Thrombocytopenia-associated mutations in the ANKRD26 regulatory region induce MAPK hyperactivation

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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 signaling.

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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, obesity development is linked to enhanced adipogenesis mediated by increased ERK and mTOR pathway activation (9). The mutations in the 5′ UTR regulatory region of ANKRD26 suggested a deregulation of its expression in megakaryocytes (MKs). Here we show a runt-related transcription factor 1/friend leukemia integration 1 transcription factor–mediated (RUNX1/FLI1-mediated) downregulation of ANKRD26 gene expression during megakaryopoiesis, leading to its near absence in platelets. The loss of RUNX1/FLI1 binding in THC2 patients leads to the persistent expression of ANKRD26 in MKs and platelets followed by an increase in TPO/myeloproliferative leukemia virus oncogene (TPO/MPL) signaling 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 signaling.

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 signaling.

Thrombocytopenia-associated mutations in the ANKRD26 regulatory region induce MAPK hyperactivation

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ubiquitinated proteins. Their presence in different pathologies, including epithelial neoplasms, suggests a link of these structures with oncogenesis (6).

ANKRD26 is the ancestral gene for the primate-specific gene family POTE (7). 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 (8). 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 partial inactivation of ANKRD26 induces obesity and gigantism (8). Obesity development is linked to enhanced adipogenesis mediated by increased ERK and mTOR pathway activation (9). The mutations in the 5′ UTR regulatory region of ANKRD26 suggested a deregulation of its expression in megakaryocytes (MKs). Here we show a runt-related transcription factor 1/friend leukemia integration 1 transcription factor–mediated (RUNX1/FLI1-mediated) downregulation of ANKRD26 gene expression during megakaryopoiesis, leading to its near absence in platelets. The loss of RUNX1/FLI1 binding in THC2 patients leads to the persistent expression of ANKRD26 in MKs and platelets followed by an increase in TPO/myeloproliferative leukemia virus oncogene (TPO/MPL) signaling, particularly in the MAPK/ERK1/2 pathway. Study of 11 Italian and French THC2 pedigrees showed no major alterations in MK differentiation, but a profound defect in proplatelet (PPT) formation, leading to thrombocytopenia. We demonstrated that the mechanism underlying this alteration in PPT formation may be ascribed
ANKRD26 was less expressed in mature (CD41+CD42+) compared to their normal counterparts, where its expression was nearly abolished (Figure 2C). Mature MKs (CD41+CD42+) from THC2 patients showed a persistent expression of the ANKRD26 gene in contrast with immature (CD41+CD42–) MKs sorted at day 9 of culture (Figure 1). When immature MKs were sorted on CD41 expression at day 6 and its expression diminished along MK differentiation (Figure 2A). The ANKRD26 gene expression during 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 −347 nt to +1 nt 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 a 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). Frequently, 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 GPla (CD49b), the α subunit (α2) of a transmembrane receptor for collagen, was detected in platelets of THC2 patients (1). Interestingly, we did not
observe a decrease in GPIa expression and in stress fiber formation upon activation of αβ1 (GPIa/GPIIIa) integrin by MK adhesion to fibrillar collagen type I (n = 3 for controls, n = 4 for patients) (Figure 4C and Supplemental Figure 1B). 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 knockdown 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.
(Figure 6, C and D). 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 (DNMEKGF) 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...
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/P) 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) supplemented with 10 ng/ml TPO, IL-3, SCF, and FLT3-L and transduced with concentrated lentiviral (shRUNX1, shFLI1, shANK1, shANK2, shSCR [control]) or retroviral (DNMEK1, MEK1a) particles for 12 hours at 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.** 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.**

**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.

**CHIP and promoter activity assays.** CHIP assays were performed with a CHIP assay kit (Merek Millipore) using the anti-RUNX1 Ab and the anti-FLI1 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.

**Luciferase reporter assay.** The 5′ UTR region of the ANKRD26 gene (from –347 nt to +1 nt) was amplified by PCR on control or patient DNA and cloned into the reporter pluc-MCS plasmid (Stratagene). HEL cells were cotransfected with the reporter plasmid plucANK without (WT) or with mutations found in 3 different TH2 pedigrees (c.119C>A, c.127A>T, c.127delAT) and with TK-Relnilla 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). The luciferase activity was measured with an GloMax 96 Microplate Luminometer with Dual Injectors (Promega). Sequences of primers used for promoter cloning are listed in Supplemental Table 2.

**Western blot assays.** For Western blot analysis, the UT7/HA-MPL transduced by lentivirus encoding for shRNA against ANKRD26 (shANK) or for control (scramble) shSCR was starved overnight (5% SVF, without cytokines) and stimulated by TPO (20 ng/ml). Primary MKs were derived from control or patient blood CD34+ cells in the presence of TPO and SCF. At day 8 of culture, they were starved for 24 hours without cytokines and stimulated by TPO (50 ng/ml). Nuclear and cytoplasmic extracts were pre-
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 Jele JEM-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.

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