

MiR-205 is downregulated in hereditary hemorrhagic telangiectasia and impairs TGF-beta signaling pathways in endothelial cells

Sebastien P. Tabruyn · Sylvain Hansen · Maria-Luisa Ojeda-Fernández · Nicolas Bovy · Roberto Zarrabeitia · Lucia Recio-Poveda · Carmelo Bernabéu · Joseph A. Martial · Luisa-Maria Botella · Ingrid Struman

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Abstract Hereditary hemorrhagic telangiectasia (HHT) is an autosomal dominant disorder characterized by arteriovenous malformations and hemorrhages. This vascular disease results mainly from mutations in 2 genes involved in the TGF- β pathway (ENG and ALK1) that are exclusively expressed by endothelial cells. The present study identified miR-27a and miR-205 as two circulating miRNAs differentially expressed in HHT patients. The plasma levels of miR-27a are elevated while those of miR-205 are reduced in both HHT1 and HHT2 patients compared to healthy controls. The role of miR-205 in endothelial cells was further investigated. Our data indicates that miR-205 expression displaces the TGF- β balance towards the anti-angiogenic side by targeting Smad1 and Smad4. In line,

overexpression of miR-205 in endothelial cells reduces proliferation, migration and tube formation while its inhibition shows opposite effects. This study not only suggests that detection of circulating miRNA (miR-27a and miR-205) could help for the screening of HHT patients but also provides a functional link between the deregulated expression of miR-205 and the HHT phenotype.

Keywords Hereditary hemorrhagic telangiectasia · microRNA · TGF-beta

Introduction

Hereditary hemorrhagic telangiectasia (HHT) or Rendu–Osler–Weber syndrome is an autosomal dominant vascular disorder characterized by recurrent nose bleeding telangiectases in mucosa and internal arteriovenous malformations (AMV-direct arterio-venous connections lacking intervening capillaries). AVMs that occur in the lungs, brain, or gastrointestinal tract can cause life-threatening complications secondary to either hemorrhages or the shunting of blood through abnormal blood vessels. No cure for HHT has been found and there is a current need to find new effective drug treatments for the disease. HHT is diagnosed on clinical grounds. To be considered as an HHT patient, three or more of the following diagnostic criteria must be present: spontaneous-recurrent epistaxis, mucocutaneous telangiectases, internal AVMs, and/or a first degree relative with HHT. The diagnosis is declared possible or suspected when two criteria are present and unlikely when they are fewer than two [1]. Since HHT is a clinically heterogeneous disorder, with symptoms differing even among the members of a same family, it is difficult to establish a proper diagnosis.

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S. P. Tabruyn · S. Hansen · N. Bovy · J. A. Martial · I. Struman (✉)
Unit of Molecular Biology and Genetic Engineering, GIGA, University of Liège, Sart-Tilman, 4000 Liège, Belgium
e-mail: i.struman@ulg.ac.be

M.-L. Ojeda-Fernández · L. Recio-Poveda · C. Bernabéu · L.-M. Botella
Centro de Investigaciones Biológicas (CIB), Consejo Superior de Investigaciones Científicas (CSIC), Madrid, Spain

M.-L. Ojeda-Fernández · L. Recio-Poveda · C. Bernabéu · L.-M. Botella
Centro de Investigación Biomédica en Red de Enfermedades Raras (CIBERER), Madrid, Spain

R. Zarrabeitia
Department of Internal Medicine, Hospital de Sierrallana, Torrelavega, Spain

There are two main types of HHT. Type 1 is due to mutations in the *endoglin* gene, encoding an accessory endothelial transforming growth factor- β (TGF- β) receptor. Type 2 is caused by mutations in *ALK1* (*ACVRL1*; activin receptor-like kinase 1) gene, encoding a TGF- β type I receptor expressed in endothelial cells. In both, HHT1 and HHT2, the TGF- β signaling pathway of endothelial cells is affected [2]. TGF β superfamily ligands mediate their effects through heteromeric complexes of type I and type II receptors. Upon ligand binding to type II receptor, the latter is activated and phosphorylates the TGF- β type I receptor, which in turn phosphorylates specific R (receptor-regulated)-Smads that can then interact with the Co (common-mediator)-Smad4 and translocates to the nucleus to regulate transcription of specific target genes, usually interacting with other transcription factors [3, 4]. In endothelial cells, TGF- β 1 can activate two distinct type I receptor/Smad signaling pathways with opposite effects on angiogenesis [5]. TGF- β 1, in most cell types, predominantly signals via the type I receptor ALK5 leading to the activation of Smad2/3 and transcription of the corresponding target genes, such as PAI-1 (plasminogen activator inhibitor-1) which in endothelial cells is associated with cell quiescence. In addition in endothelial cells, TGF β 1 can also signal via ACVRL1/ALK1 which leads to phosphorylation of R-Smad1/5/8 with the consequent activation of targets distinct from ALK5, such as ID1 (inhibitor of DNA binding 1) which is associated with cell migration, proliferation and angiogenesis.

MicroRNAs (miRNAs) are short (± 22 nucleotides long) non-coding RNAs that repress gene expression post-transcriptionally by targeting the 3'-untranslated region (3'UTR) of specific mRNAs [6]. MiRNAs play a major role in vascular biology [7–9] and “angio-miRs” (miRNAs that stimulate or repress angiogenesis) have opened up a novel aspect for therapeutics associated with deregulated angiogenesis [10] and vascular diseases [11]. Recently, blood-based miRNA detection, measuring miRNAs in the plasma, protected from endogenous RNase activity included in exosomes or in association with proteins, has emerged as a promising diagnostic tool.

In this study, we identified a circulating miRNA signature that could help identify HHT patients. We observed that levels of miR-27a are significantly higher while levels of miR-205 are significantly lower in plasma from HHT patients compared to healthy controls. The role of miR-27a in promoting angiogenesis was previously described [12] but the role of miR-205 in endothelial cells was unknown so far. We found that miR-205 reduces EC proliferation, migration and tube formation. In addition, we demonstrated that the expression of miR-205 affects TGF- β pathway, by targeting Smad1 and Smad4. This study is the first to establish a link between miRNA expression and the

HHT disorder and paves the way for developing better diagnostic tools for HHT patient screening.

Results

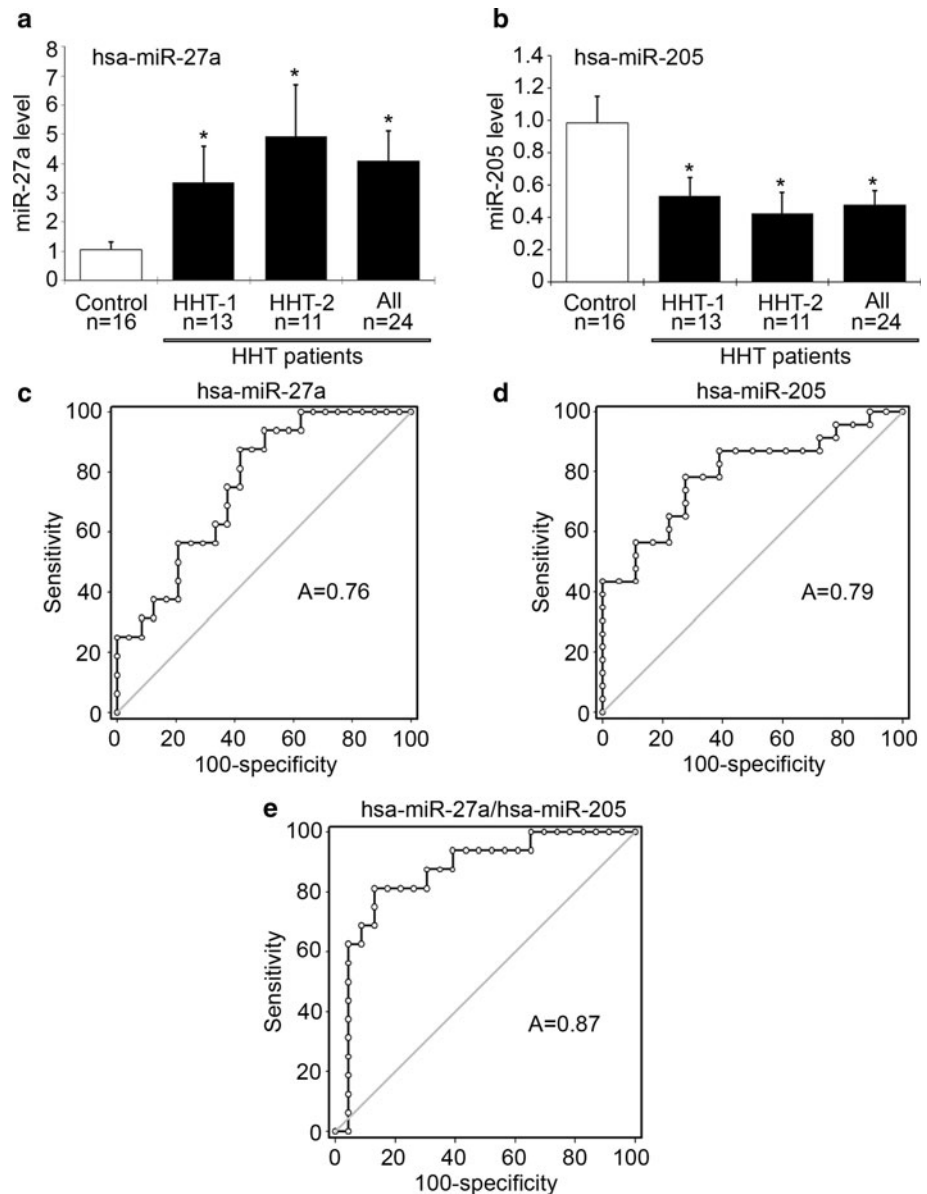
Circulating levels of miR-27a and miR-205 are altered in HHT patient plasma

In order to identify specific biomarkers of HHT, we performed a miRNA expression profiling, using miRNA PCR panels (Exiqon) of plasma samples from HHT patients (2 HHT1 and 2 HHT2) and 4 healthy controls (Supplementary Table 1). This pilot study suggests that miRNAs belonging to the miR-23a-27a-24-2 cluster were more abundant in the plasma from HHT patients while miR-205 was less abundant in plasma from HHT patients compared to healthy controls. MiR-27a and miR-205 were chosen for validation, by qRT-PCR, in the plasma samples from a cohort of 24 HHT patients (11 HHT1 and 13 HHT2) and 16 healthy controls. Our data showed that miR-27a level was significantly elevated in HHT patient plasma samples ($P = 0.021$) (Fig. 1a). Conversely, miR-205 level was significantly lower in plasma samples of HHT patients compared to healthy controls ($P = 0.006$) (Fig. 1b). We did not observe any significant differences between HHT1 and HHT2 patients for miR-27a, and miR-205. Receiver operating characteristic (ROC) curve analysis, a plot of the true positive rate against the false positive rate for the different possible cutoff values of a diagnostic test, showed that circulating miR-27a and miR-205 levels were of significant diagnostic value for HHT patients. MiR-27a and miR-205 yield an area under the curve (AUC) of 0.76 (Fig. 1c) and 0.79 respectively (Fig. 1d). Taken together miR-27a and miR-205 (ratio miR-27a/miR-205) yield an AUC of 0.87 (Fig. 1e).

MiR-205 impairs angiogenesis

Since endothelial cells are the primary cellular targets of HHT, we investigated the effect of miR-205 on endothelial cell function by overexpressing miR-205 and evaluating the impact of this ectopic expression on the endothelial proliferation, migration and tube formation. Over-expression obtained by transfection of pre-miR-205 (Fig. 2a) significantly decreased the proliferation of HUVECs compared to cells transfected with a pre-miR-control (Fig. 2b). In order to investigate whether miR-205 affects endothelial cell migration, another crucial step of angiogenesis, we performed a wound closure assay, which showed that increasing miR-205 level reduced endothelial cell capacity to close the scratch (Fig. 2c). The role of miR-205 as a modulator of endothelial cell organization

Fig. 1 HHT patients show altered levels of miR-27a and miR-205. Levels of miR-27a (a) and miR-205 (b) were measured in plasma samples of a total of 24 HHT patients [HHT1 (n = 11) and HHT2 (n = 13)] and in 16 healthy controls by TaqMan qRT-PCR. Data are expressed as relative miRNA levels normalized to two spikes-in *C. elegans* miRNAs and are expressed as mean \pm SEM. * $P < 0.05$ versus healthy patients. ROC curve representing the sensitivity and the specificity of miR-27a (c) and miR-205 (d) to discriminate between healthy controls (n = 16) and HHT patients (n = 24). e ROC curve obtained by using the ration between miR-27a and miR-205 to discriminate between control (n = 16) and HHT patients (n = 24)



into tubes was next evaluated. When seeded onto MatrigelTM, HUVECs develop into a capillary-like vessel network. Increasing levels of miR-205 in HUVECs reduced vascular network formation, as revealed by a lower number in tube branching (Fig. 2d, e). To investigate the phenotypic effect of a reduced level of miR-205 in endothelial cell, HUVECs were transfected with anti-miR-205. Blockade of miR-205 increased HUVECs proliferation (Fig. 2f), migration (Fig. 2g) and tubulogenesis (Fig. 2h) compared to cells transfected with control anti-miR.

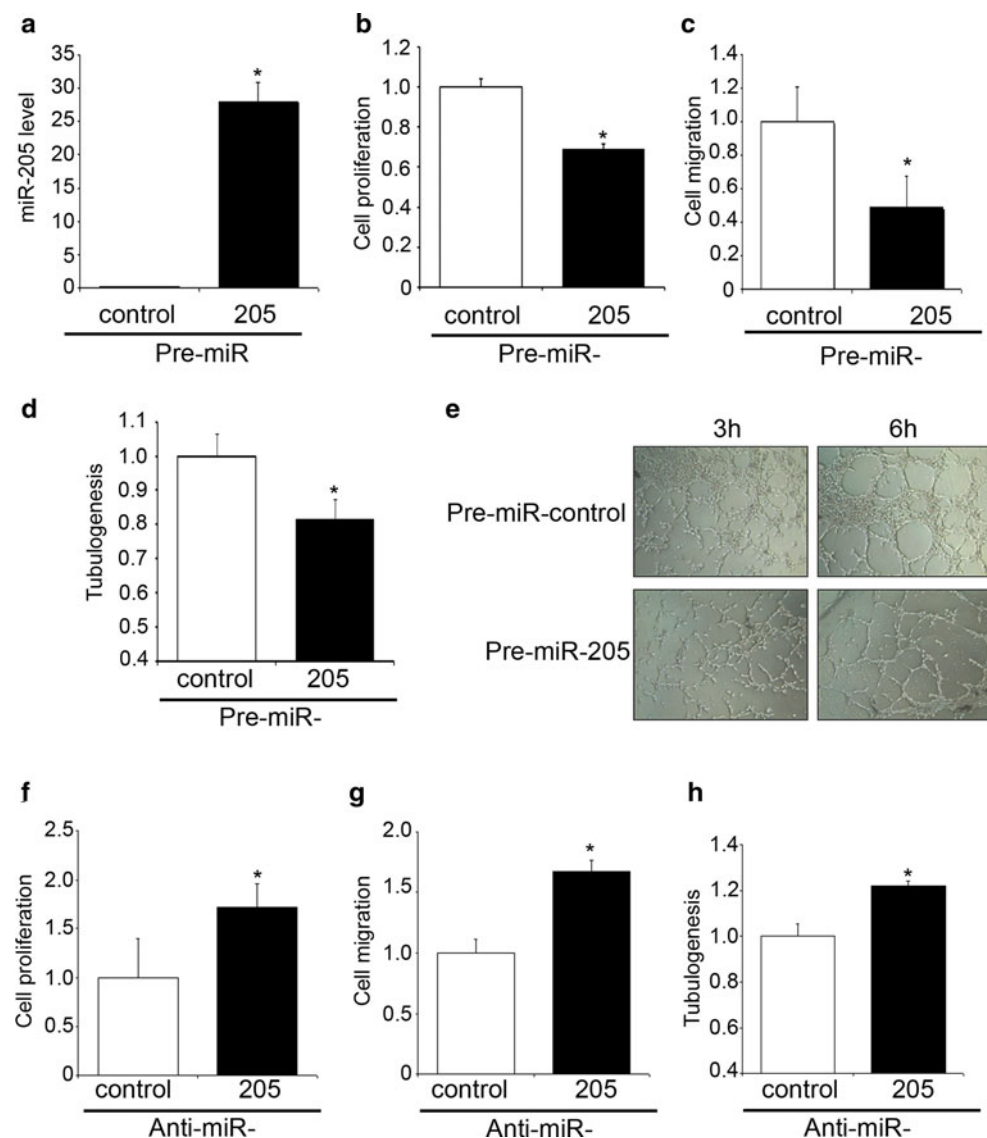
MiR-205 alters TGF- β signaling in endothelial cells

TGF- β signaling is the main pathway affected in HHT endothelial cells. As endothelial cells express two types of

TGF- β type I receptors, ALK5 and ALK1/ACVRL1, the influence of miR-205 on both pathways was first investigated by measuring, by qRT-PCR, the RNA expression levels of two downstream targets of each pathways: ID-1 whose expression is under the control of the TGF- β /ALK1/Smad1/5/8 pathway and PAI-1 whose expression is under the control of the TGF- β /ALK5/Smad2/3 pathway [5, 13, 14].

Over-expression of miR-205 by pre-miR-205 transfection in HUVECs resulted in a significant reduction of ID-1 (Fig. 3a) and a significant increase of PAI-1 mRNA levels (Fig. 3b). These results suggest that both TGF- β pathways are affected by miR-205 expression in opposite directions: the TGF- β /ALK1/Smad1/5/8 pathway, whose target is ID1, is repressed, while the TGF- β /ALK5/Smad2/3 pathway,

Fig. 2 Modulation of MiR-205 level impairs endothelial cell proliferation, migration and tube formation. **(a)** Expression level of miR-205 in HUVECs transfected with pre-miR-control and pre-miR-205 by qRT-PCR. HUVECs were transfected with pre-miR-control and pre-miR-205 before **(b)** their proliferation status was measured by measuring the amount of incorporated BrdU **(c)** their relative migration in a scratch assay was measured and **(d)** before being seeded in matrigel to determine their ability to form tube like structures. **(e)** Representative picture of HUVECs tubulogenesis after being transfected with pre-mir-control and pre-miR-205. HUVECs were transfected with anti-miR-control and anti-miR-205 before measuring their **(f)** proliferation status, **(g)** migration and **(h)** ability to form tube-like structures. Data are expressed as mean \pm SD. * $P < 0.05$ versus respective control. $n \geq 3$



targeting PAI-1, is stimulated. To further confirm these results, we analyzed the impact of miR-205 over-expression in assay reporters of the activation of the ALK1/Smad1/5/8 (BRE-Luc reporter) and of the ALK5/Smad2/3 pathway (CAGA-Luc reporter) [15]. Consistent with the results described above, over-expression of miR-205 led to a lower activation of the BRE-Luc reporter (Fig. 3c) while the CAGA-Luc reporter activity was increased (Fig. 3d). These data confirm that miR-205 affects both TGF- β pathways, in an opposite manner, displacing the TGF- β balance in EC towards the anti-angiogenic side.

MiR-205 targets Smad1 and Smad4

In order to unravel the mechanism by which miR-205 affects the TGF- β pathway, we decided to investigate the regulation of two predicted targets of miR-205, namely

Smad1 and Smad4 (TargetsCan, Fig. 4a). These two proteins play a key role in the TGF- β pathway. Over-expression of miR-205 did not significantly affect Smad1 and Smad4 (Fig. 4b) at the mRNA level. However, we observed a drastic reduction of Smad1 and Smad4 (Fig. 4c) at the protein level by miR-205 over-expression. Similarly, inhibition of miR-205 using anti-miR-205 did not significantly affect Smad1 and Smad4 mRNA levels (Fig. 4d) while their protein levels increased (Fig. 4e).

To confirm that Smad1 and Smad4 are directly regulated by miR-205, we constructed luciferase reporter vectors encoding segments of the 3'UTR of Smad1 (human) and Smad4 (human) (WT Smad1 3'UTR and WT Smad4 3'UTR), as well as a control vectors containing 4 mismatches in the predicted miR-205 binding site (Mut Smad1 3'UTR and Mut Smad4 3'UTR). Cotransfection of the Smad1 3'UTR plasmid with pre-miR-205 in HEK293T

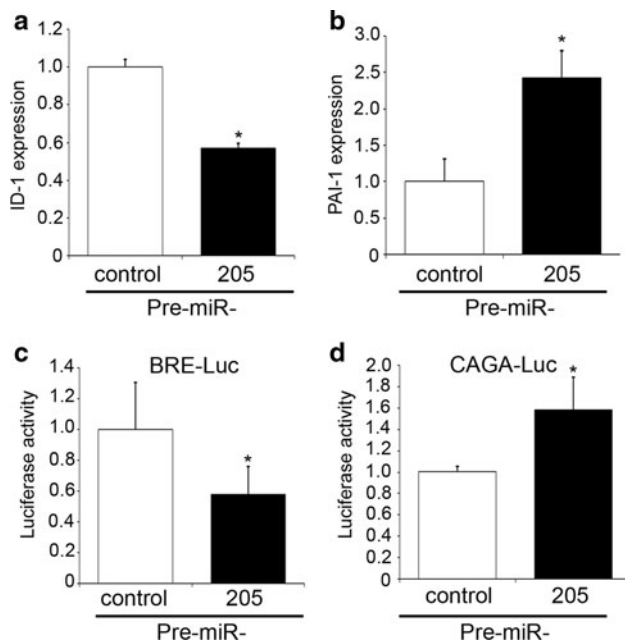


Fig. 3 MiR-205 favors ALK5 pathway in endothelial cells. qRT-PCR expression analysis of ID-1 (a) and PAI-1 (b) in HUVECs transfected with pre-miR-control and pre-miR-205. Luciferase activity in HEK293 cells transfected with (c) a BRE-LUC construct (Smad1/5-ALK1 reporter) or d a CAGA-LUC construct (Smad 2/3-ALK5 reporter) and transfected with pre-miR-control and pre-miR-205. All values are expressed as mean \pm SD, $n \geq 3$. * $P < 0.05$ versus corresponding control

cells resulted in a significant decrease in the luciferase activity compared to cells cotransfected with the pre-miR-control. Over-expression of miR-205 did not decrease the luciferase activity in cells transfected with the mutated 3'UTR target sequence (Fig. 4f). Similar results were obtained with the 3'UTR of Smad4 (Fig. 4g) indicating that both Smad1 and Smad4 are direct targets of miR-205.

TGF- β modulates MiR-27a and miR-205 in endothelial cells

In order to test if the increased level of miR-27a and the reduced level of miR-205 observed in patient plasmas could be due to a perturbation of the TGF- β pathway in endothelial cells, HUVECs were stimulated with low (1 ng/ml) and high (10 ng/ml) TGF- β concentrations before miRNA isolation. While the levels of miR-205 increased only after treatment with low TGF- β concentration, the levels of miR-27a significantly increased at 1 and 10 ng/ml in a concentration dependent manner (Fig. 5).

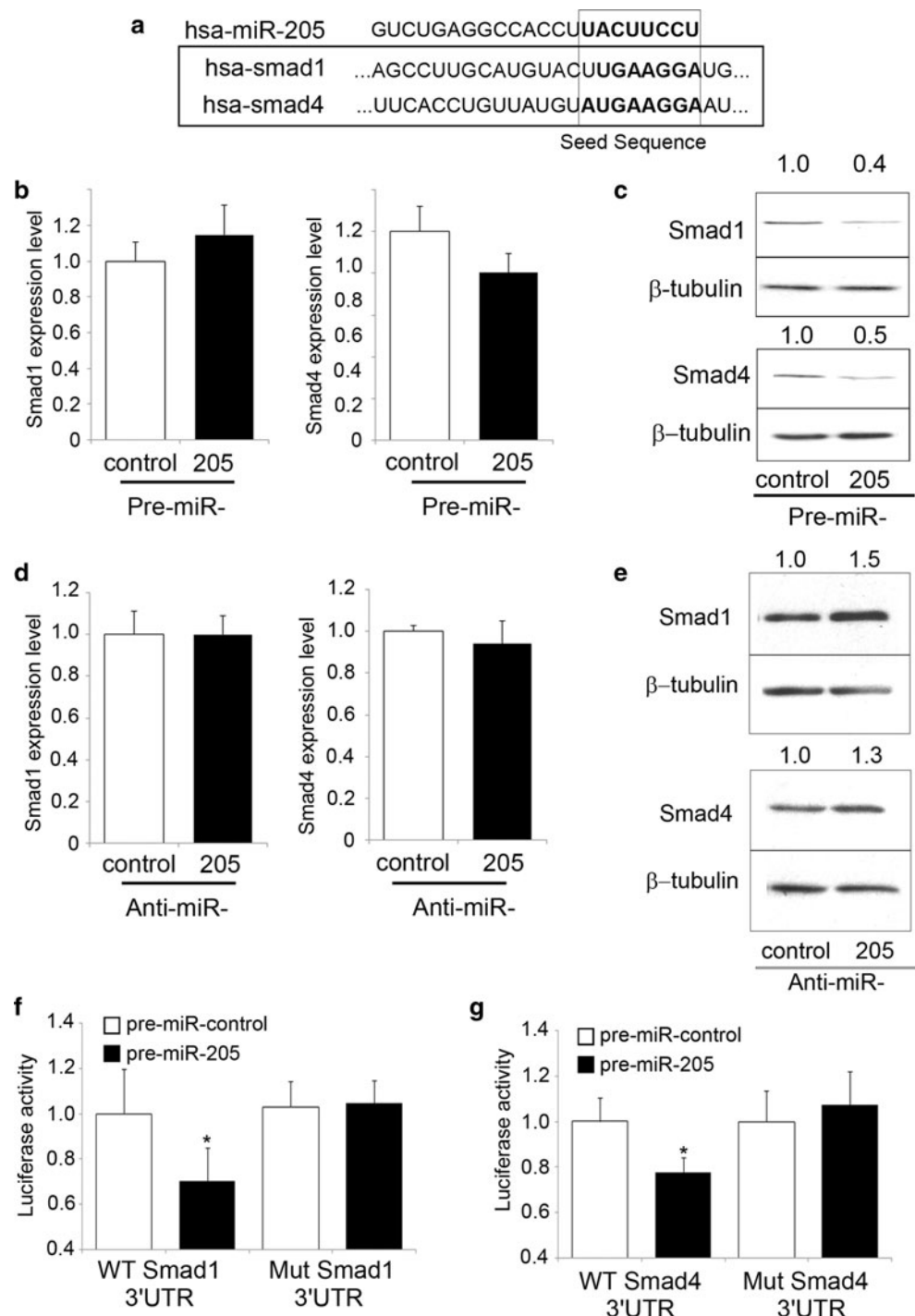
Discussion

The newly discovered accessibility and stability of the circulating miRNAs have opened the way to new

opportunities to screen and monitor a large variety of diseases non invasively [16–19]. Currently, molecular diagnosis of HHT involves sequencing of *ACVRL1/ALK1* and *ENG* coding regions, large deletion/duplication analysis, and if no mutation is identified, analysis of Smad4 coding region. Still, approximately 15 % of HHT cases have no mutations found in the coding regions of these three genes. Our study identified the miR-27a and miR-205 as new circulating biomarkers, which could help to a better screening of HHT patients. Our data show an elevated level of miR-27a and a reduced level of miR-205 circulating in plasma samples from HHT patients, compared to healthy controls. Interestingly, this observation is valid for both HHT1 and HHT2 patients suggesting that the regulation occurring at the level of miR-27a/205 is a common feature independently of the causal mutation of the disease. Further studies will be required to confirm these data including HHT patients with mutations in other genes than *ENG* and *ACVRL1/ALK1*.

It is well established that HHT syndrome is due to alterations in angiogenesis and microvessel density [20]. A further study on blood outgrowth endothelial cells (BOECs) from HHT patients compared to those from control donors, reveals an HHT gene fingerprinting where a set of genes tightly related with angiogenesis was identified [21]. The increased levels of miR-27a (proangiogenic) [12, 22] and the decreased levels of miR-205 (antiangiogenic) are thus consistent with the altered angiogenesis observed in HHT patients due to endoglin or ALK1 haploinsufficiency and will open a new window for future therapies. Other plasma soluble components were previously identified as biomarkers of HHT as sEng and Ang-2 [23], but their lower levels in plasma seemed to be a result of the haploinsufficiency in endoglin or ALK1 on endothelial cells. Since we show here that miR-205, which is expressed in EC, impairs angiogenesis, we could speculate that miR-205 plays an endogenous role in modulating EC function. Consequently, miR-205 might thus not only be a marker of HHT but also a putative therapeutic target. Endoglin and ALK1 are predominantly expressed in endothelial cells and therefore these cells are the primary cellular targets of the disease. We thus hypothesize that the reduced levels of circulating miR-205 reflects a lower miR-205 expression by the endothelial cells. However other cell targets such as smooth muscle, hematopoietic and endothelial precursor cells are also important to promote the lesion secondarily to an endothelial cell defect. Since miR-205 expression levels in endothelial cells are low (Ct value of 29) compared to other miRNAs previously described to play a role in endothelial cells such as miR-221 (Ct values 23) or miR-27a (Ct values of 24), our study does not rule out that other cell types could participate in the secretion of the deregulated miRNAs in the circulation. In addition, it has been

Fig. 4 MiR-205 targets Smad4 and Smad1 in endothelial cells. **(a)** Focus on the pairing sequences of Smad1 and Smad4 3'UTR and miR-205 in human. qRT-PCR expression levels of Smad1 and Smad4, **(b)** in HUVECs transfected with pre-miR-control and pre-miR-205. $n \geq 3$, no significant difference. Protein levels (Western blot) of Smad1 and Smad4, **(c)** in total protein extracts from HUVECs transfected with pre-miR-control and pre-miR-205. qRT-PCR expression levels **(d)** and protein levels (Western blot) **(e)** of Smad1 and Smad4 from HUVECs transfected with anti-miR-control and anti-miR-205. Luciferase activity from Smad1 3'UTR **(f)** and Smad4 3'UTR **(g)** WT and mutated reporter plasmid and the cotransfected into HEK293T cells with pre-miR-control or pre-miR-146a. Data are mean \pm SD ($n \geq 3$). * $P < 0.05$ versus corresponding pre-miR-control



recently proposed that the transfer of microRNAs by exosomes could be a new mechanism of communication between cells [24–26]. Therefore, one can speculate that the reduced level of miR-205 in the plasma of HHT patients, even if primary caused by endothelial cells, could also affect the phenotype of other target cells. In addition, the mechanisms or miR-205 regulation in EC remains to be elucidated.

We showed in vitro that treatment of endothelial cells with a low TGF- β concentration increased miR-205 level. Therefore, one possible mechanism would be that miR-205 expression in endothelial cells is regulated by the TGF- β through the ALK1/Smad1/5/8 pathway. As this pathway is reduced in the HHT patients, the resulting levels of miR-205 would be decreased. On the other hand, miR-27a level is higher after treatment with TGF- β in a concentration

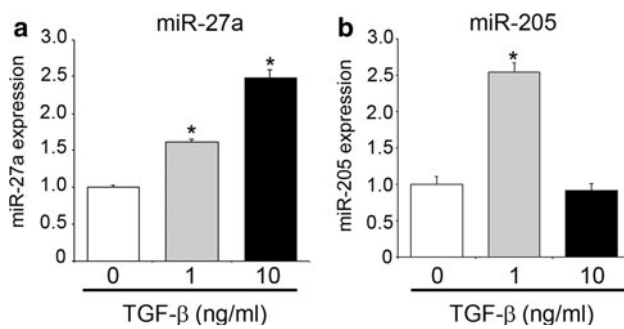


Fig. 5 TGF- β modulates miR27-a and miR-205 expression. Level of miR-27a (a) and miR-205 (b) in HUVECs treated 24 h with TGF- β . All values are expressed as mean \pm SD, $n \geq 3$. * $P < 0.05$ versus corresponding control

dependent manner, starting induction at low concentration and reaching a maximum at high concentration. This is suggestive of a miR-27a expression mainly regulated through the TGF- β /ALK5/Smad2/3 pathway. In a way, both miRNAs, miR-27a and miR-205, are found in HHT patient's plasmas according to the TGF- β pathways status of the endothelial cells. In fact, in HHT patients, the ALK1/Endoglin/Smad1/Smad4 pathway is decreased and the alternative ALK5/Smad2/3 pathway is favored. Therefore, the resulting level of miR-27a would be increased.

The HHT mutations so far reported involve components of a common signal transduction pathway that is altered in HHT [27]. Endoglin is a co-receptor for multiple receptor complexes of the TGF- β superfamily [28]. Endoglin interacts in endothelial cells with ALK-1, an endothelial-specific type I receptor that can associate with TGF- β type II receptor (TGF β RII). Interestingly, TGF β RII in endothelial cells, can associate with two different TGF- β type I receptors: TGF β RI (also known as ALK-5), or ALK-1[5]. ALK-1 and ALK-5 activate different Smad pathways, resulting in opposite endothelial cell responses in terms of pro- or anti-angiogenic gene expression [13, 14, 29, 30]. TGF- β signaling through ALK1/Smad1/5/8 is pro-angiogenic, eliciting proliferation, migration and the transcription activation of target genes such as ID1. While signaling through ALK5/Smad2/3 activates target genes involved in the inhibition of proliferation, migration, matrix deposition, such as PAI-1 and processes associated with the endothelial cell quiescence. Moreover, a fine tuning on signaling and communication of both pathways is necessary. Thus, ALK5 contributes to a TGF β -dependent recruitment of ALK1 to the receptor complex and is required for optimal ALK1 activation. Moreover, ENG recruitment to the TGF- β R2-ALK1-ALK5 receptor complex promotes signaling via the Smad1/5/8 pathway and this indirectly inhibits Smad2/3 signaling via the ALK5/Smad2/3 pathway [5, 13].

In the present work, we have described for the first time, that the miR-205 is downregulated in HHT patients and

plays an anti-angiogenic role in endothelial cells. Indeed, miR-205 expression inhibits proliferation, migration and tube formation. We also show that miR-205, by its ability to target Smad1 and Smad4, plays in EC an important role in the angiogenesis regulation by the TGF- β signaling pathway. These two targets are known to form a heterodimer Smad1/4 that is involved in the proangiogenic signaling pathway TGF- β /ALK1/Smad1/5 controlling the transcription of ID-1. Overexpression of miR-205 in EC would then result in a reduced ALK1 signaling. We suggest that the balance would then be in favor of ALK5 signaling (Fig. 6). In favor with this view is the observed regulation on PAI-1/ID-1 expression: while ID-1 is downregulated upon miR-205 overexpression PAI-1 is upregulated. MiR-205 was first described as a blocker of the EMT transition [31]. Interestingly, miR-205 has also been reported as an inhibitor of the VEGF expression in tumor cells [32]. These data are important in the context of HHT since VEGF levels are elevated in the circulation of HHT patients. We can therefore suspect that the reduced levels of miR-205 could participate to the over-production of VEGF. This excess of VEGF combined with the decrease of miR-205 and the increase of miR-27a in HHT patients would promote an excessive and abnormal angiogenesis.

Leaving aside the arteriovenous malformations which may be present in brain, liver, and lung, the rupture of which would lead to fatal hemorrhages in HHT patients, the more common and disabling problem is epistaxis. So far, attempts to treat epistaxis with pharmacological products have followed different strategies: (1) increasing the stability of the coagulation process with antifibrinolytics [21] (2) increasing the transcription of ENG and ALK1 promoters by SERMs like raloxifene [33], the only orphan drug for the HHT so far designated, or (3) suppressing of excessive and abnormal angiogenesis through antiangiogenic agents such as Bevacizumab (recombinant full-length humanized antibody active against VEGF-A). However, the currently available drugs can result in serious adverse events: frequent and unpredictable side effects for antiangiogenic strategies include thrombosis, hemorrhages, decreased wound healing, and organ perforation. Therefore, alternative therapeutic options are required and therapies based in the correction of the decreased level of miR205 in HHT appears promising.

Materials and methods

Cell culture and reagents

Isolation and cultivation of human umbilical vein ECs (HUVEC, passages 6–11) were described previously [34].

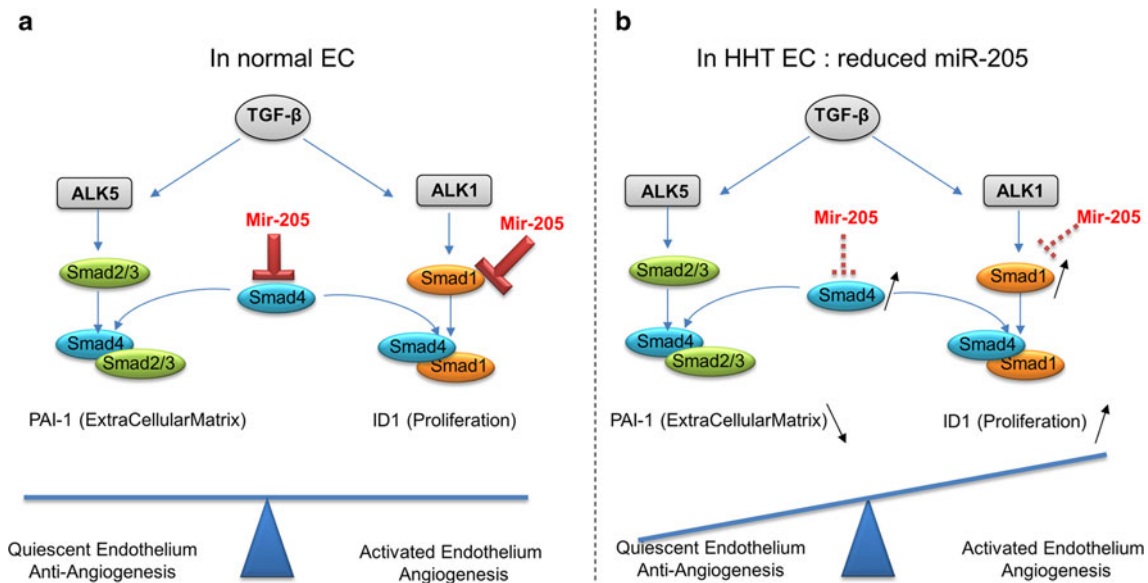


Fig. 6 Mir-205 levels contribute to modulate the equilibrium between proliferation (angiogenesis) and quiescence (deposition of extracellular matrix) in the endothelium by regulating the TGF- β pathway. **(a)** Proposed equilibrium in normal endothelial cells of both TGF- β induced pathways dependent on different type I receptors ALK5 and ALK1. Under normal conditions miR-205 downregulates the levels of

Smad1 and Smad 4. This situation is marked in the figure by the interruption bar for miR-205 over the targets Smad1 and Smad4. **(b)** In HHT patients, the lower levels of miR-205 would favor the signaling through Smad1, although this pathway is partially inactivated by the ALK1 or Endoglin haploinsufficiency, derived of the disease. The partial recovery of Smad1 and Smad4 levels is shown by the arrows

Patients

Peripheral venous blood samples were collected from all donors with EDTA as anticoagulant. Blood samples were centrifuged at 15,000g for 15 min to obtain plasma, and samples were stored at -80°C until analysis. Pilot study using miRNA PCR panels (Exiqon) was performed on 4 control and 4 HHT (2 HHT1 and 2 HHT2) patients. A total of 24 HHT patient samples were evaluated by qRT-PCR; eleven of them were HHT1 and the remaining 13 patients were HHT2. miRNAs plasma levels were also assayed by qRT-PCR in 16 control subjects to establish the normal range. All HHT patients included in the present study were clinically diagnosed following the Curaçao criteria and their genetic mutations were identified by sequencing. Genetic characteristics and clinical manifestations are summarized in Supplementary Table 1.

Transfection of pre-miR-205 and anti-miR-205 in HUVEC

Pre-miR-205 and pre-miR-control (50 nM, Ambion) or anti-miR-205 and Anti-miR-control (25 nM, miRcurry LNA power inhibitor, Exiqon) were transfected into HUVECs with Dharmafect-4 (Dharmacon Research Inc) according to the manufacturer's instructions. After transfection for 24 h, cells were washed and kept for additional

24 h in EGM-2 medium. Functional assays were performed as previously described below and in [35, 36].

Cell proliferation

Transfected cells were plated in 96-well culture plates at a density of 3,000 cells per well in 100 μl of EBM-2 (Lonza) supplemented with 0.5 % serum (for Pre-miR) or EGM-2 (for Anti-miR) and incubated for 40 h. BrdU was added for 8h and proliferation was analyzed using the Cell Proliferation ELISA, BrdU (Colorimetric) (Roche).

Scratch wound migration assay

Transfected cells were plated in 48-well culture plates at a density of 50,000 cells per well in 300 μl of EGM-2 (Lonza) and incubated for 24 h to reach confluence. Using a tip, a wound was made in the monolayer (at time 0). The cells were then washed with PBS and incubated with EBM-2 medium containing 10 ng/ml recombinant bFGF (Pro-mega Corp.) and 50 ng/ml recombinant VEGFa (RELIA-Tech GmbH) (for pre-miR) or EBM-2 supplemented with 0.5 % serum (for anti-miR) for 16 h. The distance between the two sides of the wound was measured with a graduated ocular lens coupled with an Olympus CKX41 microscope (Olympus). The distance between the two sides of the wound after 8 h of migration was subtracted from the distance at time 0 and represented on a graph.

Capillary network formation on a Matrigel matrix

Transfected cells were plated in 96-well culture plates pre-coated with 35 μ l Matrigel per well (BD Biosciences) at a density of 10,000 cells per well in 100 μ l of EGM-2 (Lonza). The cells were incubated for 16 h. Pictures were taken with an Olympus CKX41 microscope (Olympus). Quantitative analysis of network structure was performed with ImageJ software (<http://rsbweb.nih.gov/ij/>) by counting the number of intersections in the network and measuring the total length of the structures.

Luciferase assay (3'UTR reporter assays)

HEK293T cells were transfected with 30 pmol of pre-miR-Control or pre-miR-205 with DharmaFECT-4 (Dharmacon Research Inc). The next day, cells were transfected with 25 ng of the psiCHECK2 vector (Promega) encoding segments of the 3'UTR of the human Smad1 (149 pb spanning the miR-205 seed match sequence) and human Smad4 (415 pb spanning the miR-205 seed match sequence) or their mutated 3'UTR (4 mutations in the miR-205 predicted target site) with JET-PEI (Polyplus transfection) following manufacturer's instructions. Wild-type region of 3'UTR human Smad1 and Smad4 mRNA binding seed sequences of miR-205 are respectively 5'-UGAAGAA-3' and 5'-AUGAAGGA-3'. Mutated region of 3'UTR human Smad1 and Smad4 mRNA binding seed sequences of miR-205 are respectively 5'-AGUACCAU-3' and 5'-AGCAUGCA-3'. Forty-eight hours later, luciferase assay was performed using Dual-Luciferase Reporter Assay System (Promega). *Renilla* luciferase activity was normalized to Firefly luciferase.

Luciferase assay (promoter reporter assays)

HUVEC cells were transfected with 30 pmol of pre-miR-Control or pre-miR-205 with DharmaFECT-4 (Dharmacon Research Inc). The next day, cells were transfected with 25 ng of the Bre-luC [15] and CAGA-Luc [37] vectors kindly provided by Dr Peter ten Dijke (Leiden University Medical Center, The Netherlands) with JET-PEI (Polyplus transfection) following manufacturer's instructions. Forty-eight hours later, luciferase assay was performed using Dual-Luciferase Reporter Assay System (Promega). Firefly luciferase activity was normalized to *Renilla* luciferase.

MicroRNA profiling in plasma

Pilot study using miRNA PCR panels (Exiqon, human panel I, V2) was performed on 4 controls and 4 HHT (2 HHT1 and 2 HHT2) patients. RNA was extracted from plasma as previously described [26] and qRT-PCR was

performed following manufacturer instructions. miRNAs of interest were selected based on their expression levels and differential regulation in control versus HHT patients.

RNA extraction, miRNA expression analysis by TaqMan microRNA assay and quantitative real-time PCR analysis

Total RNAs were extracted with the miRNeasy kit (Qiagen). Taqman methods were used to assess miRNA expression. Briefly, 10 ng RNA were reverse transcribed to cDNA with the Taqman microRNA Reverse Transcription kit and the Taqman microRNA assay stem loop primers (Applied Biosystems). Resulting cDNAs were used for quantitative real-time PCR using Taqman microRNA assay and Taqman universal PCR master mix reagents (Applied Biosystems). Thermal cycling was performed on an Applied Biosystem 7900 HT detection system (Applied Biosystems). The relative miRNA levels were normalized to two internal controls, RNU-44 or RNU-48. For the plasma samples, the relative miRNA levels were normalized to two spikes-in miRNAs: cel-miR-39 and cel-miR-238 (Applied Biosystems).

For mRNA expression analysis, RNAs were extracted with the miRNeasy kit (Qiagen) according to the manufacturer's protocol. cDNA synthesis was performed with 1 μ g total RNA and the iScript cDNA Synthesis Kit (Biorad) according to the manufacturer's instructions. Resulting cDNAs (10 ng) were used for quantitative real-time PCR using the SYBR green method (Roche Applied Sciences). Thermal cycling was performed on an ABI Prism 7900 HT Sequence Detection System (Applied Biosystems). For all reactions, no-template controls were run, and random RNA preparations were also subjected to sham reverse transcription to check for the absence of genomic DNA amplification. Quantitative real-time PCR was performed with SYBR green method (Bioline). Thermal cycling was performed on an Applied Biosystem 7900 HT detection system (Applied Biosystems). The relative transcript level of each gene was normalized to the housekeeping genes cyclophilin-A (PPIA), β -2 microglobulin (B2M). Primers (IDT-DNA) were designed using Primer Express software and selected to span exon-exon junctions to avoid detection of genomic DNA (primer sequences are provided below).

hsa Smad1 for CTCATGTCATTTACTGCCGTGT
 hsa Smad1 rev TATTCGCTGTGTCTTGGAAACC
 hsa Smad4 for CTCATGTGATCTATGCCCGTC
 hsa Smad4 rev AGGTGATACAACTCGTTCGTAGT
 hsa PAI1 for ACGTGGTTTTCTCACCCCTATGG
 hsa PAI1 rev CATGCCCTTGTCATCAATCTTG
 hsa Id1 for CTGCTCTACGACATGAACGG
 hsa Id1 rev GAAGGTCCCTGATGTAGTCGAT

hsa B2M for GAGTATGCCTGCCGTGT
 hsa B2M rev AATCCAAATGCGGCATCT

Preparation of cell extracts

Cells were washed twice with cold PBS and scraped into lysis buffer (25 mM HEPES (pH 7.9), 150 mM NaCl, 0.5 % Triton, 1 mM dithiothreitol, 1 mM phenylmethylsulfonyl-fluoride) on ice. Insoluble cell debris was removed by centrifugation at 10,000g for 15 min. Aliquots of protein-containing supernatants were stored at -80°C . Protein concentrations were determined by the Bradford method, with the Bio-Rad protein assay reagent (Bio-Rad Laboratories).

Western blot analysis

Soluble cell lysate (30 μg) was resolved by SDS-PAGE (12 %) and transferred to a polyvinylidene fluoride membrane (Milipore Corp.). Blots were blocked overnight and probed with primary antibodies: anti-Smad1 (D59F7, Cell Signaling Technology), anti-Smad4 (sc-7966, Santa Cruz Biotechnology), and anti- β -tubulin (ab6046, Abcam). After washes with Tris-buffered saline containing 0.1 % Tween 20, antigen-antibody complexes were detected with peroxidase-conjugated secondary antibody (Cell Signaling Technology) and an enhanced fluoro-chemiluminescent system (ECL; Pierce Biotechnology).

Statistics

All values were expressed as mean \pm SD (or SEM for patient data). Comparisons between different conditions were assessed using the Student *t* test. A *P* value of <0.05 was considered statistically significant. The plasma level of the different miRNA was used as the input to plot receiver characteristics curves (ROC). ROC curves are displayed as the true positive rate (Sensitivity) versus 1 minus the false positive rate (Sensibility). The area under the ROC curve (AUC) is a measure of discrimination accuracy.

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Conflict of interest The authors declare that they have no conflict of interest.

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