TITLE

[0001] NON-REPLICATIVE TRANSDUCTION PARTICLES AND TRANSDUCTION PARTICLE-BASED REPORTER SYSTEMS

CROSS-REFERENCE TO RELATED APPLICATION

[0002] This application claims the benefit of U.S. Provisional Patent Application No. 62/041,539, filed August 25, 2014, and US Provisional Patent Application No. 62/202,653, filed August 7, 2015, the disclosures of which are incorporated herein by reference.

SEQUENCE LISTING

[0003] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on August 24, 2015, is named 29681PCT_CRF_SequenceListing.txt and is 37,642 bytes in size.

BACKGROUND OF THE INVENTION

Field of the invention

[0004] The invention relates to methods and compositions for packaging and delivery of non-replicative transduction reporter molecules into cells for detecting target genes in cells.

Description of the Related Art

[0005] A transduction particle refers to a virus capable of delivering a non-viral nucleic acid into a cell. Viral-based reporter systems have been used to detect the presence of cells and rely on the lysogenic phase of the virus to allow expression of a reporter molecule from the cell. These viral-based reporter systems use replication-competent transduction particles that express reporter molecules and cause a target cell to emit a detectable signal.

[0006] However, the lytic cycle of the virus has been shown to be deleterious to viral-based reporter assays. Carrière, C. *et al.*, *Conditionally replicating luciferase reporter phages: Improved sensitivity for rapid detection and assessment of drug susceptibility of Mycobacterium tuberculosis.* Journal of Clinical Microbiology, 1997. **35**(12): p. 3232-3239. Carrière *et al.* developed *M. tuberculosis*/bacillus Calmette-Guérin (BCG) luciferase reporter phages that have their lytic cycles suppressed at 30°C, but active at 37°C. Using this system, Carrière *et al.* have demonstrated the detection of BCG using phage reporters with a suppressed lytic cycle.

[0007] There are disadvantages, however, associated with suppressing but not eliminating the replication functions of the bacteriophage in bacteriophage-based reporter assays. First, controlling replication functions of the bacteriophage imposes limiting assay conditions. For

example, the lytic cycle of the reporter phage phAE40 used by Carrière *et al.* was repressed when the phage was used to infect cells at the non-permissive temperature of 30°C. This temperature requirement imposed limiting conditions on the reporter assay in that the optimum temperature for the target bacteria was 37°C. These limiting conditions hinder optimum assay performance.

[0008] Moreover, the replication functions of the virus are difficult to control. The replication of the virus should be suppressed during the use of the transduction particles as a reporter system. For example, the lytic activity of the reporter phage phAE40 reported by Carrière *et al.* was reduced but was not eliminated, resulting in a drop in luciferase signal in the assay. Carrière *et al.* highlighted possible causes for the resulting drop in reporter signal, such as intact phage-expressed genes and temperature limitations of the assay, all stemming from the fact that the lytic cycle of the phage reporter was not eliminated.

[0009] Reporter assays relying on the natural lysogenic cycle of phages can be expected to exhibit lytic activity sporadically. In addition, assays that rely on the lysogenic cycle of the phage can be prone to superinfection immunity from target cells already lysogenized with a similar phage, as well as naturally occurring host restriction systems that target incoming virus nucleic acid, thus limiting the host range of these reporter phages.

[0010] In other examples, transduction particle production systems are designed to package exogenous nucleic acid molecules, but the transduction particle often contains a combination of exogenous nucleic acid molecules and native progeny virus nucleic acid molecules. The native virus can exhibit lytic activity that is a hindrance to assay performance, and the lytic activity of the virus must be eliminated to purify transduction particles. However, this purification is generally not possible. In U.S. 2009/0155768 A, entitled *Reporter Plasmid Packaging System for Detection of Bacteria*, Scholl *et al.* describes the development of such a transduction particle system. The product of the system is a combination of reporter transduction particles and native bacteriophage (Figure 8 in the reference). Although the authors indicate that the transduction particle and native bacteriophage can be separated by ultracentrifugation, this separation is only possible in a system where the transduction particle and the native virus exhibit different densities that would allow separation by ultracentrifugation. While this characteristic is exhibited by the bacteriophage T7-based packaging system described in the reference, this is not a characteristic that is generally applicable for other virus systems. It is common for viral packaging machinery to exhibit headful packaging that would result in native virus and transduction particles to exhibit indistinguishable densities that cannot be separated by ultracentrifugation. Virus packaging

systems also rely on a minimum amount of packaging as a requirement for proper virus structural assembly that results in native virus and transduction particles with indistinguishable densities.

[0011] Thus, there is a need for non-replicative transduction particles that do not suffer from the deleterious effects from lytic functions of the virus and the possibility of being limited by superinfection immunity and host restriction mechanisms that target virus nucleic acid molecules and viral functions, all of which can limit the performance of the reporter assay by increasing limits of detection and resulting in false negative results.

[0012] Even where transduction particles have been engineered, methods for using the transduction particles to detect and report the presence of target nucleic acid molecules in cells have limitations. Some methods require disruption of the cell and cumbersome techniques to isolate and detect transcripts in the lysate. Detection methods include using labeled probes such as antibodies, aptamers, or nucleic acid probes. Labeled probes directed to a target gene can result in non-specific binding to unintended targets or generate signals that have a high signal-to-noise ratio. Therefore, there is a need for specific, effective and accurate methods for detection and reporting of endogenous nucleic acid molecules in cells.

[0013] Accordingly, methods and systems are needed for generating non-replicative transduction particles that allow packaging and expression of reporter molecules in cells, while eliminating replication-competent progeny virus. Effective and accurate methods for detecting molecules in cells using the expressed reporter molecules are also needed.

SUMMARY OF THE INVENTION

[0014] Disclosed herein is a bacterial cell packaging system for packaging a reporter nucleic acid molecule into a non-replicative transduction particle (NRTP) for introduction into a bacterial cell, the packaging system comprising a host cell, comprising (1) a bacteriophage genome comprising a first gene comprising a disruption, wherein in the absence of the disruption the first gene encodes a first essential component of a packaging-related enzymatic activity and comprises a first packaging initiation site sequence, wherein the packaging-related enzymatic activity recognizes the first packaging initiation site, wherein the disruption prevents recognition of the first packaging initiation site sequence by the essential packaging-related enzymatic activity, and wherein the disruption reduces the level of the essential packaging-related enzymatic activity, and (2) a reporter nucleic acid molecule comprising a reporter gene, a second gene encoding the first component of the essential packaging-related enzymatic activity, and a third gene encoding a second component of the essential packaging-related enzymatic activity, wherein the second gene comprises the non-disrupted first

packaging initiation site sequence, wherein the first packaging initiation site sequence is configured to facilitate packaging of a replicon of the reporter nucleic acid molecule into the NRTP.

[0015] In an embodiment, the bacteriophage comprises a plurality of disrupted genes, wherein in the absence of the disruptions, each encodes an essential component of the packaging-related enzymatic activity. In an embodiment, each of the plurality of disrupted genes on the bacteriophage is complemented by a functional, non-disrupted gene encoded by the reporter nucleic acid molecule. In another embodiment, the disruption is via deletion, insertion, mutation, or replacement.

[0016] In another embodiment, the reporter nucleic acid molecule comprises a small terminase gene and a large terminase gene. In a further embodiment, the terminase genes comprise a pacA gene and a pacB gene of Enterobacteriaceae bacteriophage P1. In some embodiments, at least one of said second set of bacteriophage genes comprises the sequence of SEQ ID NO:1, SEQ ID NO:4, or SEQ ID NO:6. In an embodiment, the terminase genes comprise a terS gene and a terL gene from a *S. aureus* bacteriophage φ11 or φ80α. In another embodiment, the terminase genes comprise a terA gene and a terB gene from an *E. faecalis* bacteriophage φEf11.

[0017] In some embodiments, the packaging-related enzymatic activity is a terminase activity. In an embodiment, the second gene and the third gene are each terminase genes. In an embodiment, the second gene is a pacA gene and wherein the third gene is a pacB gene. In an embodiment, the reporter nucleic acid molecule comprises the sequence of SEQ ID NO:1. In an embodiment, the second gene is a terA gene and the third gene is a terB gene. In an embodiment, the reporter nucleic acid molecule comprises the sequence of SEQ ID NO:6. In an embodiment, the second gene is a terS gene and wherein the third gene is a terL gene. In an embodiment, the reporter nucleic acid molecule comprises the sequence of SEQ ID NO:4.

[0018] In some embodiments, the second gene and the third gene are operably linked to a conditional promoter. In an embodiment, the conditional promoter comprises the sequence of SEQ ID NO: 9. In an embodiment, the conditional promoter is a native promoter of a terminase gene of the bacteriophage genome. In some embodiments, expression of the second gene or the third gene is inhibited in the absence of activation of the lytic cycle of the bacteriophage, and wherein expression of the second gene or the third gene is activated upon activation of the lytic cycle of the bacteriophage. In certain embodiments, the second gene

and the third gene are terminase genes native to the bacteriophage genome, and wherein the conditional promoter is a native promoter of the terminase genes.

[0019] In some embodiments, the bacteriophage genome comprises a reporter gene. In some embodiments, the bacteriophage genome further comprises an antibiotic resistance gene. In an embodiment, the reporter gene encodes a detectable marker or a selectable marker. In an embodiment, the reporter gene is selected from the group consisting of: enzymes mediating luminescence reactions (luxA, luxB, luxAB, luc, ruc, nluc), enzymes mediating colorimetric reactions (lacZ, HRP), fluorescent proteins (GFP, eGFP, YFP, RFP, CFP, BFP, mCherry, near-infrared fluorescent proteins), affinity peptides (His-tag, 3X-FLAG), and selectable markers (ampC, tet(M), CAT, erm). In an embodiment, the reporter gene disrupts a terminase gene. In certain embodiments, the antibiotic resistance gene is a kanamycin resistance gene. In some embodiments, the reporter gene is operatively linked to a constitutive promoter. In a further embodiment, the constitutive promoter is Pblast.

[0020] In an embodiment, the disruption comprises an insertion into or replacement of the first packaging initiation site sequence with a gene encoding a selectable marker. In certain embodiments, the gene encoding the selectable marker is operatively linked to a constitutive promoter. In an embodiment, the disruption comprises an insertion into or replacement of the first packaging initiation site sequence with a gene encoding a detectable marker. In an embodiment, the gene encoding the detectable marker is selected from the group consisting of: luxA, luxB, and luxAB. In some embodiments, the gene encoding the detectable marker is operatively linked to a constitutive promoter, e.g., Pblast. In certain embodiments, the first gene comprises a pacA gene locus, and wherein the disruption comprises a luxAB gene and a kan gene inserted into the pacA gene locus. In some embodiments, the bacteriophage genome comprises SEQ ID NO: 12.

[0021] In some embodiments, the reporter nucleic acid molecule comprises an origin of replication. In an embodiment, the replicon of the reporter nucleic acid molecule comprises a concatamer amenable to packaging into the non-replicative transduction particle. In certain embodiments, the non-disrupted first packaging initiation site sequence comprises a concatamer junction. In some embodiments, the replicon is an Enterobacteriaceae bacteriophage P1 lytic replicon.

[0022] In an embodiment, the replicon comprises a C1 repressor-controlled P53 promoter, a promoter P53 antisense, a repL gene, and an in-frame deletion of a kilA gene. In an embodiment, the replicon comprises the sequence of SEQ ID NO:2. In an embodiment, the replicon is a pBHR1 replicon or a derivative of the pBHR1 replicon. In an embodiment, the

replicon comprises the sequence of SEQ ID NO:3. In an embodiment, the reporter nucleic acid molecule comprises the sequence of SEQ ID NO:4. In an embodiment, the replicon of the reporter nucleic acid molecule is derived from a S. aureus pT181 plasmid origin of replication. In an embodiment, the replicon of the reporter nucleic acid molecule comprises the sequence of SEQ ID NO:5. In an embodiment, the reporter nucleic acid molecule comprises the sequence comprises the sequence of SEQ ID NO:6. In an embodiment, the replicon of the reporter nucleic acid molecule is derived from an Enterococcus repB plasmid origin of replication. In an embodiment, the replicon of the reporter nucleic acid molecule comprises the sequence of SEQ ID NO:7. In an embodiment, the replicon of the reporter nucleic acid molecule is derived from an Enterococcus pDL278 plasmid origin of replication. In an embodiment, the replicon of the nucleic acid molecule comprises the sequence of SEQ ID NO:8. In an embodiment, the non-disrupted first packaging initiation site sequence comprises a pac-site. In an embodiment, the non-disrupted first packaging initiation site sequence comprises a cos-site.

[0023] In an embodiment, the bacteriophage genome comprises an Enterobacteriaceae bacteriophage P1. In an embodiment, the bacteriophage genome comprises an S. aureus bacteriophage φ80α or a bacteriophage φ11. In an embodiment, the bacteriophage genome comprises an E. faecalis bacteriophage φEF11.

[0024] In an embodiment, the bacterial cell comprises an E. coli cell. In an embodiment, the bacterial cell comprises an S. aureus cell. In an embodiment, the bacterial cell comprises an E. faecalis cell. In an embodiment, the bacterial cell comprises a Gram-negative cell. In an embodiment, the bacterial cell comprises a Gram-positive cell.

[0025] In an embodiment, the reporter gene encodes a detectable marker or a selectable marker. In some embodiments, the reporter gene is selected from the group consisting of enzymes mediating luminescence reactions (luxA, luxB, luxAB, luc, ruc, nluc), enzymes mediating colorimetric reactions (lacZ, HRP), fluorescent proteins (GFP, eGFP, YFP, RFP, CFP, BFP, mCherry, near-infrared fluorescent proteins), affinity peptides (His-tag, 3X-FLAG), and selectable markers (ampC, tet(M), CAT, erm).

[0026] In an embodiment, the reporter nucleic acid molecule comprises an aptamer. In an embodiment, the reporter nucleic acid molecule comprises a nucleic acid transcript sequence that is complementary to a second sequence in the reporter nucleic acid molecule.

[0027] In an embodiment, the nucleic acid transcript sequence is complementary to a cellular transcript. In a further embodiment, the nucleic acid transcript sequence comprises a cis-repressing sequence. In an embodiment, the reporter nucleic acid molecule is operatively

linked to a promoter. In a further embodiment, the promoter is selected for contributing to reactivity of a reporter molecule expressed from the reporter nucleic acid molecule in the bacterial cell. In some embodiments, the replicon of the reporter nucleic acid molecule comprises a nucleic acid transcript sequence that is complementary to a second sequence in the replica of the reporter nucleic acid molecule.

[0028] Also provided herein is a method for packaging a reporter nucleic acid molecule into a non-replicative transduction particle, comprising (1) providing conditions to the bacterial cell packaging system as disclosed herein that induce a lytic phase of the bacteriophage genome to produce non-replicative transduction particles packaged with the reporter nucleic acid molecule; and (2) collecting the non-replicative transduction particle comprising the reporter nucleic acid molecule. In some embodiments, the non-replicative transduction particle does not contain a replicated bacteriophage genome. In some embodiments, the non-replicative transduction particle comprises a portion of the bacteriophage genome due to recombination with the reporter nucleic acid molecule, and wherein the portion of the bacteriophage genome comprises the reporter gene.

[0029] Also provided herein is a composition comprising the non-replicative transduction particle comprising a replicon of the reporter nucleic acid molecule produced by the method disclosed herein.

[0030] Also provided herein is a bacterial cell packaging system for packaging a nucleic acid molecule into a non-replicative transduction particle, the bacterial cell, comprising (1) a bacteriophage genome comprising a first packaging initiation site sequence, wherein the first packaging initiation site sequence is disrupted by a gene encoding a reporter, and (2) a reporter nucleic acid molecule comprising a second packaging initiation site sequence facilitating packaging of a replicon of the reporter nucleic acid molecule into the non-replicative transduction particle, wherein the reporter nucleic acid molecule forms a replicon configured to be packaged into the non-replicative transduction particle.

[0031] Also provided herein is a bacterial cell packaging system for packaging a reporter nucleic acid molecule into a non-replicative transduction particle (NRTP) for introduction into a cell, the packaging system comprising a host cell, comprising (1) a bacteriophage genome comprising a first pair of terminase genes, wherein at least one of the first pair of terminase genes is disrupted, rendering the disrupted terminase gene non-functional, and (2) a reporter nucleic acid molecule comprising a reporter gene and a second pair of terminase genes that complement the first pair of terminase genes, wherein each of the second pair of

terminase genes are functional, and wherein the second pair of terminase genes facilitate packaging of a replicon of the reporter nucleic acid molecule into the NRTP.

[0032] Also provided herein is a bacterial cell packaging system for packaging a reporter nucleic acid molecule into a non-replicative transduction particle (NRTP) for introduction into a cell, the packaging system comprising a host cell, comprising (1) a bacteriophage genome comprising a first pair of terminase genes, wherein at only one of the first pair of terminase genes is disrupted, rendering the disrupted terminase gene non-functional, and (2) a reporter nucleic acid molecule comprising a reporter gene and a second terminase gene that complements the first terminase gene, wherein the second terminase gene is functional, and wherein the second terminase gene facilitates packaging of a replicon of the reporter nucleic acid molecule into the NRTP.

[0033] In some non-replicative transduction particle packaging systems, viral DNA recombined with plasmid DNA can be packaged. In such systems, a lysate produced by the packaging system can contain two species of transduction particles, (1) transduction particles carrying plasmid DNA and (2) transduction particles carrying viral DNA. In such systems, the latter species of transduction particles do not contribute to signal production when using the lysate as a reporter system for the detection of target cells. As such, an improved non-replicative transduction particle-based reporter system is disclosed herein where a reporter gene has been incorporated into the viral genome such that both species of transduction particles are capable of producing signal.

BRIEF DESCRIPTION OF THE SEVERAL VIEWS OF THE DRAWINGS

[0034] These and other features, aspects, and advantages of the present invention will become better understood with regard to the following description, and accompanying drawings, where:

[0035] Figure 1 illustrates an example of pacA gene disruption in the bacteriophage P1 by insertion of a kanamycin resistance gene within the pacA gene via allelic exchange, according to an embodiment.

[0036] Figure 2 illustrates a schematic of a complementing reporter plasmid carrying pacA and pacB genes under the control of the native pacA gene promoter, according to an embodiment.

[0037] Figure 3 illustrates an example of the design and function of a packaging system comprising an *E. coli* cell lysogenized with bacteriophage P1 having a disrupted pacA, the cell also carrying a plasmid containing pacA and pacB, according to an embodiment.

[0038] Figure 4 illustrates an example of the design and function of a packaging system comprising an *E. coli* cell lysogenized with bacteriophage P1 having a disrupted pacA where the disruption is accomplished via the insertion of a kanamycin resistance gene and the bacterial luciferase luxAB genes, the cell also carrying a plasmid containing pacA and pacB, according to an embodiment.

[0039] Figure 5 depicts a system for the use of NRTPs for the detection of inducers to target gene promoters within viable cells, according to an embodiment of the invention.

[0040] Figure 6 depicts a reporter system that includes a reporter nucleic acid molecule (e.g., plasmid) that is constructed for detecting VanR, the inducer of the promoter of the vancomycin resistance (vanA) gene in *Enterococcus faecium* (or *E. faecalis*), according to an embodiment of the invention. The reporter plasmid carries a reporter gene that is operatively linked to the vanA gene promoter.

[0041] Figure 7 depicts a reporter system that includes a reporter nucleic acid molecule constructed for detecting TcdD, the inducer of the promoters of the toxins A and B genes (tcdA and tcdB, respectively) of *C. difficile*, according to an embodiment of the invention. The reporter nucleic acid molecule includes a reporter gene that is operatively linked to the tcdA gene promoter.

[0042] Figure 8 depicts a reporter system that includes a reporter nucleic acid molecule is constructed for detecting SarS, the inducer of the promoter of the Protein A gene (spa) in *S. aureus*, according to an embodiment of the invention. The reporter nucleic acid molecule includes the bacterial luciferase genes luxA and luxB operatively linked to the spa gene promoter (P_{spa}).

[0043] Figure 9 shows a diagram of base pairing between the target transcript and the cis-repressing sequence of the reporter transcript.

[0044] Figure 10 shows a table of data obtained from measuring the light production (RLU) from colonies of transduced cells. Cells that were resistant to spectinomycin (SpecR) were transduced with plasmid DNA while cells that were resistant to kanamycin (KanR) were transduced by P1 DNA. Data obtained from employing a lysate produced from a cell containing P1 without luxAB integrated into its genome (1505) resulted in KanR transductants that generally did not produce light while data obtained from employing a lysate produced from a cell containing P1 with luxAB integrated into its genome (1525) resulted in KanR transductants that did produce light.

DETAILED DESCRIPTION OF THE INVENTION

I. Definitions

[0045] Terms used in the claims and specification are defined as set forth below unless otherwise specified.

[0046] As used herein, "reporter nucleic acid molecule" refers to a nucleotide sequence comprising a DNA or RNA molecule. The reporter nucleic acid molecule can be naturally occurring or an artificial or synthetic molecule. In some embodiments, the reporter nucleic acid molecule is exogenous to a host cell and can be introduced into a host cell as part of an exogenous nucleic acid molecule, such as a plasmid or vector. In certain embodiments, the reporter nucleic acid molecule can be complementary to a target gene in a cell. In other embodiments, the reporter nucleic acid molecule comprises a reporter gene encoding a reporter molecule (*e.g.*, reporter enzyme, protein). In some embodiments, the reporter nucleic acid molecule is referred to as a "reporter construct" or "nucleic acid reporter construct."

[0047] A "reporter molecule" or "reporter" refers to a molecule (*e.g.*, nucleic acid or protein) that confers onto an organism a detectable or selectable phenotype. The detectable phenotype can be colorimetric, fluorescent or luminescent, for example. Reporter molecules can be expressed from reporter genes encoding enzymes mediating luminescence reactions (luxA, luxB, luxAB, luc, ruc, nluc), genes encoding enzymes mediating colorimetric reactions (lacZ, HRP), genes encoding fluorescent proteins (GFP, eGFP, YFP, RFP, CFP, BFP, mCherry, near-infrared fluorescent proteins), nucleic acid molecules encoding affinity peptides (His-tag, 3X-FLAG), and genes encoding selectable markers (ampC, tet(M), CAT, erm). The reporter molecule can be used as a marker for successful uptake of a nucleic acid molecule or exogenous sequence (plasmid) into a cell. The reporter molecule can also be used to indicate the presence of a target gene, target nucleic acid molecule, target intracellular molecule, or a cell, as described herein. Alternatively, the reporter molecule can be a nucleic acid, such as an aptamer or ribozyme.

[0048] In some aspects of the invention, the reporter nucleic acid molecule is operatively linked to a promoter. In other aspects of the invention, the promoter can be chosen or designed to contribute to the reactivity and cross-reactivity of the reporter system based on the activity of the promoter in specific cells (*e.g.*, specific species) and not in others. In certain aspects, the reporter nucleic acid molecule comprises an origin of replication. In other aspects, the choice of origin of replication can similarly contribute to reactivity and cross-reactivity of the reporter system, when replication of the reporter nucleic acid molecule

within the target cell contributes to or is required for reporter signal production based on the activity of the origin of replication in specific cells (*e.g.*, specific species) and not in others. In some embodiments, the reporter nucleic acid molecule forms a replicon capable of being packaged as concatameric DNA into a progeny virus during virus replication.

[0049] As used herein, a "target transcript" refers to a portion of a nucleotide sequence of a DNA sequence or an mRNA molecule that is naturally formed by a target cell including that formed during the transcription of a target gene and mRNA that is a product of RNA processing of a primary transcription product. The target transcript can also be referred to as a cellular transcript or naturally occurring transcript.

[0050] As used herein, the term "transcript" refers to a length of nucleotide sequence (DNA or RNA) transcribed from a DNA or RNA template sequence or gene. The transcript can be a cDNA sequence transcribed from an RNA template or an mRNA sequence transcribed from a DNA template. The transcript can be protein coding or non-coding. The transcript can also be transcribed from an engineered nucleic acid construct.

[0051] A transcript derived from a reporter nucleic acid molecule can be referred to as a "reporter transcript." The reporter transcript can include a reporter sequence and a cis-repressing sequence. The reporter transcript can have sequences that form regions of complementarity, such that the transcript includes two regions that form a duplex (*e.g.*, an intermolecular duplex region). One region can be referred to as a "cis-repressing sequence" and has complementarity to a portion or all of a target transcript and/or a reporter sequence. A second region of the transcript is called a "reporter sequence" and can have complementarity to the cis-repressing sequence. Complementarity can be full complementarity or substantial complementarity. The presence and/or binding of the cis-repressing sequence with the reporter sequence can form a conformation in the reporter transcript, which can block further expression of the reporter molecule. The reporter transcript can form secondary structures, such as a hairpin structure, such that regions within the reporter transcript that are complementary to each other can hybridize to each other.

[0052] "Introducing into a cell," when referring to a nucleic acid molecule or exogenous sequence (*e.g.*, plasmid, vector, construct), means facilitating uptake or absorption into the cell, as is understood by those skilled in the art. Absorption or uptake of nucleic acid constructs or transcripts can occur through unaided diffusive or active cellular processes, or by auxiliary agents or devices including via the use of bacteriophage, virus, and transduction particles. The meaning of this term is not limited to cells *in vitro*; a nucleic acid molecule may also be "introduced into a cell," wherein the cell is part of a living organism. In such

instance, introduction into the cell will include the delivery to the organism. For example, for *in vivo* delivery, nucleic acid molecules, constructs or vectors of the invention can be injected into a tissue site or administered systemically. *In vitro* introduction into a cell includes methods known in the art, such as electroporation and lipofection. Further approaches are described herein or known in the art.

[0053] A "transduction particle" refers to a virus capable of delivering a non-viral nucleic acid molecule into a cell. The virus can be a bacteriophage, adenovirus, etc.

[0054] A "non-replicative transduction particle" refers to a virus capable of delivering a non-viral nucleic acid molecule into a cell, but is incapable of packaging its own replicated viral genome into the transduction particle. The virus can be a bacteriophage, adenovirus, *etc.*

[0055] A "plasmid" is a small DNA molecule that is physically separate from, and can replicate independently of, chromosomal DNA within a cell. Most commonly found as small circular, double-stranded DNA molecules in bacteria, plasmids are sometimes present in archaea and eukaryotic organisms. Plasmids are considered replicons, capable of replicating autonomously within a suitable host.

[0056] A "vector" is a nucleic acid molecule used as a vehicle to artificially carry foreign genetic material into another cell, where it can be replicated and/or expressed.

[0057] A "virus" is a small infectious agent that replicates only inside the living cells of other organisms. Virus particles (known as virions) include two or three parts: i) the genetic material made from either DNA or RNA molecules that carry genetic information; ii) a protein coat that protects these genes; and in some cases, iii) an envelope of lipids that surrounds the protein coat.

[0058] As used herein, the term "complement" refers to a non-disrupted sequence that is in the presence of an identical sequence that has been disrupted, or to the relationship of the non-disrupted sequence to the disrupted sequence. In one embodiment, the complement comprises a gene encoded on a polynucleotide in a cell that is functional and capable of expression, and expresses a protein with the same function as a disrupted gene on a bacteriophage prior to disruption. In some embodiments, the complement gene has greater than 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% sequence identity to the disrupted bacteriophage gene prior to disruption, i.e., the native bacteriophage gene. In some embodiments, the complement gene is identical to the disrupted bacteriophage gene prior to disruption, i.e., the native bacteriophage gene. In some embodiments, the complement gene comprises a polynucleotide sequence that has been deleted from the bacteriophage. In some embodiments, the complement gene refers to a gene encoding

packaging machinery of a bacteriophage on a plasmid, where the same gene has been disrupted in a bacteriophage. Thus, the plasmid is required to be in the presence of a bacteriophage with a mutated packaging machinery gene to provide the necessary packaging machinery necessary for packaging a polynucleotide into a transduction particle.

[0059] As used herein, the term "packaging-related enzymatic activity" refers to one or more polypeptides crucial for the interaction with a packaging initiation site sequence to package a polynucleotide into a transduction particle. In some embodiments, a pair of terminase genes is required for such an interaction, wherein each terminase encodes a packaging-related enzymatic activity. In some embodiments, the enzymatic activity is encoded by a terS and/or terL gene from a *S. aureus* bacteriophage φ11 or φ80α, a terA and terB gene from an *E. faecalis* bacteriophage φEf11, or a pacA and pacB gene of *Enterobacteriaceae* bacteriophage P1. In these embodiments, each of the pair of terminase genes express a packaging-related enzymatic activity, and a functional version of both are required for packaging of a polynucleotide with the packaging initiation site. In some embodiments, disruption of one of the genes of a plurality of genes associated with a packaging-related enzymatic activity eliminates the packaging-related enzymatic activity. In some embodiments, both of a pair of terminase genes are disrupted on the bacteriophage, thus disrupting the entire set of packaging-related enzymatic activity encoding genes on the bacteriophage.

[0060] "MRSA" refers to Methicillin-resistant *Staphylococcus aureus*.

[0061] "MSSA" refers to Methicillin-sensitive *Staphylococcus aureus*.

[0062] The term "ameliorating" refers to any therapeutically beneficial result in the treatment of a disease state, *e.g.*, a disease state, including prophylaxis, lessening in the severity or progression, remission, or cure thereof.

[0063] The term "in situ" refers to processes that occur in a living cell growing separate from a living organism, *e.g.*, growing in tissue culture.

[0064] The term "in vivo" refers to processes that occur in a living organism.

[0065] The term "mammal" as used herein includes both humans and non-humans and include but is not limited to humans, non-human primates, canines, felines, murines, bovines, equines, and porcines.

[0066] "G," "C," "A" and "U" each generally stand for a nucleotide that contains guanine, cytosine, adenine, and uracil as a base, respectively. "T" and "dT" are used interchangeably herein and refer to a deoxyribonucleotide wherein the nucleobase is thymine, *e.g.*, deoxyribothymine. However, it will be understood that the term "ribonucleotide" or "nucleotide" or "deoxyribonucleotide" can also refer to a modified nucleotide, as further

detailed below, or a surrogate replacement moiety. The skilled person is well aware that guanine, cytosine, adenine, and uracil may be replaced by other moieties without substantially altering the base pairing properties of an oligonucleotide comprising a nucleotide bearing such replacement moiety. For example, without limitation, a nucleotide comprising inosine as its base may base pair with nucleotides containing adenine, cytosine, or uracil. Hence, nucleotides containing uracil, guanine, or adenine may be replaced in the nucleotide sequences of the invention by a nucleotide containing, for example, inosine. Sequences comprising such replacement moieties are embodiments of the invention.

[0067] As used herein, the term "complementary," when used to describe a first nucleotide sequence in relation to a second nucleotide sequence, refers to the ability of an oligonucleotide or polynucleotide comprising the first nucleotide sequence to hybridize and form a duplex structure under certain conditions with an oligonucleotide or polynucleotide comprising the second nucleotide sequence, as will be understood by the skilled person. Complementary sequences are also described as binding to each other and characterized by binding affinities.

[0068] For example, a first nucleotide sequence can be described as complementary to a second nucleotide sequence when the two sequences hybridize (*e.g.*, anneal) under stringent hybridization conditions. Hybridization conditions include temperature, ionic strength, pH, and organic solvent concentration for the annealing and/or washing steps. The term stringent hybridization conditions refers to conditions under which a first nucleotide sequence will hybridize preferentially to its target sequence, *e.g.*, a second nucleotide sequence, and to a lesser extent to, or not at all to, other sequences. Stringent hybridization conditions are sequence dependent, and are different under different environmental parameters. Generally, stringent hybridization conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the nucleotide sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the first nucleotide sequences hybridize to a perfectly matched target sequence. An extensive guide to the hybridization of nucleic acids is found in, *e.g.*, Tijssen (1993) Laboratory Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes part I, chap. 2, "Overview of principles of hybridization and the strategy of nucleic acid probe assays," Elsevier, N.Y. ("Tijssen"). Other conditions, such as physiologically relevant conditions as may be encountered inside an organism, can apply. The skilled person will be able to

determine the set of conditions most appropriate for a test of complementarity of two sequences in accordance with the ultimate application of the hybridized nucleotides.

[0069] This includes base-pairing of the oligonucleotide or polynucleotide comprising the first nucleotide sequence to the oligonucleotide or polynucleotide comprising the second nucleotide sequence over the entire length of the first and second nucleotide sequence. Such sequences can be referred to as "fully complementary" with respect to each other herein. However, where a first sequence is referred to as "substantially complementary" with respect to a second sequence herein, the two sequences can be fully complementary, or they may form one or more, but generally not more than 4, 3 or 2 mismatched base pairs upon hybridization, while retaining the ability to hybridize under the conditions most relevant to their ultimate application. However, where two oligonucleotides are designed to form, upon hybridization, one or more single stranded overhangs, such overhangs shall not be regarded as mismatches with regard to the determination of complementarity. For example, a dsRNA comprising one oligonucleotide 21 nucleotides in length and another oligonucleotide 23 nucleotides in length, wherein the longer oligonucleotide comprises a sequence of 21 nucleotides that is fully complementary to the shorter oligonucleotide, may yet be referred to as "fully complementary" for the purposes described herein.

[0070] "Complementary" sequences, as used herein, may also include, or be formed entirely from, non-Watson-Crick base pairs and/or base pairs formed from non-natural and modified nucleotides, provided the above requirements with respect to their ability to hybridize are fulfilled. Such non-Watson-Crick base pairs includes, but not limited to, G:U Wobble or Hoogstein base pairing.

[0071] The terms "complementary," "fully complementary" and "substantially complementary" herein may be used with respect to the base matching between two strands of a dsRNA, or between the antisense strand of a dsRNA and a target sequence, between complementary strands of a single stranded RNA sequence or a single stranded DNA sequence, as will be understood from the context of their use.

[0072] As used herein, a "duplex structure" comprises two anti-parallel and substantially complementary nucleic acid sequences. Complementary sequences in a nucleic acid construct, between two transcripts, between two regions within a transcript, or between a transcript and a target sequence can form a "duplex structure." In general, the majority of nucleotides of each strand are ribonucleotides, but as described in detail herein, each or both strands can also include at least one non-ribonucleotide, *e.g.*, a deoxyribonucleotide and/or a modified nucleotide. The two strands forming the duplex structure may be different portions

of one larger RNA molecule, or they may be separate RNA molecules. Where the two strands are part of one larger molecule, and therefore are connected by an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting RNA chain is referred to as a "hairpin loop." Where the two strands are connected covalently by means other than an uninterrupted chain of nucleotides between the 3'-end of one strand and the 5'-end of the respective other strand forming the duplex structure, the connecting structure is referred to as a "linker." The RNA strands may have the same or a different number of nucleotides. The maximum number of base pairs is the number of nucleotides in the shortest strand of the duplex minus any overhangs that are present in the duplex. Generally, the duplex structure is between 15 and 30 or between 25 and 30, or between 18 and 25, or between 19 and 24, or between 19 and 21, or 19, 20, or 21 base pairs in length. In one embodiment the duplex is 19 base pairs in length. In another embodiment the duplex is 21 base pairs in length. When two different siRNAs are used in combination, the duplex lengths can be identical or can differ.

[0073] As used herein, the term "region of complementarity" refers to the region on the antisense strand that is substantially complementary to a sequence, for example a target sequence, as defined herein. Where the region of complementarity is not fully complementary to the target sequence, the mismatches are most tolerated in the terminal regions and, if present, are generally in a terminal region or regions, *e.g.*, within 6, 5, 4, 3, or 2 nucleotides of the 5' and/or 3' terminus.

[0074] The term "percent identity," in the context of two or more nucleic acid or polypeptide sequences, refer to two or more sequences or subsequences that have a specified percentage of nucleotides or amino acid residues that are the same, when compared and aligned for maximum correspondence, as measured using one of the sequence comparison algorithms described below (*e.g.*, BLASTP and BLASTN or other algorithms available to persons of skill) or by visual inspection. Depending on the application, the percent "identity" can exist over a region of the sequence being compared, *e.g.*, over a functional domain, or, alternatively, exist over the full length of the two sequences to be compared.

[0075] For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

[0076] Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by visual inspection (see generally Ausubel *et al.*, infra).

[0077] One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al.*, J. Mol. Biol. 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov/).

[0078] The term "sufficient amount" means an amount sufficient to produce a desired effect, *e.g.*, an amount sufficient to produce a detectable signal from a cell.

[0079] The term "therapeutically effective amount" is an amount that is effective to ameliorate a symptom of a disease. A therapeutically effective amount can be a "prophylactically effective amount" as prophylaxis can be considered therapy.

[0080] It must be noted that, as used in the specification and the appended claims, the singular forms "a," "an" and "the" include plural referents unless the context clearly dictates otherwise.

II. Lysogenic and Lytic Cycle of Viruses

[0081] Viruses undergo lysogenic and lytic cycles in a host cell. If the lysogenic cycle is adopted, the phage chromosome can be integrated into the bacterial chromosome, or it can establish itself as a stable plasmid in the host, where it can remain dormant for long periods of time. If the lysogen is induced, the phage genome is excised from the bacterial chromosome and initiates the lytic cycle, which culminates in lysis of the cell and the release of phage particles. The lytic cycle leads to the production of new phage particles which are released by lysis of the host.

[0082] Certain temperate phage can exhibit lytic activity, and the propensity for this may vary with varying host bacteria. To illustrate this phenomenon, the lytic activity of two temperate *S. aureus* phages on ten MRSA clinical isolates was examined via plaque assay (Table 1). The phage φ11 exhibited lytic activity on 10 out of 10 clinical MRSA isolates and φ80α exhibited lytic activity on six of the 10 clinical MRSA isolates. Thus, reporter assays

relying on the natural lysogenic cycle of phages can be expected to exhibit lytic activity sporadically.

Table 1: Lytic activity (denoted by the letter "x") of the S. aureus temperate phages φ11 and φ80α on ten clinical MRSA isolates

MRSA isolate	ϕ11	ϕ80α
1	x	
2	x	
3	x	x
4	x	x
5	x	x
6	x	
7	x	x
8	x	
9	x	x
10	x	x

[0083] In addition, virus-based reporter assays, such as phage-based reporters, can suffer from limited reactivity (*i.e.*, analytical inclusivity) due to limits in the phage host range caused by host-based and prophage-derived phage resistance mechanisms. These resistance mechanisms target native phage nucleic acid that can result in the degradation or otherwise inhibition of the phage DNA and functions. Such resistance mechanisms include restriction systems that cleave phage DNA and CRISPR systems that inhibit phage-derived transcripts.

[0084] Both lytic activity and phage resistance can be inhibitory to assays based on reporter phages. Lytic activity can inhibit signal by destroying or otherwise inhibiting the cell in its ability to generate a detectable signal and thus affecting limits of detection by reducing the amount of detectable signal or preventing the generation of a detectable signal. Phage resistance mechanisms can limit the host range of the phage and limit the inclusivity of the phage-based reporter, similarly affecting limits of detection by reducing the amount of detectable signal or preventing the generation of a detectable signal. Both lytic activity and phage resistance caused by the incorporation of phage DNA in a reporter phage can lead to false-negative results in assays that incorporate these phage reporters.

III. Methods for Producing Non-Replicative Transduction Particles (NRTP)

Disruption/Complementation-Based Methods For Producing Non-Replicative Transduction Particles.

[0085] Disclosed herein are non-replicative transduction particle packaging systems based on disruption of a component of the genome of a virus that is recognized by the viral packaging machinery as the element from which genomic packaging is initiated during viral production. In an embodiment, this disruption disrupts a packaging initiation site from a bacteriophage, and also disrupts a terminase function. Examples of the disrupted elements include the pac-site sequence of pac-type bacteriophages and the cos-site sequence of cos-type bacteriophages. In one embodiment, when the packaging initiation site sequence within the phage is disrupted, the phage cannot produce functional terminases. In an example, the pac-site is encoded within a pacA gene sequence, and terminase functions require both a functional PacA and PacB. In the embodiment, plasmid DNA is packaged into a phage capsid by complementing said disrupted terminases and including a recognizable packaging initiation site on the plasmid DNA. The bacteriophage can be any bacteriophage, such as an *Enterobacteriaceae* bacteriophage P1 or φEF11, or an *S. aureus* bacteriophage φ80α or a bacteriophage φ11.

[0086] Packaging initiation sites are often found within coding regions of genes that are essential to virus production. In some embodiments, a region of the bacteriophage genome is disrupted by an insertion, replacement, deletion, or mutation that disrupts the packaging initiation site. Examples of disruptions that accomplish this include, but are not limited to, an allelic exchange event that replaces a sequence on the bacteriophage genome that contains the packaging initiation site sequence with another sequence such as that of the an antibiotic resistance gene, or the complete deletion of the small and large terminase genes. In an example employing the terminase genes pacA and pacB, pacA can be disrupted in a manner that causes polar effects that also disrupt pacB expression and/or overall terminase function mediated by PacA and PacB. Other examples can include terminase genes can also include terS and terL genes from S. aureus bacteriophage φ11 or φ80α, or the terS and terL genes from E. faecalis bacteriophage φEf11. In an embodiment, a terminase gene includes SEQ ID NO:10, a P1 pacA gene in which a portion of the gene sequence that contains the pac-site has been replaced by a kanamycin resistance gene. Figure 1 illustrates an example of the disruption of the pacA gene in the bacteriophage P1 by the insertion of a kanamycin resistance gene within the pacA gene via allelic exchange.

[0087] In one example, a cell's genome is lysogenized with a viral genome where the packaging initiation site has been disrupted. In some embodiments, the cell can be an *E. coli* cell, an *S. aureus* cell, or an *E. faecalis* cell. The cell can be Gram-negative or Gram-positive. A complementing plasmid (or reporter nucleic acid molecule) is introduced into the cell, and the plasmid DNA includes at least the gene that has been disrupted in the bacteriophage, as well as the packaging initiation site sequence, and optionally additional bacteriophage genes and a reporter gene, which can encode a detectable and/or a selectable marker. The plasmid can be constructed using methods found in International App. No. PCT US 2014/026536, hereby incorporated by reference in its entirety. In some embodiments, the packaging initiation site sequence includes a pac-site or a cos-site. In an embodiment, the packaging initiation site sequence includes the sequence of SEQ ID NO: 1, SEQ ID NO: 4, or SEQ ID NO: 6. One or more genes of the plasmid can be operatively linked to a promoter, such as an inducible promoter (which can be induced when packaging is initiated by inducing the bacteriophage). In some embodiments, the promoter can be a native promoter of a small terminase gene or a large terminase gene. In an embodiment, the native promoter can be controlled by the bacteriophage, and thus effectively acts as a conditional promoter induced during packaging. In an embodiment, the promoter includes the sequence of SEQ ID NO: 9.

[0088] Figure 2 illustrates a schematic of a plasmid carrying the pacA and pacB genes. Figure 3 illustrates an example of the design and function of a packaging system composed of an E. coli cell lysogenized with the bacteriophage P1 having a disrupted pacA gene. The cell also carries a plasmid that contains the pacA and pacB genes. In an embodiment, the pacA and pacB genes in the plasmid are derived from Enterobacteriaceae bacteriophage P1. When the mutated virus is undergoing a lytic cycle, the viral packaging proteins produced either from the bacteriophage genome or (if disrupted) the complementing plasmid, package a replicon of the plasmid DNA into the packaging unit because of its packaging initiation site, and non-replicative transduction particles are produced carrying the replicated plasmid DNA.

[0089] In an embodiment, the replicon is an *Enterobacteriaceae* bacteriophage P1 lytic replicon. The replicon can also be a pBHR1 replicon or a derivative of the pBHR1 replicon, derived from an *S. aureus* pT181 plasmid origin of replication, derived from an *Enterococcus* repB plasmid origin of replication, or derived from an *Enterococcus* pDL278 plasmid origin of replication. In another embodiment, the replicon includes a C1 repressor-controlled P53 promoter, a promoter P53 antisense, a repL gene, and an in-frame deletion of a kilA gene. One example of a replicon has the sequence of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, or SEQ ID NO: 8.

[0090] In some embodiments, it is preferable that the disruption/complementation is designed such that there is no homology between the mutated virus DNA and the complementing exogenous DNA. This is because lack of homology between the mutated virus DNA and the complementing exogenous DNA avoids the possibility of homologous recombination between the two DNA molecules that can result in re-introduction of a packaging sequence into the virus genome. To accomplish a lack of homology, one strategy is to delete the entire gene (or genes) that contains the packaging initiation site sequence from the virus genome and then complement this gene with an exogenous DNA molecule that preferably contains no more than exactly the DNA sequence that was deleted from virus. In this strategy, the complementing DNA molecule is designed to express the gene that was deleted from the virus. Another example of such a system is provided using the bacteriophage φ80α, a pac-type phage. The phage genome is lysogenized in a host bacterial cell, and the phage genome includes a small terminase gene where the pac-site of a pac-type prophage φ80α has been deleted. A plasmid including a complementary small terminase gene with a native pac-site is transformed into the cell. When the lytic cycle of the lysogenized prophage is induced, the bacteriophage packaging system packages plasmid DNA into progeny bacteriophage structural components, rather than packaging the native bacteriophage DNA. The packaging system thus produces non-replicative transduction particles carrying plasmid DNA.

[0091] In another embodiment, a region of the bacteriophage genome is disrupted by an insertion that disrupts the packaging initiation site. In one embodiment, the disruption comprises reporter gene incorporated into the bacteriophage genome. In one embodiment, the disruption comprises a resistance marker and a reporter gene incorporated into the bacteriophage genome. In one embodiment, the disruption is accomplished by an allelic exchange event that replaces or disrupts a sequence on the bacteriophage genome with a reporter gene. In one embodiment, the disruption is accomplished by an allelic exchange event that replaces or disrupts a sequence on the bacteriophage genome with a resistance marker and a reporter gene. In some embodiments, the resistance marker and/or reporter gene are under the control of a constitutive promoter.

[0092] Figure 4 illustrates an example of the design and function of a packaging system composed of an E. coli cell comprising bacteriophage P1 having a disrupted pacA gene in which the kan and luxAB genes have been inserted into the pac-site sequence. As in Figure 3, the cell also carries a plasmid that contains the pacA and pacB genes. Therefore, if recombination occurs between the bacteriophage and the plasmid, the replicated plasmid inserted into the P1 capsid to form the NRTP will still comprise a reporter gene.

[0093] In an embodiment, the reporter gene encodes a detectable marker or a selectable marker. In a further embodiment, said reporter gene is selected from the group consisting of enzymes mediating luminescence reactions (luxA, luxB, luxAB, luc, ruc, nluc), enzymes mediating colorimetric reactions (lacZ, HRP), fluorescent proteins (GFP, eGFP, YFP, RFP, CFP, BFP, mCherry, near-infrared fluorescent proteins), affinity peptides (His-tag, 3X-FLAG), and selectable markers (ampC, tet(M), CAT, erm). In an embodiment, the reporter gene is luxA. In some embodiments, the resistance marker comprises an antibiotic resistance gene. In some embodiments, the resistance marker is a kanamycin resistance gene (kan). In some embodiments, the constitutive promoter comprises Pblast. In some embodiments, the bacteriophage genome disruption is accomplished by an allelic exchange event that replaces or disrupts a sequence on the bacteriophage genome that contains the packaging initiation site sequence.

[0094] In some embodiments, the bacteriophage genome disruption is accomplished by an allelic exchange event that replaces or disrupts a sequence on the bacteriophage genome that contains the packaging initiation site sequence with a kanamycin resistance gene (kan) and the bacterial luciferase genes (luxAB) under the control of a constitutive promoter (Pblast). In one embodiment, the allelic exchange is accomplished in a manner analogous to that depicted in Figure 1, wherein a reporter or a reporter and a resistance marker are transferred.

[0095] In an embodiment, a pair of terminase genes on a bacteriophage genome, *e.g.*, pacA and pacB, terA and terB, or terS and terL, are disrupted in a manner that causes polar effects that also disrupt expression of one of the terminase genes and/or overall terminase function mediated by the terminase genes. In one embodiment, a construct comprising kan and luxAB inserted into the pacA gene loci is provided in SEQ ID NO: 12. In one embodiment, the disrupted bacteriophage is complemented with a plasmid comprising terminase genes, *e.g.*, pacA and pacB, terA and terB, or terS and terL, of the bacteriophage genome. In one embodiment, the plasmid is introduced into a cell lysogenized with the bacteriophage having the disrupted terminase genes. In one embodiment, the cell is an *E. coli* cell. In one embodiment, the bacteriophage is *Enterobacteriaceae* bacteriophage P1. In one embodiment, the terminase genes in the plasmid are derived from Enterobacteriaceae bacteriophage P1, i.e., pacA and pacB genes. When the mutated virus is undergoing a lytic cycle, the viral packaging proteins, produced either from the bacteriophage genome or (if disrupted) the complementing plasmid, package a replicon of the plasmid DNA into the packaging unit because it contains a packaging initiation site, and non-replicative transduction particles are produced carrying the replicated plasmid DNA.

[0096] In these deletion / complementation systems, two species of transduction particles may be produced including (1) non-replicative transduction particles carrying plasmid DNA and (2) non-replicative transduction particles carrying P1 DNA where the latter may be produced due to recombination between the plasmid DNA and the P1 DNA. In an embodiment where the P1 mutant does not contain luxAB inserted into the P1 genome, the non-replicative transduction particles carrying P1 DNA do not contribute to signal production when these transduction particles deliver DNA into target cells. However, in an embodiment where the P1 mutant does contain luxAB inserted in the P1 genome, the non-replicative transduction particles carrying P1 DNA do contribute to signal production when these transduction particles deliver DNA into target cells.

[0097] As such, an embodiment where the luxAB genes are inserted into the P1 genome results in an improved non-replicative transduction particle reporter system.

[0098]

IV. Reporters

[0099] In some embodiments, the NRTPs and constructs of the invention comprise a reporter nucleic acid molecule including a reporter gene. In some embodiments, the bacteriophage of the invention includes a reporter gene. The reporter gene can encode a reporter molecule, and the reporter molecule can be a detectable or selectable marker. In certain embodiments, the reporter gene encodes a reporter molecule that produces a detectable signal when expressed in a cell.

[0100] In certain embodiments, the reporter molecule can be a fluorescent reporter molecule, such as, but not limited to, a green fluorescent protein (GFP), enhanced GFP, yellow fluorescent protein (YFP), cyan fluorescent protein (CFP), blue fluorescent protein (BFP), red fluorescent protein (RFP) or mCherry, as well as near-infrared fluorescent proteins.

[0101] In other embodiments, the reporter molecule can be an enzyme mediating luminescence reactions (luxA, luxB, luxAB, luc, ruc, nluc, *etc.*). Reporter molecules can include a bacterial luciferase, a eukaryotic luciferase, an enzyme suitable for colorimetric detection (lacZ, HRP), a protein suitable for immunodetection, such as affinity peptides (His-tag, 3X-FLAG), a nucleic acid that function as an aptamer or that exhibits enzymatic activity (ribozyme), or a selectable marker, such as an antibiotic resistance gene (ampC, tet(M), CAT, erm). Other reporter molecules known in the art can be used for producing signals to detect target nucleic acids or cells.

[0102] In other aspects, the reporter molecule comprises a nucleic acid molecule. In some aspects, the reporter molecule is an aptamer with specific binding activity or that exhibits enzymatic activity (*e.g.*, aptazyme, DNAzyme, ribozyme).

[0103] Reporters and reporter assays are described further in Section V herein.

NRTPs and Reporter Assays

Inducer Reporter Assay

[0104] In some embodiments, the invention comprises methods for the use of NRTPs as reporter molecules for use with endogenous or native inducers that target gene promoters within viable cells. The NRTPs of the invention can be engineered using the methods described in Section III and below in Examples 1-2.

[0105] In some embodiments, the method comprises employing a NRTP as a reporter, wherein the NRTP comprises a reporter gene that is operably linked to an inducible promoter that controls the expression of a target gene within a target cell. When the NRTP that includes the reporter gene is introduced into the target cell, expression of the reporter gene is possible via induction of the target gene promoter in the reporter nucleic acid molecule.

[0106] Figure 5 depicts a genomic locus of a target cell 500 with two genes, a gene encoding an inducer 502 and a target gene 503. Also depicted is a reporter nucleic acid molecule 504 that includes a reporter gene 505 that is operatively linked to the promoter 506 of the target gene of the target cell. The reporter nucleic acid molecule 504 can be introduced into the cell via a NRTP. In the native cell, when the inducer gene 502 is expressed and produces the inducer protein 507, the inducer protein 507 is able to induce the target gene promoter 506 that is operatively linked to the target gene, thus causing the expression of the target gene and the production of the target gene product 508.

[0107] When the reporter nucleic acid molecule 504 is present within the target organism, the inducer 507 is also able to induce the target gene promoter 506 present within the reporter nucleic acid molecule 504, thus causing the expression of the reporter gene 505 resulting in the production of a reporter molecule 509 capable of generating a detectable signal.

[0108] Thus, the production of a detectable signal from the reporter molecule 509 is indicative of the presence of the cell, based on the presence of the inducer protein 507 within a target cell.

VanR Reporter System

[0109] In one embodiment, the reporter system includes NRTP comprising a reporter nucleic acid molecule (*e.g.*, plasmid). The reporter nucleic acid molecule can be constructed for detecting VanR, the inducer of the promoter of the vancomycin resistance (vanA) gene in

Enterococcus faecium (or *E. faecalis*). The reporter plasmid carries a reporter gene that is operatively linked to the vanA gene promoter.

[0110] Figure 6 outlines the design and function of a VanR reporter system. Figure 6 depicts a region of the transposon Tn1546 601 that may be present in E. faecium. The Tn1546 transposon can include the vanR inducer gene 602 and the vanA target gene 603. Also depicted in the figure is a reporter nucleic acid molecule 604 that can be packaged in a NRTP and introduced into the cell. The reporter nucleic acid molecule 604 includes a reporter gene 605 that is operatively linked to a promoter P_H 606 that controls the expression of the vanHAX operon that includes the vanA gene. In the native cell, when the vanR gene 602is expressed and produces the VanR protein 607, VanR is able to induce P_H 606 in the Tn1546 transposon, thus causing the expression of the vanA gene and thus producing the VanA protein 608. When the reporter nucleic acid molecule 603 (vector) is present within the target organism, VanR is also able to induce P_H 606 within the reporter nucleic acid molecule 603, thus causing the expression of a reporter molecule 609. Thus, the production of a reporter molecule is indicative of the presence of VanR within a target cell.

[0111] Examples of promoters that are suitable for the development of a VRE assay include: the vanA gene promoter and a vanB gene promoter. Arthur, M., et al., *The VanS sensor negatively controls VanR-mediated transcriptional activation of glycopeptide resistance genes of Tn1546 and related elements in the absence of induction.* J. Bacteriol., 1997. **179**(1): p. 97-106.

TcdD reporter system

[0112] In another embodiment of this system, a reporter nucleic acid molecule is introduced into a cell using a NRTP. The reporter nucleic acid molecule can be constructed for detecting TcdD, the inducer of the promoters of the toxins A and B genes (tcdA and tcdB, respectively) of *C. difficile*. The reporter nucleic acid molecule includes a reporter gene that is operatively linked to the tcdA gene promoter.

[0113] Figure 7 outlines the design and function of a TcdD reporter system, according to an embodiment of the invention. Figure 7 depicts a region of the transposon PaLoc 701 that may be present in C. difficile. The PaLoc transposon may contain the tcdD gene 702 and the tcdA target gene 703. Also depicted in the figure is a reporter nucleic acid molecule 704 (*e.g.*, vector) that is introduced into the cell using a NRTP. The reporter nucleic acid molecule 704 includes the reporter gene 705 that operatively linked to the tcdA gene promoter (P_{tcdA}) 706.

[0114] In the native cell, when the tcdD gene is expressed and produces the TcdD protein 707, TcdD is able to induce P_{tcdA} 706 in the PaLoc transposon 701, thus causing the expression of the tcdA gene 703 and thus producing the toxin A protein 708.

[0115] When the reporter nucleic acid molecule 704 is present within the target organism, TcdD is also able to induce P_{tcdA} 706 within the reporter vector, thus causing the expression of a reporter molecule 709. Thus, the production of a reporter molecule 709 is indicative of the presence of TcdD within a target cell.

[0116] Examples of promoters suitable for the development of a *C. difficile* assay include: the tcdA gene promoter and the tcdB gene promoter. Karlsson, S., *et al.*, *Expression of Clostridium difficile Toxins A and B and Their Sigma Factor TcdD Is Controlled by Temperature.* Infect. Immun., 2003. **71**(4): p. 1784-1793.

[0117] Target cells and inducers: Target cells can include eukaryotic and prokaryotic cell targets and associated inducers.

[0118] Vector delivery systems: The delivery of the vector containing the recombinant DNA can by performed by abiologic or biologic systems. Including but not limited to liposomes, virus-like particles, transduction particles derived from phage or viruses, and conjugation.

Bacteriophage-based SarS reporter system

[0119] In another embodiment of the invention, a reporter nucleic acid molecule is constructed for detecting SarS, the inducer of the promoter of the Protein A gene (spa) in *S. aureus.* The reporter nucleic acid molecule can be introduced into the cell in a NRTP and includes the bacterial luciferase genes luxA and luxB operatively linked to the spa gene promoter (P_{spa}). The reporter nucleic acid molecule is delivered to *S. aureus* via a NRTP, for example. If SarS is present in the cell, it will induce the expression of the luxAB genes, thus producing luciferase enzyme that is capable of generating a luminescent signal.

[0120] Figure 8 outlines the design and function of a SarS reporter system, according to one embodiment of the invention. Figure 8 depicts a region of the S. aureus genome 801 that contain the sarS gene 802 and spa gene 803. Also depicted in the figure is a reporter nucleic acid molecule (*e.g.*, vector) 804 delivered by NRTP to the cell and that includes the luxAB reporter genes 805 that operatively linked to the promoter P_{spa} 806 that controls the expression of the spa gene 803.

[0121] In the native cell, when the sarS gene 802 is expressed, producing SarS protein 807, the protein is able to induce P_{spa} 806 in the *S. aureus* genome transposon, thus causing the expression of the spa gene 803 and producing the Protein A 808.

[0122] When the reporter nucleic acid molecule 804 is present within the target organism, SarS 807 is also able to induce P_{spa} 806 within the reporter nucleic acid molecule 804, thus causing the expression of luxAB resulting in the production of the luciferase enzyme 809 that can generate a luminescent signal. Thus, the production of luciferase is indicative of the presence of SarS within a target cell.

[0123] Other reporter systems for use with the NRTPs described herein are described in International PCT Publication Number: WO 2014/160418, incorporated herein by reference in its entirety.

Mechanism of Conformational Change by Cis-Repression of the Reporter Sequence and by Binding of a Target Transcript

[0124] The general mechanisms employed in the invention are intermolecular nucleic acid molecule interactions that may result in two subsequent mechanisms: (1) a conformational change in the secondary structure of the nucleic acid molecules, and (2) a cleaving event. Described herein are methods for designing reporter transcripts that can undergo a conformational change between a cis-repressed conformation and a de-repressed conformation, such that the conformational change is induced by binding of a target transcript to the reporter transcript.

[0125] As described above, a reporter transcript can comprise a reporter sequence and be designed such that translation of the reporter gene sequence is blocked by cis-repression of the ribosome binding site (RBS) of the reporter gene.

[0126] In some embodiments, the following tools can be used for designing the reporter transcripts of the invention.

[0127] 1) RNA secondary structure is calculated using secondary structure program, such as Mfold available at a server maintained by The RNA Institute College of Arts and Sciences, University at Albany, State University of New York (Mfold web server for nucleic acid folding and hybridization prediction. Nucleic Acids Res. 31 (13), 3406-15, (2003)) (http://mfold.rna.albany.edu/?q=mfold/RNA-Folding-Form).

[0128] 2) Intermolecular RNA interactions are calculated using a software program such as RNA-RNA InterACTion prediction using Integer Programming (RactIP) available at a server maintained by the Graduate School of Information Science, Nara Institute of Science and Technology (NAIST), Department of Biosciences and Informatics, Keio University Japan (http://rna.naist.jp/ractip/).

[0129] 3) RNA secondary structure is visualized using Visualization Applet for RNA (VARNA) (http://varna.lri.fr/), which is a Java lightweight Applet dedicated to drawing the secondary structure of RNA.

[0130] A secondary structure of the target transcript can be generated based on the lowest energy conformation calculated by MFold and visualized with VARNA.

[0131] ssRNA regions or target regions can be identified within the target transcript that can be ideal for binding to a reporter transcript. In some instances, the secondary structure of the target transcript includes a consensus sequence or loop sequence that can bind to a portion of the reporter sequence. For example, in the *mecA* transcript of methicillin-resistant *S. aureus*, there is a terminal loop that includes a consensus YUNR sequence ("UUGG") that can be used to bind to a cis-repressing sequence of a reporter transcript. Analysis of the secondary structure of the target transcript can reveal these one or more ssRNA regions that can be suitable for binding to a cis-repressing sequence. The cis-repressing sequence of the reporter transcript can then be designed to bind to these one or more ssRNA regions.

[0132] In some embodiments, the cis-repressing sequence can be designed to bind to the RBS of the reporter sequence in the reporter transcript and form a stem-loop structure within the reporter transcript, such that the cis-repressing sequence blocks binding of an RNA polymerase to the RBS of the reporter sequence. Upon binding of the cis-repressing sequence to the ssRNA region of the target transcript, the RBS of the reporter sequence can be exposed and translation of the reporter sequence can be initiated.

[0133] In some embodiments, the cis-repressing sequence of the reporter transcript can be designed to be positioned at the 5' terminus of the reporter sequence and designed to generate a stem-loop structure in the reporter sequence, such that the RBS sequence of the reporter sequence is blocked. The cis-repressing stem-loop structure can be designed to block the RBS sequence based on the lowest energy conformation of the reporter transcript, as calculated by MFold and visualized with VARNA. The predicted inter-molecular interactions between the target transcript and the cis-repressing sequence of the reporter transcript can be calculated by RactIP and visualized by VARNA. A diagram can be drawn to visualize the base pairing between the target transcript and the cis-repressing sequence of the reporter transcript, as shown in Figure 9.

[0134] The interaction can include base pairing between 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50 or more nucleotides in the target sequence and cis-repressing sequence. The complementary binding between the two sequences can be fully

complementary, substantially complementary or partially complementary. The base pairing can be across contiguous nucleotide sequences or regions within the target and cis-repressing sequences, for example, as shown in Figure 9.

Transcripts

[0135] As described above, a transcript is a length of nucleotide sequence (DNA or RNA) transcribed from a DNA or RNA template sequence or gene. The transcript can be a cDNA sequence transcribed from an RNA template or an mRNA sequence transcribed from a DNA template. The transcript can be transcribed from an engineered nucleic acid construct. The transcript can have regions of complementarity within itself, such that the transcript includes two regions that can form an intra-molecular duplex. One region can be referred to as a "cis-repressing sequence" that binds to and blocks translation of a reporter sequence. A second region of the transcript is called a "reporter sequence" that encodes a reporter molecule, such as a detectable or selectable marker.

[0136] The transcripts of the invention can be a transcript sequence that can be 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 nucleotides in length. In other embodiments, the transcript can be at least 25, 30, 40, 50, 60, 70, 80, 90, 100, 500, 1000, 1500, 2000, 3000, 4000, 5000 or more nucleotides in length. The cis-repressing sequence and the reporter sequence can be the same length or of different lengths.

[0137] In some embodiments, the cis-repressing sequence is separated from the reporter sequence by 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 55, 60, or more spacer nucleotides.

Vectors

[0138] In another aspect, the transcripts (including antisense and sense sequences) of the invention are expressed from transcription units inserted into DNA or RNA vectors (*see, e.g.*, Couture, A, *et al.*, *TIG.* (1996), 12:5-10; Skillern, A., *et al.*, International PCT Publication No. WO 00/22113, Conrad, International PCT Publication No. WO 00/22114, and Conrad, U.S. Pat. No. 6,054,299). These sequences can be introduced as a linear construct, a circular plasmid, or a viral vector, including bacteriophage-based vectors, which can be incorporated and inherited as a transgene integrated into the host genome. The transcript can also be constructed to permit it to be inherited as an extrachromosomal plasmid (Gassmann, *et al.*, *Proc. Natl. Acad. Sci. USA* (1995) **92**:1292).

[0139] The transcript sequences can be transcribed by a promoter located on the expression plasmid. In one embodiment, the cis-repressing and reporter sequences are expressed as an

inverted repeat joined by a linker polynucleotide sequence such that the transcript has a stem and loop structure.

[0140] Recombinant expression vectors can be used to express the transcripts of the invention. Recombinant expression vectors are generally DNA plasmids or viral vectors. Viral vectors expressing the transcripts can be constructed based on, but not limited to, adeno-associated virus (for a review, see Muzyczka, *et al.*, *Curr. Topics Micro. Immunol.* (1992) 158:97-129)); adenovirus (see, for example, Berkner, *et al.*, BioTechniques (1998) 6:616), Rosenfeld *et al.* (1991, Science 252:431-434), and Rosenfeld *et al.* (1992), *Cell* 68:143-155)); or alphavirus as well as others known in the art. Retroviruses have been used to introduce a variety of genes into many different cell types, including epithelial cells, *in vitro* and/or *in vivo* (see, *e.g.*, Eglitis, *et al.*, *Science* (1985) 230:1395-1398; Danos and Mulligan, Proc. Natl. Acad. Sci. *USA* (1998) 85:6460-6464; Wilson *et al.*, 1988, Proc. Natl. Acad. Sci. USA 85:3014-3018; Armentano *et al.*, 1990, Proc. Natl. Acad. Sci. USA 87:61416145; Huber *et al.*, 1991, Proc. Natl. Acad. Sci. USA 88:8039-8043; Ferry *et al.*, 1991, Proc. Natl. Acad. Sci. USA 88:8377-8381; Chowdhury *et al.*, 1991, Science 254:1802-1805; van Beusechem. *et al.*, 1992, Proc. Natl. Acad. Sci. USA 89:7640-19 ; Kay *et al.*, 1992, Human Gene Therapy 3:641-647; Dai *et al.*, 1992, Proc. Natl. Acad. Sci. USA 89:10892-10895; Hwu *et al.*, 1993, J. Immunol. 150:4104-4115; U.S. Patent No. 4,868,116; U.S. Patent No. 4,980,286; PCT Application WO 89/07136; PCT Application WO 89/02468; PCT Application WO 89/05345; and PCT Application WO 92/07573). Recombinant retroviral vectors capable of transducing and expressing genes inserted into the genome of a cell can be produced by transfecting the recombinant retroviral genome into suitable packaging cell lines such as PA317 and Psi-CRIP (Comette *et al.*, 1991, Human Gene Therapy 2:5-10; Cone *et al.*, 1984, Proc. Natl. Acad. Sci. USA 81:6349). Recombinant adenoviral vectors can be used to infect a wide variety of cells and tissues in susceptible hosts (*e.g.*, rat, hamster, dog, and chimpanzee) (Hsu *et al.*, 1992, J. Infectious Disease, 166:769), and also have the advantage of not requiring mitotically active cells for infection.

[0141] Any viral vector capable of accepting the coding sequences for the transcript(s) to be expressed can be used, for example, vectors derived from adenovirus (AV); adeno-associated virus (AAV); retroviruses (*e.g.*, lentiviruses (LV), Rhabdoviruses, murine leukemia virus); herpes virus, and the like. The tropism of viral vectors can be modified by pseudotyping the vectors with envelope proteins or other surface antigens from other viruses, or by substituting different viral capsid proteins, as appropriate.

[0142] For example, lentiviral vectors featured in the invention can be pseudotyped with surface proteins from vesicular stomatitis virus (VSV), rabies, Ebola, Mokola, and the like. AAV vectors featured in the invention can be made to target different cells by engineering the vectors to express different capsid protein serotypes. Techniques for constructing AAV vectors which express different capsid protein serotypes are within the skill in the art; see, *e.g.*, Rabinowitz J E *et al.* (2002), J Virol 76:791-801, the entire disclosure of which is herein incorporated by reference.

[0143] Selection of recombinant viral vectors suitable for use in the invention, methods for inserting nucleic acid sequences for expressing the transcripts into the vector, and methods of delivering the viral vector to the cells of interest are within the skill in the art. See, for example, Dornburg R (1995), Gene Therap. 2: 301-310; Eglitis M A (1988), Biotechniques 6: 608-614; Miller A D (1990), Hum Gene Therap. 1: 5-14; Anderson W F (1998), Nature 392: 25-30; and Rubinson D A *et al.*, Nat. Genet. 33: 401-406, the entire disclosures of which are herein incorporated by reference.

[0144] Viral vectors can be derived from AV and AAV. A suitable AV vector for expressing the transcripts featured in the invention, a method for constructing the recombinant AV vector, and a method for delivering the vector into target cells, are described in Xia H *et al.* (2002), *Nat. Biotech.* 20: 1006-1010. Suitable AAV vectors for expressing the transcripts featured in the invention, methods for constructing the recombinant AV vector, and methods for delivering the vectors into target cells are described in Samulski R *et al.* (1987), J. Virol. 61: 3096-3101; Fisher K J *et al.* (1996), J. Virol, 70: 520-532; Samulski R *et al.* (1989), J. Virol. 63: 3822-3826; U.S. Pat. No. 5,252,479; U.S. Pat. No. 5,139,941; International Patent Application No. WO 94/13788; and International Patent Application No. WO 93/24641, the entire disclosures of which are herein incorporated by reference.

[0145] The promoter driving transcript expression in either a DNA plasmid or viral vector featured in the invention may be a eukaryotic RNA polymerase I (*e.g.,* ribosomal RNA promoter), RNA polymerase II (*e.g.,* CMV early promoter or actin promoter or U1 snRNA promoter) or generally RNA polymerase III promoter (*e.g.,* U6 snRNA or 7SK RNA promoter) or a prokaryotic promoter, for example the T7 promoter, provided the expression plasmid also encodes T7 RNA polymerase required for transcription from a T7 promoter. The promoter can also direct transgene expression to the pancreas (see, *e.g.*, the insulin regulatory sequence for pancreas (Bucchini *et al.*, 1986, Proc. Natl. Acad. Sci. USA 83:2511-2515)).

[0146] In addition, expression of the transcript can be precisely regulated, for example, by using an inducible regulatory sequence and expression systems such as a regulatory sequence that is sensitive to certain physiological regulators, *e.g.*, circulating glucose levels, or hormones (Docherty *et al.*, 1994, FASEB J. 8:20-24). Such inducible expression systems, suitable for the control of transgene expression in cells or in mammals include regulation by ecdysone, by estrogen, progesterone, tetracycline, chemical inducers of dimerization, and isopropyl-beta-D-1-thiogalactopyranoside (IPTG). A person skilled in the art would be able to choose the appropriate regulatory/promoter sequence based on the intended use of the dsRNA transgene.

[0147] Generally, recombinant vectors capable of expressing transcript molecules are delivered as described below, and persist in target cells. Alternatively, viral vectors can be used that provide for transient expression of transcript molecules. Such vectors can be repeatedly administered as necessary. Once expressed, the transcript binds to target RNA and modulates its function or expression. Delivery of transcript expressing vectors can be systemic, such as by intravenous or intramuscular administration, by administration to target cells ex-planted from the patient followed by reintroduction into the patient, or by any other means that allows for introduction into a desired target cell.

[0148] Transcript expression DNA plasmids are typically transfected into target cells as a complex with cationic lipid carriers (*e.g.*, Oligofectamine) or non-cationic lipid-based carriers (*e.g.*, Transit-TKO™). Multiple lipid transfections for dsRNA-mediated knockdowns targeting different regions of a single PROC gene or multiple PROC genes over a period of a week or more are also contemplated by the invention. Successful introduction of vectors into host cells can be monitored using various known methods. For example, transient transfection can be signaled with a reporter, such as a fluorescent marker, such as Green Fluorescent Protein (GFP). Stable transfection of cells *ex vivo* can be ensured using markers that provide the transfected cell with resistance to specific environmental factors (*e.g.*, antibiotics and drugs), such as hygromycin B resistance.

[0149] The delivery of the vector containing the recombinant DNA can by performed by abiologic or biologic systems. Including but not limited to liposomes, virus-like particles, transduction particles derived from phage or viruses, and conjugation.

Reporters for Transcript Assay

[0150] In some embodiments, the nucleic acid construct comprises a reporter sequence (*e.g.*, a reporter gene sequence). The reporter gene encodes a reporter molecule that produces a signal when expressed in a cell. In some embodiments, the reporter molecule can be a

detectable or selectable marker. In certain embodiments, the reporter molecule can be a fluorescent reporter molecule, such as a green fluorescent protein (GFP), yellow fluorescent protein (YFP), cyan fluorescent protein (CFP), blue fluorescent protein (BFP), or red fluorescent protein (RFP). In other embodiments, the reporter molecule can be a chemiluminescent protein.

[0151] Reporter molecules can be a bacterial luciferase, an eukaryotic luciferase, a fluorescent protein, an enzyme suitable for colorimetric detection, a protein suitable for immunodetection, a peptide suitable for immunodetection or a nucleic acid that function as an aptamer or that exhibits enzymatic activity.

[0152] Selectable markers can also be used as a reporter. The selectable marker can be an antibiotic resistance gene, for example.

EXAMPLES

[0153] Below are examples of specific embodiments for carrying out the present invention. The examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way. Efforts have been made to ensure accuracy with respect to numbers used (*e.g.*, amounts, temperatures, etc.), but some experimental error and deviation should, of course, be allowed for.

[0154] The practice of the present invention will employ, unless otherwise indicated, conventional methods of protein chemistry, biochemistry, recombinant DNA techniques and pharmacology, within the skill of the art. Such techniques are explained fully in the literature. See, *e.g.*, T.E. Creighton, *Proteins: Structures and Molecular Properties* (W.H. Freeman and Company, 1993); A.L. Lehninger, *Biochemistry* (Worth Publishers, Inc., current addition); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); *Methods In Enzymology* (S. Colowick and N. Kaplan eds., Academic Press, Inc.); *Remington's Pharmaceutical Sciences*, 18th Edition (Easton, Pennsylvania: Mack Publishing Company, 1990); Carey and Sundberg *Advanced Organic Chemistry 3rd Ed.* (Plenum Press) Vols A and B(1992).

Example 1: Allelic Exchange-Based Disruption/Complementation Packaging System

[0155] The following is an example of the design and construction of an allelic exchange-based disruption/complementation-based packaging system for producing non-replicative transduction particles.

[0156] The materials used for developing the packaging system are listed below:

[0157] Bacterial Strains:

- N1706, an E. coli K-12 P1 c1-100 Tn9 lysogen

[0158] Vectors:

- Y14439 (pBHR1 backbone)

[0159] The following GenBank accession numbers (N.B., the sequences referred to by accession number are those listed in the database as of the priority date of this application) or SEQ ID NOs. can be used for the vector backbone and cassette sequences:

- X06758 (bacterial luciferase genes luxAB)
- SEQ ID NO:1 (Native P1 pacA and pacB genes including the native pacA gene promoter)
- SEQ ID NO:2 (P1 lytic replicon containing the C1 repressor-controlled P53 promoter, the promoter P53 antisense, the repL genes, and an in-frame deletion of the kilA gene)
- SEQ ID NO:11 (Pblast promoter driving luxAB expression)

[0160] Construction of N1706(pacA::Kan): pacA mutated strain aka Strain 1505: An exemplary sequence of a pacA mutated sequence is shown in SEQ ID NO: 10. The mutation can be accomplished by constructing an allelic exchange substrate comprised of the kanamycin resistance gene flanked by pacA gene sequences that themselves flank the sequence of the pacA gene that is desired to be replaced. The allelic exchange substrate can be produced via gene synthesis and then replacing the native sequence in N1706 and inserting the Kan gene via an allelic exchange. It was determined that the disruption also disrupted the ability of the mutated P1 phage to package DNA. Induction of the mutated phage resulted in elimination of the progeny phage as determined from comparing P1 phage titers via plaque assay from cell lysates produced by inducing the native phage vs. the mutated phage. Furthermore, when complementing plasmid expressing the pacA gene was introduced into the P1 mutant lysogen and the mutant phage was induced from the transformant, transduction particles were not recovered in the lysate indicating that the phage was not able to package the complementing plasmid despite it complementing the pacA gene and pac-site.

[0161] Construction of the complementing plasmid: The complementing plasmid contains the pBHR1 origin of replication exhibiting broad Gram-negative activity, a selectable marker for spectinomycin, the native bacteriophage P1 pacA and pacB genes operatively linked to the native pacA gene promoter sequence, the luxA and luxB genes are from *Aliivibrio fischeri* operatively linked to the constitutive blasticillin promoter (Pblast), and the P1 lytic replicon containing the C1 repressor-controlled P53 promoter, the promoter P53 antisense, the repL genes, and an in-frame deletion of the kilA gene.

[0162] The plasmid can be constructed in a variety of manners that are known to one of skill in the art including obtaining the cassettes via PCR from their native sources or via gene synthesis and assembly of the vector via traditional restriction enzyme-based cloning or alternative techniques such as Gibson assembly.

[0163] Complementation-based Packaging System: The packaging system includes the pacA mutant strain 1505 complemented with the complementing plasmid. As known to one of skill in the art, the manner of constructing this system can be accomplished by transformation of 1505 with the complementing plasmid. The complementing plasmid can be maintained in cultures of the transformed 1505 by growing the transformant in the presence of 10 ug/mL of spectinomycin.

[0164] Production of Transduction Particles Carrying Plasmid DNA: Non-replicative transduction particles carrying the complementing plasmid can be produced from 1505 transformants via thermal induction at 42°C. Incubation at 42°C results in induction of the P1 lytic cycle in which the prophage produces phage structural elements, and packages complementing plasmid concatameric DNA formed by the lytic replicon in progeny phage particles. Unlike complementation using a complementing plasmid that only expressed the pacA gene that did not result in the production of transduction particles when both the pacA and pacB genes were disrupted in the bacteriophage genome, the complementing plasmid expressing both the pacA and pacB genes resulted in cell lysate containing non-replicative transduction particles, each consisting of bacteriophage P1 particles carrying a linear concatemer of the complementing plasmid and thus demonstrating that this complementing plasmid successfully complements the disruption of packaging.

Example 2: Improved Allelic Exchange-Based Disruption/Complementation Packaging System

[0165] In an example employing an *Enterobacteriaceae* bacteriophage P1 comprising terminase genes pacA and pacB, pacA was disrupted in a manner that causes polar effects that also disrupt pacB expression and/or overall terminase function mediated by PacA and PacB. The final construct in which kan and luxAB are inserted into the pacA gene loci is included in SEQ ID NO:12.

[0166] The pacAB disrupted bacteriophage genome was then complemented with the plasmid depicted in Figure 2. Figure 4 illustrates the design and function of a packaging system composed of an *E. coli* cell lysogenized with the bacteriophage P1 having a disrupted pacA gene. The cell also contained a plasmid that contains the pacA and pacB genes. In this example, the pacA and pacB genes in the plasmid were derived from Enterobacteriaceae

bacteriophage P1. When the mutated virus was in the lytic cycle, the viral packaging proteins were produced from the complementing plasmid, which packaged a replicon of the plasmid DNA into the packaging unit because of its packaging initiation site, and non-replicative transduction particles were produced carrying the replicated plasmid DNA.

[0167] In these deletion complementation systems, two species of transduction particles were produced including (1) non-replicative transduction particles carrying plasmid DNA and (2) non-replicative transduction particles carrying P1 DNA where the latter may be produced due to recombination between the plasmid DNA and the P1 DNA. When the P1 mutant did not contain luxAB inserted in the pacA gene, the non-replicative transduction particles carrying P1 DNA did not contribute to signal production when these transduction particles deliver DNA into target cells. However, when the P1 mutant did contain luxAB inserted in the pacA gene, the non-replicative transduction particles carrying P1 DNA did contribute to signal production when these transduction particles deliver DNA into target cells (*see* Figure 10).

[0168] Therefore, when we insert the luxAB genes into the P1 genome and integrated with the system NRTP generating system described herein, we have provided an improved non-replicative transduction particle reporter system.

[0169] The following provides further details of the design and construction of the allelic exchange-based disruption/complementation-based packaging system for producing non-replicative transduction particles described in this example.

[0170] The materials used for developing the packaging system are listed below:

[0171] Bacterial Strains:

- N1706, an E. coli K-12 P1 c1-100 Tn9 lysogen

[0172] Vectors:

- Y14439 (pBHR1 backbone)

[0173] The following GenBank accession numbers (N.B., the sequences referred to by accession number are those listed in the database as of the priority date of this application) or SEQ ID NOs. can be used for the vector backbone and cassette sequences:

- X06758 (bacterial luciferase genes luxAB)
- SEQ ID NO:1 (Native P1 pacA and pacB genes including the native pacA gene promoter)
- SEQ ID NO:2 (P1 lytic replicon containing the C1 repressor-controlled P53 promoter, the promoter P53 antisense, the repL genes, and an in-frame deletion of the kilA gene)
- SEQ ID NO:11 (Pblast promoter driving luxAB expression)

[0174] Construction of N1706(pacA::Kan luxAB): pacA mutated strain aka Strain 1525: was performed as follows:

[0175] An exemplary sequence of a mutated pacA sequence is shown in SEQ ID NO: 12. A pacA mutated sequence as provided in SEQ ID NO: 12 was generated by constructing an allelic exchange substrate comprised of the kanamycin resistance gene (Kan) and luxAB genes under the control of the Pblast promoter and flanked by pacA gene sequences that themselves flank the sequence of the pacA gene. The allelic exchange substrate was produced via gene synthesis. Then, the native pacA sequence in N1706 was replaced via insertion of the Kan and luxAB genes via an allelic exchange. It was determined that the disruption also disrupted the ability of the mutated P1 phage to package DNA. Induction of the mutated phage resulted in elimination of the progeny phage as determined from comparing P1 phage titers via plaque assay from cell lysates produced by inducing the native phage vs. the mutated phage.

[0176] Construction of the complementing plasmid: The complementing plasmid contained the pBHR1 origin of replication exhibiting broad Gram-negative activity, a selectable marker for spectinomycin, the native bacteriophage P1 pacA and pacB genes operatively linked to the native pacA gene promoter sequence, the luxA and luxB genes from *Aliivibrio fischeri* operatively linked to the constitutive blasticillin promoter (Pblast), the P1 lytic replicon containing the C1 repressor-controlled P53 promoter, the promoter P53 antisense, the repL genes, and an in-frame deletion of the kilA gene.

[0177] The plasmid can be constructed in a variety of manners that are known to one of skill in the art including obtaining the cassettes via PCR from their native sources or via gene synthesis and assembly of the vector via traditional restriction enzyme-based cloning or alternative techniques such as Gibson assembly.

[0178] Complementation-based Packaging System: The packaging system includes the pacA mutant strain 1525 complemented with the complementing plasmid. As known to one of skill in the art, the manner of constructing this system can be accomplished by transforming strain 1525 with the complementing plasmid. The complementing plasmid can be maintained in cultures of the transformed 1525 by growing the transformant in the presence of 10 ug/mL of spectinomycin.

[0179] Production of Transduction Particles Carrying Plasmid DNA: Non-replicative transduction particles carrying the complementing plasmid can be produced from 1525 transformants via thermal induction at 42°C. Incubation at 42°C results in induction of the P1 lytic cycle in which the prophage produces phage structural elements, and packages

complementing plasmid concatameric DNA formed by the lytic replicon in progeny phage particles. The complementing plasmid expressing both the pacA and pacB genes resulted in cell lysate containing non-replicative transduction particles, each consisting of bacteriophage P1 particles carrying a linear concatemer of the complementing plasmid and thus demonstrating that this complementing plasmid successfully complements the disruption of packaging.

[0180] In addition to transduction particles carrying plasmid DNA, the system produced transduction particles carrying P1 DNA. Transduction particles carrying P1 DNA can arise via recombination between the plasmid DNA and P1 DNA. The presence of transduction particles carrying P1 DNA was assessed by exposing target cells to lysate from this system and screening for the presence of transduced cells that propagate on selective media that incorporates kanamycin while transduction particles carrying plasmid DNA was assessed in a similar manner based on spectinomycin resistance. Figure 10 shows a table of data obtained from measuring the light production (RLU) from colonies of transduced cells. Cells that were resistant to spectinomycin (SpecR) were transduced with plasmid DNA while cells that were resistant to kanamycin (KanR) were transduced by P1 DNA. Data from 1505 was obtained from packaging lines that do not have luxAB inserted into the P1 genome while that from 1525 was obtained from packaging lines that do have luxAB inserted into the P1 genome. As can be seen from the data, all SpecR transductants produced light while all of the KanR transductants produced light only for those transduced from 1525.

[0181] As such, 1525 represents an improved non-replicative transduction particle-based reporter system where transduction particles carrying both plasmid DNA and virus DNA are capable of producing light.

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Informal Sequence Listing

> SEQ ID NO:1 pacA and pacB (bold: promoter, underlined: pacA, unformatted: pacB)

ATGTGACTTTCGTTACCCTCGCGTCAAAAAGAGTTTTTACGAAAGGAA
GCATAAGTGACCTGGGACGATCACAAGAAGAATTTTGCTCGCCTGGCGCGAGAT
GGTGGTTACACCATCGCACAGTATGCCGCCGAGTTTAATCTTAACCCTAATACCG
CACGTCGTTATCTCCGTGCCTTCAAAGAAGACACCAGGACTACGGACAGCCGCA
AGCCAAATAAGCCAGTCAGGAAGCCACTAAAAAGCATGATCATTGATCACTCTA
ATGATCAACATGCAGGTGATCACATTGCGGCTGAAATAGCGGAAAAACAAAGAG
TTAATGCCGTTGTCAGTGCCGCAGTCGAGAATGCGAAGCGCCAAAATAAGCGCA
TAAATGATCGTTCAGATGATCATGACGTGATCACCCGCGCCCACCGGACCTTACG
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CCCCAAGATGAAGTGCTTAGCGTCGAAGACGAAGCGCAGGTTGATGAAGCTCTG
GCATGGCTTAATGAATAA

> SEQ ID NO:2 P1 lytic replicon containing the C1 repressor-controlled P53 promoter, the promoter P53 antisense, the repL genes, and an in-frame deletion of the kilA gene

CACTATAGGGCGAATTGGCGGAAGGCCGTCAAGGCCGCATTTGGGCCCGG
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> SEQ ID NO:3 pBHR1 rep (bold: ORF)

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**CTCATCGGACGTTCTTTGCGGACGGTCCAATACGCAGTCAAGGACTTGGTG
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> SEQ ID NO:4 phi80alpha terS and terL genes (bold: terS ORF, underline: terL ORF)

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**TCGACAAAAAAGAAATTACTCAGAAGAATATTGAGATTAATATTGGTGAGTA
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> SEQ ID NO:5 pT181

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> SEQ ID NO:6 Ef11 terA and terB (bold: terA ORF, underline: terB ORF)

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> SEQ ID NO:7 repB

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> SEQ ID NO:8 pDL278

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> SEQ ID NO:9 nisin promoter

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> SEQ ID NO:10 pac-site and pacA gene disruption with kanR (unformatted: pacA gene seqeuence, underlined: pacA gene seqeucne included in the allelic exchange substrate, bold: Kan gene promoter, italicized: Kan gene)

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> SEQ ID NO:11 Pblast promoter

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>SEQ ID NO:12 P1 pacA gene loci with kan gene and luxAB genes inserted (lower case is native sequence, upper case is insert sequence)

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CLAIMS

1. A bacterial cell packaging system for packaging a reporter nucleic acid molecule into a non-replicative transduction particle (NRTP) for introduction into a bacterial cell, the packaging system comprising a host cell, comprising:

   - a bacteriophage genome comprising a first gene comprising a disruption, wherein in the absence of the disruption the first gene encodes a first essential component of a packaging-related enzymatic activity and comprises a first packaging initiation site sequence, wherein the packaging-related enzymatic activity recognizes the first packaging initiation site, wherein the disruption prevents recognition of the first packaging initiation site sequence by the essential packaging-related enzymatic activity, and wherein the disruption reduces the level of the essential packaging-related enzymatic activity; and
   - a reporter nucleic acid molecule comprising a reporter gene, a second gene encoding the first component of the essential packaging-related enzymatic activity, and a third gene encoding a second component of the essential packaging-related enzymatic activity, wherein the second gene comprises the non-disrupted first packaging initiation site sequence, wherein the first packaging initiation site sequence is configured to facilitate packaging of a replicon of the reporter nucleic acid molecule into the NRTP.

2. The bacterial cell packaging system of claim 1, wherein the bacteriophage comprises a plurality of disrupted genes, wherein in the absence of the disruptions, each encodes an essential component of the packaging-related enzymatic activity and wherein each of the plurality of disrupted genes on the bacteriophage is complemented by a functional, non-disrupted gene encoded by the reporter nucleic acid molecule.

3. The bacterial cell packaging system of any one of claims 1 to 2, wherein the disruption is via deletion, insertion, mutation, or replacement.

4. The bacterial cell packaging system of any one of claims 1 to 3, wherein the packaging-related enzymatic activity is a terminase activity.

5. The bacterial cell packaging system of any one of claims 1 to 4, wherein the second gene and the third gene are each terminase genes and wherein the second gene and the third gene are operably linked to a conditional promoter.

6. The bacterial cell packaging system of claim 5, wherein the conditional promoter is a native promoter of a terminase gene of the bacteriophage genome.

7. The bacterial cell packaging system of any one of claims 5 or 6, wherein expression of the second gene or the third gene is inhibited in the absence of activation of the lytic cycle of the bacteriophage, and wherein expression of the second gene or the third gene is activated upon activation of the lytic cycle of the bacteriophage.

8. The bacterial cell packaging system of claims 5 to 7, wherein the second gene and the third gene are terminase genes native to the bacteriophage genome, and wherein the conditional promoter is a native promoter of the terminase genes.

9. The bacterial cell packaging system of any one of claims 1 to 8, wherein the bacteriophage genome comprises a reporter gene encoding a detectable marker or a selectable marker and wherein the reporter gene is operatively linked to a constitutive promoter.

10. The bacterial cell packaging system of claim 9, wherein the bacteriophage genome further comprises an antibiotic resistance gene.

11. The bacterial cell packaging system of claims 9 or 10, wherein the reporter gene is selected from the group consisting of: enzymes mediating luminescence reactions (luxA, luxB, luxAB, luc, ruc, nluc), enzymes mediating colorimetric reactions (lacZ, HRP), fluorescent proteins (GFP, eGFP, YFP, RFP, CFP, BFP, mCherry, near-infrared fluorescent proteins), affinity peptides (His-tag, 3X-FLAG), and selectable markers (ampC, tet(M), CAT, erm).

12. The bacterial cell packaging system of claim 10, wherein the antibiotic resistance gene is a kanamycin resistance gene.

13. The bacterial cell packaging system of any one of claims 1 to 12, wherein the disruption comprises an insertion into or replacement of the first packaging initiation site sequence with a gene encoding a selectable marker and wherein the gene encoding the selectable marker is operatively linked to a constitutive promoter.

14. The bacterial cell packaging system of any one of claims 1 to 13, wherein the disruption comprises an insertion into or replacement of the first packaging initiation site sequence with a gene encoding a detectable marker.

15. The bacterial cell packaging system of any one of claims 1 to 14, wherein the reporter nucleic acid molecule comprises an origin of replication.

16. The bacterial cell packaging system of any one of claims 1 to 15, wherein the replicon of the reporter nucleic acid molecule comprises a concatamer amenable to packaging into the non-replicative transduction particle.

17. The bacterial cell packaging system of any one of claims 1 to 16, wherein the non-disrupted first packaging initiation site sequence comprises a concatamer junction.

18. The bacterial cell packaging system of any one of claims 1 to 17, wherein the bacteriophage genome comprises an Enterobacteriaceae bacteriophage P1, or an S. aureus bacteriophage φ80α or a bacteriophage φ11, or an E. faecalis bacteriophage φEF11.

19. The bacterial cell packaging system of any one of claims 1 to 18, wherein the reporter nucleic acid molecule comprises a nucleic acid transcript sequence that is complementary to a second sequence in the reporter nucleic acid molecule.

20. The bacterial cell packaging system of any one of claims 1 to 19, wherein the replicon of the reporter nucleic acid molecule comprises a nucleic acid transcript sequence that is complementary to a second sequence in the replica of the reporter nucleic acid molecule.

21. A method for packaging a reporter nucleic acid molecule into a non-replicative transduction particle, comprising:

- providing conditions to the bacterial cell packaging system of any of the claims 1 to 20 that induce a lytic phase of the bacteriophage genome to produce non- replicative transduction particles packaged with the reporter nucleic acid molecule; and
- collecting the non-replicative transduction particle comprising the reporter nucleic acid molecule.

22. The method of claim 21, wherein the non-replicative transduction particle does not contain a replicated bacteriophage genome.

23. The method of any one of claims 21 to 22, wherein the non-replicative transduction particle comprises a portion of the bacteriophage genome due to recombination with the reporter nucleic acid molecule, and wherein the portion of the bacteriophage genome comprises the reporter gene.

24. A composition comprising the non-replicative transduction particle comprising a replicon of the reporter nucleic acid molecule produced from the method of any one of claims 21 to 23.