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Marcello Ceci, European Brain Research Institute
Kristy Welshhans, Kent State University
Maria Teresa Ciotti, Institute of Neurobiology and Molecular Medicine, Italy
Rossella Brandi, European Brain Research Institute
Chiara Parisi, European Brain Research Institute
Francesca Paoletti, European Brain Research Institute
Luana Pistillo, European Brain Research Institute
Gary Bassell, Emory University
Antonino Cattaneo, European Brain Research Institute

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RACK1 Is a Ribosome Scaffold Protein for β-actin mRNA/ZBP1 Complex

Marcello Ceci¹, Kristy Welshhans², Maria Teresa Ciotti³, Rossella Brandi¹, Chiara Parisi¹, Francesca Paoletti¹, Luana Pistillo¹, Gary J. Bassell⁴, Antonino Cattaneo¹,⇑

¹European Brain Research Institute (EBRI), Rome, Italy, ²Department of Biological Sciences, Kent State University, Kent, Ohio, United States of America, ³Institute of Neurobiology and Molecular Medicine-CNR, Rome, Italy, ⁴Departments of Cell Biology, Neurology, Emory University School of Medicine, Atlanta, Georgia, United States of America, ⁵Scuola Normale Superiore di Pisa, Pisa, Italy

Abstract

In neurons, specific mRNAs are transported in a translationally repressed manner along dendrites or axons by transport ribonucleic-protein complexes called RNA granules. ZBP1 is one RNA binding protein present in transport RNP, where it transports and represses the translation of cotransported mRNAs, including β-actin mRNA. The release of β-actin mRNA from ZBP1 and its subsequent translation depends on the phosphorylation of ZBP1 by Src kinase, but little is known about how this process is regulated. Here we demonstrate that the ribosomal-associated protein RACK1, another substrate of Src, binds the β-actin mRNA/ZBP1 complex on ribosomes and contributes to the release of β-actin mRNA from ZBP1 and to its translation. We identify the Src binding and phosphorylation site Y246 on RACK1 as the critical site for the binding to the β-actin mRNA/ZBP1 complex. Based on these results we propose RACK1 as a ribosomal scaffold protein for specific mRNA-RBP complexes to tightly regulate the translation of specific mRNAs.

Introduction

The localization and translation of mRNAs in specific regions of the cell is an evolutionarily conserved mechanism to regulate the quantity of proteins within specific cellular compartments [1]. In neurons, the dendritic localization of mRNAs and subsequent translation at stimulated synapses is believed to be responsible for long term synaptic plasticity [2,3]. The mRNAs are transported to distal dendrites in a translational silent manner by binding to RNA-binding proteins (RBPs) within specific ribonucleic particles, called transport RNP. In these particles, the RBPs show a dual function: they act both as mRNA transport factors and as translation repressors. At their destinations, neuronal activity stimulates post-translational modifications of RBPs, which promote the release and translation of associated mRNAs.

The Zn2+ binding protein 1 (ZBP1) is one of several RBPs found in RNP whose translational regulation has been extensively studied. ZBP1 binds a wide variety of mRNAs, but only its binding to 3’UTR of β-actin mRNA has been characterized. During growth cone turning, ZBP1 binds the β-actin mRNA, represses its translation and transports it to growth cones [4]. The phosphorylation of ZBP1 by Src, stimulated by Brain-Derived Neurrophic Factor (BDNF), determines the release and the local translation of β-actin mRNA favoring the growth cone [5,6].

The local translation of mRNAs at final destinations is fast and tightly controlled to avoid aberrant protein expression, but the molecular mechanisms that regulate the process are not understood yet. The release of mRNAs occurs on transport RNP [5], which contain, besides RBPs, also eukaryotic initiation factors (eIFs) and ribosomes [5,7,8]. So far it has been established that many RBPs associate to ribosomes, but whether the binding of mRNA-RBP complexes to specific ribosomal proteins is critical to stimulate the post-translational modifications of RBPs and, consequently, the release and translation of the associated mRNAs has not been determined yet.

The role for many ribosomal proteins is mainly structural, whereas for others a double role is emerging: they also participate in the control of specific pathways, as reported by the interaction of some large and small ribosomal proteins with the tumor suppressor p53 [9]. Associated to ribosomes, there are also several proteins whose function is not clear yet. The Receptor Activated C Kinase 1 (RACK1) protein is one example. RACK1 has been identified as a scaffold protein for the activated PKCβII [10], but several reports have demonstrated its involvement in multiple biochemical pathways [11,12,13]. The presence of RACK1 on ribosomes is well documented in mammalian as well as in yeast cells [14,15,16]. Moreover by crystallographic studies of Saccharomyces cerevisiae subunit and of Tetrahymena thermophila 40S ribosomal subunit show that RACK1 localizes at head the back of 40S head region and makes direct contact with the ribosomal RNA [17,18]. RACK1 has been also demonstrated to be recruited in stress granules (SGs) [19]. These structures appear in the cytoplasm in response to stress conditions [heat stress, glucose deprivation, hypoxia] and are constituted by 40S ribosomal subunits, eIFs and many RBPs, such as ZBP1, FMRP and Staufen [20,21]. Despite the evidence showing RACK1 associated to
ribosomes, its possible role in protein synthesis has not been identified. In this study, we show that RACK1 represents a docking site on ribosomes for the β-actin mRNA/ZBP1 complex and that the binding of this complex to RACK1 is critical to the release and translation of β-actin mRNA. This study defines RACK1 as a "ribosome receptor" and provides a new insight into the molecular mechanism for translational control and the release of β-actin mRNA

**Results**

**RACK1 colocalizes on transport RNPs in vivo and in vitro**

RACK1 has been found to be abundantly and widely expressed in almost all areas of the central nervous system. Many studies concerning its scaffold function have been carried out on neuronal cultures. Previous works showed that RACK1 was distributed in cell bodies and along dendrites of adult tissue mouse [14,22]. Immunofluorescence studies conducted on cultured embryonic cortical neurons confirmed the sub-cellular localization of RACK1 in soma (Fig. 1A) and along dendrites and axons as shown by colocalization with MAP2 and Tau proteins respectively (Figure S1A and S1B). Moreover, RACK1 appeared in the form of granules in cell body and in neurites (Fig. 1A). To verify whether this granular pattern was also visible in vivo, we immunostained slices of adult mouse hippocampus by anti-RACK1 antibody. In adult tissue, RACK1 showed a granular distribution identical to that in cortical neurons (Fig. 1B). This demonstrated that RACK1 distributed in granular form both in vitro and in vivo.

To verify whether the distribution of RACK1 was affected by neuronal activity, cortical neurons were depolarized with 50 mM KCl for 15 min and, next, immunostained by anti-RACK1 antibody. KCl significantly increased the number of granules labeled by RACK1, indicating the sensitivity of its distribution to membrane depolarization (Figure S2). Many RBPs and ribosomal proteins of transport RNPs show a similar pattern to that observed by RACK1. Moreover, they redistribute as RACK1 in response to KCl stimuli [23]. Thus, we verified whether RACK1 might be part of transport RNPs. A co-immunostaining analysis in primary cortical neurons with anti-RACK1 and anti-ZBP1 antibodies, a specific marker for transport RNPs [24] revealed an extensive colocalization of RACK1 and ZBP1 proteins in the soma. Along neurites some particles stained by RACK1 were also positive for ZBP1, while others are located next to each other (Fig. 1C). To further confirm the localization of RACK1 on transport RNPs, the granular pattern of RACK1 was investigated in cortical neurons transfected with GFP-ZBP1, which is known to be recruited in RNPs [5]. We found that, in transfected neurons, the particles stained by RACK1 strongly colocalized with those of GFP-ZBP1 in soma and in neurites (Fig. 1D). Taken together, these results confirmed the localization of RACK1 on transport RNPs of cortical neurons.

**RACK1 interacts with ZBP1 through its Src phosphorylation and binding site (Y246)**

The strong colocalization of RACK1 with ZBP1 on transport RNPs prompted us to investigate whether RACK1 might interact with ZBP1. To this aim, human SH-SY5Y neuroblastoma cells, expressing low amount of ZBP1 (data not shown), were transfected with Flag-ZBP1 cDNAs and a co-immunoprecipitation assay was performed from total lysates. As revealed by western blotting analysis on eluted protein from Flag and Flag-ZBP1 immunoprecipitation, RACK1 associated to Flag-ZBP1 (Fig. 2A), indicating a specific interaction with ZBP1.

Next, we asked how the interaction of RACK1 with Flag-ZBP1 might be regulated. It has been reported that RACK1 is phosphorylated by Src kinase and that this phosphorylation is critical for the binding of Src to RACK1. Moreover, we previously reported that ZBP1 protein is a substrate of Src tyrosine kinase [6,13]. Thus, we postulated that Src kinase might control the RACK1-ZBP1 interaction. We studied the binding of RACK1 to ZBP1 in response to treatments known to activate Src, such as dibutyryl-cAMP (db-cAMP), Phosphoryl Adenylate cyclase-activating polypeptide (PACAP) or db-cAMP [25,26] in presence of the specific Src inhibitor, PP2. In the db-cAMP or PACAP stimulated cells, we found that the interaction of RACK1 to Flag-ZBP1 was reduced, while PP2 restored the complex at levels comparable to control cells (Fig. 2C). On the contrary, BDNF increased the binding of RACK1 to Flag-ZBP1, while PP2 reduced the association between the proteins (Fig. 2D). These results indicated that Src may associate/dissociate the Flag-ZBP1/RACK1 complex, depending on which extracellular signal stimulates its kinase activity.

To further investigate how Src may regulate the interaction of RACK1 with ZBP1, we co-expressed, in SH-SY5Y cells, Flag-ZBP1 with GFP-RACK1WT, which is reported to inhibit the Src kinase activity [11,13], or with GFP-RACK1 mutated in Src phosphorylation and binding site (tyrosine 246, Y246) [17,18]. Moreover, Src removes the translational repression on ZBP1 protein phosphorylated at Tyr396 [6]. The results presented so far establish that the Src phosphorylation and binding site Y246 of RACK1 is critical for the association of RACK1 to ZBP1. Therefore, we asked whether, through this site, RACK1 may represent a scaffold protein for β-actin mRNA/ZBP1 complex on ribosomes. To verify this hypothesis, we investigated the localization of Flag-ZBP1 on ribosome in GFP-RACK1Y246F overexpressing cells. Ribosomal profiles were conducted on neuroblastoma cells co-expressing Flag-ZBP1 with GFP, GFP-RACK1WT or with GFP-RACK1Y246F cDNAs. Immunoblotting with Flag, GFP and RACK1 antibodies, assessed on collected fractions, revealed that Flag-ZBP1, GFP-RACK1WT and GFP-RACK1Y246F co-sedimented in free ribosomes and polysomes as endogenous RACK1. As expected, the presence of GFP-RACK1Y246F on ribosomes greatly reduced the amount of Flag-ZBP1 on fractions corresponding to 40S and 60S/80S subunits (fractions 2–4 in Fig. 3A, and graphic in 3B). Since the Y246F mutation did not affect GFP-RACK1Y246F nor endogenous RACK1 levels in ribosomal fractions (Fig. 3A), the low amount of Flag-ZBP1 on ribosome subunits was dependent on the decrease of its binding to GFP-RACK1Y246F.
Given that Src may regulate the RACK1/Flag-ZBP1 complex formation, we evaluated whether GFP-RACK1Y246F expression also impaired the localization of Src on ribosomes. An active role of Src in translational control has been documented [27,28], but its direct association to translational machinery has not been demonstrated yet. Ribosomal profiles of SH-SY5Y cells, showed that Src co-sedimented in the same fractions containing eIF4E, an eukaryotic factor of 48S complex [29] (Figure S4A). Moreover, the binding of Src to the translational machinery was confirmed by its co-purification with RACK1 and poly(A)-binding protein (PABP), in an oligo-dT pull down assay as performed in Text S1 (Figure S4B). In SH-SY5Y co-expressing Flag-ZBP1 and GFP-RACK1Y246F cells, the localization of Src on ribosomes was reduced, indicating that the GFP-RACK1Y246F on ribosomes also impaired the binding of Src to 40S/60S and to 80S monosomes (Fig. 3A and graphic in 3C).

The binding of the β-actin mRNA to ZBP1 [5,6] and the impairment of association of Flag-ZBP1 to GFP-RACK1Y246F at the ribosome level led us to investigate whether the amount of β-actin mRNA bound to ribosomes and its translation were also affected. To this aim, the level of β-actin mRNA was measured by qRT-PCR on total RNA purified from translationally inactive (fractions 2–3 of ribosomal profile in Fig. 3A) and translationally active fractions (polysomal fractions 5–8). The assay was performed in Flag-ZBP1 overexpressing cells transfected with GFP, GFP-RACK1wt or GFP-RACK1Y246F cDNAs. In cells co-expressing Flag-ZBP1 and GFP-RACK1wt the amount of β-actin mRNA was increased in both translationally inactive and in polysomal fractions (Fig. 3D). The GFP-RACK1Y246F overexpression greatly reduced the level in both fractions compared to those of GFP-RACK1wt, indicating a low rate of translation. Moreover, the total β-actin expression mRNA was not affected by the GFP-
RACK1wt and GFP-RACK1Y246F overexpression (Figure S5). These results demonstrated that the decrease of β-actin mRNA on ribosomes and of its translation was not dependent on transcriptional control, but on the decrement of GFP-RACK1Y246F/Flag-ZBP1 complex on ribosomes.

The release of β-actin mRNA from ZBP1 is an essential step for its translation. Therefore, we asked whether GFP-RACK1Y246F might also affect the release of β-actin mRNA from ZBP1. We quantified the amount of β-actin mRNA bound to Flag-ZBP1 by qRT-PCR assay on RNA purified by Flag-ZBP1 immunoprecipitation. We conducted the assay on Flag-ZBP1 overexpressing cells transfected with GFP, GFP-RACK1wt and GFP-RACK1Y246F cDNAs. The level of β-actin mRNA associated to Flag-ZBP1 in cells co-transfected with GFP-RACK1Y246F and Flag-ZBP1 cDNAs was greater than that in cells co-transfected with Flag-ZBP1 and GFP or GFP-RACK1wt cDNAs (Fig. 3E). This suggested that the β-actin mRNA accumulated on Flag-ZBP1 protein and its release from Flag-ZBP1 was impaired.

Taken together, these results showed that GFP-RACK1Y246F, affecting the binding of ZBP1 and of Src to ribosomes, reduces the release of β-actin mRNA from Flag-ZBP1 and, consequently, its translation.

Figure 2. Src kinase regulates the RACK1/ZBP1 complex and the Y246 of RACK1 is critical for the binding with ZBP1. A, Endogenous RACK1 interacts with Flag-ZBP1 in an anti-Flag immunoprecipitation assay from total lysate of neuroblastoma Flag-ZBP1-transfected cells. Western blotting for endogenous RACK1 and Flag-ZBP1 on proteins eluted from anti-Flag immunoprecipitation assay. Flag transfected cells were used as negative control. Input represents 5% of total lysate. B and C, Src activity regulates the RACK1-ZBP1 complex formation. B, db-cAMP or PACAP treatments of Flag-ZBP1 transfected cells reduced the binding between RACK1 and Flag-ZBP1, whereas PP2 restored the binding, as in untreated cells. C, BDNF treatments increased the binding of Flag-ZBP1 to RACK1 in Flag-ZBP1 transfected cells. Src inhibition by Src inhibitor PP2 reduced the RACK1-ZBP1 complex stimulated by BDNF. The density value of immunoprecipitated RACK1 is normalized to that of immunoprecipitated Flag-ZBP1 and summarized in both graphics. Data are graphed as means plus S.D. D, The Src binding and phosphorylation site (Y246) of RACK1 is critical for complex formation. Flag-ZBP1 protein co-immunoprecipitated with GFP-RACK1wt and GFP-RACK1Y246F in immunoprecipitation assays using anti-GFP antibody, but in the presence of GFP-RACK1Y246F the binding was reduced. The figures are representative of three independent experiments. The density value of co-immunoprecipitated Flag-ZBP1 is normalized to that of immunoprecipitated GFP-RACK1wt or GFP-RACK1Y246F and summarized in both graphic. Data are graphed as means plus S.D. doi:10.1371/journal.pone.0035034.g002
The translation of β-actin mRNA in the growth cone is reduced by RACK1Y246F

The release and the translational control of β-actin mRNA by Src phosphorylation of ZBP1 plays a critical role in growth cones [6]. The results in neuroblastoma cells indicate that the decrease of the binding of β-actin mRNA/ZBP1 complex to GFP-RACK1wt on ribosomes reduces the release of β-actin mRNA from ZBP1 and, consequently, its translation. Thus, we asked whether GFP-RACK1Y246F overexpression also affected the release and translation of β-actin in growth cones. To this aim, cortical neurons were co-transfected with Flag-ZBP1 and GFP-RACK1wt or GFP-RACK1Y246F cDNAs. The growth cones were analyzed by FISH, to evaluate the amount of β-actin-mRNA, and by immunofluorescence, to detect the level of endogenous β-actin protein (as reported in Materials and Methods and in Text S1). Quantitative fluorescence analysis showed that FISH signals (Fig. 3A) in growth cones of neurons co-expressing GFP-RACK1wt and Flag-ZBP1 were similar to those of neurons co-expressing GFP and Flag-ZBP1 (control neurons). In contrast, a significant increase of the mRNA fluorescence intensity, with respect to Figure 3. RACK1Y246F impairs the binding of ZBP1 and Src kinase to ribosomes and reduces the release and translation of β-actin mRNA. A, ZBP1 and Src are less abundant in ribosomal profile fractions collected from stable GFP-RACK1Y246F overexpressing cells, transfected with Flag-ZBP1 cDNA. The histograms in B and in C summarize the ratio of density values between Flag-ZBP1 B or Src C and GFP-RACK1wt or GFP-RACK1Y246F immunoblots in 2–4 ribosomal fractions. D, The level of β-actin mRNA, measured by qRT-PCR, on RNA isolated from non translating fractions (fractions 2–3 of ribosomal profile reported in A) and from polysomal fractions (fractions 5–8) was decreased in GFP-RACK1Y246F/Flag-ZBP1 cells, as compared to that of GFP-RACK1wt/Flag-ZBP1 expressing cells. E, GFP-RACK1Y246F induced an increase of β-actin mRNA associated to Flag-ZBP1, as measured by qRT-PCR on RNA isolated from Flag-ZBP1 immunoprecipitation of GFP-RACK1Y246F/Flag-ZBP1 cells. In D and E, the values were normalized to those of 18S rRNA and the data are graphed as mean ± S.D.* = p<0.05, # and §§ = p<0.01 second t-test student. In A and D the transfection efficiency was normalized with respect to the amount of Actin protein (Figure S3). In E, the transfection efficiency was normalized with respect to immunoprecipitated Flag-ZBP1 proteins as in Figure 2B.

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Figure 3. RACK1Y246F impairs the binding of ZBP1 and Src kinase to ribosomes and reduces the release and translation of β-actin mRNA. A, ZBP1 and Src are less abundant in ribosomal profile fractions collected from stable GFP-RACK1Y246F overexpressing cells, transfected with Flag-ZBP1 cDNA. The histograms in B and in C summarize the ratio of density values between Flag-ZBP1 B or Src C and GFP-RACK1wt or GFP-RACK1Y246F immunoblots in 2–4 ribosomal fractions. D, The level of β-actin mRNA, measured by qRT-PCR, on RNA isolated from non translating fractions (fractions 2–3 of ribosomal profile reported in A) and from polysomal fractions (fractions 5–8) was decreased in GFP-RACK1Y246F/Flag-ZBP1 cells, as compared to that of GFP-RACK1wt/Flag-ZBP1 expressing cells. E, GFP-RACK1Y246F induced an increase of β-actin mRNA associated to Flag-ZBP1, as measured by qRT-PCR on RNA isolated from Flag-ZBP1 immunoprecipitation of GFP-RACK1Y246F/Flag-ZBP1 cells. In D and E, the values were normalized to those of 18S rRNA and the data are graphed as mean ± S.D.* = p<0.05, # and §§ = p<0.01 second t-test student. In A and D the transfection efficiency was normalized with respect to the amount of Actin protein (Figure S3). In E, the transfection efficiency was normalized with respect to immunoprecipitated Flag-ZBP1 proteins as in Figure 2B.

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The release and the translational control of β-actin mRNA by Src phosphorylation of ZBP1 plays a critical role in growth cones [6]. The results in neuroblastoma cells indicate that the decrease of the binding of β-actin mRNA/ZBP1 complex to GFP-RACK1Y246F on ribosomes reduces the release of β-actin mRNA from ZBP1 and, consequently, its translation. Thus, we asked whether GFP-RACK1Y246F overexpression also affected the release and translation of β-actin in growth cones. To this aim, cortical neurons were co-transfected with Flag-ZBP1 and GFP-RACK1wt or GFP-RACK1Y246F cDNAs. The growth cones were analyzed by FISH, to evaluate the amount of β-actin-mRNA, and by immunofluorescence, to detect the level of endogenous β-actin protein (as reported in Materials and Methods and in Text S1). Quantitative fluorescence analysis showed that FISH signals (Fig. 4A) in growth cones of neurons co-expressing GFP-RACK1wt and Flag-ZBP1 were similar to those of neurons co-expressing GFP and Flag-ZBP1 (control neurons). In contrast, a significant increase of the mRNA fluorescence intensity, with respect to
control neurons, was observed in growth cones of neurons co-
expressing GFP-RACK1Y246F and Flag-ZBP1. This showed that
there was an accumulation of β-actin mRNA in the growth cones
of neurons expressing GFP-RACK1Y246F, probably as a conse-
quency of an impaired release from Flag-ZBP1, as observed
neuroblastoma cells (Fig. 3E). The quantification of immunoflu-
orescence experiments (Fig. 4B) confirmed, at the protein level, the
results of FISH studies. In fact, a strong decrease of fluorescence
signal for endogenous β-actin protein was observed in growth
cones of neurons co-transfected with GFP-RACK1Y246F and Flag-
ZBP1 cDNAs. This indicated a reduction of endogenous β-actin
protein, which might affect the incorporation of β-actin protein
into actin filament and, consequently impair the growth cones.
Thus, the results from growth cones of cortical cells, as well as in
neuroblastoma cells indicated that, the release from Flag-ZBP1
and the translation of β-actin mRNA were inhibited by GFP-
RACK1Y246F over-expression.

The overexpression of GFP-RACK1 stimulates the
dendritic branching out in cortical neurons

The results obtained in growth cones prompted us to investigate
the overall morphological effects induced by RACK1Y246F in
neurons. The dendritic morphology of cortical neurons transfected
with either GFP-RACK1wt or GFP-RACK1Y246F, revealed by
anti-GFP immunofluorescence (Fig. 5A), was very striking.
Quantitative analysis of dendritic morphology measured by Sholl
analysis (as reported in Text S1) showed greater neurite branching
in GFP-RACK1wt expressing cells than in GFP and GFP-
RACK1Y246F transfected neurons. There was a higher number of
thin dendritic arborizations in GFP-RACK1wt expressing cells.
In some cells, the arborizations departed directly from the soma
and in others from the principal dendritic processing (Fig. 5A and
graphic in B). These results demonstrate that, although the Src site
on RACK1 protein is fundamental to regulate the dendritic
outgrowth by controlling the β-actin mRNA translation, RACK1
may contribute to the dendritic arbors through regulation of other
pathways.

Discussion

In this study we show that RACK1 functions as a scaffold
protein on ribosomes for the β-actin mRNA/ZBP1 complex. We
found that the binding of RACK1 to ZBP1 on ribosomes is critical
for the release of β-actin mRNA from ZBP1 and, consequently, for
its translation. The presence of RACK1 on ribosomes has been
reported by several studies [14,15]. Despite the protein sequence
of RACK1 is lacking of RNA-binding domain, the disruption of
yeast RACK1 ortholog’s (Ace1p) position at 40S ribosomal subunit
results in failure of the mRNA binding protein Scp160 to associate

Figure 4. RACK1Y246F induces accumulation of β-actin mRNA in growth cones of cortical cells and reduces its translation. A, Growth
cones of cortical cells co-transfected with Flag-ZBP1wt and GFP-RACK1Y246F show increased levels of β-actin mRNA as measured by Q-FISH. The
method to quantify the signal is reported in supplemental information and the values are summarized in the histogram in the left. B, The translation
of β-actin protein in growth cones of cortical neurons co-transfected with Flag-ZBP1wt and GFP-RACK1Y246F was reduced, as indicated by in Q-IF. All
data are reported as mean ± s.e.m. Significance was set as p<0.05. When significance was adjusted, it is referred to as alpha. β-tubulin
immunofluorescence is shown as a marker for growth cone morphology. Scale bar 10 μm.
doi:10.1371/journal.pone.0035034.g004
with ribosomes [16]. Recently, it has been reported that RACK1 can contribute to the association of miRNA complex to the translating ribosomes [30,31]. Recent papers on the three-dimensional structure of eukaryotic 40S and 80S demonstrate that RACK1 could be available for simultaneous binding to ribosomes and Src and/or PKC [17,18]. Indeed, in the structure of RACK1 bound to 40S ribosome subunit, the Src binding and the PKC binding domains of RACK1 are exposed. Thus, in this context, it is plausible to identify the function of RACK1 on ribosomes through the interaction with Src substrates such as ZBP1.

Here, we demonstrate that RACK1 binds the β-actin mRNA/ZBP1 complex through the Src phosphorylation and binding site Y246. It is well established that phosphorylation of this site by Src is a prerequisite for the binding of Src to RACK1 and for kinase inhibition [11,32]. Our results suggest that, in presence of ZBP1, ribosomal RACK1 preferentially binds ZBP1 at the Y246 site. This interpretation is confirmed by release of β-actin mRNA from Flag-ZBP1 in cells and in growth cones expressing GFP-RACK1wt. In fact, the expression of GFP-RACK1wt demonstrated to inhibit Src kinase activity [11,32], increases the release of β-actin mRNA from Flag-ZBP1 and, consequently, its translation, compared to those of GFP-RACK1Y246F. This indicates that Src can phosphorylate ZBP1 to remove the repression on β-actin mRNA, and demonstrates that Src is active and dissociated from GFP-RACK1wt. This model is fully in agreement with ZBP1 phosphorylation by Src to remove the translational repression at β-actin mRNA in specific sites of neurons [33]. Indeed, the localization of endogenous RACK1 and ZBP1 on transport RNP (Fig. 1c and D) may repress the translation of β-actin mRNA during transport to specific sites. At local destinations, activated Src removes the translational repression by phosphorylating ZBP1.

The role of Src in this molecular mechanism may be distinct depending on which extracellular stimuli induce its activity. The BDNF-activated Src may directly stimulate the association of ZBP1 to RACK1, through a direct binding to both proteins, whereas PACAP38-activated Src may indirectly induce the dissociation of ZBP1-RACK1 complex, through the activation of PKA (Fig. 6B). This latter hypothesis is supported by findings that PKA is activated by Src, following PACAP signalling [26] and by the presence of phosphorylation consensus site for PKA on ZBP1 [34]. Further studies will be essential to establish whether the regulation of ZBP1/RACK1 complex by Src kinase is a further mechanism for translational control of other mRNAs bound to ZBP1.

The translational control by Src activity has been well documented. It has been reported that Src acts on eIFs regulating the mTOR kinase [27,28,35,36]. However, in this mechanism, Src controls the translation of all cap-mRNAs and of the overall protein synthesis. Instead, in the translation of β-actin mRNA, Src, by phosphorylating ZBP1, directly acts on the translational control of specific mRNAs. Our findings show that Src localizes on ribosomes, suggesting that it may act at ribosomal level to control the translation of specific mRNAs. In the absence of ZBP1, Src may bind to ribosomes through the binding and phosphorylation site of RACK1, in agreement with proposed model in crystallographic studies on ribosomal RACK1 [17,18]. In this case, we speculate that, in correlation with the ability of RACK1 to inhibit the Src kinase [13], the binding of Src to RACK1 on ribosome may be necessary to avoid aberrant phosphorylations of some components of translational machinery. The presence of Src on ribosomes opens the possibility to consider new potential Src ribosomal substrates in the regulation of translation.

Figure 5. The dendritic branching out induced by GFP-RACK1wt. A. Immunofluorescence for GFP in cortical neurons transfected with GFP, or GFP-RACK1wt or GFP-RACK1Y246F. Reduced the dendritic arbors induced by GFP-RACK1wt overexpression Scale bar 20 μm B. Graphic reporting the values of dendritic branching seen in A. The values were measured as means of the number of neurite intersections measured by Sholl analysis. Data are graphed as mean ± S.D. doi:10.1371/journal.pone.0035034.g005
Figure 6. Molecular mechanism of RACK1/ZBP1 complex regulating the release and translation of β-actin mRNA. A, Schematic figure showing the interaction of RACK1 with the β-actin mRNA/ZBP1 complex through its Src binding site (Y246) on 40S ribosome subunit of RNPs (left). In presence of the mutation Y246F (right), RACK1 on ribosomes fails to recruit the β-actin mRNA/ZBP1 complex and Src. This impairment blocks the
Several evidences in neurons have shown that RACK1 is involved in multiple neuronal functions by the association to a variety of proteins, such as kinases, phosphatases and critical membrane receptors [23]. In neurons, RACK1 has been localized in cell bodies and along dendrites [14,22]. Here, we show that both in vitro and in vivo RACK1 appeared in granular forms corresponding to transport RNAs. Our study on RACK1 overexpression in cortical neurons indicate that it may regulate the dendritic branching out. We propose that the scaffold properties of RACK1 may favor the binding on ribosomes, besides of ZBP1, also of other protein regulating this neuronal processing. This is corroborated, as seen above, by structural studies which show that RACK1 bound to 40S subunit might bind not only Src kinase, but also PKC kinase. Although it is possible that RACK1 may regulate the branching out through the interaction with other proteins, the results observed on overexpression of RACK1 are in agreement with the critical role of ZBP1 in dendritic arborization development in hippocampal neurons [37]. The identification of which other specific mRNA/RBP complexes are associated to RACK1 and which other mRNAs are translational controlled by RACK1 will help to elucidate the function of RACK1 in neuronal cells.

Materials and Methods

Cell Culture, transfections and stable clones

Human neuroblastoma SH-SY5Y cells, obtained from American Type Culture Collection (ATCC, Rockville, MD) were cultured in DMEM/F12 medium containing 10% of FBS and antibiotics (50 U/ml penicillin and 50 µg/ml streptomycin) at 37°C in 5% CO₂/95% air. Cortical and hippocampal neuron cultures were prepared from Sprague-Dawley E18 embryos, as previously described [6,38]. For transfections, SH-SY5Y cells were transfected with Flag-ZBP1, pEGFP, GFP-RACK1wt and GFP-RACK1Y246F cDNAs using the manufacturer’s protocol of Lipofectamine 2000 (Invitrogen). Stable SH-SY5Y clone cells for GFP plasmids.

For pharmacological treatments, SH-SY5Y Flag-ZBP1 transfected cells were starved 24 hrs and then treated with 100 ng/ml BDNF (Alomone), 1 mM dibutyryl-cAMP, (db-cAMP, Sigma) or 100 nM Pituitary adenylate cyclase-activating polypeptide (PACAP, Sigma) for 30 min at 37°C. Where required, 10 µM Src inhibitor PP2 (Calbiochem) or vehicle were added to the medium for 30 min at 37°C. For cortical embryonic cells, 50 mM KCl was added to Neurobasal B27 15 min before fixation.

Fluorescent In Situ Hybridization (FISH) and Immunofluorescence (IF)

Q-FISH was performed as previously described in Text S1 and in [6]. One digoxigenin-labeled oligonucleotide probe was used to detect rat β-actin mRNA. The sequence of this probe was: 5'-TGAGGAAAGTGGGGTGAGAGCCACGTTGTGAGGATGATGTTCTC-3’. As controls, neurons were hybridized with a DIG-labeled scrambled oligonucleotide probe

Immunofluorescence (IF) experiments

IF experiments were performed essentially as previously described in Text S1 and in [6], and the following primary antibodies were used: mouse anti-RACK1 (BD biosciences, 1:100), polyclonal anti-ZBP1 mouse [39] anti-tubulin (E7, Developmental Studies Hybridoma Bank; 1:1500), rabbit anti-tubulin (Sigma; 1:1000), mouse anti-β actin (AC15, Abcam; 1:1500), rabbit anti-Flag (Sigma; 1:1000), polyclonal anti-GFP (Text S1, 1:2000).

Immunohistochemistry

Three-months-old mice were anesthetized with an excess of 2,2,2-tribromethanol (400 mg/kg) and intracardially perfused with a 4% solution of paraformaldehyde in PBS. Brains were processed for immunohistochemistry to detect RACK1 using the primary antibody seen above. Immunohistochemistry was performed according to the protocols previously described [40]. All experiments were conducted according to national and international laws for laboratory animal welfare and experimentation (EEC Council directive 86/609, OJ L 358, 12 December 1987. Experimentation was approved by Italian Department of health (approval n. 9/2006).

Ribosome profiles, immunoprecipitations and western blotting

For ribosome profiles, wild type or transfected SH-SY5Y cells were lysed in polysomal buffer (10 mM Tris-HCl, 50 mM KCl, 10 mM MgCl₂ and 0.5% NP-40). MgCl₂ was substituted with 10 mM EDTA, for ribosome profile in the presence of EDTA. Total lysate was clarified by centrifugation at 14,000 r.p.m. for 5 min at 4°C and the supernatant was loaded on a continuous sucrose gradient 15–50% in 10 mM Tris-HCl, 50 mM KCl, 10 mM MgCl₂ or 10 mM EDTA. After ultracentrifugation (Beckman) at 37,000 rpm for 2 hrs at 4°C, sucrose gradient was collected in fractions and the profile was obtained by total RNA analysis at 254 nm in Bio-radBiologic LP. Half amount of collected fractions was used to precipitate proteins with 10% trichloroacetic acid (TCA) and the other half used to isolate total RNA. Immunoprecipitations were conducted in polysomal buffer and SH-SY5Y transfected cells were lysate and clarified as seen for ribosome profiles. Next, the supernatant was incubated overnight either with polyclonal-GFP, produced as in Text S1, (1:100) or 30 µl mouse anti-Flag M2 (Sigma-Aldrich) at 4°C. For GFP immunoprecipitation, pre-equilibrated 30 µl of protein G and 30 µl of protein A sepharose resin (GE healthcare) were added and incubated for 1 hour at 4°C. The resins were extensively washed with polysomal buffer and total RNA or proteins were eluted for RNA isolation or for western blotting.
For western blotting, proteins were loaded on SDS-PAGE 10% and transferred on PVDF (Millipore) membrane and the following primary antibodies were used: mouse anti-RACK1 (1:2000), mouse anti-ZBP1 (Huttelmaier 2005, 1:1000), polyclonal anti-GFP (1:1000), mouse anti-Actin (Sigma, 1:1000), polyclonal anti-Src, polyclonal anti-eIF4E, polyclonal anti-PABP (alls from Cell signalling, 1:1000) and mouse anti-GAP43 (1:2000), polyclonal anti-p27BBB/epif6 (kindly provided by prof. Biffo Stefano, 1:1000). Secondary HRP-conjugated anti-mouse or anti-rabbit antibodies and ECL reagent (GE healthcare) were used. For RACK1, mouse HRP-conjugated anti-IgM was used.

RNA isolation and qRT-PCR

Total RNA was purified from immunoprecipitates and ribosomal fractions with TriReagent (Invitrogen) according to manufacturer’s protocol. The purified RNA was used for qRT-PCR. The first strand cDNA template was synthesized from 500 ng of total RNA using random primers and Superscript III reverse transcriptase (Invitrogen, USA). All reactions were performed with SYBR Green PCR Master Mix (BioRad) and carried out in the iCycler (BioRad). Primers for Quantitative PCR (QTR-PCR) analysis were designed with the assistance of Universal Probe Library Software (Roche Applied Science). The following primers were selected to amplify: Homo sapiens 18S (ribosomal 1 forward) 5′-GTAGTTTCGTGGATGCCAC; Homo sapiens 18S (ribosomal 1 forward) 5′-AGGCCAGGAGCTTAACCAAGCCG-3′ and reverse 5′-GTTGGTGGAGCGATTTGTC; Homo sapiens RNA, 18S (ribosomal 1 forward) 5′-AGGGCAGGGACTTAAT- and reverse 5′-GTGGTTGGAGCGATTTTGTC. Relative change of mRNA amount was calculated based DCT method, as described in [41].

Supporting Information

Figure S1 RACK1 along dendrites and axons of embryonic cortical cells. Co-immunostaining of MAP2 (A, green) or Tau (B, green) and RACK1 (red) indicated the localization of RACK1 in dendrites and axons. Scale bar 20 μm. (TIF)

Figure S2 Neuronal activity reorganizes the distribution of RACK1. 50 mM KCl for 15 min increases the number of granules stained by RACK1. In the graphic are summarized the results observed in immunofluorescence in right Scale bar 20 μM. (TIF)

Figure S3 Transfection efficiency. Western blotting for GFP, GFP-RACK1, Flag-ZBP1, RACK1, Src and Actin on total lysate from SH-SY5Y cells co-expressing Flag-ZBP1 and GFP, GFP-RACK1wt or GFP-RACK1Y246F protein. (TIF)

Figure S4 Src is part of the translational machinery. A, Src, as well as eIF4E and RACK1, localized in fractions at the top of the gradient, where 40S accumulated in the EDTA sucrose gradient from SH-SY5Y cells. B, Oligo-dT assay in cortical cells which specifically purifies proteins associated to mRNAs such as RNA binding proteins, 40S, 40S, polyribosomes and translational factors (ref 1 in Text S1). Src was specifically isolated as RACK1 and PABP proteins. p27BBB/epif6, which binds only 60S ribosomal subunit and does not bind mRNAs, was not purified, indicating that the assay was specific for proteins associated to mRNAs. The figure shows the western blots on three independent experiments. (TIF)

Figure S5 The β-actin mRNA expression in GFP-RACK1wt and GFP-RACK1Y246F overexpressing cells. Total β-actin mRNA, measured by qRT-PCR and normalized to 18S rRNA, is not affected by overexpression of GFP-RACK1wt and GFP-RACK1Y246F. (TIF)

Text S1 (DOC)

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Author Contributions

Conceived and designed the experiments: MC AC. Performed the experiments: MC KW LP. Analyzed the data: MC KW. Contributed reagents/materials/analysis tools: RB MC KW MTC FP GB. Wrote the paper: AC MC.

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11. Coyle SM, Gilbert WV, Doudna JA (2009) Direct link between RACK1 and Actin on total lysate from SH-SY5Y cells co-expressing Flag-ZBP1 and GFP, GFP-RACK1wt or GFP-RACK1Y246F protein. (TIF)


