Point mutations in the 5′ UTR of ankyrin repeat domain 26 (ANKRD26) are associated with familial thrombocytopenia 2 (THC2) and a predisposition to leukemia. Here, we identified underlying mechanisms of ANKRD26-associated thrombocytopenia. Using megakaryocytes (MK) isolated from THC2 patients and healthy subjects, we demonstrated that THC2-associated mutations in the 5′ UTR of ANKRD26 resulted in loss of runt-related transcription factor 1 (RUNX1) and friend leukemia integration 1 transcription factor (FLI1) binding. RUNX1 and FLI1 binding at the 5′ UTR from healthy subjects led to ANKRD26 silencing during the late stages of megakaryopoiesis and blood platelet development. We showed that persistent ANKRD26 expression in isolated MKs increased signaling via the thrombopoietin/myeloproliferative leukemia virus oncogene (MPL) pathway and impaired proplatelet formation by MKs. Importantly, we demonstrated that ERK inhibition completely rescued the in vitro proplatelet formation defect. Our data identify a mechanism for development of the familial thrombocytopenia THC2 that is related to abnormal MAPK hyperactivation.

Introduction

Thrombocytopenia 2 (THC2 [MIM 188000]) is characterized by autosomal-dominant transmission, a moderate thrombocytopenia, reduction of platelet α-granules, normal in vitro platelet aggregation, and mean platelet volume and predisposition to leukemia. Bone marrow examination and serum thrombopoietin (TPO) levels suggest that thrombocytopenia results from dysmegakaryopoiesis (1, 2). The THC2 locus was mapped to chromosome 10p11.1-p12 (3, 4), and more recently, different heterozygous single-nucleotide substitutions within the 5′ UTR of the ankyrin repeat domain 26 (ANKRD26) gene were described (5). It encodes for a 192-kDa protein, which is highly abundant in the brain, particularly in the hypothalamus, as well as in the liver, the adipose tissue, the skeletal muscle, and the hematopoietic tissue (6). The ANKRD26 protein is associated with the inner part of the cell membrane and contains ankyrin repeats and spectrin helices for interaction with signaling proteins. The par-
ANKRD26 was less expressed in mature (CD41+CD42+) compared to cultured until day 12 to induce differentiation, a similar decrease when immature MKs were sorted on CD41 expression at day 6 and its expression diminished along MK differentiation (Figure 2A). To predict which transcription factors bind to the ANKRD26 UTR enhances 5′ in a cell line model (5), that a mutation in 5′ obtained in primary cells confirmed what was previously observed detectable in healthy control platelets (Figure 2E). These results expressed in platelets from THC2 patients while being hardly abolished (Figure 2D). Similarly, the ANKRD26 gene remained expressed in platelets from THC2 patients whereas its expression was nearly abolished (Figure 2D). Similarly, the ANKRD26 gene remained expressed in platelets from THC2 patients while being hardly detectable in healthy control platelets (Figure 2E). These results obtained in primary models confirmed what was previously observed in a cell line model (5), that a mutation in 5′ UTR enhances ANKRD26 gene expression during megakaryopoiesis.

ANKRD26 gene is negatively regulated by the RUNX1 and FLI1 transcription factors. To predict which transcription factors bind to the 5′ UTR region of the ANKRD26 gene and could be affected by mutations, we used the TRAP (10) and the CHipMapper (11) online software. Two transcription factors, RUNX1 and FLI1, which are known to coregulate megakaryopoiesis (12) were found to potentially bind this affected region (Figure 3A). shRNA knockdown of RUNX1 and FLI1 (Figure 3, B–D) led to an increase in ANKRD26 gene expression in normal MKs, demonstrating that these 2 transcription factors could repress ANKRD26 gene expression (Figure 3E). ChIP assays demonstrated that RUNX1 or FLI1 bound the 5′ UTR ANKRD26 gene region encompassing THC2 mutations in MKs (Figure 3F), which led us to test the functional relevance of this binding site. For that purpose, the ANKRD26 gene region from +347nt to +1nt was cloned upstream of the luciferase gene, and this reporter construct was cotransfected into K562 cells with an empty vector or vector expressing RUNX1 gene or FLI1 gene. Individually, RUNX1 and FLI1 overexpression showed a moderate inhibitory effect on ANKRD26 gene expression, while their simultaneous overexpression showed an synergistic inhibitory effect (Figure 3G). To confirm that the mutations found in the 5′ UTR of ANKRD26 gene of THC2 patients led to the loss of inhibitory regulatory function of RUNX1 and FLI1, we performed luciferase assays in K562 cells using reporter constructs encoding for the 5′ UTR ANKRD26 region with the c.-119C>T, the c.-127A>T, or the c.-127delAT mutations. These 3 different mutations led to a significant increase in luciferase activity in comparison with the WT sequence (Figure 3H).

Persistent ANKRD26 expression induces a deep defect in PPT formation. To understand how the persistent expression of the ANKRD26 gene could contribute to thrombocytopenia, we further studied the phenotype of patient MKs. We used 2 techniques in parallel to derive mature MKs. In the first, MKs were derived from purified blood CD34+ cells in the presence of TPO and SCF; in the second, blood CD45+ cells were isolated and MKs were obtained after culture with TPO, IL-6, and IL-11. Both techniques gave very similar results. The percentage of mature CD41+CD42+ MKs was evaluated at day 10 (when derived from CD34+ cells) or 14 (when derived from CD45+ cells) of culture. No difference in MK differentiation was detected between patients and healthy donors (n = 14 for controls, n = 19 for patients) as shown in Figure 4A, except a slight decrease in ploidy level (n = 11.4 for controls [n = 4] to n = 9.5 for patients [n = 5], P = 0.0079) (Figure 4A and Supplemental Figure 1A). Electron microscopy analysis was performed for 2 patients’ MKs after 10 days of culture (Figure 4B). In controls, mature MKs showed homogeneously distributed granules and demarcation membranes (DMS) with typical organization of DMS that form platelet territories. On the contrary, patient MKs showed a decreased concentration of granules (PD1_3, PD1_2). MKs showed thick and short cytoplasmic extensions with heterogeneous distribution of granules (PD3_3) or fragile extensions with very thin attachment to the MK body (PD1_2). Frequently, within the MK cytoplasm with deformed elongated shape, the DMS system appeared to delineate areas of fragmentation instead of formation of long pseudopods (PD1_3, PD1_2). These results suggested a defect in PPT formation (Figure 4B)

Previously, a decrease in the expression of GPIa (CD49b), the α subunit (α2) of a transmembrane receptor for collagen, was suggested a defect in PPT formation (Figure 2D).
observe a decrease in GPIa expression and in stress fiber formation upon activation of αβ1 (GPIa/GPIIa) integrin by MK adhesion to fibrillar collagen type I (n = 3 for controls, n = 4 for patients) (Figure 4D). Finally, the ability to form PPTs by MKs generated by the 2 protocols was investigated in liquid medium and after adhesion on poly-L-lysine or fibrinogen substrates. In all experimental designs, a profound decrease in the number of PPT-forming MKs in patients compared with controls (n = 14 for controls, n = 22 for patients, P < 0.0001) was observed (Figure 4D). Moreover, the branching area of PPT was significantly decreased in MKs of patients (Figure 4E), as demonstrated by a 4.6-fold decrease in the bifurcation number compared with controls (n = 10 for controls, n = 17 for patients, P < 0.05) (Figure 4E). To confirm that the ANKRD26 overexpression led to the defect in PPT formation, the CD34+ cells of 2 controls and 2 THC2 patients were transduced by an shRNA of ANKRD26 (shANK1). The inhibition of ANKRD26 expression in patients’ MKs led to a rescue of the defect in PPT formation (Supplemental Figure 2). Overall these results demonstrated that the persistent ANKRD26 expression in MKs of THC2 patients does not alter MK differentiation, but leads to a profound defect in PPT formation, which could be at the origin of the thrombocytopenia.

Persistent ANKRD26 expression induces increased MAPK/ERK1/2 activation in patient MKs. ANKRD26 gene knockout was reported to modulate the ERK pathway in mouse embryo fibroblasts (MEF) (9). Through its receptor MPL, TPO is the principal physiological regulator of MK differentiation and platelet production. To understand how the preserved expression of the ANKRD26 gene could alter PPT formation through a signaling defect, we focused on the activation of JAK/STAT, MAPK, and PI3K in response to TPO. First, the UT7 megakaryocytic cell line maintained under GM-CSF was transduced with HA-tagged MPL (HA-MPL) to make it sensitive to TPO. As these cells express the ANKRD26 gene, contrary to primary mature MKs, we subsequently transduced them with an shRNA targeting ANKRD26 (shANK1), which decreased its expression by about 80% compared with control cells transduced with an irrelevant shRNA (shSCR) (Supplemental Figure 3, A and B). ANKRD26 knockdown led to a decrease in TPO/MPL signaling pathways as attested by a diminution in phosphorylation of STAT5, AKT, and ERK1/2 (Figure 5, A–D). These results were confirmed by using a second shRNA against ANKRD26 (shANK2, data not shown). Subsequently, peripheral blood CD34+ cells from a THC2 patient and a healthy individual were cultured for 8 days in the presence of TPO and SCF. The cells were then starved for 24 hours and stimulated with TPO. Activation of the 3 signaling pathways was increased in MKs of patients compared with MKs of controls (Figure 5, E–H), without changes in the kinetics. This increased signaling was more pronounced for the ERK1/2 pathway, which was confirmed for 2 other patients (Supplemental Figure 3, C–F).

Decrease in MAPK signaling is necessary for PPT formation. To understand whether an increase in MAPK activation could alter PPT formation, we analyzed the ERK pathway during MK differentiation from CD34+ cells: early in MK differentiation (day 6 to 7 of culture), during terminal maturation prior to PPT formation (day 10), and at time when mature MKs start to or display PPTs (day 14). As illustrated in Figure 6A, ERK activation induced by TPO dramatically decreased at late stages of megakaryopoiesis. Indeed, at day 6, a sustained and strong ERK activation could be detected 5 minutes after TPO stimulation and reached its maximum after...
10 to 30 minutes. At day 10, the ERK activation started to decrease and at day 14, when MKs began to shade PPTs, a weaker and transient activation of ERK was detected (Figure 6A). This result was confirmed by measuring ERK1/2 phosphorylation by flow cytometry in the CD41+ cell population. A more transient and less intense ERK activation was detected at day 10 of culture in the CD41+ cell population in comparison with day 7 (Figure 6B). These results strongly suggested that ERK activation by TPO is downregulated during MK differentiation. To further demonstrate ERK downregulation involvement in PPT formation, the MEK inhibitor PD98059 was used. The CD34+ cell–derived MKs were sorted at day 6 on the expression of CD41. The inhibitor was added at day 8, prior to PPT formation. An important increase in the percentage of PPT-forming MKs was observed in the presence of PD98059.
Importantly, PD98059 is not entirely specific of MEK, but also inhibits cyclooxygenase-1 (13). To demonstrate that PD98059 increases PPT formation through the MAPK pathway and not through cyclooxygenase inhibition, we used indomethacin, an inhibitor of cyclooxygenase-1 at a 10-μM concentration. When added at day 8 of culture, indomethacin did not affect MAPK pathway activation and PPT formation, whereas PD98059 at 10 μM in presence of indomethacin almost completely inactivated ERK1/2.
and increased the number of PPT-forming MKs (Supplemental Figure 4, A and B). Then, we verified that, at a concentration of 10 μM, PD98059 does not affect MK maturation and does not induce apoptosis. The inhibitor was added to the culture at day 0 and day 3, and the analysis was performed at day 7; no differences with the controls were observed (Supplemental Figure 4, C and D).

To clearly demonstrate that inhibition of the MAPK/ERK pathway negatively regulates PPT formation, we overexpressed a dominant-negative (DNMEK1) (14) or active (MEKa) (15) form of MEK1 in primary MKs and showed that DNMEK1 leads to a 2-fold increase in the percentage of PPT-bearing MKs while, in opposition, MEKa leads to a decrease (Figure 6, E and F). This result demonstrated that ERK1/2 activation at late stages of MK differentiation inhibits PPT formation, as previously postulated (16).

**Discussion**

THC2 is one of the rare inherited pathologies with a mutation in the regulatory region of a gene, the deregulation of which affects megakaryopoiesis and early stages of hematopoiesis, as attested...
by thrombocytopenia and the leukemic predisposition (2). Only 2 other inherited platelet disorders with such mutations in regulatory regions have been reported till now: (a) a mutation in the 5′ UTR region of the GPIbβ gene inducing a loss of GATA1 binding to this promoter region in MK results in Bernard-Soulier syndrome (17); and (b) recently, 2 regulatory SNPs leading to a diminished expression of a subunit Y14 of exon junction complex in platelets have been described as responsible for the thrombocytopenia–absence of radius (TAR) syndrome (18).

Here, we demonstrated that mutations in the 5′ UTR of the ANKRD26 gene prevent the transcription factors RUNX1 and FLI1 from repressing ANKRD26 gene activity. Consequently, ANKRD26 remained expressed in the platelets of THC2 patients. RUNX1, FLI1, SCL, GATA1, and GATA2 are known coregulators of megakaryopoiesis (12, 19) that simultaneously bind promoter regions of key regulators of MK differentiation and functions (19). Importantly, analysis of these ChIP-seq data revealed only an enrichment in RUNX1 and FLI1, but not in GATA and SCL, in the 5′ UTR region of ANKRD26 gene (19), strongly supporting our findings. We recently reported the silencing of MYH10 by RUNX1 during MK differentiation (20). Consistently, MYH10 was demonstrated to remain expressed at high levels in mature MKs and in platelets from patients with familial platelet disorder with predisposition to acute myeloid leukemia (FPD/AML) characterized by RUNX1 mutations, but also from patients with the Paris-Trousseau syndrome associated with a FLI1 deletion.

Figure 6
Decrease in MAPK signaling pathway is necessary for PPT formation by MKs. MKs were differentiated from CD34+ cells in the presence of TPO. (A and B) Analysis of the MAPK pathway. Starved MKs were stimulated by TPO (100 ng/ml) for 5, 30, 60, and 120 minutes. (A) Western blot analysis of ERK and PERK performed at days 6, 10, and 14. (B) Flow cytometry analysis of PERK at days 7 and 10. The ratio of fluorescence intensity represents the ratio between the value obtained using PERK and control IgG isotype Abs for each time point of TPO stimulation. For A and B, experiments were performed 3 times with similar results. (C) Inhibition of MAPK pathway increases PPT formation. The CD41+ cells were sorted at day 6, the PD98059 inhibitor was added at day 8, and the percentage of PPT-bearing MKs was evaluated at days 11–13. One of 3 independent experiments with similar results is presented. Data were collected from triplicate wells and represent mean ± SD of triplicate. *P < 0.05, Student's t test. (D) PPT-forming MKs cultured in presence or absence of PD98059 at day 13. (E and F) Inhibition or activation of MAPK pathway displayed an opposite effect on PPT formation. (E) CD34+ cells were transduced by retroviruses encoding for a dominant negative form of MEK1 and GFP (DNMEKGFP) or (F) for an active form of MEK1 (MEKa) and GFP. A retrovirus MIGR encoding for GFP was used as control. CD41+GFP+ cells were sorted at day 10 and the percentage of PPT-bearing MKs was evaluated at day 13 of culture. Data were collected from triplicate wells and represent mean ± SD.
suggesting that RUNX1 and FLI1 cooperate in MYH10 downregulation. The repression of both ANKRD26 and MYH10 during megakaryopoiesis might be achieved by a recruitment of Polycomb repressor complex 1 by RUNX1/FLI1 complex to the regulatory region of both genes (22). RUNX1 mutations also increased expression of ANKRD26 in platelets of FPD/AML patients (Supplemental Figure 5). Based on these observations, screening the expression of both MYH10 and ANKRD26 in platelets could be used to distinguish between these 2 close clinical disorders. In FPD/AML, both MYH10 and ANKRD26 will persist in platelets, while only ANKRD26 will be detected in THC2 platelets. Thus studies of ANKRD26 gene expression together with MYH10 in platelets could be an interesting biomarker for THC2 diagnosis.

Finally, we showed that the persistent expression of ANKRD26 in MKs leads to an increased activation of TPO/MPL–mediated signaling, including the PI3K, STAT5 and MAPK/ERK1/2 pathways, this last pathway being more activated than the 2 others. The role of MAPK activation during megakaryopoiesis, particularly in the polyploidization process, remains controversial (16, 23–25). The differences probably depend on the cell type (cell lines, murine, or human primary cells) and the stage of maturation in the case of primary cells and on the experimental protocols. In various MK cell lines, the induction of differentiation in response to PMA or TPO showed a rapid and sustained activation of ERK1/2 (26–29), suggesting that the MAPK/ERK1/2 pathway plays an important role in MK differentiation. Similar results were obtained in human and

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**Figure 7**

Inhibition of sustained MAPK pathway in MKs of patients leads to the correction of PPT formation defect. In vitro MK differentiation was induced from control or patient peripheral blood CD34+ progenitors in the presence of TPO. At day 8, the DMSO (−PD98059) or the MAPK inhibitor PD98059 (+PD98059) was added to the cultures performed in liquid medium. The percentage of PPT-forming MKs was estimated by counting MKs exhibiting 1e or more cytoplasmic processes with areas of constriction at different days of culture. A total of 200 cells per well were counted. The histograms show 1 experiment for each THC2 patient with its respective control performed in triplicate. Data represent mean ± SD of triplicate. (A–C) Histograms show the percentage of PPT bearing MKs before and after inhibition of MAPK pathway with PD98059 inhibitor. (A) PD3_2 and PD5_II4 patient with their respective control, (B) PD5_II2 and PD5_IV1 patients, (C) PD3_3 patient and its respective control. (D and E) Representative microscopic images of PPT formation by control and patient MKs before and after addition of PD98059 inhibitor. (D) PD5_II2 and PD5_IV1 patients. (E) PD3_3 patient and its respective control.
ANKRD26 is localized in the inner part of the cell membrane and can interact with transmembrane receptors (31). An attractive hypothesis would be that ANKRD26 controls MPL signaling through its trafficking. In conclusion, our data show that the loss of inhibitory regulatory function of RUNX1 and FLI1 leads to ANKRD26 overexpression in MKs. ANKRD26 accumulation at the inner part of the MK membrane may alter the TPO/MPL, which is confirmed by the increase in MAPK/ERK pathway activity in patients’ MKs. ERK1/2 overactivation will, in turn, alter PPT formation and contribute to thrombocytopenia in THC2 patients (Figure 8).

TPO/MPL regulates not only MK differentiation, but also the HSC and progenitor (HSC/HP) compartment. Thus, we cannot exclude that the ANKRD26-mediated deregulation of signaling pathways might also take place in HSC/HP and promote leukemic transformation of hematopoietic progenitors. MAPK signaling pathway upregulation in many cancer cells leads to increased proliferation and cell survival. Several MEK inhibitors have been developed for use in clinical trials and a recent phase III study of MEK1/MEK2 inhibitor Trametinib in patients with metastatic cutaneous melanoma showed improved survival (32). Therefore, this MAPK sustained activation in THC2 patients’ MKs could be considered, in the future, as a therapeutic target for controlling thrombocytopenia.
**Methods**

**Patients.** Blood samples from TH2 patients, healthy subjects, and individuals after mobilization were collected.

**Samples.** Peripheral blood CD34+ and CD45+ cells were separated by double-positive selection using a magnetic cell-sorting system (AutoMACS; Miltenyi Biotec SAS). The platelet-rich plasma was prepared by centrifugation at 170 g for 10 minutes. Platelets were pelleted by centrifugation at 2,100 g for 10 minutes.

**In vitro MK differentiation.** Two different protocols were used for in vitro MK differentiation. In the first, patient or control CD34+ cells were grown in serum-free medium as previously reported (33). The medium was supplemented with TPO (10 ng/ml; Kirin Brewery) alone or with TPO and stem cell factor (SCF 25 ng/ml; Biovitrum AB). In the second, patient or control CD45+ cells were cultured in Stem Span medium (Stem Cell Technologies) supplemented with 10 ng/ml TPO, IL-6, and IL-11 (PeproTech EC Ltd.) (34).

**Flow cytometry analysis.** Cells were stained with directly coupled mAbs: anti-CD41 APC, anti-CD42 PE, and anti-CD49b FITC (BD Biosciences) for 30 minutes at 4°C. Depending on the experiments, MKs were sorted according to CD41 or CD41 and CD42 expression using an Influx flow cytometer equipped with 5 lasers (BD). For phospho-ERK staining, cells were fixed in 2% paraformaldehyde for 10 minutes, permeabilized with 0.2% Triton X-100 for 5 minutes, and incubated for 1 hour at 4°C with anti–p-ERK Ab (Cell Signaling) followed by incubation with Alexa Fluor 488–conjugated goat anti-rabbit IgG (Molecular Probes) for 30 minutes.

**Ploidy analysis.** At day 10 of culture, Hoechst 33342 (10 μg/ml; Sigma-Aldrich) was added in the medium of cultured MKs for 2 hours at 37°C. Cells were then stained with directly coupled mAbs: anti-CD41 APC and anti-CD42 PE (BD Biosciences) for 30 minutes at 4°C (20). Ploidy was measured in the CD41+CD42+ cell population by means of an Influx Flow Cytometer (BD) and calculated as previously described (20).

**Fluorescence microscopy.** Fibroblast collagen type I (Horm) from equine tendons (Nycodenz) was incubated at a concentration of 50 μg/ml on coverslips overnight at 4°C. After washing, primary MKs grown in serum-free medium were plated on coated coverslips for 2 hours at 37°C (5% CO2 in air). Cells were then fixed in 2% paraformaldehyde for 10 minutes, permeabilized with 0.2% Triton X-100 for 5 minutes, and incubated for 1 hour at 4°C with anti–vWF Ab (Cell Signaling) followed by incubation with Alexa Fluor 548–conjugated goat anti-rabbit IgG (Molecular Probes) for 30 minutes. Finally, slides were mounted using Vectashield with Dapi (Molecular Probes). The MK (cells expressing vWF) exhibiting α-tubulin–positive long filamentous structures. The extent of branching and platelet-like structures on MKs were evaluated. The number of branching and platelet-like structures on MKs were measured with an GloMax 96 Microplate Luminometer w/Dual Injector (Promega).

**Luciferase reporter assay.** The 5′ UTR region of the ANKRD26 gene (from −347nt +1nt) was amplified by PCR on control or patient DNA and cloned into the reporter plLuc-MCS plasmid (Stratagene). HEL cells were cotransfected with the reporter plasmid plucANANK without (WT) or with mutations found in 3 different THC2 pedigrees (c.-119C>A, c.-127A>T, c.-127delAT) and with TK-Renilla reporter (Promega) for normalization of transfection efficiency. Cells were harvested 48 hours after transfection. A dual luciferase assay was performed according to the manufacturer’s instructions (Promega).

**ChIP and promoter activity assays.** ChIP assays were performed with a ChIP assay kit (Merek Millipore) using the anti-RUNX1 Ab and the anti-FL11 Ab (ab23980 and ab15289, respectively; Abcam). Assays were performed using chromatin prepared from human MKs and analyzed as previously described (36, 37). Immunoprecipitated DNA was analyzed on a PRISM 7700 sequence detection system using SYBR green (Applied Biosystems) in duplicate. Two independent experiments were performed. Primer sequences are listed in Supplemental Table 2.

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**Quantitative RT-PCR.** mRNA isolation, reverse transcription, and quantitative RT-PCR (qRT-PCR) analyses were performed as described (36). The expression levels of all genes studied were expressed relative to housekeeping genes PPIA and HPRT, with stable expression level during MK differentiation. Primer sequences are listed in Supplemental Table 2.

**Western blot assays.** For Western blot analysis, the UT7/HA-MPL cells were transfected with the reporter plucANANK without (WT) or with mutations found in 3 different THC2 pedigrees (c.-119C>A, c.-127A>T, c.-127delAT) and with TK-Renilla reporter (Promega) for normalization of transfection efficiency. Cells were harvested 48 hours after transfection. A dual luciferase assay was performed according to the manufacturer’s instructions (Promega). Luciferase activity was measured with an GloMax 96 Microplate Luminometer w/Dual Injector (Promega). Sequences of primers used for promoter cloning are listed in Supplemental Table 2.

**Cell culture and transduction.** Lentiviral vector encoding for shRUNX1 was already described (35). shANK1, shANK2, and shFL11 (Supplemental Table 2) were cloned into the sniPRPL-PGK-GFP lentivirus. The dominant negative of MEK1 (DNMEK1) and the active form of MEK1 (MEKa) were cloned into the bicistronic retrovirus, which also encoded for GFP (14, 15). Viral particle production and cell transduction were performed, as previously described (36).

Control CD34+ cells (10^6/ml) were prestimulated for 24 hours with TPO, IL-3, SCF, and FLT3-L and transduced with concentrated lentiviral (shRUNX1, shFL11, shANK1, shANK2, shSCR [control]) or retroviral (DNMEK1, MEK1a) particles at 12 hours after an MOI of 10 followed by a second transduction. Cells were then cultured in the presence of TPO alone.

Human factor-dependent cell line UT7/HA-MPL was maintained in DMEM supplemented with 10% heat-inactivated FCS, antibiotics, and 5 ng/ml of rhGM-CSF. Lentiviral particles (shANK1, shANK2, shSCR) were added for 12 hours at an MOI of 10.

Both CD34+ cells and UT7/HA-MPL cells were sorted by flow cytometry (FACS Vantage; BD Biosciences) 48 hours after transduction on GFP expression.

**ChIP and promoter activity assays.** ChIP assays were performed with a ChIP assay kit (Merek Millipore) using the anti-RUNX1 Ab and the anti-FL11 Ab (ab23980 and ab15289, respectively; Abcam). Assays were performed using chromatin prepared from human MKs and analyzed as previously described (36, 37). Immunoprecipitated DNA was analyzed on a PRISM 7700 sequence detection system using SYBR green (Applied Biosystems) in duplicate. Two independent experiments were performed. Primer sequences are listed in Supplemental Table 2.

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pared as previously described (38). Western blot analyses were performed by using the following Abs: rabbit anti-ERK, anti-phospho-ERK, anti-AKT, anti-phospho-AKT, anti-phospho-STAT5 (Cell Signaling), mouse anti-β-actin (Sigma-Aldrich), rabbit anti-RUNX1, and rabbit anti-FLI1 (ab23980 and ab15289 respectively; Abcam). All protein blots were analyzed using Image Quant LAS 4000 (GE Healthcare) and protein expressions were quantified using ImageQuant TL 8.1 software.

Electron microscopy. In vitro–cultured MKs were fixed in 1.25% glutaraldehyde (Fluka Chemie) and diluted in 0.1 M phosphate buffer (pH 7.2) for 1 hour at room temperature. Samples were processed for EM by standard procedures previously described (39). Sections were observed with a JEOI-1010 transmission electron microscope at 80 kV.

Statistics. Data are presented as mean ± SD or ± SEM. Statistical significance was determined by Student's t test or Mann-Whitney test. A P value of less than 0.05 was considered as statistically significant.

Study approval. Informed written consent was obtained from all human subjects in accordance with the Declaration of Helsinki. The study was approved by the Ethics Committee of INSERM RBM 01-14 for the project Network on the inherited diseases of platelet function and platelet production in France and by the IRBs of the IRCCS Policlinico San Matteo Foundation and of the Department of Pediatrics at the Second University of Naples.

Acknowledgments

This work was supported by French grants from the Agence Nationale de la Recherche (ANR-physiopathology, ANR-jeunes chercheurs to H. Raslova), the Ligue contre le Cancer (équipe labellisée à Villejuif cedex, France. Phone: 33.1.42.11.46.71; Fax: 33.1.42.11.52.40; E-mail: hraslova@igr.fr).

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Received for publication June 28, 2013, and accepted in revised form October 31, 2013.


