Claims

1. A method for creating a new gene in an organism without the need to provide a foreign DNA template, characterized by comprising the following steps:

simultaneously generating DNA breaks at two or more different specific sites in the organism's genome, wherein the specific sites are genomic sites separating the prommoters and the coding regions of two genes with different expression patterns, and the DNA breaks are ligated to each other by a non-homologous end joining (NHEJ), generating a combination of the promoter of one of the two genes with different expression patterns and the coding region of the other gene, thereby creating the new gene; and

wherein the method results in events of inversion or duplication-doubling of the fragments between the targets on the same chromosome, and/or the exchange of chromosome fragments between targets on different chromosomes.

2. The method according to claim 1, characterized in that said two or more different specific sites locate on the same chromosome or on different chromosomes, or may be specific sites on at least two different genes, or may be at least two different specific sites on the same gene, wherein said at least two different genes may have the same or different transcription directions.

3. The method according to claim 1 or 2, characterized in that said DNA breaks are achieved by delivering a nuclease with targeting property into a cell of the organism to contact with the specific sites of the genomic DNA.

4. The method according to claim 3, characterized in that said nuclease with targeting property is selected from the group consisting of Meganuclease, Zinc finger nuclease, TALEN, and CRISPR/Cas system.

5. The method according to claim 3 or 4, characterized in that the nuclease with targeting property is in the form of DNA, or exists in the form of mRNA or protein, but not DNA.

6. The method according to any one of claims 3-5, characterized in that the nucleases with targeting property are delivered into the cell by: 1) a PEG-mediated cell transfection method; 2) a liposome-mediated cell transfection method; 3) an electric shock transformation method; 4) a microinjection; 5) a gene gun bombardment; or 6) an *Agrobacterium*-mediated transformation method.

7. The method according to any one of claims 1-6, characterized in that the combination is a combination of the region from the promoter to 5'UTR of one of the two genes with different expression patterns and the CDS of the other gene.

8. The method of claim 7, wherein the combination is a combination of the coding region of HPPD, EPSPS, PPO or GH1 gene and an endogenous promoter of the organism with a higher expression activity as compared to the endogenous promoter of the HPPD, EPSPS, PPO or GH1 gene.

9. The method according to claim 7 or 9, characterized in that the different expression patterns are different levels of gene expression, different tissue-specificities of gene expression, or different developmental stage-specificities of gene expression.

10. The method according to claim 1, wherein the organism is an animal, a plant, a bacterium or a fungus.

11. An editing method for increasing the gene expression level of a target endogenous gene in an organism, which is independent of an exogenous DNA donor fragment, which comprises the following steps:

simultaneously generating DNA breaks separately at selected sites between the promoter and the coding region of each of the target endogenous gene and an optional endogenous highly-expressing gene, wherein the promoter of the endogenous highly-expressing gene has a higher expression activity as compared to that of the target endogenous gene; ligating the DNA breaks to each other by means of non-homologous end joining (NHEJ), thereby generating an in vivo fusion of the coding region of the target endogenous gene and the optional endogenous highly-expressing promoter to form a new highly-expressing endogenous gene with a higher expression level as compared to the target endogenous gene, wherein the target endogenous gene and the optional endogenous highly-expressing gene are located on the same chromosome or different chromosomes.

12. The editing method according to claim 11, which is used for knocking up the expression of the endogenous HPPD, EPSPS or PPO gene in a plant, comprising fusing the coding region of the HPPD, EPSPS or PPO gene with an endogenous highly-expressing promoter of a plant in vivo to form a new plant endogenous HPPD, ESSPS or PPO gene, respectively, wherein the endogenous highly-expressing promoter exhibits a higher expression activity as compared to that of the target endogenous gene.

13. The editing method according to claim 12, characterized in that it comprises the following steps: simultaneously generating DNA breaks respectively in selected specific sites between the promoter and the coding region of each of the HPPD, EPSPS or PPO gene and the endogenous highly-expressing gene , ligating the DNA breaks to each other through an intracellular repair pathway, generating in vivo a fusion of the coding region of the HPPD, EPSPS or PPO gene and

the endogenous highly-expressing promoter to form a new highly-expressing HPPD, EPSPS or PPO gene, respectively.

14. The editing method according to claim 12 or 13, characterized in that it comprises fusing the coding region of the HPPD gene with an endogenous highly-expressing promotor of a rice, wherein the endogenous highly-expressing promoter is a promoter of ubiquitin2 gene,

it comprises fusing the coding region of the EPSPS gene with an endogenous highly-expressing promotor of a rice, wherein the strong promotor is a promotor of TKT gene, or

it comprises fusing the coding region of the PPO gene with an endogenous highly-expressing promotor of a rice or an *Arabidopsis*, wherein in rice, the endogenous highly-expressing promotor is a promotor of CP12 gene, and in *Arabidopsis*, the endogenous highly-expressing promotor is a promotor of ubiquitin10 gene.

15. A rice endogenous HPPD gene being expressed at a higher level as compared to a wildtype rice endogenous HPPD gene, which has a sequence selected from the group consisting of:

(1) the nucleic acid sequence as shown in SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 18 or SEQ ID NO: 19 or a complementary sequence thereof;

(2) a sequence having an identity of at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98% or at least 99% to any one of the sequences as defined in (1); or

(3) a nucleic acid sequence capable of hybridizing to the sequence as shown in (1) or (2) under a stringent condition.

16. A rice endogenous EPSPS gene being expressed at a higher level as compared to a wildtype rice endogenous EPSPS gene, which has a sequence selected from the group consisting of:

(1) the nucleic acid sequence as shown in SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13 or SEQ ID NO: 14 or a complementary sequence thereof;

(2) a sequence having an identity of at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98% or at least 99% to any one of the sequences as defined in (1); or

(3) a nucleic acid sequence capable of hybridizing to the sequence as shown in (1) or (2) under a stringent condition.

17. A rice endogenous PPO gene being expressed at a higher level as compared to a wildtype rice endogenous PPO gene, which has a sequence selected from the following:

(1) the nucleic acid sequence as shown in SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, or SEQ ID NO: 26 or a complementary sequence thereof;

(2) a sequence having an identity of at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98% or at least 99% to any one of the sequences as defined in (1); or

(3) a nucleic acid sequence capable of hybridizing to the sequence as shown in (1) or (2) under a stringent condition.

18. A DNA comprising the gene according to any one of claims 15-17.

19. A recombinant expression vector, which comprises the gene according to any one of claims 15-17, and a promoter operably linked thereto.

20. An expression cassette comprising the gene according to any one of claims 15-17.

21. A plant host cell, which comprises the expression cassette according to claim 20.

22. A plant regenerated from the plant host cell according to claim 21.

23. A method for producing a plant with an increased resistance or tolerance to an herbicide, which comprises regenerating the plant host cell according to claim 21 into a plant and a progeny derived therefrom.

24. A rice resistant to a herbicide, which comprises one or a combination of two or more of the rice endogenous HPPD gene according to claim 15, the rice endogenous EPSPS gene according to claim 16, and the rice endogenous PPO gene according to claim 17.

25. A method for controlling a weed in a cultivation site of a plant, wherein the plant is selected from the group consisting of the plant according to claim 22, a plant prepared by the method according to claim 23, or the rice according to claim 24, wherein the method comprises applying to the cultivation site one or more of HPPD, EPSPS or PPO inhibitory herbicides in an amount for effectively controlling the weed.