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Review

RNA interference: a pathway to drug target identification and validation in trypanosome

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RNA interference (RNAi) is a phenomenon through which double stranded RNA (dsRNA) induces potent sequence-specific degradation of homologous transcripts. Besides its function in cellular defense and developmental regulation, it has emerged as an invaluable tool for elucidation of gene function and drug target validation. This is particularly useful when substantial genome sequence data are available. Gene silencing using RNAi can aid translation of raw genomic sequence data into biologically relevant information toward the development of new and/or improved control strategies. Here, we review the current status of RNAi in trypanosome research focusing on challenges involved in the utilization of the technique as well as its potential application in drug target discovery and validation.

Key words: RNA interference, trypanosomes, gene silencing, RNAi library, drug targets

INTRODUCTION

RNA interference (RNAi) is the phenomenon where double stranded (ds) RNA induces sequence-specific silencing of genes by degradation of complimentary RNA in a cell. This silencing phenomenon is widespread in eukaryotes and has been previously linked to post-transcriptional gene silencing (PTGS) in plants (Jorgensen, 1990; Napoli et al., 1990; Flavell, 1994; Matzke et al., 2000; Baulcombe, 2004) and quelling in fungi (Romano and Macino, 1992; Fagard et al., 2000; Vaucheret et al., 2001). It has also been reported in *Caenorhabditis elegans* (Fire et al., 1998), mammalian cells (Montgomery et al., 1998; Elbashir et al., 2001a) and insects (Caplen et al., 2001). It is thought to be an evolutionarily conserved mechanism that inhibits the replication and expression of selfish DNA elements and viruses (Caplen et al., 2001; Chi et al., 2003; Matzke et al., 2002) and hence maintains genome integrity. Although its protective role against pathogens would be very important in plants and worms such as *Caenorhabditis elegans* (Milhavet et al., 2003) which lack humoral defense system analogous to that found in animals, its role in mammalian cells remains unclear. It is suggested that it must have evolved as a cellular defense mechanism against foreign DNA and RNA regulating the expression of endogenous genes (Milhavet et al., 2003). In addition, the process has been implicated in cellular processes such as gene expression (Iorio et al., 2005), differentiation (Song and Tuan, 2006; Callis et al., 2007), proliferation, apoptosis (Jovanovic and Hengartner, 2006), metabolism and signaling (Yoo and Greenwald, 2005) hence involved in animal and plant development (reviewed by Carrington and Ambros, 2003; Harfe, 2005; Kloosterman and Plasterk, 2006).

The biological role of RNAi in disease causing trypanosomes is not clear. Although abolition of RNAi by deletion of genes responsible of the process cause a transient defect in chromosome segregation and mitosis (Durand-Dubief and Bastin, 2003) and augment levels of retroposon transcripts (Shi et al., 2004), parasites lacking RNAi are fully capable of undergoing a complete life cycle (Janzen et al., 2006). The discovery of RNAi in trypanosomes has provided a basis for the elaboration of powerful research tools in reverse genetics studies and utilization of raw and rapidly accumulating information available in the trypanosome genome database. The technique is of immense power in functional genomics. Its ability to specifically ablate the function of individual genes makes RNAi an invaluable tool in drug target discovery and validation. In this review, advances and chal-

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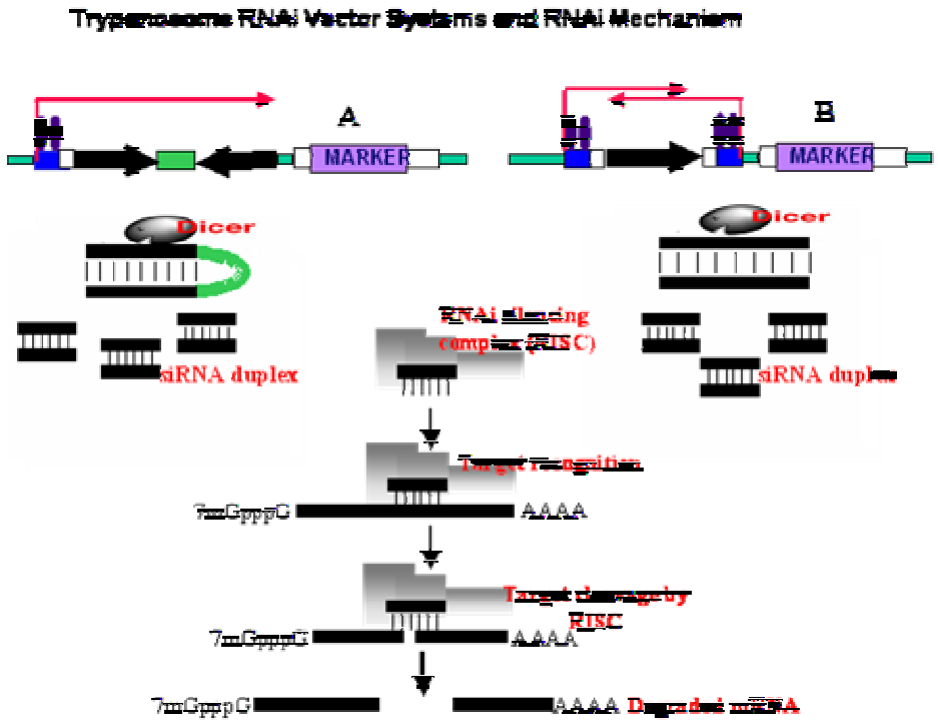

Figure 1. The two types of trypanosome double stranded RNA expression constructs. A: single inducible promoter driving head to head arranged gene fragments. B: two opposing inducible promoters controlling the expression of a single copy gene fragment. Double stranded RNA is cleaved by dicer into 21- to 23-nt siRNAs, which is complexed with a RNA silencing complex, the RISC. RISC unwinds the siRNA to help target the appropriate mRNA. The siRNA-mRNA hybrid is cleaved, releasing the siRNA, and the mRNA is degraded by endo and exonucleases.

lenges of RNAi in trypanosome research with respect to drug target validation are discussed.

RNAi mechanism and classes of small RNAs

Studies over the last several years have demonstrated that RNAi is mediated by the generation of 21- to 23-nucleotide dsRNA molecules, termed small interfering RNA (siRNA) (Elbashir et al., 2001a; Dillin, 2003; Dykxhoorn et al., 2003). They have a characteristic structure, with 5'-phosphate/3'- hydroxyl ends and a 2-base 3' overhang on each strand of the duplex (Dykxhoorn et al., 2003) . Upon entry into the cell, dsRNA is cleaved into siRNAs by the action of RNase- III-type enzyme Dicer (Jones et al., 2004; Pauls and Esté, 2004). The siRNAs are incorporated into a protein-RNA complex, the RNA-induced silencing complex (RISC) (Nykanen et al., 2001; Schwarz et al., 2002; Schwarz et al., 2003; Dykxhoorn et al., 2003). There is a strict requirement for the 3' siRNA to be 5' phosphorylated to enter into RISC, and siRNAs that lack a 5' phosphate are rapidly phosphorylated by an endogenous kinase (Dykxhoorn et al., 2003). The duplex siRNA is unwound, leaving the antisense strand to guide RISC to the homologous target mRNA for endonucleolytic cleavage (Pauls and Esté, 2004). The target mRNA is cleaved at a single site in the centre of the duplex region between the guide siRNA and the target mRNA, 10-nt from the 5' end of the siRNA. Mismatches >1-2bp within the 21- to 23-nt siRNA effectively disrupts proper degradation of the target mRNA (Dillin, 2003). The synthesis of the protein encoded by the mRNA targeted by the siRNAs is thus prevented and that protein is selectively depleted from the cell. The RNAi process is shown in Figure 1.

Presently, four major classes of small RNAs that mediate RNA silencing have been described. They include small interfering RNAs (siRNAs) (Elbashir et al., 2001a; Elbashir et al., 2001b), microRNAs (miRNAs) (Nelson et al., 2001; Lagos-Quintana et al., 2001; Lau et al., 2001), small heterochromatic RNAs (Reinhart et al.,, 2002) and Piwi-interacting RNA (piwiRNAs) (Aravin et al., 2006; Lau et al., 2006; Brower-Toland et al., 2007). Small interfering RNAs (siRNAs) are 21-23 nucleotide dsRNAs and are the hallmark of `classical` RNAi. MicroRNAs are pro-cessed by the RNase III enzyme Drosha to produce a hairpin RNA of ~70 nucleotides (Lee et al., 2002). The hairpin is subsequently exported into the cytoplasm by

exportin-5 (Jones et al., 2004). Pre - miRNA is then cleaved by the Dicer to produce a double stranded 21- to 23- nucleotide RNA duplex (Grishok et al., 2001; Hutvagner et al., 2001). Like siRNAs, they direct silencing as in siRNA-mediated mRNA cleavage in case of complete complementarity to the target transcript (Ambros et al., 2003; Doench et al., 2003; Chen et al., 2004). In case of incomplete complementarity, miRNA blocks mRNA translation through imperfect complementary binding of the antisense sequence to the miRNA recognition elements (MREs) within the 3` untranslated region (UTR) (Jones et al., 2004). This miRNA translation repression process is distinct from siRNA-directed mRNA cleavage. Doench et al., (2003) have however shown that siRNAs can mediate miRNA-dependent translation repression. In eukaryotes, centromeric silencing has been reported to occur via small heterochromatin RNAs (Volpe et al., 2002). In *Schizosaccharomyces pombe,* they have been implicated in epigenetic modification (Reinhart et al , 2002; Volper et al., 2002) through hetero-chromatic silencing thought to occur through RNA-directed transcriptional silencing involving histone H3 methylation and heterochromatin formation (Stevenson and Jarvis, 2003). The mechanism of this type of RNA interference has been suggested by Volpe et al. (2002). Piwi-interacting RNAs, which utilize piwi-interacting RNA complex (piRC) have been isolated in rat testes (Lau et al., 2006) and Drosophila (Saito et al., 2006) and are implicated in posttranscriptional gene silencing (Carthew, 2006) and defense of genomes from transposons (Saito et al., 2006; Aravin et al., 2007).

RNAi in trypanosome genome studies

Characterization of putative coding regions is a prerequisite for converting raw genomic sequence data into biologically relevant information (Gopal et al., 2003). With the completion of trypanosome and leishmania genome projects (Berriman et al., 2005; El-Sayed et al., 2005a; Ivens et al., 2005), a wealth of information is available at the genome database at GeneDB (http://www.geneDB.org) (Arnaud Kerhornou and The Sanger Institute Pathogen Sequencing Unit, 2002; Hertz-Fowler et al., 2004). This can be exploited using techniques such as RNAi, which has been shown to occur in *Trypanosoma brucei* (Ngô et al., 1998) and *T. congolense* (Inoue et al., 2002) but not in *T. cruzi* (DaRocha et al., 2004) or *Leishmania spp.* (Robinson and Beverley, 2003).

RNAi in *T. brucei* was first reported in abstracts presented by Elisabetta Ullu and co workers in the Molecular Parasitology Meeting at Woods Hole, MA, in 1997. Ullu et al., (2004) have given a comprehensive review of RNAi mechanism in *T. brucei*. The RNAi technique is used to knock down the expression of a specific mRNA in African trypanosomes for the purpose of examining the function of its genes (DaRocha et al., 2004). It circumvents the necessity of generating double knockouts, which is a requirement for such studies in diploid organisms; hence it is a simpler and faster method. Additionally, there is no need of prior knowledge on the chromosomal location of gene(s) under study. It works well in *T. brucei* due to the presence of Dicer (Shi et al., 2006) and a member of argonaute (AGO) protein family, TbAGO1 (Durand-Dubief and Bastin, 2003; Shi et al., 2004). The RNAi mechanism is also functional in *T. congolense* (Inoue et al., 2002). Since this finding, more has been done on utilization of this technique in trypanosome gene functions studies (Wang et al., 2000; Morris et al., 2001; Hendriks et al., 2003), development of cell lines (Wirtz et al., 1999; Chen et al., 2003; DaRocha et al., 2004; Alibu et al., 2005; Alsford et al., 2005), construction of plasmid vectors for RNAi delivery (Wirtz et al., 1999; Wang et al., 2000; LaCount et al., 2000; Gull et al., 2002; Wickstead et al., 2002; Motyka et al., 2004; DaRocha et al., 2004; Alibu et al., 2005), *in vivo* analysis (Tschudi et al., 2003), RNAi library construction (Morris et al., 2002; Drew et al., 2003; Englund et al., 2005) and designing siRNAs (Redmond et al., 2003). Redmond et al., (2003) have developed a web-based tool for designing RNAi targets in *T. brucei*. This *T. brucei* functional genomics project (TrypanoFAN: http://trypanofan.path.cam.ac.uk/trypanofan/main/) aims to utilise the information from the *T. brucei* genome project to produce a research resource and systematic collection of mutants by targeted gene inactivation using RNAi. Trials by Subramaniam and coworkers (2004) on open reading frames (ORFs) in chromosome 1 have demonstrated its applicability as a robust and systematic functional annotation tool. These developments are important in the utilization of genome sequence for valuable functional studies and drug target discovery and validation.

Vehicles of siRNA delivery in trypanosomes

The success of RNAi in potential drug target discovery and validation depends on the efficient delivery of siRNA *in vivo*. Principally, two modes of delivery (plasmid/vector-based and chemically synthesized siRNA) are utilized. Direct siRNA transfections have the advantage of high efficiency and immediate initiation of gene silencing when compared to plasmid DNA transfections. Plasmid based siRNA on the other hand allows storage of trypanosomes with inducible RNAi and is much less expensive.

In trypanosome research, two types of plasmid-based double stranded RNA expression constructs have been developed. The first type has a single inducible promoter driving head to head arranged gene fragments (Ngô et al., 1998; Shi et al., 2000) (Figure 1, panel A), while the second has two opposing inducible promoters controlling the expression of a single copy gene fragment (Wang et al., 2000; LaCount et al., 2000) (Figure 1, panel B). Additionally, they have another promoter that drives the

expression of a selectable marker (Biebinger et al., 1996; Wirtz et al., 1999), usually a gene that confers antibiotic resistance. Where two opposing bacteriophage T7 promoters are used, control of expression is by binding of the tetracycline (*tet*) repressor to *tet* operators (Wang et al., 2000; Morris et al., 2001; LaCount et al., 2002). Examples of this type of inducible RNAi vectors are pZJM (Wang et al., 2000) and p2T7^{Ti} (LaCount et al., 2002). They are widely used because they allow a single ligation of PCR-generated fragments of any target gene between the opposing tetracycline-inducible T7 promoters (Wang et al., 2000; Motyka et al., 2004). Transcription of the insert in both directions is activated by induction with tetracycline.

Type two constructs are the stem-loop vectors and include pLEW79, pLEW100, pHD1145 (for procyclics), pHD1146 (for blood stream forms) and pHD1336 (Wirtz et al., 1999; Wang et al., 2000; Estévez et al., 2003). They involve cloning of the insert twice in opposite direction on either sides of a 'stuffer' fragment. The transcription of the (target) -stuffer-(reverse-target) construct generates a stem-loop RNA that mediates RNA interference (Alibu et al., 2005). A linearized construct allows integration by homologous recombination into the ribosomal DNA (rDNA) spacer region, a transcriptionally inactive segment of the *T. brucei* genome (Morris et al., 2001; LaCount et al., 2002; Motyka et al., 2004; Alibu et al., 2005). Transcription occurs on induction with tetracycline, hence producing mRNA homologs to the target the gene.

Challenges of RNAi in trypanosome research

Various limitations have been experienced in RNAi in trypanosomes. These generally involve the generation and maintenance of recombinants. First, "background" expression from the "repressed" tetracycline-inducible opposing T7 promoters affects selection of suitable transformants (Wirtz et al., 1998; Wang et al., 2000; Chen et al., 2003; Alibu et al., 2005). This has been an important limitation to knockdown studies of several genes essential to trypanosomes (Chen et al., 2003; Alibu et al., 2005). To overcome this, the use of stem loop constructs under the control of tightly regulated inducible EP promoters has been undertaken (Shi et al., 2000; Alibu et al., 2005) . This approach however requires several cloning steps and some sequence combinations resist cloning (Drozdz et al., 2002; Alibu et al., 2005). In addition, the EP promoter is down regulated in blood stream forms (Biebinger et al., 1996; Alibu et al., 2005). To mitigate against this, Alsford and colleagues (2005) have developed bloodstream cell lines that exploit the strengths of inducible rRNA promoter.

The second limitation involves the development of RNAi revertants through deletion of target gene inserts (Chen et al., 2003). No appropriate solution has been achieved to this problem. However, precautionary measures taken involve the use of stem loop vectors, clonal RNAi populations (Motyka et al., 2004) and avoiding selection of transformants over long periods of time since the revertants begin to occur after the third day of induction (Alsford et al., 2005).

The third limitation is the variation in regulation of expression of constructs due to availability of various sites for integration (Biebinger et al., 1996; Alsford et al., 2005) and integration into an unintended region (Motyka et al., 2004). In the latter, Motyka et al. (2004) observed a change in orientation of dual T7 promoters in non stem-loop vectors resulting in transcription of distant genes. Since regulation is chromosomal and position dependent (Biebinger et al., 1996), variations occur in the clones generated. To circumvent this position effect, Alsford et al. (2005) propose using a locus tagged with a unique sequence that allows constructs to be reproducibly inserted into the same genomic location. In their attempts to use this approach, they reported an advantage in reducing the amount of DNA used for transfection from 10 g to ~5 g. In addition, they developed a new blood stream cell line that allows high efficiency DNA-mediated transformation, addressing the fourth limitation of difficulties in generating recombinant bloodstream-forms.

The fifth limitation is the possible integration of the constructs in unanticipated regions rather than the transcriptionally inactive rDNA locus hence transcriptional up- regulation of the genes upstream and downstream of the integration sites as observed by Motyka et al., (2005). This knockdown affects more than one protein. They suggested a complete *Not I* digestion of constructs prior to transfection to avoid integration via circular plasmid and confirmation of integration sites in the clones developed.

The sixth shortfall is the inability to achieve a complete abolishment of gene function (Balana-Fouce and Reguera, 2007) hence the undetectable levels of the respective protein present (Motyka et al, 2004) can rescue the cells from potential lethal effects. Therefore, resulting phenotypes with no significant changes in morphology or organelles organization or growth rate, do not necessarily depict an unimportant gene in viability. In addition, high expression levels and stability of the some protein enables residual effects, resulting in false negative phenotypes. To overcome this shortfall, the development of live-cell reporter strains suggested by Subramaniam *et al.* (2004) could be an option for improving sensitivity and better interrogations. Precautionarily, RNAi experiments on both procyclic and bloodstream forms of the parasites should be encouraged since certain genes are developmentally regulated.

These drawbacks indicate that the success of various studies is pegged back by important limitations. Hence, efforts to develop an optimized RNAi toolkit that will allow an exhaustive analysis of gene function in trypanosomes need to continue. This would significantly enhance our knowledge of the biology of other members of disease

causing kinetoplastids, *T. cruzi* and *Leishmania spp.* which share 76% of genes with *T. brucei* (El-Sayed et al., 2005b).

The RNAi Library

Englund et al. (2005) have developed an RNAi library as a forward genetics approach to high throughput screening of trypanosomes genes. This involves the cloning of short random genomic fragments (approximately 0.7 kb) into a double T7 vector, transfection, generation and selection of clones with desired phenotypes. They applied this approach successfully in discovery of new genes for kDNA replication. It opens a wide window for a speedy characterization of genes responsible for important phenotypes and those essential for viability, leading to the identification of novel potential drug targets and biochemical processes. This overcomes the ap-proach of reciprocal BLAST searches used in identi-fying orthologous and paralogous genes that are limited when the nature of proteins or pathways are unknown, as is the case for many biological processes in trypa-nosomes.

The RNAi library approach has a number of limitations, especially with regard to choosing the appropriate inserts. First, in cases where fragments have a *Not I* restriction site(s), integration of the constructs could occur in undesired sites as explained above. Second, it will be difficult to generate appropriate insert sizes (about 500bp) from digested total genomic DNA hence high possibilities of non-specific knockdowns. Third, though ideally rare, the criteria of not including the initiator ATG codon but using the region close to it hence the risk of forming a truncated protein is a possibility (Clayton et al., 2005). Fourth, generation of a library that covers a 26 megabase genome (Berriman et al., 2005) is not easily achievable because large numbers of recombinant trypanosomes will be required to cover a small percent-tage of the genome.

RNAi library approach should thus be applied with great caution but its use and improvement will be invaluable in genomics studies. One potential application could be to develop a cDNA based RNAi library similar to yeast two-hybrid cDNA library. This would allow investi-gation of genes expressed during specific develop-mental stages, and offer an alternative to the use of micro-arrays, which require considerable skill and the invest-ment.

RNAi and drug target validation in trypanosomiasis

African trypanosomiasis remains among the most neglected tropical diseases in terms of drug development (Morel, 2003; Fairlamb, 2003; Pink et al., 2005). With none of the current control strategies being completely effective and resurgence of the disease (Legros et al., 2002), there is a great need for improvement of current approaches and development of new ones. Chemotherapy, which remains the mainstay for control is becoming increasingly compromised by drug resistance and toxicity (Verlinde et al., 2001). This is due to continued use of the few available drugs, which have resulted into multiple resistance (Matovu et al., 2001; Geerts et al., 2001) , yet development of new drugs remains extremely slow.

Developing a new drug involves the identification and early (pre-clinical) validation of novel biological targets, a process termed target discovery (Lindsay, 2003; Knowles et al., 2003) . In trypanosomes, various potential drug targets have been investigated. They include glycolysis (Verlinde et al., 2001), redox metabolism (Hunter et al., 1992; Stoll et al., 1997; D`Silva et al., 2000), purine metabolism (Chowdhury et al., 1999; Soulére et al., 1999), glycosylphosphatidylinositol (GPI) synthesis and myristate (Ferguson et al., 1999; Kimberly et al., 2001; Smith et al., 2004), fatty acid and sterol metabolism (Urbina, 1997; Urbina et al., 2002; Roberts et al., 2003), RNA editing, gene expression (Denker et al., 2002) and RNA splicing machinery (Denker et al., 2002; Owino et al., 2006). Barrett et al., (1999) and Wirth (2001) have given comprehensive reviews on potential drug targets in trypanosomes and leishmania. Using RNAi, a better understanding of these processes can be achieved. In addition, our knowledge of some of the processes has greatly improved. For example, based on the robustness of the technique, trypanosomes have been shown to synthesize fatty acids using the enzyme elongase (Lee et al., 2006) rather than a type II synthase (Kimberly et al., 2001), showing the potential to identify significant differences between parasite and host.

Comparative analysis of the trypanosome genome and those of hosts (or their relatives) can allow discovery of new targets, including genes or processes that are either absent in hosts (trypanosome specific) or, if present, are either sufficiently different to allow selective inhibition or non-essential for host survival. Switching off these genes by RNAi is an approach that can be used to determine if they are essential for growth or survival of trypanosomes, hence informing on their potential as targets for control.

Conclusion

The availability of the trypanosome genome sequence allows better understanding of known drug targets and identification of new targets. With clues of gene function available through annotation, a lot more should be done towards the conclusive determination of biological functions of these genes with priority to those that could be potential drug targets. This can be achieved using RNA-mediated RNA interference, which is fast and does not need prior knowledge of gene function. RNAi offers new hope for high throughput screening of the trypanosomes genome, with the potential discovery of new targets that can result in tools for control.

REFERENCES

Alibu VP, Storm L, Haile S, Clayton C, Horn D (2005). A doubly inducible system for RNA interference and rapid RNAi plasmid construction in *Trypanosoma brucei.* Mol. Biochem. Parasitol. 139: 75-82.

Alsford S, Kawahara T, Glover L, Horn D (2005). Tagging a *T. brucei RRNA* locus improves stable transfection efficiency and circumvents inducible expression position effects. Mol. Biochem. Parasitol. 144: 142-148.

Ambros V, Bartel B, Bartel DP, Burge CB, Carrington JC, Chen X, Dreyfuss G, Eddy SR, Griffiths-Jones S, Marshall M, Matzke M, Ruvkun G, Tuschl T (2003). A uniform system for microRNA annotation. RNA. 9: 277-279.

Aravin A, Giadatzis D, Pfeffer S, Lagos-Quintana M, landgraf P, Iovino N, Morris P, Brownstein MJ, Kuramochi-Miyagawa S, Nakano T, Chien M, Russo JJ, Ju J, Sheridan R, Sander C, Zavolan M, Tuschi T (2006). A novel class of small RNAs bind to MILI protein in mouse testes. Nature. 442: 203-207.

Aravin, AA, Sachidanandam R, Girard A, Fejes-Toth K, Hannon GJ (2007). Developmentally regulated piRNA clusters implicate MILI in transposon control. Science. 316: 744-747.

Arnaud K, The Sanger Institute Pathogen Sequencing Unit (2002). GeneDB: a repository for genome resource. JOBIM 185.

Balana-Fouce R, Reguera RM (2007). RNA interference in *Trypanosoma brucei*: a high-throughtput engine for functional genomics in trypanomastids? Trends Parasitol. 23: 348-351.

Barrett MP, Mottram JC, Coombs GH (1999). Recent advances in identifying and validating drug targets in trypanosomes and leishmanias. Trends Microbiol. 2: 82-88.

Baulcombe DC (2004). RNA silencing in plants. Nature. 431: 356-363.

Berriman M, Ghedin E, Hertz-Fowler C, Blandin G, Renauld H, Bartholomeu CD, Lennard NJ, Caler E, Hamlin NE, Haas B, Böhme U, Hannick L, Aslett MA, Shallom J, Marcello L, Hou L, Wickstead B, Alsmark UCM, Arrowsmith C, Atkin RJ, Barron AJ, Bringaud F, Brooks K, Carrington M, Cherevach I, Chillingworth T, Churcher C, Clark NL, Corton HCI, Cronin A, Davies RM, Doggett J, Djikeng A, Feldblyum T, Field MC, Fraser A, Goodhead I, Hance Z, Harper D, Harris BR, Hauser H, Hostetler J, Ivens A, Jagels K, Johnson D, Johnson J, Jones K, Kerhornou AX, Koo H, Larke N, Landfear S, Larkin C, Leech V, Line A, Lord A, MacLeod A, Mooney PJ, Moule S, Martin DMA, Morgan GW, Mungall K, Norbertczak H, Ormond D, Pai G, Peacock CS, Peterson J, Quail MA, Rabbinowitsch E, Rajandream M, Reitter C, Salzberg SL, Sanders M, Schobel S, Sharp S, Simmonds M, Simpson AJ, Tallon L, Turner CMR, Tait A, Tivey AR, Aken S, Walker D, Wanless D, Wang S, White B, White O, Whitehead S, Woodward J, Wortman J, Adams MD, Embley TM, Gull K, Ullu E, Barry JD, Fairlamb AH, Opperdoes F, Barrell BG, Donelson JE, Hall N, Fraser CM, Melville SE, El-Sayed, NM (2005). The Genome of the African trypanosome *Trypanosoma brucei.* Science. 309: 416-422.

Biebinger S, Rettenmaier S, Flaspohler J, Hartmann C, Peña-Diazw J, Wirtz LE, Hotz H, Barry JD, Clayton C (1996). The PARP promoter of *Trypanosoma brucei* is developmentally regulated in a chromosomal context. Nucleic Acids Res. 24: 1202-1211.

Brower-Toland B, Findley SD, Jiang L, Liu L, Yin H, Dus M, Zhou P, Elgin SC, Lin H (2007). Drosophila PIWI associates with chromatin and interacts directly with HP1a. Genes Dev. 21: 2300-2311.

Callis TE, Chen JF, Wang DZ (2007). MicroRNAs and cardiac muscle development. DNA Cell Biol. 26:219-225.

Caplen NJ, Parrish S, Imani F, Fire A, Morgan RA (2001). Specific inhibition of gene expression by small double-stranded RNAs in invertebrate and vertebrate systems. PNAS 98: 9742-9747.

Carrington JC, Ambros V (2003). Role of microRNAs in plant and animal development. Science. 301:336-338.

Cathew RW (2006). A new RNA dimension to genome control. Science. 313: 305-306.

Chen CZ, Li L, Lodish H, Bartel DP (2004). Micro-RNAs modulate hematopoietic lineage differentiation. Science. 303: 83-86.

Chen Y, Hung CH, Burderer T, Lee GS (2003). Development of RNA interference revertants in *Trypanosoma brucei* cell lines generated with a double stranded RNA expression construct driven by two opposing promoters. Mol. Biochem. Parasitol. 126: 275-279.

Chi JT, Chang HY, Wang NN, Chang DS, Dunphy N, Brown PO (2003). Genomewide view of gene silencing by small interfering RNAs. PNAS. 100:6289-91.

Chowdhury SF, Villamor VB, Guerrero RH, Leal I, Brun R, Croft SL, Goodman J M, Maes L, Ruiz-Perez LM, Pacanowska DG, Gilbert IH (1999). Design, synthesis, and evaluation of inhibitors of trypanosomal and leishmanial dihydrofolate reductase. J. Med. Chem. 42: 4300-4312.

Clayton CE, Estevez AM, Hartmann C, Alibu VP, Field M, Horn D (2005) Down-regulating gene expression by RNA interference in *Trypanosoma brucei*. Methods Mol. Biol. 309: 39-60.

DaRocha WD, Otsu K, Teixeira SM, Donelson JE (2004). Tests of cytoplasmic RNA interference (RNAi) and construction of a tetracycline-inducible T7 promoter system in *Trypanosoma cruzi.* Mol. Biochem. Parasitol. 133:175-86.

Denker A, Zuckerman M, Moroney A, Nilsen N (2002). New components of the spliced leader RNP required for nematode trans-splicing. Nature. 417: 667-670.

Dillin E (2003). The specifics of small interfering RNA specificity. PNAS. 100: 6289-6291.

Doench JG, Petersen CP, Sharp PA (2003). siRNAs can function as miRNAs. Genes Dev. 17: 438-442.

Drew ME, Morris JC, Wang Z., Wells L, Sanchez M, Landfear SM, and Englund PT (2003). The adenosine analog tubercidin inhibits glycolysis in *Trypanosoma bruce*i as revealed by an RNAi library. J. Biol. Chem. 278: 46596-46600.

Drozdz M, Quijada L, Clayton CE (2002). RNA interference in trypanosomes transfected with sense and antisense plasmids. Mol. Biochem. Parasitol. 121: 149-152.

D'Silva C, Daunes S (2000). Structure-activity study on the in vitro antiprotozoal activity of glutathione derivatives. J. Med. Chem. 43: 2072-2078.

Durand-Dubief M, Bastin P (2003). TbAGO1, an Argonaute protein required for RNA interference, is involved in mitosis and chromosome segregation in *Trypanosoma brucei.* BMC. Biol. 1:2.

Dykxhoorn D, Novina C, Sharp P (2003). Killing the messenger: short RNAs that silence gene expression. Nature. 4: 457-467.

Elbashir SM, Harborth J, Lendeckel W, Yalcin A, Weber K, Tuschl T (2001b). Duplexes of 21-nucleotide RNAs mediate RNA interference in cultured mammalian cells. Nature. 411: 494-498.

Elbashir SM, Lendeckel W, Tuschl T (2001a). RNA interference is mediated by 21-and 22-nucleotide RNAs. Genes Dev. 15: 188-200.

El-Sayed NM, Myler JP, Bartholomeu DC, Nilsson D, Aggarwal, G, Tran A, Ghedin E, Worthey EA, Delcher AL, Blandin G, Westenberger SJ, Caler E, Cerqueira GC, Branche C, Haas B, Anupama A, Arner E, Åslund L, Attipoe P, Bontempi E, Bringaud F, Burton P, Cadag E, Campbell DA, Carrington M, Crabtree J, Darban H, da Silveira JF, de Jong P, Edwards K, Englund PT, Fazelina G, Feldblyum T, Ferella M, Frasch AC, Gull K, Horn D, Hou L, Huang Y, Kindlund E, Klingbeil M, Kluge S, Koo H, Lacerda D, Levin MJ, Lorenzi H, Louie T, Machado CR, McCulloch R, McKenna A, Mizuno Y, Mottram JC, Nelson S, Ochaya S, Osoegawa K, Pai G, Parsons M, Pentony M, Pettersson U, Pop M, Ramirez JL, Rinta J, Robertson L, Salzberg SL, Sanchez DO, Seyler A, Sharma R, Shetty J, Simpson AJ, Sisk E, Tammi MT, Tarleton R, Teixeira S, van Aken S, Vogt C, Ward PN, Wickstead B, Wortman J, White O, Fraser CM, Stuart KD, Andersson B (2005a). The genome sequence of *Trypanosoma cruzi*, etiologic agent of Chagas disease. Science. 309: 409-415.

El-Sayed NM, Myler PJ, Blandin G, Berriman M, Crabtree J, Aggarwal G, Caler E, Renauld H, Worthey EA, Hertz-Fowler C, Ghedin E,

Peacock C, Bartholomeu DC, Haas BJ, Tran AN, Wortman JR, Alsmark UC, Angiuoli S, Anupama A, Badger J, Bringaud F, Cadag E, Carlton JM, Cerqueira GC, Creasy T, Delcher AL, Djikeng A, Embley TM, Hauser C, Ivens AC, Kummerfeld SK, Pereira-Leal JB, Nilsson D, Peterson J, Salzberg SL, Shallom J, Silva JC, Sundaram J, Westenberger S, White O, Melville SE, Donelson JE, Andersson B, Stuart KD, Hall N (2005b). Comparative genomics of trypanosomatid parasitic protozoa. Science. 309:404-409.

Englund PT, Agbo EE, Lindsay ME, Liu B, Liu Y, Motyka SA, Yildirir G, Zhao Z (2005). RNAi libraries and kinetoplast DNA. Biochem. Soc. Trans. 6:1409-1412.

Estévez A, Lehner B, Sanderson C, Ruppert T, Clayton C (2003). The roles of intersubunit interactions in exosome stability. J. Biol. Chem. 37: 34943-34951.

Fagard M, Boutet S, Morel J, Bellini C, Vaucheret H (2000). AGO1, QDE-2, and RDE -1 are related proteins required for post-transcriptional gene silencing in plants, quelling in fungi, and RNA interference in animals. PNAS. 97: 11650-11654.

Fairlamb AH (2003). Chemotherapy of human African trypanosomiasis: the current and future prospects. Trends Parasitol. 19: 488-494.

Ferguson MA, Brimacombe JS, Brown JR, Crossman A, Dix A, Field RA, Guther ML, Milne KG, Sharma DK, Smith TK (1999). The GPI biosynthetic pathway as a therapeutic target for African sleeping sickness. Biochem. Biophys. Acta. 1455: 327-340.

Fire A, Xu S, Montgomery M, Kostas S, Driver S, Mello C (1998). Potent and specific genetic interference by double-stranded RNA in *Caenorhabditis elegans*. Nature. 391: 806-811.

Flavell RB (1994). Inactivation of gene expression in plants as a consequence of specific sequence duplication. PNAS. 91:3490-3496.

Geerts S, Holmes PH, Eisler MC, Diall O (2001). African bovine trypanosomiasis: the problem of drug resistance. Trends Parasitol. 1:25-28.

Gopal S, Cross G, Gaasterland T (2003). An organism-specific method to rank predicted coding regions in *Trypanosoma brucei.* Nucleic Acid Res. 20: 5877-5885.

Grishok A, Pasquinelli AE, Conte D, Li N, Parrish S, Ha I, Baillie DL, Fire A, Ruvkun G, Mello CC (2001). Genes and mechanisms related to RNA interference regulate expression of the small temporal RNAs that control *C. elegans* developmental timing. Cell. 106: 23-34.

Gull K, Ersfeld K,Wickstead B (2002). Targeting of a tetracycline-inducible expression system to the transcriptionally silent minichromosomes of *Trypanosoma brucei*. Mol. Biochem. Parasitol. 125: 211-216.

Harfe BD (2005). MicroRNAs in vertebrate development. Curr. Opin. Gen. Dev. 15:410-415.

Hendriks E, Abdul-Razak A, Matthews K (2003). tbCPSF30 Depletion by RNA interference disrupts polycistronic RNA processing in *Trypanosoma brucei.* J. Biol. Chem. 278: 26870-26878.

Hertz-Fowler C, Peacock C, Wood V, Aslett M, Kerhornou A, Mooney P, Tivey A, Berriman M, Hall N, Rutherford K, Parkhill J, Ivens A, Rajandream M, Barrell B (2004). GeneDB: a resource for prokaryotic and eukaryotic organisms. Nucleic Acids Res. 32: D339-D343.

Hunter WN, Bailey S, Habash J, Harrop SJ, Helliwell JR, Aboagye-Kwarteng T, Smith K, Fairlamb AH (1992). Active site of trypanothione reductase. A target for rational drug design. J. Mol. Biol. 227:322-333.

Hutvagner G, McLachlan J, Pasquinelli AE, Balint E, Tuschl T, Zamore PD (2001). A cellular function for the RNA-interference enzyme Dicer in the maturation of the let-7 small temporal RNA. Science. 293: 834-838.

Inoue N, Otsu K, Ferraro D, Donelson J (2002). Tetracycline-regulated RNA interference in *Trypanosoma congolense*. Mol. Biochem. Parasitol. 120: 309-313.

Iorio MV, Ferracin M, Liu C, Veronese A, Spizzo R, Sabbioni S, Magri E, Pedriali M, Fabbri M, Campiglio M, Ménard S, Palazzo JP, Rosenberg A, Musiani P, Volinia S, Nenci I, Calin GA, Querzoli P, Negri M, Croce CM (2005). MicroRNA gene expression deregulation in breast cancer. Cancer Res. 65:7065-7070.

Ivens CA, Peacock SC, Worthey AE, Murphy L, Aggarwal G, Berriman M, Sisk E, Rajandream M, Adlem E, Aert R, Anupama A, Apostolou Z, Attipoe P, Bason N, Bauser C, Beck A, Beverley MS, Bianchettin G, Borzym K, Bothe G, Bruschi VC, Collins M, Cadag E, Ciarloni L, Clayton C, Coulson MRR, Cronin A, Cruz KA, Davies MR, De Gaudenzi J, Dobson ED, Duesterhoeft A, Fazelina G, Fosker N, Frasch CA, Fraser A, Fuchs M, Gabel C, Gob A, Goffeau A, Harris D, Hertz-Fowler C, Hilbert H, Horn D, Huang Y, Klages S, Knights A, Kube M, Larke N, Litvin L, Lord A, Louie T, Marra M, Masuy D, Matthews K, Michaeli S, Mottram CJ, Müller-Auer S, Munden H, Nelson S, Norbertczak H, Oliver K, O'Neil S, Pentony M, Pohl MT, Price C, Purnelle B, Quail AM, Rabbinowitsch E, Reinhard R, Rieger M, Rinta J, Robben J, Robertson L, Ruiz CJ, Rutter S, Saunders D, Schäfer M, Schein J, Schwartz CD, Seeger K, Seyler A, Sharp S, Shin H, Sivam D, Squares R, Squares S, Tosato V, Vogt C, Volckaert G, Wambutt R, Warren T, Wedler H, Woodward J, Zhou S, Zimmermann W, Smith FD, Blackwell MJ, Stuart DK, Barrell B, Myler JP (2005). The genome of the kinetoplastid parasite, Leishmania major. Science. 309: 436-442.

Janzen CJ, van Deursen F, Shi H, Cross GAM, Matthews KR, Ullu E (2006). Expression site silencing and life cycle progression appear normal in Argonaute1-deficient *Trypanosoma brucei*. Mol. Biochem. Parasitol. 14: 102-107.

Jones SW, Souza PM, Lindsay MA (2004). siRNA for gene silencing: a route to drug target discovery. Curr. Opin. Pharmacol. 4:522-527.

Jorgensen R (1990). Altered gene expression in plants due to trans interactions between homologous genes. Trends Biotechnol. 8: 340-344.

Jovanovic M, Hengartner MO (2006). miRNAS and apoptosis: RNAS to die for. Oncogene. 25:6176-6187.

Kimberly SP, Jiang D, Morita YS, Englund PT (2001). Fatty acid synthesis in African trypanosomes: a solution to the myristate mystery. Trends Parasitol. 17: 381-386.

Kloosterman WP, Plasterk RHA (2006). The diverse functions of microRNAs in animal adevelopment and disease. Dev. Cell. 11:441-450.

Knowles J, Gromo G (2003). A guide to drug discovery: target selection in drug discovery. Nat. Rev. Drug. Discovery. 2: 63-69.

LaCount DJ, Barrett B, Donelson JE (2002). *Trypanosoma brucei* FLA1 is required for flagellum attachment and cytokinesis. J. Biol. Chem. 277:17580-17588.

LaCount DJ, Bruse S, Hill KL, Donelson JE (2000). Double-stranded RNA interference in *Trypanosoma brucei* using head-to-head promoters. Mol. Biochem. Parasitol. 111: 67-76.

Lagos-Quintana M, Rauhu R, Lendeckel W, Tuschl T (2001). Identification of novel genes coding for small expressed RNAs. Science. 294: 853-858.

Lau NC, Lim LP, Weinstein EG, Bartel DP (2001). An abundant class of tiny RNAs with probable regulatory roles in *Caenorhabditis elegans.* Science. 294: 858-862.

Lau NC, Seto AG, Kim J, Kuramochi-Miyagawa S, Nakano T, Bartel DP, Kingston RE (2006). Characterization of the piRNA complex from rat testes. Science. 313: 363-367.

Lee PL, Nelson CL, Earl GW, Aliaa A, Soraya Y, Matthew WR, Christopher BB, David PB (2003). The microRNAs of *Caenorhabditis elegans.* Genes Dev. 17: 991-1008.

Lee SH, Stephens JL, Kimberly SP, Englund PT (2006). Fatty acid synthesis by elongases in trypanosomes. Cell. 126: 691-699.

Lee Y, Jeon K, Lee JT, Kim S, Kim VN (2002). MicroRNA maturation: Stepwise processing and subcellular localization. EMBO. J. 21: 4663-4670.

Legros D, Ollivier G, Gastellu-Etchegorry M, Paquet C, Burri C, Jannin J, Büscher P (2002). Treatment of human African trypanosomiasis-present situation and needs for research and development. Lancet. Infectious Diseases. 2: 437-440.

Lindsay MA (2003). Target discovery. Nat. Rev. Drug Discovery. 2: 831-838.

Matovu E, Seebeck T, Enyaru JC, Kaminsky R (2001). Drug resistance in *Trypanosoma brucei spp.,* the causative agents of sleeping sickness in man and nagana in cattle. Microbes Infect. 9:763-770.

Matzke MA, Aufsatz W, Kanno T, Mette MF, Matzke AJ (2002). Homology- dependent gene silencing and host defense in plants. Adv. Genet. 46:235-275.

Matzke MA, Mette MF, Matzke AJM (2000). Transgene silencing by the host genome defense: implications for the evolution of epigenetic control mechanisms in plants and vertebrates. Plant Mol. Biol. 43: 401 - 415.

Milhavet O, Gary D, Mattson M (2003). RNA interference in biology and medicine. Pharm. Rev. 55: 629-648.

Montgomery MK, Fire A (1998). Double-stranded RNA as a mediator in sequence-specific genetic silencing and co-suppression. Trends in Genetics. 14: 255-258.

Morel C (2003). Neglected diseases: under-funded research and inadequate health interventions. EMBO reports. 4: S35-S38.

Morris J, Wang Z, Drew ME, Paul KS, Englund PT (2001). Inhibition of bloodstream form *Trypanosoma brucei* gene expression by RNA interference using the pZJM dual T7 vector. Mol. Biochem. Parasitol.

117: 111-113.
Morris JC, Wang Z, Drew ME, Englund PT (2002). Glycolysis modulates trypanosome glycoprotein expression as revealed by an RNAi library. EMBO. J. 21:4429-38.
Motyka S, Zhao Z, Gull K, Englund P (2004). Integration of pZJM library plasmids into unexpected locations in the *Trypanosoma brucei* genome. Mol. Biochem. Parasitol. 134*:* 163-167.
Napoli C, Lemieux C, Jorgensen R (1990). Introduction of a chimeric chalcone synthase gene into petunia results in reversible co-suppression of homologous genes in plants. Plant Cell. 2: 279-289.
Nelson CL, Lee PL, Weinstein EG, Bartel DP (2001). An abundant class of tiny RNAs with probable regulatory roles in *Caenorhabditis elegans.* Science. 294: 858-862.
Ngô H, Tschudi C, Gull K, Ullu E (1998). Double-stranded RNA induces mRNA degradation in *Trypanosoma brucei*. PNAS. 95: 14687-14692.
Nykanen A, Haley B, Zamore P (2001). ATP requirements and small interfering RNA structure in the RNA interference pathway. Cell. 107:309-321.
Owino VA, Limoh MK, Masiga, DK (2006). Cloning and analysis of trans-splicing factors in *Trypanosoma brucei.* Proceedings of Egerton University research Week. Egerton University Press. pp. 210 – 222.
Pauls E, Esté J (2004). RNA interference as a tool for target validation. Drug Disco. Today Tech. 3: 1-6.
Pink R, Hudson A, Mouriès M, Bendig M (2005). Opportunities and challenges in antiparasitic drug discovery. Nat. Rev. Drug Discovery. 4: 727-740.
Redmond S, Vadivelu J, Field M (2003). RNAit: an automated web-based tool for the selection of RNAi targets in *Trypanosoma brucei.* Mol. Biochem. Parasitol. 128: 115-118.
Reinhard BJ, Weinstein EG, Rhoades MW, Bartel B, Bartel DP (2002). MicroRNAs in plants. Genes & Dev 16: 1616-1626.
Roberts CW, McLeod R, Rice DW, Ginger M, Chance ML, Goad LJ (2003). Fatty acid and sterol metabolism: potential antimicrobial targets in apicomplexan and trypanosomatid parasitic protozoa. Mol. Biochem. Parasitol. 126: 129-142.
Robinson KA, Beverley SM (2003). Improvement of transfection efficiency and tests of RNA interference (RNAi) approaches in the protozoan parasite Leishmania. Mol. Biochem. Parasitol. 128: 217-228.
Romano N, Macino G (1992). Quelling: transient inactivation of gene expression in *Neurospora crassa* by transformation with homologous sequences. Mol. Microbiol. 6: 3343-3353.
Saito K, Nishida KM, Mori T, Kawamura, Y, Miyoshi, K, Nagami, T, Siomi H, Siomi MC (2006) Specific association of Piwi with rasiRNAs derived from retrotransposon and heterochromatic regions in the Drosophila genome. Genes Dev. 20: 2214-2222.
Schwarz D, Hutvágner G, Du T, Xu Z, Aronin N, Zamore P (2003). Asymmetry in the assembly of the RNAi enzyme complex. Cell. 115: 199-208.
Schwarz D, Hutvágner G, Haley B, Zamore P (2002). Evidence that siRNAs function as guides, not primers, in the Drosophila and human RNAi pathways. Mol. Cell. 10: 537-548.
Shi H, Djikeng A, Mark T, Wirtz E, Tschudi C, Ullu E (2000). Genetic interference in *Trypanosoma brucei* by heritable and inducible double-stranded RNA. RNA. 6: 1069-1076.
Shi H, Djikeng A, Tschudi C, Ullu E (2004). Argonaute protein in the early divergent eukaryote *Trypanosoma brucei*: control of small interfering RNA accumulation and retroposon transcript abundance. Mol. Cell Biol. 24: 420-427.
Shi H, Tschudi C, Ullu E (2006). An unusual Dicer-like1 protein fuels the RNA interference pathway in Trypanosoma brucei. RNA. 12: 2063-2072.
Smith TK, Crossman A, Brimacombe JS, Ferguson MAJ (2004). Chemical validation of GPI biosynthesis as a drug target against African sleeping sickness. The EMBO J. 23: 4701-4708.
Song L, Tuan RS (2006). MicroRNAs and cell differentiation in mammalian development. Birth Defects Res. C. Embryo Today. 78:149-149.
Soulère L, Hoffmann P, Bringaud F and Périé J (1999). Uptake of NO-releasing drugs by the P2 nucleoside transporter in trypanosomes. Brazillian J. Med. Biol. Res. 32: 1447-1452.
Stevenson DS, Jarvis P (2003). Chromatin silencing: RNA in the driving seat. Curr. Biol. 13: R13-R15.
Stoll VS, Simpson SJ, Krauth-Siegel RL, Walsh CT, Pai EF (1997). Glutathione reductase turned into trypanothione reductase: structural analysis of an engineered change in substrate specificity. Biochemistry. 36: 6437-6447.
Subramaniam C, Veazey P, Redmond S, Hayes -Sinclair J, Chambers E, Carrington M, Gull K, Matthews K, Horn D, Field MC (2006). Chromosome-wide analysis of gene function by RNA interference in the African trypanosome. Eukaryot. Cell. 5: 1539-1549.
Tschudi C, Djikeng A, Shi H, Ullu E (2003). *In vivo* analysis of the RNA interference mechanism in *Trypanosoma brucei*. Methods. 30: 304-312.
Ullu E, Tschudi C, Chakraborty T (2004). RNA interference in protozoan parasites. Cell Microbiol. 6: 509-519.
Urbina JA (1997). Lipid biosynthesis pathways as chemotherapeutic targets in kinetoplastid parasites. Parasitology. 114 Suppl: S91-999.
Urbina JA,Concepcion JL, Rangel S, Visbal G, Lira R (2002). Squalene synthase as a chemotherapeutic target in *Trypanosoma cruzi* and *Leishmania mexicana.* Mol. Biochem. Parasitol. 125:35-45.
Vaucheret H, Béclin C, Fagard M (2001). Post-transcriptional gene silencing in plants. J. Cell Sci. 114: 3083-3091.
Verlinde C, Hannaert V, Blonski C, Willson M, Périé J, Fothergill-Gilmore L, Opperdoes F, Gelb M, Hol W, Michel M (2001). Glycolysis as a target for the design of new antitrypanosome drugs. Drug Resist. Update 4: 1-14.
Volpe TA, Kidner C, Hall IM, Teng G, Grewal SIS, Martienssen RA (2002). Regulation of Heterochromatic Silencing and Histone H3 Lysine-9 Methylation by RNAi. Science. 297: 1833-1837.
Wang Z, Morris J, Drew M, Englund P (2000). Inhibition of *Trypanosoma brucei* gene expression by RNA interference using an intergratable vector with opposing T7 promoters. J. Biol. Chem. 275: 40174-40179.
Wickstead B, Ersfeld K, Gull K, (2002). Targeting of a tetracycline-inducible expression system to the transcriptionally silent minichromosomes of *Trypanosoma brucei.* Mol. Biochem. Parasitol. 125: 211-216.
Wirth D (2001). A harvest not yet reaped: genomics to new drugs in Leishmania and trypanosome. Correspondence: drugs for neglected diseases working group, Médecins Sans Frontières, 12 rue du Lac Geneva 33-39.
Wirtz E, Hoek M, Cross AM (1998). Regulated processive transcription of chromatin by T7 RNA polymerase in *Trypanosoma brucei*. Nucleic Acids Res. 26:4626-34.
Wirtz E, Leal S, Ochatt C, Cross GA (1999). A tightly regulated inducible expression system for conditional gene knock -outs and dominant negative genetics in *Trypanosoma brucei*. Mol. Biochem. Parasitol. 99: 89-102.
Yoo AS, Greenwald I (2005). LIN-12/notch activation leads to microRNA-mediated down-regulation of Vav in *C. elegans*. Science. 310: 1330-1333.