Claims

1. An isolated recombinant cell comprising one or more genes selected from the group consisting of *dmaW, easF, easC, easE, easD, easA*$_{isomerase}$, *easG,* and *cloA*, wherein each gene codes for an enzyme from the biosynthetic pathway from tryptophan to D-lysergic acid (DLA).

2. The isolated recombinant cell according to claim 1, comprising at least one *easE,* at least one *easA*$_{isomerase}$ and at least one *cloA.*

3. The isolated recombinant cell according to claim 2, wherein the *easE* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to a sequence selected from the group consisting of SEQ ID NO: 6 to SEQ ID NO: 14, the *easA*$_{isomerase}$ comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to a sequence selected from the group consisting of SEQ ID NO: 15 to SEQ ID NO: 18, and the *cloA* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 22, 23, 24, 27 or 28.

4. The isolated recombinant cell according to claim 2, wherein the *easE* comprises *easE* from *Epichloe coenophiala* (easE_Ec), *easE* from *Aspergillus japonicas* (easE_Aj) and/or *easE* from *Aspergillus indologenus,* the *easA*$_{isomerase}$ comprises *easA*$_{isomerase}$ from *Neotyphodium lolii* (easA_Nl), *easA*$_{isomerase}$ from *Periglandula ipomoeae* (easA_Pi), *easA*$_{isomerase}$ from *Claviceps purpurea* (easA_Cp) and/or *easA*$_{isomerase}$ from *Epichloe coenophiala* (easA_Ec), and the *cloA* comprises *cloA* from *Claviceps paspali* (CloA_Cpas), *cloA* from *N. lolii* (CloA_Nlol), *cloA* from *P. ipomoeae* (CloA_Pipo), *cloA* from *E. coenophilia* (CloA_XN6) and/or *cloA* from *C. purpurea* (CloA_Cpur).

5. The isolated recombinant cell according to claim 4, wherein the *easE* from *Epichloe coenophiala* (easE_Ec) comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 14 and the *easE* from *Aspergillus japonicas* (easE_Aj) or the *easE* from *Aspergillus indologenus* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 6, the *easA*$_{isomerase}$ from *Neotyphodium lolii* (easA_Nl) comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 15, the *easA*$_{isomerase}$ from *Claviceps purpurea* (easA_Cp) comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 18, and the *easA*$_{isomerase}$ from *Epichloe coenophiala* (easA_Ec) comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 17, and the *cloA* from *E.*

coenophilia (CloA_XN6) comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 27 or 28 and the *cloA from C. purpurea* (CloA_Cpur) comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 22, 23 or 24.

6. The isolated recombinant cell according to claim 2, wherein the *easE* comprises *easE* from *Aspergillus japonicas* (easE_Aj) or *easE* from *Aspergillus indologenus*, the $easA_{isomerase}$ comprises $easA_{isomerase}$ from *Epichloe coenophialia* (easA_Ec) and the *cloA* comprises *cloA* from *C. purpurea* (CloA_Cpur).

7. The isolated recombinant cell according to claim 6, wherein the *easE* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 6, the $easA_{isomerase}$ comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 17 and the *cloA* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 23.

8. The isolated recombinant cell according to any one of claims 2 to 7, wherein the *easE* expresses an enzyme which catalyses conversion of 4-Dimethylallyl-*L*-abrine to Chanoclavine I, the $easA_{isomerase}$ expresses an enzyme which catalyses conversion of Chanoclavine-I aldehyde to agroclavine, and the *cloA* expresses an enzyme which catalyses conversion of agroclavine to D-lysergic acid.

9. The isolated recombinant cell according to any one of claims 2 to 8, wherein the recombinant yeast cell further comprises at least one *dmaW*, at least one *easF*, and at least one *easD*.

10. The isolated recombinant cell according to claim 9, wherein the *dmaW* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 1, the *easF* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 2; and the *easD* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 4.

11. The isolated recombinant cell according to claim 9 or 10, wherein the *dmaW, easF* and *easD* each expresses a respective enzyme, wherein each respective enzyme is functional.

12. The isolated recombinant cell according to any one of claims 9 to 11, wherein the recombinant yeast cell further comprises at least one *easC* and/or at least one *easG*.

13. The isolated recombinant cell according to claim 12, wherein the *easC* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 3 and the *easG* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 5.

14. An isolated recombinant cell comprising at least one *dmaW*, at least one *easF*, at least one *easE* or *easC*, at least one *easD*, at least one $easA_{isomerase}$ or *easG*, and at least one *cloA* gene.

15. An isolated recombinant cell comprising at least one *dmaW*, at least one *easF*, at least one *easE*, at least one *easD*, at least one $easA_{isomerase}$, and at least one *cloA* gene.

16. An isolated recombinant cell comprising at least one *dmaW*, at least one *easF*, at least one *easC*, at least one *easD*, at least one $easA_{isomerase}$, at least one *easG*, and at least one *cloA* gene.

17. The isolated recombinant cell according to claim 14, wherein the *dmaW* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 1; *easF* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 2; *easE* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 6; *easC* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 3; *easD* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 4; $easA_{isomerase}$ comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 17; *easG* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 5; and *cloA* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 23.

18. An isolated recombinant cell according to any one of claims 9 to 17, further comprising multiple copies of *FAD1* and *PDI1* genes, wherein the *FAD1* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 35 and *PDI1* comprises a sequence at least 80%, at least 85%, at least 90%, at least 95% identity to SEQ ID NO: 36.

19. An isolated recombinant cell according to any one of claims 1 to 18, capable of expressing the one or more genes, wherein expression of the one or more genes produces respective gene product(s), wherein the respective gene product(s) are respective enzyme(s).

20. A method of culturing the recombinant cell according to any one of claims 1 to 19 in an appropriate culture medium for preparing D-lysergic acid.