Differential Trypanosome Surface Coat Regulation by a CCCH Protein That Co-Associates with procyclin mRNA cis-Elements

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Abstract

The genome of Trypanosoma brucei is unusual in being regulated almost entirely at the post-transcriptional level. In terms of regulation, the best-studied genes are procyclins, which encode a family of major surface GPI-anchored glycoproteins (EP1, EP2, EP3, GPEET) that show differential expression in the parasite’s tsetse-fly vector. Although procyclin mRNA cis-regulatory sequences have provided the paradigm for post-transcriptional control in kinetoplastid parasites, trans-acting regulators of procyclin mRNAs are unidentified, despite intensive effort over 15 years. Here we identify the developmental regulator, TbZFP3, a CCCH-class predicted RNA binding protein, as an isoform-specific regulator of Procyclin surface coat expression in trypanosomes. We demonstrate (i) that endogenous TbZFP3 shows sequence-specific co-precipitation of EP1 and GPEET, but not EP2 and EP3, procyclin mRNA isoforms, (ii) that ectopic overexpression of TbZFP3 does not perturb the mRNA abundance of procyclin transcripts, but rather that (iii) their protein expression is regulated in an isoform-specific manner, as evidenced by mass spectrometric analysis of the Procyclin expression signature in the transgenic cell lines. The TbZFP3 mRNA–protein complex (TbZFP3mRNP) is identified as a cis-regulator of differential surface protein expression in trypanosomes. Moreover, its sequence-specific interactions with procyclin mRNAs are compatible with long-established predictions for Procyclin regulation. Combined with the known association of TbZFP3 with the translational apparatus, this study provides a long-sought missing link between surface protein cis-regulatory signals and the gene expression machinery in trypanosomes.

Introduction

The pathway of mRNA control in eukaryotes involves regulatory steps at multiple stages. This is reflected by the large investment of eukaryotic genomes in RNA binding proteins, with hundreds of genes in yeasts and mammals being devoted to functions requiring RNA interaction. As the diverse roles of these proteins, and their interactions with specific subsets of mRNAs, are investigated, it is becoming clear that post-transcriptional control represents a regulatory network of a complexity and importance likely greater than transcriptional control [1].

Perhaps the most extreme example of a group of organisms with emphasis on post-transcriptional control is the kinetoplast parasitises. These organisms are of medical, veterinary and economic importance because they are responsible for an enormous burden of disease within the tropics, including a variety of cutaneous and visceral diseases (caused by Leishmania spp.), Chagas disease (caused by Trypanosoma cruzi) and African sleeping sickness (caused by Trypanosoma brucei). Here, an absence of detectable RNA II polymerase promoters for protein coding genes and the general organisation of transcription units into polycistrionic arrays necessitates almost complete reliance on post-transcriptional control for regulated gene expression [2]. Supporting this, the genome of these parasites reveals a complexity and composition of encoded RNA binding proteins exceeding, and distinct from, that found in the crown group of eukaryotic organisms [3,4].

Gene regulation is particularly important in kinetoplastid parasites because their life cycle is complex, involving passage through a mammalian host and within distinct compartments of an arthropod vector [5]. One of the best-characterised life-cycle differentiation events involves exchange of the major surface antigens as African trypanosomes passage from mammalian blood to the midgut of their haematophagous vector, the tsetse fly [6]. In the bloodstream trypanosomes stay ahead of the immune response by expressing, sequentially and hierarchically, thousands of different antigenic surface coats comprised of variant surface glycoprotein (VSG) [7]. However, upon differentiation in the tsetse, the VSG coat is replaced by a family of glycoprophosphatidyl inositol (GPI)-anchored proteins known as Procyclins. There are two types of Procyclin proteins, which mainly differ by the type of amino acid repeats they contain at their C-termini. One set of proteins, the EP isoforms (encoded by the EP1-1, EP1-2, EP2 and EP3 genes) contain 22–30 [E-P] internal repeat peptides whereas
Author Summary

Trypanosomes, the tropical parasites that cause African sleeping sickness, show a number of biological peculiarities that distinguish them from other eukaryotes. One is the unusual way in which they regulate gene expression. Unlike most eukaryotes, trypanosomes do not regulate gene expression by controlling the rate of messenger RNA synthesis, but, instead, control the stability of messenger mRNAs (and, hence, their abundance) and also their rate of translation into protein. The best-studied model for this "post-transcriptional" gene expression control in trypanosomes is the procyclin mRNAs, which encode the major surface proteins of the parasite in the tsetse fly. In this study we demonstrate that a small kinetoplastid-specific protein (TbZFP3) co-associates with the mRNAs for some procyclin isoforms (EP1, GPEET procyclin) but not others (EP2, EP3 procyclin). Furthermore, we show that this is dependent upon sequences in the EP1 procyclin 3′ untranslated region known to govern its mRNA turnover and protein synthesis. Finally, we demonstrate that limited over-expression of TbZFP3 causes a change in the surface protein expression profile on cultured parasites from GPEET to EP1 Procyclin. Our data identify TbZFP3 as an important post-transcriptional regulator of Procyclin expression, the first such protein factor identified.

GPEET Procyclins (encoded by one copy of GPEET) contain 6 [G-P-E-E-T] repeats, which can be phosphorylated at the Thr residues. In the tsetse, Procyclins follow a programmed expression and their C-terminal repeat peptides, together with their complex GPI anchors, may provide protection for the parasite from the action of tsetse gut hydrolases [8–11].

Sequence-dependent signals in the 3′ untranslated region (3′ UTR) of each procyclin mRNA govern their expression and have been the subject of intense investigation, providing the paradigm for gene expression control in kinetoplastid parasites [2]. Although the 3′ UTRs of EP1, 2 and 3 and GPEET procyclin mRNAs are highly similar, the genes are differentially regulated in distinct phases of tsetse infection or in vitro. For example, the GPEET procyclin 3′ UTR contains an element, absent in the closely related EP1 3′ UTR, that differentially regulates its expression in response to glycerol and the activity of mitochondrial enzyme activities [12,13]. However, whilst the cis-acting control sequences for procyclin mRNAs are very well characterised [14–17], protein factors that recognise these regulatory domains have remained unidentified, despite considerable effort. Here we establish the specific association and regulation of procyclin mRNA isoforms by a kinetoplastid-specific protein factor that associates with polyribosomes, providing the first example in these organisms of surface protein regulation by an mRNA-associated regulatory factor.

Results

TbZFP3 immunoprecipitation differentially selects procyclin isoform mRNAs

Previous immunoprecipitation experiments using an antibody specific for a small CCCH-protein implicated in developmental control, TbZFP3 (Tb927.3.720), demonstrated co-precipitation of mRNA for the procyclic-form specific surface proteins, Procyclins [18]. Since different Procyclin isoforms exhibit distinct profiles of mRNA and protein expression in the tsetse fly [8,11,19] we investigated whether each isoform mRNA was co-precipitated with equivalent efficiency by TbZFP3. Figure 1A shows a typical experiment where immunoprecipitation from cell extracts resulted in a selection for TbZFP3 (lane 1), this being blocked in the presence of the peptide immunogen used to raise the TbZFP3-specific antibody (lane 2). The resulting co-selected mRNAs were then reverse transcribed and subjected to quantitative real-time (qRT) PCR using primers specific for each procyclin transcript isoform [11] (Figure 1B). In parallel reactions, total RNA from the starting cultures was also analysed with each primer set, allowing us to compare the relative level of each procyclin isoform mRNA in different stages of the cell cycle.

Figure 1. Co-immunoprecipitation of EP1 and GPEET procyclin mRNA, but not EP2 and EP3 mRNA, by TbZFP3. (A) Schematic representation of TbZFP3 immunoprecipitation. Cell extracts were subject to a clearing spin and immunoprecipitated in the presence or absence of the peptide immunogen against which the TbZFP3 antibody was raised ("Peptide blocked"). Western blotting with anti-serum to TbZFP3 was used to detect selection in the absence (Lane 1) or presence (Lane 2) of blocking peptide. (B) Three replicate immunoprecipitations from three distinct trypanosome procyclic lines were carried out, with the selected material being subject to reverse transcription and amplification using primers specific for EP1, EP2, EP3, or GPEET mRNAs. Values are normalised in unselected and selected material to the level of EP1 mRNA. Error bars = SD. doi:10.1371/journal.ppat.1000317.g001
unselected and TbZFP3-immunoprecipitated material. In total mRNA of the cell extracts, both EP2 and EP3 were present at 66% of EP1 levels (EP1 is normalised to 100% in Figure 1B), approximating to their observed relative abundance in culture and in the tsetse midgut [11]. As expected in this parasite strain [12,20,21], GPEET mRNA was also abundant (191% with respect to EP1) in the unselected material. In contrast to unselected cDNA, TbzZFP3-immunoprecipitated material showed a strikingly differential abundance of the isoforms, such that EP1 and GPEET were the dominant selected transscripts, with EP2 and EP3 selected at much lower level (3.3% and 6.2% of immunoprecipitated EP1, respectively). Importantly, use of the peptide block prevented the immunoprecipitation of each procyclin mRNA isoform, demonstrating specificity of the selection. Supporting this qRT-PCR data, non-selective amplification and cloning of procyclin cDNAs derived from TbzZFP3-immunoprecipitated material isolated 21/27 (78%) EP1 sequences and 6/27 (22%) GPEET sequences, with no clones containing EP2 or EP3 derived sequences. We conclude that although EP1, EP2, EP3 and GPEET procyclin mRNAs are each abundant in the unselected mRNA pool, TbzZFP3 is preferentially associated with EP1 mRNA, but also GPEET procyclin mRNAs.

Procyclin mRNA association requires integrity of the CCCH domain in TbzZFP3

To determine whether the co-immunoprecipitation of procyclin mRNAs with TbzZFP3 was dependent on its predicted RNA-binding domain we examined a cell line expressing a mutant form of TbzZFP3 lacking the CCCH zinc finger domain (TbzZFP3 ΔCCCH; [18]). This mutant incorporated a C-terminal Ty1 epitope tag to allow it to be specifically immunoprecipitated in the context of endogenous TbzZFP3 using the BB2 antibody which detects the Ty1 epitope [22]. As a control, wild type TbzZFP3 was also expressed with a C-terminal Ty1 tag with the relative expression of each ectopically expressed protein being examined by Western blotting using either the antibody against TbzZFP3 (this detecting endogenous and ectopically expressed TbzZFP3) or BB2 (detecting only the ectopically expressed protein). Figure 2A shows the relative expression of each ectopically expressed protein in each cell line, confirming their approximately equivalent abundance. Thereafter, cell extracts from each line were used in immunoprecipitation experiments to select the ectopic TbzZFP3 using the BB2 antibody, and the co-selection of procyclin EP1 mRNA assayed. This demonstrated selection of EP1 mRNA with TbzZFP3-Ty, as expected, whereas deletion of the CCCH domain prevented co-precipitation of EP1 mRNA (Figure 2B). Thus, the integrity of the predicted RNA binding domain in TbzZFP3 is necessary for co-immunoprecipitation of EP1 mRNA.

Sequence-specific affinity selection of EP1 mRNA via TbzZFP3 immunoprecipitation

The sequences which regulate procyclin gene expression have been very well characterised in transgenic parasites by use of reporter genes linked to wild type or mutant forms of the EP1 mRNA 3’ UTR. This has identified a number of regulatory regions that act to either positively or negatively control expression [14,23–26]. Minimally, three domains contribute to EP procyclin regulation: a positive control element in the first 40 nt after the stop codon (“Loop I”), a negative element contained within 101–173 nt (“Loop II”) and a further positive element comprising a highly conserved 16 nt loop structure (“Loop III”). To determine whether TbzZFP3 RNA-immunoprecipitation generated sequence-specific selection of EP1 procyclin mRNA, we generated a series of cell lines transfected with previously characterised reporter constructs (kindly provided by Professor I. Roditi, University of Bern). These comprised a GARP coding region reporter [27] linked to either the wild type EP1 procyclin 5’UTR or mutants lacking each regulatory domain (ΔI0, ΔII or Δ16mer) (Figure 3A). Initially the anticipated effects on reporter gene expression for each construct were confirmed by analysing the GARP mRNA and protein levels in the resulting transfected cell lines (Figure 3B). Matching previous analyses of these deletions...
the mRNA abundance of GARP was reduced in the Δ40 (62% of wild type levels) and Δ16mer cell lines (26% of wild type levels), but significantly elevated in the ΔLII cell line (210% of wild type levels). Similarly, Western blotting of protein extracts from these cell lines with a GARP antiserum [28] confirmed that the levels of GARP protein translated from the expression constructs matched previous observations, with abundant GARP generated in the ΔLII cell line and little detectable protein when the 16mer element was deleted.

Having generated cell lines stably transfected with each reporter construct, extracts from each were subjected to TbZFP3-immunoprecipitation, either in the presence or absence of blocking peptide and analysed for the selection of TbZFP3, (Figure 4A, “TbZFP3 IP”) or of the reporter GARP mRNA (Figure 4A; “GARP-RT-qPCR”). Importantly, in each case the relative selection of GARP mRNA was compared with, and normalised to, the selection of endogenous EP1 procyclin, ensuring the efficiency of immunoprecipitation from each extract was equivalent (Figure 4A and 4B). In the cell line containing GARP linked to wild type EP procyclin 3’UTR, efficient selection of the reporter mRNA was observed with this being abolished in the presence of the blocking peptide (80% and 1% respectively, normalised to the relative immunoprecipitation of endogenous EP1 mRNA). When the Δ40 cell line was examined efficient selection of GARP transcripts was also observed (81% of endogenous EP1, with 3% of endogenous EP1 in the presence of the peptide block). However, when either the negative control element contained in Loop II of the EP1 procyclin 3’UTR, or the 16mer stem-loop structure were deleted, selection with TbZFP3 was reduced to only 1.5% or 9% of endogenous EP1 mRNA, respectively. This did not represent inefficient immunoprecipitation since endogenous EP1 procyclin mRNA was selected at an equivalent level in all cell lines (Figure 4B and data not shown). Moreover, it was not simply dependent on target mRNA abundance because the ΔLII–derived GARP mRNA was highly expressed (Figure 3B). This demonstrated that TbZFP3 immunoprecipitation showed sequence-specific selection of the EP procyclin 3’UTR, this being individually dependent upon integrity of the Loop II and the 16mer regulatory domains.

TbZFP3 is a positive regulator of EP1 Procyclin operating at the protein level

Having demonstrated that EP1 procyclin mRNA co-selects with TbZFP3 via known regulatory domains we determined if TbZFP3 could specifically regulate EP procyclin mRNA abundance. Initially, we made use of transgenic procyclic and bloodstream form lines that ectopically over-express TbZFP3 under tetracycline control. Figure 5A (lanes 1–4) shows endogenous and ectopically expressed TbZFP3 mRNA in each cell line, whereas lanes 5–8 shows hybridisation to the same RNAs of a generic EP procyclin riboprobe. This revealed no evidence for a specific enrichment of any EP mRNA in response to TbZFP3 induction in procyclic forms nor appearance of EP mRNA in bloodstream forms (where Procyclin is not normally expressed). Furthermore, quantitative RT-PCR specific for EP1, EP2, EP3 procyclin revealed no specific change of EP1 mRNA with respect to EP2 or EP3 mRNAs,
although the expression of all mRNAs increased slightly (~20%; Figure 5B). Similarly, RNAi directed to TbzZFP3 (resulting in 60% reduction of protein expression; Figure 6A) resulted in no specific regulation of any procyclin mRNA isoform, although all procyclin mRNAs as well as several housekeeping genes showed an overall reduction of mRNA abundance. This suggests non-specific or indirect effects or, potentially, a more widescale consequence of TbzZFP3 knock-down on mRNA abundance (Figure 6B and data not shown). Nonetheless, the analysis demonstrated that there was no differential change in the abundance of procyclin isoform mRNAs caused by enhanced or reduced TbzZFP3 expression.

To monitor the relative protein expression of individual Procyclin isoforms we made use of an established mass spectrometry approach to detect Procyclins. Thus, cell lines induced to ectopically express TbzZFP3 for 48 h, 72 h or 1 week were subject to delipidation and butanol extraction followed by aqueous HF treatment to release the Procyclin proteins from their GPI-anchors. The released full length Procyclins were then further subject to mild acid treatment [29], a procedure that cleaves the EP isoforms at the Asp-Pro bonds and partially cleaves GPEET between Asp-Gly. The resulting extracts were analysed by negative ion MALDI-TOF-MS to detect the pseudomolecular ions representing C-terminal fragments of the [M-H]− of the [M-H]− pseudomolecular ions representing C-terminal fragments of GPEET and EP1-1, EP1-2, EP2 and EP3 proteins. Consistent with expectation for this parasite strain, the dominant surface protein was GPEET Procyclin [20,21], with lower expression of the EP Procyclin isoforms (Figure 7A–7C). However, ectopic expression of TbzZFP3 (generating 1.5 and 2.3 fold overexpression at 48 h and 72 h, respectively), progressively elevated EP1-1 and EP1-2 Procyclins (Figure 7D–7F) above either uninduced controls (Figure 7A–7C) or the parental cell line grown in the presence of tetracycline (Figure S1). Furthermore, expression of GPEET was progressively reduced (~5 fold) from being the dominant surface molecule to being a minor component with respect to EP1 after 7 days of induction (Figure 7F). In contrast to these two proteins, both allelic variants of EP3 procyclin (EP3-1 and EP3-5) remained relatively unchanged, whereas EP2 was not detected in any cell population matching previous studies. Consistent with the specific regulation of Procyclin expression by TbzZFP3, examination of the Procyclin protein signature of the cell lines expressing the ΔCCCH mutant of TbzZFP3, which does not co-select procyclin mRNAs, did not reveal any change in the profile of

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**Figure 4. Sequence specific co-precipitation of EP1 3' UTR with TbzZFP3.** (A) Co-immunoprecipitation of each GARP reporter mRNA with TbzZFP3 either in the presence or absence of blocking peptide (“GARP RT-qPCR”). qRT-PCR values are normalised to the value for co-selected endogenous EP1 mRNA in each cell line. Control amplifications lacking input RNA or reverse transcriptase failed to amplify any product. Above each bar chart is shown Western blots for TbZFP3 (“GARP-PCR”). The co-selection of endogenous EP1 with the products visualised on ethidium bromide stained agarose gels of the real-time PCR data generated in a separate immunoprecipitation, These confirm specificity of the selection. (B) Independent confirmation of the real-time PCR data generated in a separate immunoprecipitation, with the products visualised on ethidium bromide stained agarose gels (“GARP-PCR”). The co-selection of endogenous EP1 mRNA is also shown (“EP1-PCR”).

doi:10.1371/journal.ppat.1000317.g004

**Figure 5. Effect of ectopic over-expression of TbzZFP3 on procyclin mRNA levels.** (A) Northern blots of procyclic forms (PCF) and bloodstream form (BSF) transgenic trypanosome lines that induce the ectopic expression of TbzZFP3 under a tetracycline regulatable promoter. Lanes 1–4 show the expression of the ectopic TbZFP3 (arrowed) in the absence or presence of induction. Endogenous TbzZFP3 mRNA is also shown (arrowhead). Lanes 5–8 ("EP") show the same RNAs hybridised with a riboprobe detecting all EP procyclin isoforms. The relative loading is indicated by rRNA below each panel. (B) Relative expression of EP1, EP2, and EP3 mRNAs after ectopic expression of TbzZFP3 as determined by quantitative RT-PCR. Values are normalised to actin. All procyclin isoform mRNAs showed an approximately 20% increase in abundance, but no specific isoform showed a consistent change with respect to another. GPEET mRNA levels were also not affected (data not shown). Error bars = SD. doi:10.1371/journal.ppat.1000317.g005
The experiments in this paper identify the developmental regulator, \textit{TbZFP3}, as an isform-specific regulator of Procyclin surface coat expression in trypanosomes. Specifically, we demonstrate (i) that endogenous \textit{TbZFP3} shows sequence-specific co-association with distinct \textit{procyclin} mRNA isoforms, (ii) that ectopic overexpression of \textit{TbZFP3} does not enhance the mRNA abundance of selected transcripts, but rather that (iii) their protein expression is regulated in an isform-specific manner, as evidenced by mass spectrometric analysis of the Procyclin expression signature in transgenic cell lines. Unlike the wild type \textit{TbZFP3} protein, a mutant form of \textit{TbZFP3} lacking its C.\textit{x}8C.\textit{x}5C.\textit{x}3H predicted RNA-interaction motif and which cannot co-associate with \textit{procyclin} mRNAs does not alter Procyclin expression. We have already demonstrated that \textit{TbZFP3} promotes differentiation when associated with the translational machinery (this being dependent upon its predicted RNA and protein interaction motifs) and that this occurs only in the parasite life cycle stage at which Procyclin proteins are expressed [18]. Hence, our work provides a long-sought ‘missing link’ between the intensely studied cis-regulatory signals for the \textit{procyclin} gene family and the general gene expression machinery, this being the translational apparatus.

\textit{TbZFP3} shows specific co-association in vivo with \textit{EP1} and \textit{GPEET} \textit{procyclin} mRNA, whereas the distinctly regulated transcripts \textit{EP2} and \textit{EP3} are not co-immunoprecipitated. Although deletion of the predicted RNA-binding domain in \textit{TbZFP3} prevents the co-association with \textit{EP1} mRNA, our studies do not formally distinguish between direct intermolecular contact between \textit{TbZFP3} and target mRNAs and indirect contact dependent on other protein factors. Hence, we use the term \textit{TbZFP3mRNP} to define the composition of the immunoprecipitated material comprising \textit{TbZFP3}, \textit{procyclin} mRNAs and, possibly, other identified (e.g. [18]; see below) and unidentified co-operating factors. Nonetheless, by using an immunoprecipitation approach employing an antibody directed to the endogenous \textit{TbZFP3} protein in wild type parasites we demonstrate that the observed co-association with \textit{procyclin} mRNAs is physiological, and directed by \textit{TbZFP3} in its normal cellular context. Interestingly, the differential selection of different \textit{procyclin} mRNA isoforms by the \textit{TbZFP3mRNP} matches their overall sequence similarity, with \textit{EP1} and \textit{GPEET} 3’UTR sequences being significantly more closely related than \textit{EP2} and \textit{EP3} (Figure S3). Nonetheless, \textit{EP1} and \textit{GPEET} are differentially regulated in vivo, with \textit{GPEET} expression being repressed as \textit{EP1} is upregulated during differentiation to late procyclic forms in vitro and in the tsetse fly [8,12]. Significantly, this matches the observed effects of \textit{TbZFP3} ectopic overexpression, whereby \textit{EP1} expression is elevated to become the dominant surface protein and \textit{GPEET} expression is repressed, correlating with enhanced association of the \textit{TbZFP3mRNP} with \textit{EP1} mRNA and diminished association with \textit{GPEET} mRNA. Although copy number control of Procyclins on the parasite surface could accentuate this switch, it is significant that the inverse control of these surface molecules is regulated by only subtle changes in the abundance of \textit{TbZFP3} (~1.5–2.5 fold). This suggests exquisitely regulated control of Procyclin isofrm expression in response to \textit{TbZFP3} levels.

In addition to isform-specific selection, the \textit{TbZFP3mRNP} exhibits sequence-specific association with the \textit{EP1} mRNA 3’UTR, this being dependent upon the integrity of two well-characterised regulatory regions - the ‘Loop II’ and the 16mer stem loop region. Previous analyses have demonstrated that these sequences provide negative and positive control elements for \textit{EP1} \textit{procyclin} expression, respectively. The Loop II region acts as a translational repressor and mRNA destabilisation element in procyclic forms, whereas the 16mer is a translational enhancer, which suppresses the action of the Loop II region [23,24]. In insect stages, it was predicted that a macromolecular complex would associate with both elements and so shield the ‘Loop II’ element from recognition by a negative regulator, thereby promoting gene expression [23]. Our findings are compatible with this, invoking a model (Figure 9) in which \textit{TbZFP3} competes with a negative regulator binding ‘Loop II’, such that \textit{TbZFP3} over-expression
promotes EP1 Procyclin expression (at the expense of GPEET), whereas RNAi mediated removal of \textit{Tb}ZFP3 results in reduced \textit{procyclin} mRNA abundance. Interestingly, expression of the Loop II deletion reporter construct revealed that \textit{Tb}ZFP3mRNP-binding is not necessary for efficient mRNA or protein expression (Figure 3B), suggesting that the \textit{Tb}ZFP3mRNP acts primarily as an anti-repressor (Figure 9), matching earlier predictions for the \textit{procyclin} regulatory machinery [2,17,23,30]. This is analogous to the regulation of \textit{nanos} RNA during \textit{Drosophila} embryogenesis, whereby overexpression of Oskar displaces the translational repressor Smaug bound to the \textit{nanos} 3’UTR [31].

CCCH proteins in eukaryotes are involved in all levels of gene expression through RNA recognition, usually this being dependent upon the integrity of at least two juxtaposed CCCH fingers [32]. \textit{Tb}ZFP3, however, has only a single CCCH motif and is a member of a family of small CCCH zinc finger proteins (\textit{Tb}ZFP1, \textit{Tb}ZFP2 and \textit{Tb}ZFP3), unique to kinetoplastids, and each <140 amino acids long. These proteins interact in yeast 2-hybrid assays and co-immunoprecipitate \textit{in vivo}, suggesting that they provide a modular function in order to confer specificity of binding [33]. Whether this is part of a single mRNP complex, or distinct complexes with differential specificities for different genes or in different life cycle stages, remains to be determined. This complexity of interactions may define the specificity of different mRNA classes selected by the \textit{Tb}ZFP3mRNP, or moderate their differential efficiency of selection and hence regulation, as observed with \textit{EP1} and \textit{GPEET} mRNA regulation under conditions of \textit{Tb}ZFP3 ectopic expression. To be understood in depth, such interactions will need to be analysed on a case-by-case basis for individual RNAs as has been done here for \textit{procyclin} mRNAs. Nonetheless, analogous combinatorial interaction between RNA binding proteins in kinetoplastid parasites to confer target specificity and regulation has previously been proposed for the small RNA binding proteins \textit{Tb}UBP1 and \textit{Tb}UBP2 [34], homologues of the regulators of mucin gene expression in \textit{T.cruzi} [35].

\textit{Tb}ZFP2 and \textit{Tb}ZFP3 are constitutively expressed and associate with the translation apparatus in procyclic forms but not in bloodstream forms [18]. Our demonstration here that the \textit{Tb}ZFP3mRNP co-associates with \textit{procyclin} mRNA regulatory elements that control translation, thus promoting EP1 surface protein expression without enhancing \textit{EP1} mRNA abundance, suggests a role for \textit{Tb}ZFP3 in translational control. Supporting this, a mutant \textit{Tb}ZFP3 lacking the predicted RNA-interaction domain neither co-associates with \textit{procyclin} mRNAs (Figure 2) nor

Figure 7. Procyclin isoform regulation by \textit{Tb}ZFP3. Negative ion MALDI-TOF mass spectra of Procyclin isoforms extracted from cells uninduced (A–C) or induced (D–F) to express ectopic \textit{Tb}ZFP3 to a level ~2-fold its endogenous abundance. In response to elevated \textit{Tb}ZFP3 levels, the expression of EP1-1 and EP1-2 (which share an identical 3’UTR) is elevated, whereas GPEET expression is reduced. (A) and (D) show uninduced and induced cells after 48 h, (B) and (E) show cells after 72 h, and (C) and (F) show cells after 1 week. EP3-5 is an allelic copy of the EP3 gene in the 427 strain [42]. EP C-terminal polypeptides (I) and (II) represent forms containing the sequence P (EP),G-EtN and PDP (EP),G-EtN, respectively. GP (FL), (-4), and (-13) indicate full-length GPEET and its polypeptides lacking four and thirteen N-termini amino acids, respectively. P, indicates levels of peptide phosphorylation.

doi:10.1371/journal.ppat.1000317.g007
The translational apparatus [18] and induces no consistent change in procyclin expression (Figure S2). Temporally-regulated translational control is a key aspect of cell-type development in the Plasmodium parasite, whereby translational repression via the DDX6 RNA helicase family member DOZI regulates gametocyte mRNA expression and life-cycle differentiation [36]. Interestingly, these transcripts share a 47 nt U-rich control element [37], similar to the regulatory U-rich 20mer elements enriched in procyclin form-specific transcripts [30] and comprising part of the Loop II region of EP1 procyclin recognised by TbZFP3. This points to common mechanisms of developmental control among widely divergent eukaryotic protozoan pathogens.

Translational control is believed to be a major mechanism of gene regulation in trypanosomatid parasites [39,40]. Although the general mRNA degradation and translational machineries are broadly conserved in these evolutionarily ancient eukaryotic organisms [3], it is the kinetoplastid-specific trans-acting regulators that provide the key to understanding their extreme emphasis on post-transcriptional control. Moreover, targeting unique components of the translational machinery in pathogens is a major strategy in antimicrobial therapies. Thus, discovering novel regulators interacting with this apparatus provides both new understanding of gene expression and new possibilities to intervene in the virulence and spread of these devastating parasites.

Materials and Methods

Cell Lines

Procyclic form or bloodstream form T. brucei Lister 427 trypanosomes were used throughout. Cell lines engineered for TbZFP3 ectopic expression in procyclic or bloodstream forms have been described previously and were cultured in SDM-79 or HMI-9, respectively [18].

Immunoprecipitation and qRT-PCR

Immunoprecipitation using TbZFP3-specific antisera, RNA extraction and reverse transcription have been described previously [18]. Blocking peptides used were N-DSSQMQQVGHDPMPA-C for TbZFP3 and N-EVHTNQDPDL-C for Ty1, each being titrated prior to use. SYBR green qRT-PCR reactions were performed using Roche reagents as per specifications for the LightCycler system. The 5′ primers for actin, ep and gpee and 3′ primers specific to EP1, EP2, EP3, GPEET, or the Anchor sequence were described previously [11,18]. cDNA was amplified as follows: 10 min, 95°C; 30×[8 s, 95°C; 9 s, 55°C; 12 s, 72°C] with fluorescence acquired at 82°C. The amplification was followed by a melting temperature analysis that measured PCR product fluorescence during a temperature increase from 65°C to 95°C at 0.1°C/s to determine product melting temperature and confirm specificity. Product identities were further verified by gel electrophoresis and DNA sequencing. In all cases, serial dilutions of input cDNAs confirmed the quantitative efficiency of the reactions and “no reverse transcriptase” controls confirmed the absence of contaminating genomic DNA in the RNA preparations.

Northern and Western blotting

Northern blotting involved resolution of 3–5μg of total trypanosome mRNA on formaldehyde agarose gels resolved in MOPS buffer. Hybridization of blots used digoxigenin labelled riboprobes, detected using anti-DIG alkaline phosphatase-conjugated antibody and visualised using CDP-star as a reaction substrate (Roche). Western blots were detected and quantitated using a Li-COR Odyssey system, using alpha-tubulin as an internal standard.

Mass spectrometry

Mass spectrometry was carried out according to the methodology described in [8,19,29]. Briefly, parasite pellets were freeze-
dried and then extracted twice with 200 μl of Chloroform/Methanol/Water, 10:10:3 (V/V/V), under sonication (10 min). After centrifugation, the delipidated pellets were then extracted 3 times with 150 μl of 9% butanol (ButOH), also under sonication. The ButOH fractions contain the Procyclins. All ButOH fractions were then freeze-dried and submitted to dephosphorylation using 50 μl of 48% aqueous hydrofluoric acid (aq.HF), at 0 uC for 24 h. After aq.HF incubation the samples were freeze-dried again and washed twice with water. The samples were then dried and further incubated with 200 μl of 40 mM TFA, 20 min at 100 uC (mild acid conditions), in order to assist visualization of the Procyclin C-termini and the identification of each isoform. Under this condition, the Asp-Pro bonds of most of the EP isoforms are cleaved whereas GPEET partially releases 13 amino acids at its N-terminus. Equivalent amounts of each sample were mixed with a-cyano (matrix) and analysed by negative-ion MALDI-TOF-MS using a Voyager-DE STR instrument.

Supporting Information

Figure S1 Procyclin isoform expression in parental procyclic forms. Found at: doi:10.1371/journal.ppat.1000317.s001 (0.51 MB DOC)

Figure S2 Procyclin isoform expression in transgenic cells expressing the ACCCH mutant of TbZFP3-Ty. Found at: doi:10.1371/journal.ppat.1000317.s002 (0.58 MB DOC)

Figure S3 Overall similarity between the 3’UTRs of EP1, EP2, EP3, and GPEET procyclin mRNAs. Found at: doi:10.1371/journal.ppat.1000317.s003 (2.22 MB DOC)

Acknowledgments

We thank Douglas Lamont (Proteomics Facility, Dundee University) for access to the MALDI mass spectrometer, Professor Judi Allen (University of Edinburgh) for Lightcycler access, and Dr. Toni Aebischer (University of Edinburgh) for thoughtful comments on the manuscript. Reporter constructs and GARP antiserum were kindly provided by Professor Isabel Roditi, University of Bern.

Author Contributions

Conceived and designed the experiments: AAS KRM. Performed the experiments: PW AP AAS. Analyzed the data: PW AP AAS KRM. Wrote the paper: PW AAS KRM.

References


