CLAIMS

1. A *Talaromyces pinophilus* strain with the deposition no. PTA-125750 for producing a cellulolytic enzyme complex.

2. An active mutant of the *Talaromyces pinophilus* strain of claim 1, wherein the active mutant comprises at least one mutation in one or more genes, wherein the active mutant has cellulolytic activity.

3. The active mutant of claim 2, wherein the one or more genes are selected from the group consisting of MFS monosaccharide transporter gene, monocarboxylate permease gene, MFS transporter Liz1/Seo1 gene, general substrate transporter gene, zinc transporter gene, C2H2 transcription factor gene, MAP kinase kinase kinase gene, CaaX farnesyltransferase alpha subunit Ram2 gene, biotin:apoprotein ligase gene, Dihydrodipicolinate synthetase protein gene, response regulator-like (hhk1) gene, annexin ANXC3.2 gene, actin binding protein gene, tannase and feruloyl esterase gene, acid phosphatase gene, copper-exporting ATPase gene, ubiquitin biosysthesis protein gene, Proteasome activator subunit 4 gene and THO complex subunit Tho1 gene, wherein the active mutant has cellulolytic activity.

4. The active mutant of claim 2, wherein the active mutant comprises at least one mutation in a gene including a polynucleotide sequence set forth in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19, wherein the active mutant has cellulolytic activity.

5. The active mutant of claim 2, wherein the active mutant comprises a gene including a polynucleotide sequence having at least 80% identity with a polynucleotide sequence set forth in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19, wherein the active mutant has cellulolytic activity.

6. The active mutant of claim 5, wherein the polynucleotide sequence set forth in SEQ ID NO: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19 comprises at least one mutation, wherein the active mutant has cellulolytic activity.

7. The active mutant of claim 6, wherein the at least one mutation comprises a single nucleotide polymorphism and/or a point mutation.

8. The active mutant of claim 2, wherein the active mutant comprises at least one mutation in a gene encoding a polypeptide having an amino acid sequence set forth in SEQ ID NO: 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37 or 38.

9. The active mutant of claim 2, wherein the active mutant contains a gene encoding a polypeptide includes of an amino acid sequence having at least 85% identity with an amino acid sequence set forth in SEQ ID NO: 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37 or 38.

10. The active mutant of claim 9, wherein the amino acid sequence set forth in SEQ ID NO: 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37 or 38 comprises at least one mutation, wherein the strain has cellulolytic activity.

11. The active mutant of claim 10, wherein the at least one mutation comprises an amino acid substitution, insertion and/or deletion.

12. An isolated culture of the *Talaromyces pinophilus* strain of claims 1 or active mutant of claim 2 having cellulolytic activity and capable of producing a cellulolytic enzyme complex.

13. A method of obtaining a supernatant from the strain of *Talaromyces pinophilus* of claim 1 or the active mutant of claim 2, comprising steps of:

contacting the strain of *Talaromyces pinophilus* or active mutant with a medium to produce a suspension;

incubating the suspension;

fermenting the suspension; and

centrifuging the suspension to obtain the supernatant.

14. The method according to claim 13, wherein the medium comprises inorganic salts and nutrients suitable for growth of the strain of *Talaromyces pinophilus* or active mutant.

15. The method according to claim 14, wherein the inorganic salts is selected from the group consisting of potassium dihydrogen phosphate, magnesium sulphate, calcium chloride, iron(II) sulphate, manganese sulphate and zinc sulphate.

16. The method according to claim 14, wherein the medium further comprises inorganic ammonium salts and organic ammonium salts.

17. The method according to claim 13, wherein the medium comprises a substrate selected from the group consisting of cellulosic material, grass material, herbaceous material, agricultural residue, forestry residue, waste paper, and pulp and paper mill residue.

18. A method for degrading lignocellulosic material to fermentable sugar, comprising steps of:

pre-treating the lignocellulosic material;

washing the pre-treated lignocellulosic material with distilled water;

drying the pre-treated lignocellulosic material; and

contacting the pre-treated lignocellulosic material with a supernatant obtained from the method of caim 13.

19. The method according to claim 18, further comprising a step of recovering the degraded lignocellulosic material.

20. The method according to claim 18, wherein the lignocellulosic material is selected from the group consisting of grass material, herbaceous material, agricultural residue, forestry residue, waste paper, and pulp and paper mill residue.