32A bound to unmodified histone H3 and inhibited H3 acetylation⁷. Thus, ANP32A downregulation may potentially alter global epigenetic modifications.

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Author details

¹College of Life Sciences, Hubei Key Laboratory of Cell Homeostasis, Wuhan University, Wuhan, China. ²Department of Hematology, Tongji Hospital of Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China. ³Institute of Hematology, Union Hospital of Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China. ⁴Feinberg School of Medicine, Northwestern University, Chicago, IL, USA. ⁵Chicago Stritch School of Medicine, Loyola University, Chicago, IL, USA

Competing interests

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References

- Malinge, S, Izraeli, S. & Crispino, J. D. Insights into the manifestations, outcomes, and mechanisms of leukemogenesis in Down syndrome. *Blood* **113**, 2619–2628 (2009).
- Tallman, M. S. et al. Acute megakaryocytic leukemia: the Eastern Cooperative Oncology Group experience. *Blood* **96**, 2405–2411 (2000).
- Wen, Q. et al. Identification of regulators of polyploidization presents therapeutic targets for treatment of AMKL. *Cell* **150**, 575–589 (2012).
- Wilson, N. K. et al. Combinatorial transcriptional control in blood stem/progenitor cells: genome-wide analysis of ten major transcriptional regulators. *Cell Stem Cell* **7**, 532–544 (2010).
- Bagger, F. O. et al. BloodSpot: a database of gene expression profiles and transcriptional programs for healthy and malignant haematopoiesis. *Nucleic Acids Res.* **44**, D917–D924 (2016).
- Opal, P. et al. Generation and characterization of LANP/pp32 null mice. *Mol. Cell Biol.* **24**, 3140–3149 (2004).
- Kular, R. K., Cvetanovic, M., Siferd, S., Kini, A. R. & Opal, P. Neuronal differentiation is regulated by leucine-rich acidic nuclear protein (LANP), a member of the

- inhibitor of histone acetyltransferase complex. *J. Biol. Chem.* **284**, 7783–7792 (2009).
8. Sun, X. et al. Novel function of the chromosome 7 open reading frame 41 gene to promote leukemic megakaryocyte differentiation by modulating TPA-induced signaling. *Blood Cancer J.* **4**, e198 (2014).
 9. Lu, B. et al. Novel function of PITH domain-containing 1 as an activator of internal ribosomal entry site to enhance RUNX1 expression and promote megakaryocyte differentiation. *Cell. Mol. Life Sci.* **72**, 821–832 (2014).