CLAIMS

[Claim 1]

A bacterium for targeting tumors and treating cancer, each comprising:

a nucleic acid system; and

a gene that encodes a cytotoxin that kills tumor cells,

wherein the nucleic acid system comprises:

a first DNA fragment that encodes a toxin that kills the bacterium;

a second DNA fragment that encodes an antidote that negates the toxin, the second DNA fragment being transcribed at tumor tissues but not transcribed at non-tumor tissues;

a promoter of an antidote gene that is operably linked to the second DNA fragment and represses transcription of the second DNA fragment under control of a glucose level such that the antidote is expressed at the tumor tissues but not expressed at the non-tumor tissues; and

a constitutive promoter of a toxin gene that is operably linked to the first DNA fragment and causes constitutive transcription of the first DNA fragment such that the toxin is expressed at the tumor tissues and the non-tumor tissues.

[Claim 2]

The bacterium according to claim 1, wherein the cytotoxin that kills tumor cells is selected from a group consisting of Pseudomonas aeruginosa exolysin, Bacillus cereus non-hemolytic enterotoxin, Vibrio cholera hemolysin A and Escherichia coli alpha-hemolysin.

[Claim 3]

The bacterium according to any one of claims 1 - 2, wherein the tumor tissues have a glucose concentration lower than 0.424 mM, and the promoter of the antidote gene initiates the transcription of the second DNA fragment when the glucose level is lower than 0.424 mM.

[Claim 4]

The bacterium according to any one of claims 1 - 3, wherein the non-tumor tissues have a glucose concentration higher than 1.22 mM, and the promoter of the antidote gene represses the transcription of the second DNA fragment when the glucose level is higher than 1.22 mM.

[Claim 5]
The bacterium according to any one of claims 1 - 4, wherein the promoter of the antidote gene is located immediately upstream of the second DNA fragment.
[Claim 6]
The bacterium according to any one of claims 1 - 5, wherein the constitutive promoter of the toxin gene is located immediately upstream of the first DNA fragment.
[Claim 7]
The bacterium according to any one of claims 1 - 6, wherein the promoter of the antidote gene is selected from a group consisting of a lac promoter, a gltA promoter, an sdhADC promoter and a tnaB promoter.
[Claim 8]
The bacterium according to any one of claims 1 - 7, wherein a pair of the toxin and the antidote is selected from a group consisting of a CcdB-CcdA pair, an AvrRxo1-Arc1 pair, a Hha-TomB pair, and a PaaA2-ParE2 pair.
[Claim 9]
The bacterium according to any one of claims 1 - 8, wherein the first DNA fragment is shown as SEQ ID No. 1, and the second DNA fragment is shown as SEQ ID No.2.
[Claim 10]
The bacterium according to any one of claims 1 - 9, wherein the promoter of the antidote gene is shown as SEQ ID No.3.
[Claim 11]
The bacterium according to any one of claims 1 - 10, wherein the bacterium further includes a random sequence that consists of 5 – 6 nucleotides, and replaces original 5 – 6 nucleotides of the bacterium that are located immediately upstream of the second DNA fragment.
[Claim 12]
The bacterium according to claim 11, wherein the random sequence is GCCTT or TGTCT.
[Claim 13]
The bacterium according to any one of claims 1 - 12, wherein the bacterium further includes a third DNA fragment that encodes a chloramphenicol

resistance cassette, wherein the third DNA fragment is shown as SEQ ID No. 4.

[Claim 14]

The bacterium according to any one of claims 1 - 13, wherein the bacterium is derived from a bacterial strain selected from a group consisting of *Escherichia coli*, salmonella and Shigella.

[Claim 15]

The bacterium according to any one of claims 1 - 14, wherein the bacterium is derived from *Escherichia coli* MG1655.

[Claim 16]

The bacterium according to any one of claims 1 - 15, wherein the nucleic acid system is shown as SEQ ID No. 7 or SEQ ID No.8.

[Claim 17]

A bacterium for targeting tumors and treating cancer, comprising:

a nucleic acid system; and

a gene that encodes a cytotoxin that kills tumor cells,

wherein the nucleic acid system comprises:

a first DNA fragment that encodes a toxin that kills the bacterium, the first DNA fragment being transcribed at non-tumor tissues but not transcribed at tumor tissues;

a second DNA fragment that encodes an antidote that negates the toxin;

a constitutive promoter of an antidote gene that is operably linked to the second DNA fragment and causes constitutive transcription of the second DNA fragment; and

a promoter of a toxin gene that is operably linked to the first DNA fragment and causes transcription of the first DNA fragment under control of a glucose level, wherein expression of the toxin is higher than constitutive expression of the antidote under the control of the glucose level such that the toxin kills the bacterium at the non-tumor tissues.

[Claim 18]

The bacterium according to claim 17, wherein the cytotoxin that kills the tumor cells is selected from a group consisting of Pseudomonas aeruginosa exolysin,

Bacillus cereus non-hemolytic enterotoxin, Vibrio cholera hemolysin A and Escherichia coli alpha-hemolysin.

[Claim 19]

The bacterium according to any one of claims 17 – 18, wherein the tumor tissues have a glucose concentration lower than 0.424 mM, and the promoter of the toxin gene represses the transcription of the first DNA fragment when the glucose level is lower than 0.424 mM.

[Claim 20]

The bacterium according to any one of claims 17 – 19, wherein the non-tumor tissues have a glucose concentration higher than 1.22 mM, the promoter of the toxin gene initiates the transcription of the first DNA fragment and the expression of the toxin is higher than the constitutive expression of the antidote when the glucose level is higher than 1.22 mM.

[Claim 21]

The bacterium according to any one of claims 17 – 20, wherein the promoter of the toxin gene is located immediately upstream of the first DNA fragment.

[Claim 22]

The bacterium according to any one of claims 17 – 21, wherein the constitutive promoter of the antidote gene is located immediately upstream of the second DNA fragment.

[Claim 23]

The bacterium according to any one of claims 17 – 22, wherein the promoter of the toxin gene is selected from a group consisting of a ptsG promoter, a fruB promoter and an ackA promoter.

[Claim 24]

The bacterium according to any one of claims 17 – 23, wherein a pair of the toxin and the antidote is selected from a group consisting of a CcdB-CcdA pair, an AvrRxo1-Arc1 pair, a Hha-TomB pair, and a PaaA2-ParE2 pair.

[Claim 25]

The bacterium according to any one of claims 17 – 24, wherein the first DNA fragment is shown as SEQ ID No. 1, and the second DNA fragment is shown as SEQ ID No.2.

[Claim 26]

The bacterium according to any one of claims 17 – 25, wherein the bacterium further includes a random sequence that consists of 5 – 6 nucleotides, and replaces original 5 – 6 nucleotides of the bacterium that are located immediately upstream of the first DNA fragment.

[Claim 27]

The bacterium according to any one of claims 17 – 26, wherein the bacterium further includes a third DNA fragment that encodes a chloramphenicol resistance cassette, wherein the third DNA fragment is shown as SEQ ID No. 4.

[Claim 28]

The bacterium according to any one of claims 17 – 27, wherein the bacterium is derived from a bacterial strain selected from a group consisting of *Escherichia coli*, salmonella and Shigella.

[Claim 29]

The bacterium according to any one of claims 17 – 28, wherein the bacterium is derived from *Escherichia coli* MG1655.

[Claim 30]

The bacterium according to any one of claims 1 - 29, wherein the bacterium is derived from a strain JY1 deposited at the China General Microbiological Culture Collection Center (CGMCC) under deposit no. 14577, a strain JY6 deposited at CGMCC under deposit no. 14578, a strain SH1 deposited at CGMCC under deposit no. 14580, or a strain JYH1 deposited at CGMCC under deposit no. 14579.

[Claim 31]

A drug delivery composition, comprising a bacterium of any one of claims 1 - 30.