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ORIGINAL RESEARCH

Role of Shwachman-Bodian-Diamond syndrome protein in translation machinery and cell chemotaxis: a comparative genomics approach

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Abstract: Shwachman-Bodian-Diamond syndrome (SBDS) is linked to a mutation in a single gene. The SBDS proinvolved in RNA metabolism and ribosome-associated functions, but SBDS mutation is primarily linked to a defect in polymorphonuclear leukocytes unable to orient correctly in a spatial gradient of chemoattractants. Results of data mining and comparative genomic approaches undertaken in this study suggest that SBDS protein is also linked to tRNA metabolism and translation initiation. Analysis of crosstalk between translation machinery and cytoskeletal dynamics provides new insights into the cellular chemotactic defects caused by SBDS protein malfunction. The proposed functional interactions provide a new approach to exploit potential targets in the treatment and monitoring of this disease.

Keywords: Shwachman-Bodian-Diamond syndrome, wybutosine, tRNA, chemotaxis, translation, genomics, gene proximity

Introduction

Shwachman-Bodian-Diamond syndrome (SBDS) is an autosomal recessive disorder characterized by pancreatic exocrine insufficiency, bone marrow dysfunction, and skeletal abnormalities.[1]

The SBDS gene (*sbds)* encodes a member of a highly conserved protein family of unknown function, with orthologs in diverse species, including Archaea, plants, and eukaryotes, but not Eubacteria.[2] Structural and functional aspects of SBDS link this protein to a group of proteins involved in RNA metabolism with ribosome-associated functions.[3,4] For example, the yeast SBDS ortholog clusters with RNA-processing enzymes and ribosomal RNA-processing factors in gene expression analyses,[5,6] and in the SBDS sequence homolog in *Saccharomyces cerevisiae*, YLR022C, was shown to be physically associated with proteins involved in ribosome biosynthesis.[7]

The N-terminal domain of the SBDS protein, which is most prone to mutations leading to disease, contains a novel mixed α/β fold that was also suggested for a single domain yeast protein, Yhr087wp, implicated in RNA metabolism.[1] The βαββαβ folding topology of the SBDS C-terminal domain III (Glu^{162}–Gly^{234}) is structurally close to domain V of *S. cerevisiae* elongation factor 2 (Eft2p/Ydr385wp).[8] It is also typical for a ferredoxin-like fold and characteristic of a number of heterogeneous nuclear ribonucleoproteins, eg, factors involved in regulation of alternative splicing.[9] Although SBDS links to RNA metabolism are apparent, an association has also been observed between the SBDS protein and cell locomotion, in that polymorphonuclear leukocytes isolated from SBDS patients are unable to orient correctly in a

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spatial gradient of chemoattractants.[10] SBDS protein was also shown to localize to the pseudopod of Dictyostelium amoebae during chemotaxis.[11] The interaction of SBDS and a structural or regulatory cytoskeletal component is more than likely responsible for the observed defect in polymorphonuclear leukocyte chemotaxis. Nonetheless, no specific candidate for such an interaction has been suggested.

The complexities of the myriad defects associated with SBDS have made it difficult to relate the diverse biochemical and phenotypic properties of the SBDS syndrome on an experimental basis. A way forward on how mutations of the SBDS gene (*sbds*) may relate to its altered functions is via a functional genomics approach and phylogenetic analysis of gene proximity in *sbds* loci. Functionally related genes are commonly found clustered in prokaryotic and eukaryotic genomes,[12–17] and predicting gene function based on physical proximity to other genes has been used successfully in a number of studies. Therefore, we treated consistency of gene proximity in *sbds* loci in evolutionary distant genomes as an indication of functional relatedness, which led to a prediction of SBDS protein involvement in initiation of translational wybutosine metabolism. The crosstalk between the translation machinery and elements of the cytoskeleton provides an explanation as to how cell chemotactic defects may be caused by SBDS malfunction.

Materials and methods

We used the Seed database (http://theseed.uchicago.edu/FIG/index.cgi) for chromosome alignment and phylogenetic analysis of gene positional clusters.[18] The "Compare Regions" resource provided by Seed allows alignment of chromosome loci that contain open reading frames for homologous proteins, or, in other words, to pin these loci through genes that are homologous to a query sequence. It can be used in a text or graphic format. We used the latter to illustrate phylogenetic conservation of gene proximity. The typical graphic window presents a selected number of chromosome loci from different genomes. The first line of Compare Regions is a graphical display of the chromosomal neighborhood of the features in its genome. All proteins are shown as colored arrows, where the direction depicts the strand of the feature. RNAs and other features are small boxes on the line. Feature overlaps are resolved by drawing the overlapping feature in a new line. The graph is centered on the selected feature, always numbered 1 and colored red. Below, there is the same region for orthologs in other organisms, also colored in red. The colors of the other features (as well as the numbers) also represent ortholog (or sometimes also paralog) features. Whenever there are at least two ortholog or paralog features of a kind, a color (and a number) is assigned to them. The selection of genomes to show in the graphics can be made by similarity or the pair of close homologs pin. We used similarity, which means that the genomes are chosen using the similarity of the selected genes to its orthologs in other genomes. The E value cutoff for selection of pinned coding sequence depicts the minimum similarity in order for its region to be displayed. We used the e-20 E value threshold to obtain all the presented data sets.

There are numerous queering and display options that allow customization of the size of displayed regions, selection of organisms, similarity thresholds for pinning of regions, and coloring of features that we implemented to deliver the illustrations accompanying this paper.

Results

Conservation of gene proximity in SBDS gene loci

Phylogenetic analysis of archeal *sbds* loci (Figure 1) shows conservation of *sbds* gene proximity. *Sbds* orthologs are shown as red arrows (N1) in the centers of all the selected regions, where one can also see repetitive occurrence of colors/numbers depicting other orthologous genes in different genomes. Almost all of these co-occurring genes are related to RNA modification and degradation, ie, probable exosome complex exonuclease 2 (EC 3.1.13.-)/tRNA nucleotidyltransferase (N2) , proteasome subunit α (EC 3.4.25.1) (N3), probable exosome complex RNA-binding protein 1 (N4), large ribosomal subunit protein L37 Ae (N5) large ribosomal subunit protein L15e (N7), ribonuclease P (tRNA processing) protein component 3 (EC 3.1.26.5) (N8), ribonuclease P protein component 2 (EC 3.1.26.5) (N9), prefoldin, chaperonin cofactor (N10), and a predicted exosome subunit containing the IMP4 domain present in small nuclear ribonucleoprotein (N11). An archeal *sbds* locus that includes all or part of the genes encoding the listed functions is surrounded by a variable region (gray arrows), suggesting that clustered genes related to the archeal exosome complex indeed represent a functionally coupled group or even an operon, and that *sbds* can be a part of this group.

Chromosome loci with vertebrate orthologs to human *sbds* (ENSG00000126524) have also been aligned. In the human genome, *sbds* spans a start for *tyw1* (ENSG00000198874), which encodes tRNA-wybutosine synthesizing protein (TYW1) from the opposite string. In all vertebrate genomes analyzed (from the SEED database collection), *sbds* (red, N1)

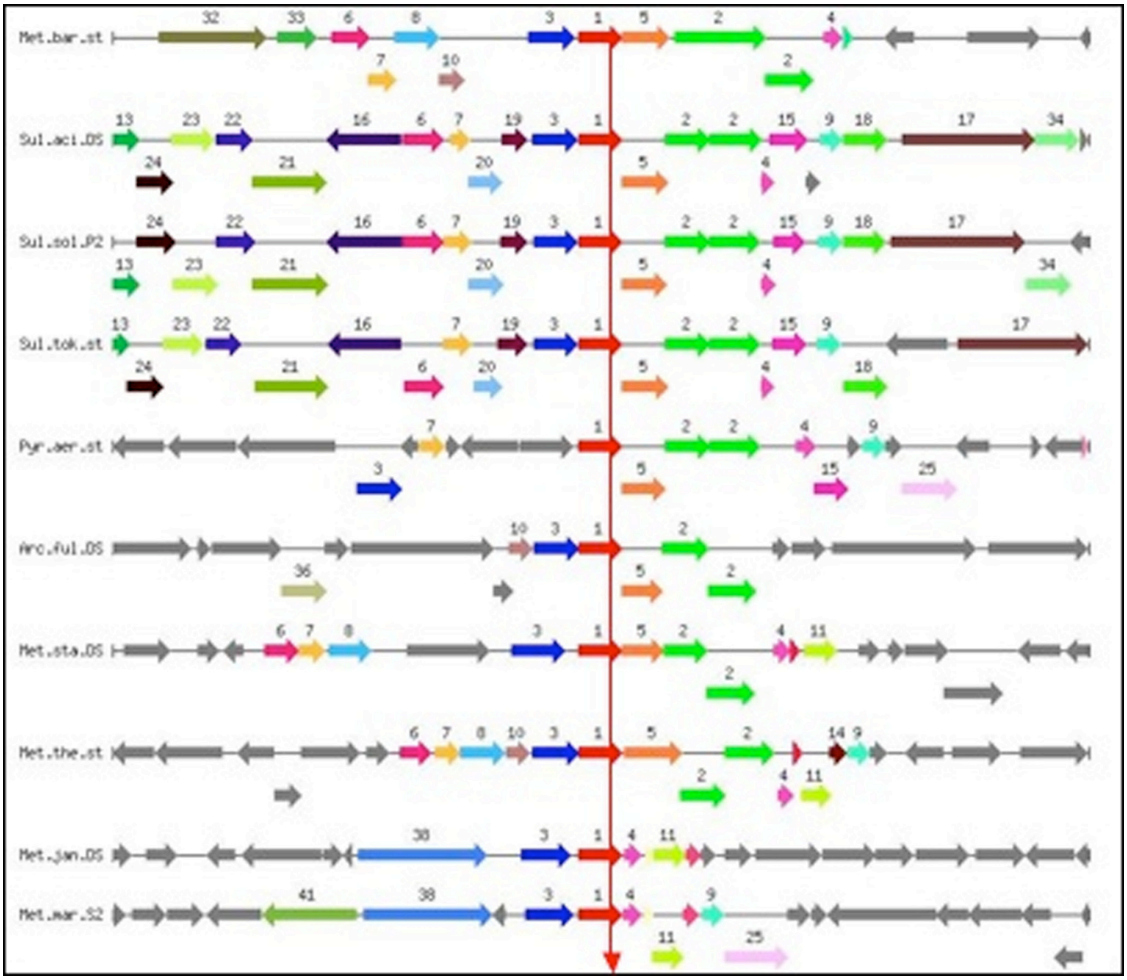

Figure 1 Graphical display of the chromosomal neighborhood of *sbds* genes in archeal genomes. Arrows correspond to open reading frames, same color and number depicts gene orthology. Vertical arrow connects pinned genes (red arrows), ie, orthologs of *sbds* gene from *Methanosarcina barkeri* (upper line). Genes encode 1-SBDS protein (AAB90746.1 and its orthologs), 2-probable exosome complex exonuclease 2 (EC 3.1.13.-)/tRNA nucleotidyltransferase, 3-proteasome subunit α (EC 3.4.25.1), 4-probable exosome complex RNA-binding protein 1, 5-large ribosomal subunit protein L37 Ae, 7-large ribosomal subunit protein L15e, 8-ribonuclease P (tRNA processing) protein component 3 (EC 3.1.26.5), 9-ribonuclease P protein component 2 (EC 3.1.26.5), 10-prefoldin, chaperonin cofactor, and 11-predicted exosome subunit containing the IMP4 domain present in small nuclear ribonucleoprotein. 16 kbp regions are shown.

Abbreviations: Met. sta.DS, *Methanosphaera stadtmanae DSM 3091*; Met.the.st- *Methanothermobacter thermautotrophicus*; Met.mar.S, *Methanococcus maripaludis S2*; Arc.ful, *Archaeoglobus fulgidus DSM 4304*; Pyr.aer.st, *Pyrobaculum aerophilum str. IM2*; Met.bar.st, *Methanosarcina barkeri str. Fusaro*; Sul.aci.ds, *Sulfolobus acidocaldarius DSM 639*; Sul.sol. P2, *Sulfolobus solfataricus P2*; Sul.tok.st, *Sulfolobus tokodaii str. 7*.

is colocalized with a gene encoding the TYW1 homolog, annotated in SEED as wybutosine biosynthesis reductase (green, N2, Figure 2). A small gap between these two genes in the different vertebrate genomes suggests that they may share a regulatory region. The gene region downstream of *sbds* is not conserved, even in narrower phylogenetic groups, because one can see it for the displayed regions from several mammalian genomes.

In the *Plasmodium falciparum* and *Ciona intestinalis* genomes, *sbds* genes are also colocalized with genes encoding functions related to translational initiation and mainly with tRNA-regulated components of translational initiation complexes, ie, a gene for predicted GCN1 (general control of amino-acid synthesis 1) (XP_002120729.1) is immediately downstream and a gene for tRNA/RNA cytosine-C5-methylase (EC 2.1.1.-) is immediately upstream from the human *sbds* ortholog (XM_002124782.1) in the *C. intestinalis* genome (Table 1). The *aIF2β* gene is the second gene upstream from the *sbds* ortholog (XP_001348280.1) in a *Plasmodium* genome (Table 2).

In *Schizosaccharomyces pombe,* the *sbds* ortholog (O14179, SDO1) is proximal to a gene encoding the L26e ribosomal protein, followed by a gene for the mRNA capping enzyme subunit. Gene encoding RNA processing factor 1 is immediately downstream, followed by one for S23e (Table 3).

No specific functional gene overrepresentation at the *sbds* locus in *S. cereviciae* was observed, apart from a noticeable but comparatively distant proximity to genes

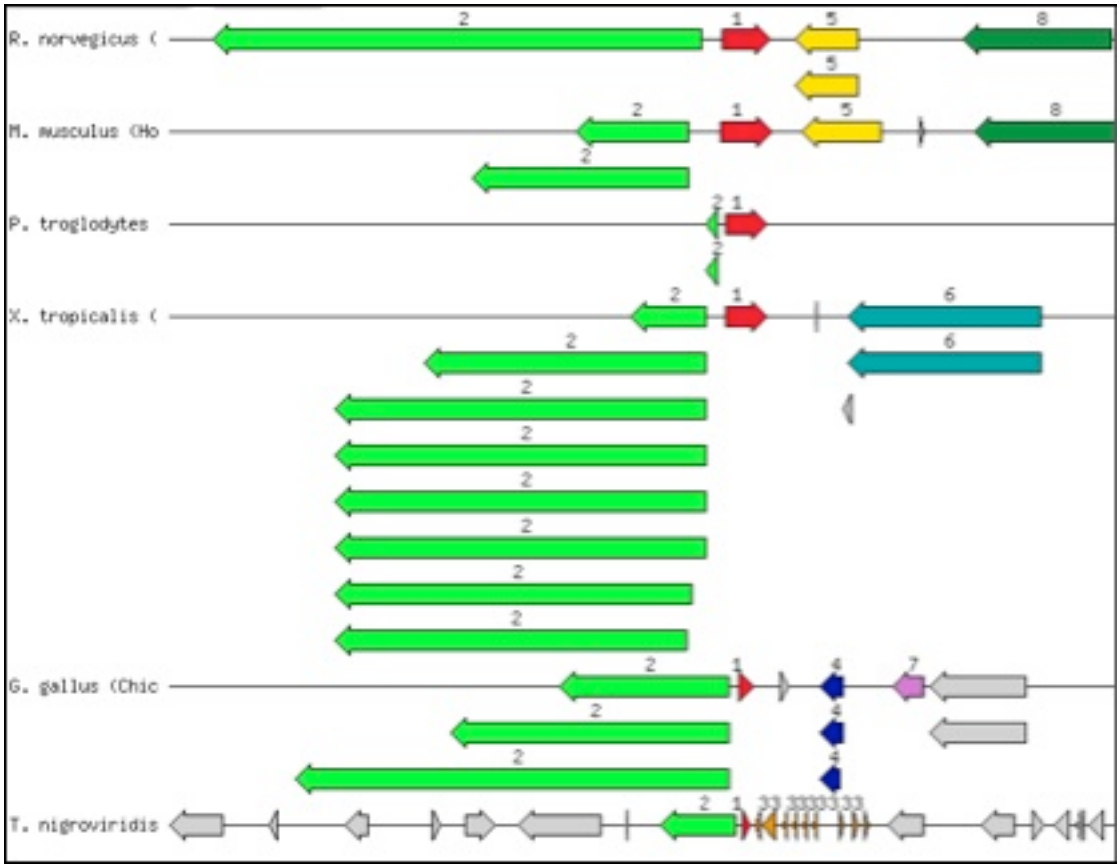

Figure 2 Graphical display of the chromosomal neighborhood of *sbds* genes in genomes of vertebrates. Arrows correspond to open reading frames encoding: red, Shwachman-Bodian-Diamond syndrome (NM_001008289.1 and pinned orthologs, green), tRNA-YW synthesizing protein (NP_001100607.1 (in *Rattus norvegicus*) and ortholog, multiple arrows in *Xenopus tropicalis* correspond to known transcripts), 3-claudin, 4-septin, 5-0610007 L01Rik protein, 6-hypothetical protein, 7-putative dual specificity testis-specific protein kinase 2 (EC 2.7.11.1), and 8-RABX5 (NP_001185988.1). 200 kbp regions are shown. Organisms are *R. norvegicus*, *Mus musculus*, *Pan troglodytes*, *X. tropicalis*, *Gallus gallus*, *Tetraodon nigroviridis*.

encoding RNA-related functions. However, *sbds* orthologs (XP_387070.1, XP_956795.1, XP_360288.1) are proximal to genes encoding L18e in fungal (*Gibberella zeae*, *Neurospora crassa*, and *Magnaporthe oryzae*) genomes (Figure 3).

Discussion

SBDS is a complex disease linked to mutation in a single gene. Recent advances in genomics and functional bioinformatics are providing a new avenue for studying this and similar phenomena, complementing traditional hypothesis-driven laboratory research. Our bioinformatics approach undertaken in this study provides a new insight as to how a single gene mutation may affect diverse molecular functions, such as RNA metabolism, translation initiation, and cytoskeletal dynamics leading to complex disease.

Phylogenetic conservation of gene proximity may manifest itself in the presence of sets of orthologous genes in gene loci from different genomes. However, even in prokaryotes, it often comes up as conservation of positional connections between and inside particular pathways, not exactly the same representatives of the pathways.[12,18] Therefore, integration of genomic data may uncover trends in gene positional clustering and the underlying functional links between genes and pathways. Analysis of our data points to initiation of translation as the main functional

Table 1 Tabular display of the chromosomal neighborhood of *sbds* gene in *Ciona intestinalis* genome (SEED db IDs)

ID	Start	Stop	Size (nt)	Strand	Function
Fig|7719.3.peg.1816	37845	18631	19215	–	GCN1-like protein 1
Fig|7719.3.peg.1817	**46144**	**45386**	**759**	–	**Shwachman-Bodian-Diamond syndrome protein**
Fig|7719.3.peg.1818	77340	70503	6838	–	tRNA/RNA cytosine-C5-methylase (EC 2.1.1.-)
Fig|7719.3.peg.1819	94790	77229	17562	–	Protein kinase C, beta type (EC 2.7.11.1)

Note: Line corresponded to a gene for SBDS protein ortholog is highlighted.

Table 2 Tabular display of the chromosomal neighborhood of *sbds* gene in *Plasmodium falciparum* genome (SEED db IDs)

Fig|36329.1.peg.1979	427190	428587	1398	+	Eukaryotic translation initiation factor 2 γ subunit
Fig|36329.1.peg.1980	430860	429689	1005	–	Hypothetical protein
Fig|36329.1.peg.1981	433950	435317	519	+	Hypothetical protein
Fig|36329.1.peg.1982	**437223**	**439465**	**1917**	**+**	**Shwachman-Bodian-Diamond syndrome protein**
Fig|36329.1.peg.1983	440540	447009	5856	+	Hypothetical protein
Fig|36329.1.peg.1986	458795	460450	1656	+	Hypothetical protein
Fig|36329.1.peg.1987	467450	461400	6051	–	DNA polymerase I (EC 2.7.7.7)
Fig|36329.1.peg.1988	468987	472015	2832	+	Hypothetical protein
Fig|36329.1.peg.1989	472942	474825	1884	+	GTP-binding protein, putative
Fig|36329.1.peg.1990	475248	477296	2049	+	Putative ribosomal RNA small subunit methyltransferase J (EC 2.1.1.-)

Note: Line corresponded to a gene for SBDS protein ortholog is highlighted.

connection for SBDS (Figure 3), with particular TYW1 and SBDS functional coupling as characteristic of all the studied vertebrate genomes.

Wybutosine is a hypermodified guanosine with a tricyclic base found at the 3′-position adjacent to the anticodon of eukaryotic phenylalanine tRNA. The UUU phenylalanine codon is highly prone to frameshift in the 3′ (rightward) direction at pyrimidine 3′ contexts,[19] and wybutosine supports reading frame maintenance by stabilizing codon–anticodon interactions during decoding on the ribosome.[20,21] Wybutosine synthesis might proceed through sequential reactions in a multiple protein complex assembled with the precursor tRNA and may be linked to exosomal/proteosomal structure that includes the SBDS protein. Comparative analysis of archeal *sbds* loci stresses the potential involvement of SBDS in the exosomal complex where functions of translation, RNA processing, and degradation are tightly coupled.[22]

The SBDS protein has a thioredoxin fold, which might be directly coupled to the function of wybutosine reductase. Not all stages of wybutosine biosynthesis are known. There is some ambiguity surrounding the source of the C2 atom in wybutosine, suggested to originate from an intermediate in lysine metabolism. Interestingly, SBDS was shown to interact physically (Reactome db) with methylmalonate semialdehyde dehydrogenase, the enzyme in the branched-chain amino acid degradation pathway. It would be too speculative to go further, but the possible involvement of the SBDS protein in biosynthesis of wybutosine merits experimental validation.

Considering an alternative link between wybutosine and SBDS, we may suggest involvement of SBDS in degradation of noncharged or not properly modified tRNA. The tRNA surveillance pathway has been shown to exist in yeast and requires the exosome for polyadenylation and degradation of hypomodified pre-tRNA(i)(Met).[23] Analogously, tRNA(Phe) without a modified wybutosine residue may be subject to degradation, and therefore SBDS may play some role in this process. The N-terminus of the Yhr087wp yeast protein has a fold similar to that in SBDS. It also has 2.4e-06 and 100.00% homology with bacterial tRNA pseudouridine 13 synthase, that may support an involvement of Yhr087wp itself and SBDS protein in tRNA modification. Genes do not cluster in *S. cerevisiae* orthologs of SBDS (Q07953, SDO1) and TYW1 (Q08960, Tyw1p). However, the *tyw1* locus in *S. cerevisiae* also contains a gene for tRNA pseudouridine synthase 1 (YPL212C) and a number of genes encoding proteins of ribosomal biogenesis.

Establishing a link between SBDS and tRNA modification provides an interesting aspect of crosstalk between cytoskeleton function and translation machinery that may explain a faulty chemotactic phenotype of SBDS malfunction.

Table 3 Tabular display of the chromosomal neighborhood of SBDS-encoding genes in *Schizosaccharomyces pombe* genome (SEED db IDs)

Fig |4896.1.peg.3836	2660945	2660505	–	SSU ribosomal protein S12p (S23e), mitochondrial
Fig |4896.1.peg.3837	2661984	2662340	+	LSU ribosomal protein L40 mt, mitochondrial
Fig |4896.1.peg.3838	2663620	2662700	–	RNA processing factor 1
Fig |4896.1.peg.3839	**2665276**	**2664342**	**–**	**Shwachman-Bodian-Diamond syndrome protein**
Fig |4896.1.peg.3840	2666151	2666990	+	LSU ribosomal protein L24p (L26e), mitochondrial
Fig |4896.1.peg.3841	2667934	2667270	–	Putative breast adenocarcinoma marker
Fig |4896.1.peg.3842	2669311	2670276	+	Putative mRNA capping enzyme subunit
Fig |4896.1.peg.3843	2671220	2670798	–	Deoxyuridine 5 and 39;-triphosphate nucleotidohydrolase (EC 3.6.1.23)
Fig |4896.1.peg.3844	2673717	2671936	–	Mitosis inducer protein kinase cdr1

Note: Line corresponded to a gene for SBDS protein ortholog is highlighted.

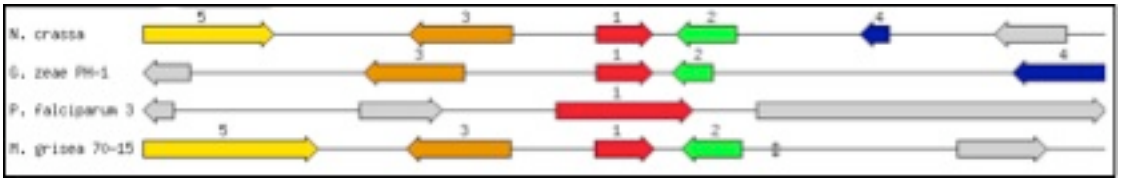

Figure 3 Graphical display of the chromosomal neighborhood of *sbds* genes in fungal genomes. Arrows correspond to open reading frames encoding: 2- SSU ribosomal protein S18e (S13p), 3-carboxypeptidase precursor, and 4- and 5-hypothetical proteins. 100 kbp regions are shown. Organisms are *Neurospora crassa*, *Gibberella zeae*, *Plasmodium falciparum*, and *Magnaporthe grisea*.

In the *P. falciparum* and *C. intestinalis* genomes, SBDS genes are colocalized with functions associated with tRNA-regulated components of translational initiation complexes.[24] GCN1 is a translational activator and regulator of Gcn2p kinase activity. It forms a complex with Gcn20p and is proposed to stimulate Gcn2p activation by an uncharged tRNA.[24,25] The second gene colocalized with *sbds* in the sea squid genome is a gene for tRNA/RNA cytosine C5 methylase, which is required for initiating tRNA(i) (Met) modification. Eukaryotic and archeal initiation factors 2 are heterotrimeric proteins where only the γ subunit of the *aIF2αβ* heterodimer contacts tRNA.[26] Intriguingly, the *aIF2β* gene is colocalized with *sbds* in a genome of *Plasmodium* (Figure 3).

Indirect evidence implicates actin as a cofactor in eukaryotic protein synthesis. The principle function of EF-1α is to bind aminoacyl-tRNA to the ribosome. EF-1α also interacts with the cytoskeleton by binding and bundling actin filaments and microtubules, and can alter the assembly of F-actin, a filamentous scaffold on which nonmembrane-associated protein translation take place[27] (Figure 4). F-actin and aa-tRNA compete for EF-1α, and

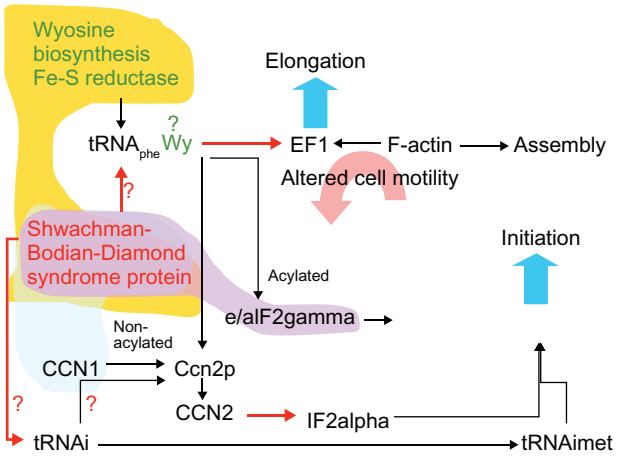

Figure 4 Hypothetical functions of SBDS protein, and their effect on chemotaxis. Clouds represent gene proximity in different groups of organisms, ie, vertebrates (yellow), *Ciona intestinalis* (blue), and *Plasmodium falciparum* (purple).

their binding is pH-dependent and mutually exclusive. Release of EF-1α from actin binding was suggested to cause a transient increase in local concentration of the factor to facilitate polypeptide elongation. This interrelationship may ensure that cell proliferation and steady-state protein synthesis is separated from cell migration caused in primitive eukaryotic ancestors by starvation or by an avoidance response to other stressors.

There is also a crosstalk between the two systems in establishing cell polarity during chemotaxis. It has been proposed that the EF-1α-F-actin complex is an important scaffold for anchoring of β-actin mRNA to sites of active actin polymerization.[28] Translation only occurs when the RNA-protein complex reaches its destination at the periphery of the cell.[29] Nothing is known about localization of exosome complexes to cellular lamella, but the processes of translation and degradation of RNA species are likely to be colocalized and to be coordinated by cell locomotion.

It can be suggested that binding of tRNAphe with or without wybutosine modification differentially affects EF-1α. For example, tRNAphe without wybutosine modification can bind to EF-1α with a higher affinity, and eventually lead to cell polarization/arrest of movement. In this case, the function of the SBDS protein would be in downregulation or destruction of EF-1α, thereby inhibiting tRNA(s). It was shown recently that SBDS protein is also required for release and recycling of the nucleolar shuttling factor, Tif6, from pre-60S ribosomes,[30] and also for pre-rRNA modifications and final maturation of the ribosome.[31] Both processes can be regulated and coordinated with ribosomal transport to the cell periphery where actin translation and assembly takes place.[32,33]

We suggest a multiple involvement of SBDS protein in initiation and stability of translation in vertebrates. The suggested roles for this protein in wybutosine/tRNA metabolism would complement its potential involvement in the ribosome assembly recently reported for yeast and would crosstalk tightly, with establishment of cell polarity

and cell locomotion. Experimental validation of the relationship between SBDS, wybutosine synthesis, and/or degradation of tRNAphe seems plausible, and we hope that our suggestions will attract the attention of biologists in related fields.

It is still not clear what functional features of a gene pair (structural or functional specificity of the encoded proteins, topology of their interaction, presence of a direct protein–protein contact) correlate significantly with their colocalization. Validation of genomic clustering of genes encoding metabolic functions demonstrates 90% correlation for yeast and just slightly less for a human genome. A high correlation was also shown between gene colocalization and their temporal and spatial expression profiles.[14,16] All the existing studies point to phenotypic associations between genes clustered in genomes, but more information is required for a proper large-scale statistical analysis of the correlation. We hope that case-by-case analysis will support the general validity of this method and lead to a routine automatic approach to functional classification of eukaryotic proteins via systematic comparative genomics.

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Disclosure

The author reports no conflict of interest in this work.

References

1. Shammas C, Menne TF, Hilcenko C, et al. Structural and mutational analysis of the SBDS protein family. Insight into the leukemia-associated Shwachman-Diamond syndrome. *J Biol Chem*. 2005;280:19221–19229.
2. Bateman A, Birney E, Cerruti, et al. The Pfam Protein Families Database *Nucleic Acids Res*. 2002;30:276–280.
3. Boocock GR, Morrison JA, Popovic M, et al. Mutations in SBDS are associated with Shwachman-Diamond syndrome. *Nat Genet*. 2003;33:97–101.
4. de Oliveira JF, Sforça ML, Blumenschein TM, et al. Structure, dynamics, and RNA interaction analysis of the human SBDS protein. *J Mol Biol*. 2010;396:1053–1069.
5. Wu LF, Hughes TR, Davierwala AP, Robinson MD, Stoughton R, Altschuler SJ. Large-scale prediction of *Saccharomyces cerevisiae* gene function using overlapping transcriptional clusters. *Nat Genet*. 2002;31:255–265.
6. Peng WT, Robinson MD, Mnaimneh S, et al. A panoramic view of yeast noncoding RNA processing. *Cell*. 2003;113:919–933.
7. Savchenko A, Krogan N, Cort JR, et al. The Shwachman-Bodian-Diamond syndrome protein family is involved in RNA metabolism. *J Biol Chem*. 2005;280:19213–19220.
8. Jorgensen R, Ortiz PA, Carr-Schmid A, Nissen P, Kinzy TG, Andersen GR. Two crystal structures demonstrate large conformational changes in the eukaryotic ribosomal translocase. *Nat Struct Biol*. 2003;10:379–385.
9. Oubridge C, Ito N, Evans PR, Teo CH, Nagai K. Crystal structure at 1.92 A resolution of the RNA-binding domain of the U1A. *Nature*. 1994;372:432–438.
10. Stepanovic V, Wessels D, Goldman FD, Geiger J, Soll DR. The chemotaxis defect of Shwachman-Diamond syndrome leukocytes. *Cell Motil Cytoskeleton*. 2004;57:158–174.
11. Wessels D, Srikantha T, Yi S, Kuhl S, Aravind L, Soll DR. The Shwachman-Bodian-Diamond syndrome gene encodes an RNA-binding protein that localizes to the pseudopod of Dictyostelium amoebae during chemotaxis. *J Cell Sci*. 2006;119:370–379.
12. R Overbeek R, Fonstein M, D'Souza M, Pusch GD, Maltsev N. The use of gene clusters to infer functional coupling. *Proc Natl Acad Sci U S A*. 1999;96:2896–2901.
13. Vasieva O, Wolf R. Unraveling functional networks: does gene clustering have a meaning? *BMC Sys Biol*. 2007;1(Suppl v1):84.
14. Lee JM, Sonnhammer EL. Genomic gene clustering analysis of pathways in eukaryotes. *Genome Res*. 2003;5:875–882.
15. Volpi EV, Chevret E, Jones T, et al. Large-scale chromatin organization of the major histocompatibility complex and other regions of human chromosome 6 and its response to interferon in interphase nuclei. *J Cell Sci*. 2000;113:1565–1576.
16. Hurst LD, Pal C, Lercher M. The evolutionary dynamics of eukaryotic gene order. *Nat Rev Genet*. 2004;5:299–310.
17. Vasieva O. The many faces of glutathione transferase pi. *Curr Mol Med*. 2011;11:129–139.
18. Overbeek R, Begley T, Butler RM, et al. The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. *Nucleic Acids Res*. 2005;33:5691–5702.
19. Schwartz R, Curran JF. Analyses of frameshifting at UUU-pyrimidine sites. *Nucleic Acids Res*. 1997;25:2005–2011.
20. Noma A, Kirino Y, Ikeuchi Y, Suzuki T. Biosynthesis of wybutosine, a hyper-modified nucleoside in eukaryotic phenylalanine tRNA. *EMBO J*. 2006;25:2142–2154.
21. Salomon R, Giveon D, Kimhi Y, Littauer UZ. Abundance of $tRNA^{Phe}$ lacking the peroxy Y-base in mouse neuroblastoma. *Biochemistry*. 1976;15:5258–5262.
22. Koonin EV, Wolf YI, Aravind L. Prediction of the archaeal exosome and its connections with the proteasome and the translation and transcription machineries by a comparative-genomic approach. *Genome Res*. 2001;11:240–252.
23. Kadaba S, Krueger A, Trice T, Krecic AM, Hinnebusch AG, Anderson J. Nuclear surveillance and degradation of hypomodified initiator tRNAmet in *S. cerevisiae*. *Genes Dev*. 2004;18:1227–1240.
24. Olsen DS, Savner EM, Mathew A, et al. Domains of eIF1 A that mediate binding to eIF2, eIF3 and eIF5B and promote ternary complex recruitment in vivo. *EMBO J*. 2003;22:193–204.
25. Kubota H, Ota K, Sakaki Y, Ito T. Budding yeast GCN1 binds the GI domain to activate the eIF2alpha kinase GCN2. *J Biol Chem*. 2001;276:17591–17596.
26. Yatime L, Mechulam Y, Blanquet S, Schmitt E. Structural switch of the γ subunit in an archaeal aIF2αγ heterodimer. *Structure*. 2006;14:119–128.
27. Liu G, Tang J, Edmonds BT, Murray J, Levin S, Condeelis J. F-actin sequesters elongation factor from interaction with aminoacyl-tRNA in a pH-dependent reaction. *J Cell Biol*. 1996;135:953–963.
28. Liu G, Grant WM, Persky D, Latham VM Jr, Singer RH, Condeelis J. Interactions of elongation factor 1a with F-actin and b-actin mRNA: Implications for anchoring mRNA in cell protrusions. *Mol Biol Cell*. 2002;13:579–592.
29. Hüttelmaier S, Zenklusen D, Lederer M, et al. ZBP1 enhances cell polarity and reduces chemotaxis. *J Cell Sci*. 2005;120:3173–3178.

30. Menne TF, Goyenechea B, Sánchez-Puig N, et al. The Shwachman-Bodian-Diamond syndrome protein mediates translational activation of ribosomes in yeast. *Nat Genet*. 2007;39:486–495.
31. Savchenko A, Krogan N, Cort JR, et al. The Shwachman-Bodian-Diamond syndrome protein family is involved in RNA metabolism. *J Biol Chem*. 2005;280:19213–19220.
32. Mirra SS, Miles ML, Jacobs J. The coexistence of ribosome-lamella complex and annulate lamellae in chronic lymphocytic leukemia. *Ultrastruct Pathol*. 1981;2:249–256.
33. Sigler E, Shvidel L, Shtalrid M, Berribi A, Shaft D, Resnitzky P. Ribosome-lamella complexes in a patient with aggressive chronic lymphocytic leukemia. *Leuk Lymphoma*. 2007;48:434–436.