AN IN VIVO GENE EXPRESSION SYSTEM

The present invention relates generally to an *in vivo* system for gene expression and, more particularly, to the use of the system to screen for molecules which are capable of inhibiting, reducing, altering or otherwise modulating the expression of a target nucleotide sequence or the activity of a gene product. The *in vivo* system of the present invention is particularly but not exclusively useful for screening for antisense, sense or ribozyme constructs or transdominant polypeptides, small peptides or other chemical compounds and which are capable of inhibiting, reducing, altering or otherwise modulating expression of target genes or target genetic sequences or the activity of target gene products of commercial importance such as in the medical, agricultural and industrial fields.

Sequence Identity Numbers (SEQ ID NOs.) for the nucleotide sequences referred to in the specification are defined just prior to the claims.

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

The rapidly increasing sophistication of recombinant DNA technology is greatly facilitating the efficacy of many commercially important industries including areas of medicine, agriculture, horticulture and fermentation. An important tool in recombinant DNA technology is the use of antisense molecules, sense molecules, ribozymes and other genetic sequences and/or non-nucleotide molecules such as peptides or chemical agents to affect expression of genetic sequences.

Ribozymes are RNA molecules which possess highly specific endoribonuclease activity. In particular, they comprise a hybridising region which is complementary in nucleotide sequence to at least part of a target RNA and a catalytic region which is adapted to cleave the target RNA. An example where ribozymes are well described is Haseloff J. and Gerlach W *Nature 334:* 586-591, 1988 and in International Patent Application No. WO 89/05852. Antisense molecules are genetic constructs which are generally complementary in nucleotide sequences to target mRNA. Although the exact mode of action of antisense molecules is unclear, it is possible that they form a duplex with all or part of target mRNA with a consequential interferring effect on the mRNA transcript. Sense nucleotide constructs are used in co-suppression and have been shown to be effective in reducing expression of, for example, plant genes.

There is a need to develop effective approaches for rapidly evaluating molecules such as antisense, sense and ribozyme constructs, transdominant polypeptides, small peptides and other chemical compounds as potential effector molecules in modulating expression of target genetic sequences or the activity of products encoded thereby.

Microorganisms have previously been considered as a convenient *in vivo* model system for testing for compounds which affect, for example, their viability or ability to grow. Microorganisms are advantageous experimental hosts for molecular and genetic analysis. Their assets include a short generation time, readily available techniques for growing and analysing large numbers of cells and the relative ease of introducing and recovering nucleic acids from these cells. More than 10^{11} microorganisms can readily be grown on inexpensive nutrients whereas the production of even 10^{8} mammalian cells is slow and expensive. However, while bacterial cells have been used in the elucidation of many basic aspects of gene expression, they lack many of the fundamental features of eukaryotic RNA physiology. Bacterial cells have no nuclear compartment, contain a reduced number of completely distinct RNA and DNA binding proteins, have few or no spliced mRNAs, no spliceosomal machinery for intron removal, and use a different system for the initiation of protein translation.

Yeast cells, on the other hand, have greater benefits as experimental models because they have all the basic features of higher eukaryotes such as plant and animal cells plus a generation time reminiscent of bacteria. There is a large set of molecular and genetic techniques available for introducing, analyzing and recovering nucleic acids in these cells making them amenable to genetic as well as biochemical investigations. It is possible to generate populations of yeast cells that are large and complex enough to facilitate thorough genetic analysis.

However, many laboratories have attempted unsuccessfully to use antisense and ribozyme technology in the budding yeast *Saccharomyces cerevisiae*. This yeast has been studied more thoroughly than any other eukaryotic microorganism and a large range of genetic and molecular tools are currently available. To date, there have been no reports of the completely successful use of antisense and/or ribozyme constructs to suppress gene expression in *S. cerevisiae* even using target systems which have worked well in animal and plant cells. It is surprising that *S. cerevisiae* is apparently so recalcitrant to, for example, antisense and ribozyme inhibition. Artificial antisense approaches have been successfully explored in virtually every other eukaryotic system available for molecular genetic studies such as in mammalian cells, *Drosophila*, plants and the slime mould *Dictyostelium discoidium*.

The fission yeast *Schizosaccharomyces pombe* also has a highly characterised genetic system. There are a number of features of *S. pombe* that render these cells more similar to human and other higher eukaryotic cells than *S. cerevisae* including chromatin structure and behaviour, intron distribution and small nuclear ribonucleoprotein particle RNAs and proteins. Furthermore, *S. pombe* cell division cycles are very similar to those of higher eukaryotic organisms. This makes *S. pombe* a potentially valuable model for studying higher eukaryotic gene expression including expression of animal and mammalian (e.g. human) genes, insect genes and plant genes.

In work leading up to the present invention, the inventors sought to evaluate *S. pombe* as a potential model for studying altered expression of target genes. The inventors discovered that certain genetic constructs are expressed in *S. pombe* and lead to altered

modulation of expression including suppression of target genes. The present invention, therefore, provides for the first time, a suitable microbial model of gene expression for the efficient screening of genetic constructs such as antisense, sense and ribozyme constructs and molecules such as transdominant polypeptides, small peptides and other chemical compounds as potentially effective agents capable of modulating expression of target genes of eukaryotic, prokaryotic or viral origin or capable of modulating activity of products of such genes. The present invention is useful, for example, in screening bacteriophage display libraries for novel protein, polypeptide or peptide encoding sequences for effectors of gene expression. The present invention is particularly useful in the screening of potential diagnostic and therapeutic molecules for the medical and animal health industries as well as a range of agrochemical molecules for the plant and crop industries.

Accordingly, one aspect of the present invention contemplates a method of identifying molecules capable of inhibiting, reducing or otherwise modulating expression of a target gene or activity of a target gene product, said method comprising generating a strain of *Schizosaccharomyces pombe* capable of expressing said target gene, introducing to said strain of *S. pombe* an effective amount of said molecule to be tested and determining the effect of said molecule on expression of said target gene or activity of the product of the target gene.

The molecules are preferably genetic constructs such as antisense, sense nucleotide sequences or ribozymes relative to a target gene, or other nucleotide sequences such as oligonucleotides, random nucleotide sequences or nucleotide sequences selected for cleavage *in vitro*. The present invention extends, however, to non-nucleotide molecules such as transdominant polypeptides, small peptides and chemical compounds as well as to synthetic nucleotide molecules or nucleotide analogue molecules. The term "modulating expression" and other like expressions includes up-regulating and down-regulating activity of a product of a target sequence. Accordingly, molecules which so modulate expression or activity may be agonists or antagonists. Furthermore, the present invention extends to identifying agents, such as for example, ribozymes, antisense and sense nucleotide molecules who activity is regulated by cellular factors including

switching mechanisms and intracellular address signals. Addtionally, in some circumstances, the level of effect on expression may be enhanced by increasing the level of modulating molecules such as antisense, sense or ribozyme molecules.

The method of the present invention may also be used in conjunction or in combination with or as an adjunct to *in vitro* evaluation experiments to identify target molecules of interest. Accordingly, the method of the present invention may be used in random as well as rational drug design. This would be particularly useful, for example, for the further evaluation of a ribozyme which is effective *in vitro*. In one embodiment, further nucleotide sequences are added to the ribozyme to facilitate, for example, targetting the ribozyme to a particular sequence, penetration of the cell or to otherwise facilitate is activity.

The term "gene" is used in its most broadest sense to include a classical genomic gene as well as a genetic sequence comprising only the coding portions of a gene (i.e. exons) and a cDNA sequence corresponding to a mRNA transcript. A "gene" as contemplated herein especially in relation to a target gene includes a naturally occurring gene, a partial gene, a synthetic gene and a fusion between a target gene and another gene or genetic sequence. A "gene", therefore, is considered herein to include any target nucleotide sequence and may be of eukaryotic, prokaryotic or viral origin. Preferably, the target gene is "exogenous" or "non-indigenous" to *S. pombe* meaning it is a heterologous gene which has been introduced by transformation, conjugation, electroporation or other means to the yeast cell. However, the target gene may alternatively be "endogenous". Particularly preferred endogenous or homologous (also referred to herein as "indigenous") *S. pombe* genes are those which encode cell cycle proteins, modulate cell cycles and/or are involved in programmed cell deaths. Such genes and in particular antagonists thereof identified in accordance with the present invention may be useful in the treatment of cancers in mammals such as humans. Other important endogenous genes are *S. pombe* homologues of mammalian (e.g. human) genes. A particularly useful yeast in accordance with this aspect of the present invention has *S. pombe* genes replaced by a mammalian (e.g. human) homologues or comprise homologous animal, mammalian or plant genes or have homologous functions to animal, mammalian or plant

genes. An example of such a yeast is a yeast carrying a mutation which is functionally complemented or otherwise substituted by homologous of animal, mammalian or plant genes.

In a particularly preferred aspect of the present invention, the target gene construct comprises either a target sequence or a portion thereof fused to or otherwise operably linked to a nucleotide sequence encoding a reporter molecule. Alternatively, a reporter gene may be inserted in an operable location adjacent to an *S. pombe* gene such as a *S. pombe* homologue of a heterologous (e.g. mammalian) gene. Such a genetic construct when expressed in *S. pombe* may in one form direct the synthesis of a fusion polypeptide having a target gene encoded portion and a reporter molecule portion. In accordance with this aspect of the present invention, a molecule such as a genetic sequence is tested for its ability to alter the expression of the target gene by reference to expression of the reporter gene sequence or activity of the reporter molecule.

In accordance with this aspect of the present invention, there is provided a method of identifying genetic sequences capable of inhibiting, reducing or otherwise regulating expression of a target gene, said method comprising generating a strain of *S. pombe* capable of expressing said target gene in a genetic construct which further comprises a reporter gene capable of providing an identifyable signal, introducing to said strain of *S. pombe* an effective amount of a genetic construct to be tested and assaying for an inhibition, reduction, or down-regulation of expression of said reporter gene. In some assays up-regulation may also be tested. In an alternative embodiment, chemical agents including transdominant polypeptides, small peptides or other chemical compounds are tested for their modulatory ability.

The rationale behind this method is the production in the yeast cell of a single mRNA transcript encoding both the target gene product or a portion thereof and reporter molecule. Generally, the reporter molecule will be encoded by a nucleotide sequence placed downstream of the nucleotide sequence encoding the target gene product. A genetic sequence is then tested by reference to a change in the detectable reporter molecule.

In a preferred embodiment, the genetic sequence to be tested is an antisense molecule comprising five or more nucleotides, a ribozyme, a triplex, an RNA or protein decoy, a sense molecule for use in sense or co-suppression, transdominant mutant nucleotides, defective interfering RNAs or DNAs or proteins and the like such as naturally occuring or synthetic chemical compounds. In a most preferred embodiment, the genetic sequence to be tested is an antisense molecule, a sense molecule or a ribozyme.

The reporter molecule may be any molecule capable of giving an identifiable signal and may be an enzyme (e.g. β-galactosidase and horse radish peroxidase), confer antibiotic resistance, confer non-antibiotic compound resistance, be a fluorogenic compound, a fluorescent protein, a chemiluminescent compound, a biotynolated compound, an essential growth factor, cell cycle protein or a molecule capable of giving a cell a defined phenotype such as size, colour and cell surface phenotype (e.g. rough or smooth edges, concave or convex colonies). The β-galactosidase gene is a particularly useful reporter molecule. The reporter molecule may also be a fusion reporter molecule between the above reporter molecules or between *S. pombe* homologous and heterologous genes. Particularly, useful reporter molecules include chloramphenicol acetyl transferase (CAT) [Jones *et al Cell 53:* 659-667, 1988], β-glucuronidase (GUS [Pobjecky *et al Mol. Gen. Genet. 2220:* 314-316, 1990], firefly luciferase (LUX), phleomycin resistance gene (*ble*) [Prentice and Kingston *Nucl. Acids. Res. 20:* 3383-3390, 1992], green fluorescent protein (GFP) [Chalfie *et al Science 263:* 802-805, 1994], neomycin phosphotransferase (Neo) which confers resistance to G418 (Gmunder and Kohli *Mol. Gen. Genet. 220:* 95-101, 1989) and the *S. pombe ura4* gene and fusion derivatives thereof (for example see Myers *et al Current Genetics 27:* 243-248, 1995). Another suitable reporter molecule is adenosine phosphoribosyl transferase (APRT).

The target gene including a fusion target gene construct may be integrated into the chromosome of *S. pombe* under the control of an endogenous promoter or exogenous promoter or may exist as an extrachromosomal, replicating element. Any number of exogenous promoters may be used such as the SV40 promoter. A suitable endogenous promoter is the regulated *S. pombe adh1* promoter.

The genetic sequences to be tested (e.g. an antisense or sense molecule or ribozyme construct) may be introduced to the yeast cell by any number of means including transformation, conjugation, electroporation, amongst others. The genetic sequence may be expressed under an endogenous or exogenous promoter or may be introduced without a promoter.

The present invention permits the rapid screening of genetic sequences having an effect on expression of target genes. The target genes include eukaryotic, prokaryotic and viral genes. Examples of eukaryotic genes include mammalian growth factors and cytokines and their receptors and cancer specified genes and plant genes. Examples of prokaryotic genes include β-galactosidase and pathogen-specific genes. Examples of viral genes include HIV and Hepatitis genes. The subject invention is particularly applicable for the development of a disease model system suitable for screening for useful genetic sequences to target viral, cancer and aberrant "self" genes. The method of the present invention may also be useful as drug screening reagents. For example, receptor genes are engineered and expressed in a reporter gene-dependent manner. The modified yeast is then used in high through-put assays for agonists or antagonists of the receptors.

Although the present invention is exemplified using *S. pombe* as the *in vivo* model and β-galactosidase gene as both the target and reporter molecule, the present invention clearly extends to and encompasses other suitable eukaryotic organisms and other reporter molecules.

Other aspects of the present invention include an *in vivo* model system for screening of molecules capable of inhibiting, reducing or otherwise modulating expression of a target gene or activity of a target gene product, said *in vivo* model system comprising a strain of *S. pombe* capable of expressing said target gene wherein molecules to be tested are introduced into said *S. pombe* and screened for inhibition, reduction or down regulation of said target gene.

The present invention is further described by the following non-limiting figures and examples.

In the figures:

Figure 1 is a representation showing genotypic analysis of *S. pombe* β-galactosidase strains. The β2-1* ura 4/β-galactosidase locus was used to construct KC4-6.

Figure 2 is a representation showing regulated gene expression in *S. pombe*.

Figure 3 is a diagrammatic representation showing β-galactosidase antisense and control sense orientation genes.

Figure 4 is a diagrammatic representation showing that antisense RNA inhibits gene expression in *S. pombe*.

Figure 5 is a diagrammatic representation showing that β-galactosidase gene suppression is transcription-dependent.

Figure 6 is a diagrammatic representation showing long and short-armed *lacZ* ribozymes containing a single hammerhead cleavage domain.

Figure 7 is a representation showing *in vitro* cleavage by the short-armed *lacZ* ribozymes.

Figure 8 is a photographic representation showing expression of long and short-armed *lacZ* ribozymes in *S. pombe* transformants. Cells transformed with plasmids containing *lacZ* ribozyme genes showed expression of the respective ribozymes with comparable steady-state levels.

Figure 9 is a graphical representation showing *in vivo* assay of long and short-armed *lacZ* ribozymes. The inclusion of a hammerhead ribozyme in the short 5' *lacZ* antisense RNA resulted in differential elimination of antisense RNA-mediated suppression. The short-armed *lacZ* ribozymes did not significantly reduce β-galactosidase activity.

Figure 10 is a graphical representation showing the antisense RNA inhibits gene expression in *S. pombe* strain RB3-2.

Figure 11 is a diagrammatic representation showing that the *ura4* locus in strain RB3-2 containing the *adh1* promoter-β-galactosidase-*ura4* 3′ expression cassette.

Figure 12 is a schemmatic diagram showing the *lacZ* target gene and antisense and control plasmids.

Figure 13 A is a photographic representation of a Northern blot of total RNA isolated from KC4-6 cells transformed with each of the expression vectors shown in Figure 12.

Figure 13 B is a photographic representation of a northern blot of total RNA isolated from independent pGT2 transofrmants of strain KD4-6 (GT2, GT2-2 and GT2-3) grown in the presence (+) and absence (-) of 4 μM thiamine.

Figure 14 is a graphical representation showing reduction of β-galactosidase activity in *lacZ* antisense transformants.

Figures 15 A-D are graphical representations showing that reduction in β-galactosidase activity by long *lacZ* antisense RNA is transcription-dependent. The middle panel summarizes the experimental design. Single colonies from three independent transformants of pREP1 and pGT2 were split and streaked onto (A) EMM+U (*nmt1* promoter ON) or (B) EMM+TJI+U (*nmt1* promoter OFF). In the second stage of the experiment (C) cells of each transformant on EMM+U were streaked to EMM+THI+U (*nmt1* promoter OFF), and (D) cells of each transformant growing on EMM+THI+U were streaked to EMM+U (*nmt1* promoter ON). Each sample in the histogram represents the average of three independent transformants and the standard deviation is indicated by the error bars.

Figure 16 is a graphical representation showing the role of antisense RNA level on the suppression of the *lacZ* gene in RB3-2.

EXAMPLE 1

CONSTRUCTION OF pREP1

Plasmid pREP1 was constructed according to Maundrell, K., *J. Biol. Chem. 265:* 10857-10864, 1990.

EXAMPLE 2

INHIBITION OF β-GALACTOSIDASE EXPRESSION

The present invention is conveniently exemplified using the β-galactosidase gene from *E. coli* as a target. This gene has the advantage of having a well characterised and easily detected cellular phenotype. Cells expressing β-galactosidase turn blue or become fluorescent when incubated with appropriate substrate analogues. This permits rapid visual identification or fluorescence-activated cell sorting and quantitation of cells expressing the gene. Moreover, there are very sensitive solution enzyme assays which permit accurate quantitative assessment of β-galactosidase expression using extracts of cell populations. β-Galactosidase has been used as a reporter gene in molecular biology experiments in many systems and is an excellent building block for gene fusions. β-Galactosidase can be used to tag a wide variety of cellular or viral genes and monitor their expression and physiology.

In accordance with an exemplified embodiment of the present invention, the β-galactosidase gene has been put under the control of the SV40 early promoter. This has been integrated into the *ura*4 gene locus of *S. pombe* to create KC4-6, a stable constitutive strain of yeast expressing β-galactosidase. Figure 1 shows a diagram of the wild-type *ura*4 locus at the top. The middle of the diagram is a representation of the integrated β-galactosidase gene and the bottom of the figure shows a Southern blot confirming the integrity of the chromosomal β-galactosidase gene in β2-1 (the strain used to derive KC4-6) and other similar strains. Clearly, other target genes may be inserted into the *ura*4 or another locus. Furthermore, the target gene may also be expressed from extra-chromosomal episomes or plasmids.

Regulated expression of antisense genes has been achieved using episomal vectors with conditional promoters. Figure 2 shows the structure of the vector pREP1 which contains the *nmt* (*n*o *m*essage in *t*hiamine) promoter. Sequences cloned downstream of this promoter are expressed at a very high level when grown in the absence of thiamine. Transcription is almost undetectable in the presence of thiamine. The right hand panel in Figure 2 shows a representative RNA blot probed with a double stranded β-galactosidase probe which documents the high level of expression of antisense β-galactosidase RNA in the absence of thiamine (in the "-" lanes). In the presence of thiamine ("+" lanes), only the target, sense-orientation β-galactosidase transcript is detected. Other expression systems may also be used.

Figure 3 shows diagrams of the antisense gene constructs used in the present disclosure. Antisense or reverse orientation fragments encompassing the protein-coding domain (long), the 5′ end of the gene and the 3′ end of the gene were each cloned behind the *nmt* promoter in the pREP1 expression plasmid. A set of plasmids were constructed as controls for potential non-specific effects on the pattern of gene expression, cell growth or β-galactosidase levels. These included sense orientation fragments of β-galactosidase from the coding region (long), the 5′ end and the 3′ end as well as a sense oriented fragment from a non-related reporter gene luciferase. A frame shift mutation was inserted in the long sense control gene to eliminate the production of spurious additional β-galactosidase. Other fragments of the β-galactosidase gene or other reporter and target genes may also be used in such a system.

The antisense gene expression vectors are introduced into the β-galactosidase-expressing target strain by electroporation although other methods of gene transfer may also be used. The cells are grown in media lacking thiamine to promote expression of the antisense genes. Log phase cells at a constant cell density are assayed for β-galactosidase activity using solution assays and the chromophore substrate O-nitrophenol β-D-glactropyranside (ONPG). Reporter enzyme levels are determined by observing the OD 420 nm after 30 minutes. Multiple independent transformants have been assayed in triplicate and the results from several experiments are compiled in Figure 4. The schematic diagram on the left depicts the protocol for the experiment and the histogram indicates the average level of β-galactosidase activity in cells transformed with each of

the antisense constructs. The error bars indicate the standard deviation of the population. It can be seen that the parental pREP1 plasmid and all of the plasmids having sense orientation gene fragments (labelled controls) have within the experimental error of this system, the same level of β-galactosidase activity. *S. pombe* cells containing the long antisense plasmid reproducibly show a 45% reduction in β-galactosidase level while the 5′ and 3′ antisense cells show a 20% and 10% reduction, respectively. This experiment is the first documentation of antisense gene suppression in yeast cells and demonstrates the relative activity of the long, 5′ and 3′ fragments for artificial gene regulation.

To confirm that the observed inhibition is due to the expression of the antisense β-galactosidase RNA a series of experiments documented in Figure 5, was performed. Parallel cultures of the long antisense strain and the control pREP1 strain were alternately grown in thiamine-containing medium to inhibit antisense production and then in thiamine-free medium to "turn on" antisense expression (right side of middle diagram in Figure 5). Reciprocal experiments were performed where cultures were grown in thiamine-free and then in thiamine-containing medium (left side of middle diagram Figure 5). As shown in the flanking histograms, cells which showed significant inhibition of β-galactosidase in the absence of thiamine showed no inhibition when grown in thiamine (left two histograms in Figure 5) while cells which showed no inhibition of β-galactosidase when grown in thiamine showed approximately 55% inhibition (right two histograms in Figure 5) when grown in the absence of thiamine (conditions which turn on antisense RNA transcription). These on-off/off-on experiments indicate that the long β-galactosidase plasmid produces transcript-dependent and sequence specific antisense suppression of the β-galactosidase gene in the KC4-6 type reporter gene strain of *S. pombe*. This system is valuable for genetic and biochemical explorations of artificial gene regulation technology.

From this, it is clear that one skilled in the art can now develop and use gene inactivation methods to inhibit gene activity in *S. pombe*. The present demonstration shows utility for antisense RNA transcripts but it will be appreciated by persons skilled in the art that it is applicable to other genes, synthetic antisense and ribozyme oligonucleotides, triplex, RNA and protein decoys, sense co-suppression, transdominant

mutant approaches, defective interfering RNAs and DNAs, etc. This system is also applicable to the identification and development of small molecule therapeutics and pharmaceutical formations. Furthermore, it is applicable to a disease model system. All that is required is simple genetic constructions and demonstration of assay tests for effects on gene activity.

One application of this technology is the rapid and reliable screening on large scale of gene inactivation approaches and combinations of them to determine effective constructs for application through genetic engineering and genetic manipulation in the human, medical, animal, plant and fermentation application areas.

EXAMPLE 3

CONSTRUCTION OF AN *S. POMBE* STRAIN EXPRESSING THE TARGET *lacZ* GENE AT HIGHER STEADY-STATE LEVELS COMPARED TO STRAIN KC4-6.

The β-galactosidase gene was placed under the control of the *S. pombe adh1* promoter and the *S. pombe ura4* 3′ processing region. This *adh1* promoter-β-galactosidase-*ura4* 3′ expression cassette was integrated at the *ura4* locus of *S. pombe* to produce strain 599-2. Figure 6 shows the integrated cassette at the *ura4* locus in strain 599-2. This strain was crossed to a leu⁻ *S. pombe* strain to create the ascospore isolate RB3-2. This strain also contains the integrated *adh1* promoter-β-galactosidase-*ura4* 3′ expression cassette at the *ura4* locus as indicated in Figure 11 and exhibited a 20-fold increase in β-galactrosidase mRNA expression over KC4-6. Strain RB3-2 was transformed with the set of antisense and control plasmids represented in Figure 3 (Example 2) and assayed for β-galactosidase activity. Multiple independent transformants were assayed in triplicate and the results for these experiments are summarized in Figure 10. The protocol for this assay is as for Figure 4 (Example 2). Cells of *S. pombe* expressing the long antisense RNA show a 55% reduction in β-galactosidase activity while the short 5′ antisense RNA- and short 3′ antisense RNA-expressing cells show a 22% and 4% reduction, respectively. As indicated, the control plasmid transformants exhibited similar levels of β-galactosidase activity to the pREP1 transformants. All RB3-2 transformants containing antisense or control plasmids have been shown to express the expected

plasmid-derived RNA. The primary advantage of RB3-2 over KC4-6 is that single colonies of RB3-2 turn blue on X-gal medium. This reflects the higher level of expression of β-galactosidase in RB3-2 compared to KC4-6.

EXAMPLE 4

INHIBITION OF GENE EXPRESSION IN *S. POMBE* STRAIN RB3-2

The yeast strain RB3-2 described in Example 3 was tested for antisense inhibition of β-galactosidase. The results are shown in Figure 10. Long and 5' antisense molecules were more effective at inhibiting β-galactosidase expression than 3' antisense molecule. A diagrammatic representation of the target gene in RB3-2 is shown in Figure 11.

EXAMPLE 5

RELATIONSHIP BETWEEN BIOCHEMICAL ACTIVITY ASSAY AND PHENOTYPE READER

Analysis of *lacZ* expression can be completed by incubation of transformants on media containing Xgal. Xgal is a chromogenic substrate of the enzyme β-galactosidase and confers a blue phenotype to the colonies when hydrolysed. RB3-2 transformants described in Figure 10 were plated on media containing 50, 100, 150 and 200μg/ml of Xgal. After 5 days of growth an obvious reduction in the intensity of the blue colour of the strains expressing the full-length and 5' antisense was detectable when compared to the control transformed strain. This result demonstrates a relationship between *lacZ* expression and phenotype and illustrates how the *S. pombe* strain RB3-2 can be used in a genetic screen to identify genetic sequences, from libraries encoding random genetic sequences, that reduce the expression of the target *lacZ* expressing yeast strain when hydrolysed. Phenyl-β-d-galactropyranoside is a candidate compound for such a suicide substrate and is currently under investigation.

EXAMPLE 6

ANTISENSE MEDIATED REGULATION OF *lacZ* EXPRESSION IN *S. pombe*

Yeast Strains and Media

Schizosaccharomyces pombe strain 972 (*h-*) was used as the host for integration and expression of the *Escherichia coli lacZ* gene. Strains NCYC 1913 *(h-, leul-32)* and NCYC 1914 (*h+, leul-32*) were obtained from the National Collection of Yeast Cultures (AFRC Institute of Food Research, Norwich, UK). Yeast matings were performed according to standard procedures (Alfa *et al.*, Experiments with fission yeast: A laboratory course manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1993). The transformation of *S. pombe* cells with episomal plasmid DNA or linearized plasmid DNA was carried out using electroporation (Prentice, H.L. *Nucleic Acids Res. 20:* 621, 1992). Gene replacement at the *ura4* locus in *S. pombe* was achieved as described by Grimm *et al., Mol. Gen. Genet. 215:* 81-86, 1988.

Yeast cells were grown on standard YES medium (BIO 101 Inc., Vista, CA) or synthetic dextrose (SD) medium containing biological supplements (Rose *et al.*, Methods in yeast genetics: A laboratory course manual. Cold Spring Harbor Press, Cold Spring Harbor, New York, 1990). Thiamine-free EMM medium (BIO 101 Inc., Vista, CA) was used to obtain maximum expression from the promoter in yeast transformants. Repression of transcription from this promoter was achieved by the addition of thiamine (Sigma) to EMM medium at a final concentration of 4μM (Maundrell, K., *J. Biol. Chem. 265:* 10857-10864, 1990). Conjugation and sporulation of *S. pombe* cells was performed using nutrient deficient ME agar medium (BIO 101 Inc., Vista, CA) (Moreno *et al., Meth. Enzymol. 194:* 795-823, 1991). To examine the blue colony colour of yeast integrants expressing the *E. coli lacZ* gene, cells were plated onto SD or EMM media buffered with potassium phosphate (to pH 7.0) and containing Xgal at final concentrations ranging from 50 to 200 μg/ml (Rose *et al.*, Methods in yeast genetics: A laboratory course manual. Cold Spring Harbor Press, Cold Spring Harbor, New York, 1990).

Plasmids and Yeast Strain Construction

All standard DNA manipulations were carried out as described by Sambrook *et al.*, 1989, Molecular Cloning: A laboratory manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York. The *E. coli lacZ* gene under control of the SV40 early promoter and 3' processing signals was integrated into the *S. pombe* genome using *ura4* flanking DNA sequences and homologous recombination at the wild type *ura4* gene locus. The *ura4* DNA sequences flanking the *ura4* transcriptional unit were isolated from pCG5 (Prof. J. Kohli, University of Bern, Bern, Switzerland) as a 1.8 kb *BamHI-EcoRI* fragment (Grimm *et al., Mol. Gen. Genet. 215:* 81-86, 1988). This fragment was filled using the Klenow fragment of DNA polymerase and subcloned as a blunt end fragment into the HindII site of pNEB194 [a version of pNEB193] (New England Biolabs Inc., Beverly, MA) from which the region between the *Pst*I and *Hin*dIII sites in the polylinker was deleted] to create pNEB 195. The *lacZ* expression cassette containing the SV40 early promoter, the *E. coli lacZ* gene and the SV40 early gene 3' processing sequence was subcloned from the plasmid pSVβ (Clontech Laboratories Inc., Palo Alto, CA). The *Eco*RI site 5' to the SV40 promoter in pSVβ was modified to include a HindIII site by inserting an *Eco*RI-HindIII-*Eco*RI adaptor. The above cassette was then subcloned as a HindIII fragment between the *ura4* L 5' and 3' sequences in pNEB 195 to produce plasmid pNEBD2 with an orientation such that the SV40 early promoter was located adjacent to the *ura4* 3' fragment. A PacI-PmeI double-digest released the lacZ expression cassette flanked at either end by *ura4* sequences. This fragment was used to transform *S. pombe* strain 972 (*h-*) and 5-FOA resistance was used to identify yeast transformants having undergone a disruption of the *ura4* locus. Putative integrants were then characterized with respect to the structure of the *ura4* locus and expression of the SV40 early promoter-driven *lacZ* gene. The structure of the integrated *lacZ* expression cassette at the *ura4* locus in chromosome III of the *S. pombe* genome is depicted schematically in Figure 12.

Plasmid pREP1 (Maundrell, 1990) was used as the expression vector for construction of *lacZ* antisense gene-containing plasmids and sense controls. All fragments used were subcloned into pREP1 at the unique BamHI site and are represented schematically in Figure 12. The long lacZ BamHI fragment spans positions -56 to +3419 of the SV40

early promoter-driven *lacZ* expression cassette. In order to construct the long sense control plasmid, a frameshift mutation was introduced at base +909 in the *lacZ* BamHI fragment. The fragment was linearized with ClaI, filled and religated. The frameshift was confirmed by DNA sequencing and the *lacZ* BamHI fragment subcloned into pREP1 in the sense orientation relative to the nmt1 promoter. This plasmid was designated pGT62 and served as a control for pGT2 which contains the long *lacZ* BamHI fragment in the antisense orientation.

The short 5′ and 3′ *lacZ* fragments were generated using the polymerase chain reaction (PCR) and pNEBD2 plasmid DNA as a template. The primers used for amplification of the short 5′ fragment were 5′-AAGAGATCTGCCTCTGAGCTATTCCAGAAGTAGTG-3′ [SEQ ID NO:1] and 5′-AAGAGATCTCATCGATAATTTCACCGCCGAAAGGC-3′ [SEQ ID NO:2]. For the short 3′ DNA fragment these sequences were 5′-AAGAGATCTTCAGTATCGGCGGAATTACAGCTGAG-3′ [SEQ ID NO:3] and 5′-AAGAGATCTCAATGTATCTTATCATGTCTGGATCC-3′ [SEQ ID NO:4]. In each case a BglII restriction site was added to both the 5′ and 3′ ends of the amplified DNA fragments. The short 5′ fragment spanned positions -299 to +912 while the short 3′ DNA was located between +3093 and +3454 with the TAA stop codon of the *lacZ* gene at +3141. PCR amplified DNA was cloned into the BglII site in pSP72 (Promega Corp., Madison, WI) and subcloned as BglII fragments into the BamHI site of pREP1 in both the sense and antisense orientations. The plasmid designations were as follows: pGT58 (short 5′ sense), pGT59 (short 5′ antisense), pGT60 (short 3′ sense), and pGT61 (short 3′ antisense). A non-sequence specific plasmid control pGT68, containing the luciferase gene, was constructed by linker ligating the StuI-BamHI fragment of pGEM-luc (Promega Corp., Madison, WI) into pREP1.

DNA:RNA Isolation and Hybridization

Total genomic DNA was isolated from *S. pombe* cells using glass beads as described by Hoffman and Winston (1987) *Gene 53:* 659-667. These DNA samples were used for Southern analysis of chromosomal DNA and copy number analysis of plasmids. Yeast total RNA was purified using a standard procedures. Nucleic acid electrophoresis and

hybridization were as described (Sambrook *et al.*, Molecular Cloning: A laboratory manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York, 1989) with the exception of Northern blots which were hybridized using Express Hybridization solution (Clontech Laboratories Inc., Palo Alto, CA). DNA used as probes included the long *lacZ* BamHI fragment and the 405 bp BamHI-PacI fragment from the *nmt1* 3' sequence in pREP1. All DNA probes used for hybridization were ^{32}P-labelled using the Megaprime labelling kit (Amersham International, Amersham, UK). The radioactive hybridization signal was detected by autoradiography and quantified using a phosphorimager (Bio-Rad Laboratories, Hercules, CA).

β-Galactosidase Enzyme Assay

The enzyme activity of the *E. coli lacZ* gene-encoded product, β-galactosidase, was assayed using a cell permeabilization method (Ausubel *et al.*, Current protocols in molecular biology. Green Publishing Associates and Wiley-Interscience, New York, 1987). For *S. pombe* strains 972 and NCYC 1913, $1x10^8$ cells were assayed for β-galactosidase activity following growth of yeast transformants in EMM or EMM media containing thiamine to a cell density of $10x10^7$ cells/ml. Triplicate assays were performed for each transformant and β-galactosidase units calculated according to the formula described in Ausubel *et al.*, Current protocols in molecular biology. Green Publishing Associates and Wiley-Interscience, New York, 1987).

Results

In order to examine the suitability of fission yeast as a model system for the analysis of antisense RNA-mediated gene regulation, the *E. coli lacZ* reporter gene was chosen as a target. This gene offers the advantages of the availability of rapid and sensitive solution enzyme assays for the gene product β-galactosidase (Ausubel *et al.*, Current protocols in molecular biology. Green Publishing Associates and Wiley-Interscience, New York, 1987) and confers a blue colony colour to *S. pombe* on medium containing the chromogenic substrate Xgal (Kudla *Nucleic Acids Res. 16:* 8603-8617, 1988). The *E. coli lacZ* gene was expressed at a low constitutive level in *S. pombe* placing it under control of the SV40 early promoter and 3' processing sequences. This mammalian viral promoter has been shown to function effectively in *S. pombe* with transcription initiating

from the precise site used in mammalian cells (Jones *et al., Cell 53:* 659-667, 1988). The *lacZ* gene expression cassette was integrated into *S. pombe* chromosome III to create a stable β-galactosidase-expressing strain. Integration was accomplished by replacement of the DNA sequence at the *ura4* locus with the *ura4*-flanked *lacZ* expression cassette and identification of a stable integrant using 5-FOA selection (Fig. 12). The integrity of the chromosomally integrated single copy plasmid DNA was confirmed by Southern analysis on genomic DNA isolated from strain β2-1 (*h-, ura4::SV40-lacZ*) and the chromosomal structure of the *ura4* locus of this strain is shown in Figure 12. Expression analysis on this *lacZ* gene-containing strain revealed that the strain expressed *lacZ* mRNA and produced an average of 1.8 units of β-galactosidase per $1x10^8$ cells assayed. To facilitate transformation with episomal expression vectors the *leu1* mutation was introduced into β2-1 by crossing with NCYC 1914 (*h+, leu1-32*) and a random ascospore isolate designated KC4-6 (*ura4::SV40-lacZ, leu1-32*) was identified. This strain was shown to express β-galactosidase at levels similar to that of the parental strain β2-1.

All *lacZ* antisense genes were expressed from the episomal plasmid pREP1 (Maundrell, K. *J. Biol. Chem. 265:* 10857-10864, 1990) using the conditional *nmt1* promoter. This promoter is repressed in the presence of thiamine at concentrations greater than 0.5 μM and maximally derepressed in the absence of exogenous thiamine (Maundrell, K. *J. Biol. Chem. 265:* 10857-10864, 1990). A set of antisense genes were constructed to produce antisense RNAs of varying sizes complementary to different regions of the target message (Fig. 12). The long *lacZ* antisense gene was designed to produce an antisense RNA complementary to 56 bases of the 5′ untranslated sequence, the entire coding region of the target mRNA and 288 bases of the 3′ untranslated region. The shorter antisense genes were designed to produce RNA complementary to either the 5′ or 3′ ends of the *lacZ* mRNA. Control expression plasmids were constructed in order to examine non-specific effects of high level *nmt1* promoter-driven transcription on β-galactosidase enzyme levels (Fig. 12). These controls included the sense-oriented fragments for each of the antisense genes and the firefly luciferase gene in the sense orientation (Fig. 12) The long *lacZ* sense control plasmid was prepared by introducing a frameshift mutation into the *lacZ* gene to eliminate β-galactosidase activity of any resultant gene product. β-Galactosidase enzyme assays on pGT62 plasmid transformants

of strain NCYC 1913 (h-, leul-32) confirmed that transcripts produced from the long sense control gene were not translated into active β-galactosidase.

The target strain KC4-6 was transformed with each of the plasmid constructs described above and three independent transformants were analyzed to detect RNA transcripts expressed from the plasmid-borne genes. Northern analysis was completed using an *nmtl* 3′ processing region DNA fragment as a probe. All RNAs produced from the *nmtl* promoter on pREP1 contain 144 bases of the *nmtl* message at their 3′ ends. Figure 13A indicates that each of the transformants produced an RNA species of the expected size. Analysis of each RNA species relative to the chromosomally-encoded *nmtl* mRNA indicated that the expression levels of all these RNAs were similar. Figure 13B shows that the expression of *lacZ* antisense RNA is conditionally dependent on thiamine and the expression level of long *lacZ* antisense RNA, as for all the antisense RNAs, is 20-fold greater than that of the target *lacZ* mRNA.

β-Galactosidase enzyme assays were used to monitor the effect of antisense RNA synthesis on target *lacZ* gene expression (Ausubel *et al.*, Current protocols in molecular biology. Green Publishing Associates and Wiley-Interscience, New York, 1987). Three independent transformants for each plasmid construct were grown in thiamine-free medium to derepress the *nmtl* promoter (Fig. 14). Cells of *S. pombe* expressing the long *lacZ* antisense RNA showed a 45% reduction in β-galactosidase activity, while cells expressing the short 5′ or short 3′ complementary transcripts produced 20% and 10% less β-galactosidase activity, respectively. In contrast, all transformants containing plasmids with the sense-orientated gene fragments exhibited levels of β-galactosidase activity comparable to the pREP1 transformants. This suggests that the decrease in β-galactosidase activity observed was due to the presence of *lacZ* antisense RNA and was not due to non-specific interference with gene expression or cell physiology.

To confirm that the observed reduction of β-galactosidase activity was dependent on *lacZ* antisense RNA transcription, yeast transformants were grown under conditions that would repress or derepress the *nmtl* promoter prior to assaying for β-galactosidase activity. Independent transformants, containing either control plasmid pREP1 or the

long *lacZ* antisense plasmid pGT2, were initially grown on thiamine-free medium to permit antisense RNA expression (ON; Fig. 15) and thiamine-containing medium to inhibit antisense RNA production (OFF; Fig. 15). *lacZ* antisense plasmid pGT2-containing cells grown in the absence of thiamine produced 40% less β-galactosidase than the pREP1 transformants (Fig. 15A). Cells from the same culture grown in the presence of thiamine showed control levels of β-galactosidase activity (Fig. 15B). The reversibility of antisense RNA regulation was demonstrated by transferring cells from thiamine-free medium (ON) to thiamine-containing medium (OFF), and cells from medium containing thiamine (OFF) onto medium lacking thiamine (ON). The pGT2 transformants previously showing 40% reduction in the absence of thiamine exhibited no inhibition of β-galactosidase activity in the presence of thiamine (Fig. 15C). This indicates that repressing *lacZ* antisense RNA transcription permitted target gene expression to return to the same levels as observed in control pREP1 transformants. In contrast, pGT2 transformants previously exhibiting normal levels of β-galactosidase when grown in the presence of thiamine revealed a 55% decrease in β-galactosidase activity when grown on thiamine-free medium (Fig. 15D). The experiment confirms that the decrease in *lacZ* gene expression is dependent on transcription of the *lacZ* antisense gene and the observed reversibility eliminates the involvement of additional genetic effects such as target gene rearrangement.

To further assess the effectiveness of antisense RNA regulation in the present system, partial inhibition of β-galactosidase activity was examined by the long *lacZ* antisense RNA to determine whether it could modulate the blue colony colour phenotype associated with expression of the *lacZ* gene in *S. pombe*. Cells containing the *lacZ* antisense plasmids or the appropriate control vectors were plated on thiamine-free media containing a range of Xgal concentrations. Following extended incubation at 30°C there was no detectable qualitative difference in the blue colour phenotype exhibited by the long *lacZ* antisense RNA-expressing cells and those expressing control RNAs. It is concluded that a 55% reduction in β-galactosidase enzyme activity in *S. pombe* in insufficient to alter the visible cellular phenotype.

However, phenotypic readout is still a valuable parameter in the screening process. This

was shown in Example 5.

EXAMPLE 7

ANTISENSE SUPPRESSION OF THE *lacZ* GENE OF *S. POMBE* STRAIN RB3-2 IS DEPENDENT ON THE ANTISENSE RNA LEVEL

Strain RB3-2 was transformed with the combinations of plasmids shown in Table 1 with the expected ratios of antisense RNA indicated for each transformation. Three independent transformants for each plasmids combination were assayed in triplicate as hereinbefore described. The data are summariseed in Figure 16. The data show that for the *lacZ* target gene, the level of suppression is dependent upon the leve of antisense RNA. For example, the highest level of suppression of approximately 65% is seen when RB3-2 is transformed with the two antisense-encoding plasmids. The plasmids pREP42 and pREP82 encode derivatives of the *nmt1* promoter in which mutations have been introduced which result in weaker levels of transcription.

Table 1

Transformant	Plasmid 1	Plasmid 2	Ratio (Antisense:Target)
1	pREP1	pREP4	0:1
2	pREP1	pREP82::antisense	0.025:1
3	pREP1	pREP42::antisense	0.3:1
4	pREP1	pREP4::antisense	2-4:1
5	pREP1:antisense	pREP4::antisense	4-8:1

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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APPLICANT (OTHER THAN US): GENE SHEARS PTY LIMITED

(ii) TITLE OF INVENTION: AN IN VIVO GENE EXPRESSION SYSTEM

(iii) NUMBER OF SEQUENCES: 4

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(E) COUNTRY: AUSTRALIA
(F) ZIP: 3000

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: PCT INTERNATIONAL
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(A) APPLICATION NUMBER: PM5169/94 (AU)
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGAGATCTG CCTCTGAGCT ATTCCAGAAG TAGTG 35

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGAGATCTC ATCGATAATT TCACCGCCGA AAGGC 35

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGAGATCTT CAGTATCGGC GGAATTACAG CTGAG 35

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAGAGATCTC AATGTATCTT ATCATGTCTG GATCC 35

CLAIMS:

1. A method of identifying molecules capable of inhibiting, reducing or otherwise modulating expression of a target gene or activity of a target gene product, said method comprising generating a strain of *Schizosaccharomyces pombe* capable of expressing said target gene, introducing to said strain of *S. pombe* an effective amount of said molecule to be tested and determining the effect of said molecule on expression of said target gene or activity of the product of the target gene.

2. A method according to claim 1 wherein the molecule to be tested is a genetic sequence.

3. A method according to claim 1 wherein the molecule to be tested is a peptide, polypeptide, or a chemical compound.

4. A method according to claim 2 wherein the genetic sequence is an antisense molecule relative to all or part of the target gene.

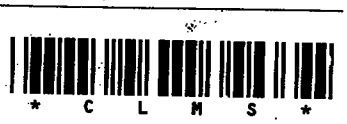
5. A method according to claim 2 wherein the genetic sequence is a sense molecule relative to all or part of the target gene.

6. A method according to claim 2 wherein the genetic sequence is a ribozyme.

7. A method according to claim 1 wherein the target gene is an exogenous gene of eukaryotic, prokaryotic or viral origin.

8. A method according to claim 1 wherein the target gene is a *S. pombe* homologue of an exogenous gene of eukaryotic, prokaryotic or viral origin.

9. A method according to claim 7 or 8 wherein the eukaryotic gene is a mammalian gene.



10. A method according to claim 9 wherein the mammalian gene encodes all or part of a growth factor, a cytokine, a growth factor or cytokine receptor or a cancer-specific gene.

11. A method according to claim 7 or 8 wherein the eukaryotic gene is a plant gene.

12. A method according to claim 7 or 8 wherein the viral gene is of HIV or hepatitis origin.

13. A method according to claim 1 wherein the target gene or a portion thereof is fused to a genetic sequence encoding a reporter molecule capable of providing an identifyable signal.

14. A method according to claim 13 wherein the reporter molecule is an enzyme, confe: ntibiotic resistance, confers resistance to a chemical compound, a fluorogenic compound, a fluorescent protein, a chemiluminescent compound, a biotynolated compound, an essential growth factor, a cell cytokine protein or a molecule giving a cell a defined phenotype.

15. A method according to claim 13 wherein the reporter molecule is adenosine phosphoribosyl transferase, *Neo, Gus, Cat, Lux* or *GFP* or functional parts thereof.

16. A method according to claim 13 wherein the reporter molecule is a fusion reporter molecule between an *S. pombe* homologous and heterologous gene.

17. A method according to claim 1 wherein the target gene is under the control of an endogenous *S. pombe* promoter.

18. A method according to claim 17 wherein the endogenous promoter is the *S. pombe adh1* promoter.

19. A method according to claim 1 wherein the target gene is under the control of an exogenous promoter.

20. A method according to claim 19 wherein the exogenous promoter is the SV40 promoter.

21. A method of identifying genetic sequences capable of inhibiting, reducing or otherwise regulating expression of a target gene, said method comprising generating a strain of *S. pombe* capable of expressing said target gene in a genetic construct which further comprises a reporter gene capable of providing an identifyable signal, introducing to said strain of *S. pombe* an effective amount of a genetic sequence to be tested and assaying for an inhibition, reduction, or other regulation of expression of said reporter gene.

22. A method according to claim 21 wherein the genetic sequence to be tested is an antisense molecule relative to the target gene and which comprises 5 or more nucleotides.

23. A method according to claim 21 wherein the genetic sequence to be tested is a ribozyme, triplex, RNA, transdominant mutant nucleotides, defective interfering RNAs or DNAs or is a sense construct relative to the target gene.

24. A method according to claim 21 wherein the target gene is a mammalian gene or an *S. pombe* homologue of a mammalian gene.

25. A method according to claim 24 wherein the mammalian gene encodes all or part of a growth factor, a cytokine, a growth factor or a cytokine receptor, or is a cancer specific gene.

26. A method according to claim 21 wherein the target gene is of plant origin.

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27. A method according to claim 21 wherein the target gene is of viral origin.

28. A method according to claim 27 wherein the virus is HIV or a hepatitis virus.

29. A method according to claim 21 wherein the reporter gene encodes an enzyme, confers antibiotic resistance, confers resistance to a chemical compound, a fluorogenic compound, a fluorescent protein, a chemiluminescent compound, a biotynolated compound, an essential growth factor, a cell cytokine protein or a molecule giving a cell a defined phenotype.

30. A method according to claim 21 wherein the reporter gene encodes adenosine phosphoribozyl transferase, or is *Neo, Gus, Cat, Lux* or *GFP* or functional parts thereof.

31. A method according to claim 21 wherein the reporter gene is a fusion reporter molecule between an *S. pombe* homologous and heterologous gene.

32. A method according to claim 21 wherein the target gene is under the control of an endogenous *S. pombe* promoter.

33. A method according to claim 21 wherein the endogenous promoter is the *S. pombe adh1* promoter.

34. A method according to claim 1 wherein the target gene is under the control of an exogenous promoter.

35. A method according to claim 19 wherein the exogenous promoter is the SV40 promoter.

36. An *in vivo* model system for screening of molecules capable of inhibiting, reducing or otherwise modulating expression of a target gene or activity of a target gene product, said *in vivo* model system comprising a strain of *S. pombe* capable of expressing said target gene wherein molecules to be tested are introduced into said *S.*

pombe and screened for inhibition, reduction or other regulation of said target gene.

37. An *in vivo* model system according to claim 36 wherein the molecule to be tested is a genetic sequence.

38. An *in vivo* model system according to claim 36 wherein the molecule to be tested is a peptide, polypeptide or a chemical compound.

39. An *in vivo* model system according to claim 37 wherein the genetic sequence is an antisense molecule relative to all or part of the target gene.

40. An *in vivo* model system according to claim 37 wherein the genetic sequence is a sense molecule relative to all or part of the target gene.

41. An *in vivo* model system according to claim 37 wherein the genetic sequence is a ribozyme.

42. An *in vivo* model system according to claim 36 wherein the target gene is an exogenous gene of eukaryotic, prokaryotic or viral origin.

43. An *in vivo* model system according to claim 36 wherein the target gene is a *S. pombe* homologue of an exogenous gene of eukaryotic, prokaryotic or viral origin.

44. An *in vivo* model system according to claim 42 or 43 wherein the eukaryotic gene is a mammalian gene.

45. An *in vivo* model system according to claim 44 wherein the mammalian gene encodes a growth factor, a cytokine, a growth factor or cytokine receptor or a cancer-specific gene.

46. An *in vivo* model system according to claim 42 or 43 wherein the eukaryotic gene is a plant gene.

47. An *in vivo* model system according to claim 42 or 43 wherein the viral gene is of HIV or hepatitis origin.

48. An *in vivo* model system according to claim 36 wherein the target gene or a portion thereof is fused to a genetic sequence encoding a reporter molecule capable of providing an identifyable signal.

49. An *in vivo* model system according to claim 48 wherein the reporter molecule is an enzyme, confers antibiotic resistance, confers resistance to a chemical compound, a fluorogenic compound, a fluorescent protein, a chemiluminescent compound, a biotynolated compound, an essential growth factor, a cell cytokine protein or a molecule giving a cell a defined phenotype.

50. An *in vivo* model system according to claim 48 wherein the reporter molecule is a denosine phosphoribozyl transferase, *Neo, Gus, Cat, Lux* or *GFP* or a functional part thereof.

51. An *in vivo* model system according to claim 48 wherein the reporter molecule is a fusion reporter molecule between an *S. pombe* homologous and heterologous gene.

52. An *in vivo* model system according to claim 36 wherein the target gene is under the control of an endogenous *S. pombe* promoter.

53. An *in vivo* model system according to claim 52 wherein the endogenous promoter is the *S. pombe adh1* promoter.

54. An *in vivo* model system according to claim 36 wherein the target gene is under the control of an exogenous promoter.

55. An *in vivo* model system according to claim 54 wherein the exogenous promoter is the SV40 promoter.