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DESCRIPTION

Description

Technical Field

[0001] The present invention relates to a mutant filamentous fungus and a method of producing a substance using the mutant filamentous fungus.

Background Art

[0002] A filamentous fungus is a collective name for fungi constructed of tubular cells called hyphae, and is used for fermentative production of: low-molecular-weight compounds, for example, chemical products such as an organic acid, a pigment, and an agricultural chemical bulk, and pharmaceutical products such as penicillin and statins; and industrial enzymes such as amylase, cellulase, protease, and lipase.

[0003] For example, in JP 2010-227032 A, there is a description of a method of producing cellulase, including the steps of: producing a disaccharide-containing solution by adding thermophilic fungus-derived β -glucosidase to a glucose-containing solution and subjecting the mixture to a condensation reaction; and producing cellulase by culturing a filamentous fungus using a medium containing the disaccharide-containing solution.

[0004] In addition, in JP 2010-172343 A, there is a description of a method of producing phospholipase, including a step of processing a fungal peptide to truncate a peptide from the C-terminus and/or a peptide from the N-terminus, to thereby produce a core peptide formed of a specific amino acid sequence having phospholipase activity.

[0005] In addition, in JP 2001-46078 A, JP 2005-52116 A, JP 2009-118783 A, JP 11-506025 A, and JP 2007-508022 A, with a view to increasing efficiency of substance production using the filamentous fungus, there is a description of an expression vector constructed so that the filamentous fungus functions as a host, there is also a description of a method involving preparing a transformant by introducing, into the filamentous fungus, a plasmid in which a gene encoding a homologous or heterologous protein is functionally linked to the expression vector, and there is also a description that utilization of the transformant contributes to increased production of enzymes such as amylase and cellulase and low-molecular-weight compounds such as penicillin.

[0006] As described above, the filamentous fungus has an advantage of being able to produce a wide variety of useful substances. However, the filamentous fungus causes a problem in that the filamentous fungus cannot be cultured at a high density because of entanglement of hyphae and aggregation of cells in its liquid culture step, a problem in that a production amount of a useful substance lowers, and a problem in that a production step of a useful substance becomes complicated (e.g., JP 2002-218970 A and JP 2010-227031 A).

[0007] Under such circumstances, the inventors of the present invention have found that, when a mutant filamentous fungus lacking expression of α -1,3-glucan is used, aggregation of cells during culture is suppressed more than in the related art and the cells are relatively homogeneously dispersed in a medium, and thus have developed a method of producing a substance (WO 2014/073674 A1). However, although the use of the mutant filamentous fungus suppresses the aggregation of the cells more than in the related art, there is a demand for development of a filamentous fungus that is still less liable to form an aggregate.

[0008] Non-Patent Literature 10 discloses filamentous fungus *Aspergillus oryzae* having genes encoding α -1,3-glucan synthase knocked out has better hyphal dispersion in culture and increased recombinant protein production (see abstract). The introduction explains that the aggregation of hyphae is thought to be related to cell wall

polysaccharides and polypeptides. Also explained is the similarity between cell wall of *A. oryzae* and the human pathogen *Aspergillus fumigatus* (see p.1853, column 2).

[0009] Non-Patent Literature 11 discloses *A. fumigatus* mutants deficient in the production of α -1,3-glucan (see p. 1702-1703). *A. fumigatus* mutants having genes sph3 or uge3 knocked out being defective in the production of galactosaminogalactan (GAG) are review. Gene sph3 is indicated to be also present in *A. oryzae* (see end of p.1704 and first paragraph of p 1705). It is explained that GAG and α -1,3-glucan play major roles in hyphae aggregation (see p 1705, column 1, paragraph 1).

[0010] Non-Patent Literature 12 discloses overlapping and distinct roles of *Aspergillus fumigatus* UDP-glucose 4-epimerases in galactose metabolism and the synthesis of galactose-containing cell wall polysaccharides.

[0011] Non-Patent Literature 13 is directed to sph3, which is a glycoside hydrolase required for the biosynthesis of galactosaminogalactan in *Aspergillus fumigatus*.

Non-patent Literature

[0012]

NPL 1: Fontaine T. et al. (2011) Galactosaminogalactan, a New Immunosuppressive Polysaccharide of *Aspergillus fumigatus*, PLoS Pathogens, 7: e1002372

NPL 2: Rappleye C.A. et al. (2004) RNA interference in *Histoplasma capsulatum* demonstrates a role for α -(1,3)-glucan in virulence. Mol. Microbiol. 53: 153-165.

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NPL 4: Maubon D. et al. (2006) AGS3, an α (1-3)glucan synthase gene family member of *Aspergillus fumigatus*, modulates mycelium growth in the lung of experimentally infected mice. Fungal Genet. Biol. 43: 366-375.

NPL 5: Henry C. et al. (2011) α 1,3 glucans are dispensable in *Aspergillus fumigatus*. Eukaryot. Cell 11: 26-29

NPL 6: Mizutani O. et al. (2008) A defect of LigD (human Lig4 homolog) for nonhomologous end joining significantly improves efficiency of gene-targeting in *Aspergillus oryzae*. Fung. Genet. Biol., 45: 878-889.

NPL 7: Zhang S. et al. (2017) Self-excising Cre/mutant lox marker recycling system for multiple gene integrations and consecutive gene deletion in *Aspergillus oryzae*. J. Biosci. Bioengin. 123: 403-411

NPL 8: Gomi K. et al. (1987) Integrative transformation of *Aspergillus oryzae* with a plasmid containing the *Aspergillus nidulans* argB gene. Agric. Biol. Chem. 51: 2549-2555

NPL 9: Natalie et al (2015) Sph3 Is a Glycoside Hydrolase Required for the Biosynthesis of Galactosaminogalactan in *Aspergillus fumigatus*. J Biol Chem 290, 27438

NPL 10: Ken Miyazawa ET AL: "Increased enzyme production under liquid culture conditions in the industrial fungus *Aspergillus oryzae* by disruption of the genes encoding cell wall α -1,3-glucan synthase", Bioscience Biotechnology Biochemistry, vol. 80, no. 9, 1 September 2016 (2016-09-01), pages 1853-1863,

NPL 11: Akira Yoshimi ET AL: "Cell wall structure and biogenesis in *Aspergillus* species", Bioscience Biotechnology Biochemistry, vol. 80, no. 9, 3 May 2016 (2016-05-03), pages 1700-1711

NPL 12: Mark J. Lee ET AL: "Overlapping and Distinct Roles of *Aspergillus fumigatus* UDP-glucose 4-Epimerases in Galactose Metabolism and the Synthesis of Galactose-containing Cell Wall Polysaccharides", The Journal of Biological Chemistry, vol. 289, no. 3, 17 January 2014 (2014-01-17), pages 1243-1256

NP 13: Natalie C. Bamford ET AL: "Sph3 Is a Glycoside Hydrolase Required for the Biosynthesis of Galactosaminogalactan in *Aspergillus fumigatus*", Journal of Biological Chemistry, vol. 290, no. 46, 13 November

2015 (2015-11-13), pages 27438-27450

Summary of Invention

Technical Problem

[0013] An object of the present invention is to provide a filamentous fungus mutant strain that is still more suppressed in aggregation of cells (hyphae) in a medium than a related-art filamentous fungus.

Solution to Problem

[0014] Under such circumstances, the inventors of the present invention have made extensive investigations on a wide variety of factors in filamentous fungi from the viewpoint of the aggregation of cells, and as a result, have found a galactosaminogalactan (GAG) biosynthetic cluster to be a novel factor. In Non-patent Literature 9, a disruption strain of the GAG biosynthetic cluster is obtained using *Aspergillus fumigatus*, and is analyzed for evaluating the effect of the cluster disruption. In Non-patent Literature 9, it is reported that GAG is not observed on the cell wall surface of the disruption strain, but that there is no difference in germination or growth between the disruption strain and a wild-type strain. The inventors of the present invention have caused a filamentous fungus modified so as to be deficient in at least one α -1,3-glucan synthase gene comprising *agsB* and to be deficient in at least one galactosaminogalactan biosynthetic gene selected from the group consisting of *uge3*, *sph3*, *ega3*, *agd3*, and *gtb3* so that the at least one gene responsible for the expression of galactosaminogalactan is knocked out, and as a result, have observed a further decrease in expression of galactosaminogalactan, and besides, have surprisingly found that the aggregation of cells is suppressed and the cells are completely dispersed. The present invention is based on such novel findings.

Advantageous Effects of Invention

[0015] According to the present invention, the filamentous fungus mutant strain that is still more suppressed in aggregation of cells in a medium than the related-art filamentous fungus can be provided. When cells aggregate during culture, the inside of the aggregate becomes anaerobic to kill the cells. Therefore, the filamentous fungus of the present invention suppressed in aggregation and the method using the same contribute to efficient culture and substance production of the filamentous fungus, and hence are extremely useful.

Brief Description of Drawings

[0016]

[Figs. 1] Estimation of GAG biosynthetic gene cluster in *A. oryzae* (A) A GAG biosynthetic gene cluster in *A. oryzae* was predicted on the basis of the sequences of a GAG biosynthetic gene cluster in *A. fumigatus*. (B) The results of sequence alignment with ClustalW of *sph3* in *A. fumigatus*, *A. clavatus*, *A. oryzae*, *Marssonina brunnea*, *Ralstonia pickettii*, and *Physarum polycephalum*. Also in predicted *sph3* of *A. oryzae*, there was a highly conserved region.

[Figs. 2] Production of *uge3/sph3* gene disruption cassette, strain deficient only in GAG, and AG-GAG-deficient strain (A) A *uge3* downstream (5' side) region (amplicon 1) and an *sph3* downstream (3' side) region (amplicon 2) were amplified by PCR using genomic DNA of *A. oryzae* as a template. In addition, *AnadeA* gene (amplicon 3) was amplified from a plasmid TOPO-2.1-*adeA* by PCR (1st round of PCR). PCR was performed again from both sides of amplicons 1 and 2 to link the three fragments (2nd round of PCR). A main band of the PCR product was gel-

extracted, and used as a *uge3/sph3* gene disruption cassette. Next, an AG-deficient strain was used as a parental strain and transformed with the *uge3/sph3* gene disruption cassette. Selection was performed with *adeA*-free CD agar plate medium to acquire a strain deficient only in GAG and an AG-GAG-deficient strain. (B) The acquired AG-GAG-deficient strain was confirmed by PCR amplification to have the construct introduced therein.

[Figs. 3] Comparison of culture properties of wild-type strain, AG-deficient strain, AG-GAG-deficient strain, and GAG-deficient strain. A wild-type strain, the AG-deficient strain, the AG-GAG-deficient strain, and a GAG-deficient strain were used and subjected to liquid shaking culture in YPD medium for 24 hours. (A) Photographs of flasks are shown in an upper row, cells observed after transfer to 6 cm dishes are shown in a middle row, and stereoscopic micrographs are shown in a lower row. In all cases, observation was performed at 24 hours of culture. (B) Microscopic observation was performed at 10 hours of culture. The length of a bar in each figure is as follows: left of Figs. 3(B): 200 μm , center of Figs. 3(B): 200 μm , right of Figs. 3(B): 100 μm . (C) 1.0×10^3 conidia were inoculated at the center of agar medium, and subjected to static culture at 30°C for 5 days.

[Figs. 4] Production of strain highly expressing cutL1 for AG-GAG-deficient strain (production of AG-GAG-deficient strain highly expressing cutL1) (A) A method of producing an AG-GAG-deficient strain highly expressing cutL1 is illustrated. Arrows indicate primer positions for construct introduction confirmation. (B) The results of construct introduction confirmation by PCR amplification. (C) A halo formation test was performed by inoculating conidia at the center of CD medium containing 1% PBSA and performing static culture at 30°C for 4 days.

[Figs. 5] Evaluation of CutL1 productivity in AG-GAG-deficient strain (A) Dry cell weights in the case of culturing the wild-type strain, the AG-deficient strain, and the AG-GAG-deficient strain (each of which is a strain highly expressing cutL1) in YPM medium (24 hours, 100 rpm, and 1×10^4 conidia inoculated). (B) CutL1 secretion amounts in the wild-type strain, the AG-deficient strain, and the AG-GAG-deficient strain (each of which is a strain highly expressing cutL1). Culture conditions were the same as above, i.e., YPM medium, 24 hours, 100 rpm, and 1×10^4 conidia inoculated.

[Fig. 6] The putative amino acid sequence of AgsA of *Aspergillus oryzae* (SEQ ID NO: 1) is shown.

[Fig. 7] The base sequence of a nucleic acid molecule encoding AgsA of *Aspergillus oryzae* (SEQ ID NO: 2) is shown.

[Fig. 8] The base sequence of a nucleic acid molecule encoding AgsA of *Aspergillus oryzae* (SEQ ID NO: 2) is shown.

[Fig. 9] The putative amino acid sequence of AgsB of *Aspergillus oryzae* (SEQ ID NO: 3) is shown in Fig. 9.

[Fig. 10] The base sequence of a nucleic acid molecule encoding AgsB of *Aspergillus oryzae* (SEQ ID NO: 4) is shown.

[Fig. 11] The base sequence of a nucleic acid molecule encoding AgsB of *Aspergillus oryzae* (SEQ ID NO: 4) is shown.

[Fig. 12] The putative amino acid sequence of AgsC of *Aspergillus oryzae* (SEQ ID NO: 5) is shown.

[Fig. 13] The base sequence of a nucleic acid molecule encoding AgsC of *Aspergillus oryzae* (SEQ ID NO: 6) is shown.

[Fig. 14] The base sequence of a nucleic acid molecule encoding AgsC of *Aspergillus oryzae* (SEQ ID NO: 6) is shown.

[Fig. 15] The putative amino acid sequence of AgsA of *Aspergillus nidulans* (SEQ ID NO: 7) is shown.

[Fig. 16] The base sequence of a nucleic acid molecule encoding AgsA of *Aspergillus nidulans* (SEQ ID NO: 8) is shown.

[Fig. 17] The base sequence of a nucleic acid molecule encoding AgsA of *Aspergillus nidulans* (SEQ ID NO: 8) is shown.

[Fig. 18] The putative amino acid sequence of AgsB of *Aspergillus nidulans* (SEQ ID NO: 9) is shown.

[Fig. 19] The base sequence of a nucleic acid molecule encoding AgsB of *Aspergillus nidulans* (SEQ ID NO: 10) is shown.

[Fig. 20] The base sequence of a nucleic acid molecule encoding AgsB of *Aspergillus nidulans* (SEQ ID NO: 10) is shown.

[Fig. 21] The putative amino acid sequence of AgsA of *Aspergillus sojae* (SEQ ID NO: 11) is shown.

[Fig. 22] The base sequence of a nucleic acid molecule encoding AgsA of *Aspergillus sojae* (SEQ ID NO: 12) is shown.

[Fig. 23] The base sequence of a nucleic acid molecule encoding AgsA of *Aspergillus sojae* (SEQ ID NO: 12) is shown.

[Fig. 24] The putative amino acid sequence of AgsB of *Aspergillus sojae* (SEQ ID NO: 13) is shown.

[Fig. 25] The base sequence of a nucleic acid molecule encoding AgsB of *Aspergillus sojae* (SEQ ID NO: 14) is shown.

[Fig. 26] The base sequence of a nucleic acid molecule encoding AgsB of *Aspergillus sojae* (SEQ ID NO: 14) is shown.

[Fig. 27] The putative amino acid sequence of AgsC of *Aspergillus sojae* (SEQ ID NO: 15) is shown.

[Fig. 28] The base sequence of a nucleic acid molecule encoding AgsC of *Aspergillus sojae* (SEQ ID NO: 16) is shown.

[Fig. 29] The base sequence of a nucleic acid molecule encoding AgsC of *Aspergillus sojae* (SEQ ID NO: 16) is shown.

[Fig. 30] The putative amino acid sequence of AgsE of *Aspergillus niger* (SEQ ID NO: 17) is shown.

[Fig. 31] The base sequence of a nucleic acid molecule encoding AgsE of *Aspergillus niger* (SEQ ID NO: 18) is shown.

[Fig. 32] The base sequence of a nucleic acid molecule encoding AgsE of *Aspergillus niger* (SEQ ID NO: 18) is shown.

[Fig. 33] The putative amino acid sequence of Ags1 of *Aspergillus fumigatus* (SEQ ID NO: 19) is shown.

[Fig. 34] The base sequence of a nucleic acid molecule encoding Ags1 of *Aspergillus fumigatus* (SEQ ID NO: 20) is shown.

[Fig. 35] The base sequence of a nucleic acid molecule encoding Ags1 of *Aspergillus fumigatus* (SEQ ID NO: 20) is shown.

[Fig. 36] The putative amino acid sequence of Uge3 of *Aspergillus oryzae* (SEQ ID NO: 21) and the base sequence of a nucleic acid molecule encoding Uge3 thereof (SEQ ID NO: 22) are shown.

[Fig. 37] The putative amino acid sequence of Sph3 of *Aspergillus oryzae* (SEQ ID NO: 23) and the base sequence of a nucleic acid molecule encoding Sph3 thereof (SEQ ID NO: 24) are shown.

[Fig. 38] The putative amino acid sequence of Ega3 of *Aspergillus oryzae* (SEQ ID NO: 25) and the base sequence of a nucleic acid molecule encoding Ega3 thereof (SEQ ID NO: 26) are shown.

[Fig. 39] The putative amino acid sequence of Agd3 of *Aspergillus oryzae* (SEQ ID NO: 27) and the base sequence of a nucleic acid molecule encoding Agd3 thereof (SEQ ID NO: 28) are shown.

[Fig. 40] The putative amino acid sequence of Gtb3 of *Aspergillus oryzae* (SEQ ID NO: 29) is shown.

[Fig. 41] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus oryzae* (SEQ ID NO: 30) is shown.

[Fig. 42] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus oryzae* (SEQ ID NO: 30) is shown.

[Fig. 43] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus oryzae* (SEQ ID NO: 30) is shown.

[Fig. 44] The putative amino acid sequence of Uge3 of *Aspergillus nidulans* (SEQ ID NO: 31) and the base sequence of a nucleic acid molecule encoding Uge3 thereof (SEQ ID NO: 32) are shown.

[Fig. 45] The putative amino acid sequence of Sph3 of *Aspergillus nidulans* (SEQ ID NO: 33) and the base sequence of a nucleic acid molecule encoding Sph3 thereof (SEQ ID NO: 34) are shown.

[Fig. 46] The putative amino acid sequence of Ega3 of *Aspergillus nidulans* (SEQ ID NO: 35) and the base sequence of a nucleic acid molecule encoding Ega3 thereof (SEQ ID NO: 36) are shown.

[Fig. 47] The putative amino acid sequence of Agd3 of *Aspergillus nidulans* (SEQ ID NO: 37) and the base sequence of a nucleic acid molecule encoding Agd3 thereof (SEQ ID NO: 38) are shown.

[Fig. 48] The putative amino acid sequence of Gtb3 of *Aspergillus nidulans* (SEQ ID NO: 39) is shown.

[Fig. 49] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus nidulans* (SEQ ID NO: 40) is shown.

[Fig. 50] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus nidulans* (SEQ ID NO: 40) is shown.

[Fig. 51] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus nidulans* (SEQ ID NO: 40) is shown.

[Fig. 52] The putative amino acid sequence of Uge3 of *Aspergillus sojae* (SEQ ID NO: 41) and the base sequence of a nucleic acid molecule encoding Uge3 thereof (SEQ ID NO: 42) are shown.

[Fig. 53] The putative amino acid sequence of Sph3 of *Aspergillus sojae* (SEQ ID NO: 43) and the base sequence of a nucleic acid molecule encoding Sph3 thereof (SEQ ID NO: 44) are shown.

[Fig. 54] The putative amino acid sequence of Ega3 of *Aspergillus sojae* (SEQ ID NO: 45) and the base sequence of a nucleic acid molecule encoding Ega3 thereof (SEQ ID NO: 46) are shown.

[Fig. 55] The putative amino acid sequence of Agd3 of *Aspergillus sojae* (SEQ ID NO: 47) and the base sequence of a nucleic acid molecule encoding Agd3 thereof (SEQ ID NO: 48) are shown.

[Fig. 56] The putative amino acid sequence of Gtb3 of *Aspergillus sojae* (SEQ ID NO: 49) is shown.

[Fig. 57] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus sojae* (SEQ ID NO: 50) is shown.

[Fig. 58] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus sojae* (SEQ ID NO: 50) is shown.

[Fig. 59] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus sojae* (SEQ ID NO: 50) is shown.

[Fig. 60] The putative amino acid sequence of Uge3 of *Aspergillus niger* (SEQ ID NO: 51) and the base sequence of a nucleic acid molecule encoding Uge3 thereof (SEQ ID NO: 52) are shown.

[Fig. 61] The putative amino acid sequence of Sph3 of *Aspergillus niger* (SEQ ID NO: 53) and the base sequence of a nucleic acid molecule encoding Sph3 thereof (SEQ ID NO: 54) are shown.

[Fig. 62] The putative amino acid sequence of Ega3 of *Aspergillus niger* (SEQ ID NO: 55) and the base sequence of a nucleic acid molecule encoding Ega3 thereof (SEQ ID NO: 56) are shown.

[Fig. 63] The putative amino acid sequence of Agd3 of *Aspergillus niger* (SEQ ID NO: 57) and the base sequence of a nucleic acid molecule encoding Agd3 thereof (SEQ ID NO: 58) are shown.

[Fig. 64] The putative amino acid sequence of Gtb3 of *Aspergillus niger* (SEQ ID NO: 59) is shown.

[Fig. 65] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus niger* (SEQ ID NO: 60) is shown.

[Fig. 66] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus niger* (SEQ ID NO: 60) is shown.

[Fig. 67] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus niger* (SEQ ID NO: 60) is shown.

[Fig. 68] The putative amino acid sequence of Uge3 of *Aspergillus fumigatus* (SEQ ID NO: 61) and the base sequence of a nucleic acid molecule encoding Uge3 thereof (SEQ ID NO: 62) are shown.

[Fig. 69] The putative amino acid sequence of Sph3 of *Aspergillus fumigatus* (SEQ ID NO: 63) and the base sequence of a nucleic acid molecule encoding Sph3 thereof (SEQ ID NO: 64) are shown.

[Fig. 70] The putative amino acid sequence of Ega3 of *Aspergillus fumigatus* (SEQ ID NO: 65) and the base sequence of a nucleic acid molecule encoding Ega3 thereof (SEQ ID NO: 66) are shown.

[Fig. 71] The putative amino acid sequence of Agd3 of *Aspergillus fumigatus* (SEQ ID NO: 67) and the base sequence of a nucleic acid molecule encoding Agd3 thereof (SEQ ID NO: 68) are shown.

[Fig. 72] The putative amino acid sequence of Gtb3 of *Aspergillus fumigatus* (SEQ ID NO: 69) is shown.

[Fig. 73] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus fumigatus* (SEQ ID NO: 70) is shown.

[Fig. 74] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus fumigatus* (SEQ ID NO: 70) is shown.

[Fig. 75] The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus fumigatus* (SEQ ID NO: 70) is shown.

[Fig. 76] The putative amino acid sequence of AgsB of *Penicillium chrysogenum* (SEQ ID NO: 71) is shown.

[Fig. 77] The base sequence of a nucleic acid molecule encoding AgsB of *Penicillium chrysogenum* (SEQ ID NO: 72) is shown.

[Fig. 78] The base sequence of a nucleic acid molecule encoding AgsB of *Penicillium chrysogenum* (SEQ ID NO: 72) is shown.

[Fig. 79] The putative amino acid sequence of Uge3 of *Penicillium chrysogenum* (SEQ ID NO: 73) and the base sequence of a nucleic acid molecule encoding Uge3 thereof (SEQ ID NO: 74) are shown.

[Fig. 80] The putative amino acid sequence of Sph3 of *Penicillium chrysogenum* (SEQ ID NO: 75) and the base sequence of a nucleic acid molecule encoding Sph3 thereof (SEQ ID NO: 76) are shown.

[Fig. 81] The putative amino acid sequence of Ega3 of *Penicillium chrysogenum* (SEQ ID NO: 77) and the base sequence of a nucleic acid molecule encoding Ega3 thereof (SEQ ID NO: 78) are shown.

[Fig. 82] The putative amino acid sequence of Agd3 of *Penicillium chrysogenum* (SEQ ID NO: 79) is shown.

[Fig. 83] The base sequence of a nucleic acid molecule encoding Agd3 of *Penicillium chrysogenum* (SEQ ID NO: 80) is shown.

[Fig. 84] The putative amino acid sequence of Gtb3 of *Penicillium chrysogenum* (SEQ ID NO: 81) is shown.

[Fig. 85] The base sequence of a nucleic acid molecule encoding Gtb3 of *Penicillium chrysogenum* (SEQ ID NO: 82)

is shown.

[Fig. 86] The base sequence of a nucleic acid molecule encoding Gtb3 of *Penicillium chrysogenum* (SEQ ID NO: 82) is shown.

[Fig. 87] The base sequence of a nucleic acid molecule encoding Gtb3 of *Penicillium chrysogenum* (SEQ ID NO: 82) is shown.

[Figs. 88] Test results on the Congo red (CR) sensitivity of the WT strain, the AGΔ strain, and the AG-GAGΔ strain are shown.

[Figs. 89] Analysis results of the cell wall constituent saccharides of a wild-type (WT) strain, AGΔ strain, AG-GAGΔ strain, and GAGΔ strain of an *Aspergillus* are shown.

[Fig. 90] Results of sulfuric acid hydrolysis and monosaccharide component analysis of the wild-type (WT) strain, AGΔ strain, AG-GAGΔ strain, and GAGΔ strain of an *Aspergillus* are shown.

[Figs. 91] (A) A GAG biosynthetic gene cluster in *Cochliobolus heterostrophus* is illustrated and (B) electrophoresis results of PCR products of genomic DNAs extracted from gene disruption strain candidates are shown.

[Figs. 92] Culture properties of a wild-type strain and GAGΔ strain of *Cochliobolus heterostrophus* are shown.

[Figs. 93] (A) A GAG biosynthetic gene cluster in *B. fuckeliana* is illustrated and (B) electrophoresis results of PCR products of genomic DNAs extracted from gene disruption strain candidates are shown.

[Figs. 94] Culture properties of a wild-type strain and GAGΔ strain of *B. fuckeliana* are shown.

[Fig. 95] The putative amino acid sequence of uge3 of *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*) (SEQ ID NO: 89), the base sequence of a nucleic acid molecule of uge3 thereof (SEQ ID NO: 90), the putative amino acid sequence of sph3 thereof (SEQ ID NO: 91), and the base sequence of a nucleic acid molecule of sph3 thereof (SEQ ID NO: 92) are shown in Fig. 95.

[Fig. 96] The putative amino acid sequence of ega3 of *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*) (SEQ ID NO: 93), the base sequence of a nucleic acid molecule of ega3 thereof (SEQ ID NO: 94), the putative amino acid sequence of agd3 thereof (SEQ ID NO: 95), and the base sequence of a nucleic acid molecule of agd3 thereof (SEQ ID NO: 96) are shown in Fig. 96 and Fig. 97.

[Fig. 97] The putative amino acid sequence of ega3 of *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*) (SEQ ID NO: 93), the base sequence of a nucleic acid molecule of ega3 thereof (SEQ ID NO: 94), the putative amino acid sequence of agd3 thereof (SEQ ID NO: 95), and the base sequence of a nucleic acid molecule of agd3 thereof (SEQ ID NO: 96) are shown in Fig. 96 and Fig. 97.

[Fig. 98] The putative amino acid sequence of gtb3 of *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*) (SEQ ID NO: 97) and the base sequence of a nucleic acid molecule of gtb3 thereof (SEQ ID NO: 98) are shown in Fig. 98 to Fig. 101.

[Fig. 99] The putative amino acid sequence of gtb3 of *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*) (SEQ ID NO: 97) and the base sequence of a nucleic acid molecule of gtb3 thereof (SEQ ID NO: 98) are shown in Fig. 98 to Fig. 101.

[Fig. 100] The putative amino acid sequence of gtb3 of *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*) (SEQ ID NO: 97) and the base sequence of a nucleic acid molecule of gtb3 thereof (SEQ ID NO: 98) are shown in Fig. 98 to Fig. 101.

[Fig. 101] The putative amino acid sequence of gtb3 of *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*) (SEQ ID NO: 97) and the base sequence of a nucleic acid molecule of gtb3 thereof (SEQ ID NO: 98) are shown in Fig. 98 to Fig. 101.

[Fig. 102] The putative amino acid sequence of ags1 of *Botrytis cinerea* (SEQ ID NO: 99) and the base sequence of a nucleic acid molecule of ags1 thereof (SEQ ID NO: 100) are shown in Fig. 102 to Fig. 104.

[Fig. 103] The putative amino acid sequence of ags1 of *Botrytis cinerea* (SEQ ID NO: 99) and the base sequence of a nucleic acid molecule of ags1 thereof (SEQ ID NO: 100) are shown in Fig. 102 to Fig. 104.

[Fig. 104] The putative amino acid sequence of ags1 of *Botrytis cinerea* (SEQ ID NO: 99) and the base sequence of a nucleic acid molecule of ags1 thereof (SEQ ID NO: 100) are shown in Fig. 102 to Fig. 104.

[Fig. 105] The putative amino acid sequence of uge3 of *Botrytis cinerea* (SEQ ID NO: 101), the base sequence of a nucleic acid molecule of uge3 thereof (SEQ ID NO: 102), the putative amino acid sequence of sph3 thereof (SEQ ID NO: 103), and the base sequence of a nucleic acid molecule of sph3 thereof (SEQ ID NO: 104) are shown in Fig. 105.

[Fig. 106] The putative amino acid sequence of ega3 of *Botrytis cinerea* (SEQ ID NO: 105), the base sequence of a nucleic acid molecule of ega3 thereof (SEQ ID NO: 106), the putative amino acid sequence of agd3 thereof (SEQ ID NO: 107), and the base sequence of a nucleic acid molecule of agd3 thereof (SEQ ID NO: 108) are shown in Fig. 106 and Fig. 107.

[Fig. 107] The putative amino acid sequence of ega3 of *Botrytis cinerea* (SEQ ID NO: 105), the base sequence of a nucleic acid molecule of ega3 thereof (SEQ ID NO: 106), the putative amino acid sequence of agd3 thereof (SEQ ID NO: 107), and the base sequence of a nucleic acid molecule of agd3 thereof (SEQ ID NO: 108) are shown in Fig. 106 and Fig. 107.

[Fig. 108] The base sequence of a nucleic acid molecule of gtb3 of *Botrytis cinerea* (SEQ ID NO: 109) and the base sequence of a nucleic acid molecule of gtb3 thereof (SEQ ID NO: 110) are shown in Fig. 108 to Fig. 111.

[Fig. 109] The base sequence of a nucleic acid molecule of gtb3 of *Botrytis cinerea* (SEQ ID NO: 109) and the base sequence of a nucleic acid molecule of gtb3 thereof (SEQ ID NO: 110) are shown in Fig. 108 to Fig. 111.

[Fig. 110] The base sequence of a nucleic acid molecule of gtb3 of *Botrytis cinerea* (SEQ ID NO: 109) and the base sequence of a nucleic acid molecule of gtb3 thereof (SEQ ID NO: 110) are shown in Fig. 108 to Fig. 111.

[Fig. 111] The base sequence of a nucleic acid molecule of gtb3 of *Botrytis cinerea* (SEQ ID NO: 109) and the base sequence of a nucleic acid molecule of gtb3 thereof (SEQ ID NO: 110) are shown in Fig. 108 to Fig. 111.

[Fig. 112] The results of staining with AGBD-GFP for various cells are shown.

[Fig. 113] The results of staining with AGBD-GFP for various cells are shown.

Description of Embodiments

[0017] The present invention provides a mutant filamentous fungus which is deficient in at least one α -1,3-glucan synthase gene comprising agsB, and is deficient in at least one galactosaminogalactan biosynthetic gene selected from the group consisting of uge3, sph3, ega3, agd3, and gtb3 so that the at least one gene responsible for the expression of galactosaminogalactan is knocked out.

Mutant Strain of Filamentous Fungus

[0018] Examples of the filamentous fungus include the genus *Aspergillus*, the genus *Penicillium* (e.g., *Penicillium chrysogenum*), the genus *Trichoderma*, the genus *Cephalosporium*, the genus *Acremonium*, the genus *Neurospora*, the genus *Botrytis*, the genus *Cochliobolus*, and the genus *Monascus*. Of those, the genus *Aspergillus*, the genus *Botrytis*, or the genus *Cochliobolus* is preferred, and the genus *Aspergillus* is more preferred. Examples of the filamentous fungi of the genus *Aspergillus* to be used in the present invention include *Aspergillus oryzae*, *Aspergillus sojae*, *Aspergillus nidulans*/*Emmericella nidulans*, *Aspergillus niger*, and *Aspergillus fumigatus*. Of those, *Aspergillus oryzae*, *Aspergillus sojae*, *Aspergillus nidulans*, or *Aspergillus niger* is preferred, *Aspergillus oryzae* or *Aspergillus*

sojae is more preferred, and *Aspergillus oryzae* is still more preferred. Examples of the filamentous fungi of the genus *Botrytis* to be used in the present invention include *Botrytis cinerea* (teleomorph: *Botryotinia fuckeliana*), *Botrytis allii*, *Botrytis squamosa*, and *Botrytis byssoides*. Examples of the filamentous fungi of the genus *Cochliobolus* to be used in the present invention include *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*), *Cochliobolus carbonum*, *Cochliobolus miyabeanus*, and *Cochliobolus victoriae*. Examples of the genus *Monascus* include *Monascus purpureus*, *Monascus ruber*, and *Monascus pilosus*.

[0019] The filamentous fungus mutant strain, which is deficient in at least one α -1,3-glucan synthase gene, comprises agsB according to the present invention. Examples of the α -1,3-glucan synthase gene ags include: agsA (Genbank accession No. AN5885) and agsB (Genbank accession No. AN3307) of *Aspergillus nidulans*; agsA, agsB, and agsC of *Aspergillus oryzae*; agsA, agsB, and agsC of *Aspergillus sojae*; ags1 (Genbank accession No. AFUA_3G00910) of *Aspergillus fumigatus*; agsE (Genbank accession No. ANI_1_360084) of *Aspergillus niger*, and agsB (Genbank accession No. Pc16g06130) of *Penicillium chrysogenum*. In this connection, agsA, agsB, and agsC of *Aspergillus oryzae* are registered in the *Aspergillus* database AspGD (<http://www.aspergillusgenome.org>) with the following gene numbers: agsA (AOR_1_956014), agsB (AOR_1_2634154), and agsC (AOR_1_1350024). The putative amino acid sequence of AgsA of *Aspergillus oryzae* (SEQ ID NO: 1) is shown in Fig. 6, and the base sequence of a nucleic acid molecule encoding AgsA of *Aspergillus oryzae* (SEQ ID NO: 2) is shown in Fig. 7 and Fig. 8. The putative amino acid sequence of AgsB of *Aspergillus oryzae* (SEQ ID NO: 3) is shown in Fig. 9, and the base sequence of a nucleic acid molecule encoding AgsB of *Aspergillus oryzae* (SEQ ID NO: 4) is shown in Fig. 10 and Fig. 11. The putative amino acid sequence of AgsC of *Aspergillus oryzae* (SEQ ID NO: 5) is shown in Fig. 12, and the base sequence of a nucleic acid molecule encoding AgsC of *Aspergillus oryzae* (SEQ ID NO: 6) is shown in Fig. 13 and Fig. 14. The putative amino acid sequence of AgsA of *Aspergillus nidulans* (SEQ ID NO: 7) is shown in Fig. 15, and the base sequence of a nucleic acid molecule encoding AgsA of *Aspergillus nidulans* (SEQ ID NO: 8) is shown in Fig. 16 and Fig. 17. In addition, the putative amino acid sequence of AgsB of *Aspergillus nidulans* (SEQ ID NO: 9) is shown in Fig. 18, and the base sequence of a nucleic acid molecule encoding AgsB of *Aspergillus nidulans* (SEQ ID NO: 10) is shown in Fig. 19 and Fig. 20. Examples of the amino acid sequences of AgsA, AgsB, and AgsC of *Aspergillus sojae* include amino acid sequences estimated from gene sequences registered in GenBank (Genbank accession Nos. DF093557 to DF093585) on the basis of homology with *Aspergillus oryzae*. The putative amino acid sequence of AgsA of *Aspergillus sojae* (SEQ ID NO: 11) is shown in Fig. 21, and the putative base sequence of a nucleic acid molecule encoding the above-mentioned AgsA of *Aspergillus sojae* (SEQ ID NO: 12) is shown in Fig. 22 and Fig. 23. In addition, the putative amino acid sequence of AgsB of *Aspergillus sojae* (SEQ ID NO: 13) is shown in Fig. 24, and the base sequence of a nucleic acid molecule encoding AgsB of *Aspergillus sojae* (SEQ ID NO: 14) is shown in Fig. 25 and Fig. 26. In addition, the putative amino acid sequence of AgsC of *Aspergillus sojae* (SEQ ID NO: 15) is shown in Fig. 27, and the base sequence of a nucleic acid molecule encoding AgsC of *Aspergillus sojae* (SEQ ID NO: 16) is shown in Fig. 28 and Fig. 29. The putative amino acid sequence of AgsE of *Aspergillus niger* (SEQ ID NO: 17) is shown in Fig. 30. The base sequence of a nucleic acid molecule encoding AgsE of *Aspergillus niger* (SEQ ID NO: 18) is shown in Fig. 31 and Fig. 32. The putative amino acid sequence of Ags1 of *Aspergillus fumigatus* (SEQ ID NO: 19) is shown in Fig. 33. The base sequence of a nucleic acid molecule encoding Ags1 of *Aspergillus fumigatus* (SEQ ID NO: 20) is shown in Fig. 34 and Fig. 35. The putative amino acid sequence of AgsB of *Penicillium chrysogenum* (SEQ ID NO: 71) and the base sequence of a nucleic acid molecule encoding AgsB thereof (SEQ ID NO: 72) are shown in Fig. 75.

[0020] Examples of the mutant filamentous fungus include mutant filamentous fungi each deficient in one or two or more of those α -1,3-glucan synthase genes. Of those, a mutant filamentous fungus deficient in all the three genes is preferred.

[0021] In the present invention, examples of the deficiency in α -1,3-glucan synthase gene ags include: a deletion of the whole or part of the coding region of α -1,3-glucan synthase in a genome; an insertion of another nucleic acid molecule into the whole or part of the coding region; and a substitution of the whole or part of the coding region by another nucleic acid molecule. In addition, the deficiency in α -1,3-glucan synthase gene ags encompasses an addition, deletion, and substitution of a predetermined nucleic acid molecule to the above-mentioned coding region. Also disclosed is a conditional gene deficiency designed so that α -1,3-glucan is expressed only under a certain condition.

[0022] The filamentous fungus mutant strain according to the present invention is deficient in at least one

galactosaminogalactan biosynthetic gene selected from the group consisting of *uge3*, *sph3*, *ega3*, *agd3*, and *gtb3* so that the at least one gene responsible for the expression of galactosaminogalactan is knocked out, and the mutant filamentous fungus is deficient in at least one α -1,3-glucan synthase gene comprising *agsB*.

[0023] Galactosaminogalactan is an extracellular polysaccharide identified in *Aspergillus fumigatus* in 2011, and is formed of galactose (Gal), N-acetylgalactosamine (GalNAc), and galactosamine (GalN) (Non-patent Literature 1). In addition, genes constituting the GAG biosynthetic cluster include *uge3*, *sph3*, *ega3*, *agd3*, and *gtb3*.

[0024] Therefore, an example of the filamentous fungus mutant strain deficient also in at least part of the GAG biosynthetic cluster according to the present invention is a filamentous fungus mutant strain deficient in at least one gene selected from the group consisting of *uge3*, *sph3*, *ega3*, *agd3*, and *gtb3*. In one embodiment of the present invention, an example of the filamentous fungus mutant strain deficient also in at least part of the GAG biosynthetic cluster is a filamentous fungus mutant strain deficient in at least *uge3* and *sph3* out of those genes.

[0025] Examples of those genes constituting the GAG biosynthetic cluster include: *uge3* (Genbank accession No. AOR_1_2588174), *sph3* (Genbank accession No. AOR_1_2586174), *ega3* (Genbank accession No. AOR_1_2584174), *agd3* (Genbank accession No. AOR_1_2582174), and *gtb3* (Genbank accession No. AOR_1_2580174) of *Aspergillus oryzae*; *uge3* (Genbank accession No. AN2951), *sph3* (Genbank accession No. AN2952), *ega3* (Genbank accession No. AN2953), *agd3* (Genbank accession No. AN2954), and *gtb3* (Genbank accession No. AN2955) of *Aspergillus nidulans*; *uge3*, *sph3*, *ega3*, *agd3*, and *gtb3* of *Aspergillus sojae*; *uge3* (Genbank accession No. ANI_1_1578024), *sph3* (Genbank accession No. ANI_1_3046024), *ega3* (Genbank accession No. ANI_1_1582024), *agd3* (Genbank accession No. ANI_1_3048024), and *gtb3* (Genbank accession No. ANI_1_3050024) of *Aspergillus niger*; *uge3* (Genbank accession No. AFUA_3G07910), *sph3* (Genbank accession No. AFUA_3G07900), *ega3* (Genbank accession No. AFUA_3G07890), *agd3* (Genbank accession No. AFUA_3G07870), and *gtb3* (Genbank accession No. AFUA_3G07860) of *Aspergillus fumigatus*; *uge3* (Genbank accession No. Pc20g06140), *sph3* (Genbank accession No. Pc20g06130), *ega3* (Genbank accession No. Pc20g06110), *agd3* (Genbank accession No. Pc20g06090), and *gtb3* (Genbank accession No. Pc20g06080) of *Penicillium chrysogenum*; *uge3* (Gene ID: COCHEDRAFT_1185586), *sph3* (Gene ID: COCHEDRAFT_1023805), *ega3* (Gene ID: COCHEDRAFT_1023806), *agd3* (Gene ID: COCHEDRAFT_1146217), and *gtb3* (Gene ID: COCHEDRAFT_1146218) of *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*); and *uge3* (Gene ID: Bcin01p05750.1), *sph3* (Gene ID: Bcin01p05740.1), *ega3* (Gene ID: Bcin01p05730.1), *agd3* (Gene ID: Bcin01p05720.1), and *gtb3* (Gene ID: Bcin01p05710.1) of *Botrytis cinerea*.

[0026] The amino acid sequence of *Uge3* of *Aspergillus oryzae* (SEQ ID NO: 21) and the base sequence of a nucleic acid molecule encoding *Uge3* thereof (SEQ ID NO: 22) are shown in Fig. 36. In addition, the amino acid sequence of *Sph3* of *Aspergillus oryzae* (SEQ ID NO: 23) and the base sequence of a nucleic acid molecule encoding *Sph3* thereof (SEQ ID NO: 24) are shown in Fig. 37. In addition, the amino acid sequence of *Ega3* of *Aspergillus oryzae* (SEQ ID NO: 25) and the base sequence of a nucleic acid molecule encoding *Ega3* thereof (SEQ ID NO: 26) are shown in Fig. 38. In addition, the amino acid sequence of *Agd3* of *Aspergillus oryzae* (SEQ ID NO: 27) and the base sequence of a nucleic acid molecule encoding *Agd3* thereof (SEQ ID NO: 28) are shown in Fig. 39. In addition, the amino acid sequence of *Gtb3* of *Aspergillus oryzae* (SEQ ID NO: 29) is shown in Fig. 40, and the base sequence of a nucleic acid molecule encoding *Gtb3* of *Aspergillus oryzae* (SEQ ID NO: 30) is shown in Fig. 41 to Fig. 43.

[0027] The amino acid sequence of *Uge3* of *Aspergillus nidulans* (SEQ ID NO: 31) and the base sequence of a nucleic acid molecule encoding *Uge3* thereof (SEQ ID NO: 32) are shown in Fig. 44. In addition, the amino acid sequence of *Sph3* of the above-mentioned *Aspergillus nidulans* (SEQ ID NO: 33) and the base sequence of a nucleic acid molecule encoding *Sph3* thereof (SEQ ID NO: 34) are shown in Fig. 45. In addition, the amino acid sequence of *Ega3* of *Aspergillus nidulans* (SEQ ID NO: 35) and the base sequence of a nucleic acid molecule encoding *Ega3* thereof (SEQ ID NO: 36) are shown in Fig. 46. In addition, the amino acid sequence of *Agd3* of *Aspergillus nidulans* (SEQ ID NO: 37) and the base sequence of a nucleic acid molecule encoding *Agd3* thereof (SEQ ID NO: 38) are shown in Fig. 47. In addition, the amino acid sequence of *Gtb3* of *Aspergillus nidulans* (SEQ ID NO: 39) is shown in Fig. 48, and the base sequence of a nucleic acid molecule encoding *Gtb3* of *Aspergillus nidulans* (SEQ ID NO: 40) is shown in Fig. 49 to Fig. 51.

[0028] In the present invention, examples of the amino acid sequences of Uge3, Sph3, Ega3, Agd3, and Gtb3 of *Aspergillus sojae* include amino acid sequences estimated from gene sequences of *Aspergillus sojae* registered in GenBank (Genbank accession Nos. DF093557 to DF093585) on the basis of homology with *Aspergillus oryzae*. The putative amino acid sequence of Uge3 of *Aspergillus sojae* (SEQ ID NO: 41) and the putative base sequence of a nucleic acid molecule encoding Uge3 thereof (SEQ ID NO: 42) are shown in Fig. 52. The putative amino acid sequence of Sph3 of *Aspergillus sojae* (SEQ ID NO: 43) and the putative base sequence of a nucleic acid molecule encoding Sph3 thereof (SEQ ID NO: 44) are shown in Fig. 53. The putative amino acid sequence of Ega3 of *Aspergillus sojae* (SEQ ID NO: 45) and the putative base sequence of a nucleic acid molecule encoding Ega3 thereof (SEQ ID NO: 46) are shown in Fig. 54. In addition, the putative amino acid sequence of Agd3 of *Aspergillus sojae* (SEQ ID NO: 47) and the putative base sequence of a nucleic acid molecule encoding Agd3 thereof (SEQ ID NO: 48) are shown in Fig. 55. In addition, the putative amino acid sequence of Gtb3 of *Aspergillus sojae* (SEQ ID NO: 49) is shown in Fig. 56, and the putative base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus sojae* (SEQ ID NO: 50) are shown in Fig. 57 to Fig. 59.

[0029] The putative amino acid sequence of Uge3 of *Aspergillus niger* (SEQ ID NO: 51) and the base sequence of a nucleic acid molecule encoding Uge3 thereof (SEQ ID NO: 52) are shown in Fig. 60. The putative amino acid sequence of Sph3 of *Aspergillus niger* (SEQ ID NO: 53) and the base sequence of a nucleic acid molecule encoding Sph3 thereof (SEQ ID NO: 54) are shown in Fig. 61. The putative amino acid sequence of Ega3 of *Aspergillus niger* (SEQ ID NO: 55) and the base sequence of a nucleic acid molecule encoding Ega3 thereof (SEQ ID NO: 56) are shown in Fig. 62. The putative amino acid sequence of Agd3 of *Aspergillus niger* (SEQ ID NO: 57) and the base sequence of a nucleic acid molecule encoding Agd3 thereof (SEQ ID NO: 58) are shown in Fig. 63. The putative amino acid sequence of Gtb3 of *Aspergillus niger* (SEQ ID NO: 59) is shown in Fig. 64. The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus niger* (SEQ ID NO: 60) is shown in Fig. 65 to Fig. 67. The putative amino acid sequence of Uge3 of *Aspergillus fumigatus* (SEQ ID NO: 61) and the base sequence of a nucleic acid molecule encoding Uge3 thereof (SEQ ID NO: 62) are shown in Fig. 68. The putative amino acid sequence of Sph3 of *Aspergillus fumigatus* (SEQ ID NO: 63) and the base sequence of a nucleic acid molecule encoding Sph3 thereof (SEQ ID NO: 64) are shown in Fig. 69. The putative amino acid sequence of Ega3 of *Aspergillus fumigatus* (SEQ ID NO: 65) and the base sequence of a nucleic acid molecule encoding Ega3 thereof (SEQ ID NO: 66) are shown in Fig. 70. The putative amino acid sequence of Agd3 of *Aspergillus fumigatus* (SEQ ID NO: 67) and the base sequence of a nucleic acid molecule encoding Agd3 thereof (SEQ ID NO: 68) are shown in Fig. 71. The putative amino acid sequence of Gtb3 of *Aspergillus fumigatus* (SEQ ID NO: 69) is shown in Fig. 72. The base sequence of a nucleic acid molecule encoding Gtb3 of *Aspergillus fumigatus* (SEQ ID NO: 70) is shown in Fig. 73 to Fig. 75. The putative amino acid sequence of Uge3 of *Penicillium chrysogenum* (SEQ ID NO: 73) and the base sequence of a nucleic acid molecule encoding Uge3 thereof (SEQ ID NO: 74) are shown in Fig. 79. The putative amino acid sequence of Sph3 of *Penicillium chrysogenum* (SEQ ID NO: 75) and the base sequence of a nucleic acid molecule encoding Sph3 thereof (SEQ ID NO: 76) are shown in Fig. 80. The putative amino acid sequence of Ega3 of *Penicillium chrysogenum* (SEQ ID NO: 77) and the base sequence of a nucleic acid molecule encoding Ega3 thereof (SEQ ID NO: 78) are shown in Fig. 81. The putative amino acid sequence of Agd3 of *Penicillium chrysogenum* (SEQ ID NO: 79) is shown in Fig. 82. The base sequence of a nucleic acid molecule encoding Agd3 of *Penicillium chrysogenum* (SEQ ID NO: 80) is shown in Fig. 83. The putative amino acid sequence of Gtb3 of *Penicillium chrysogenum* (SEQ ID NO: 81) is shown in Fig. 84. The base sequence of a nucleic acid molecule encoding Gtb3 of *Penicillium chrysogenum* (SEQ ID NO: 82) is shown in Fig. 85 to Fig. 87.

[0030] The putative amino acid sequence of uge3 of *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*) (SEQ ID NO: 89), the base sequence of a nucleic acid molecule of uge3 (SEQ ID NO: 90), the putative amino acid sequence of sph3 thereof (SEQ ID NO: 91), and the base sequence of a nucleic acid molecule of sph3 thereof (SEQ ID NO: 92) are shown in Fig. 95. The putative amino acid sequence of ega3 of *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*) (SEQ ID NO: 93), the base sequence of a nucleic acid molecule of ega3 thereof (SEQ ID NO: 94), the putative amino acid sequence of agd3 thereof (SEQ ID NO: 95), and the base sequence of a nucleic acid molecule of agd3 thereof (SEQ ID NO: 96) are shown in Fig. 96 and Fig. 97. The putative amino acid sequence of gtb3 of *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*) (SEQ ID NO: 97) and the base sequence of a nucleic acid molecule of gtb3 thereof (SEQ ID NO: 98) are shown in Fig. 98 to Fig. 101.

[0031] The putative amino acid sequence of ags1 of *Botrytis cinerea* (SEQ ID NO: 99) and the base sequence of a nucleic acid molecule of ags1 thereof (SEQ ID NO: 100) are shown in Fig. 102 to Fig. 104. The putative amino acid

sequence of *uge3* of *Botrytis cinerea* (SEQ ID NO: 101), the base sequence of a nucleic acid molecule of *uge3* thereof (SEQ ID NO: 102), the putative amino acid sequence of *sph3* thereof (SEQ ID NO: 103), and the base sequence of a nucleic acid molecule of *sph3* thereof (SEQ ID NO: 104) are shown in Fig. 105. The putative amino acid sequence of *ega3* of *Botrytis cinerea* (SEQ ID NO: 105), the base sequence of a nucleic acid molecule of *ega3* thereof (SEQ ID NO: 106), the putative amino acid sequence of *agd3* thereof (SEQ ID NO: 107), and the base sequence of a nucleic acid molecule of *agd3* thereof (SEQ ID NO: 108) are shown in Fig. 106 and Fig. 107. The base sequence of a nucleic acid molecule of *gtb3* of *Botrytis cinerea* (SEQ ID NO: 109) and the base sequence of a nucleic acid molecule of *gtb3* thereof (SEQ ID NO: 110) are shown in Fig. 108 to Fig. 111.

[0032] In the present invention, examples of the deficiency in at least part of the GAG biosynthetic cluster include: a deletion of the whole or part of a coding region out of the GAG biosynthetic cluster in a genome; an insertion of another nucleic acid molecule into the whole or part of the coding region; and a substitution of the whole or part of the coding region by another nucleic acid molecule. In addition, the deficiency in at least part of the GAG biosynthetic cluster encompasses not only an addition, deletion, and substitution of a predetermined nucleic acid molecule to the above-mentioned coding region but also a conditional gene deficiency designed so that GAG is expressed only under a certain condition.

[0033] In addition, in the present invention, examples of the deficiency in *uge3* include: a deletion of the whole or part of a *Uge3* coding region in a genome; an insertion of another nucleic acid molecule into the whole or part of the coding region; and a substitution of the whole or part of the coding region by another nucleic acid molecule. In the present invention, examples of the deficiency in *sph3* include: a deletion of the whole or part of an *Sph3* coding region in a genome; an insertion of another nucleic acid molecule into the whole or part of the coding region; and a substitution of the whole or part of the coding region by another nucleic acid molecule. In the present invention, examples of the deficiency in *ega3* include: a deletion of the whole or part of an *Ega3* coding region in a genome; an insertion of another nucleic acid molecule into the whole or part of the coding region; and a substitution of the whole or part of the coding region by another nucleic acid molecule. In the present invention, examples of the deficiency in *agd3* include: a deletion of the whole or part of an *Agd3* coding region in a genome; an insertion of another nucleic acid molecule into the whole or part of the coding region; and a substitution of the whole or part of the coding region by another nucleic acid molecule. In the present invention, examples of the deficiency in *gtb3* include: a deletion of the whole or part of a *Gtb3* coding region in a genome; an insertion of another nucleic acid molecule into the whole or part of the coding region; and a substitution of the whole or part of the coding region by another nucleic acid molecule.

[0034] In addition, also for *uge3*, *sph3*, *ega3*, *agd3*, and *gtb3*, the deficiency in each of these genes encompasses not only an addition, deletion, and substitution of a predetermined nucleic acid molecule to the above-mentioned coding region but also a conditional gene deficiency designed so that GAG is expressed only under a certain condition. According to the invention, the mutant filamentous fungus is deficient in at least one galactosaminogalactan biosynthetic gene selected from the group consisting of *uge3*, *sph3*, *ega3*, *agd3*, and *gtb3* so that the at least one gene responsible for the expression of galactosaminogalactan is knocked out.

[0035] The filamentous fungus mutant strain deficient in at least part of the GAG biosynthetic cluster according to the present disclosure but not part of the present invention encompasses not only a filamentous fungus mutant strain completely lacking expression of GAG but also a filamentous fungus mutant strain substantially lacking expression of GAG. More specifically, the mutant strain substantially lacking expression of GAG refers to a mutant strain that expresses only a small amount of GAG and shows significant suppression of aggregation of cells and an example thereof is a strain having an expression amount of GAG of 30% or less with respect to that of a wild-type strain, more preferably 10% or less with respect to that of the wild-type strain.

[0036] A method of the present invention may be used for the production of useful substances, for example, enzymes such as amylase and cellulase and low-molecular-weight compounds such as penicillin that the filamentous fungus originally has abilities to produce. In the method of the present invention, transformation may be performed so as to enhance the expression of the useful substances that the filamentous fungus originally has abilities to produce, or so as to express substances that the filamentous fungus originally has no abilities to produce. As such transformation method, a method known per se (e.g., methods described in JP 2001-46078 A, JP 2005-52116 A, JP

2009-118783 A, JP 11-506025 A, and JP 2007-508022 A) may be used, the method involving utilizing an expression vector constructed so that the filamentous fungus can function as a host, and a plasmid constructed by functionally linking a gene encoding a homologous or heterologous protein to the expression vector.

[0037] A method of producing such mutant strain may be performed by subjecting a filamentous fungus to, for example, the following, by appropriately using a method known per se (e.g., methods described in Non-patent Literatures 2 to 5): the construction of a disruption cassette for α -1,3-glucan gene and the introduction of the cassette into a genome gene; and the construction of a disruption cassette for a gene constituting the GAG biosynthetic cluster and the introduction of the cassette into a genome gene. In the present invention, as the filamentous fungus to be subjected to such genetic manipulation, there may be used, for example, a filamentous fungus having a mutation of gene *ligD* disruption and/or gene *adeA* disruption (preferably both thereof) introduced in advance in order to enable gene introduction into a target site at a high probability. Here, *ligD* is a gene associated with nonhomologous recombination repair in DNA repair, and is preferred because a transformant having the gene introduced into the target site through homologous recombination can be acquired with relatively high efficiency by disrupting the gene. An example of the mutation that disrupts the gene is a *ligD::sC* mutation obtained by disruption using an *sC* marker (Non-patent Literature 6). In addition, *adeA* is an adenine auxotrophic gene, and an example of the mutation that disrupts the gene is *adeA Δ ::ptrA* obtained by disruption with pyrithiamine resistance gene (*ptrA*) (Non-patent Literature 7). Therefore, examples of the filamentous fungus mutant strain of the present invention also include filamentous fungus mutant strains further having those mutations.

[0038] The filamentous fungus mutant strain according to the present invention may be used for the production of a substance, and may be used for, for example, the following method.

Method of Producing Substance

[0039] The present invention provides a method of producing a substance, including the steps of:

culturing the above-mentioned filamentous fungus mutant strain to allow the filamentous fungus to produce a substance; and

collecting the resulting substance.

[0040] The useful substances that can be produced by the method of the present invention are not particularly limited as long as the substances can be produced by the filamentous fungus, and examples thereof include: low-molecular-weight compounds such as penicillin, statins, cephalosporin, kojic acid, citric acid, and malic acid; and high-molecular-weight compounds such as amylase, cellulase, protease, lipase, peptidase, esterase, hydrophobin, and oxidase. In addition, examples of the useful substances include chemical products such as an organic acid, a pigment, and an agricultural chemical bulk, and various substances to be used as pharmaceutical products. In addition, the method of the present invention is also applicable to, for example, the production of bioethanol through biomass decomposition (e.g., one using a mold genetically modified so as to highly produce cellulase or the like). By the method of the present invention, a cell wall constituent component or a hydrolysate thereof may be produced, but a substance other than the cell wall constituent component or the hydrolysate thereof may also be produced. Examples of the cell wall constituent component or the hydrolysate thereof include α -1,3-glucan, β -1,3-glucan, polygalactose, glucose, galactose, glucosamine, amino acid, mannose, N-acetylglucosamine, N-acetylgalactosamine, and chitin. In the present invention, the "substance" that can be produced by the method of the present invention is understood not to encompass: a compound that harms or kills the filamentous fungus; living cells; a substance that can only be obtained by chemical synthesis; and the like.

Culturing Step

[0041] The method of the present invention includes a step of culturing a mutant filamentous fungus, which is

deficient in at least one galactosaminogalactan biosynthetic gene selected from the group consisting of *uge3*, *sph3*, *ega3*, *agd3*, and *gtb3* so that the at least one gene responsible for the expression of galactosaminogalactan is knocked out, and the mutant filamentous fungus is deficient in at least one α -1,3-glucan synthase gene comprising *agsB* to allow the filamentous fungus to produce a substance. A medium to be used in the step is not particularly limited, and there may be used a wide range of media that may be used for the culture of a filamentous fungus. Examples thereof include CD minimal medium, YPD medium, TSB medium, malt medium, and PDA medium. To the medium, glucose, starch, soluble starch, or the like may be added as a carbon source. The addition amount of such carbon source is not particularly limited and may be appropriately set within a range of, for example, from 0.5% to 10%, more preferably from 1% to 4%. A culture temperature is not particularly limited and may be appropriately set within a range of from 20°C to 45°C, more preferably from 25°C to 37°C. A culture time is also not particularly limited and may be appropriately set within a range of, for example, from 12 hours to 72 hours, more preferably from 24 hours to 48 hours. In addition, as described above, the filamentous fungus mutant strain according to the disclosure but not part of the present invention relates to a filamentous fungus mutant strain having a conditional gene deficiency designed so that α -1,3-glucan and/or GAG is expressed only under a certain condition. Therefore, the method of the present disclosure but not part of the present invention also relates to a method including a step of culturing a mutant strain having the conditional gene deficiency under such a condition that α -1,3-glucan and GAG are not expressed (or their expressions are suppressed).

Collecting Step

[0042] A method of collecting the useful substance from the culture medium is not particularly limited, and there may be appropriately used a method known per se (e.g., centrifugation, recrystallization, a distillation method, a solvent extraction method, or chromatography). The method of the present invention is a method of collecting a useful substance. Therefore, a method of decomposing and detecting constituent components of a filamentous fungus mutant for the purpose of analyzing constituent components of cells of a filamentous fungus itself or the like for research thereof is essentially different from the method of the present invention.

[0043] Now, an embodiment of the present invention is more specifically described by way of Examples, and the action and effect of the present invention are demonstrated.

Examples

Example 1

Materials and Methods

Strain

[0044] In this study, a modified strain of an NS4 strain (genotype; *niaD*⁻, *sC*⁻) was used as a wild-type strain of a filamentous fungus *A. oryzae*. The NS4 modified strain used in this study is a strain having introduced therein a *ligDΔ::sC* mutation capable of gene introduction into a target site at a high probability and an *adeAΔ::ptrA* mutation having adenine auxotrophy (*ligDΔ::sC, adeAΔ::ptrA*). In addition, a strain deficient in three kinds of α -1,3-glucan synthase genes (*agsAΔagsBΔagsCΔ*) was used as an AG-deficient strain. Other produced gene mutant strains and genotypes thereof are as shown in Table 1.

Table 1

Strain	Genotype	Reference
<i>A. oryzae</i>		

NS4 <i>ligDΔ :: sC, adeAΔ :: ptrA</i>	<i>ligDΔ :: sC, adeAΔ :: ptrA, niaD⁻, adeA⁺</i>	Mizutani <i>et al</i> (2008) Fungal. Gent. Biol. 45, 878-889.
<i>agsAΔagsBΔagsCΔ</i>	<i>ligDΔ :: sC, adeAΔ :: ptrA, niaD⁻, adeA⁺, agsA :: loxP, agsB :: loxP, agsC :: loxP</i>	Miyazawa <i>et al</i> (2016) Biosci. Biotechnol. Biochem. 80, 1853-1863.
<i>agsAΔagsBΔagsCΔ sph3Δuge3Δ</i>	<i>ligDΔ :: sC, adeAΔ :: ptrA, niaD⁻, agsA :: loxP, agsB :: loxP, agsC :: loxP, sph3Δuge3Δ :: adeA</i>	This study
<i>sph3Δuge3Δ</i>	<i>ligDΔ :: sC, adeAΔ :: ptrA, adeA⁺, niaD⁻, sph3Δuge3Δ :: loxP</i>	This study
NS4 O/E <i>cutL1</i>	<i>ligDΔ :: sC, adeAΔ :: ptrA, adeA⁻, PglA142-cutL1-TagdA :: niaD</i>	Miyazawa <i>et al</i> (2016) Biosci. Biotechnol. Biochem. 80, 1853-1863.
<i>agsAΔagsBΔagsCΔ</i> O/E <i>cutL1</i>	<i>ligDΔ :: sC, adeAΔ :: ptrA, adeA⁺, agsA :: loxP, agsB :: loxP, agsC :: loxP, PglA142-cutL1-TagdA :: niaD</i>	Miyazawa <i>et al</i> (2016) Biosci. Biotechnol. Biochem. 80, 1853-1863.
<i>agsAΔagsBΔagsCΔ sph3Δuge3Δ</i> O/E <i>cutL1</i>	<i>ligDΔ :: sC, adeAΔ :: ptrA, agsA :: loxP, agsB :: loxP, agsC :: loxP, sph3Δuge3Δ :: adeA, PglA142-cutL1-TagdA :: niaD</i>	This study

Medium

[0045] In this study, Czapek-Dox (CD) medium was used as a selection minimal medium for *A. oryzae*. In addition, YPD medium was used as a nutrient-rich medium. Herein, CD medium having added thereto 70 mM sodium glutamate in place of sodium nitrate as a nitrogen source was used in the culture of a *niaD⁻* strain (this medium is hereinafter referred to as CDE medium). In addition, in the culture of an *adeA⁻* strain, adenine sulfate was added at a final concentration of 0.01% (this medium is hereinafter referred to as CDEA medium). The compositions of media and culture solutions are as shown in Table 2. In the case of using a medium as an agar plate medium, agar was added to the medium at a final concentration of 1.5% (w/v).

[0046]

Table 2

Compositions of media used in this study

For plate culture, 1.5% agar added			
<i>A. oryzae</i>			
Czapek-Dox (CD) medium (/liter)			
10×stock solution	100 ml		
1000×trace elements solution	1 ml		
1 M MgSO ₄	2 ml		
Glucose	20 g		
10× stock solution (/liter)		1000×trace elements solution (/liter)	
NaNO ₃	60 g	FeSO ₄ ·7H ₂ O	1.0 g
KCl	5.2 g	ZnSO ₄ ·7H ₂ O	8.8 g
KH ₂ PO ₄	15.2 g	CuSO ₄ ·5H ₂ O	0.4 g
Adjust to pH6.5 with 10N KOH		MnSO ₄ ·4H ₂ O	0.15 g
		Na ₂ B ₄ O ₇ ·10H ₂ O	0.1 g
		(NH ₄) ₆ Mo ₇ O ₂₄ ·4H ₂ O	0.05 g
10× stock solution (Glutamate) (/liter)			
C ₁₂ H ₂₁ NNaO ₆	130.9 g		
KCl	5.2 g		
KH ₂ PO ₄	15.2 g		
Adjust to pH6.5 with 10N KOH			
YPD medium (/liter)			
Peptone	20 g		
Yeast extract	10 g		
Glucose	20 g		
YPM medium (/liter)			
Peptone	20 g		
Yeast extract	10 g		
Maltose	20 g		

Culture

[0047] In this study, the culture of *A. oryzae* was performed at 30°C, unless otherwise stated. In the case of agar plate culture, a plate was left to stand still, and in the case of liquid culture, rotary shaking culture was performed at 120 rpm.

Spore Suspension

[0048] Conidia of *A. oryzae* were inoculated into agar plate medium of CD medium satisfying the auxotrophy of each kind of mutant strain, and were cultured at 30°C for about 7 days until conidia were sufficiently formed. Further, the conidia were subcultured in malt medium at 30°C for about 4 days until conidia were sufficiently formed. 10 mL per plate of a sterilized conidial suspended solution (150 mM NaCl, 0.1% Tween 20, 10 mM phosphate buffer (pH 7.2)) was poured on agar plate medium, and the conidia were scraped with a cell spreader to be suspended. For the purpose of removing hyphae mixed in the suspension, the suspension was filtered using a sterilized cell strainer (pore size: 70 µm) or sterilized MIRACLOTH (Calbiochem), and only the conidia were collected in a Falcon tube having a volume of 50 mL or a volume of 15 mL to prepare a conidial suspension. The number of the conidia was measured using a Thoma hemocytometer.

Production of uge3/sph3 Gene Disruption Cassette

[0049] The *uge3* and *sph3* genes of *A. oryzae* are adjacent to each other. Therefore, a disruption cassette for disrupting both the genes at once was produced. First, a *uge3* downstream (5' side) region (amplicon 1) and an *sph3* downstream (3' side) region (amplicon 2) were amplified by PCR using genomic DNA of *A. oryzae* as a template. In addition, *AnadeA* gene (amplicon 3) was amplified from plasmid TOPO-2.1-*adeA* by PCR (1st round of PCR). PCR amplification was performed using: primers Sph3+Uge3-LU and Sph3+Uge3-LL+Ade for amplicon 1; primers Sph3+Uge3-RU+Ade and Sph3+Uge3-RL for amplicon 2; and primers Sph3+Uge3-AU and Sph3+Uge3-AL for amplicon 3 (Table 3). The primers Sph3+Uge3-LL+Ade, Sph3+Uge3-AU, Sph3+Uge3-RU+Ade, and Sph3+Uge3-AL each contain, on the 5' side, a homologous sequence to a complementary strand, for linking by fusion PCR. The PCR product was gel-extracted, and subjected to PCR using the primers Sph3+Uge3-LU and Sph3+Uge3-RL to link those three fragments (2nd round of PCR). A main band of the PCR product was gel-extracted, and used as a *uge3/sph3* gene disruption cassette.

Table 3

Sequences of PCR primers used for production of <i>uge3/sph3</i> gene				
Name	Sequence 5' -3'	Direction	nt	Gene
Sph3+Uge3-LU	TCTCCATAGTGTTACCA	Forward	18	<i>uge3</i>
Sph3+Uge3-LL+Ade	ATATACCGTGACTTTTTAGCACAAATTGGAGCTACT	Reverse	37	<i>uge3</i>
Sph3+Uge3-RU+Ade	AGTTTCGTGAGATACTGCGCGTTGTCATATTTGCAAG	Forward	38	<i>sph3</i>
Sph3+Uge3-RL	AGGGCTCAGAATACGTATC	Reverse	19	<i>sph3</i>
Sph3+Uge3-AU	AGTAGCTCCAATGTTGTGCTAAAAAGTCACGGTATATCATGAC	Forward	43	<i>AnadeA</i>
Sph3+Uge3-	TTGCAATATGACAACGCGCAGTATCTCGACGAACTACCTAA	Reverse	43	<i>AnadeA</i>

Sequences of PCR primers used for production of uge3/sph3 gene				
Name	Sequence 5' -3'	Direction	nt	Gene
AL				

Transformation of *A. oryzae* by Protoplast-PEG Method

[0050] Transformation of *A. oryzae* was performed using a protoplast-PEG method (Non-patent Literature 8). The wild-type strain and the AG-deficient strain (agsAΔagsBΔagsCΔ) were each used as a host strain. 2×10^8 conidia of the host strain were inoculated into 200 mL of YPD liquid medium in an Erlenmeyer flask having a volume of 500 mL, and were subjected to rotary shaking culture at 30°C for 20 hours. The cells were filtered through sterilized MIRACLOTH (Calbiochem) to collect the cells. The cells were washed with distilled water, and the cells were dehydrated by being pressed with a sterilized spatula. The collected cells were placed in a Falcon tube having a volume of 50 mL, and suspended by adding 25 mL of a protoplast forming solution [10 mg/mL Lysing Enzymes (Sigma), 5 mg/mL Cellulase Onozuka (Yakult Pharmaceutical Ind. Co., Ltd), 2.5 mg/mL Yatalase (TaKaRa), Lysing enzyme buffer (Table 4)] that had been filtered through a filter DISMIC-25CS (ADVANTEC) having a pore size of 0.20 μm. The suspension was shaken at 30°C and 83 rpm for 3 hours to digest cell walls, to thereby prepare protoplasts. After the reaction, undigested cells were filtered through sterilized MIRACLOTH, and the filtrate was centrifuged at 4°C and 2,000×g for 5 minutes to collect the protoplasts. The collected protoplasts were washed with 0.8 M NaCl, and centrifuged at 4°C and 2,000×g for 5 minutes to precipitate and collect the protoplasts. The protoplasts were added to Sol. I (Table 4) at 2×10^8 protoplasts/mL and suspended therein. After that, a 1/5 amount of Sol. II (Table 4) was added, and the contents were mixed well. 240 μL of the protoplast liquid was dispensed in a Falcon tube having a volume of 15 mL, a DNA solution was added in an appropriate amount (from about 1 μg to about 10 μg), and the contents were mixed well and left to stand in ice for 25 minutes. Next, 1 mL of Sol. II (Table 4) was added, and the contents were mixed well and then left to stand at room temperature for 20 minutes. 10 mL of Sol. I was added, and the contents were mixed well and then centrifuged at room temperature and 2,000×g for 5 minutes. The supernatant was removed, and 300 μL of Sol. I was added. The protoplasts were homogeneously suspended, and seeded into CD selection medium (Table 2) containing 0.8 M NaCl. After that, 5 mL of soft agar medium of the same composition [0.6% (w/v) Agar] that had been warmed to 55°C was poured from the periphery and overlaid so as to quickly and homogeneously suspend the protoplasts. After that, the protoplasts were cultured at 30°C until colonies were formed.

Table 4

Buffers used in genetic experiment in this study		
Buffer		
TE buffer		
	10 mM	Tris-HCl
	1mM	EDTA
50×TAE buffer		
	2 M	Tris base
	0.1M	EDTA
Adjustto pH8.0 with glacial acetatic acid		
Spore suspension buffer		
	150 mM	NaCl
	0.1%	Tween20
	10 mM	Phosphate buffer(pH7.2)
For fungal transformation		
Lysing enzyme buffer		
	0.8 M	NaCl
	10 mM	Sodium phosphate buffer (pH 6.0)

For fungal transformation		
Lysing enzyme buffer		
Sol. I		
	0.8 M	NaCl
	10 mM	CaCl ₂
	10 mM	Tris-HCl (pH 8.0)
Sol. II		
	40%	PEG 4000
	50mM	CaCl ₂
	50mM	Tris-HCl (pH 8.0)

Selection of Transformed Strain Candidate

[0051] In order to confirm whether the genomic DNA of the resulting transformed strain candidate had been transformed as intended, the genomic DNA was simply extracted from the conidia of the strain, and the transformed strain was selected by PCR using designed primers. 500 µL of YPD liquid medium was taken in a 1.5 mL Eppendorf tube, and the conidia of the transformed strain candidate were poked with a sterilized toothpick and inoculated, followed by culture at 30°C until cells were grown. After centrifugation, the medium was removed. Glass beads in an amount equal to that of the cells and 150 µL of Nuclei Lysis Sol. (Promega) were added, and the cells were pulverized with Micro Smash™ MS-100R (TOMY) at 4,500 rpm for 2 minutes. The resultant was left to stand at 65°C for 15 minutes, 100 µL of Protein Prep. Sol. (Promega) was added, and the contents were mixed well. The mixture was left to stand at room temperature for 5 minutes and centrifuged at 4°C and 15,000 rpm for 5 minutes, and then the supernatant was transferred to another 1.5 mL tube. A 1/10 amount of 3 M sodium acetate and a 2.5-fold amount of ethanol were added, and the contents were mixed. After centrifugation at 4°C and 15,000 rpm for 20 minutes, the pellets were washed with 1 mL of 70% ethanol and dissolved in 50 µL of RNase-containing TE. The resulting solution was defined as a genomic DNA solution, and stored at 4°C until being used as a template for PCR.

Nucleus Purification

[0052] The transformed strain candidate of interest was grown on minimum agar plate medium, and the collected conidial suspension was passed through a mononucleation filter (ISOPORE™ MEMBRANE FILTERS, 5.0 µm TMTP, Millipore) that had been sterilized by autoclave treatment in advance, to thereby collect mononucleate conidia. The conidial suspension subjected to the mononucleation treatment was appropriately diluted, and grown on minimum agar plate medium. The resulting strain candidate was confirmed again by PCR. Thus, the transformed strain of interest was purified.

Liquid Shaking Culture in YPD Medium

[0053] The wild-type strain, the AG-deficient strain, or the AG-GAG-deficient strain was used and subjected to liquid shaking culture in YPD medium for 24 hours. The temperature was set to 30°C, the number of revolutions was set to 120 rpm, the scale of the medium was set to a 50 mL/200 mL Erlenmeyer flask (without baffles), and conidia were inoculated at 1×10^5 conidia/mL.

Polybutylene Succinate-co-adipate (PBSA) Decomposition Ability Test with Strain Highly Expressing cutL1

[0054] The produced AG-GAG-deficient strain highly expressing cutL1 was subjected to a PBSA decomposition ability test in order to confirm the introduction of the plasmid for highly expressing cutL1. CDE (2% maltose) medium containing 1% PBSA was used for the test. Conidia were inoculated at the center of the medium and subjected to static culture at 30°C for 4 days, and formed halos were observed. As controls, a wild-type strain highly expressing cutL1 and an AG-GAG-deficient strain not highly expressing cutL1 were used.

Quantification of CutL1 Secretion Amount

[0055] Proteins in 100 µL of the culture supernatant were purified by TCA precipitation, appropriately diluted, and subjected to SDS-PAGE (buffer compositions were as shown in Table 5). As a standard, 0.4 µg to 2 µg of purified α-amylase (derived from *A. oryzae*, Sigma-Aldrich) or 0.2 ng to 1 ng of purified CutL1 quantified by a BCA method was used. An image of a gel detected by SDS-PAGE was taken into ImageJ, and a band of interest was converted into a pixel value. A calibration curve was prepared from the standard to quantify an endogenous amylase or CutL1 secretion amount.

Table 5

Buffers used in SDS-PAGE		
SDS-PAGE Sample buffer		
	Tris-HCl (pH 8.8)	0.12 M
	Glycerol	10% (v/v)
	SDS	5% (w/v)
	2-mercaptoethanol	5% (v/v)
	Bromophenol blue	0.05% (w/v)
SDS-PAGE running buffer		
	Tris base	50 mM
	Glycine	384 mM
	SDS	0.10%

Liquid Shaking Culture in YPM Medium

[0056] The wild-type strain highly expressing cutL1, the AG-deficient strain highly expressing cutL1, or the AG-GAG-deficient strain highly expressing cutL1 was used and subjected to liquid shaking culture in YPM medium (Table 2) for 24 hours. The temperature was set to 30°C, the number of revolutions was set to 100 rpm, the scale of the medium was set to a 50 mL/200 mL Erlenmeyer flask, and conidia were inoculated at 1×10^4 conidia/mL.

Experimental Results

Estimation of GAG Biosynthetic Gene Cluster in *A. oryzae*

[0057] On the basis of five gene cluster sequences considered to be responsible for GAG biosynthesis in *A. fumigatus*, a database (AspGD) was searched as to whether or not the same gene cluster was also present in *A. oryzae*. As a result, it was suggested that the cluster gene sequences were also present in *A. oryzae*, and the ORFs of gtb3 (AOR_1_2580174), agd3 (AOR_1_2582174), ega3 (AOR_1_2584174), sph3 (AOR_1_2586174), and uge3 (AOR_1_2588174) were GAG biosynthetic genes in *A. oryzae* (Fig. 1A).

Production of Strain Deficient Only in GAG and AG-GAG-deficient Strain (Figs. 2)

[0058] The wild-type strain and the AG-deficient strain were each used as a parental strain, and the *uge3/sph3* gene disruption cassette was introduced into the genome thereof by a protoplast-PEG method. The selection of transformants was performed with *adeA*-free CDE agar plate medium. The resulting transformants were subjected to nucleus purification, and confirmed by PCR amplification using primers *Sph3+Uge3-LU* and *Sph3+Uge3-RL*.

Culture Properties of Strain Deficient Only in GAG and AG-GAG-deficient Strain (Figs. 3)

[0059] The strain deficient only in GAG formed a large hyphal aggregate as compared to the wild-type strain. In addition, the hyphae aggregated to form a hyphal aggregate in each of the wild-type strain and the AG-deficient strain, whereas the AG-GAG-deficient strain did not show aggregation of hyphae and was observed to be in a state in which the hyphae were completely dispersed in liquid medium. Hitherto, a mutant strain of *A. oryzae* showing culture properties of being completely dispersed as described above has not been known. In addition, on agar plate medium, the AG-GAG-deficient strain showed growth comparable to that of the wild-type strain.

Acquisition of Strain Highly Expressing cutL1 for AG-GAG-deficient Strain (Figs. 4)

[0060] The AG-GAG-deficient strain was used as a host strain and transformed with pNGA-gla-cut (Takahashi et al., 2005), a plasmid for highly expressing cutL1. For the selection of a strain highly expressing cutL1, CD medium containing 0.8 M NaCl was used, and a transformed strain candidate showing nitric acid autotrophy was acquired. The resulting transformant was subjected to nucleus purification, and confirmed by PCR amplification using primers *niaD-tail-Fw* and *cutL1-RT-F*.

[0061] Further, a halo formation test was performed using CDE (2% maltose) medium containing 1% PBSA. As a result, in the AG-GAG-deficient strain highly expressing cutL1, halo formation comparable to that of the wild-type strain highly expressing cutL1 used as a control was observed. This suggested that the plasmid for highly expressing cutL1 had been properly introduced.

Evaluation of CutL1 Productivity of AG-GAG-deficient Strain

[0062] As a result of culture in YPM medium, the dry cell weight at 24 hours of culture had increased in the order of the wild-type strain, the AG-deficient strain, and the AG-GAG-deficient strain. In particular, the dry cell weight of the AG-GAG-deficient strain had significantly increased to be about 10 times that of the wild-type strain (Fig. 5A). In addition, the CutL1 production amount had also increased in the order of the wild-type strain, the AG-deficient strain, and the AG-GAG-deficient strain, and the CutL1 production amounts of the AG-deficient strain and the AG-GAG-deficient strain had significantly increased to be about 2.5 times that of the wild-type strain and about 5 times that of the wild-type strain, respectively (Fig. 5B). The results suggested that the AG-GAG-deficient strain showing complete dispersibility had properties suitable for high production of a substance in high-density culture.

CR Sensitivity Test on AGΔ and AG-GAGΔ Strains

[0063] 2 μL of a conidial suspension of the WT strain, the AGΔ strain, or the AG-GAGΔ strain prepared at 5×10^3 /μL was spotted (a total of 1×10^4 conidia/plate) at the center of CD agar medium containing Congo red (CR) at 0 ug/mL, 10 ug/mL, 20 ug/mL, 40 ug/mL, 80 ug/mL, or 120 ug/mL, and incubated at 30°C for 3 days. A colony diameter after the 3 days was measured, and a growth rate on CR-containing medium was calculated with reference to a colony diameter in the case of no CR (Figs. 88). The results were as follows: the AG-GAGΔ strain had lower growth rates than the wild-type strain and the AGΔ strain at all concentrations. This suggested that not only AG but also GAG was associated with CR sensitivity.

Analysis of Cell Wall Constituent Saccharides of *Aspergillus* AG-GAGΔ Strain

[0064] The cell wall components of the wild-type (WT) strain, AGΔ strain, AG-GAGΔ strain, and GAGΔ strain of an *Aspergillus* were analyzed by fractionating the polysaccharide components of cells through the use of a hot water/alkali extraction method, and quantifying monosaccharide components contained in a sulfuric acid hydrolysate of each fraction. First, conidia of each strain were inoculated into 200 mL of YPD medium (2% peptone, 1% yeast extract, 2% glucose) at a final concentration of 1.0×10^5 /mL, and subjected to shaking culture at 30°C and 120 rpm for 24 hours. After the culture, the culture solution was filtered through MIRACLOTH. The resulting cells were washed with water. The cells were lyophilized, and then pulverized with a mixer mill. Next, 1 g of dry cell powder of each strain was fractionated into a hot-water-soluble (HW) fraction, an alkali-soluble/water-soluble (AS1) fraction, an alkali-insoluble (AS2) fraction, and an alkaliinsoluble (AI) fraction in accordance with the method of Yoshimi et al. (Yoshimi et al., PLoS ONE, 2013) (Table 6).

Table 6.

Hot water/alkali extraction				
(%)	HW	AS1	AS2	AI
WT	32.0 ± 2.8	7.0 ± 0.6	14.8 ± 0.4	46.2 ± 2.4
AG Δ	35.7 ± 1.4	6.9 ± 0.5	12.1 ± 2.1	45.2 ± 0.8
AG-GAG Δ	35.5 ± 0.4	7.8 ± 0.3	12.0 ± 0.3	44.8 ± 0.7
GAG Δ	36.6 ± 0.5	7.5 ± 0.3	17.6 ± 1.1	38.2 ± 0.7

It is known from the report of Yoshimi et al. that α-1,3-glucan is mainly contained in the AS2 fraction, and β-1,3-glucan and chitin are mainly contained in the AI fraction (Yoshimi et al., PLoS ONE, 2013). 10 mg of each of those four fractions was used and heated in the presence of 2 N H₂SO₄ at 100°C for 12 hours to decompose the polysaccharide components in the fraction into monosaccharides. Each of the hydrolyzed fractions was neutralized with barium carbonate, and centrifuged to provide a supernatant. The monosaccharide components contained in the hydrolysate of each fraction were separated using an anion-exchange column Carbo PAC PA-1 (4×250 mm, DIONEX) and a guard column Carbo PAC under the conditions of a flow rate of 1 mL/min, a column temperature of 35°C, a compartment temperature of 20°C, and an eluent of 18 mM NaOH, and were detected using a pulsed amperometric detector. The monosaccharide components were quantified using 1 ug/mL to 100 ug/mL galactosamine, glucosamine, galactose, glucose, and mannose as standards. In addition, 10 ug/mL fucose was used as an internal standard. As a result, no significant difference was found among the monosaccharide components of the HW, AS1, and AI fractions of each strain (Figs. 89). In contrast, in the AS2 fraction, the AGΔ strain and the AG-GAGΔ strain were remarkably reduced in glucose amount as compared to the wild-type strain (Figs. 89). This suggested that the cell walls of the AGΔ strain and the AG-GAGΔ strain hardly contained α-1,3-glucan.

[0065] In addition, 50 μg of the HW fraction of each strain was subjected to sulfuric acid hydrolysis and monosaccharide component analysis by the same methods as described above. The results were as follows: the wild-type strain and the AGΔ strain contained 0.25 mg and 0.60 mg of galactosamine per 1 g of grown cells, respectively, whereas no galactosamine was detected in the AG-GAGΔ strain (Fig. 90). No previous study has reported a polysaccharide containing galactosamine other than GAG in the cell wall of a filamentous fungus of the genus *Aspergillus*. This revealed that the cell wall of the AG-GAGΔ strain contained no GAG.

Example 2

Generation and Culture Properties of GAG Disruption Strain in *Cochliobolus heterostrophus*

[0066] *Cochliobolus heterostrophus* (anamorph: *Bipolaris maydis*) has in its genome a gene cluster homologous to the galactosaminogalactan biosynthetic gene cluster (sequence information, Fig. 1A). This cluster includes five genes, and a construct for substituting regions corresponding to sph3 and uge3 out of those genes by hygromycin

resistance gene was produced (Fig. 91A). First, a HIT07711 strain serving as a wild-type strain of *Cochliobolus heterostrophus* was subjected to shaking culture (120 rpm) in complete medium (CM: 1.5 g $\text{Ca}(\text{NO}_3)_2 \cdot 4\text{H}_2\text{O}$, 0.5 g $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.5 g KCl, 0.4 g KH_2PO_4 , 30 mg K_2HPO_4 , 10 g glucose, 1.0 g tryptone, and 1.0 g yeast extract per liter) at 25°C for 36 hours, and the cells were collected by filtration through MIRACLOTH. Next, the cells were treated with a protoplast forming liquid (50 mg/mL lysing enzyme, 5 mg/mL Cellulase onozuka, 2.5 mg/mL Yatalase in 10 mM Na phosphate buffer, pH 6.0) to produce protoplasts. The produced protoplasts were used and transformed by a protoplast-PEG method in accordance with the method of Yoshimi et al. (Yoshimi et al., 2004, Mol. Gen. Genomics 271: 228-236). Genomic DNA was extracted from one gene disruption strain candidate thus obtained, and gene disruption was confirmed by PCR. As a result, bands of about 3.5 kb and about 5.5 kb to be amplified only in the case of successful gene disruption were found (Fig. 91B), and thus the strain was confirmed to be a GAG disruption strain having the regions corresponding to sph3 and uge3 deleted as designed.

[0067] Next, the GAG disruption strain thus obtained was subjected to shaking culture in YPM medium using maltose as a carbon source (2% peptone, 1% yeast extract, 2% maltose) (25°C, 120 rpm, 72 hour), and culture properties were observed. The results were as follows: the wild-type strain grew while forming aggregates of hyphae (Fig. 92A), whereas the hyphae of the GAG disruption strain tended to be dispersed (Fig. 92B). This characteristic is similar to that of the AG-GAG-deficient strain of *A. oryzae*, and hence it is suggested that GAG deficiency provides a culture characteristic suitable for high-density culture also in *C. heterostrophus*.

Example 3

Generation and Culture Properties of AG-GAG Disruption Strain in *Botryotinia fuckeliana*

[0068] *Botryotinia fuckeliana* (anamorph: *Botrytis cinerea*) has in its genome a gene cluster homologous to the galactosaminogalactan biosynthetic gene cluster (sequence information, Fig. 93A). This cluster includes five genes, and a construct for substituting regions corresponding to sph3 and uge3 out of those genes by hygromycin resistance gene was produced (Fig. 93A). First, an AG disruption strain of *Botryotinia fuckeliana* was subjected to shaking culture (120 rpm) in complete medium (CM: 1.5 g $\text{Ca}(\text{NO}_3)_2 \cdot 4\text{H}_2\text{O}$, 0.5 g $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.5 g KCl, 0.4 g KH_2PO_4 , 30 mg K_2HPO_4 , 10 g glucose, 1.0 g tryptone, and 1.0 g yeast extract per liter) at 25°C for 36 hours, and the cells were collected by filtration through MIRACLOTH. Next, the cells were treated with the protoplast forming liquid described above to produce protoplasts. The produced protoplasts were used and transformed by a protoplast-PEG method in the same manner. Genomic DNA was extracted from 24 gene disruption strain candidates thus obtained, and gene disruption was confirmed by PCR. As a result, bands of about 3.5 kb and about 5.5 kb to be amplified only in the case of successful gene disruption were found (Fig. 93B) in two strains, and thus these strains were each confirmed to be a GAG disruption strain having the regions corresponding to sph3 and uge3 deleted as designed.

[0069] Next, the GAG disruption strain thus obtained was subjected to shaking culture in YPM medium using maltose as a carbon source (2% peptone, 1% yeast extract, 2% maltose) (25°C, 120 rpm, 72 hour), and culture properties were observed. As described later, when AG expression on the cell surface of the GAG disruption strain of *B. cinerera* was detected with an α -1,3-glucanase-glucan binding domain-GFP fusion under the above-mentioned culture conditions (Fig. 112), it was found that no expression of AG was detected, which was substantially comparable to that of the AG-GAG disruption strain of *A. oryzae*. Accordingly, under the above-mentioned culture conditions, although the GAG disruption strain of *B. cinerera* is deficient only in GAG, whereas the wild-type strain grew while forming aggregates of hyphae (Fig. 94A), the hyphae of the GAG disruption strain of *B. cinerera* tended to be more dispersed than those of the wild-type strain (Fig. 94B). This property is similar to that of the AG-GAG disruption strain of *A. oryzae*, suggesting the possibility that *Botryotinia fuckeliana* can be made suitable for high-density culture merely by GAG disruption.

AGBD-GFP Method and Results

[0070] Cells (WT or AG-GAGΔ of *Aspergillus oryzae*; WT or GAGΔ of *Botrytis cinerea*; or WT or GAGΔ of *Cochliobolus heterostrophus*) were mounted on a slide glass, and fixed by being incubated at 65°C for 15 minutes. The fixed cells were immersed in 10 μL of an AGBD-GFP solution (100 ug/mL in 50 mM potassium phosphate buffer) and incubated at 30°C for 3 hours. AGBD-GFP is a recombinant protein obtained by fusing the α-1,3-glucan-binding site of α-1,3-glucanase and GFP, and can specifically stain α-1,3-glucan (Suyotha et al (2013) Biosci. Biotechnol. Biochem. 77: 639-647.). After the 3 hours of reaction, the cells were washed with 50 mM potassium phosphate buffer 3 times, and observed with a fluorescence microscope. As a result, definite fluorescence derived from α-1,3-glucan was observed in the cells of *A. oryzae* serving as an *Aspergillus*, whereas no fluorescence was observed in the AG-GAGΔ strain (Fig. 112). In addition, also in the case of *B. cinerea*, no fluorescence was observed in each of the wild-type strain and the GAGΔ strain (Fig. 112). Therefore, it was suggested that *B. cinerea*, though having α-1,3-glucan synthase, did not express α-1,3-glucan under the culture conditions in question.

[0071] In addition, as a matter of course, no fluorescence derived from α-1,3-glucan was observed in *C. heterostrophus* having no α-1,3-glucan synthase (Fig. 113).

Industrial Applicability

[0072] According to the present invention, in the method of producing a substance using a filamentous fungus, the production amount of a useful substance can be drastically increased. In addition, a wide variety of useful substances can be produced without any particular limitation by the method of the present invention. Thus, the method of the present invention is extremely useful in industry.

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P a t e n t k r a v

1. Mutant filamentøs svamp, som opfylder begge af de følgende krav (1) og (2):

- 5 (1) den mutante filamentøse svamp mangler mindst ét galactosaminogalactan-biosyntesegen valgt fra gruppen bestående af uge3, sph3, ega3, agd3 og gtb3, således at det mindst ene gen, der er ansvarlig for ekspressionen af galactosaminogalactan, er inaktiveret, og
- 10 (2) den mutante filamentøse svamp mangler mindst ét α -1,3-glucansyntasegen omfattende agsB.

2. Filamentøs svamp ifølge krav 1, hvor den filamentøse svamp tilhører en slægt *Aspergillus*.

- 15 3. Filamentøs svamp ifølge krav 2, hvor den filamentøse svamp er *Aspergillus oryzae*, *Aspergillus sojae*, *Aspergillus nidulans*, *Aspergillus niger* eller *Aspergillus fumigatus*.

- 20 4. Fremgangsmåde til fremstilling af et stof, omfattende trinene: dyrkning af den filamentøse svamp ifølge et hvilket som helst af kravene 1 til 3 for at gøre det muligt for den filamentøse svamp at producere et stof; og opsamling af det resulterende stof.

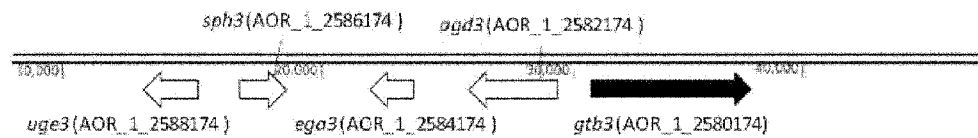
- 25 5. Fremgangsmåde ifølge krav 4, hvor stoffet er et andet stof end en cellevægsbestanddel af den filamentøse svamp eller et hydrolysat deraf.

DRAWINGS

Drawing

Figs. 1

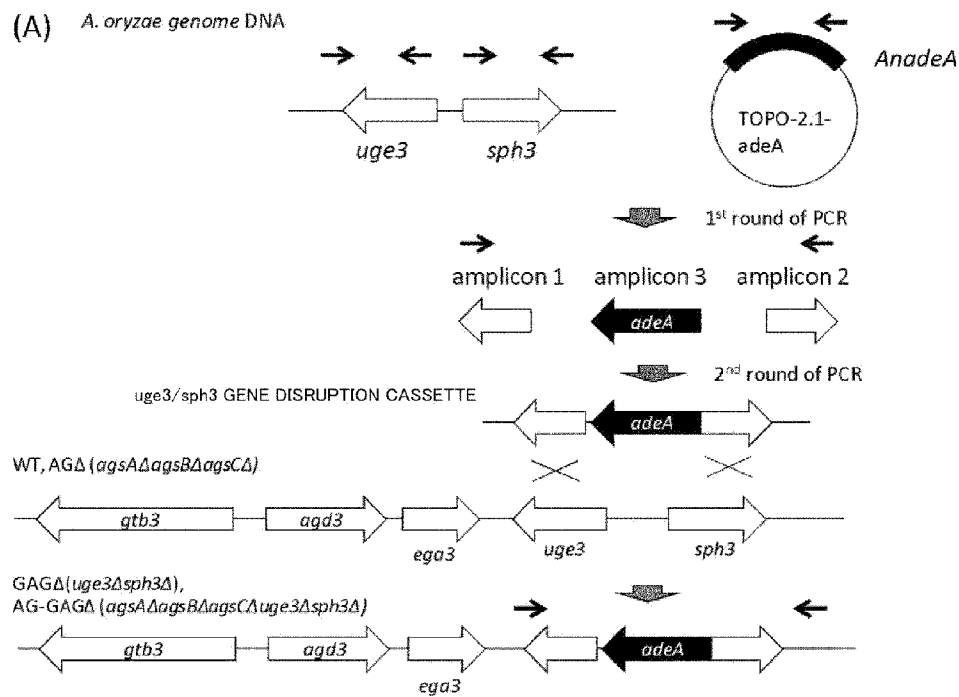
(A)

GAG BIOSYNTHETIC CLUSTER OF *A. fumigatus*GAG BIOSYNTHETIC CLUSTER OF *A. oryzae*

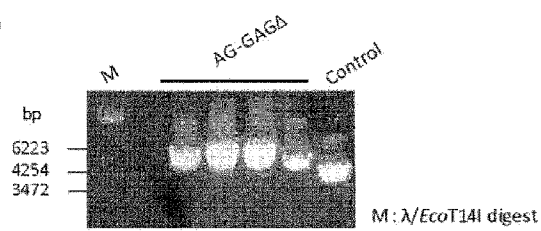
(B)

<i>Sph3_{af}</i>	100%	156 G L F F D E T	194 V H N P G A I	212 T V V F E A
<i>Sph3_{ao}</i>	87%	162 G L F F D E T	200 V H N P G A I	218 T V V F E A
<i>Sph3_{ao}</i>	77%	157 G L F F D E T	185 V H N P G A V	213 T V V L E A
<i>Sph3_{ao}</i>	37%	125 G L F F D E S	163 I H N P G T V	182 T T I F E T
<i>Sph3_{op}</i>	22%	90 G F F I D E M	125 T G N P G T N	145 L V V F E D
<i>Lav8-1</i>	21%	155 G L F F D E A	222 I L N P G T Q	240 I V I F E A

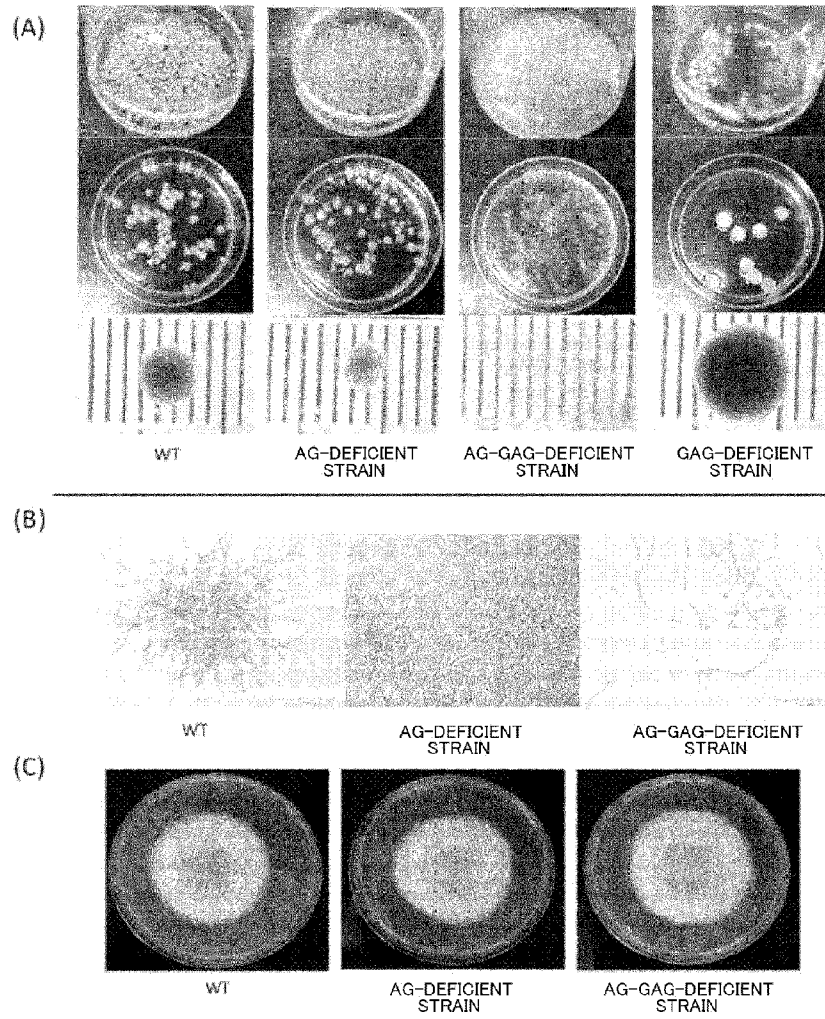
Figs. 2

(A) *A. oryzae* genome DNA

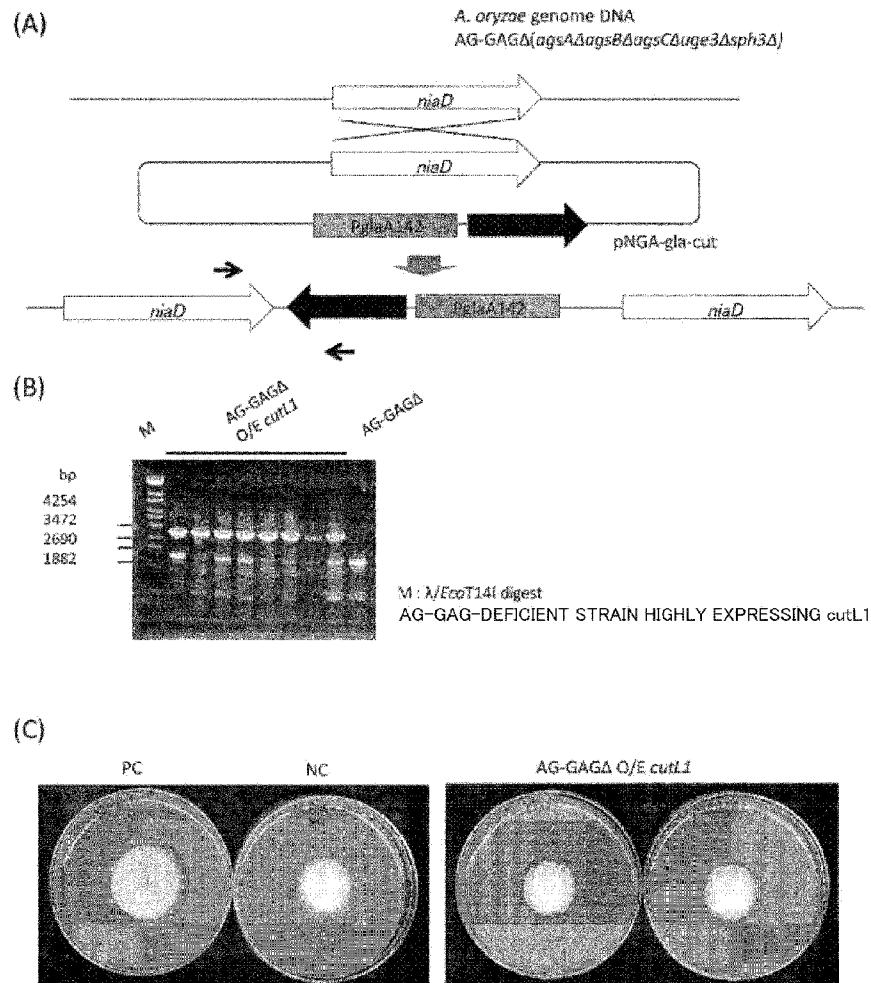
(B)



Figs. 3

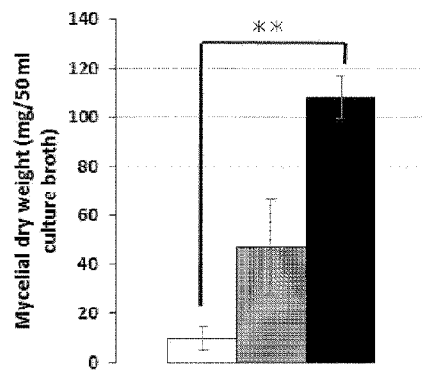


Figs. 4



Figs. 5

(A)



(B)

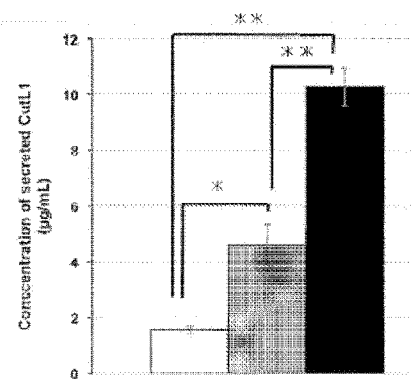


Fig. 6

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus oryzae* AgsA (Genbank accession No. AOR_1_956014)

MKWGFTGPLLALLAATAAGWPYDESLVDYNLVNNDTTNPAEYTHAEWKGEYNPSPKSWRFPFYTLFIDRFVNGDPTND
 NINGSLFEHDLNSNQMRHGGAAGLVDTLDYLGGMGIKGIYLAGTILMNQPWGSDGYSILDITLLDQHYGTIGTWDAIT
 EIHKRGMYVLFNDTIATMGDLIGFEGYLNTPFSVKEHKALWKSQRQYVDFRFDNEYNNNTCEYPRFWNETGYPVQDKDVT
 DELVGCYNSDFDQYGDREAFGVYPDWERQLAKFASVQDRLREWHPSVKERLIRHSCMIKALDIDGFRYDKATQATVDAL
 GDMSHAYRECARSVGKDNFFLPGEITGGNNFGSIYLRGRQPNQYPDSSLASMNLTNTSDHQYFLRDDGLQALDAAAFHY
 SVYRTLTRFLGMDGNLAAGYDTPLDWTDWNIMVLSNDMINANTGKFDPRHMYGTINQDVFRWPAIELGVERQLLGHFIT
 TLHLPGIPILLWGEEQAFYILDSTADNYIYGRQAMSPSTAWKTHGCYSLGSSQYYNWPVSAGREGCHDEAVAYDHRDPSH
 PVHNIKHMFMQRQDFVLNDGYSVVKLSKQTREIQYPGSNGTATEVGVWSVLRDLVSNIQDFGDSGNNPEVWL VYQNDN
 KTYEYSFDCGSNDALISPFITGTIVNLFYPHDEHELDGPKSLHLNGTNATNGCLDTLKLKPFEFRAVVPKANFVKPR
 PMITQFEPGHDVQPLSKVGPDESEDIDVSIYFSTKMDQDQVTKSISFESSTEAGKTPSISNNSVSCDKAQDDPKWTGQI
 PNAWVWTAKLTVYNGIHRITVKNATSSDGHSSQTATDHFLIRVGGQDNPLVFTSANYSTSLNQYDNGTLYIQHRAAGA
 NKYRYSTNFGSSFSDDWKDYHGGNDTIEELPWSGTDKQKWKHVRVEYWNKL TGSSDYAQEGDSGYDHPRRFPHLFFNGP
 FNQYGYDAGLDNVVRQDSGLWKFRMAEFPAQGGFNWGMNPDGQPDQSYVFGDVDDGVLDRMPSSLSSTIINITDI
 PPSPYLAWNLGVDGTLRVHLLPTGSRTIQMVVYFLLWFVPLVTAIACVYAFVKSFYQVKFNQVGVSEKKSILPLAFRRK
 LSRDGSOGSINPFMRLANKSGFLQSTPAFGAVASRRRTTLIATMEYDIEDWAIKIKIGGLGVMAQLMGKHLGGQDLIWVV
 PCVGGVDYPVDQPAEPMFVTVLGNSEYVKVQYHVLNNIKYVLLDAPVFRQQTSEYPARMDDLSAIYSAWNQCIQA
 IRRFPIDLYHINDYHGSIAPLYLLPQTIPVCLSLHNAEFQGLWPMRTQKERDEVCSVFNLDLDTAKRYVQFGEVFNMLHA
 GASYLRVHQGGFAGVGSRKYGKRSYARYPIFWGLKKVGNLPNPDSDTGEWNKELPKDSEIRVDPNYEASRGELKROAQ
 EWAGLDQNPADLLVFVGRWSMQKGVDLIADVMPAVLEARNVQLICVGPVIDLYGKFAALKLDHMMRLYPGRVFSKPEF
 TALPAYIFSGAEFALIPSRDEPFGLVAVEFGRKGALGIGARVGGLGMPGWYNIESTTTSHLLHQFKLAIGSALNSKPQ
 VRAMRARSQKQRFVVAQWVEDLEILQTTAMRIHSGQAQKSNGGPLSPSGYNTPSEVITPSGMMTPTIASTGTTTPTGMQ
 TPPIAHSREGSYTNLSVNRDSAYGPQQRNTIVYSRDPSPGGNDEPRLSLGRQLSLGFRAGPGHINLRGRRLKRRSQMTNE
 ESGTATEESSDDDYFRGEEEVITIREQADEGRHQRNAPRSLASPPNSYFEEGITSGRPPWAQPGNRLSSASVLSVDSVVG
 EKKDYKLQKVPFFIDGTGEYYRMFDQRLEKLNQSNSESQLCIEEYLMKSEKKWFDKFRDARLGRNQSPASSIFQTKGEN
 NTPMSSISHEDLGSNESGSDPRAEKDEFLLGRDYVPPSGLRKWMQIRIFGWVYVSFFLGLGQIIAANSYQITLLAGENGQ
 TAEKLYGIATVYLVTSIIWWFFFRFFKSVFVLSIPWFLYGASFVIIGLAHFESNGSARGWIONVGSVYAAASSSGSLFF
 ALNFGDESQVQKDVVFRACLIGGTQQAYVIGLWYWGTTISSAVANGVTNVNGGIVNSWKMTAICMPIAAFLWAIGLIIF
 FGLPNYYRQSPGKVPsfyKSVFRKIVLWNFVVVILQNFFLSAPYGRNWAFWSSNHAEAWQVIGLVVVFVGVVWVAVLT
 LFGYLSKRHSWILPVFACGLGAPRWAQIWWGVSGMGLFPWAGSSVSGALASRSLWLWLGLDALQGLGFGMILLQTLTR
 VHIAFTLLASQVLGSIATIVARACAPNNIGPGPISPDVTAGGSSVANAWFWIALFFQLICAGFLLFRKEQLTKP

Fig. 7

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus oryzae* agsA (Genbank accession No. ADR_1_956014)

ATGAAGTGGGATCTACTGCCCCCTTGGTTGGCTTGGCTGGCAGCAACAGCAGCAGGCTGGCCCTATGATGAGTCCCTAGT
 CGATTATAACTTGAATGTGAACAAGGATACAGCAATCCGGCTGAATATAGTCACGCAGAAATGGAAGGGCCATAGTATATA
 ATCCCTCTCCAAAAAGCTGGCGATTCCCTTCTATACCCCTGTTTCATTGACCGGTTTGTCAATGGCGATCCTACTAACGAT
 AACATCAACGGGTCACTCTTTGAACATGATCTTAATCAAACCAATGCBTCACGGTGGTGAATGACAGCTGGCTTGGTGBA
 TACACTAGACTACCTACAAAGTATGGGCATAAAGGTTGGTAGCAATGATCTCCGTGTTGTTCTTGTCTTGGTATTGCTTAC
 GGCATATGGCTGACTGACCTCTACAGGGGATCTATTGGCTGGTACTATCTTGGTGAATCAAGCATGGGGTGAAGACGGT
 TACTCGATTGGGATAGTACCGTGGTGGATCAGCATTATGGTGAATCAAACCTGGAGAGACGGGATCACCAGAGATTCA
 TAAGCGGGGATGTATGCTCTCTTTGACAATAGTATCGCAACGTAAAGTGGTGGCCCTCAGCTAAGTGGTTATATCCGAG
 AGCTGACATGAACACAGCATGGGGGATTGGATGGATTTGAAGGTTATTGAAATACACACGGCTTTCTCAGTCAAGGA
 GCACAAAGCATTGTGAAATCTGACCGTCAATGATCTGACCTTCCGTTTGAACAATGATACAAACACACTTCCGAATACC
 CTGATTCTGGAAAGAGCTGGCTATCCGGTGGATAAGGATGTACAGATGAGCTGGTGGATGGTATGAACAGTGGATTTC
 GACCAATAGGTCAGACAGAAAGCTTTGGTGTCTACCGAGACTGGAGGGCCAGTTGGCCAAATTCGGCTCAGTTCAAGGA
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 ATGGCTTCGGCTACGATAAAGCGACGACGGCCACAGTGGATGGCTTGGAGACATGGCCATGGCTATAGAGAGTGTGGT
 CGCAGTGTGGCAAGGATAACTCTCTCTTCCGGAGAAATTAAGTGGTGGAAATAACTTTGGTCTATTTACCTGGACG
 TGGAGAGCAGCGCAACCAATACCGAGACTCTCTCTTGGCTTGGTGAACCTGACGAACACCTCGCATCATCAGTATTCT
 TACGTGATGACGGTCTACAGCGGTAGATTGAGCAGCTTTCCATTATTGGGTGACCGTACCGTCACTCGATTCTAGGT
 ATGGATGGCAATCTGGGTGGGGCTATGACACACCGTTGGACTGGACGGACTCCTGGAAATTTATGGTATTGAGCAACGA
 TATGATCAATGCTAACACTGGCAATTTGACCCCGGCAATATGATGGTACTACAACCAAGGATGTTTTCCGTGGCCCTG
 CCATCGAGCTCGGAGTCGAGAGACAGCTTTGGGTCACTTCATCACAACCTTGCACTCTCCGGGCATCCCAATTTTGGT
 TGGGGAGAGGAACAGGCTCTGATCTGAGACTCTACTGGGATAAATATATCTATGGGGCCCAAGCAATGTCTCCCTC
 CACTGGCTGGAAACACAGGATGTTATTCCTTGGTGGTCCCAATACTACAACCTGGCTGTGATGCAAGTGGGAGG
 GATGTGATGATGAAGCTGTGGCTTATGATCATCGAGATCGGTCTGATGGAGTGCAGAAATGATCAAGATATGTTCCAG
 ATGGCAGAGGACTTCCTGTACTAAATGATGGATCTCAGTTGTCAAAGTGTCAAACAGACTCGTGAGATTCAATACG
 TGGTTCGAATGGCAGGGCAACGGAAAGTGGGGCTGTGGTCACTGGCTGGTGGTCTTGTCTCCAACTTCAAGACTTTGGT
 ACAGCGGCAACAGCAAGCTGTCTGGCTGGTCTATCAAAATGACAACAAGACCGTGGAAATAGCTTTGATTTGGGAGT
 AACGATTGGGCTTGAATTTCCCGATTACTACGGGAACACTGTTGTTAATCTCTTCTACCGCACAGATGAACACGAGCT
 TAAAGATGGCGCCCAATCACTTCACTGAAACGGCACCATGCAACAACGGTTGTGGATAGTTTGAAGTTGAAGCCCT
 TCGAGTTCAAGGCTTACGTTCGAAAGGCTAACTTTGTTAAGCTCGTCCGATGATCAGCCAGTTGGAGGCTGGTCAAGAT
 GTGCCGCAAGTGTCTAAAGTGGAGCTGACGAATCAGAAATATGAGCTGAGCATTTACTTTCCACCAAGATGGATTG
 TGATCAGGTTACGAATTCATTTCAATCGAATCGAGTACGAAAGCTGGCAAGACTCCCTCTATCAGTAAACAGTGTCA
 GGTGGAAAGATGCCAGGGTGGATGATCGAAGTGGACTGGTCAATTCGCAAGCGCTGGGTCTGGACAGGGAAGTTGACT
 GGGCTTTACAACGGTATCCATCGCTTGACCGTCAAAAAATGCCACTAGCTGGATGGCATAGTTCTACCCAGGCAACTGA
 TCAGTCTTTGATCGAGTGGGGCAAGGGATAATCGGTTGGTGTTCAGATCTGCGAAGTACTCGAGCTCCTTGTAAAGC
 AGTATGACAATGGCAGCTCTACATCCAACATCGTGGCAGGTGGCAACAAATACCGCTATTCAACAAAGTTTGGTTCG
 TCATTTCTGACTGGAAAGACTACCGGAGGGAAAGGATCTATTGAAGAACTGGCTGGAGTGGAAAGGACGACAAAGAA
 GTGGCAAGGGAAGCAGTGGAGTGGAACTAGTGAATAGTTAACGGGACGAGTGAATAGCTCAGGAAAGGCACTCTG
 GATATGACCATCCAAGAGGCTTTCCGATCTTTCTTCAACGGGCAATCAACCAATGGATATGATGGGGCTTGGAG
 AACGTTGTGAGGCAAGACAGTGGTCTTTGGAAAGTTCAGATTCAATGGCTGAGTTTCCAGCACAAGGACAGTTCAATGT
 TTGGGGAATGAATCCAGATGGTCAACGACGACGAGCTAGTGTGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 TGGCTCCTTCTTGGCTTATGTTCCAGGATAAATAACATCAGGATATCCCTCCATCTCCATACTTGGCTGGAACTTGGT
 GTTGAAGATGGAACTCTGGGTGTTCTATCTTGGCAACGGGTTCAAGGACCATGCAAAATGGTTGTGATCTTCTGCTG
 GTTGTGTTCCCTTGTCAAGGCAATCGCTTGTGTCTATGGCTTGGTGAATCCTTCTACCAAGTCAAGTTCAACCAAGTGG
 GGGTCAAGGCAAGAAATCAATCTTCCATGGCATTCGAAAGGAACTGAGGCTGATGGAAAGGGGATCAATCAAT
 CCTTTGATGGGCTTGGCAATAAGTGGGATTCTTGAAGGACACAGCTGTTTTGGAGCAGTGGCTTCAAGAGACGGAC
 GACCTTGAATGGCAGCATGGAATATGATATTGAGGACTGGGCAATCAAGATTAATAATCGGTGGTGGTGGTGGTGGT
 AGTTGATGGGCAAGACCTTGGGACGAGGATGTAATTTGGGTTGTTCCATGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 CAGGCAAGCTGAGCTATGTTTGTGACAGTGGTGGGAAATTCCTAGGAAGTCAAGGTCAGTATCAGCTCTGATTAATAT

Fig. 8

TAAATATGTCCTTTTATGATGCTCCTGTTTTTCGTCAACAGACCAATCTGAGCCTTATCCGCGCCGAATGGACGATTTGG
 ACAGCGCAATCTACTATTCCGCTTGGAACCAAGTCGATTCGACAAGCAATCAGACGTTTCCCAATTGATCTTTATCATATT
 AACGACTAGCATGGATCCATTGGCCCTCTTTATCTTACCTCAAAACCATGCCGTGATGTCTGTGCTGCAATGCCAATGCCGA
 GTTCCAAGGACTGTGGCCTATGCGCACCCAGAGGAGAGGGATGAAGTCTGTTCTGTTTTCAACCTTGATCTTGACACTG
 CAAAGCGCTACGTCGAATTTGGCGAAGTTTTAACATGCTTCATGCTGGAGCAAGCTACCTACGCGTCATCAACAAGGG
 TTTGGTGCAGTGGCGTTTTCTCGAAAGTACGGTAAACGTTCTTATGCCCGGTACCCAATCTTTGGGGTCTGAAGAAGGT
 TGGAAATGTCACGCAACCGGACCGCTTCAGACACTGGCGAATGGAACAAGGAGTTACCAAAGGACAGCGAGATTGGGGTTG
 ACCCGAAGCTACGAGGCTAGCAGAGGAGAGCTTAAGCGCGAGGGCAGGAATGGGCAAGGCTTGATCAAAACCGCTGATGCC
 GACCTGTTGGTGTGTTGTTGGAAAGATGGTCTATGCGAAGGGCGTGGACCTTATTGCTGATGTGATGCCCTGCCGTCTGGA
 AGCAGCTCCCAATGTTCAACTCATCTGTGTTGGTCCAGTCATTGATCTTTATGGTAAATTTGCTGCTTAAAGCTGGATC
 ATATGATGAGGTTATATCTTGGGCGTGTCTTCTCAAAGCCTGAGTTTACTGCACTCCGACGATATATCTTCTCTGGCGCC
 GAATTCGCGCTGATTCCATCTCGTGATGAACCTTTTGGTCTTGTGCTGTCGAATTTGGTCGAAAGGGCGCTCTTGGTAT
 TGGTGCTGCTGTTGGTGGTCTGGCCAGATGCCGTGGTGGTATAATATTGAGTCTACAACAACCTTCCCATCTCTTGC
 ATCAATTCAGGCTTGGATTGGAAAGCGCGTTAACTCGAAGCCCAAGTTGCTGCAAGATGCTGACAGCTCCGCAAG
 CAACCGCTTCTGTTGCTCACTGGGTGGAAAGATTGGAAATTCGCGAGCCACTGCTATCGGATTGACAGCAAGGGAG
 GGGAAATCGAAGCGTGGACCTCTCTCGCTTCTGGTTACAAACACCAAGTGAAGTAATAACACCAAGTGGAAATGATGA
 CACCTACGATTGATCCACTGGTACCAAGCCCAACGGGAATGCAAGCCGCTCCAATCCGACACTCACGGGAAGCGAGT
 TACACGAATCTCAGCGCTCAATCGGACAGTGCATACGGGCCCAACAGCGCAACACAATTTGTGACAGCGGTGACCGAAG
 CCTGGAGGTAATGACGAACCTAGGTTAAGCCTTGGTCGGCAACTGTCATTGGATTCAAGGCTGGACCAAGGACATATTA
 ATCTCCGTGCTGCTCGCTTAAAGAAAGAGCCAGATGACCAACGAGGAGGTGGTACAGCGACCAAGAAAGCAGTGAT
 GACGATTATTTCCGCGGAGAGGAAGAGTTACGATTACGAGGGAGCAAGCAGATGAAGGACGTCATCAACGCAATGCTCC
 GAGGTGCGTTGATCTCCTCCCACTCTTACTTTGAAGAAGGCATAACATCCGGAAGGCCACCTTGGGCTCAACCTGGGA
 ATCGACTCAGTATGTCATCGGTTCTTTCTGTTGATTCTGTGCTGGGCAAAAGAAAGACTATAAGCTGCAGAAAGTTGAT
 CCTATTCTCAGACGCTACTGGCGAATACTATCGAATGTTTATCAGAGACTCGAAAGCTCAACGGAATCTAATCTGA
 ATCCCAAGCTTTGTATAGAGGAGTATCTGATGAAGAGCGAAAGAGTGGTTTGACAAGTTGAGAGCGCAAGATTGGGGC
 GCAACCAATCTCCGCTTCTTGGATTTTCCAAACCAAGGGCGAAACACACACCTATGAGCTCAATCTCCACGAGGAT
 CTGGGTTCAAACGAAGTGGCAGCGATCCACGCGCAGAAAGGATGAGTTCTTCTGGACGAGACTATGTTCCCCCTC
 GGGCTTAAGGAAATGGATGCAATTCGAATCTTTGGCTGGCTGTGATTCTGTTTTCTAGGCTCGGTCAGATCATTG
 CGGCCAATCATACCAATTAACCTTCTTGGCGGTGAAACGGCCAGACAGCTGAGAAGCTCTATGATTGCGACAGTA
 TACCTTGTCACTTCAATCATCTGGTGGTTTTCTTCCGCTTCTCAAATCGGTGTTTGTCTTTCCATACCTTGGTCTT
 ATACGGCGCATGTTTGTATCTGATTGATGACACACTTTGAGTCAAAATGGCTCCGCTCGTGATGATCCAGAATGTGG
 GAAGCGGTGTTTACGCTGCTGCTTCTCAAGCGGATCACTGTTCTTGGCTCTCAATTTTGGCATGAAAGCGGTGTTGAG
 GTTAAAGACTGGGTTTTCCGGGATGCTCATCCAAGGAACCGCAAGCATATGTTATTGAGCTGTGGTACTGGGGAAC
 GACAATCTCTAGCGCTGTCCCAATGGAGTTACCAACGTCAACGGCGGCTTGTCAACTCCTGGAAATGACGATATGTTT
 CACCTTTATCACTATGATTACAATTGCTAACGGCTCTTCTAGCGCAATCTGCATGCCAATGCTGCTCATTCTCTGGGCC
 ATTGGTCTGATAATCTCTTCCGGCTGCCCAATTACTACGCGCAGTCACCTGGAAAAGTCCATCATTTCTACAAGTCTGT
 CTTCCGGCGCAAGATGCTGCTGGAAGTCTGGTGGTATTTGCAAAATTTCTTCTCGCGGACCTTATGAGCGAA
 ACTGGGCTGTAAAGTACATCAGACCTATACCTCCAAAGAGCCACTAATTATGCTGCTCATACAGTCTTTGGAGCTC
 AAACCATGCCGAAGCTGGCAAGTGGCATCCTGCTGCTGCTCTTCTGCTGCTATCTGGGTAGCAGTGTAAACCTAT
 TTGGATATCTCTCGAAGCGCATAGCTGATTCTACCTGTATTTGATGCGGTTTGGGAGCTCCACGTTGGGCCAGATA
 TGGTGGGTGCTCCGGAATGGGTCTCTTCTTCCCTGGCTGGCAGTTCTGTTAGCGGAGCACTGCGATCACGAAGTCT
 ATGGCTCTGGCTGCTGATCTTGTATGCTTACAGGGTCTCGGCTTCCGCTGATTTCTTCCAGACCTCACACAGATAC
 ATATAGCTTACCGCTGCTTGCATCTCAAGTGTGGGATCCATCGCGACAATCGTGGCAGAGCATGTGCTCCAAATAAC
 ATCGGTCTTGGCAATCTCGCGGATGTGATGCGGCTGGCAGTTCGTTGCAAAACGCTTGGTTCTGGATCGCTTATT
 CTTCCAGCTCTTGTATCTGTAAGTCACTGATCCGCTACAATCCATTTACAGGCGCAAAATGCTAACAAAGCCCGAGC
 GCGGATTCTCTGTTCTTCCGGAAGAGCAACTACCAAGCCCTAA

Fig. 9

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus oryzae* AgsB (Genbank accession No. AOR_1_2634154)

MKWAFSSAVLALFATTVKAWPYEESLSAYNLNENKSATNPAQYWGEWPDHKGKYFSPDNWRFVYTLFMDRFVNGDPTN
 DNINGTLFEHDISSQMRHGGDVAQLVDTLDYLQGMGIKAIYLAGTILMNQPWGSDGYSALDTLLDQHFQDIATWRNAI
 DEIHKRGMYVIFDNTIATMGDLIGFEGHLNDITPFSVKEHKALWKSNNRYVDFDIGNDYNQTCDYPRFWYEDGYPVQQSM
 TEGLVGCGYDSDFDQYGDIEAFGVFPDWQRQLAKFASVQDRLREWHPSVRERLIRHSCMIYQLDIDGFRYDKATQSTVDA
 LGDMSMAYRECARAVGKENFFISGEITGGNTFGSIYLRGRQPNQYPETAEKAMKMTNESESQYFLREAGHEAIDGAAFH
 YSTYRALTRFLGMDGNLAAGYDVPVDWYDAWNLMQLSNDFINPNTGKFDPRHMFGATNQDVFRWPTVEKGVERQLLGLYI
 TLLLPGLPLLLWGEEQAFYILDATASNYIYGRQAMSPATAWRDHGCFSLDSSQYYQWPIQAGREGCHDPTAAYDHRDPA
 HPVRNIKHKMYQLREDFPVLNDGYSVQKLSNLTTEEYFPGSNGTATETGLWSILRDVNADVQDLGSDAKNQPVWL VYHNT
 NRTIDFKFNCKDNETALISPFATGKVRNLFYPYDEHTLIDGPVKLGLNGSTELNGCLANMTLDAYEFRAYVPSARFTKP
 RPMITQFTPGHDVPVRSTVAPNLDES VKIELYFSEEMDCDSVTKAISISSSTESKKVPTLDEKTVDCGIPASNTSWTGG
 LPSVFMWAANLTGVYNGIHRVTYKNASSTNGNATTNAVDFHFRIGQIDNPMVFTSANYSTSLHEESNGTLFIQHHAAG
 ADKWRYSNTNWGTFSEWKDYTGNDTITELWSGTTKKQRWKHHVRVEYWSKWTGSSDYVQEGDAGVHSNVPRRPFHIF
 NGPYNQYGYDGGLDNVVRQDSKDGWLKYHFTAEPWAQALNIWGMNPDGKPDQSWVLGDADNDSVLD RMPSSSLSATLIN
 ITEHPPKPYLAWNIYINDATMKFQLFPVGHQNTQIAMFVLFWIIPVITGAACVYIFMKSFYKVKFNQIGVSEKATLIPLA
 LRRKFKRNRGGDEERMNPLMRLANKSGFLQNTAIGGAASGKRRMVL IATMEYDIEDWQIKIKIGGLGVMAQLMGKTLGH
 QDLIWWVPCVGGVEYPVDKPAEPMNVTILGNSYEVQVQYHVLNNITYVLLDAPVFRQQSKSEPYPARMDLNSAIYYSAW
 NQCIAEACKRFPIDLYHINDYHGSLAPLYLLPDTVPACLSLHNAEFQGLWPMRTQKEKEEVCSVFNLIDIVRRYVQFGE
 VFNLLHSGASYLRVHQGFAGVGVSKYKRSYARYPIFWGLRKVGNLPNPDPSDVGEWSKEKAIGNADEVHVDPDYEAG
 RADLKRQAQEWAGLDVNPADLMVFVGRWSMQKGVDLIADVMPAVLEARNVQVICVGPVIDLYGKFAALKLDHMMKVYP
 GRVFSRPEFTALPPYIFSGAEFALIPSRDEPFGLVAVEFGRKGALGIGARVGGLGQMPGWWYNVESTATSHLLYQFKLAI
 DAALNSKQETRAMMRARS AKQRFPAQWVEDLEILQTTAIQVHNKELVKHNGRPFTPTGTTTPSGLMTQPASPLGTPGMQ
 TPLAHSRESSYSLNRLSEYVTQPKTSYSRDPSPSGTEKPKSGLQRQLSLGVRSGPGHQSRGRARQRDSIPEHEDTQEA
 HGGAITDVEEESDDDIVNHYADDEYTLTPAQVEEGRRLQAAQQQAGGRRYSQDSLHPRNVQPPSSPGTPPAASQSLLPP
 PRLLDPGSRLSSASVLSLDSVVGKKDFKLQKVDPPFTDSTGEYYKIFDKKLDELNGSNSESQLCIEEYLKSEKEWFDK
 FRDARLGRTKSPTSVYRDKHGASPIGSFYDDNGSRMSGSDGPHSNDSDEDFLLGKDYVPPTGLKKWMQIRIGDWP IYS
 LFLALGQIIAANSYQITLLTGEVGQTAEKLYGIATTYLITSILWWLVFRYFKSVVCLSA PWFLYGI AFIFIGSAHFESNS
 FTRGWIQNVGSGFYAAASSSGSFFALNFGDEGGAPVETWIFRACLIQGIQSAYVIALWYWGSTLSQAQSEGLLTPTNNI
 SNSWKISAI CYP IAAALFGIGLLTFGLPNYYRQTGKVASFYKSVFRRKIVLWNFVAVILQNFFLSAPYGRNWQFLWTS
 HHAHHWQIVILCVFYGFVWAGFLVVSRYFKSHSWFLPVFACGLGAPRWAQIWWGVSGIGYYLPWVTGGYTGGALVSRS
 VWLWLGVLDSIQGLGFGIILLQTLTRMHMLFCLVCSQVLGSIATICARAFAPNNVGPVSPDPTFGGSAVANAWFWVAL
 FCQLLVACAGYILFFRKEQLSKP

Fig. 10

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus oryzae* agsB (Genbank accession No. A0812634154)

ATGAAGTGGGCTTTCTCGAGTGGGCTGCTGGGCTTTTCCACCAACAGTAAAAGCCTGGCTTACGAAGATCTCTCTC
 CGCATACAACTTAAAGCAAAACAAATCGCGACCAAGCCGGCTCAATATTGGGGAGAAATGGCCGGACCAAGGGGAAAT
 ACTTCCCTTCTGCCGACAAATGGCGATTTCCCGTCTATAGTCTGTTTCATGGACCGCTTTGTCAACGGAGACCCCTACGAAC
 GACACATCAATGGAACCTCTTCCAGCAGATATCTCTCGACACAAATCGCGCATGGTGGAGATGTGGCTGGTCTAGT
 GGAATCTTGGATTATCTTCAGGGAAATGGGTATCAAGGTTCTGTCATTGTTTCAAGTTAATTAGGTGGCATGCCATCTGA
 GAATTCCTAGGGCATCTATCTCGCAGGAACCATCTTGTATGAACGAGCATGGGGCTCTGATGGTTATTTCGGCTCTCGATA
 CGACATGCTCGATCAAGATTTGGGTGACATTGGGACATGGCGTAATGCTATGGAAGGATTTCATAAGCGGGGATGTAT
 GTCATCTTCCATAACAGGATTCTACGTAGTCTGCCGATCCACGGTACATATGAGATGATTGTTAACGCTTGTATT
 AGGATGGGTGATCTCATCGGCTTCGAGGGCATCTGAATGATACGACCCGTTTTTCGGTTAAGGAGCATAAAGCACTTTG
 GAAGAGCAATCTGCTATGTGGATTTGATATAGGAACGACTATAACGACATGCGACTACCCCGCTTTCTGGTACG
 AGGACGGTTATCCAGTTCAACAGTCTATGACTGAAGCGCTTGTGGTTGTTATGACAGCGACTTTGATCAATAGTGAT
 ATTGAAGCTTTCGGGTGTTCCCTGATTGGCAACGTGAGTATGCAAAATTCGGCTCGCTCGAAGATCTCTCGGAGAAATG
 GCACCCCTCGGTCGGGAGCGGTTGATTCTGCTATCTGTTATGATTATTACCACTTTGGATATCGACCGTTTCGGTTATG
 ATAGGGCTACTCAAGTCACCGTGGATGCGGTAGGAGATATGTGATGGCTTATCGCGAATGGCGCGTGGCTTGGCAAG
 GAGAAATTTCTCATCTCCGTTGAAATTAAGTGTGTAACACTTTTGGTTCCATCTATTTGGGCCGAGGTADACAGCCGAA
 CGAGTATCTGAGAGCGGGGAGAGGGCATGAAATGACCAAGGAGTGGAGTCCGAACTCTCTGCTGCTGAAAGTGGAC
 ATGAGGGCATCGACGGTGGGGCTTCCACTATTGACATATCTGGCGCTGACTCGGTTCTTGGGTATGGAGGGTAAGTTG
 GCGCGCGGTTACGATGACCTGTGGATTGGTGGATCGGTGGATCTGATGTTGCAAGTCAAGCACTTCTCAACCCCTAA
 CACAGGCAAGTTGATCCCGCCATATGTTGGGGCGACCAACCGAGATGTTTTCCGCTGGCGCAGTGGCAAAAGGGTG
 TGGAAAGCAGTGTGTTGGGCTGTATATCACTACCTTACTTCTTCGGGTATTCCGCTCTCTTGGGGCGAGGACAG
 GCAATCTATATCTTGGATGGCAGGGCATCAACTATATCTATGGCGCTCAAGCAATGTCGCCCGGACTGGGTGGAGAGA
 CCAGGTTGGTTTTGCTTGGATTCTCACAGTATTACAGTGGCTTTCAGGCGGTCGTGGAGGTTGGCATGACCCAA
 CTGGTGGGTAGCATGTGATCGGGCGACCGGGTGGCGAACAATATCAAGCACATGTACAGCTGCCGGGAAGACTTC
 CGTGTCTGAATGATGGTACTCGGTCCAGAAACTCTCGAAGCTGACCGAGGAGGTTCTTATCCGGGTTCCAAAGGTAC
 CGCTACAGAAACGGGTTTGTGGTCTATCTCTACGTGATGTCAATGGCGATGTGAGGAGCTAGGCTCCGACGCGAAGAACT
 AAGCGGTGGGCTGGTCTACGACAAACCAACCGGTACAATTGACTTCAAGTTCAAGTGAAGSACAAGGAGACTGCACTA
 ATCTCGCCCTTCCGACCGGACCAAAAGTTGAAATCTGTTCTATCCCTATGACGAGCACACCTTGATTGATGGCGCGT
 CAAGGTTGGACTGAAGGATCTACGAGCTCAATGGGTGGGTGGCGAAGATGACATTGGAGGGCTATGAGTTGGCGCGT
 ACGTCCCGAGTGAAGCTTTCACTAAGCCTGGTCCAATGATCAAGCAATTCACCTCCGGCCATGACCTCCCTGTTGGCTCC
 ACGGTGGCTCCCAATCTGGATGAAGCGTGAAGATTGAGCTGATTCTCGGAAGAGATGGACTGGCATCTGTGACCAA
 AGCGATTTCCATCAGCTCATCTACGGAATCTAAAAGGTCCCGAGCTGGATGAGAAAGCTGTAGACTGCAAGGGAAATTC
 CAGCAAGCAACACCTCCTGGACTGGGCAAGTTCTTCAAGCTCTTCTATGTGGGCTGCCAACCTGACGGGAGTGTATAACGGC
 ATCCACCGAGTCAAGGTTAAGAACGCTAGCACTAATGGAAGCGGACAAACAGCGGTGGACCACTTCTCTTCCG
 TATCGGACAAATCGATAACCCCATGGTCTTTACATCGCCCAACTATTGCACTAGTTTGTCTCCAGAGGAATCGAAATGGCA
 CCGTATTCTACAGCAGCAGCAGCTGGTGTGATAAGTGGCTTATTCACCAATTTGGGGCCACCACTTTCTCGAGTGG
 AAGGATTACAGAGTGGTAATGACACTATCAGGAGTTAGAAATGGTCTGGAACCAAGAAACAGAGATGGAAGGGACACCA
 TGTGGGGTGGAGTACTGGAGCAATGGAAGGAGGAGGATACGTTGAGGAGGGGATGCTGGAATGATTCGAATG
 TGGCAGCGGGCTTCCCGCATATCTTCTTCAAGCGGCTTACAAATCAGTATGGGATATGACGGTGGTCTTGATAAGGTGGTG
 ACGCAGGACTCCAAAACAGGACTCTGGAAATATCACTTCAAGCGGAGTGGCGGCTCAAGCCGAGCTGAACATCTGGGG
 CATGAATCGGATGGAAGGCTGATCAAAAGCTGGGTGCTGGGTGATGCGGATAATGATTCCGTTCTGGATGGAATGCCAC
 CCTCTCTCTCTGCAACCTTGATTAACATCACCGAGCATCGGCTAAGCCATATCTGGCTTGGAAATATCTACATCAAC
 GATCGGACATGAAGTTCCAGCTCTTCCGTTGGGACACCAAGACGAGATCGCCATGTTCTGCTCTTCTGGATCAT
 CCTGTCTATCAGCGGTGACGATGGTCTACATTTTCATGAAGTCTTTCTATAAGGTCAGGTTCAAGTTCAACCAATCGGTGTGA
 GTGAAAAGCCACATGATCCGTTGGCTTGGGAGAAAGTTCAAGAGGAATCGGTGGTGGATGAGGAAAGGATGAAC
 CCGTTGATGCTGTGGGCAACAGTCCGGTTTCTGCGAGACCAACAGCGCTATTGGCGGCGTGGCTCTGGCAAGCGACG
 CATGGTTCTTATCGCGACAAATGGAGTATGATATGAGGATTGGCAGATTAGATCAAGATTGGTGGTCTTGGTGTCTAG
 CCGAGCTTATGGGGAAGACTCTGGACATGAGGACCTGATCTGGGTTGTTCCCTGTGTGGGGGAGTCAATACCCAGTG
 GATAAACCCGCTGAGCGCATGATGTACGATCTTGGCACTCTTATGAGGTTCAAGTCCAGTACCATGTCTTGAACAA

Fig. 11

ATACCACTACGTTCTACTAGACGCCCGTGTGTTTCGCCGACGAAATCGAAGTCGGAAGCCGTATCCGAGCCGATATGGATGACCT
 TCAACAGTGCTATACAGCTTCTGCTTCTGCTTGGAAATCAGTGTATCGCTGACAGCTGCAAGACCGTTTCCGCGATGACCTGTACCAT
 ATCAACAGATTTACAGGTTCTCTAGCTTCGCTCGCCTCATCTCTTCGCCGATACAGATCCGCGGTGTCTGTTTCCTCTCAACAGCG
 TGAATTTCCAGGCTGTCTGCCCCAATGCTGCATACACAGAAAGAAAGAGGAGGAGTGTGCTCGCTGTTAAACCTAGATATTTGAT
 TTGTCAGACGTTATGTGCAGTTCCGTAAGGTTTTCAAACTGCTGCATCTCAGGTGCTAGTTATCTTGTTGTTTCCAGCAGAG
 GGTTTTCGGTTCGGTTCGGTTGTTCAGAAAGATCGAAGAAAGCGGTCTGTCGCCCGTTATTCCCATCTCTCGGGTTTGAAGAA
 GGTCCG6CAACATTTGCCATACCTGATCTCTCGGATGTGGGAGATTTGGGATTAAGGAAAGAAAGGATTTGGTAACCGCTGCAGGAG
 TCGATGTGGATTCGGGATCTATGAGCGCGGAGGCGACAGCTCTCAAAACGCGAGCTGACGAATAGGGGTGGTTGTGATGACAG
 CCTGACGCTGATCTAATGGTGTTCGTTGGTGGTTGGTCCATGCAAGAAAGGTGCGATTAAATCGCCGATGTGATGCCACG
 TGTCTTGAAGCTCCGCTCAAGGTGCACGTTAAATGTGTGTTGAGCCTGTTATGCTATCTTTATGGTAAATTCGCTGCCCTGCA
 AGTGTGAACCAACATGATGAAGGTTTACCCTGAGCGTGTGTTCTGAGACGCTGAATTTACCGCTGTCTCCGCTTATATCTTCT
 CTGGTGTGTAATTCGCGCTTATTTCTTCTCGTGACGAGCGCTTTGGTCTAGTGCAGTCTGAGTTTCGCGCGTAAAGGAGC
 CTGTGGTATTCGGTTCGGCTGTTCGGTGTCTCGGTGCAGATGAGTGTGGTGTGTTAATGTCGCAATCTGCTGCGATCTCT
 ATCTCTTCTGACCAAGTTCAAGTTGCGCTGCGGCGCAGCTAACTGCTGGAAGCAAGAGACAGAGCAATGATGCTGCTGGCCT
 TCTGCTAAACAGGATTCGCGCTGCCCAATGGTGCAGGACTTGGAAATCTTGCAAAACACCGCAATCCAAAGTACACAA
 CAAAGGAAATTTGCTCAACACCAAGCGGTGCTGCCCTGACCTCCGAGCTGGAAGCAAGCTACTCTGATGGCGTTATAGCTCAACCGTG
 CGAGCCCTCTCGGACCGCCAGGAATGAACAATCCTCTTGCTATTCTAGBGAAGAAGCATGCAATCTGCAACCTCAACCGCTTCA
 AGTGAATACGTTACCCAGCCAAAGACAGCTACAGCAGAGATCCGACCGCTAGGGCAGCGGAAGCCGAAATCAGGACT
 TCAGGCGACAGCTTTCGCTGGTGTTCGCTGTGAGCTTGCTGATCAGAGCGCGTGGTGGTCGGCTCGCGCAGCTGACAGCA
 TCCGACAGCAGCAAGAACACAGGAAGCTCACGGTGGCGCATCTGATGTTGGAGCAAGAAGCATGACGACAGCATTT
 GTCAACCAATACGCGGATGACAGGATATCTCTTACAGCTGCCCAAGTTCGAAGAAGGCCGTGAGTTACAGGCCGCCCAAGCA
 ACAGGCTGGTGTGCGCATGCGGTTGAGTGCAGGTTGGTAGCGCTACAGGCCAGCTGTTGCTCTCGCGAGAAATGTCCGAGT
 CTGCTTCGAGTTCGCGCAACACCGCCAGCGGTTCCGAGAGCTGCTTCTCGCCGCTCGCTGATGCTCGCGAGCTGT
 CTTCAGTACGCAATCCGCTTCTCTCACTTGACTCGGTTGTGGTGAAGCAAGAGCATTTCAAGCTCGCAAAAGBTGATTCGTT
 TCTCACTGTATAGGACCGCGAGATTTACAGAGTATTTGATAGAAGCTTGATGAATCAATGGATCGAATCGGATCGC
 AACTGTGATCGAAGAAATCTGATCAAGAGTGAAGAAAGATGTTGCAGAAAGTTCGTCGACAGCTAGACTTGGTCCGACT
 AAATGCCCAATCCCTCAGTCTATCTGATGAAGCAGCGCGCTTCGCTTCTCGGCTCGTTCTACAGATGATAAGCGCTCCCG
 TATAGTGTGATAGCATGCGCCCTCACTCCAAATGACATGAAGCAGAGAGTTCCTCTCGGAAAGGATATGCTCCCTCCCA
 CAGGCTCTCAAGAGATGATGACAGATTCGATCGGTTGACTGGGCTTCTACTCTGTGTTCTCGCTTTAGGCAAAATCTG
 GTTGGCCAACTCGTACCAGATCGATGCTGCTCAGGCGCAAGTCGCTCAAACTCGCGGAACTGTACGGAATTCGCAACCG
 CATTGTTGATCGAGATTTCTCTGCTGAGTGTGTTTCCGCTGATTTCAAACTCCGCGATCTGTGTGCTGTGCTGATGCTT
 TGTACGATATCGCCTTCATCTCAATGATGCGGCCATTTTGAAGAGCAACTTTTCACTCGGGGATGGAATCAAAAATGTC
 GGTAGTGGGTTCTACCGCGCGGCTCTGCTCATGTGTTCTTTCTCTCCGCTTAACTTCGATGTGAAGTGGTGGCCACC
 TGTGGAAACATGATCTTCGGTGGATGTCTCATTTCAAGGTTTCGACTTCGCGCTTATGTTATGTTGCTCTGTGATCGTGGGTT
 CAACCCCTGTCAAGGACAAAGATGAGGTTGCTTGTGACTCTCAAAAATATCTCCAATTCTGGAGAAATAGGATGAGTT
 ATATTGATTTGTTGTTGTTATTTCACTAGCTAATAATATTCCAGTGCATCTGTATGCCCATTCGCTCGCGCGCCCTTT
 TCGGAATGGTTTGGCTCTTGACATTTGGCCTGCCCAACTATTCCAGTCAAAACCCTGGCAAGTGGCTTCCTCTTCAAAA
 TCCGTTGTTCCGCTGAAGATGCTGCTCTGGAACCTTGTGCGGCTGATCCTTCAGAACTCTTCTCAGCGCCCGCTACGG
 CGCGCAATCGGAGTGTAAGTTGACCCCTGTATAACGGTTTCATCATATCAGACCAAGCAATAGTGTGTTTCTGAGCTGT
 CTGTGBCAATCCCAACGCBGACATGACATGBCAAATGCTCATCTGTGTTGTTTTCATGCGCTTCGATGBCGACAGCT
 CCTATTGCTGTCAGTGCCTACTTCAAATCACACAAGCTGGTTCCTCGCGGTGTTGCGCTGTGCGCTCGAGCTCCGCGCT
 GGGCACAAGATCTGTGTTGGGTTGTGTGTCGATTTGGCTATGCTACTGCTGGGTGACAGAGAGATATACGCGGCGCGCTGT
 GTCTCCGCAAGTGTCTGCGCTGTGGCTGGCGCTGCTGAGCTGATCCGAGGCTGCGGCTGCGGATCTGCTGCTCTGCAAA
 CCGTAGCTGCAATGCACATGCTTTCTGCTGTTGTTTCTGCTCAAGTCTTGGTCTGATGCTGATGCTGATGCTGATGCTG
 TCGGCTGCTGCTGTTTTCAGTTGTTGCTGTGTAAGTTATTACGATCTATGAACATTTGTTATATCAACGATCCCTGAA
 CBTGTGATGATTACAGTGCGGCTTACATCTCTTCTCGGAAAGAACAGCTGTCAAGCGCTTAAGGGCCATGCTTAACT
 GTGTGGTGTGTTGTTGTTAGTACTACCTCGGAATGTATACATGTGCGAGCTCTGTGAGCGTTACTGCTCATCTAATATAAT
 CCTTTGTATATAGATGACCAATACTGAACATATTCAGATC

Fig. 12

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus oryzae* AgsC (Genbank accession No. AOR_1_1350024)

MFLTVMQRSAILILSLLSATALSWPYTESLVDYNLNENKTAEPIDYWGEWPDHEYHPSPDNWRFPITYIFLDRIANGDP
 KNDDINGTAFEHVVGSNQMRHGGDLVGLIDTLDYIRGMGFKGIYFAGTYLMNLPWAYDGYSPVDTTLLDMHHGTLEDWRR
 TITEIHKRDMYVIVDNTLATMSNLIGFKGHLNDSADFRADYEYVQWISDRQYADFKFGNEYNETCNFPKFWNETGYPLTS
 GGVEELKGCYNPDFDQFGELEAFGNFPDWKRQLTKFASVQDRLREWHKPIRDVITKHSCIQIASLDIDGFRFDKAVQTTL
 EPLSEITAVYRECAKKYGKHNFLLPGEITSGNTFGSLYLGRGRQPDQQPESADAGVKLKNSSDGYFLRDDGQALDSAAF
 HYTIYRSMTRFLGMDGNLVAGFDLPTDFIEAWNGLVSNDFLNAYTGEVDPRHMFVSNQDNFRWPAIVNGTEKYLLGLY
 IVTLELPGIPLILWGEEQAMYVFESTASNYLFGROPMTYQTAWWTHGCMTLNTSKFYDFPNEKGLHGCEditvtyDQRNP
 AHPLRNINKRMFEIREQYPVANDGFYQLTSLQTKDYYLPGSTDTPTVTGLWSVLSYFPGVQKEASKNSQNLWLKDTAL
 LSPFKSGTKLKNLFYPYDELTEDEGGEIAVHNSTESYGCIRSMKLLPWEYRAYIEAENFVEPGPTVTEFVPGHDARLLS
 TDDSGQTVDIQLGYSKEMDCDKIADAIISLNSTTVKGVASLDTSSVSCNKISPRTSNDNFVGEVPTVWTSAKLKNVHHG
 IHQLTVKNVSTSGVHTDAVDQFLFRVGSQNNPLLSPLSNYSTSLVQKSDNGSFYIQHDAAGADKFRYSTDFGLNWSNW
 TYTGDNTLVDFPEWTGTDAQKWGTHIRVQYFSRLTGSSDYIQEGDHGWEKGVARRFPNLFWNGPFNQYGYDAGLDNKM
 YDTKDHWRKYDFVYEWPAIGQMSVWGLKDGPRPDVTEVYGDVNDSSVVQKLPPSYLSSNVINITKLPFPFLGWTITLND
 ANLRYEMLPVGSGWAQLVLYILLWVLPILMGFAGIFIFIRTYRVKLNTDGDVAKEDKLPLLFWRVRREKFSGDDESDKS
 ISDKDIPTDIAIAGAPEQRRTVLATMEYNIEDWKVKVIGGLGVMAQLMSQHLKHQNLIWVVPVCGDIEYPQDTPSEPF
 VVTILDKPYFINVQYHIVDNITYVLLDAPVFRQQTAEPPYPRMDDLDSAIYSAWNQCAETIKRFPSIDLYHINDFHG
 CLAPLYLLPTRTIPVGLSLHNAEFQGLWPLRNPQEKKEVCSVFNLPJETATKYSQFGNVFNLLHTGASYVRFYQRFQAV
 GVSCKYGKRWARYPFIWSLEKIGSLPNPDSDTGDMTNNADAEVPIQSYEERINDKLQAQKWAGLNEDRDADLLVFVGR
 WSKQKGVDLIADVMPAILSARPHVQLICVGPVLDLYGRLAATKLERIMEMFPGRVFSKPEFTVLPYVFSGADFALIPSR
 DEPFGLVAVEFGRKGALGIGSRIGGLGQMPGWYTVESDATHLLHQLKTAIKQALDSSQDAREEMRANSVRQHFPVLEW
 IQKLEALQRTAIQIHHTKNKNTVTGPMPESONYWETQSVRMSTLGLPGPTQSVTEGLDTPGRLTPGQSRFAELQLEGA
 DGNRNSSLGRKLSLGRSGPGQDRKRPKSPRESQILGEDLEGENTDAEEEGTTTPQVNYISPEEAMAAVNNTLTGTQDI
 GMAHTNNSHSLAGPQGSTYMSVPGSPNMSRASSMPGTPGLPQYPFQFALGSGGNTPFTHSRNVSMLSLPSVVADHNQ
 PVFELQKVDPTFTDSTRHFTRRFEEILNNLNKKNSMTDCCITETLYMKSERKFYDMYNDACLKQPDRAVSDSNSDTQDN
 RASYATVTGGSDNDPDEIDLWLSRLGYKRIAIIQRFMRRLGKWPVYALFLGLGQIIATNSAQMILLVGGVGETATKLY
 IIATIIYCISSICWLLFYRFPSVIVLTLPWFIYCMAFIIIGVSPFALTSLGRAWAQNVAAAGVYSAASSSGSLFFALNFGD
 QGAVPIKDWMFASLIQGIQQLYTVALWYSSKVTEAEVGGVSTAALSSWRLTAVVMPIAAYCFIVGVLLALGLPKYYRQ
 SPGRILFFYTSLFRRLIVLWFFFMVIVQNWFLSAAFGRNWSFLWSSQHAKAWEVVLVIFFFVVLWVILIIIFRALSKEH
 SWILPVFGLSLGAPRWAQTWWGTSNIGYYLPWAGSLTSGALVSRVWLWLGVLDEIQQVGLGMILLQTLTRVHVCFVLLA
 AQALGSIATICARGFAPNKLGPAGISPNVGTSLDTVGNWFWIALFFQLLASWGFLFYRREQLNRP

Fig. 13

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus oryzae* spC (Genbank accession No. AOR_I_1350024)

ATGTTCTCCACGGTGTATGCAAGCGCTCAGCGATCCTTATCTCTCTTACTGAGCGCTACCGCTTAAAGCTGGCCATACAC
 TGAGTCGGTCTGTGACTATAAGCTGAATGAAATAAAGCCGCGGAAGCGCGGATTGATTATTGGGGAGAGTGGCGGATC
 ATGAATATACCGCGTCCCGGATAGTGGCGCTTCCGATCTATACCATCTTTTGGACCGCATCGCTAACGGTGACCGG
 AAGAAATGATGATATCAATGGCAGCGCTTGGAGATGTGGTGGCTCGAATCAATGGCGCAGCGGGCGATTGGTTGG
 TCTAATTGATACGGTGGATTATATTAGGGGATGGGTTCAAGGTGGTTGAGCGGATTGTGATCGGATCTTGGTGCTTA
 CTCGGTAGGGGCACTTACTTCGGTGGAACTGCTGATGAACCTTCGGTGGCGCTACGATGGCTACTACCGGTTGATAC
 CACTTTGGCTGGACATGCACCATGGGACAGTCGAGGATTGGAGACGGAGCATCACTGAGATCGAGAAAGGAGATATGTATG
 TGTATGGGATAAATACACTGGCAAGCTAACTACATATCGGAGCTGTCTCAGATCAACACTGGTTGACGAGTATATGCAAG
 ATGAGCAACCTTATTGGTTTCAAAGGACATCTCAACGATTGAGCGGATTTGAGGCGAGATGAATATGAAGTGCAGTGGAT
 CTCAGATAGACAGTACGCGGACTTCAAATTCGGAATGAGTACAACGAGACCTGCAACTTCCGGAAGTTTGGAAATGAGA
 CTGGGTATCGGTTGACATCAGGTGGTGGTGGAGAGCTGAAAGGGTGGTATAATAGCGATTGCGATCAATTGGAGAGCTG
 GAGGGCTTGGTAACTTCCGAGCTGGAAAGGGGAGCTTACCAAGTTGGCTGGTGGAGATGGTCTGGGTGAATGGCA
 CAAGGCTATTGGTGTATGCTACTTAAGACTTCTGCAATTCGATAGCTAGCTAGATATCGATGGTTCCGTTTCGATA
 AAGCGGTTGAGACAACTTCGAGCGGCTTAAGTGAATAACCGCGCTGACGGTGAATGGGAGAAATATGGCAAGCAT
 AACTTTTCTTCCCGGTGAGATCAGTCAAGAAATACCTTTGGCAGTCTTACCTTGGACGGGTCTGACGGCAGATCA
 GCGGCTGAATCTGAGATGCTGGTGGTAAAGTTGAAGAAATAGTTGCGGACGGATATTTCTCAGAGACGATGGATACGAGG
 CGTTGGACTCAGCCGCGTTTCACTAGACGATGACCGTTGAGTACTGGTTTCTGGGAAATGGATGGTAACTAGTGGCT
 GGGTTTGACTTGGCTACTGATTTTATCGAGGGCTGGAATGGATGCTGCTGAGCAACGACTTCTCAATGCAATACAGGG
 TGAAGTAGCCGAGGACACATGTTGGTGTCTCAAAACGAGGCAACTTTGGCTGGCCAGCAATCGTAAATGGCAGCGAGA
 AATATCTTCTGGGCTTTATATCGTCACTTGGAGCTCCCTGGAAATCTCTGATCTCTATGGGCGAAGAGGAGCGGATG
 TATGTTTTGAACTACTGGTTCTAACTACCTGTTCCGGCCGGCAGCAATGACGATATCAGACGGCATGGTGGACACATGG
 ATGCACTGACTTTGAATACATCCAAATGTACGATTTCCCTAAAGAGAGGAGTACAGGGTGGAGGATATCAACGTTA
 GCTATGATCAGCGGAATCGGGACAGCGCTCGGCAATATGATGAAGCGCATGTTGGAAATTCGGGAGCATATCGGGTA
 GCAAAATGATGGGTTTATCTTCAAGCGCTTCTCAGCTGACAAAGGATGTGACTTCTCTGGTTCAACGGACACCGGGAC
 TGTACTGGCTATGGTGGTTCTGGCGAGCTACTTCCGAGGGCTCCAGAGGAGGCAAGCAAGAACAGTCAAGAACCTTT
 GGGTTGTATCATAAATGCTAACAACCTGAAACCTACGGTGGTGAAGTCAAAAAAGAGATACGGCTTGGTGTGGCT
 TTCAAGTCCGGGAGCTAAGCTGAAGAAATCTCTCTATCGGTACGATGAGCTCACTTTAGAAGATGGTCCGCGCAAAATCGG
 AGTCCACAATAGCACTGAGAGCTATGGATGCAATCGGAGTATGAAATGGTTCCATGGGAATACGGTGGCTACATAGAGG
 CGGAGAACTTCGTTGAGCGCGGCGCTACTGTTACTGAGTTGGTTCTGGCCAGGACCGCGGATTGTTGTCTAGGGATGAC
 AGTGGCCAAACTGTGCACATCCAGCTCGGATATTCAAAGAGATGGAGCTGTGACAGATCGCGGATCGCATCTCTTTGAA
 CTCACAGAGAGTGAAGGGAGTTACAGCTTCCGTTGACAGATCTAGCGTGTCTTGAACAAATCTGCCAAGGACAGGA
 GTGATAACTTTGTTGGGGAGGTTCCAAACGCTTGGACATGGTCTGCCAAGCTGAAAAATGTCCACCAGGAAATCCATCAG
 CTGACAGTTAAGAACGTTTCCACGAGCTGTGGAGTTATACCCATGCGGTTGACCACTTCTATTCCGTGTGGAGTCA
 AAACAAATCCGCTTTTATCGCGAGTGTCCAAATTTCCAGCAGCTGTGTGCGAGAAATCGGACAACGGCAGCTTGTATGCG
 AGCATGACCGCGCTGGTGGTGAATAATTTGGCTACTGAGTGAATTTGGGCTTAACTGGTCCAACCTGGACAAAGTATACC
 GGTGACAAACACCTAGTGCAGTTCCGAGAGTGGACCGGAACAGAGCTCAGAGTGGAAAGGGAAGTCAATTCGGGTACA
 GTACTTTTCAAGGCTCACCAGGAGTGGTATTACATTCAGGAAGGTGATCATGGCTGGGAAAAAGGTGTTGGTGGAGAT
 TTCTTAAGCTCTTTTGGAAAGGTCGGTTCAATGAATATGGTTACGATGCGGAGCTGGATAACAGATGAGATACGATACC
 AAGSAGTATCGTTGGAAAGTACGATTTTGTCTACGAGTGGCGCGGCTTGGACAAATGAGTGTCTGGGGAATGTTAAAGGA
 TGGCGCGCGGAGGTACAGAGGTGTATGGTGTATGTGACAACTCATCTGATGTGAGAACTTCTCCGCTTACCTAT
 GGTCCAAGCTGATCAATATCACAAGCTGGCTCCATTCGGGACCTCGGCTGGACCATCAGGCTCAATGACGGCAACTTG
 AGATATGAGATGCTTCCGGTGGGATCTGGATGGGCGCAGGCTGGTGTATACATTTCTCTGGGTGGTTGAAATTCAT
 GGGATTTGGTGGTATCTTATCTTCAATGAGCATTTACCGGTGTTAAACTCAATACCGATGGCGATGTGGCCAAAGAG
 ATAAGCTACCGCTCGTCTTTTGGCGAGGGTCAGAGAAAAAGTTCTCGGGCAGGACGAGTGGATAAGTGGATATCAGAT
 AAGSAGTATCCGACAGACATTTGCTATCGCGGAGCGGCTGAGCAAGCTGTACAGTATTGATCGCCACCATGGAAACAA
 CACTGAAGAGTGGAAAGGTCAAGGTCAAGATCGGGGCTGATGGCGTCAATGGCACAACATCATGTCTCAGCATGTGAAGCATC
 AAAGCTGTATCTGGGTTGTTCTTGGCTTGGTGGATTAATATCTCAGGACAGGCAATCGGAGCTTTTGGTGGTCACT
 ATCCTGGACAGGCAATATTTATCAATGTGCAATATCATATAGTTGATAACATCAGCTATGCTGGCTGACGGTCCAGT

Fig. 14

TTTCGCCCCAACAGACCAAAGCAGAGCCATATCCTCCTCGCATGGATGATCTTGACAGTGCATCTACTATTGGGCATGGA
 ACCAATGTATCGCAGAGACGATCAAAAGGATCCCGTCAATCGATCTCTATCATATCAACGATTTCATGGTTGTTAGCA
 CCACTGTATTTGCTCCACGCGTACCATCCGGTGTGGCTGTCTTACATAATGCTGAATCCAGGGTCTTTGGCCGCT
 GAGAAACCCCGAGGAAAAGAGGAGTCTGTTGGTCTTCAACCTTCCCATCGAAACTGCAACCAAGTACAGTCAATTTG
 GAAACGTCTTCAACCTTCTTACACTGGTGGAGGTATGTGGGATTTACCAACGCGGTTTGGGCGCAGTAGGTGTGTGG
 AAAAGTATGGAAAGCGCTCATGGGCTAGATACCCGATTTTCTGGAGTCTTGAAAGATTGGCAGTCTTCCAAACCCAGA
 CCGCTCCGACACAGGGGACATGACAAATAACGCGAGCGCGAGGTTCCAATCCAGTCTACGAAGAAGCAATCAATGATA
 AGCTACAGGCCAGAGTGGGCTGGTTGAATGAAGATCGTGATGCTGACCTACTTGTGTTCTGGGCGATGGTGGAAAG
 CAGAAGGGAGTGGATTGATTGAGATGTCTATGCCAGCGATATTATCGGCGAGCCCGACGTGCAATTGATCTGGGTTGG
 ACCTATCGTTGATCTCTATGGTAGCTGGCTGCTACAAAGCTAGAGCGCATCATGGAATGTTCCCTGGTGGGCTCTTCT
 CTAAGCGAGAGTTCAACGTTTTGCTCCATACGATTTTCTGGTGGGACTTGGCTCTGATTCCCTCCAGAGACGAACCA
 TTTGGGTTAGTGGTGTAGAGTTGGGCGTAAGGGTGCATGGGAATGGTTCTCGCATTGGAGGTTTAGGGCAGATGGC
 AGGTTGGTGTACACCGTGAATCCGACGCAACCCGCGCATCTTCTGCATCAGTTGAAGACCGCTATCAACAAAGCGTTGG
 ACTCATCACAGGAGCTCGTAGGAGATGCGCGCAATTCCTCAGGCAACATTTCCCGTTCTTGAATGGATTGAGAAA
 CTCGAAGGCTTGCAACGACAGCGATCCAAATCCATCACCCAAGAAACAGACCGCTGACAGGCGCGATGCCAGAGTGC
 GAGAACTATTGGGAGACTCAAAGCTACGAATGTCTACGCTGGGCTTCCAGGACCTACCCAGTGGGTGACAGAGGGTT
 TGGATACACCGCGAGGAGGCTTTTACGCGCGCGGAGTCTGATTTGAGAAATTGCAATTGGAGGGAGCTGATGGCAAC
 AGGAACAGGAGCTGGTGGCAACTCTCGCTGGTGGGCGATCTGACCTGCTCAGGACAGAAACGTCGCGCAAGAG
 CCGCGCGCGGAGAGCCAGATCTAGGAGAGGATTTGGAAGGTGAGAACCGGATGCCGAAGAGAGGGCAGCCACTACGC
 CGCAGGTGAACATAATTTCACTGGAAGAGCTATGGCTGCAATTACAACACTTTGGGAACCTCAGATATCGGAATGGCA
 CACAGCAACATAGTACTCACTCGCTCGCTGGTCTCAAGGATCTACTTACATGTCTGGTGGCAGGCTACCAAAACAACAT
 GTCAGCGGCTCTCTCTCAATGCCAGGAACCCCGGGCTGCGCGCAATACCGATTCCAGTTCTGCAATTGGGTTCTGGCGAA
 ATACTCCTTCACTCACTCCCGCAATGTGCCATGCTTTCTTGCCTTCACTCGTGGCGGACCAACAGCGGTTTTT
 GAGCTGCAAAAGGTTGATCGGACCTTTACAGACAGCACAGCCACTTCAGCGGAGCTTCGAAGAGATTCTCAACAACCT
 GAACAGAGAACTCGATGACAGACTGCTGTATCGAGACGTACCTAATGAAGAGCGAGCGTAAATTTACGACATGTACA
 ACGATGCACAATTAAGAAACAGCCGATGATCGTGCAGTGTCTGATTGGAATTCAGACACTCAAGATAACCGCGCTCG
 TAGCGCACTGTCACTGGAGGTTGGGACTCGAATGATCGGATGAGATTGATTATGGCTCTCTCGACTGGGGTATAAAGC
 ACCGATTGCTATTCAAAGATTATGAGAAGCGCTTTGGCAATGGCTGTCTACGCTCTATTCTGGGTTCTTGGACAAA
 TCAATCGGACCAACTCCGCTCAAAATGACCTGTTGGTGGTCAAGTAGGAGAAACAGCAACCAAGTTGTACATTATCGCG
 ACGATCTACTGCCATTTCTCTATCTGTTGGTGGCTCTCTCTATCGATTCCCGTCACTAATCGTCTCACTCTCCCGTG
 GTTCATTTACTGCATGGCAATTTATCATGATTGGGCTCTCTCCATTGCTCTCACATCTCTGGTGGAGCTGGGCGCAGA
 ACGTGGCTGCAGGTGTGATTCCGCGCGCATCTATGCGGCTCGTTATTCTTCCGCGCTCAACTTGGTGTATCAGGGTGGC
 GTTCTCTATAAAGGATTGGATGTTCCGGCGAAGTCTCATCCAGGGAATCCAGGAGCTCTACACCGTGGCTTATGGTACTG
 GAGCTCGAAGGTGACCGAAGCAGAGGTTGGGAGGCTGTCCACCGCGGCTCTAAGCTCATGGAGACTCACAGCTGTGGTGA
 TGGCCATCGCGCAGTATGTTTCATAGTGGGCTGCTTCTCGCGCTGGGCTACCAAAATACTACCGCAATCCCGCGGT
 AGGATCCTCTTCTTACACATCGCTCTTCCGCGCGGATTTGCTCTGGTTCTTCTTATGTTAATAGTCCAGAACTG
 GTTCCTCTCGCGAGCATTTGGTGGCAATTGGTCAATTCCTCTGGTCTCCCAACAGCTAAGGCATGGGAGGTCGTATCC
 TAGTCATCTTTTCTTCTGCTGCTCTGTTGATCATCTCTCATCATATTCCGCGCGCTATCCAAGGAACACAGCTGGATT
 CTACCGGATTTGGTCTGAGTCTCGGCGCACCGCGTGGGCGCAACATGGTGGGGAACGTCCAACATAGGCTACTACCT
 GCGATGGGCGGGAAGTCTGACATCGGCTGCGCTGCTGCGAGATGCGTCTGGCTCTGGCTGGTGTGCTTGACGAAATCC
 AGCAAGTCGGCTGGGATGATCCTCTACAGACACTGACCAGAGTCCAGCTGTGCTTCTGTTGTTGGCGCACAGGCT
 CTCGGATCCATCGCTACGATCTGGCGCGGTGGATTGCGCGCAATAAGCTGGGCGCGCGGGAATCTCGCGCAACGTGGG
 AACGTCTCTAGATACAGTTGGAATGCGTGGTTCTGGATCGCGCTCTTCTTCCAGCTTCTGGCTAGGTAGGCTTCTGTA
 TTCCCGGCTTCAATGATTCAATACTAATGTGGTTCATAGTTGGGCTTCCCTTTGTTCTATCGTGTGAGCAGCTTAAT
 AGGCGTTAA

Fig. 15

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus nidulans* AgaA (Genbank accession No. AN5885)

MRWRPLNPLLPLLAATAAGWPYEEVLVDYNLVNKNAAATPADYYAPEWRNHTYMPSPENWRFPFYTLFLDRFVNGDPTND
 NINGTVYEHDLNSNQMRHGGDAQGLVDLTDYLGQMGIKGIYLAGTILMNQPWGADGYSILDITLLDQHFGTIQTWRNAIT
 EIHKRGMYVLFNDNTIATMGDLIGFKGYLNVSAFVSKEHEAVWKSDDRYVDFDFGNTYNGTCEYPRFWNETGWPVDKDVR
 DELQGCYSSDFDQYGDREAFGVYPDWQRQLAKFASVQDRLREWNPSVRERLIRHSCMIKALDIDGFRYDKATQATVDAL
 GDMSSAYREITGGNNFGSIYLGRRQPNQYPDSAMDSMAMNNESSHQYFLREDGLQALDSAAFHYSIYRSLTRFLGLDGN
 LAAGYDTPIDWTDWVNMVMTNDMINANTGKFDPRHMFATNQDVFWRWPAIKQGIERQLLAMFITTLLHLPGIPILLWGEE
 QGFYILDATADNYVYGRQAMSPATAWKTHGCFQLTADQYHNWPI SKGREGCHDET VTYDHRDP SHPLRNIIKHMYQLRQD
 YQVLNDGYSVQKLSNQTRQIFYPGSGTATETGMWSVLRDSYKIQELHNEQPVWLVYQNDNKTVEYNFDCSDNDTALIS
 PFATKTTVVNLFYPHDEYDLKDGPKKLHLNGSAEFNGCLDSMTLKPFEKAFVPKERFVKPRPMITKITPGHDQPIISKV
 VASEAEDLDSIYFSAEMDCDSVTKAIKVQSTTEVNKTALIDKDSVKCRRIDPNETRWTAQLPSVWAWSSKLTGVYNGIH
 RLTVTNATSEVGGSTQAVDHLIRIGQIDNPMVFTTANYSTDLLHQHENGTLYIRHKAAGADKYRYSTNWGSSFSNWREY
 KGGDEFIEEQWPGSKKKQKWNKGKVRVEYWSKLTGSSSYVQEGDYDTKHQRRFPHLFFNGPYNQYGYDAGLDNEVKQDSD
 GYWKYRLRAEFPAQGQFNWGMNPDGKPDQSFVFGDLDSGVLDRMPPSSLNTLSINVTD RPPSSYLSWNIWVDDGTMSI
 QFQPTGSRTIQMVVYFLLWFVPLVTAIGCVYAFMKSFYQVKFNQIGISQKRSLFGFSVGRKPSLNLPLTRLANKSGFLQST
 PVFGTSSRRRSVL IATMEYDI EDWGI RIKIGGLGVMAQLMGKNLGHQDLIWVVP CAGD VDY PEDQPAEPMFVTVLGN IY
 EVKVQYHVLNNITYVLLDAPVFRQSKAEYPARMDDLSAIYSSAWNQCIAETIKRFPIDLYHINDYHGSIAPLYLLPQ
 TIPVCLSLHNAEFQGLWPMRTQKERDEVCSVFNIDVDVARRYVQFGEVFNMLHAGASYLRVHQQGF GAVGVS RKYGKRSY
 ARYP IFWGLKKVGNLPNPDSDTAEWNKELPKESI QVDQNYEASRAELKRQAQEWAGLEQNPADLMVFVGRWSMQKGI
 DLIADVMPAVLEAHPNVQLICVGPVIDLYGKFAALKLDRMMQLYPGRVFSKPEFTALPPYIFSGAEFALIPSRDEPFGLV
 AVEFGRKGALGIGARVGGLGQMPGWYNVESTTTAHLHQQFLAIGCALNSKPQVRARMRARS AKQRFPAQWVEDLEIL
 QSTAMRIHSGKLAKASYQPYNSGSNTPLGMMTPPIASTGTVTPTGIQTPPLAHSRSGSYSNINRLSAYGPQQRNTIIYSR
 DPSPGGEDQPRSGIRQLSLGVRAGPGHLMRRGRRRLRRNSHAGTDENASVSMTESSDDDIIPSFYGEEEYLTPEQAE
 VRRADMT PQQEQNHGVSVDFFTRRHSSQSSILSRVLSPASSTTFDGD ETVFPAPPFAEPGNRLSSASVLSVDSVVG EK
 KDYKLQKVDPTFTDSTGEFYKVFERKLEKLNGSNSISQLCIEEYLEKSEKKWDFRFRDARLGRKQSPSSSIFRTKFE GSS
 PMALVSNDVEVGRASGSEPRMRPDEFCLGNDYVPPSGLKKWMQVRIFDWPIYSFILGLGQIIAANSYQITLLTGEVGQRP
 EKLYGIATVYLVSIVWWFLFRFCKSVVLSLPWLFYGFVFLIGVAHYEGDSFARAWIQNVGAGVYAAASAGSLFFAL
 NFGDENGAPVKNWVRACIIQGTQQAYIIGLWYWGTSISQAVTRGVDPVQAHITETWRMTTICMPIAVFLWVLGILVFFG
 LPNYYRQTGKVP SFYQSVCRKIIILWNFVVILQNFFLSAPYGRNWSFLWSSVHAEPWHIGLLVVAFFGVAWVLILCIF
 ARLSKSHSWILPVFACGLGAPRWAQIIWWGVSGMGLFLPWAGSYTTGALVSRSLWLWLGLDLSLQGLGFGMILLQTLTRMH
 ICFTLLASQVLGSIATICARAFAPNNIGPGPISPDITDGAGAVANAWFWIALFFQLLICSFIDVMS

Fig. 16

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus nidulans* agoA (Genbank accession No. AN5885)

ATGAGGTGGAGGGCTTTAAACCGGTACTTGGGTGGTTGGACGACCGGACGAGGCTGGCGGTACGAAAGATCATTAGT
 TGATTATAATCTCAACGTAACAAAAACCGTGGCACCACGAGATTATACGCCCGGAATGGAGAACACACATATA
 TGCGGTGGCAGAGAACTGGAGGTTTCCATTCTACACCGCTGTTTCTGGACAGATTCTGTCAACGGCGACCCCTACTAACGAT
 AATATTAAAGGGAACCTGTCTATGAACATGATTTGAAGTCCAAACGAGATGGACACGGCGGTGATGCACAAGCGCTGGTAGA
 CACACTCGACTACCTTCAAGGAATGGGAATCAAGGTCTGATTTTGTGTTCTGCTCAGCTTACGCTTGGCTAACACGAT
 GTTGTATTAGGGGATCTAGCTCGCGGGTACTATTCTCATGAATCAACCGCTGGGCGGAGACGTTATTTCGATTTTGGACAC
 TAGCTGCTGGATCAGCACTTGGGACCATCGAAACCTGGAGAAATGCAATCACAGAGATTACAAAGCGTGGGATGTAGG
 TCTTATTCCGCAACACTATCGCTAGGTGCTGCTGCTGCTTTCGAAGTCAAAATGCGCGAATGCTTAACCTACACCGCAAGGAT
 GGGCGATTGATCGGATTCAAAGGTTATTTGAACGTTAGGCGCCCGTCTCTGTCAAAGACGACGAAGCTGTTTGGAAAGT
 CTGACCGTGGCTACGTCGATTTTGTATTTTGGAAACACCTACAATCAGACCTGGGATACCGCTCGATTCTGGAACGAGACT
 GGTGGCGGCTGTGATAAGAGCGTTCTGTATGAGCTACAAGGTGCTATAGTAGTGATTTTCGATCAATACGGTGCACAGGA
 AGCTTTCGGTGTATATCAGAGCTGGCAGCGACAGCTGGCCAAGTTTCATCAGTCCAGGATCGTCTCCGTGAATGGAACC
 CAAAGGTTCCGAGAGACTAATCAGACATTCTGCTATGATTATCAAAGCTCTTGACATTGACGGATTTCCGCTATGACAAA
 GCGACGCGGCGACAGTGGACGCGCTTGGAGACATGTGAGTGTCTATCTGAGTGTGCGCGGTGAGGTGGTAAAGACAA
 CTTTTTCTCCCGGTTGAGATTACTGGTGGAAACAATTTGGGCTCGATCTATCTCGGACGAGGAAGACGCGCAACCAAT
 ACCGAGACTCTGCTATGGAATCTATGGCCATGAACAACGAGTGGATACCAATATTTCTGTGGAAGATGGTTACAG
 GCGCTCGATAGCGCTGGCTTCCACTAGTCAATCTATGATCGCTGACCGGTTCTTGGGCTGGACGGAATCTTGTGCG
 TGGTTACGATACGCGGATTGACTGGACAGATGCTGGAATGTAAATGGTGATGACCAATGACATGATAACGCGAATACGG
 GTAAATTTGACCGCGACACATGTTTGGTGGCAGACCAAGATGTTTTCTGTGGCAGCCATCAAAACGAGGTATCGAA
 GCGCACTCTTGGCGATGTTGATTACAACACTTCACTCCCGGTTTCCAAATATGTTGTGGGGTGAAGGCAAGGTTT
 CTATATCTTGGACGCGCTGAGACAACTATGCTACGGCGCGCAGGCGATGTCAACGCGCACAGCTTGGAAACCGCATG
 GATGCTTCCAATTGACACAGATCACTACCAAACTGGCTATCAGCAAGGACGTGAAGGCTGTCTATGACGAGACAGTA
 ACCATGACCAACCGGACCGGCTCTCATCCGCTCGGAATATCATCAACATATGTACCACTTGGCAAGATTACCGGT
 TTTGAACGACGGAATTCTGTGCGAGAACTCTGCAATCAAACCGCGGAGATTTCTATCGAGGTCGAACGGAACGGCTA
 CGGAGACGCGAATGTGGTCTGTCTTACGAGACTCAGTTTACAAGATCCAGGAGCTACACAACGAGCAACCGGTTTGGCT
 GTATACGAGATGACAACAAGACGGTGGAAATACAATTTGACTGCAATGATAATGACACGGGCTTGATATCCCGCTTTGC
 CACCAAAACCGGTTGTCAATCTCTTTACCGCATGACGAATATGACTTGAAGGACGGTCCAAAGAGGTCGATCTTA
 ATGGCTCAGCGGAGTTCAATGGATGCTTGTATGATGACGCTGAAGGCTTTGCAATTCAGGGCTTCTGTCCGAAAGAG
 CGATTTGTGAAGCGTAGACCGATGATTACCAAAATCACACCAAGGACGACGACCAACCGATCATTTCCAAAGTCGTGGCGAG
 CGAGCGAGAGATCTTGATTTGAGCATTTACTTCTCTCGGAGATGGACTGCGACTCAGTCAAAAAGCGATCAAAAGTGC
 AGTCCACACAGAGTCAATAGACAGCTTTGATTGACAAAGACAGCGTGAATGCGAGGAGATTGATCCAAACGAAACG
 GGTGGACTGCGGAGCTACCGAGGCTCTGGGGTGGTGGTCAAAGTTGACGGAGTATACAATGGAATTCATCGGCTGAC
 CGTCAACCAATGCCACGAGCGAGGTTGGAGGCTCAACACAGGCTGTTGATCACTTCTCATTCGATTTGGTCAAAATAGACA
 ATCGCATGCTTTCACCGCGCAATTACTCCACTGACCTACTTCAACGACGAGAGACGGAACACTCTATATTCCGACAC
 AAAGCGGCTGGTGTCTATAAATATCGTTATTCCACCAATTGGGGAAGCTCTTTTCAAACCTGGCGCAATACAAAGGTGG
 CGACGAATTCATTGAAGAACACCATGGTCCGGAATAAAGACGAATGGAATGGGAAGCATGTCCCGGTTGAGTACT
 GGAGCAAGTTGACTGGTAGCAGAGCTATGTCCAAGAGGTGACTATGATACCAAGCATCAAAGACGCTTCCGCGACCTC
 TTCTCAATGGGCTTACAACAGTATGGATAGGATGACGAGCTGGAGAAATGAGGTGAACAGGACAGTACGCGGTACTG
 GAAATATCGGCTCCGAGCGGAATTCCTGCTCAGGAGACAGTTAATGTTTGGGGTATGAACCCAGACGGGAAGCCGAGC
 AGAGTTTTGTGTTTGGTGATCTTGATTTCTGACGGTGTGTTGGACCGCATGCCACCATGCTCCCTGAACAGGCTTTCTATT
 AAGCTCAGCGACAGGCGCCGCTGCTCTATCTTGAATATTTGGTTCGATGACGGTACCATGAGCATCCAGTTTCA
 ACCGACTGGCTCGAGGAGCAATCGAGATGATGTTTATTGTTGCTTGGTTCGTACCGGTTGTGACAGCTATCGGATGG
 TATATGCTTTCATGAATCGTTTACCAGGTCAAATTCAAACGAGATTGGAATCAGCCAGAAAGCGGTCAATTTCGGTTTC
 TCAGTGGCGCGGAAGGCTTCATTGAATCGACTGACCGGCTTCCCAATAAATCCGATTTCTCCAAAGCAGCGCTGTCTT
 TGGAAACAGGCTCTTCTCGCAGGCGAGTGTCTCATCGCCACTATGGAATATGACATTGAGGACTGGGGTATCAGGATTA
 AAATTTGGTGGCTTGGAGTCATGGCAGCTCATGGGCAAGAACCTCGGGCATCAAGATCTCATTTGGGTTGTCCCATGT
 GCGGGGAGCTAGACTACCGAGAGGATCAGCCAGCTGAGCCAAATGTTTGTGAGTGTCTCGGGAACATCTACGAAGTCAA
 GGTTCAGTATCATGTCTGAAACAATATTACATATGTTCTTCTCATGCGCCGCTTTTCGCTCAACAGTCAAAGGCTGAGC
 GCTACCGCTGCTCGATGGAGGACCTTGATAGTGCATATGATTTCCGCGTGGAAATGAGTGCATGCTGAGACCATCAAG

Fig. 17

CCGTTCCGCTATCGACCTTTATCATATCAATGATTATCATGCTTCTATTGCGGCTCTCTACCTTCTTCCCGAGACGATCCG
 TGTTTTGTCTTTCCGCTTTCACAAACGCGGAATTTCAAGGCTCTCTGCGCCATGCGCACACAAAAGGAAGGGATGAGGTTTGTCT
 CTGTTTTCAATATCGACGTCGATGTGCGCAAGGCGATATGTCCAATTTGCGGAAGTTTTTAACTGCTCCATGCCGCTGCT
 AGCTACCTTCTGTCCACCAACAAAGGTTTCCGCGCTGTAGGTGTTTCCAGGAAATATGGAAGACGCTGCTACGCGCGCTA
 TCCCATCTCTTGGGGTCTCAAGAAAGTTGGGAATCTTCCGAACCCAGATGCTTCTGACACGCGTGAATGGAAACAAAGAAC
 TGCCTAAAGAAAGTGAAGTCCAGGTAGACCAAGCACTACGAGGCAAGCAAGGCGAGGCTGAACCGCAAGCGCGAGGAATGG
 GCGGGCTTGAACAAACCCCAAGTGGACCTTATGGTTCGACGCTTATGGTTCGACGCTTATGGTTCGACGCTTATGGTTCGACGCT
 AGCTGATGTTATGCCGCTGTTTGGAGGCTCATCCCAATGTTCAAGCTGATCTGTGTCGCGCCAGTCAATTGACCTTTATG
 GAAATTTGCGGCGCTGAAGCTTACCGGATGATGACGCTTACGCTGCGGCTGTTGTTCTCAAGCGCGAGTTTACAGCA
 CTTCCTCCATACATATTTTCAGGAGCGGAGTTTGCCTTATCCCATCCCGTACGCAACCGTTCCGAGCTGTTGCCGTTGA
 ATTTGGTCGCAAGGGAGCTTGGGAATCGGTGACGCTTGGAGGCTTGGCCAGATGCCGCTTGGTGGTATAATGTTG
 AATCAACAACACTACTGCCATCTGCTTCACTCAATTTAACTAGCTATCGATGTGCTTGAAGTCAAGAACCCCAAGTTAGG
 GCAAGGATGCTGCAAGATCTGCAAGCAAGCGTTTCCCTGTTGCTCAATGGGTTGAGGACCTCGAGATTCTACAGTCAAC
 GGCCATGCGAATCCACAGCAAAAGGCTTGGCTAAGCGAGCGCTCGAGCCCTATAACTCAAGAAAGCAACAGCCGCTTGGCA
 TGTATGACGCGCGCTATTGCTGCACTGGGACTGTTACCGCGACGGAATCGAGACAGCTCCTCTTGGCCATTCGCGATCA
 GAGAGCTACTCAAACTATCAACGCGCTCAGTGTCTTATGGGCTCAGCAACGTAACACGATATCTACAGCCGAGCCCAAG
 CCGAGCGCGCAAGACAGGCTAGATCTGCTTATCGACGTTATCACTTGGTGTATGGGCTGGGCTTGGACATCTTATGC
 GTCTTGGCGCGCGGAGGTTGAGAAAGAAATAGCCACGCGGAGCGAGCGAGAAAGCCAGCGCTCTCCATGACGGAGGAGAG
 AGCGACGAGGATATAATGCCAAGTTTCTACGGGGAAGAGGAGTACAGCGCTTACCGCTGAACAGGCTGAGGAAGTACGTCG
 CCGAGATATGACACACAGAGGAAACAGAAATCATGGCTCGGTTAGGGAAGCTTCTTACCGCTGCTCACTCGAGTCAAGGCT
 CGATTTTGTCTGCTAGTGTCTTGTCTCCAGCCAGTTGCACTAGCTTTGACGCGGAGCGAGGCTTGTCTCCAGCCGACCA
 CGGTTTGCAGAACTTGAAGAACGCTCAGCAAGTGTCTGCTGCTCTCTGTTGCTGCTAGTGTGGCGGAGAGAAAGATTA
 CAAAGTCCAAAGATTTGATCTACATTTACCGATAGCACTGGCGAATTTACAAAGGTTTTTGAAGAAAGCTAGAAAGG
 TCAATGGCTCGAAGCTCCATCTCCCACTTTGCAATCGAGCAATATCTGAGAGAGCGAAAGAAATGGTTGACCGATTG
 CGTATGACGAGCTTGGCGGCAACAGTCCCGCTGCTTTCGATTTTCCGACCAAGTTTGAAGGCTCCTGCGCTATGGG
 ACTCGATCAAGAGATGAAGTGGATCGGCGCGGATGGAAGCGAGCGCGCTATGAGGCTGACGAAATTTGTCTTGGAA
 ACAGCTATGTTCTCCCTCTGCGGCTCAAGAAAGTGGATGCAAGTTGCGAATTTGCACTGGGCTTTACTCCTTCACTCTC
 GGAGTGGGCAAAATATAGCAAGCAAGCTCTTACGAGATCAGCTTGTGCTGAGCAAGTGGCGAGCGGCTGAGAAAGCT
 CTATGGTATTGCAACAGTATACCTCGTGAGCTCTATAGTCTGGTGGTTTCTTTCCGCTTTTGCAAATCTGTCTGTGTAC
 TGTCTCTGCGCTGGCTGTTCTACGGTTTCCGCTTTGTTCTTATGGAGTCGCACACTATGAGGCGGATAGCTTGGCTGCT
 GCTTGGATCCAGAACGTTGAGGCGGCTGTATAGCGCGCTGCATAGCGGAGTGGCTCATTGTTTTTCCGCTTTAACTTCGG
 AGACGAAAGCGGTGCACGAGTCAAGATTTGGGTGTGGGCTGCTTGCATCATACAGGTACCCAGCAAGCTTACATCATCG
 GTCTTTGGTACTGGGGGACTTCTATATCGCAAGCAGTACAGAGGCGCTTCCGAGTGTTCAGGCCATATACGAGAGACA
 TGGAGAAATGACGTACGTGCTCCATCTCTCCACAGGCTCCTTACTAACTCTATATTGCACTATCTGTATGCGGATA
 CAGGCTTTCTCTGGGCTAGCTGGGCTGCTTGTCTTTTGGCTACCAAACTATTACCGCGAGCGGCTGGAAAGTCCG
 TTCTGTTCTACCAATCTGTCTGCGGTGGAAAGTCACTCTGGAAGTGTGATGCTTCTGCAAAATTTCTTCTCTCA
 GCGCGCCCTACGAGCAAACTGGAGCTGTAGTCCCAAAAGAACTCACTTTATGTTCCGAACTAACTAAGGAAGCAAGT
 CCTCTGGAGCTCCGTCACGCGGAACCTGGCACATCGGCTTCTGCTGCTGCGCTTCTTGGAGTGGCTGGGTTCTCA
 TCGCTGTATCTTCCGCGGCTTTCCAAATCCGACAGTTGGATCCTCCGCTTTTGGCTGCGGCTTGTGGTGGCGCGGA
 TGGGACAGATCTGGTGGGGGCTCTGGGAATGGGCTTATTCCTGCTTGGGAGGAGGCTACAGAGCGGCGGCTAGT
 ATCTCGCTCTCTGCTGCTATGGCTGGGTATTCTCGACTCCCTGCAAGGCTTAGGCTTTGGTATGATTCTATTACAAACAC
 TCACACGAGTGCATATCTGCTTACGCTTTTGGGAGTCAAGCTCTAGGCTCTATTGGGACGATCTGCGGCAAGGCTTTT
 GCGCGGAATATATCGGCGCAAGGCGGCTCTCTCTGATATTAGGATGGAGCGGCGGCTTGGAAAGCGGTGGTTCTG
 GATTGGGTTGTTCTTCCAGTTTGGATTGGTATGCTTCTCTACTATATAATTGGAGGCTAGTGGGACGTAAGCTAATAG
 TTCGATCTAGTGGTGGTTCTCATGTTCTTCCGAAAGAGGAGCTTACGAAACCTTAATACCATCGCACTCGACCTC
 GGCATTGGCAATACCTGGTACTTGTCAATTTCTGACATAACTACAGCGGGAATCTACCGGTTGGCGGCTTAT
 GCTGCAATTTGCTCTCGAATCTCTCCATTGTCCTATAGGCTATTACTCTACGCTTTATTGATCTTGTGTGCTATC
 GACGAGCGGTGCATATTGCAACTTCTGAGGATATTGACCTGAGCTTCTGAAACGAAAGAAATGACTGCTATGAGTCAA
 CCTAATGATTGGATGTTATATGGTCTCTTATTCTCTATGGAAGTGAATATCATGTCGCGCGGATGAGGCTGATTGAT
 GTGGGTGAGATGTGGGTGATGTAGCTAATGATAGTACTTGTGTTGATTAGTCTCTGCTCTTGTATGTTATGCTATAA

Fig. 18

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus nidulans* AgsB (Genbank accession No. AN3307)

MGRLLQLSSGLKAIALLTFAATATCWPYDESLVDYNNVNTNKSATNPADYWGWEWSHKYHPSPENWRFPFYTLFMDRFVNGD
 PTNDNINGTTFEHDLNSNQMRHGGDVAGLVDTLDYLQGMGIKGLYLAGTPLMNQPWGSDGYSALDTLLDQHFGTIQVWR
 DAITEIHKRGMVYVLFNDTIATLGDLIGFEGHLNDTTPFSEKEHKALWKSNNRYVDFDIGNTYNATCDYPRFWYEDGMPVN
 ESLTAGLVGCYDSDFDQYGDIEAFGVWPDWKRQLAKFASVQDRLREWYPPVRERLIRHTCMIIASFDDIDGIRYDKATQAT
 VDALGDMASKAYRECARAVGKENFFIAGEITGGNTFGSIYLRGRQSNQVDSVGNIDAMKLTNESDPQLFLREVGEAID
 AGAFHYSTYRALTRFLGMDGQLEAGYDVPLDWVQAWGNMTVNDLINANTGKFDPRHMYGVTNQDVFRWPAIEWGVERQM
 LGSFITLLMLPGIPLLLWGEQAFYVLDATAENYIYGRQAMSSATAWKTHGCFSESSQYYQWPLVAALDGCNDETVTYD
 HRDPSPHVRNI IKHMYQMRQYPMNDGFI IETLSNQTEPVYYPGSGNGTETETGMWSVRRDRNEETQDFGSSDDNEPIWL
 VYSNMNRTHDYTFDCSDNETALIAAFPSGKVRNLFHPYDTLTLGDGPKEMVYGNSTELVGCLPNLTLTRYEFRAVYKNE
 LWKKPRPMITKFQPGDDEANGHDSPLRSTVAPDASETVRLTLQFSEAMGCDSTDSISFNSSTETGKIPSIDASTVQCGN
 ITEVANSNATGHIPGKWQAAADLRGVNGIHRVTVNNASNADGDDSTHAVDHFLFRIGQIDNPMVFTSANYSSSLLHEKE
 DGTIFYIQHHAAGADKYRYSTNWGTTFSDWKTYKGGNDTIITMLPWNGTKAQEWEGHHIRVEYWSRWTSSSSHVQEGDSGWK
 YKTPRRFPFAFFNGPYNQYGYDGLDNQIKLDAGAGDGYWKYHFTSEWPAVGQVNVWGIPDGEPPQSWVMGDVDGDKV
 LDRMPPSALSATLINITDHPHPIYISWKLYINDATMRYLIPAGHQSGQIAMFVLFWIIPLLSGSACVYIFMKSFYKVKF
 NEIGAAGASTEMKSLVPLALRRRMKQLASGNKGNGPSFNPLMRLAEKSGFMQSTTALAGAASGKRRMVL IATMEYDIEDW
 GIKIKIGGLGVMAQLMGKTLGHQDLI WVVPVGGVDYPVDTPAEPMTVTILGQAYQVNVQYHVLKNITYVLLDAPVFRQQ
 TKSEPYPARMDLDSAVYSAWNQCI AEAIKRFPPVDLYHINDYHGSVAPLYLLPGTIPACLSLHNAEFQGLWPMRTQKEK
 EEVCSVFNLDEVVRNYVQFGEVFNLHAGASYLRVHQGGFAGVGSKKYGKRSYARYPIFWGLRKIGNLPNPDPSDVGE
 WTKEDSLIKDEDIKVDPEFEAGRAELKRAQEWAGLDONPDADLLVFVGRWSMQKGVDLIADVMPAVLEARPNVQLICVG
 PVIDLYGRFAALKLDRMMKVYPGRVFSRPEFTALPPYIFSGAEFALIPSRDEPFLVAVEFGRKGALGIGARVGGGLQMP
 GWWYNVESVSTSHLLMQFKLAEALSSKTETRAMMRARSQKRFPAQWVEDLEILQSTAIQVHEKEVSRGHAGGRPMT
 PMTPSGATTTPSGMMTPITGSRGLKPLSQGVGMGLSVPHSRESSYSLNRLSEYVAQKTPGESQPRESSGLQSRSLSLQVRS
 GPGHRGRARKQKPGADNIPGNEGDSSTDESIPDYDDDEYTLTPAQIEESRRAQATRSISFSPETLQPPRSPLPAPMS
 PGTPPSVEQTLPPPKPFAAADAGNRLSSASVLSLDSVVGKKDFKLQKVPFFTDSTNGEYARNFEQQLENLNGSNSSEQ
 LCIEEFLVKSERRWFNKFDRDLRLRSPTPSVFRDNHSHGRGSPDGS MYVDEAGHRNSGDVHONGSDDTDDFEFLGKD
 YVPPTGLKKWMQIKIGDWPVYTLFLALGQIIAANSYQITLLTGEVGQTAEKLYGIATTYAITSAWLVFRYFKSIVCLS
 TPWFLYGI AFLFIGSAHFESDSFTRGWIQNVGSGFYAAASSSGSIFFALNFGDEGGAPVSKWIFRACVIQGIQQVYVIVL
 WYWGSTMHQSSQGLLTADNTISNTWKMTAICYPIAMLLWAIGLLLIFGLPNYYRQKPGKVP SFYKSLFRRKIVLWNFVA
 VILQNFFLSAPYGRNWSFLWTSSHTKPWQIVILCVIFFGLLWCAFLYIVAVLSKQHSWFLPVFACGLGAPRFLQIWWGVS
 GIGHYLPWWAGGYTGGALVSRSIWLWLGVLDISQGLGFGIILLQTLTRMHMCFTLIVSQVLGSIATIVARACAPNNVGP
 PVSPDITKGAGELANAWFWVALFCQLLVCAFLFFRKEQLAKP

Fig. 19

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus nidulans* agsB (Genbank accession No. AN3307)

ATGGGAGGGCTCCAGCTCTCAAGCGGGCTGAAGGCCATAGCCCTGCTCACATTGCACGCGACGCAACATGCTGGCCATA
CAGCAGGCTCCCTGGTGGACTACAGCTCAACGTCAGACGAAATAGTGGGCGCACTACCCCGCCGACTCTGGGGAGAGATGGTCGGG
ATCCAGGATACCTCATCGCTGGCGACGCAACAGCTGGCGGCTTTGCGTTTTCACACGCTTCGATGGACAGATTCTGGATAGGGGAT
CGAACCAATGATTAACATACACGGGACACGGTCTTGACGACGATGTCAAATCAAAATCAGATGGCTCATGGCCGGTGATGTGGC
TGGGCTGGTTGATACCGTGATACCTGACTGTCAGGAGGATGGGATACCGATGGGTGGCCGATATATTCTGCAATCTGGTGA
AAGATATAGTTAGTGTACGATGACATGAGTATAGGAGTACGCTTCTGGAAGTCCGCGCTGATGAACACCGCGCTGGGGCTGGAG
TGGGATTTCGCGCGCTGGACGACACCGCTTCTGGACACGAGACTTGGACAGATCGARRGTGGCGCGGACGCCATCAGCGAAAT
TGCACAAAGCGGGGATGACGTTGCTGTTGGACAAATCAATCGCTACGATGGATGACTGGCCCTGCGCTTGTGGCATGCGGAT
TTTGTAAAAAAGTTGGGGCTGACATGACTATCTGACGCGCTGGATGACTCATTTGGTTTGAAGGTCATCTCAAGACGAC
CAGCGGCTCTCTCGGAGAAAGAACACAGGCCGCTTTGGAAATCTCAACACAGCGTGATCGCATTTGCGATTGGCAACACT
ACACCGCCACTGCTGATTATTCGCGCGTCTCTGTGATCAGAGACGGATAGCGATCAATGATGATCGACCGCGCGCGCTGCTG
GGGTGTATGATAGTGACTTTGACCGAGTACGGTAGACTGGAAAGCTTTGGGTGCTTGGCGAGACTGGAAAGGTCGAATCGGCGGT
GAAGTTTGGCGCTGCTCGAGATCGAGCTGGAGAGATGTTCCAGAGAGCTTACCGGAGACGGCTGATCGACACACATGATGATGATG
TAAGTTTCGCTGCTTTGATATTCGACGATATTCGATACGACACAGCGACCCAGCGAGGCTGCGATGCGTTGGGGAGACATGCTCC
AAAGCGTATCGGGAATGCGCGCGGGCTGTGCGCAAGGAGAACTTTTTCAATTGCGGGTGAGATCAGAGAGGCCAATAGCTTT
TGGGCTATGCTATCTATGCTGACGAGAGAGGGGACTGCAACACGGAGTGAATTTGGTGGGGAATTTCTAGCGACGCAATGAAGCTGAT
CAACAGAGTCGATCGCGAGCTTTTCTGGCGGCAATCTGAGTGGGGTGTGAGAGGGCGATGTGCTGGGCTGCTTTATACCCAGCGAT
ATGCTGGCGGGCATCGCCGCTGCTGCTTTGGGGAGAGGAGCAAGGCTTTACGTGCTCGATGGCAGCGGCTCAAACTACAT
ATATGACGACGAGATGAGGTTGCTGCTCGAGCGGCTGGAGAGAGCCAGCGCGCTGCTTTCTCACTGGAATCGAGCGAGTACAT
AAGTCGGCGCTGGTGGCGGCACTCGAGGTTGCAACGAGGAGAGGCTGACCTGACGACGCGGAGCCGCGACCGCGGTTG
CGCAACATCATCAAGCAGATGTACGAGATGGAGGAGATACCGAATGCTGCAACAGTGGTTGATCATCGAGACGCTTTCT
TAACACAGAGCGAACGTTGTACTACTCGCCGGTTCGAACGCGGACGAGACGAGACAGGCTATGATGCTGGCTGCGTGGCGCTGACC
GGAAAGAGAGAGACCGAGCTTTGGCTCGAGTGACGACCAAGCAACCCATCTGGCTAGTCTATAGCAACATGCAACCGCAGC
CGCTACATACACATTTATGTTGCTCGAATGAGACGGGCACTATTGGGCTTCCGCTCGAGGACAGAGBTGAGAGACT
CATTGACGCGCTGACGACGCTGAGCGTAGCGGACGGGCGAAAGAGATTTATATGGAACATGGACTGAACTGGGTAGGCT
GCTTACCGAAGCTGACGCTTAGCGGCTACGAGTTCCGTTGCTATGTCAAGAGCAAGGCTCTGGAAAAAGCGCGGGCGATG
ATACCGAAGTGGCGGCGCGAGCGATGAGCGCAACCGGACGAGCTGAGGCTCGAGCTGACCACTTTCTCTCGGATGGGGAGATGAGCA
ACCCCATGGCTTTTACCTTGTGGCAACTTCTCGAGCAGTTTGTGTCGATGAGAGAGGAGAGCGGACGTTCTATATCCACAC
CAGCGCTCGCGGTGCTGACAGTACGCTATTTCGAGCAATTTGGGGACCAAGCTTCTGCTGATGGAAGATCTCAAGGGAGG
TAACGACGAGTATAGCATGTTGCTGATGAAATGAGCTAAGGCGAGGAATGGAGGGAGATCAATCCGGGTGGAGTACT
GGTCCGCGTGGAATGGACAGTAGGCAAGCTGAGCAGTGAAGAGGCAATTTCCGGTGAGGATCAAGAGCGGACGCTGCTTCCGCG
TACGCTTTTTCATGGGCTGATCAACAGCATGCGGATAGCAGCGCGTTGGACAGAGATCAAGCTGGAGCGGCGGACG
CGGCGCGACGAGTACTGAGAGTACGATTTTCACTCGGATGGCTGGCGCTGGCGAGGTGAATGTTCTGGGGATCAATC
CGGATGGGCGGCGGACGATGACAGCTGGGTGATGGGCGAGCTGGAGCGGAGATGGGTGCTGACGCGGACATCCGACGCGGAC
CTCTGTGCAACGTTGATTAAGCATGATGATCCACACAGCAAGCTTATGCTGTTGATGGAGGTTGATCAATAAGCAGCGGAC
GATGGGCTACTATCTATCCCGCTGGCCACAGAGCGGCGAGATCGGATGTTGGTGGTCTGTGATCATCGCTCTCGCT
TTCGGCGCTCGCGCTGGCTATTTGCTGTTGATGAGTCTCTGATGAGTCAATTCAGCGAGCTGCGGCTGGGAATGGCGAG
AGCGAGAAATGAGTCAATGTTTCCCGGCTGCTGCTGGTGGAGCGGATGAAGCGAGCTGCGCTGGGAATGGGACAGCGAG
TGGCTCATTCAGCGCGCTGATGGCGTTGCTGAAAAAGTGGGCTTTATGCGAGACGAGCTGCTTGGCGGCTGCGGCT
CGGGCGAGAGAGCGGCTGCTGCTGATGGAGACGATGGATACGATTTGAAGACTGGGGATCAAGATCAGATCTGGGGTGT
CTGGGAGTATGAGGCGGAGTATGGTGAAGACATCGGCCACAGCAACTTATGGTGGTGGCTTGTGTGGGCGGCT

Fig. 20

[illegible]

Fig. 21

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus sojae* AgsA

MKWGF TGSLLALLAATAAGWPYDESLVDYNLVNNDTTNPAEYTHAEWKGHYHPSPE SWRFPFYTLFIDRFVNGDPTND
 NINGSLFEHDLNSNQMRHGGDAAGLVDTL DYLGGMGIKGIYLAGTILMNQPWGSDGYSJLDITLLDQHYGTIQTWRDAIT
 EIHKRGMYVLFNDTIATMGDLIGFEGYLNTPFSVKEHKALWKS DRQYIDFRFDNEYNNTC EYPRFWNETGYPVDKDVT
 DELVGCYNSDFDQYGDREAFGVYPDWERQLAKFASVQDRLREWHPSVKERLIRHSCMIKALDIDGFRYDKATQATVDAL
 GDM SHAYRECARSVGKDNFFIPGEITGGNNFGSIYLRGRQPNQYPDSSLASMNLTNTSDHQYFLRDHGLQALDSAAAFHY
 SVYRTLTRFLGMDGNLAAGYDTPLDWTDSWNIMVLSNDMINANTGKFDPRHMYGTTNQDVFRWPAIELGVERQLLGHFIT
 TLHLP GIPILLWGEEQAFYILDSTADNYIYGRQAMSPSTAWKTHGCYSLGSSQYYNWPISAGREGCHDEAVAYDHRDP SH
 PLHNI IKHMFQMRQDFPVLNDGYSVVKLSKQTHEIQYPGSNGTATEVGWVSVMRDIVSNIQDFGDSGNNEPVWL VYQNDN
 KTVESYFDCGSND SALSIPFTTGTTVNLFYPHDEHELKDGPKSLHLNGTNATNGCLDSLKMKPF EFRA YVPKANFVKPR
 PMITQFEPGHDPQLSKVGPDESEDIDVSIYFSTKMDCDQVTKSISFESSTEAGKTPSISNNSVSCKDAKGDDPKWTGQI
 PNAWVTAKLTGVYNGIHR LTVKNATSSDGHSSQTATDHFLIRVGQRDNPLVFTSANYSTSLNQYDNGTLYIQHRAAGA
 NKYRYSTNFGSSFDWKDYHGGNDTIEELPWSGTDKQKQGHVVRVEYWNKLTGSSDYAQEGDSGYDHPRRFP HLLFFNGP
 FNQYGYDAGLDNVVRQSDGLWKFRFMAEFPAQGQFNWGMNPDGQPDQSYVFGDIDDDGVLD RMPPSSLSSTIINITDI
 PPSPYLAWN LGVDDGTLRVHLLPTGSR TIQMVVYFLLWFVPLVTAIACVYAFVKSFYQVKFNQVGVSEKKSILPLAFRRK
 MNPDGSGGSINPFMR LANKSGFLQSTPAFGAVASRRRTTLIATMEYDIEDWAIKIKIGGLGVMAQLMGKHLGQQDLI WVV
 PCVGGVDYPVDQPAEPMFVTVLGNSYEVQVQYHVLNIIKYVLLDAPVFRQQT KSEYPARMDDLSAIYYSAWNQCIAQA
 IRRFPIDLYHINDYHGSIAPLYLLPQTIPVGLSLHNAEFQGLWPMRTQKERDEVCSVFNLDLDTAKRYVQFGEVFNMLHA
 GASYL RVHQGF GAVGVSRKYGKRIYARYPIFWGLKKVGNLPNPDPSDIGWNKELPKDSEIQVDANYEASRGELKRQAAQ
 EWAGLDQNP DADLLVFVGRWSMQGVDLIADVMPAVLEARNVQLICVGPVIDLYGKFAALKLDHMMRLYPGRVFSKPEF
 TALPAYIFSGAEFALIPSRDEPGLVAVEFGRKGALGIGARYGGLGQMPGWYNIESTTTSHLLHQFKLAIGSALNSKPQ
 VRAKMRARS AKQRFPVAQWVEDEILQTTAMRIHSGQA KSNGGPLSPSGYNTPEVITPSGMMTPTIASTGTTTPTGMQ
 TPPIAHSREGSYTNLSVNRDSAYGPQQRNTIVYSRDPSPGGNDEPRLSLGRQLSLGFRAGPGHINLRGRRLKRRSQMGNE
 ESGTATEESSDDDYFRGEEVITITREQADEGRHQRNPLRSLASPTNSYFEEGITSGRPPWAQPGNRLSSASVLSVDSVVG
 EKKDYKLQKVDPFFTDGTGEYRYRFDQRLEKLNGSNSESQLCIEEYLMKSEKKWFDKFRDARLGRNQSPASSIFQTKGEN
 NTPMSSISHEDLGSNESGSDPRAEKDEFLLGRDYVPPSGLRKWMQIRIFGWPVYSFFLGLGQIIAANSYQITLLAGENGQ
 TAGKLYGIATVYLVTSIIWWFFFRFFKSVFVLSIPWFLYGASFV IIGLAHFESNGFARGWIONVGS GYVYAAASSSGSLFF
 ALNFGDES GVGQKDWVFRACLIGGTQQAYVIGLWYWGTTISSAVANGVTNVNGGI VNSWKMTAICMPIA AFLWAI GLIIF
 FGLPNYYRQSPGKVP SFYKSVFRRKI VLNWFV VVILQNFFLSAPYGRNWAFLWSSNHAEAWQVGILVVVFFGVIVVAVLT
 LFGYLSKRHSWILPVFACGLGAPRWAQIWWGVSGMGLFLPWAGSSVSGALASRSLWLWLGILDALQGLGFGMILLQTLTR
 VHIAFTLLASQVLGSIATIVARACAPNNIGPGPISPVDYTAGGSSVANAWFWIALFFQLLICAGFLFFRKEQLTKP

Fig. 22

BASE SEQUENCE (PUTATIVE) OF NUCLEIC ACID MOLECULE OF *Aspergillus sojae* agsA

ATGAAGTGGGATTCACTGGCTGGTTGCTTGGCTGCTGCAAGCAACAGCAGCAGGCTGGCCCTATGATGAGTCCCTAGT
 CGATTATAACTTTGAATGTGAATAGGATACACCAATCCGGCTGAATATACACGAGAAATGGAAAGGGCCATACGTATC
 ATCCCTCTCCAGAAAGCTGGCGTTTCCCGTTCTATACCGCTGTTCATTGACCGGTTTGTCAATGGTGATCCCACTAACGAT
 AACATCAACGGGTCACTCTTTGAACATGATCTTAATCAAATCAAAATCCGTACCGGTGGTGTATGACGCTGGCTTGGTGA
 TACACTAGCTACCTACAGGAATGGGCATAAAGGTTGGTGGCAATGATTTGGCTGTGTGTTCCTTGGCTATTGGTGTITAC
 AGCATATGGCTGACTGAGCTCTACAGGGGATCTATTTGGCTGGTACTATCTTAATGAATCAACGATGGGGCTCAGACGGT
 TACTCGATTTTGGATCTACCGTGGCTTGGATCAGCATTATGGTACAATTGAACCTGGAGAGACGCAATCACCGGATTTGA
 TAAGCGGGGCTATGTATGCTCTTTGACAACTACTATCGCAACGTAAGATGCTGGCCCTGGCTAAGTGGTTACATTCAG
 CGCTGACATGAACACGAGATGGGCGATTGGATGGATTGGAGGTTATTTGAATACACGAGCTTTCTGAGTCAAGGA
 GCACAAAGCATTTGGAAATCTGACCGTCACTATACGATTCGCTTTTGAATGATGATCAACACGCTTGGCAATACC
 CTGGATTTGGAAACGAGACTGGCTATCCAGTCGATAAGGATGTCAGAGATGAGCTAGTGGGATGCTATAACAGTGGTTTC
 GACGAGTACGGTGAACGAGAGCTTTGGGTGTCTACCGAGCTGGGAGCGTCAAGTTGGGCAATTCGGTTCAAGTCAAGA
 TCGTCTACGTGAATGGGACCTAGCGTTAAAGAGAGACTTATTCGGGACCTGGTGTATGATATAAAAGGCGCTGGATATTG
 ATGGCTTCGGCTACGATAAAGCGACCGGACGACAGTGGATGCTTTGGTACATGTCCCATGCTTATAGAGAGTGTGCT
 CGGATGTGTGGCAAGGAACTCTTCATTCATTCCTGGGAAATCACTGGTGGGAAATCACTTTGGTGTATTTACCTCGAGC
 TGGAGAGACGGCGAAGCAATACCGAGACTGGTGGTGGCTGGATGAACCTGAGCAACGCTGTGATCATCAGTATTTCT
 TACGTGATCAGCGTCTACAAAGCGCTAGATTGAGCAGGTTTCCATTATTCGGTGTACGCTACCGTCAACGATTCCTAGGT
 ATGGATGGCACTGGCTGGCGGCTATGACACAGCTTGGACTGGACGGACTCTGGAAATATATGGTATTGAGCAACGA
 TATGATCAATGCTAACACTGGCAATTCGAGCCCGGCAATATGATGGTACTACAACCAAGGATGTTTCGGTTGGCTG
 CCACTCGAGCTCGGAGTCGAGAGACACTCTTGGGTCACTTCAACCAAGCTTACATCTCCCGGCACTCCGATTTGGCTG
 TGGGAGAGAGAAACGCTTCTACATTCTAGACTCTACTGGCGGATAACTATATCTATGGCGGTGAAGCAATGTCTCCCTC
 CACTCGCTGGAAACACAGGATGTTATTCGCTTGGTTGGTGGCAATACTACAAGTGGCTATCAGCGCAGGTAGGGAG
 GATGTACAGATGAAGCTGTGGCTTATGATGATCGAGATCGCTGTGATCGACTGGCAATATGATCAAAACAGATGTGGAG
 ATCGACAGGACTTCCCTGTACTGAATGATGGATCTCAGTTGTCAAGTTGTCCAAACAGACTCATGAGATTGAGTATCC
 TGGTTGCAATGGCACGGCAACGGAAGTGGCGCTGTGGTCAATTATGGGTGATTTGTCTCCAACTTCAGGACTTTGGTG
 ACAGCGGCAACCAACGAGCGCTGGCTGGCTATCAAAACGCAACAGAGCGTGGAAATATAGCTTTGATTGTGGGAGT
 AAGGATTCGGGCTTGTATTTCTCGATTACTAGGGGAGCTAGTGTGTTAATCTCTTCTACCGCACAGATGAACAGGAGCT
 GAAAGATGGCGGCAAACTCACTTCACTGAAAGCGGACCAATGCAACAAATGGTTGTCTGGATAGTTTGAAGATGAAGCGCT
 TCGAGTTCAGAGCTTACGTTCCAAAGGCTAACTTTGTTAAGGCTCGTCCCATGATCAACGAGTTCGAGGCTGGTCAAGAT
 GTGGCGGAGCTGTCTAAAGTCGGGCTGACGAATCAGAAATATGACGTTAGCATTGACTTTTCCACTAAGATGGATTG
 TGATCAGGTTACGAAATCGATTTGATTGCAATCCAGTACTGAGGTGGCAAGACTCGCTCTATCAGTAATAAGAGTGTCA
 CGTGCAGGATGGCAAGGCTGATGATCCGAGTGGAGTGGTCAAAATCCCAACGCTTGGGTCTGGACGCGAAGTTGACT
 GCGGTTTACAACGCTATCCATCGCTTGACCGTCAAAATGCAACTAGTTGCGATGGCATAGTTCTACCCAAGCAACTGA
 TCACCTTCTTGATCGGAGTGGGCAAGGGATAATCCGTTGGTGTTCACATCTGGCAACTACTCGACCTGCTTTGTTAAAGC
 AATATGACAAATGGCAGCTCTACATCCAACATCGTGCAGCAGGCGCAACAAATACCGCTATTCAACAAATTTGGTTCC
 TCATTCTCTGACTGGAAAGACTACCAAGGAGGAAGCATACTATTGAAGAACTGCCCTGGAGTGGAAAGGCAAGCAAAA
 GTGGCAAGGGAAGCAGTGGGAGTGGAAATAGTGAATAAGTTAACGGGACGAGTACTAGCTCAGGAAGGCGACTCTG
 GATATGACCATCGACGAGCTTTCCGCTATTTCTTCAAGGGGCAATTAAGCAATATGGATATGATCGGGGCTTAGAC
 AAGCTTGTGAGGCAAGACAGTGTATGGTCTTTGGAAGTTGAGATTGATGGCTGAGTTTCCAGCACAAAGGACAGTTCAATGT
 TTGGGGAATGAATCCAGATGGTCAACGAGCAGAGCTACGTTGTGGTGTATATGATGATGACGGAGTTTGGACGTA
 TGGCTGCTTCTTGGCTTGTTCACGATAATAAATCATCAGGATATCCCTCCATCTCCATACTTGGCTGGAAATCTTGGT
 GTTGACGAGGAACTCTGGCTGTTCACTCTTCTGCAACGGGTTCAAGGACCATCCAGATGGTTGTGTACTTCTGCTCTG
 GTTTGTTCCGCTTGTACAGGATCGCTTGTGTCTATGGCTTGGTGAATCTTCTACCAAGTCAAGTTCAACCAAGTGG
 GGGTACGCAAAAGAAATCAATCTTCCATTGGCATTCGCAAGGAAATGAACCGGATGGAGCGGGGATCAATCAAT
 CCTTTCATGGCGCTTGGCAATAGTCCGGATTCTTGCAAAAGCACACTGCTTTTGGAGCAGTACTTCAAGAGACGGAC
 GACCTTGATTGCCACCATGGAATATGATATGAGGACTGGGCCATCAAGATTAATCGGTGGTCTGGGTGTTATGGCTC
 AGCTTATGGGCAACAGCTTGGGACGAGGATCTAATTTGGGTGTTCATGCGTGGGAGGAGTTGACTACCGGGTAGAT
 CAGCCAGCTGAGGCTATGTTTGTGACAGTGTGGGAAATTCGACGAAGTCCAGGTGGCAATACGCTCTGTAATACAT

Fig. 23

TAAATATGTCCTTTTAGATGCTCCTGTTTTTCGTCAACAGACCAATCTGAGCCTTATCCGCGCCGAATGGACGATTTGG
 ACAGCGCAATCTACTATTCCGCTTGGAACCAAGTCGATTCGACAAGCAATCAGACGTTTCCCAATTGATCTTTATCATATC
 AAGCACTAGCATGGATCCATTGGCCCTCTTTATCTTGCCTCAAAACCATGCCGTGTTTGTCTGCTGCAAAATGCCGA
 GTTCCAAGGACTGTGGCCATGCTACCCAGAGGAGAGGGATGAAGTCTGTTCTGTTTTCAACCTTGATCTTGACACTG
 CAAAGCGTTACGTCGAGTTTGGCGAAGTTTTAACATGCTTCATGCTGGAGCAAGCTACCTACGCGTGCATCAACAAGGG
 TTTGGTGCAGTGGGCGTTTCTCGGAAGTATGGTAAACGTACTTATGCCGCGTACCTATCTTTTGGGGTCTGAAGAAAGT
 TGGAAATGTCACGAAACCGGACCGCTTCAGACACTGGCGAATGGAACAAGGAGTTACCAAAGGACAGCGAGATTCAAGTTG
 ACGCGAACTACGAGGCGAGAGAGGGGAGCTTAAGCGCGCAAGGCGAGGAATGGGGGCGCTTGATCAGAACCCTGATGCT
 GACCTGTTGGTGTGTTTGTGGAAAGATGGTCTATGCAGAGGGCGTGGACCTTATTGCTGATGTGATGCTGCGCTTCTGGA
 AGCAGCTCCCAATGTTCAACTCATCTGTGTTGGTCCAGTCATTGATCTTTATGGTAAATTTGCTGCGCTTAAGCTCGACC
 ATATGATGAGGTTGATCTGCGCGTGTCTTCTCAAAGCCTGAGTTTACTGCACTTCAGCATATATCTTCTCTGGCGCT
 GAATTGCGCCTGATTCCATCTCGTGATGAACCTTTTGGTCTTGTGCTTGAATTTGGTCGAAAGGGCGCTCTTGGTAT
 TGGCGCTGCTGCTGGTGTCTGGCCAGATGCTGGTTGGTGGTATAATATTGAGTCTACAACAACCTTCCCATCTCTTGC
 ATCAATTCAGGCTTGGATTGGAAAGCGCGCTTAACTCGAAGCCCAAGTTGCTGCAAGATGCTGACAGCTCTGCAAG
 CAACGCTTTCTGTTGCTCAGTGGGTGGAAAGATTTAGAAATTCGCAAGCACTGCTATCGGATTGACAGCAAGGGGA
 GGGAAATCGAACGCTGGCGCTCTCTCGCTTCTGGTTACAAACACCAAGTGAAGTAATAACACCAAGTGGAAATGATGA
 CAGCTACGATTGATCGACTGGTACCAAGCCCAACAGGGATGCAGACACCTCCAATCGCAGACTCACGGGAAGCGAGT
 TACACGAATCTCAGCGCTCAACCGGCGACAGTGCATACGGGCGCAACAGCGCAACACAATTTGTGACAGCGCTGACCGAAG
 TCGTGGAGGTAACGACGAACCTAGGTTAAGCCTTGGTCGGCAACTGTCATTGGATTCCGGGCTGGACCAAGGACATATTA
 ATCTCCGCTGCTGCTGGCTTAAAGAGAAGAGCCAGATGGGCAACGAGGAGAGTGGTACCGGACCGAAGAAAGCAGTGAT
 GAGGATTATTTCCGCGGAGAGGAAGAGTTACGATTACGAGGGAGCAAGCAGATGAAGGACGGCATCAACGCAATCCTCT
 GAGGTCGCTTGCATCTCCTACCACTCTTACTTTGAAGAAGGCATAACATCCGGAAGGCCACCTTGGGCTCAACCTGGGA
 ATCGACTCAGTAGTGCATCGGTTCTTTCTGTTGATTCTGCTGCTGGGGAAGAAAGACTATAAGCTGCAGAAAGTTGAT
 CCAATCTTCACAGACGCTACTGGCGAATACTATCGAGTGTGTTGATCAGAGACTCGAGAAGCTCAACGGATCTAACTCTGA
 ATCTCAGCTTTGTATAGAGGAGTATCTGATGAAGAGCGAAAGAGTGGTTTGACAAGTTTAGAGACGCAAGATTGGGCG
 GCAACCAATCTCCGCTTCTTGCATTTTCCAAACCAAGGGCGAAACACACACCTATGAGCTCAATCTCCACAGAGGAT
 CTGGGTTCAAACGAAGTGGCAGCGATCCACGCGCAGAAAAGGACGAGTTCTCTGGGACGAGACTATGTTCCCGCTC
 GGGCTTAAGGAAATGGATGCAATTCGAATCTTTGGCTGGCTGTGATTCTGTTTTCTAGGCTCGGTCAGATCATTG
 CGGCCAAGCTCGTACCGATTACCTTCTTGGCGGTGAAAACGGCCAGACAGCTGGGAAGCTCTATGTTATTGCGACAGTA
 TACCTTGTCACTTCAATCATCTGGTGGTTTTCTTCCGCTTCTTCAAATCGGTGTTTGTCTTTCCATACCTTGGTCTT
 ATACGGCGCATGTTTGTATCTTGGATTAGCACACTTTGAGTCAAAATGGCTTGGCTGCTGATGATCCAGAAATGTGG
 GAAGCGGTGTTTATGCTGCTGCTTCTTCAAGTGATCACTGTTCTTGGCTCTCAATTTTGGCATGAAAGCGGTGTTGAG
 GTTAAAGACTGGGTTTTTCGCGCATGCTCATCCAAGGAACCTCAGCAAGCATATGTTATTGGGCTGTGGTACTGGGGAAC
 GACAACTCTAGCGCTGTCCGCAATGGAGTTACCAACCTCAACGGTGGCATTGTCAACTCTGGAAAAATGACGTACGTTT
 CACCGTTATCATTATGATTACAATTGCTAACAGGCTCTTGTAGCGCAATCTGCATGCCAATCGCTGCACTTCTCTGGGCG
 ATTGGTCTGATAATCTCTTCCGCGTGGCCCAATTACTACGCGCAGTCACCTGGAAAAAGTCCATCATTCTATAAGTCTGT
 CTTCCGCGCAAGATCGTTTTGTGGAAGTCTGGTGTGATGATTTTGCAAAAGTCTTCTCTCAGCGCACCTTATGAGCGGA
 ACTGGGCGCTGAAGTACATCAGACCTATACCTCCAAAGAGCCACTAATTATCTGCGCCCATACAGTCTTTGGAGCTC
 AAACCATGCCGAAGCTGGCAAGTGGCATCCTGCTGCTGCTCTTCTGCTGCTATCTGGGTAGCAGTGTAAACCTGT
 TTGGATATCTCCAAAGCGCATAGCTGATTCTACCTGTATTGCGATGTGGTTTGGGAGCTCCACGTTGGGCGCAGATA
 TGGTGGGTGCTCCGGAATGGGTCTCTTCTTCCCTGGGCTGGCAGTCTGTTAGCGGAGCACTGCGATCAGGAAGTCT
 ATGGCTCTGGCTCGTATCTTGTATGCCCTTACAGGGTCTCGGCTTGGCATGATTCTTCTCAGACCTCAGACAGATAC
 ATATAGCTTACCGCTGCTTGCATCTCAAGTGTGGGTTCCATCGCGACAATCGTGGCAGAGCATGTGCTCCAAACAAC
 ATCGGCGCTGGACCAATCTCCCGAGATGTGATGCGGCTGGCAGTTCGCTGCCAAACGCTTGGTTCTGGATCGCTTATT
 CTTCCAGCTCTTGTATCTGGTAAGTCACTGATCCCGCTACAATCCATTTACAGGAAGCAAAATACTAAACAAGCCCGAGC
 GCTGGATTCTCTGTTCTTCCGGAAGAGCAACTACCAAGCCCTAA

Fig. 24

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus sojae* AgsB

MKWAFSSTVLALFATTATAWPYEESSLAYNLNENKSATNPAQYWGEWPDHKGKYFSPDNWRFVYTLFMDRFVNGDPTN
 DNINGTLFEHDISSQMRHGGDVAGLVDTLDYLGGMGIKAIYLAGTILMNQPWGSDGYSALDTLLDQHFQDIATWRNAI
 DEIHKRGMVIFDNTIATMGDLIGFEGHLNDTTPFSVKEHKALWKSRRRYVDFDLGNDYNQTCDYPRFWYEDGYPVQQSM
 TEGLVGCGYDSDFDQYGDIEAFGVFPDWQRQLAKFASVQDRLREWHPSVRERLIRHSCMIYQLDIDGFRYDKATQSTVDA
 LGDMSMAYRECARAVGKENFFISGEITGGNTFGSIYLGRRQPNQYPKTAEEAMKMTNESESQYFLREAGHEAIDGAAFH
 YSTYRALTRFLGMDGNLAAGYDVPVDWVDWVDAWNMLQSNDFINPNTGKFDPRHMFATNQDVFRWPTVEKGVERQLLGLYI
 TLLLPGLPLLLWGEEQAFYILDATASNYIYGRQAMSPATAWRDHGCFSLDSSQYYQWPIQAGREGCHDPTAAYDHRDPA
 HPVRNI IKHMYQLREDFPVLNDGYSVQKLSNLTEEVYPGSGTATETGLWSVLRDVNAEVQDLGSDAKNQPVWL VYHNT
 NRTIDFKFDCKDNETALISPFPTGKVRNLFYPYDEHTLIDGPVKLGLNGSTELNGCLANMTLDAYEFRAYVPSTRFTKP
 RPMITQFTPGHDVPRSTVAPDMDES VKIELYFSEEMDCDSVTAKAISITSSTESRKVPTLDEKTVDCGIPASNTSWTGQ
 LPSVFMWAANLTGVYNGIHRVTVKNASSTNGNATTNAVDFLFRIGQIDNPMVFTSANYSTLLHEESNGTLFVQHHAA
 ADKWRYSNTWGTTFSEWKDYTGNDTITELEWSGTTKQRWQGHVVRVEYWSKWTGSSDYVQEGDVGVHNSLPRRPFHIF
 NGPYNQYGYDGGLDNVYRQDSKDLWKYHFTAEPQAQALNIWGMNPDGKPDQSWVLGDADNDSVLD RMPSSLSATLIN
 ITEHPPKPYLAWNIIYINDATMKFQLFPVGHQNTQIAMFVLFWIIPVITGAACVYIFMKSFYKVKFNQIGVSEKATLIPLA
 LRRKFKNRNGGDEEKMNPLMLANKSGFLQNTAIGGAASGKRRMVL IATMEYDIEDWQIKIKIGGLQVMAQLMGKTLGH
 QDLIWWVPCVGGVEYPYDTPAEPMNVTILGNSYEVQVYHVLNNITYVLLDAPVFRQQSKSEYPARMDDLNSAIYYS
 AWNQCIAEACKRFIDLYHINDYHGLAPLYLLPDTVPACLSLHNAEFQGLWPMRTQKEKEEVCSVFNLDIDIVRRYVQFGE
 VFNLLHSGASYLRVHQGGFAGVGVSKKYGKRSYARYPIFWGLRKVGNLNPNPDSDVGEWSKEKAIGNADEVHVDPDYEAG
 RADLKRQAQEWAGLEVNPADLMVFVGRWSMOKGVDLIADVMPAVLEARNVQVICVGPVIDLYGKFAALKLDHMMKVYP
 GRVFSRPEFTALPPYIFSGAEFALIPSRDEPFGLVAVEFGRKGALGIGARVGGGQMPGWYNNVESTATSHLLYQFKLAI
 DAALNSKQETRAMMRARSQKRFPAQWVEDLEILQTTAIQVHNKELVKHNGRPFTPTGTITPSGLMTQPASPPMTPGMQ
 TPLAHSRESSYSLNRLSEYVTQPKTSYSRDPSPSGTEKPKSGLQRQLSLGVRSGPGHQSRGRARQRDSIPEHEDTQEA
 HGGAITDVEEESDDDIVNHYADDEYTLTPAQVEEGRRLQAAQQAGGRRYSQDSLHPRNVQPPSSPGTPPAASQSLLPP
 PRLLDPGSRLSSASVLSLDSVVGKKDFKLQKVDPFFTDSTGEYYKVFDKKLDELNGSNSESQLCIEEYLKSEKEWFDK
 FRDARLGRKTSPTSPVYRDKHGASPIGSFYDDNGSRISGSDGPHSNDSEDFLLGKDYVPPTGLKKWMQIRIGDWPIYS
 LFLALGQIIAANSYQITLLTGVEGQTAEKLYGIATTYLTITSILWWLVFRYFKSVVCLSAWFLYGIAFIFIGSAHFESNS
 FSRGWIQNVGSGFYAAASSSGSFFALNFGDEGGAPVETWIFRACLIQGIQSAYVIALWYWGSTLSQAQSEGLLTPTNNI
 SNSWKMSAICYPIAAALFGIGLLLTGFLPNYYRQTPGKVASFYKSVLRRKIVLWNFVAVILQNFFLSAPYGRNWQFLWTS
 HHVHHWQIVILCVVYGFVWAGFLFVVSRYFKSHSWFLPVFACGLGAPRWAQIWWGVSGIGYYLPWVTGGYTGGALVSR
 VWLWLGVLDSIQGLGFGIILLQTLTRMHMVFCLVCSQVLGSIATICARAFAPNNVGPVSPDPTFGGSAVANAWFWVAL
 FCQLLVCAGYILFFRKEQLSKP

Fig. 25

BASE SEQUENCE (PUTATIVE) OF NUCLEIC ACID MOLECULE OF *Aspergillus sojae* agsB

ATCAAGTGGGCTTTCGCAAGTACGGTGGTGGGCTTTTCGCAACACAGCAAGGGCTTACGAGGAATCACTATC
 CGCATACAACTTAAGGAAACAAATCGGGACCAACCGGCTCAATATTGGGGAAGATGCGCGACACAAAGGGAAAT
 ACITCCCTTCGCGGACAAATGGGGAATTTCCGCTATACCGCTGTGATGGACCGCTTTGTCAACGGAGACCGTACGAAT
 GACAACATTAATGGGACCGCTTCGAGACGATATCTCTCGACACAGATGCGCCATGGTGGAGATGTGGCTGGCTAGT
 GGATACITTTGGATATCTTCAGGGAAATGGGTATCAAGGTGGCTCATTCGTTGATTTCAATACGTGGGATGGGATACATGA
 GAATTGCTAGGGCATCTATCTCGGAGGAACATCTTGGATGAACGAGCCATGGGGCTGTGATGGTTATTCGCTCTCGATA
 CGACCGCTGCTCGACCAACACTTCGCTGACATTCGACATGGCTAATGCTATCGACGAGATTCTAAGCGCGGATGTAT
 GTCATCTTTGATAACAGGATGCTACGTAAGTCTTGGCGCATCCAGATAGTACATATGAGGTGATTGTAAAGGTGTGA
 TTTCAAGATGGGTGATCTCATCGGCTTCGAGGGCCACTTGAATGATACGACCGCGTTTTCGTTAAGGAGCATAAAGCGCT
 TTGGAAGAGCGATCGTCCCTATGTGGATTTGATCTCGGAACGACTATAACGACATGCGACTACCCCGGTTCTGGT
 ACGAGGACGCTTACGATTCGACAGTCCATGACGAGGGCTTGTGGTTGTTATGACAGTGACTTTGATCAATATGGT
 GATATTGAGGGCTTCGGGTGTTCCCTGATTGGCAACGTGAGCTAGCAAAATTTGCGTCCGTCAAGATCGCTACGAGA
 ATGGACCGCTCGGTGCGGAGACGGCTGATTGCGCATTCGTGTATGATTATCTACGAGTTGGATATCGACGGTTTCGCT
 ATGATAGGGGACCTGAGTCGACCGTGGATGGGCTGGGAGATATGTCGATGGCTTATCGGGAATGGCGCGTGGCGTTGGC
 AAGGAGAAATTTCTCATCTCGGTGAAATTAAGTGGTGAACACTTTGGTTCTATTTTGGGCGAGGACAGCAACG
 TAACGAGTATCTTAAGACGGGCGAGGAGGCGCATGAAATGACCAAGGAGTGGGATCGCAATACCTTCGCTGGTGAAGCTG
 GACATGAGGCGATCGACGGCGCGGCTTCCACTATTGACATATCGTCTGCTGACTCGGTTCTTGGGTATGATGGTAACT
 TTGGCGCGGGTTACGATGTTCTGTGGATTGGGTCGATGGTGGAAATTTGATGTTGCACTGCAACGACTTCAACAGCC
 TAACAGGGGCAAGTTGATCCCGGCGCATATGTTTGGCGGACCAACGAGGATGTTTCCGCTGGCGAAGCTGAAAGAG
 GTGTGGAAGCGGAGTTGCTTGGGCTGTATATCACTACCTTACTTCTTCGGGGCATTCGCTCTCTCTTTGGGGCGAGGA
 CAGGCAATTCATATCTTATGATGCGACGACATCTAATATATCTATGGCGGTCAAGCAATGTCGCGCGCGACTGGGTGGAG
 AGACCAAGGTTGCTTTTCCTTGGATTCTTCACGATATTATGATGGCGGATTCAGCGCGGTCGTGAGGGTTGGCATGATC
 GAGTGGTGGTACGATGATCGTGGTGGGCGGCGGCTGGGCAAGATTATTAAGGACATGACGAGTGGGGAAGAC
 TTCCCTGTTCTGACGATGAGTACTCGGTTCAAGAACTCTGCAACTTGGCGAGGAGGCTTCTATCGGGGCTCCAAAGG
 TACCGCTACGAAACGGGTTTGTGGTCTGCTGCTGCTGATGTCATGGGAGGTGCAAGGACTGGGCTCCGACGCAAGA
 ATCAAGCGGTTTGGCTGCTGACGACACACCAAGCGTACAATTGACTTCAAGTTCGACTGCAAGGACAACGAGCTGCA
 CTAATCTCCCGCTTCGCGACCGGACCAAGGTCGAAATCTGTTCTATCCCTATGACGAGCACACCTTGATTGATGGCGC
 CGTGAAGCTTGGACTGAAGGATCTACCGAGCTCAACGGCTGGCTGGGCAACATGACATTGCAAGCGCTATGAGTTCCGGC
 CCTACGTCGCGAGTACAGGTTTCACTAAGCGCGCGCGATGATACCGAGTTTACTCCGCGCATGACGTCCCTGTTGGC
 TCCACGGTGGCTCCGATATGATGAAGCGTGAAGATTGAGCTCTATTTCTCGAAGAGATGAGCTGTATTCCGTGAC
 TAAAGCAATCTGATACGCTTCTACGGAATCTAGAAAAGTCCGACACTGGATGAGAAAGCTGATGATTGCAAGGGAA
 TTCCGGCAAGCAACATCGGTGGAGTGGGAGCTCCCTAGGCTCTTCTATGGGCTGCCAACCTGACGGGAGTGTACAAC
 GGCATTACCGGGTTACGTTAAGAAAGCTAGCACTACTAATGGAAGCGGACGCAAAAGCGGCTGCCCACTTCTCTT
 CGGATTTGGCAAAATGATATCGGATGGTCTTTAGATGGGCGAGTATTGGAGTATTGCTCCAGGAGGATCGAATG
 GTACCGCTGTTCTGACGATACCGGCTGGTGGTGAATGAGTGGGTTTCTACCAATTTGGGGCACCACTTTCTCCGAG
 TGGAAAGGATTACACAGTGGCAATGACACTATCACGGAGTTAGAATGGTCTGGAACCAAGAAACAGAGATGGCAGGGACA
 CCGATGCGGGTGGAGTATTGGAGCAATGGAACGGTAGGAGCGATTACGTTACGAGGGGCGATGTTGGAGTGCATTGGA
 ATCTGCTGCGGCTTCCCGCATATCTTCTTCAAGCGGCGTTAGAATCAGTACGGCTATGACGGTGGCTTTGATAAGCTG
 GTGAGGAGGAGTCCAAAGACGGTCTCTGGAATATCACTTCAAGGGGGAATGGCTGGCTCAAGCTCAGCTGAACATTGG
 GGGCATGAATCGGATGGAAGCGCTGATCAAGGCTGGGTGCTGGGTGATCGGATATGATTCCGTTCTGGATGAAATGC
 CACCGCTCTCTCTGTTGGAAGCTTGTCAACATCACCGAGCATCGGCTAAGGCTTATCTGGCTTGGAAATCTACATC
 AAGGATGCGACCATGAAGTTCAGGCTCTTCCCTGTGGGGACGAGAAACGCGAGATCGCCATGTTCTGTGCTCTGTGGAT
 CATCCGTGTCATCACCGGTGCAAGCATGGTCTACATTTTCATGAAGTCTTTCTATAAGGTCAAGTTCAACGAGATCGGTG
 TGAAGTAAAGGCGCATGATCCCTTTGGCTTTGGGAGAAAGTTCAAGAGAAATCGTGGTGGTGAAGGAAAGAGTGA
 AATCCCTTAATGGCTGCGGCAAGAAAGTCCGGTTTCTGCGAGCAACACCGCTATTGGCGGCGCTGCTTCTGCAAGAG
 ACGCATGGTTCTGATCGGACCATGAGTATGATATCGAGGATTGGCAGATTAAAGTCAAGATTGGTGGTCTTGGTGTCA
 TGGCGCAGGTTTATGGTTAAAGTCTCGGACATCAGGAGTGTGTTGGTTGTTCCCTGTGTCGGGAGTGGAAATACCGCA
 GTGATACCGCGCTGAGCGCATGAATGTGACGATTCTTGGCACTGCTATGAAGTTCAAGTCCAGTACCATGTGTTGAA

Fig. 26

AATAATACCTACGTTTTCGTAGACGCCCTCTGTGTTCCGTGACGAATCGAAGTCCGAACCTATCCAGCCCGATGGATG
 ACCTCAACACGTGCTATCACTTACTCCGCTGGAATCAGTGTATTTGTCAGGGCTCGAAAGCGTTCCGCATCTGCTT
 CATTCACAGCATATACAGGTTTCGCGATCCGCTCTACTCTTCCGATATGTCAGGCGTTGTCCTTACCTTACAA
 TCGTGAATTCAGGGTCTCTGGCCAAATCGCTACACAGAAAGAAAGGAAGAGTGTGCTCCGCTTTTAACCTGGATATTG
 ATATTGTCAGAGCTTATGCGATTTGCGGTGAGGTTTCAACTTGTCTGCACTGGGTGTGATATTCTTCGTTGTCCACG
 CAGGGTTTCGTCGCGCTGGGTGTGTGCTCAACAAAGTACGGAAAGCGTTCTCGCCGCGTTATCCCATCTTCTGGGGTTGAG
 AAAGGTTGCGAACCTGCTTACCCCTGATCTTTCAGATGTGTCGAGAAATGGATGAAGAAAGGCTATTGCGAACCGTGACG
 AGGTTCACTGTGGATCCGCACTTGAAGCCGGCAGAGCCGACTCAAAAGCCAGGCTCGAATAGGGTGGTGTGTGAAGTG
 AACCCGACGAGCTGCTATTATGGTTGTCGTTGGTGGTGGTGCATGCAAGAAAGTGTGTTAATTAATCGCGATGTGATGCC
 CGCTGTTCTTGAAGCTCGTCTTAACGTCCAAAGTGATTTGTGTTGACCTGTTATCGATCTTTATGGTAAATTCGCCGCT
 GAAAGTTAGACAGAGCTGATGAAGGTTTACGCTGACAGCTGTGTTTTCGAGACGCTGAATTCACCGCTGTCTCCGCTTATATC
 TTCTGTGTCGTGAATTCGCGCTATTCCCTTCTGTGACGACGAGCCCTTGGTCTATGTCGAGTCGAGTTTCGCGCTATAAGG
 AGCCTTGGGTATTGGTGCCTGCTTTGGTGGTCTGGTCAGATGCTTGGTTGGTGGTTAAACGTCGAATCTACTGCGACAT
 CTGATCTTATGTCACGAGTTCAAATTCGCAATGACGTGACGCCBACTGAAGTCAAGAACAGACGAGCATGATGCGTGCC
 CGTTCGCTGAACACAGGATTCGCCGTCGCCCAATGCTGTGCGAGCACTGGAGATCTGCGAACACCGGCAATTGAAGTACA
 CAACAAGGAACGTGGTTAAGCACAAAGGTCGCGCGTTCCTCTACTGGAACAATTATCTCTAGTGGCTTTATGACTCAGC
 TCGAGCCGCGCCGCTTACCTCCGGGTATGCAAACTCGCTTGGCTATTCGCGAACAGAGCAGCTACTCCAACCTCAACCGC
 TTAAGTGAATCACTTCCACCGCAAGACAGCTACAGCAGAGATCCCAAGCCCTAGCGCAGCGGAAGCCGAATCAGG
 ACTTCAGCGACAGCTTTCACTTGGTGTTCGCTGGTCTGGTATCATCAGAGCCGTGGTGGCGCTGCGCAGCGTGACA
 GTATCCGAGAACACGAAGACACTCAGGAAGCGCACGCTGCGCCATTACTGATGTTGAGGAAGAAAGCAGTACGACGAT
 ATTCGACAGCTTATGCGAGCAGCGATGATGTTTACCGCGCAAGTCAAGAGAGGCGAGGCTAGCGAGCCGCCCA
 GGAAGACCGCTGGTGTGCGGATGCGGTTACTCTCCAGGTTGTAAGCGTGGCAGCAAGCACTTGAATGTCGAGAAATGTCC
 AGCCTCCTTCAAGTCCCGGAACACCGCCAGCCGCTTCCCAAGGCTCCTTCTCTCCCTTAGGCTCCTCGATCCGCGACG
 CGCTTCGATAGGCGATCCGTTCTCTCCTCACTTGAAGCTCGGTTGTGCGTGGCAAGAGGACTCAAGCTGCGAAGAGTTGATC
 GTTCTTCCAGGATAGCCAGCGCAGATTACAAGGTCCTTTGATAAGAACTTGTAAGACTCAATGGATGCAACTCGACCT
 CGCAACTGTGATACGAAGAAATCTGATCAAGAGTGAAGAAAGAAATGGTTCGATAAGTTCGCTGACGCGCAGACTTGGTGG
 CCAAAATCGCAAACTCCCTCAGTCTACCGCTGATAAGCAAGCGGCCCTCAGCATTCTCGCTCTTTTACGATGATACGCTC
 CGCATATAGTGGTAGGATGGCGCTCAGCTCGAATGACAGTGAAGACGAGGAGGAGTTCCTTTCGGAAGAGGACATGTCCGCT
 CCACTGCTCTCAAGAAAGTGAATGACAGATCCGATCGCTGACTGBCCTATCTACTCTTCTTCTCGCTCTAGCGCAATCT
 ATGTGTCGCAACCTGCTACGAGATCAGATTGCTCAGGGGTGAAGTCCGTCAGATCGCGAGAACTCGCGAAGACTTGAAC
 CAGCTGTTGATCAGTCACTATTCTTGTGCTGGTGTGCTGCTGCTTCAAACTCCGCTGCTGTGCTGTCTGCGCATGCGC
 TCTGTACGCTATTGCTTCTATTTCATTCGATCGGCCATTGTGAAGCAACTCTTTCAGTCCGGGATGGATTCAAAT
 TGCAGTATGTCGCTCTACGCTGCGGCTCTGTATGAGTGTCTTCTTCTTCGCAATGAACTTCGCTGATGAGAGTGGTGG
 ACTGTTGAAACATGGAATTTCCGTCGACCTTGATTCAGGAGTTACGATCGGCTATGTTATTCGCTGATGAGATCTGG
 GTTCAACCGCTGTACAGGCAAGAAAGTGAAGGCTCTCTGACTCTCAACAACAATTTTCCAATCTCGAAGATGAGGTT
 GTTCTTATGAATCAATGCTTAATCTTACATGACTACGATGAGGCTTTCAGAGTGCATCTGTTAGCCCATCTGCGCCGCC
 CTTTTTAAACTCGGCTGTGCTGTGACATCTGCTGTGCCAAATTATTCGACGAGACTCTGGCAAGAGTCCGTTCCCTCTCA
 CAAGTCGCTGTCGCTGTAAGATCGTCCTTGAACCTTTGTGCGGTCATCCTTCAGAACTCTTCTCGACGCCGCCCT
 ACGCGCGCAACTGGCAGCTGTAAGTGAACCTGTATATACGCTCTGTCTCACGACGCAAACTCAACTGCTTCTTATC
 GTTCTTATGACTTGGCTGCTGATCACTGCAATCACTGCTCTGCTTGTGTTTCTACGGCTTCGATGAGGACG
 AGTTCCTATTGCTGTGACGTGCTCACTCAAATCAACAGTTGGTTCCTGCCCTGTTCCGCTGTGCGCTCGGAGCGGCC
 CGCTGGGCAACAATGTGTGGGTTGTGTTGCACTTGGCTACTACTTCTTGGTGAACAGAGATGATACACGCGCGCGC
 CTTGCTCTCCGCGAGTGTCTGCTCTGCTGCGCGCTGCTGACCTGATCGATCGGCTCGGCTAGGATATCATCTCTGGA
 AAACGCTCACTGCGATGCACATGTTTTGTTGTTGTTGTTTCAAGTCTGGTTCGATGCTCATCTATGCGCGAGGA
 GCTTCCGCGCTTAATAATGTGGGCGGAGGCGGTTTTCGCTGTATCTGACTCTGCTGGGTAGCGCTGTGCGCAATGCGCT
 GTTCTGGTGTGCTGTTTGTGATGATGTTGGTGTGTAAGTTATTCACATCTCTTAAACTCGGTTATATAGGATAAT
 GCTAACGTGTGCTGTTTGAAGTCGGGTTACATGCTCTTCTCGGAAAGAACAGCTGTCAAAGCGGTAA

Fig. 27

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus sojae* AgsC

MFLTVMQRSAILILSLLSATALSWPYTESLVYDNLNENKTAEPIDYWGEWPDHEYHPSPDNWRFPITYIFLDRIANGDP
 KNDDINGTAFEHVVGSNQMRHGGDLVGLIDTLDYIRGMGFKGIYFAGTYLMNLPWAYDGYSPVDTLLDMHHGTLEDWRR
 TITEIHKRDMYVIMDNLTATMSNLIGFKGHLNDSADFRADYEYVQWISDRQYADFKFGNEYNETCNFPKFNETGYPLTS
 GGVEELKGCYNPDFDQFGELEAFGNFPDWKRQLTKFASVQDRLREWHKPIRDVITKHSCIQIASLDJGGFRFDKAVQATL
 EPLSEITAVYRECAKKYKGHNFFLPGEITSGNTFGSLYLGRGRQPDQQPESADAGAKLKNSSDGYFLRDDGGYQALDSAAF
 HYTIYRSMTRFLGMDGNLVAGFDLPTDFIEAWNGLVSNDFLNAYTGEVDPRHMFVSNQDNFRWPAIRNGTEKYLLGLY
 IVTLELPGIPLILWGEEQAMYVFESTASNYLFGROPMTYQTAWWTHGCMTLNTSKFYDFPNEKGLHGCEITVTYDQRNP
 AHPLRNIMKRMFEIREQYPVANDGFYQLTSLQTKDYYLPGSADTPTVTGLWSVLRSYFPGVQKEASKNSQNLWLKDTAL
 LSPFKSGTKLKNLFYPYDELTEDEGPGEVAVHNSTESYGCIRSMKLLPWEYRAYIEAENFVEPGPTVTEFVPGHDARLLS
 TDDSGQTVDIQLGYSKEMDCOKIADAISLNSTTVKGVTASLDTSSVSCNKISARTSSDNFVGEVPTVWTSAKLKNVHHG
 IHQLTVKNVSTTSQVHTDAVDQFLFRVGSQNNPLLSPLSNYSTSLVQKSDNGSFYIQHDAAGADKFRYSTDFGLNWSNWT
 TYTGDNLTLVNFPWETGTDAQKWKGTJIRVQYFSRLTGSSDYIQEGDHGWEKGVARRFPNLFWNGPFNQYGDAGLDNKMR
 YDTKEHRWKYDFVYEWPAIGQMSVWGMKDGPRPDVTEVYGDVDNSSVVQKLPPSYLSSNVINITKLPPFPHLGWTITLND
 ANLRYEMLPVGSGWAQLVLYILLWVLPILMGFAGIFIFIRTFYRVKLNTDGDVAKEDKLPLLFWRRVREKFSGGDESOKS
 ISDKDIPTDIAIAGAPEQRRTVLATMEYNIEDWKVKVKGIGGLGVMAQLMSQHLKHQNLIWVVPVCGDIEYPQDTPSEPF
 VVTILDKPYFINVQYHIVDNITYVLLDAPVFRQQTAEPPYPRMDDLDSAIYYSAWNQCIAETIKRFPSIDLYHINDFHG
 CLAPLYLLPTRTIPVCLSLHNAEFQGLWPLRNPHEKKEVCSVFNLPJETATKYSQFGNVFNLLHTGASYVRFYQRGFAGV
 GVSCKYKGRSWARYPIFWSLEKIGSLPNPDPSDTGDMTNNPDAEVPISQSYEERINDKLQAQKWAGLNEDRDADLLVFVGR
 WSKQKGVDLIADVMPAILSARPHVQLICVGPVVDLYGRLAATKLERIMEMFPGRVFSKPEFTVLPPYVFSQADFALIPSR
 DEPFGLVAVEFGRKGALGIGSRJGGLQMPGWYTTVESDATRHLLHQLKTAIKQALDSSQEAAREEMRANSVRQHFPVLEW
 IQKLEALQRTAIQIHHTKNKNTVTGMPESQNYWETQSVRMSTLGLPGPTQSMTEGLDTPDRLLMPGQSRFTELQLEGA
 DGNRNSSLGRKLSLGRRSGPGQDRKRLGKSPPRESQILGEDLEGENTDAEEEGTATPHVNYISPEEAMAAVNNTLTGTQDI
 GTAHTNNSTHSLAGPQGSTYMSAPGSPNNMSRASSPMPGTPALPQYPFQLALGSGGNTPFAHSRNVSMLSLPSVVAHDNQ
 PVFELQKVDPTFTDSTRHFTRRFEEILNNLNKKNSMTDCCITETLYLMKSERKFYSMYNDAQLKKQPDRAVSDSNSDTQDN
 RASYATVTGGSDSNPDDEIDLWLSRLGYKRPIAIQRFMRRLGKWPVYALFLGLGQIIATNSAQMTLLVGQVGETATKLY
 IATIYCISSICWLLFYRFPSVIVLTLFPWFIYCMAFIIIGVSPFALTSLGRAWAQNVAAAGVYSAASSSGSLFFALNFGD
 QGAVPIKDWMFRASLIQGIQQLYTVALWYWSKVTAEVGGVSTAALSSWKLTAVVMPAAVCFIVGVLLALGLPKYYRQ
 SPGRILFFYTSLFRRLIVLWFFFMVIVQNWFLSAAFGRNWSFLWSSQHAKAWEVVILVIFFFVILWVILIFRALSKEH
 SWILPVFGLSLGAPRWAQTWWGTSNIGYYLPWAGSLTSGALVSRGVWLWLGVLDEIQQVGLGMILLQTLTRVHVCFVLLA
 AQALGSIATICARGFAPNKLGPAGISPNVGTSLDTVGNWFWIALFFQLLASWGFLLFYRREQLNRP

Fig. 28

BASE SEQUENCE (PUTATIVE) OF NUCLEIC ACID MOLECULE OF *Aspergillus sojae* agsC

ATGTTCTCAGCGGTGATGCGCGCTCAGCGGATCTTATCTCTGCTTACTGAGCGCTACCGGCTTAAAGTGGCCCTACAC
 TGAGTCGCTCGTGTGATTATACTTGAATGAAATAAAACCGCGGAAGCGCGGATTGATTATGGGGAGAGTGGCCGGATC
 ATGAATATACCGCGTCGCCCGATAAAGTGGCGCTTCCGATCTATACCATCTTTTGGACCGCATCGCTAACGGTGACCCG
 AAGAAATGATGATTAATAGCGACCGCGCTTGGAGCATGTGGTGGGCTCGAATCAATGGCCACGGGGCGATCTAGTTGG
 TCTAATTGATACGCTGGATTATATTAGGGGCATGGGTTCAAGGGTGTGTAAGCCGCTGTGTGATCCGATCTTGGTGCTTA
 CTATAGTAGGGTATTACTTGGCTGGAACTGCTTGTATGAACCTTCCCTGGGCTACGATGGCTACTACCGGTTGATAC
 CACTTTGCTCGACATGCACATGGCAGCTCGAGGATTGGAGACGGACCATCACCGAGATCCACAAACGAGATATGTAAG
 TGATCATGGATAATACACTGGCAAGTAAATACATACCCAGATGTCTCAGATCAACACTGGTGACAAATATATCGAGA
 ATGAGCAACCTTATTGGCTTCAAGGACATCTAAACGATTTCAGCCGATTTTGGAGCAGATGAATATGAAGTGCAGTGGAT
 CTCAGATAGACAGTACCGGACTTCAAAATTCGGAATGAGTACAATGAGACCTGCAACTTCCCGAAGTTTGGAAATGAGA
 CCGGGTACCGGTGACATCAGGTGGTGTGCGAGGCTGAAAGGGTGTACAATAGTGATTTCGATCAATTTGGAGAACTG
 GAGGCGTTGGTAACTTTCCAGACTGGAAGCGGCGAGCTTACCAAGTTCCGCTCGGTGCAAGATCGTCTGGCGGAATGGCA
 CAAGGCTATTCTGATGTCTACACCAAGCTTCTGCAATTCAGATCGCCAGTCTAGATATCGATGGTTTTCGGTTGATAT
 AAGCGCTCAGGCAACCGCTCGAGCCCTAAGTGAGATAACCGCTGTCTATCGTGAATGTGCAAGAAATATGGCAAGCAT
 AACTTTTTCTTCCCGCGGAGATCACATCAGGAAATACCTTTGGCAGTCTTTACCTTGGACCGCGTGTGACGCCAGATCA
 GCGAGCTGAATCAGCAGATGCTGGTGTCAAGTTGAAGAAATAGTTGCGGACGATATTTCTCAGAGATGATGGATACGAGG
 CGTTGGACTCAGCGCGGTTTCACTACACGATCTACCGTTGCGATGACTGCTTCCCTGGGAATGGATGGTAACTGATGGCT
 GGGTTTACTTGGCTACTGATTTTATCGAGGCTGGAATGGATGCTGCTGAGCAACGACTTCTCAATGCAATACAGCGG
 TGAAGTAGCCGAGCGGACATGTTGGTGTCTAAATCAGGCAACTTTCGTTGGCCAGCAATCAGGAATGGCACCGAGA
 AATAGCTTCTGGGCTTTTATATCGTCAACCTGGAGCTCCCTGGGATTCCTGATCTCTATGGGGCAAGAGCGCGATG
 TATGTTTTGAATCTAGTGTCTAAGTACCTGTTCCGCGCGGAGCGCAATGAGCTATCAGACTGCTATGGAGCGCATGG
 ATGATGACTTTGAATACATCTAAATCTACGATTTCCCTAATGAGAAAGGACTACAGCGCTCGGAGGATATCAACGTTA
 CGTATGATCAGCGGAATCCGGCACACCTCTGCGCAATATCAAGAGCGCATGTTGGAAATCGGGAGCAGTATCCGGTA
 GCGAAATGATGGGTTCTATCTTCAACGCTTTCTCAGCTGACAAAGGATGTGTACCTCCCTGGTTCAAGCGGACACTCGAC
 TGTGACTGGTTTATGCTGGTCTGCGGAGCTACTTCCAGGGCTCCAGAAAGGAGGCAAGCAAGAACAGTCAGAACTTT
 GGGTGTGTATCATATGCTAAGCAAACTGAAACCTACGGTGGTGAAGTCAAAAAGAAAGATACCGGCTTGGCTGTGGCT
 TTCAAGTCCGGGAACGAGCTAAAGAAATCTCTTCTATCCTTACGATGAGCTCACTTTAGAAGATGGTCCGGCGAAGTCCG
 AGTCCACACAGCGACCGAGAGCTATGGATGCATCCGAGTATGAAATTCCTTCCGTGGGAATACCGTGGCTACATAGAGG
 CCGAGAACTTCGTTGAGCCCGCGCTACGTTTACGAGTTCGTTGCTTGGCCATGAGCGCGGATTTGTTGCTACGGAAGAC
 AGTGGCCAAAGTGTGAGATCCAGCTCGGATATTCAAAAGAGATGGAGTGTGACAAGATCGCGGATGCCATGCTTTGAA
 CTCAAGGACAGTGAAGGAGTTACAGCTTCCGTTGACACATCTAGCGTGTCTTGGCAACAAATCTCGGCAAGGACAAAGCA
 GTGATAACTTTGTTGGGAGGTTCAACCGTTTGGAGCTGGTCTGCCAAGCTGAAAAATGTCCACGACGGGAATCCATCAG
 CTGACGGTTAAGAACTTTCCACGAGCTCGGAGTTATACCGATGCGGTTGACCAAGTCTTCTTCCGTGTGGAAGTCA
 AAACAAATCCGCTTTTATCCGCACTGTCCAAATTTCCACCGAGTCTTGTGCAAGAAATCCGACAACGGCAGCTTCTATATCC
 AGCATGACCGCGCTGGGGCTGACAAATTCGCGTACTCGACTGATTTTGGCCTTAACTGGTCCAAGTGGCAACAGTATACC
 GGTGACAAACCCCTAGTCAACTTCCAGAGTGGACCGGAACAGAGGCTCAGAAATGGAAGGGAAGTCAATTTGGGTACA
 GTACTTTTCAAGGCTACCGGAGTGTGATTACATTCAAGGAAGGTGATCAGCGCTGGGAAAAAGGTGTTGCTCGAAGAT
 TTCTTAACCTCTTTTGGAAAGGTCGGTTCAATCAATATGGTTATGATGCGGGACTGGATAACAGATGAGATACGATACC
 AAGGAACATCGTTGGAAATACGATTTTGTCTACGAGTGGCCGGCCATTGGACAAATGAGTGTCTGGGGAATGTTAAAGGA
 TGGGCGCCCGACGTTACAGAGGTGTATGGTGTGTTGACAACTCATCTGTAGTTGAGAAACTTCTCCGCTTACCTGT
 CGTCCAAGCTGATCAATATCACAAGCTCGCTCCATTCGCGGACCTCGGCTGGACCATCACGCTCAATGACGCCAACTTG
 AGATATGAGATGCTTCCGGTGGATCTGGATGGGCGGAGCTCGTGTATACATTCTTGTGTTGGTGTGCAATCTCAT
 GGGATTTGCTGGTATCTGATCTTCATCAGGACATTTACCGTGTAAACTCAATACCGATGGCGATGTGGCTAAAGAAAG
 ATAAGCTGCGGCTCGGTTTTTGGCGAGGGTCAGAGAAAGTGTCTCGGCGACGACGATGGATAAGTGGATATCTGAT
 AAGGATATACGACAGACATTTGCTATCGCGGAGCGGCTGAGCAACGACGACTGATTTGATCGCCACCATGGAAATACAA
 CATCGAAGACTGGAAGGTCAAGGTCAAGATCGGCGGTCTAGGGGTCTAGGGGTATGGGCAAACTCATGTCCAGCATCTGAAGCATC
 AAAACCTGATCTGGGTTGCTTCCGTTGGTGACATTGAATATGCTCAGGACAGCCCATCCAGGCTTTGGTGGTTACT
 ATCGTGCAAGCGATTTTATCAATGTGCAATATCAGATAGTGAATACATCAGCTATGTCTGCTGACGCTCCAGT

Fig. 29

TTTCCGCCAACAGACCAAGCAGAGCGGTATCCTCCTCGCATGGATGATCTTGACAGTGCAATCTACTATTGGGCATGGA
 ACCAATGTATCGCAGAGACGATCAAGCGATTCCCGTCGATCGATCTCTATCATATCAACGATTTCATGGTTGTTTGA
 CCACTGTATTTGCTTCCACACGATACCATCCCGGTGTGCCGTGCTTACATAATGCTGAATCCAGGGTCTGTGGCCCT
 GAGAAACCCCCAGCAAAAGAGGAGTCTGTTCCGTCTTCAACCTTCCCATCGAACTGCAACCAAGTACAGTCAGTTTG
 GAAACGCTCTCAACCTGCTTACAGCCGGTGCAAGCTACGTGCGATTCTACCAACGGGTTTGGCGCAGTAGGTGTGTGG
 AAAAAGTATGAAAGCGCTCATGGGCTAGATACCCGATTTTCTGGAGCGCTTGAAAGATTGGCAGTCTTCCAAACCCAGA
 TCCCTCCGATACAGGGGATATGACAAATAACCCAGACGCCGAGGTCCCAATCCAGTCTACGAAGAAGCAATCAACGATA
 AGCTGCGAGGCCAGAGTGGGCTGTTTGAATGAAGATCGTGACGCTGACCTACTTGTGTTGTCGGACGATGGTCGAAG
 CAGAAGGGAGTGGATTGATTGGAGATGTCATGCCAGCGATATTATCCGCCACGCCACGTCGAATTGATTGCGTTGG
 ACCTATCGTTGATCTCTATGTAAGCTAGCTGCTACAAAGCTAGAGCGCATCATGGAAATGTTCCCTGGTCCGTTTCT
 CTAAGCGGAGTTCAACGTTTTGCTCCATACGATTTTCTGGTCCGACTTCGCCCTGATTCCCTCCAGAGACGAGCCA
 TTTGGGTTAGTCGCTGTAGAATTCCGCCGTAAGGGTGCACTGGGAATCGGCTCTCGCATCGGAGGTCTAGGCCAGATGCC
 AGGTTGGTGTACACCGTGAATCCGACGCCAACCCGCCATCTTCTGCATCAGTTGAACACCGCTATAAAACAAGCGTTGG
 ACTCATCACAAGAGCTCGTAGGAGATGCGGCCAATTCCGTCAGGCAACATTTCCCGTTCTTGAATGGATTGAGAAA
 CTCGAAGGCTTGCGAGCAACAGCAATCCAATCCATCACCAAGAACAAGAACCCGTCAGACGGCCGATGCCAGAATC
 GCGAATATTATGGGAGCTCAAAAGCTACGGATGCTACGCTGGGCTTCCAGGGCTACCCAGTCGATGACAGAGGGTT
 TAGATACACCGCCAGACAGGCTTTTGTATCCCGCCGAGTCTCGATTTACAGAACTGCAATTTGGAGGGAGCTGATGGCAAC
 AGGAACAGTAGGCTGGGTCGCAACCTCTCGCTCGGTGCGCGATCTGGACCTGGTCAGGACAGAAACGCTCTCGCAAGAG
 CGGACCGCGCGAGAGCCAGATTCTTGGCGAGGATCTGGAAGGTGAGAACCGGATGCCGAAGAAGAGGGCAGCGCTACGC
 CGCATGTGAACATAATTTCCGCTGAAGAAGCTATGGCTGCAGTTAACAAACATTTGGGAACCTCAGATATCGGAACGGCA
 CACAGCAACACAGTACTACTCGCTCGCAGGTCCTCAAGGATCTACTTACATGTCGCGCCAGGCTCACCACCAACAT
 GTCAGGGGCTTCTCTCGCATGCCAGGAACCCCGGCGCTGCTCAATACCCATTCCAGTTAGCATTGGGTTCTGGCGAA
 ATACTCCTTTCGCTCACTCCCGCAATGTGCCATGCTTTCTGCTTCACTCGTGGCGGACCATACCCAGCGCTTTT
 GAGCTGCAAAAGGTTGATCGGACCTTACAGACAGCACAGCCACTTCAGCGACGCTTCGAAGAGATCCTCAACAATTT
 GAACAGAAGAACTCAATGACAGACTGCTGTATCGAGACGTACCTGATGAAGAGCAACGTAATTTACAGCATGTACA
 ACGATGCACAATTAAGAAACAGCCGATGATCGTGCAATCTGATTGCAATTCAGACACTCAAGATAACCGCGCTCA
 TACGCCACTGTCACTGGAGGTTCCGACTCAAATGATCCGGATGAGATTGATCTATGGCTCTCTCGACTGGGTTAAAGCG
 ACCGATTGCTATTGAGAGATTGATGAGAAGCGCTCTCGGCAATGGCTGTTACGCTCTATTCTGGGTTCTTGACAAA
 TCATCGCGACCAACTCCGCTCAAATGACCGCTTTGGTCGGTCAGGTAGGAGAAACAGCAACGAAATTGTACATTATCGCA
 ACGATCTACTGTATTTCTCCATCTGTTGGTGGCTCCTCTCTATCGATTCCCGTCAGTAATCGTCTCACTCTCCCGTG
 GTTCATTTACTGATGGCATTCAATCATGATTGGGCTCTCTCCATTGCTCTCACATCTCTCGGTGAGGCTGGGCCAGA
 ATGTCGCTGCAGGTGTGATTCCCGCGCATCATCTAGCGGCTCGTTATTCTTCCCGCTCAACTTCGGTGACCAAGGTGGC
 GTCCTATAAAGGATTGGATGTTCCGGCGAGTCTCATCCAGGGAATCCAGCAGCTCTATACCGTCGCCCTATGTAAGT
 GAGTTCGAAGGTAACCGAAGCAGAAAGTGGGAAGCGTGTCCACCGCTGCTCTAAGCTCATGGAACCTCACAGCTGTGGTGA
 TGCCCATGCGCGAGTATGTTGATAGTGGGCTGCTTCTCGCGCTCGGCTACCAAAATACTACCGTCAATCCCGCGGT
 AGGATCCTCTTCTTACACATCGCTCTTCCCGCGCGTATCGTCTGTTCTTCTTCAATGGTGATCGTCCAGAACTG
 GTTCCTCTCGCGAGCAATCGGTGCAATTTGGTCATTCTCTGGTCTCCAGCACGCCAAAGCATGGGAGGTTGTATCC
 TAGTCATCTTCTTCTGTCATGCTCTGGTAATCATCTCTATCATCTTCCGCGCGCTGTCCAAGGAACACAGCTGGATT
 CTACCGCTCTTCCGCTGAGTCTCGGCGCACCGGCTGGGCCCAACATGGTGGGGAACCTCCAACATAGGCTACTACCT
 GCGATGGGCAAGGCTGACATCGGCTGCCCTCGTGTGAGATGCGTCTGGCTCTGCTCGGTCTCTTGGACGAAATCC
 AGCAAGTCGGCTGGGATGATGCTCTACAGACCTGACAAGAGTCCAGCTGTGCTTTGTTCTGTTGGCGCACAGGCT
 CTGGATCCATCGCTACGATCTGTGCGCTGGATTGCGCGCAATAAGCTCGGCTCTCGGGTATCTCGCCAAATGTGGG
 CACGCTTTGGATACAGTTGAAATGCGTGGTTCTGGATCGGCTCTTCTCCAGCTCTGGCTAGGTAGGCTTTTGAA
 TTTTACGGGTTTAAATAATCAATCTAATGTGATTATAGTTGGGCTTCTTTTGTCTATCGTGGAGCAGCTTAA
 TAGGCCTTAA

Fig. 30

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus niger* AgsE (Genbank accession No. ANI_1_360084)

MKWAISGTLACFATTATAWPYDESLVDYNFNQNSATNPADYWGTPWNHTGDYFPPSPDNWRFPVYTLFLDRFVNGDPTN
 DNINGTLFEHDLRSNQMRHGGDVAGLLDTLDYLOGMGIKGLYLAGTILMNQPWGSDGYSALDTLLDQHYGNLQWTRNAI
 TEIHKRGMVYIFDNTIATMGDLIGFDGYLNTTTPFSVKEHQTVWKTDRRYVDFDIGNDYNETCDYPRWFEDGYPVQASV
 TEELVGCSNSDFDQYGDIEAFGVFPDWQRQLAKFASVQDRLREWVPSVRERLIRHSCII IQSLDIDGFRYDKATQATVDA
 LGDMSNAYRECARAVGKENFFIAGEITGGNTFGSIYLRGRQPNQFPDSAEAAAMKLNTSDAQYFLREVGHAEIDGAAFH
 YSIYRALTRFLGMDGNLAAGYDVPVDWVDAWNLMLQSNLDVNANTGKFDPRHMYGATNQDVFRWPTVEKGVERQLLGLYI
 TTLPLPGIPLLLWGEEQAFYVLDATASNYIYGRQAMSPATAWRDHGCFSESSQYYNWP IESGRQGGCHDPTVAYDHRDPS
 HPVRNI IKHMYQMRQEPVLDNGYTIQKLSNHTEDVYVLGSGTATETGLWSILRDVNADVQDLGSDAKNQPVWL VYHNT
 NRTIDYKFDSCDNDTAL IAPFDSGTWVKNLHPYDEHQLIDSPTKLGNGSTAYSGCLANMTMSAYEFRAVVPKTRFTKP
 RPMITKFTPGHDVPIRSTVAPNADENVEVEIYFSEEMDCDSVTKSITLSSSTEIGKAPSVDGSGVNCXSVPATNTSWTGO
 IPGVWMAANLTGVYNGIHLRLTVNNVSTESGNATTNAVDFLFRIGQIDNPMIFSSANYSTSLHKNESNGTLFIQHAAG
 ADKYRYSTNWGTTFSWDIDYRGNDTIEELEWSGTKKQSKGNHVRVEYWSRWTGSSDYVQEGDAGWNENVPRRFPVFF
 NGPYNQYGYDAGLDNVVRQDSVDGLWKYHFTAEPQAQALNIWGMNPDGEPDQSWVLQDADNDSVLD RMPSSLSATLIN
 ITEHPPSPYISWNIFIDOGTMRFLFPVGHQNTQIAMYYLFWIIPVITGAAGVWAFMKSFYKVKFNQVGVSEKHQMIPLA
 LRRKFKRNRNRGGDEENSNPLMRLANKSGFLQTDTAIGGAASGKRRMVL IATMEYDIEDWAIKIKIGGLGVMAQLMGKTL
 GHQDLIWVPCVGGVDYPVDKPAEPMHVTILGNSYEVQVQYHYLNNITYVLLDAPVFRQSKSEPYPARMDDLNSAIYYS
 AWNQCIAEACKRFPIDLYHINDYHGLAPLYLLPDTVPACLSLHNAEFQGLWPMRTQKEKEEVCSVFNLDIETVRHYVQF
 GEVFNLLHSGASYLRVHQGGFAGVGSKKYGKRSYARYPIFWGLRKVGNLNPNPDSVGEWSKEQASAMGDNVSVDPITYE
 AGRGDLKRQAQEWAGLEQNPDADLLVFVGRWSMQKGVDL IADVMPAVLEARPNVQLICVGPVIDLYGKFAALKLDHMMKV
 YPGRVFSRPEFTALPPYIFSGAEFALIPSRDEPFGLVAVEFGRKGALGIGARVGGLGQMPGWWYNVESTATSHLLVQFKL
 AIDAALSSKTETRAMMRARSQKRFPAQWVEDLEILQTTAIQVHNKELVKHNRPFTPSGTTTPGGILSQPSSPLMPPG
 MQTPLAHSRESSYSLNRLSEYVTPKTNYSRDISPSGTEKPRSGLRQLSLGVRSGPGHQERRRRGRQRDSIPEHEDT
 AGAMTDVEEDHEDIGDQDADDEYTLTPAQVEEGRRLQAVQQGGVGMPTSPGVRRYSQDSLHPRQLPSSPGVPVPPTQSL
 LPPPRLGDAGSRLSSASVLSLDSVVGTKDFKLQKVDPFFTDSTGEYYKAFDKRLVGLNGSNSESQLCIEEYL IKSEKEW
 FDKFRDARLGRLLKSPASSVFRDKHGASPVGSYYDDTGSRVSGDYDRESRDTEDEFLLGKDYVPPTGLRKWMQIRVGDWP
 VYSLFLALGQIIAANSYQVTLTGEVGETAEKLYGIATTYLTITSILWWLVFRYFKSVVCLSAFWFFYGLAFLLIQSAHFE
 PNSFNRGWIQNIIGSGCYAAASSSGSIFFALNFGDEGGAPVETWIFRACLIQGIQSAYIIGLWYWGSTLTAKASSQGLLTST
 NNIANSWKMTAICYP IAI FLWAVGLLLFGLPNYYRQTGKVASFYKSVFRRKIVLWNFVAVILQNFFLSAPYGRNWGFL
 WSSNHAKAWQIVILCIVFYGFVWAGFLFVVSRYFKSHSWFLPVFACGLGAPRFIQIWWGVSGIGYFLPWVSGGYLGALA
 SRSLWLWLGLVDSIQGLGFGIILLQTLTRMHMLFTL ICSQVLGSIATICARAFAPNNVGGPGVPSPDPTFGGSAVANAWFW
 VALFCQLLVCAGFLFFRKEQLSKP

Fig. 31

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus niger* agsE (Genbank accession No. AN1_1_360084)

ATGAAGTGGGCTATTTCGGGACGGCTGCTGGCTGTTCGCAACCACTGCAACGGCTTGGCTTACGACGAGTCCCTGCT
 CGACTACAGCTTCAATCAGAACCACTGGCTAGCAACCGGGGAGCTATTGGGGAACATGGCCCAATCATACCGGGGAGCT
 ACTTCCCGCTGGCGGACAAATGGCGCTTGGCGCTTACACCGCTCTTCTGGAGCGCTTGGTCAACGGGTGACCCCAAAAC
 GACAACATCAATGGCAGCTGTTCGAACATGACCTCCGCTCGAATCAGATGGCGCATGGTGGCGATGTTGGCGGCTGCT
 GGAACCTTGGATAGTTCGAGGGCAIGGGAATCAAGGTGCGTCCTGTGGCTTGGCGATGCTGCAATCAATACATGAC
 GATGGTTTAGGGTCTCTATCTTGGCGGAACAATCCTCATGAACCAAGCGCTGGGGAATCTGACGGTTATTGGGCTTTGGACA
 CGAGATTGTTGGATCAACAGTATGGTAACCTGCAGAGCTGGCGCAATGGATGACGGAAATTCACAAGCGGGGATGTAT
 GTGATCTCGATAACACCATCGCAACGTAAGTTTCCGCTGCTCTTTCCTACCCAAACCACTAAGCTGCAA
 TTTTAAAGATGGGTGATTTGATCGGATTTGATGGCTATCTGAACACCAACCGCTTCTCGGTGAAGGAACCAACG
 GTGTGGAAGACTGACCGCGCTATGTGGACTTGGACATTGGCAATGACTACAAAGAGAGCTGGGACTACCCCGCTTCTG
 GTTGGAGATGGCTACCGCTTCAAGCGTCACTACCGAGAGCTTGTGGATGTTACAAAGTGTATTTCGACGATAG
 GTGATATTGAGGCTTTGGTGTCTTCCCGATTGGCAAGCTCAGCTGGCAAAATTCGCTCGGTTCAGGATCGACTCGGT
 GAATGGCTTGGCTCGGTGGCGAGCGTTGATCGCGCATCTCGATCATTATTCACTGCTCGATATTGACGGTTTCGG
 GTACGACAAAGCGACTCAGGCAACCGTGGACGCTCGGAGATATGTCCAATGGGTACCGGAGTGGCGCGCGCGCTAG
 GAAAGAGAACTTCTTCACTGGCGGGAATCAGGGTGGTAATACCTTTGGTCCATCTACTTGGCGCGAGGAAGACA
 CGCAACAGTTCCTGACTGGCGGAGGGACGCTGAAGTGGACCAACTTGGAGCGCGATTTCTCGGTGAAGT
 GGGACATGAGGGGATGATGGTGGAGCTTGGACTACTCTATTACCGAGCGCTGACCGCTTCTCGGTGGATGGTGA
 ACTTGGCTGGCGTTACGATGTGGAGTCACTGGTTGATGGCTGGAACTCATGCTGCACTCCAAAGTATCTGGTCAAT
 GCGAATACAGGCAAGTTCGACCCCGCGACATGTACGGGCTACCAACGAGATGCTTCTGGTTGGCGCAAGGTGGA
 GGGCTGGAGGCTCAGTTGGTTGGATTGTACATCAGAGCTTCTGCTGGCGGGAATTCGCTCTCTCGGGGCGAGG
 AACAGGGCTTTTACGTACTGGATGGCAGCGCATCGAAGTCACTACGGTGGGCGGGCATGCTGCTGGCGCATGG
 AGGGATCATGGCTGTTCTCTTGGAACTCGTCTGACTATAATGGCCCATGAGTGGCGGCTCAGGGCTGGCAGG
 CGCGAGGTGGGCTAGGATCATGCTGACGGCTCTATCGCGGTGGGAATATGATTAAAGGATATGATCAGATGGCGGAG
 AGTTCCCGCTGCTCAATGACGGCTATACTATTCAAAGCTCTGGAACCAACGAGAGGAGTGTACTATCTGGTTCCAA
 GGCACAGCCAGGAGCGAGCTGCTGGCTGATTCTTCTGATGTGAACGGGATGTGGAGGATTTGGGCTCCGATGCGAA
 GAACGAGGCTGTCTGGCTGGTTACGACAGAGGAGCGGACCATGATTACAAGTTTGAATGCTGCTGGATAATGATACAG
 CTCTGATTTGGCGCTTTCGATAGTGGGAGCTGGGTCAAAAAGCTGTTCCACCGGATGACGAGCAGGAGCTGATCGATTGG
 CCGACGAAGTTGGGATTGAACGGATCAACTGCATACAGTGGCTGCTTGGCTAATATGACCATGTCCGGCTATGAATTCGG
 GGGCTACGTGGCTAAAAGCGCTTTACTAAACCGAGCGGATGATTACAAGTTCACTCGGGACACGATGTCCCGATGG
 GCTCGACCGTGGCGCGAGACGAGAGGAGTGGAGGTGGAATTTACTTCTCGGAAGAAATGGATTGGGATCGGATCGGTG
 ACAAGTCCATTACGCTTTCGTATCGAGCGAATTTGGAAGGGCGGCTCTGTGGATTCTGGCAGTGTCAACTGCAAGTCA
 AGTCCCGGCGACTAACACAGCTGGAGCGGCGAGTTCCCGGGGTGGGATGTGGCGGCGCAACCTGACAGGTGTGTACA
 ACGGCATTCATGCTCTCACAGTCAACATGTACGACAGAGAGTGGGAACCAACCAACCGCGTCAACCATTTCTCTC
 TTCCGCTATCGGCGAGATTGATAATCGGATGATTTTCAGCAGTGGGAACTATTCAACTAGTTTGTCCATAAGGAATCCAA
 CGGACCGCTTTTCTCAAGCAGCAGCGCGGGTCTGATAGTATCGCTATTCTCAAGATTTGGGATACCACTTTCTCGG
 ATTGGATTGACTACAGGGGCGGAATGACACTATTGAGGAAGTCAATGGTGGGAGCAAGAGCAGTATGGAAGGA
 AACGAGCTTGGCTGGAGTATTGGAGTGGTGGACGGGAGGAGGATTACGTCCAAGAGGAGAGCGGGCTGGAAAGGA
 GAATGTTCCAGCGGTTTCCGCTACGCTCTTCTCAAGGAGCGCTACACCAAGTATGGGATGATGCAAGTCTGGACACG
 TGGTCCGCGAGGACAGCGTTGACGGTCTCTGGAAATATCATTTCAAGCGGGAATGGCTGCTCAAGCTCAATTGAACATT
 TGGGATGAAACCTGATGGGAGGCTGACCAAGTGGGTCTGGGAGATGGGATAATGATTGGGTTCTCGATCGCAT
 GCGCGCTCTTGGGTGTGGGAGACTTGAATACATCACTGAACAGCGCGCTCTGGCTACATTTGGTGAATATCTTCA
 TTGATGACGGGAGCATGGCTTCCAGCTGTTCCGCTGGGATCAGAACTACTGAGATCGGATGATATGTGCTCTTTGG
 ATCATCCCGTCACTACGGCGGAGCGGCTGTGGGCTTTCATGAAGTCTTTCTACAAGGTCAAAATTCACCAAGGTTGG
 TGTGAGCGAAGAACCAAGATGATCCATTGGCTTGGGCGGAAGTTCAAGGCAATCGAATGCTGGCGGTGATGAGG
 AAAACTCAAGCGCTCTCATGGCTTGGCGAACAAGTGGGCTTCTCCAGACTGACAGGCGGATTGGTGGTGTGCTAGC
 GGCAGCGTGGATGGTCTGATGGCAGCATGGAGTACGACATTGAGGATTGGGCGATCAAGATCAAGATGGTGGTCT
 TGGTCTATGGCGCAACTCATGGTAAGACTCTGGCTCATCAAGACTTGTATGGTGGTGGCTTGGCTTGGGCTGGTGG
 ATTACCGGTGGACAAGCGCGAGGAGGATGATGTCACGATTCTTGGCAATTCGTACGAGGTCCAGGTCGAGTATCAG

Fig. 32

[illegible]

Fig. 33

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus fumigatus* Ags1 (Genbank accession No. AFUA_3600910)

MKWGWGTGALLAWFATTTSCWPYDESLVGYNLNENKEAKSPVEYWGEWPDHKGYFSPENWRFPFYTLFLDRFVNGDPEN
 DNINGTQFEHDISSNQMRRHGGDVAGLVATLDYLQGMGIKGIYLAGTILMNQPGADGYSTLDTLLDQHFNGNIDTWRNAI
 TEIHKRGMVYIFDNTIATMGDLIGFEGYLNITTPFSVKEHKALWKTDRRYVDFDIGNDYNSTCDYPRFWYEDGLPLPSEQ
 ADQLVGCYNSDFDQYGDIEAFGVFPDWQRQLAKFASVQDRLREWIPSVRERLIRHSCIIIASLDIDGFRYDKATQATVDA
 LGEMSMAYRECARAVGKNFFISGEITGGDYFGSIYLGRRGQONQWLDPDSQGPMTNESSAQYFLREAGHEALDSAAFH
 YSVYRTLTRFLGMDGNLAAGYDVPLDWVDMWRQMLRSNDLVNANTGKFDPRHMYGATNQDVFRWPTVQWGVVERQLLSYI
 TTLPLPGIPLLLWGEEQAFYVLDAATNYIYGRQAMSPATAWRDHGCFSLNSSQYYKWP IQAGREGCHDDTVAYDHRDPS
 HPVRNILKHMVQLREQFPVLNDGYTLNLSKSTFPVQYPGSNGTETETGMWSVSREANLEVDQFGSDDLNSPVMMVYQND
 NHTVDYKFCNSETDALIAPYPADTVKNLFPWDEFTLTAGPTKRTFGNATLPAGCYGNLTAKAFEFRAYVPKLRKRP
 RPMITKFSFGHDVPIASTVAPDASENVPIELHFSEEMDCDGVTKSISLTSSTESLKVPSIDAGSVHCERITNFNTSWTAQ
 IPSMWWQATLTNVYNGIHQITVKEPTSSGNASTNSTDHLFRIGQVDNPMVFTRANYSTLLHEYENGTLFIQHHAAG
 ADKYRSTNWGTWSSWTKYHGNDTIEELPWQGTKEQRWEGKHVRVEYWSGLTGSSDYQEGQDVGWPHQVPRRFPFIHF
 NGPFNQFGYDGLPNKLLDTTTTGHWKYHFTYEWPAQAQINVWGMNPDGRPDQSWVLQDIDGDHVLDRMPPSSLATMIN
 ITDLPPSPHLAWIISINDGTMRYTLEPTQDQSTQMAMYILFWIVPLLTGAVCVYVFMKSFYQVKFNQVGVSEKRTLPLA
 LRRKLKRARNGEGEAMNPLMLRANKSGFLQSATDLTAASGGSKRRMVLATMEYDIEDWAIKIKIGGLGVMAQLMGKTLG
 HQDLIWVYPCVGGVDYVDRPAEPMIVTILGKPYEVQVQYHILQNITYVLLDAPVFRQQSKSEPPPRMDDLDSAIYSSA
 WNNQIAQTIKRFPIDLYHINDYHGSLAPLYLLPQTIPACLSLHNAEFQGLWPMRTEKEKEEVCSVFNLDEKIEITRRYVQFG
 EVFNLLHAGASYLRVHQGGFAGVGSKKYGKRSYARYPIFWGLKKVGNLPPDPDSVGEWNKEKALAKSEDPPVDQFEFA
 GRAELKRQAQEWAGLEQNPADLLVFVGRWSMQKGVDLIADVMPAVLEARNVQLICVGPVIDLYGKFAALKLDRMMKVY
 PGRVFSRPQFTALPPYIFSGAEFALIPSRDEPFLVAVEFGKRGALGIGARVGGLQMPGWWYNVESMTTAHLHQFKLA
 IEGALNSKPEVRAKMRARSQKRFPAQWIEDLEILOSTSIIRHNKEASKSNNRPVPTGPMTPRGLGTMSPTFPGSGTQ
 TPVGTHSREASYVNLRLQSEIGPQQRDTIISYSNNNAGREMTEKPAAGLSRKLSLGVRSGPGHINRPGRRGGQQLALP
 DRRDGGQVSDIEESEDDEFIDQYYGDEEYTLTPEQAEEGRRLONNPQSQSGRATPRELTRSSQFPSSPSVHSDMGLAPPT
 RPFLEPGNRLSSASVLSVDSVVGDKKDFKLQKVDPFITDSHGEYARLFENSLNLAANSETQLCIEEFLVKSEKEWFDK
 FRDAKLGRNLNSPAPSVFRGKRGPSPVDSYGGDASSRMSPDDEQSQEDDEFLLGKDYVPPTGLRKWMQLRIGDWPVYSLL
 LGLGQIIAANSYQITLLTGEVGQTAEKLYGIATTYLITSILWWFVFRYFKSIVCLSVPWFFYGLAFLLIIGLAHFDHNEFS
 RGWIONVASGFYATASSSGSIFFALNFGDESGAPVKEWVFRACVIQGTQQAYVIALWYWGSTLTAKASSQGLLTAETNIAN
 TWKMTAICVPITVFLWCVGLLMFFGLPNYYRQSPGKVPSFYRSVFRRKIVIWNAFVVIQNFLLSAPYGRNWNFLWSSAH
 AKTWQIVILCIVFFGFVWAGFLFVLSHLKHSWILPVFACGLGAPRWAQIWWGVSGIGYYMPWVAGGLTGALASRSIW
 LWLGVLDAIQGLGFGMILLQTLTRMHMCFTLIVCQVLGSIATIGARAFAPNNVGPPISPDPTYGASAVANAWFWIALIF
 QLLICAGFLFFRREQLAKP

Fig. 34

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus fumigatus* ags1 (Genbank accession No. AFUA_3600910)

ATGAAGTGGGGATGGACGGGGCGTTGCTGGCGTGGTTTGGGACAACCATCATGCTGGCGTATGACGAGAGCCCTGGT
 CCGGTACAACTCAACGAGAAATAAGAGGCCAAAGCCCGTGGAGTACTGGGGAGAAATGGCGGACATAAGGGCAAAAT
 ACTTTCCCTCCCGGGAAGACTGGCGGTTTGCATTTACACCGCTGTTTTGGATCGATTGGTGAACGGTGAACCGGAGAAT
 GATAATATCAACGGGACGCACTTCGAGCATGATATCAGCTCCAAACGAGATGCGTCACGGTGGTATGTCCCGGGTTGGT
 CGCTAGTTTGGACTACTTACAGGGCATGGGGATCAAGTAGGTTTTCTGACCTGACTGATCTGTGGCGCAATGAGATG
 CTGACTCGGACAGGGCATTTATGTGGCGGGAACGATCCTTATGAACGAGCGCTGGGGCGCAGACGGTTAGTCGCAATTGG
 ATACAACGCTTTGGATGACATTTTGGTAACATCGACACCTGGCGCAACCGGATCACGGAGATCCACAAGCGGGGATG
 TATGTGATATTCGACAATACTATTGGCAGTAAGTCTGCCAAACCCCAATTCTCTGCGTGGGACTGACGCAATAACAAG
 CATGGGTGATCTCATTTGGCTTCGAAGGCTATCTCAACACCCACCCCGCTTCTCGGTCAAGGACACAAAGGCCCTCTGGA
 AGACCGATCGTCGCTACGTGGATTTTGACATTGGCAACGACTATAACTCAACCTGGGATTACCCCGGTTTTTGGTATGAG
 GACGGTCTTCGGCTTCCTCGAGGAGGGCGATCAGCTGGTGGCTGCTACAACAGGATTTGACACGATACGGTACAT
 TGAAGCGTTCGGTGTGTTCCCGGATTGGCAGGTCAGTTGGCGAAGTTGGCGTCCGTGCAGGATCGTCTGGGGAATGGA
 TCCGAGCGTGGCAGAGCGCACTGATCCGTCACTCTTGCAATAATCATCGCTCCCTGGATTTGATGGTTTTCCGGTACGAT
 AAAGCCACCGAGGGACGGTTGATGCTCTCGGCAAAATGTCATGGCATACCGGGAGTGTCCCGTGGCTGGGCAAGAA
 CAACTTCTTCATCTCGGGAGAAATACCGGTGGTATTACTTCGGTTCCATCTACCTCGGACGGGGCAGACAGCAGAACCC
 AGTGGGTTCCGGACCGCTTCCAGGGTCCCAAGATGACGAATGAGTCCAGCGGCCABTTTCTGCGGGAGGGCGGCGCAT
 GAAGCCCTTGATAGTGTGCTTCCACTATTCCGTTTACCGCACCTTGACCCGTTTCTGGGTATGGACGGCAATCTCGC
 CGCCGGTTACGATGTCCCTCTGATTGGGTGGCATGTGGCGGCAATGCTCGGTGCAACGACCTCGTTAATGCGAACA
 CAGGCAAGTTGACACCGCCCGGCACTGTACGGTGGCAGCAACCGAGATGTCTTCGGTGGCAACTGTGCAATGGGGCGTG
 GAACGGCAATTGTTGGGTAGTTATATCACAACTGCTCCTTCCCGCATCGCTCTTTGCTCGGGTGAAGGACAGGC
 CTCTATGTGGTGGATGCACTGCTACTAATTATATTTACGGTGGTGGCAATGTGGCTGCAACTGGCTGGAGAGAC
 ATGGCTGCTTCACTGAACTCTCGGAGTACTACAATGGGGGATTCAAGCTGGCGGGAGGTTCCGACGATGATAGA
 GTGGCTATGATCATCGGGACCGTTCTCAGCGAGTGGCGCAACTGCTCAAGCACATGATCAGTTGGCTGAGCAATTTCC
 CGTCTTAAATGACGGTTACACCGTCAACAACTGTGCCAAGTCGACCTTCCCGTGGATACCGCGGTTTCAACGGAAACCG
 AGACCGAGACGGGAATGTGGTCTGTCACTGGCGAAGCCAACTGGAAAGTCAGGATTTGGATCGGATGACCTGAATTCG
 CCTGTTTGGATGGTCTACGAGAAATGATAACCATACGGTGGATTACAAGTTGATTGCAACAGCGAGACCGATGCTTTGAT
 TGCTCCCTACCGTGGCGACACCGTGGTCAAGAACTTTGTTTACCGCTGGGATGAGTTACCTTGACCGCGGGCGCAACCA
 AACGGACCTTTGGAATGGCACTATGCTGCTGGTGGTATGGCAATCTGACCGTCAAAAGCATTGAGTTCCGGGCTAC
 GTGCCAAAGAAAGTTACATCGGAAGCTCGCGGATGATACCAAAATTCAGCCGGGGCACGAGTTCCCATTTGCTTCCAC
 GGTGGCGCTGATGCTTGGAGAAATGTGGCGATTGAGCTGCAATTTCTCGGAGGATGGATTGGATGGGGTGAACAAAT
 CGATTTCCCTGACCTCCTCCACGGAGTCACTCAAAAGTGGCATGCAACGCTGGCTCTGTACATTGGGAGCGCTATTACC
 AACTTCAACACCTGTGGACTGCTGAGATGCTAGCATGTGGAAAGTGGCAGGCTACTTTGACGAATGTCTACAAAGGAT
 CCACGAGATCACTGTGAAGGAACCCAAAGACTAGCAGTGGCAACGCTCCACCAACTCCACCGATCACTTCCTTTTCGCA
 TTGGCAGGTCGATTAATCGGATGGTCTTCCAGAGGCGAACTACTCGACTAGTTTGTCCATGATATGAGAAACGGGACT
 CTGTTTCATCGAGCACCAAGCTGCAAGCGCGGATAAATACCGCTACTCGACCAACTGGGGAACCACTGGTGGAGCTGGAC
 CAAGTACCATGGCGGTAACGACACCATCGAAGAGCTGGGTGGCAAGGACCAAGAACAGCGGTGGGAAGGCAACAGG
 TCCCGGTGGAATACTGGAGCGGCTTGACCGGTAGCAGCGACTACTACCAAGAAAGTATGTGGGTGGCGGCAACAGTG
 CCGCGTCAATTCCTCATATCCATTTCAACGGTCTTTCAACGAGTTTGGCTACGATGGCGGCTCGCGCAACAGCTCAA
 GCTGGACACCGACCTGGGCTATGGAAGTACCACTTCACTACGAGTGGCTGCAACAGCTGAGATCAACGTCTGGGGCA
 TGAACCGCGATGGCAGGCGGACGAGATTTGGTGTGGCGGATCGAGGGTGAACAGTTTGGACGGATGGCGCG
 TCGTCTGTGGCGGACGATGATCAATATCAGGGACCTTCCGGCGTCACTCACTCGCGTGGATCATCTGATCAACGA
 CGGGACCATCGGTATACGTTAGAACCCACCGGTGATCAAGATACGAGATGGCGATGATACATTCTTCTGGATTGTGC
 CCGTGGTCAAGGTTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGTGTGGGT
 GAAAGCGGACCGCTATTCCCTGGCGCTTGGCGGAAAGCTGAAGCGTGGCGTAATGGCGAGGGTGAAGCAATGAACCG
 CCTGATGGCGCTGGCGCAACAGTGGGTGCTGCGAGAGCGGACGGATGTCAACAGCGCTTGGGGCGTTCCAAACGCG
 CGATGGTCTCATTTGCCAGATGGAATACGATACGAGACTGGCGCATCAAGATGAAATCGGTGGTGTGGGTGTCAATG
 GCTCAACTGATGGGCAAGACCTCGGGCCACGAGATCTCATTTGGGTGTTCCCTGGGTGGGTGGATGGAGTACCTGCT

Fig. 35

[illegible]

Fig. 36

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus oryzae* Uge3 (Genbank accession No. AOR_1_2588174)

MESPRQSDASTPVEPYSPGCVDTPATQSSVLFDGNLEELLRNFLDQYILVTGGLGFIGSHTTLELLKANYNVIVIDNLS
NAFQNVFDRIKLLASKHHEQGGTKMPEMHLHAHDYRDSVALRKLEQYQIQSRWGTPTKISGVIHFAAHKAVEESIRNP
LKYYANNVGGIDFATTLGEFGIKTFVFSSSATVYGTLATSGPLKEELCVHKDEIFEDRDGSKKLMPEGGTGITNPYGR
TKWICEAILADLAASDPEWTIVALRYFNPVGCDESGLLGEDPKQIPTNLLPVVVKVMTGQYKELQMFQTDWDTEDGTAVR
DFIHVTDLARGHIAALSAANEGKLEKFNFTFNLGTGTGHSVMEVVNTMESVSSKAIPRRAADRRAGDVGSCVAVATRSQE
ELQWKTEKLTDAACASLCNFLAVSGLSS

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus oryzae* uge3 (Genbank accession No. AOR_1_2588174)

ATGGAGAGCCCTCGACAGTCTGACGCAAGTACTCCCGTGGAGCCTTATTCTCCAGGATGCGTCGATACACCAGCGACGCA
GTATCCGTCTTGTTCGATGGAATCTTGAAGAGTTGCTGCGCAACTTCCCCTGGATCAATACATCCTCGTCACCGGCG
GTCTCGGTTTCATTGGAAGTCACACAACATTGGAGCTACTCAAGGCCAATTATAACGTAATCGTCATTGACAACCTTAGC
AATGCTTTCCAGAACGCTTCGATCGCATCAAACCTCGGCTTCCAAGCACCATGAGCAACAAGGAACCAAAATGCCCGA
GATGCATCTGCATGCCATGATTACCGCGACAGTGTGCTCTTCGCAAGCTTCTTGAGCAATATCAAATCCAGTCGAGGT
GGGGTACACCTAAGACCAAGATCTCCGGCGTCATCCATTTTGTGCCCCACAAGGCGGTTGAGGAGAGTATCAGGAATCCT
TTGAAGTACTACGCAACAATGTGCGCGGCTCATCGACTTTGCCACGACGCTGGGTGAGTTTGGTATCAAGACCTTCGT
CTTCTCGTCATCCGCCACCGTATACGGAACCTTGGCAACCTCCGGTCTTCTCTTAAGGAGGAGCTTTGTGTCCACAAGG
ATGAGATCTTGAAGACCGTGACGGGTCCAAGAAGCTCATGGAGCCTGGGTGCACAGGTATCACAACCCCTATGGACGC
ACAAAATGGATCTGCGAAGCCATCTTAGCCGACCTCGCGGCTCCGATCCAGAGTGGACCATCGTGGCTCTACGATACTT
CAACCCAGTTGGATGCGATGAATCCGGCCTTCTCGGTGAAGATCCCAAGCAAATACCTACCAACCTTCTCCAGTTGTCTG
TCAAGGTCATGACTGGGCAGTACAAGGAGCTGCAGATGTTTGAACCGACTGGGACACGGAAGATGGCACAGCTGTCCGT
GACTTCATCCACGTACCGATCTGGCTCGAGGACATATCGCAGCCCTCAGTGCTGCCAATGAAGGGAAGCTCAAGGAGAA
TTTCCGCACATTCAACCTCGGAACCGGTACAGGCCATTCCGTAATGGAGGTGGTGAACACTATGGAGAGTGTCTTCCA
AAGCAATTCGAGAAGAGCTGCTGACCGCGTCCGGGTGATGTGGTTCTGCGTTGCTGTGGCCACCAAGGTCACAGGAG
GAGCTGCAGTGAAGACCGAGAAGACATTGACCGATGCCTGTGCCAGTTTGTGCAATTTCTGGCTGTGAGCGGACTGTC
CTCTTAG

Fig. 37

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus oryzae* Sph3 (Genbank accession No. AOR_1_2586174)

MATMGPDKHVSGRRCLQSRRSRIILGAFVFIAILAVVIPPVVVTLRKKNSMGPKANIFVPLYVYPAPGAWDPLEAEISS
HPEANFIVVINPSSGPGPNALPDANYTREIPKLASYDNVRLGYVPTTWAKRNISAVRRDIATYAEWPTNSSNPKLAVRG
IFFDETQQYDADALSYLQELTSFVKGLSGLGPDNFIVHNPGAVPDSRYMSSADSTVVFEAAYDTFNERDGTQKQFDVLPK
SDRGRGQLCIVHSVPDQVEGSKLRDLVKKLRKTADEIFITHLSTDYYANFGDRWGEFVDWMAK

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus oryzae* sph3 (Genbank accession No. AOR_1_2586174)

AATCCACTTTCTTGCCTCCTTTCGTTGCATTCTAAGGCATTACATTTTAATTGCCTACCTCACATGGCAACGATGGG
CCAGACAAACACGTGAGCGGTGCTGTTGCCGTCAAAGCCGACGTTCTCGAATCATTTTGGGGGCCTTTGTCTTTATTGC
TATCCTCGCGGTGCTTATACCTCCCGCAGTCGTGTCACCTACGCAAGAAGAACAGCATGGGCCCTAAAGCTAACATTT
TCGTCCCTCTCTATGTGTACCTGCCCTGGCGCCTGGGATCCATTGGAAGCAGAGTATGTCTGATTTTTTTTTTATG
TCTATTTGTATTTCTAATTCTTACCTTCAATTTACCCCACTACTCCCTCACCCTCCAAAGCCCAATATGTTCTGGT
CCCTGGGGTATATACATTATACACCATAAGCAAGCTGAAAGCCAATTGCATGATGCATGCAAGCGGGAAGCTATAATTTT
GGGGGAAAGTAAGCAAGCGCCACAGGATCTCTTACATCCGAGGCCAACCTTACCGTTGTGATTAAACCTAGCAGCGGC
CCAGGGCCCAATGCCCTGCCGATGCTAATTATACCGAGAGATTCCCAAGCTCGCCTCTTATGACAACGTGCGTCTCTT
AGGTTATGTCCCTACAACCTGGGCTAAACGCAACATCTCGGCCGTGCGTCGCGACATCGCAACCTACGCGAGAATGGCGA
CCAACAGTTCGAACCTAAGCTCGCGGTTCGGGGTATATTCTTTGATGAGACGCCCAACAGTATGATGCCGATGCGTTG
TCATATTTGCAAGAGCTCACCTCATTGCGAAAGGCCTTTCTGGTCTTGGTCCAGACAACCTTGTATGTGTGACCGTTCT
CTTTACCCCTCTGTAATTTGTATTACCGCTCGGTATTCATGGTAATTTACATGGGTACATACCTCATGCCCTCTGATT
CCTTCTCCACCTCTGTTTACTTTCTTTTATGCTTTTCACTTTTGCCTCTCGGACAGTCAATATGGCCCATACCTGT
CTTTTGTATGGCGCTAGGTTCTATTACGGTTTCCAAGTCAACTCCGACAACCTCATTGGGTCAAGTTGGTCAACGATGA
TGCTAATAGTGAAGTGGCTAGATTGTCCATAACCCGGGAGCCGTTCCAGACTCTCGTTACATGTCTTCAGCTGAAGTGA
GTCGTATTCGAAGCGGCTTATGACACCTTCAACGAGCGTGATGGCAGCAAGCAATTCGACGTTCTTCGAAGAGCGATCG
CGGTGCGCGTCAAGCTCTGCATTGTGATCCACTCCGTTCCGGATGGGGTTGAAGGTTGCAAGCTTCGTGATCTCGTCAAGA
AGCTTCGCAAGACCGCGGATGAGATTTTCATTACCCACCTGAGCAGCGATTACTATGCCAACTTCGGGGATAGGTGGGGC
GAGTTTGTGATTGGATGGCTAAATAATTCCTACGGCGCGGCTTTTCGAGCATACCTGATGCAACATTGCTTATGATCA
GGGCCCGATTGGCGTCGACTGATAATATATGCGCGCGGCTTTCTTTGATGGATTGGATTGACTAATTAACCTACGACC
TGTCTATACTGTATGAACGTCTATATCCTGTATGATGATTCTACTGATAATATGCTATTTGACTTTGGCGTTGGGACTA
TCAAATGATACCTAGAATTACGATAGAGTTTACGATCGTCAAGATTTCTTTTGTCTTC

Fig. 38

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus oryzae* Ega3 (Genbank accession No. AOR_1_2584174)

MAGIDEALPLKKGQAASGWKTSVKKRMLIIGAIALVIALAIGLGVGLGVGLNKGGGDDGEVPPITGGGVTTAKWQPA
VGTKWQIELLYALNDTSVDADIYDIDLFNNDKSTITDLQKQGRKVICYFSAGSYENWRPDKDKFKDSMDGNTLDGWPNEK
WLDLNSKNVRSIMTSRLDMAVEKNC DGVD PDNV DAYDNDNGLDMKKEDSANFMMWLANEAHARNMSIGLKNAGAIISAVI
DNMQWSVNEQCAQYEECDTYAAFIDKNKPVFHI EYPKGGDTNNNDLVSTSQKKSACDFEGSSNFSTVIKNMNLNDNWIGTC

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus oryzae* ega3 (Genbank accession No. AOR_1_2584174)

CCGCAGGTGACCTCGAAACAACAGCCACTGTGGCAGAGTCCATTATTTGGACATTGACTGCCGCAGTCTGTAAGGCATTG
ACTTGCCCTTTAATTCACCCAGGACAGGCGTCTCTGCATCCGATTCCCGGACCACTCAACGCAATCTCTGAACGAGC
CACTTCATAGTTTCAGTGTAACCGCGGAGAGAGGGATTCTTTGTCCTCTCCTAGCCTATACATTTAACGGTTGCGCTGT
AACCCCTGTGGTTCTACTCCGGAATACGCCACTTCATTTGCTTCTTTATCTGATCGTTTGATCTTCCTCTCAGGTCCTCT
TTATATTTTCCCTGCTTACCCCCACCTTACCCTGTGGTTTGTGAGAATCAAATCGCAGGTCGTACCTTTCTTTCTCGG
AATTCCCTTCTTTGAACATTTCTTTCTTTAGTCGTTCTGTTTACAGGAATTTTCTTTGTGAAATCTATTGCACTATGGC
GGGTATTGATGAAGCGCTGCCCTTGAAGGGTAAGGGACAAGCCGCGTCCGCTGGAAGACTTGGTCCGTCAAGAAGCGCA
TGCTGATTATCGGCGCTATCGCTCTCGTGATCGCTCTCGCTATTGGTCTAGGAGTTGGCTTGGGAGTCGGTCTGAATAAG
GGTGGAGGGGATGACGAAGGCGAGGTTCCGCCCACTACCGGAGGAGGCGTGACCACAGCCAAGTGGCAACCGGCCGTAGG
AACGAAATGGCAGATCGAGCTTCTGTACGCGCTCAACGACACTTCAGTAGACGAGATATCTACGACATTGATCTCTTCA
ACAATGACAAGTCGACCATCACCGATCTACAAAAGCAAGGACGCAAGGTGATCTGCTACTTCTCCGCTGGGAGCTACGAG
AACTGGAGGGCCGACAAGGACAAGTTCAAGGACTCCGATATGGGTAAACCGCTGGATGGGTGGCCGAATGAGAAATGGCT
TGACCTCAACTCCAAGAAGTGCAGGACATTATGACGTGCGCTCTGGATATGGCGGTCGAGAAGAACTGCGATGGAGTTG
ACCCGGATAACGTGATGCTATGACAACGACAACGGTCTCGATATGAAGAAGGAGGATTCCGGCAATTTTCATGATGTGG
CTCGCCAATGAAGCGCATGCACGCAATATGTCCATTGGTCTGAAGAATGCCGGGGCGATCATCTCCGCAGTGATCGACAA
CATGCAGTGGAGCGTGACGAGCAATGCGCGCAATATGAGGAGTGCATACCTATGCCGCATTTCATGATAAGAACAAGC
CGCTCTCCACATCGAGTACCCCAAGGGCGACGACACCAACAACAACGATTTGGTCAGCACGAGCCAGAAGAAGAGTGCT
TGGGACTTCGAGGGATCCTCCAACCTTCTCGACGGTCATCAAGAATATGAATCTGGATAACTGGATCCAGACCTGCTAGTC
GCACAATTGATCCGCATCTAAATACTCTGTTGATCAGCAAGGGCGCGGGAGTTTGAGATTGGGGTTCACCATCCGCT
TACCATCTATATAGTTTGACTATGATGTAATCTCGCTCATTTAATTAAGTTGGACATTGCTCTTTCA

Fig. 39

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus oryzae* Agd3 (Genbank accession No. AOR_1_2582174)

MWLPLWLLRTGCGVGLITCDPQGVPIQGVPSVIAIPVPSRISGVITNSPFGTSVLSFTSSSPVPTGSSSVFVITITTLAS
 STSTSTSLPSFSTSLPSTLTVSYSTPVSASTMSLIPSPSSSIIPATSPASASALINAGNAGNLIIVAKDTAAANVAATSGNLGY
 IGFPTTLLPVSGVLPGLNGLTSGNGGGLVIVASEYVYDGAQGSALITDQWNLVYATQLEYVSRVNVQYVPPGPNV
 ASAYGGGCGDSSGVEQLVSFSDVDFKEAQLTKAGVYSTGLNHPYASVNDATTKEIARFAANGNVGSETTAAVINNFUG
 RQMAAFSLFDITSPSTSNLYHAGNINWLLTRGLYAGHRRVNLITQIDMFLEITDIYPNGTIFRTITADMDQSSWLPIT
 NGKMGAGSSYFVYGVHNGNIVLEAAAGGADAAGNAGGIEHDSAPLGTCEKPKLGTIGTLWPKDLEFYNTWTEGTLKIDLE
 FVWWTTPANRDKYQHISHTFHEEQNNATYNDVKRESFNQAWLRSQGYDQAKYFTSNQIIPPAITGLHNGDALRAYEN
 GTTCVGLNDRITPLPGLNGQNSMPLTASGSDGDMQVNPATRIIYNCDTACTVQWIEIDTSAGSDGSFNLALTEKAD
 TRMHLFGLTRDPYMFHAGNLRNVGYDPSVINGETGQWSINQAWVEINQVGFVRLVDQVPIVITHQEMSANLLDRYNRDQC
 NYSLYQITGNKIGTVELSADKNTGNAPIPVSPVAPDTKGFTEQYSGSFTLVVQGLSGSPVFTSLSTIPL

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus oryzae* agd3 (Genbank accession No. A012582174)

AGGTGCTACCGGTGGTTGCGAGGAACATGGTTGATTCTCGGACCTTATAACTTGCAGCAACTCCCCAGGTTGTTTGGCCTGA
 AGGTGTCGCCAAGTACGATCGCTCGTCTGGCTCCCTCAGCGACATCTGGATGTCAGCAACTCTCCGGCTTACTTCTCGT
 CGGTGCTGTCGGTGCATCTTGTTCTTGGCGTCTGACGGGGTCATGGTTCGTTACGACTAGCTGCGCTTACTTGGTTCGTC
 TCCACTTCCACTTCTACTTCAACCTCTCTACCTTCGTTTACTAGGACAGCTCGTTTCTGTGACGACTCCCGTGAGTGGCTC
 GACCAAGATGTCTGATTAATCTCTCTGCTTTCGAGTATGATTCCTTCGCGAAGACCTTGGCGTCTCTGTCAATGGCATG
 CTAAATTCGCGGGTACATCTTGGTATTCGGAAGACACCGCGTCTGCTGAATTTGGTTCATCGCTCGCGCGCTCAATGGCTAT
 GGTATTTCTTTTACTACGTTGCTGGTTCGCGAGTCTGGTGATCTTGGCAAGTCTGCTGCTGATTTGGTTCATCGCTCGCG
 TGGCGGATCTGGTGTTCGGAAGCGGCTGAGCTACGACTAGTGGTGGCCAAAGGCTTCCAGAGGCGCTTGACTACCGCAACT
 GGAATCAACTCTAGCGGCTACGAGTCGAGTACGATGATTCAGCATGAGTACGACGCTTACCGCGGACCCAATCGGTT
 GCGCTTTCGCGGTGGTGGCGGATGCTGTGACTCTCGGGCTGGAGCGAGCTTGTTTCTTTCTCAGAGAGTCACTGATGATTCGAAGA
 AGCCGCGCTGAAGAGCTGGTGGCGGTGTGAGTACGACAGGCCCTTGGCACTACCGCACTCGATTAATGATCTGATCTACCA
 CCAAGGAATTTGGCTGTGTTTCGCGCGCAACGGCAAGCTACGCGACGAGCAAGCTCTGCACTGATCAAGCAATCTCAATGGT
 AGACAGCAAAATGGCTTTGCTTCTGCTTTTTCGACATACCTGGAGTGGAACTTCCAACTACTTGCAGCGAGCCTGGATGAA
 CTGCGCTACTCGGGGCTCTACGCTGGCCAGCTCGCGTCAAGCTGAAACCCGAGATGATGATGTTGCTCGCGAACTG
 ATATCTACTCGCCCAATGGAAGAGCTTCGGTATATACCGAGCTTATGGATGGTATCTCGAGGTCGCTCGGACGCTC
 AACCGCAAGATGAACGCCGCTAGCTCATACTTGTGGTGAAGTCGGACACAAACGGTAAACGGTGTCTCGAAACCGCGTCGCGG
 CAAGGTCGCGATGCTGCAACGGAGGTGGCAATGAACAGCACTCGCCCGCTGATACCTCTCGAGGTTTGAAGAAGCTCT
 TGGCGACGCGGATGACTCTTGGCCCAAGGACTGACCGGATGACAGTACCTGGCACTCAAGTACGCCAAATTCGAGAGCTT
 TTGCTCTGGTGGACAGCGCCCGGCTAACCGCGCAAGTATGGTGCATCTTTCAGTCACTTTCAGTCAATGAAGAGCAACAA
 TGGCCACTACAACAGCGTGAAGAGGAGATCTCTTTTCCCAAGGCTTGGTTGAGACAGAGGTCTTCTATGATGCCAAT
 ATTTCACATCAACAGBTATACCTCTCGGCACTTACGGGTTGCACAAAGGCGATCGCTTGGGCGGCTGTGATCAAGAA
 GGCATGACCAACTGTGTTGGTGATAACTGTCGCAACCGGCTCGCTCAACGACGAGAACAGTATGTGGCGCTTCTCTACTAC
 CTCGCACTCGGATGGATTCGATGGTATGCAAGTGACAAACCCCGTTGGGCCACTGCBATCTCTACCAACTGCGATACCCGCT
 CCGTGCACGCTTCAGGAATGAGTTGACACTCGCCGCGGCGGTCGTACTCAGCAACTCTGTCGCGACGAGGAAGBGCAG
 AGCATGCGGCATCTCTTTCGGTCTTCATGCGGACCTTACATATGTTCCAGCGGCAACTTTCGCAATGTGCGGCGTTGACCC
 GTGGTAGATCAACGGTGAGTGGCCAACTGAGGCTCACTCATGCGGGCGGGTGGGAGAACCATGGTCGAGGAATGGTGGTG
 TGGTAGACTGGGCGATCTTACCATCAGGCAAGGAGGAGTAACTGATGGAGATCTTAGAAAGCTCTCTAAGCAACGGCGCA
 ATTGCTAATTAATACCCCGAGATGTCCGCCAATCTCTCGACCGGTACAAACCGGATGATGATGCAACTTCTCGCTGCACT
 CAGCATCGGCAACAGAGATTAATCGGGTCACTCTGCGGCGCAAGGCAAGCTGATACCTGCGCGTCTCCGCTCGAGCT
 TCGCTTTCGCGCCCGCGACCAACGGGCTCACCAACGAAAGCTACGCGAGTGAACCACTGCGCTCGGCTGACGCTG
 TCGGGCTCGCGCGTCACTTTCGCTCTCGACCGCTTCTGGTGTAAATGGATTGAACAGATTTGAATTAAGGAAGGGC
 TTGAAGGATTCCTGGACCAATATCATGATTTAATGGGTTTGAATGGAGCTTTGGAAATAGGGGAAGAGATGAAT
 GAAATGTTAGGTACATACATACATACTCAATGATGATGATACATACATACATA

Fig. 40

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus oryzae* Gtb3 (Genbank accession No. AOR_I_2580174)

MAEILHVSALGWDKMKDHWQFVFIAILACVATGSLWLLYS6TKRLRNYIKTRPRSEKVPLNVSQLVTLNKLKLSVPN
 IQRRKPSSFGVYLGFSFSPDRDQLRLNEWDLIVDPFQSGTAQAIRYVEGKQLLGRVDLDRILSKDESTLSAIEKIEN
 LLTGTFDSANFSGMVLNWEKGKFTPVFVKLVEIDELGLAVYLETAPPDFLKDHNMQNPAISGIVIQNASILPEGQKR
 DYFQLVKMQPTIKAFVSEACVRDFVVMWETIDDNAALSNVAVQRSIQWCFYSAIPWIGQKSALTNAALNVKISEPLSS
 FGWLKDAEIIKAHDRWRSNLHLKDVASDTNAWNLTLLPFFPTLEELLTSSEYGQPESNELTTKLDRDPEWVAQVKSLSGSL
 SISMAGIEYNLSGCFPLGSEATALAFAEVLQSQRLRLKSLGLLHPVPASKIQSIGLLKKFHESYLLPNATSSDPYVIPNA
 TSDQLATTIKELSNLATNGSLQVNLGLDSGLRKSVDVRFWAVYQMDSDGFVFAKKAQGLAGTVLHTFLSAKGYPRHVC
 FEVETALAKWSQDLVKDTGLPRRLVEDIDMLSPEERLLLFQHLSLTDSYSELSDTICAYIRRLIDAPSLAQLKELNTVS
 YLEGSASPEILVNTRIKWYREGGQHPSPSKCALFYQTDAAFTQILREHREGDLALISKGFCQLLQNDHIDITYDIMAL
 ALFCAARKGAIDEITYEVTDRNPLFNNQSDQAAAFSESFALGSRCEVYFDVQPSAFGKLLSDRFRRREYNDEKLPDWINGA
 PEMATSYAGAGIDVNPDKHKVSPGYQRFITFLGVFAFPALIDIIILLTIIIGRGLYLSAFMTHDELQSATIALMISLLSGA
 IGTMIACGGPYLISMAFAASNMFVIRLIAGVAFIAAGLIGFIVISGVKSPQAGIIFYLYLVALTIYLTTFATLASFS
 YPGTGFLSGRKVIFSCPIILFVSPITITWSGHDSAILYLAVLYVFIGFLLGLRSVASKWVTWYQNIIRRTDDTEIRKWIJA
 TYGNNDKVFNGMNDPAVLKMSDALYKDYLAEKSRSFSSKPTTDLVRELARDWDSTNLLDWYCRYADVPRPIPFSSS
 WNIQTQKGLDVLNRNSQKIRLHNAFIHWRQSSKEIGCGILYFIALLDKWVELLSGGQLVGLSTSLSDANRMAVGGLAY
 YLIGAVLIDTKAQELHDLVQGHSAVAVGSAKEIRPSQKRDVRFKRVYWKTFKFLMWLVWSLAIALIATLITFQAPVQAM
 IMFFAYVLSYTGLLWYQYTKIFTGPHALIPMTGVVVGLPVGIKLVCLGNFLYSQVIGLGAATWTVAILSLFTAKMGM
 PKKVDSPVELGKTFHAYTAPWADPEWSQQLQTFEFGVSVVPADARLKLVPGSHPGVEVKTILLSRKIEPRIEEAFPESE
 KLISMAIGAWETGEISLELVPLGSLGPNIALSCSMGHLQIAICVGRGLDERIDVSANCOVIAETLLHAVAESMMRMPH
 EYAVLSESLVTAQVTETTARQLREEDTPLVVRWSKKELLRQLCLGFEVDSHWEKLPENVRNMLLDRCLGRPCLLSEGSQ
 QWLQTSLCRFDTSDLVNHVARGNLGAATAVSIIDYANYGTGEAGAIKDEPIPIYIPEIPKKLPMAMSI IQKPLSYVYHSI
 GSGVKFFIAALLADSEFQREFDHVMSEHRTLIRVPLVFLNMVWLYFKTVQDQIGL SFFLFHGRSNVKRLWNETKGITVSI
 KKSRLFVQSLQGTFAAFRHNEDPGGFKVYYSGEHKTEPEGMKLLKYVSTYSKDMLLLIRQEFKDGKVLNEYHYDYRAPT
 KKSFTLSKAWATRIPLGRRRCVRGQNNLQSVQYNNRGLIEAGSYMKGDLIRFKYHYRKNPRFGDELLRAEFSLTHITCTV
 SWCAPPLRHPEKVERWIPHSKVTEATFVQGADVYEARNLYDHKFHPTIFTTLN6QKVQTPPMIENDFIGVLAKPKQTSFA
 NDNPLLYCDSLSSNTVTRFLGLTTKRFPVSTSRARSLLWKSWKDRVDFDAIMVRWMDERLLRREKTLAPYWRARNRGDLA
 AAKKYELRLADAITASADLDNISSWTPLAVKISDLFNFPGGGDAVVHTRSKDFGSDTDKSMHVMAADNGTWPNEGGSVS
 ACRRDMINSLRTVKWHMICESANDFGIPKHQTEQNVLSLKVPLWGLDFTPTHGLFRNKLDSEVDNVTASDMDIKLNF
 IPILTALVKGARATHLSKADIHQATRALVNLNTYFQDSRHWTQIWNSDIVKESWRDLWLTOEMPNTVPSSQWFRTELPTL
 TSLDTALELWYRYLFIPIPIEPIPSVFQASHHSVSASYGVVCKMKRNLQIWDHAIWRETNLCLSSALCKLSPFVR
 NALLGLMRITSAITLHADIIILPCADFFNPGWEVEIGTCQGTIEHRNVFRKRVDPVVGITDMQKFAPVKEIKSERPTVT
 MLSHVWYAKDIKJALLAADIINQWKFDYHLDIYGAIKAPTSTECQEI IASKGLRGKVTLRGTADPMKVLNTWFL
 NSSLSEGLPLALGEAALTGAPVVCTDVGASLRVLSOPDDFSRYSAVVAPNDAAHALAKAGITMLGLLGEWSKYTDDTEPAP
 VLTSSPTPEDYAKITRRMYEKSDYRRKLGMMDTRDIVQKSFSGDRYLREHEQMLWIGKSAKIMANRVGGAITEPTDIATAM
 ROTLPIEEEVITIPRSVHWSRSSAASGMSTVYSEVSNFPMNLNGYHRPSSIRSGISGMSTDTESFLPLPSNASLPVFAPR
 QTLGYPSTPDGRLSPSGRLSPLPNRNSGRRSMSTAGREQLRGLGREELNPYRNSDVSTIMRDEFLKSSYKNIIEGSNST
 PNM

Fig. 41

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus oryzae* gtb3(Genbank accession No. AOR_1_2580174)

CGGACCTGTGAGGTTGGCTGCAATATCTAATCAGGATGGCGAAATCCTCCAGCTCTCAGCCCTC66CTGGGATAAAAT
 GAAAGATCATTTGGTGGCAGTTTGTAAAGTAGTATTGATATATACGTTTCAGATATCACTGACTAATGCTATGCTAGGTGTT
 CATCGCTATCTTAATAGCGTGTGTAGCTACAGGATCCTTGTGGCTTCTGTACTGTGGGACGAAGAGACTGGGCACTACA
 TTAAGGTAGGGCTTCTTTGATATGCTTGTGAATGTATATGTATCTGTCACTACCTGATTCAAAATCATAGACAAGGCCA
 CGTTCAGAGAAAGTGGCGTCAATGTAATCTCAACGTTTGGTACTCTTTCCAAAGATTTGGTCAATGTGGCAAAACATTC
 AAGACGCAAGCGCTCTTCTTTTGGCGTCTATCTGGGTTTCATTAGTTCCCGCCAGATCGGGATCAGCTTCGGCTTCTGA
 ATGAATGGGACCTGTGTATAGTTGACGCTTTTCAGTCGGGCACGGCCCAAGCAATCGGTTATGTGGAGGGTAAGCAGTTA
 TTGGGAAGAGTTGACCTTGATCGTATCCTCTCAAAAGGACGAGTCCACATTTGTCAAGCAATTGAAAGATTGAAACCTTCT
 CACCGGCACATTTGATAGTGTAACTTCAGCGGCATGCTACTGGCCAACTGGGAAGGAAGTTTCCACCCCGGTTTTCA
 CTAAGCTTGTGAGGTGATCGATGAGTTGGGTTTGGCAGTGTACCTGGAGACGGCACCCCGGACTTTCTAAAGGACCAC
 AACTCCATGAGAACCCGTGCAATTTCCGGAACTGTTATTCAAAATGGCAGTATACCTGGCAGAGGCCAGAAAGCGGACTA
 TTTTCAAGTCTGTGAAGATGCAACCCAGCATCAAGGGCTTCTGTCTCGAAGCTTGTGTAGGGATTTCGTGGTATGGGT
 GGGAGACAATCGATGACATGCGCGCTTATCAAAATGCTGTGTCTCAAAAGATCTCTCAGTGGTGAACCTTTTATAGTGGG
 ATCCGCTGATAGGCGAGAGTGGCTCTCAGAAATGCTGGCTTAAATGTCAAGATCTCAGAGGCTCTCTCCTCTTTTGG
 ATGGCTGAAGATGGCGAAATCATCAAGGCTCAGGATCGGTGGCGCTCAAAATTTAGATCTCAAGGATGTTGATCCGACA
 CGAGCGCTGGAAATCATTTTGGCGTTTTTCCCGACCGCTGGGAAGATTTGCTTACCTGCTGGAATATGGTCAGGCTGAG
 AGCAACGAGTTGACGACAAAACCTCGGTGATCCACGGAGTGGGTAGCAGGTAAATCTCTAGGAGTCCACTTTCCAT
 ATCAATGGCGGCAATGAAATATACTGCTTTGTTGCTTGGCGCTTGGATCTGAAGCGACAGCAGTTGGCTTTGCTGAAG
 TCGTTCACTCTCAATTTGGCGCTTAAATCACTGGGCTTGGTCCACCCGGTTCTGCTTCCAAAGATTCAGAGCATCGGTCTG
 CTCTCTCAAGAAATTCAGGAATCTTATTTGCTTCCCAAGCAGCAGCTCAGATCTTACGTTATTTCCAAACGCAACCTC
 GGACCAACTGGCGACTACGATCAAGGAACCTGCGAATGTGGCACTAACGGCTCATTTGCAGGTCAACCTTGGATTGGACT
 CAGGACTTCTGAAGAGCGTGCAGTGGCTTTTGGGAGTTTATCAGATGGACTCAGATGGATTGAAGTTTTGCTTGG
 AAAAAGGCGCAAGTTTACGAGGAGCTGTACTGCATACATTTCTGTCTGCAAAAGCTTACCGCGCCAGCTTTGTTTGA
 GGTAGAAACCGCTTTAGCCAAATGGTCCGAGGACCTCTCAAGGATACAGGGCTTCTCTCGCGACTCTGTGAAAGACATCG
 ACATGCTGAGCCGAGAGAGGAGCTGCTTTCTATTTCAAGCATCTCTCTTGGCAGCTCATACAGTGAAGCTCTCGGATCT
 ATCTGTGCTTACATTCGGAGACTGCTTATCGATGGACCTTCACTCGCTCAGCTGAAGGAGCTTAACACGGTCTCATATCT
 TGAAGGCTCGGCTTCTCCGGAATTTTGGTTAATACCGCATCAAAATGGTACCGAGAACAGGGATGCCAACATCCGTCAC
 CATGCCAAATGCTCGCATTTATCTACCAAGCGGATGCTGCTTTTACTCAGATCCTAAGGGAGCATCGGAGGGAGAGCTT
 GCTTTGATATCAAAAGGGCTTGTGCGAGCTGCTCAAAATGATGACATCGATACGTATACATGATATCATGGCATTTGGACT
 TTTCTGCGCTGGCGGAAAGGAGCAATCGATGAGATTTAATGAGATTTACGTAAGTTACCGATCGTAACCGGTTTGTCAACAAICAGI
 CAGACCAAGCGGCTGCTTTCTCAGAAATGCTTTGCTTTAGGGTACGTTGTAGGTTCTACTTTGATGTTTCAAGCTAGCGCT
 TTTGGAAGCTGCTCTCGGATCGTTTCAGAAAGGAGTACACCGATGAAAGGCTCCCGGATGGATCAATGGCGCGCTGA
 GATGGCCAGATGTTATGGCGGTGGCAAAATGACGTTAAGCGGATCAGAGGTTAAATGGATGGCTGTTTACGAGCGAT
 TTACTTTCTCGGTGTTTTGCGATTCCGCGGATTTGATCGACATGATTCTGCTCACAATATCGGCGGTGGTCTCTACCTT
 TCAGGCTTCATGACCATGACGAGCTGCAAAAGTGGCACCATCGCTTTGATGATCTCTCTTCTCTATCTGTTGCAATCGG
 TACGATGATTGGCTGTGGAGGACCTACTATCTCATTTGATGGCTTTGCGAGCTTCAAAACATGTTTGTCTTATCGGAC
 TAATTGCTGGTGTGGCTTTACAATGCTGCTGTTTAAATGGGATTCATGTTATCTCTGGCGTGAAGAGCCACAGGCT
 GGAATATCTCTATCTGTACCTAGTGGCTTGGACATTTACCTGACGAGCTTGGCTACCGCTGGTAGCTTTAGTTAGCG
 TGGAACCGGTTTTCTTCTCGGAGCGAAAGTGTCTTCAAGTGCATCCGATTTCTTTCTGCTCAGCTATCATCACTACTT
 GAGCGCGCCAGGATTCAGCTATTTACCTCGCTGTCTATAGGTGTTTCTGCTTCTGCGCTTGCAGTCACTT
 GCTTCAAAATGGGTGACCTGGTATCAAAACATTAAGAGGACGGAGCATACGGAATTCGGAATTTGATACATTTGCCAGTA
 CGGTAATAATGACGAGAGGTTTTTGGAAACATGAGTGACCGGGGTGCTTTGAAATGTCAAGAGATGCTGCTATAAGG
 ATGCTTTGGCTGAGAAAGTCCCGAAGCTTCTCTTAAGCCCAACACTGATACGCTGGTCCCGAGCTTGGCAGGGAGCTGG
 GATTGCAAAATTTCTCTCGACTGGTACTGTGCTTATGCTGATGTGCTCGGCGGATTCGGTTCAGTTCTTCTTGGAA
 TATCCAGACCAAGTCCGACTAGAGTTCTTCGGAATTCGAGAAAGGAATCCGGTTGCATAATGCTTGCATCCATTTGGC
 GCCAATCGAGCAAAAGAAATAGGCTGTGGAATCTGTACTTTATCATAGCCCTCTTGGCAAAATGGGTTGAGTTATTGAGT
 GGTGGACAACCTGTTGGTCTCTGCAAGCTGCTTTGATGACCAATGGAATGGAGTGGATTGGAGTGGGTTACTAGCT
 GATTGGGCGCTTCTCATGATACCAAGCGCAGGAAGCTCCATGATCTTCTGGCGAGGATTGGCTCTGCTGTGGAT

Fig. 42

[illegible]

Fig. 43

GTCACTTTCCGAAGGTCTGCCCTTAGCTTTAGGTGAAGCTGCTCTGACCGGTGCCCGTGTTTGACTGATGTCGGTG
CATCTCTTCGTGTTCTGAGCGACCCAGACGACTTCTCTCGTTACAGTGCCGTCGTGCGACCCAATGAGGCTCAGCGCCTC
GCAAAAGCGCAGATCACCATGCTTGGCCTTCTGGGAGAATGGAGCAAGTATACTGATGACACTGAGCGCGCACCTGTGCT
CACTTCATCTCCAACACGAGAGGATGTTGCCAAGATCACCGCGGCATGTACGAGAAGAGCGATTATGTCGCAAACTCG
GCATGATGACCCGCGATATCTCTCAGAAATCATTCAGCGCGCAGCGATACCTCCGTGAGCAGCAGCAAAATGCTGTGGATC
GGCAAGTCTGCTAAGATTATGGCCAACCGAGTTGGAGGAGCCATCACCGAGCCACAGACATTGCAACAGCCATGCGCCA
GACTCTCCGATTGAAGAAGAAAGTCATACCATCCCTCGCAGCGCCGTGCACTCGTGGCGTTCGTCTGCTGCATCGGGCA
TGTGACAGTATACAGTGAGGTTTCCAATTTCCAATGCTCAATGGCTACCACGCGCCATCCTCTATTGCTCAGGTATA
AGCGGTATGTCAACGGATACAGAGTCTTTCCCTTCTCTCCCGAGCAACGCCTCTCTCCCTGTCTTCGTCCTCTGTCAGC
CCTGGGCTACCCGAGCAGCCCTGACGGTCTGCTCTCAGCTTGGGGGGCTCTCTCAGCGCTACCAAACCAAGGAACAGTG
GTGACGATCCATGTCAACCGCTGGCCGCGAGCAGCTACGTGGTCTCGGACGCGAAGAATTGAACCCTTACCGCAATTCC
GACGTCAGTACCATCATGAGAGACGAATTTCTTAAATCAAGCATCTACAAGAACATAGAAGGCAGCAACAGCACCCCAA
CATGATCTAAACGAAAAAGGAAAAAGAAACAGAAAAATCCCATCTAGTTCTCTTGTTTTTACACTTTTTTTTTTTCTTT
TTTTTTTTGCATCATATGATTGATTCTTGGGTTAACTCCCGGCCCTGGCAATAATTGCTAATCTGTCTATTGCTATACC
AACCATATACCCGAGATGATGAAGTGCTGTTGTAAATACCTGCATCTTGCATATACTTTCGTTATTTTGCATCTAAC
TTCATCATTA

Fig. 44

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus nidulans* Uge3 (Genbank accession No. AN2951)

MDSPRRSDASSPAEPCSPVCVDTPATQSSVLFDGNLDDLRRNFPLROYILVTGGLGFIGSHTTLELLKASYNVVVIDNLS
NSFQSVFDRIKHLAQKHDERGTEMPALHLAAHDYRDTAALRQLLDQYQVDSRWGTPKSKISGVIHFAAYKAVEESIKNP
LKYYANNVSGLIDFASTLGKYGIKTFIFSSSATVYGTLATSGLPLKEELCAHKDEIYHDADGVAQTIRAGSTGITNPYGR
TKWMCEAILADLAASDPEWTIVALRYFNPIGCDSEGLLGEDPKQTPTNLLPVVVKVMTGEYNELSMFGTDWETEDGTAVR
DFIHVTDLARGHIAALDAANERKLAENFRAFNLGTGRGHSVKEVVDAMESVSRKQIPVRAAPRRPGDVGSCVAVATRSQQ
ELRWKTEKSLTDACGSLCKFLEVSGVTL

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus nidulans* uge3 (Genbank accession No. AN2951)

ATGGATAGTCCTCGACGATCAGATGCAAGCTCTCCTGCGGAGCCCTGCTCTCGGTATGCGTGGACACACCAGCGACACA
GTCCTCTGTCTGTTTCGACGGCAATCTGGATGACTTGTTCGCGAACTTCCCTCTTCGTCAGTACATCCTGGTCACTGGCG
GGCTCGGGTTTATCGGAAGTCACACAACATTAGAGCTGCTGAAGGCCAGCTATAACGTGGTTGTGATCGACAATCTCAGC
AATTCTTCCAAAGTGTCTTCGACCGCATCAAGCACTTGGCGCAGAAGCACCATGACGAGCGAGGAACTGAAATGCCAGC
TCTGCATCTGGCTGCTCAGGACTACCGAGACACTGCCGCTCTCAGGCAGCTTCTCGACCAGTATCAGGTGATTCTAGAT
GGGGCACTCCCAAGTCCAAAATTTCCGGCGTGATCCACTTTGCTGCGTATAAAGCAGTCGAGGAGAGCATAAAAATCCG
TTGAAGTACTATGCAACAACGTTAGTGGTCTCATTGACTTTGCCTCGACACTCGGAAAGTACGGCATCAAAACATTCTAT
ATTTTCCTCATCGGCAACCGTTTATGGCACTTTAGCCACTTCTGGTCTTCCACTCAAGGAAGAGCTCTGCGCCACAAAG
ATGAAATTTACCACGACGCGAGATGGAGTCGCTCAAACCATCAGAGCAGGGTCTACGGGAATTACCAATCCCTATGGCGCG
ACCAAGTGGATGTGCGAAGCCATACTGGCGGATCTTGCAAGCTTCTGATCCGGAGTGGACGATTGTTGCGCTCCGGTATTT
CAACCCAATCGGCTGCGACGAGTCGGGATTGCTCGGTGAGGATCCGAAACAGACCCCTACGAATCTTTTGGCGGTGGTCG
TAAAGGTCATGACCGGAGAGTACAATGAAGTCTCAATGTTCCGCACTGACTGGGAGACGGAAGATGGCACCGCCGTACGT
GACTTCATCCACGTAACCGACTTAGCCCGAGGGCATATAGCTGCTCTTGACGCTGCCAACGAAAGAAAGTTAGCTGAGAA
CTTCCGCGCCTTCAACTTGGGAAGTGGCGCGGACACTCAGTCAAGGAGGTAGTGGACGCTATGGAAGCGGTGTGCGCGCA
AACAAATCCCTGTTAGAGCAGCCCTCGTCGCCCTGGGGATGTTGGATCCTGCGTTGCCGTTGCTACAGATCGCAGCAG
GAGCTCCGATGGAAGACTGAAAAATCACTTACGGACGCATGTGGAAGTCTGTGCAAGTTCTTGGAAAGTTAGCGGTGTTAC
TTTATGA

Fig. 45

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus nidulans* Sph3 (Genbank accession No. AN2952)

MAVLIFVA1LAIVLPTSIIIVTRRKNNNMGPKAKVFVPLYVYPAPGAWDPLVNVITAHDPVNFVTVVNPVPGSGP6PNPLPDR
 NYTQEIPRLTAHDNVRVLGYVATTYAKRNISSVRNDIETYAAWPTISANPKLAVRGIFDETPQQYNASDLAYLEELTSV
 VKNTPGLGPDHFVFNHNP6VVPDPRYLSTADSTVVFEATYDTFQDRDGARLFETIPNSNRSQLCAVVHVSVPDSVEGSELRK
 FVKQARRVADEIFVTHLSTNYASF6DKWDDFVRLMAQ

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus nidulans* sph3 (Genbank accession No. AN2952)

ATGGCCGTCCTCATATTTGTCGCTATTCTTGCAATCGTTCTCCCGACATCAATTATAGTAACCCGACGCAAGAATAATAA
 TATGGGCCCGAAAGCAAAGGTCTTTGTCCCTCTCTATGTGTACCTGCTCCCGGTGCGTGGGATCCCTAGTGAATGTGT
 AAGTTTCCTTTGACCTGGGTGCGTTTTTATTTGCCCTCGCTTTTTCGGAACGAACCCGAACCCCTGTAGGTGAGACA
 GGTGACCTAGATTCTGGAATCATGCGAAGCCATCAGCGCGCTGCAGAGGCACCGGCGTGGGACAGAAGGCGCCTTTGT
 TTTTTCGGGGGCTGCAGCTAAACGCGCTGTAGGATCAGGCGACACCCCGATGTCAACTTCAGGTCGTGGTAAACCCCTG
 GCAGCGGGCGGGTCCGAATCCCTGCTGATAGAAATTATACGCGAGGAAATTCCTCGGTTGACGCGCGCATGACAATGTG
 CGCGTTCTCGGCTATGTGCGCACTACATACGCGAAGCGCAACATTTGTCGGTGCGCAATGACATTGAGACCTACGCGCG
 CTGGCTACAATCAGCGCTAACCCCAAGCTTGCCGTTGCGGGAATATTCTTCGACGAAACACCGCAGCAGTACAATGCCA
 GCGATCTGGCGTACCTAGAGGAGCTCACCTCGGTGGTGAAGAACACCCCTGGGCTCGGGCCCGACCATTTGTAAGTTTG
 ACGCTGTTTGTGATGAGCACCACGCGGATCTGCCTAATTCGAGTGAGCCTCTTGTTGGGGCGATATCTCATATCCATCT
 CCAACATCTACAATCTATTTTCCCTTGGCAGTGTGGTTGGATGTCTTAGTCTGTGACTTGTCTAGCCTTGGAAATCGGAC
 CGATCTCTGTCAATCACTACCGGTGCCGCGGTGTGGCCGGTAGATTGGGTACTAGCCATGCTAACTGGCGAATGCAATA
 GGTTCCTCCACAACCCCTGGAGTTGTCCAGACCCTCGCTACCTGTCGACGGCTGACTCGACTGTGGTGTGAGGCAACGT
 ATGACACCTTCAGGATCGCGATGGGGCCAGGCTGTTGAGAGCAATTCCCAACAGCAACCGTAGCCAGCTCTGCGCGGTG
 GTCCACTCGGTGCCGGACAGCGTGAAGGGTCAGAGCTGCGAAAATTTGTCAAGCAGCGCGCGGAGTCGCCGACGAGAT
 TTTTGTACCCATCTCAGCACGAATTACTACGCCAGCTTCGGAGACAAGTGGGACGACTTTGTTGCTCTGATGGCTCAAT
 AG

Fig. 46

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus nidulans* Ega3 (Genbank accession No. AN2953)

METLKAPSTGWKSWTAKKKALLISSILIFIIALAVGLGVGLGLNLKGSNDNESGGNNTPTTPNNTAIWQPAVGTSWQ
 IVLRYALNDTSYDQVDYDIDLFDNKKAIIDELHSDGRKVICYFSAGTYEDWRDDADKFPEDDIGDNLDEWEGESWVDIRS
 SKIRDIMLDRLDIAVQKGCQGVDPDNDGYDNQNGLDLTQDDTVDMNFLADEAHSRNLISGLKNAGAVIPRVISRMQWS
 VNEQCAQYDECPTYAAFVRRGKPVFHIIEPKGDDTNNEVQVTGQKKATACDFDDSNFSTLIKMDLDNLQESGAYLPI
 QVPPQTPQVRTQCHGQTTLIRAPTTGPTLHSQSSSPLLSRERQIRRPYLLPQT

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus nidulans* ega3 (Genbank accession No. AN2953)

ATGGAAACCTCAAGGCTCCGAGCACGGCTGGAAATCCTGGACGGCCAAGAAGAAAGCTCTCCTAATCTCGTCGATTCT
 CATCTTCATAATCGCCCTCGCTGTTGGTCTCGGCGTCGGTCTTGGCCTCGGCCTCAACAAGGGGAGCGATAATGACAATG
 AGAGCGGCGGTAAACAACACCACCCGACCCCAACAACACCGCCATTTGGCAGCCTGCCGTGGGCACCTCCTGGCAG
 ATCGTGCTGGCGTATGCCCTGAATGATACCTCATATGACGTTGATGTATACGACATCGACCTCTTCGATAACAAGAAGGC
 GATCATCGACGAGCTCCACTCCGACGGCCGCAAGGTGATCTGCTATTTCTCAGCAGGCACGTACGAGGACTGGCGGACG
 ATGCAGACAAGTTCGCCGAAGACGATATCGGCGATAACCTTGATGAATGGGAAGGCGAGAGCTGGGTTGACATCGGCTCG
 TCCAAAATCGGCGACATCATGCTCGACCGGCTCGATATCGCCGTGCAAAAAGGCTGCGACGGAGTCGATCCAGACAACGT
 TGACGGGTACGACAACCAGAACGGGCTTGACCTCACTCAGGATGATACGGTTGACTATATGAATTTCTGGCGGATGAGG
 CGCACTCAGCAATTTGTGATCGGACTCAAGAACGGCGGCGCGTGATCCCGCGCGTGATTAGCAGGATGCAGTGGAGC
 GTCAACGAGCAGTGGCGCAGTATGACGAGTGGGATACATATGCGGCATTTGTCCGGCGCGTAAGCCGGTCTTTTCATAT
 TGAGTATCCGAAGGGGGATGACACGAATAATGAGGTCCAGGTTACGGGGCAGAAGAAGGCGACGGCCTGTGACTTTGACG
 ACTCGAATGAGTTCTCAACCTTGATCAAGACATGGACTTGGATAACTGGCTGCAGGAATGTTAGCTCTTACTGTCTACT
 CTAAGGTTATGTTGAGAACGAGCAGGGGTTCTGTTGATCTTGATCTAGATACTAGTGTAATATTCATACCCGATATTGT
 ACTTCATTACTTTGTAACCGGGCTCGGCCATCATCAGAAACCTTCAATCGCCAACGTCTTACTGGAACTCAGTTCCTA
 CCGTATACTATAGCCGGAGCCTACCTTCCCATTCAGTTCCACACAGACCCGCAAGTTCCGACGCAATGTCAGGGTCA
 GACCACACTCATTAGGGCCCCAACGACAAGGCCTACCTTCATTCTCAGTCTTCGTACCCCTTTTGTCAAGAGAACGAC
 AAATACGCAGACCTCGGTATCTCCTGCCCCAGCCGACGTAG

Fig. 47

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus nidulans* Agd3 (Genbank accession No. AN2954)

MVAPTLVIQTGGFFGIFTCDTPRGVWPFGRPTVI SPWPPSPSSSTSTSVPPAASSASTISVPTVTGPTPTVTVTATSS
ASTLLTTLTLPSTDSATASASTSADSTTISSTSSASDPAOSSTLYPTSEPSASEPTSEPSSTGTPTSTSDPDPT
SATEPSSSTSTPEPSQIVTSSSTSSPSTSPSTSSSTSPSSTLTSTSSPSTSTLTPTSASPTPTTIVTSPSMSVT
STSVAPSATGSLANNILVIARDSTQASVASSGLNGYGIPTFTLLVPDAGVELPALNSSGGNFGGIYVAGEVSYDYGNDN
WRSALTDDGNQLYAYQLAYGVRWVQYDVPFQPNFGASSIGNGCCADGVEQLVYFTDTSDFPTAGLKTGSSAGVSTSGL
WHYIASVTDTNTKAIASFASGGGVDGESVAIVNFDGRQWAFIIGFDIVWSQSYLQHAHITWIRGLHAGYRRYN
LNTQIDDMFLETDIYQPSGITFRITTDMDGITNWLPSIRAKLNAGSTYFVEIGHNONGNIEAGTTAAGESTCGGGAIEY
DSPPDTALEFVKPIGTQTDVNPSTPTNFTWITTCMNADSLIWFQNHLDQYAYISHTFTLEQNATYSOIYKEISFNQV
WLERAGTSAASKFTSNGIIPPAITQLHNGDALRANWONGITNCVDNTRPVLLNSENMNPFYTTAAADGAGMQVNPRT
ATRIYNNCDTPACTGQWIDTISAGAGDFNLLDTERAEVLRHLFGLHRDPYMFHQANLRNKGIDPITVQSETGQFSIFQA
WVETIVAEFTRLVDWPIVITTHQEMSAEFLARYTRDHCYGLNYILDNGAITQVITVANQNTCDANIPVTFPTAPTDLG
FATEQLGSDPFTVWAOLSGSPVTFSLATPJAL

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus nidulans* agd3 (Genbank accession No. AN2954)

ATGGTCGCTCCACGCTGGTGCTGCAGATCGGCTGTTTCTTTGGGATATTACCTGCGACAGCGCCCGGGAGCTGGCC
TGAAGGACGCCGACGTGTTCTTTCCGCTGGCTGCCAGTCCGAGCTCGACGAGCTCAACTACTTCGGTGGCCCGGCTG
CTTCGTCTGCATCTACGATCAGTGTCCGACACATCACCGGCCGACTGAGCTACAGTACGAGTACTGCAACGCTCTCT
GGATCTACTACTCTGACGAGCTCAGGACTGTGCCCTGCGCCACAGACTCTGCTACTGCGCACTTCTGCTTCTACTCTG
TGATTCCAGTACTACTCTCCAGCACATCCAGTGCTTCTGACCGCGCTGGCTCTTCCACTCTGTTCCACCTCAGAGCCTA
GCGGCTCTGAGCCTAGCAGCTTCAAGGCCAGTTTCTATCCGCTACTCCAGGACTTCGACCACTGATCTGATCCGAG
AGTGGCACTGAGCGCTCCAGTACTTCGACCTCGACTCCGAGGCTTCAGGACTGTGACTTCAAGTACTTCGACTTCGAG
TCCAGTACTAGCCCGCCGACACTTCCAGCACTTCCAGCACTAGCCGCTAGTACCTTGGCTTACCTTACCTTACCTTCCCT
CTAGCTCTCTAGCTTACGCGGAGTGGCAGGCTACCGGCTCTACTACAGTCAAGCGCTCCGCGGAGCATGTCTGTACT
TCCAGTACGGTGGCAGCGCTCGGCGAGCGGCTCCCTGGCCAAACACATCCTGTGATCGCCGCGGACTCTGACGAGGCCAG
CGTTGCTCTGTCGCGGCTGAAATGGCTACGGAATCCGCTTACGAGCGTCTGCTGCTCGCTCAGCGCGGCTCGAGCTCGCG
CGCTGAACCTCTCTCAGGCGGCAACTTTGGCGGTATCGTCTGCTGCGCGGCAAGTACGCTACGACTACGCTAACGATAAC
TGGCGCTCGCGCTGACGAGCAGCAGTGGAAACGAGCTGTACGCTACGAGCTCGCTACGCGTGGCGATGGTCCAGTA
GAGCTCTCTCGCGGTCCCAACTTGGCGGCTCTGCTCATCGGCAAGCGGCTGCTGCGCGGAGCTGTCGAGCAGCTCG
TCTACTTCAAGGATACGAGCACTTCCGACGCGCGGCTCAAGAGCGGCTCGAGCGCGGCTCTCGACTCGGCTCTC
TGGCACTACAGGCTTGGCTCAGCGACACGACACGACGCAAGCGGATTGGGTGCTTTGCTCGCGCGGCGGCTTACG
CGAGCTGTGTGCGCGGCTCATCAGAACTTCGATGCGCGCAGCAGATGGCTCTTCTACGCTTCCAGCTGTCTGCT
CGGAGACTCCAACTACTTCAGCAGCGCTGGATCAGCTGATCAGCGCGGCTTCCAGCGCGGCTACCGCGGCTGAAC
CTGAACACCGAGATTACGACATGTTCTTGGAGCGGATATCTACAGCGGAGCGGAACTCTTCCGATCAGCGGAG
TGATATGAGCGGATCAGCAACTGGCTGCGCGAGCATCCGCGGCAAACTCAAGCTTGAAGCAGCTACTTTGTGAGATCG
GCGCAACGCGCAACGCAACATCGAAGCGCGCACCGCGCGGCTGAGAGCAGCTGCTCGCGCGGCGGATCGAGTAC
GACTCGCTCCGCGACAGCGGCTCGAATTTGTCAAGCTATCGGACCGGCACTGAGCTGCGCAAGCTCGCGGACCA
CTTCACTGGCAACAGCTGCTGATGAACGCGGAGGCTGCTCATATGTTCCAGAACCACTGGAGCACTACGCTACA
TCAGCGCACGCTTCAACCACTTGGAGCAGAACACGCGACCTACAGCGACATGTACAAGGAGATCTCCTTCAACGAGTC
TGGCTGAGCGTGTGCTTCTCGCGCGGCTCGAAGTTCAGCTCGAAGGATATCATCGCGCGGCTACCGCGGCTGCA
CAAGGTCAGCGCTCTCGCGGCTGCTGGACAATGGCATCAGCAACTGCTCGCGGATACACGCGCTGCTGCTCTCA
ACAGCGAGAACGAGATGTGGCGCTACTTCAACCACTGAGCGCGCGGCTTGGCGGATGCGAGTCAACCGCGCTTC
GCGACTCGAATCTACTCAACTGCGACACCGCTGCTGCAAGCAGCAAGGATGGAICGATACCTTCTCGCGCGGCGGAG
CTTCAATGAGCTTCTGACACAGAGCGCGGAGGCTCTGCTGCTGCTTGTTCGCGCTGCTGCGGAGCGGATGATGCTTCC
ACAGCGCAAGCTGCGGAATGTGGGATCGAGCGCATCAGCGTGGCTCTGAGACGGCGAGTTCTGCTGCTTCCAGGCG
TGGGTGAGAGCATGCTTCCGAGTTGACCGGCTGCTGAGTGGCGCTTGTACGATTACGATCAAGAGGATACACTT
CGCTGCTGCTTCCGCTGCTTCCGCTGCTTCTACGCTGCTGCTTAAATCTTGGCTGCTTCTGCTCATAGTTACAGCT
TGCTAACTAAGTAGATGTCGCGGAAATCTCGCGGCTACAGCGCGGAGCACTGCGACTACGGGCTCACTACATCT
CGCAACGCGCTACAGCGGCTACCGGCTGACTGCAAGCGGCAACAGCTGCGAGCGCAACATCCCGCTTACCTTCCG
CGCGGCTACGGAACAGCTAGGCTTGGCGAGGAGCAGCTGGCGAGCGAGCGCTTACCGATGAGGCGAGCTCTCGG
TCCGCTGAGCTTCTGCTTGGCAGCGCAATTCAGCTGAG

Fig. 48

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus nidulans* Gtb3 (Genbank accession No. AN2955)

MTQILHVSPVGDHMKNHWWQFSRRRPEKVSPPRSVAKIDGLANRHLNLANRPTGQKPSSVGIYLGGLDEHLSDYQRRFLD
 EWDMLIVDPYQSGVVEAVATAAGKQILGRDLQDVASKEDAALAAIEKIDSALSQVFERSAFSGILLANWENKLSSECWA
 SLLQAIQKLGSLVLETPAPPDFLPDRVLQQAISGLVVKNASILPNGQKRDFYQLQSMKSTIKAFVSEACMRDFTVVAV
 ETIDDDASLNAVVRRLQWCFYSAIPWIGCRAALKDVKLNKLEPLSSFSWLKEPEIMSAHWRWRANSSIEDVNGVV
 SSGWDELLPFFPTLSNLIASSERDNGAHEDLTMAIRDPPDWVSLTKSQTNPLSTSIGGLEYNFSGCFPLGAEATAGSFAE
 ILKSQQLKSLGLLHPVPLAKMQSLATLLRQFHDFALSAWGSSDPVPGHIKELSNLAANEQLRVYLGLDGFRKNTDIR
 FWGVYHMDSEGFDFVSKKVOGLAGTVLHTYLSAKGCPRHVCFGAETALAKWTKDLVEEIGLPRRLVQDIDVLSPEERLL
 LLQHLSLTDAPSDLTKSICAYLQQQLIEGTSVLQKQVNTVSYLEGSASPELTVNSRVKWKYREQGCSYSPSPSVCLSLFRE
 VEATFPQILKERREADLAQISRGLCQLMQGKQVDAYTDILALALFCAARKGALDEIYQEVTDNRNPLFNAHSDQAAAFES
 FALGSRCESYFDISPSAFGKLLSDFRKRSYKDGDLDPWINGAPEMATSYAGAQIDVNPDDKVKPMRGYQRTFSLVFAFP
 ALIDIIILLTLIGRGLYLSAFMTYEEQNSATTAIMISLLSGGIOTWIAACGGPYLISMAFAATNMVFVIRLIAGLAFTIA
 GGLIGFVVVSGVNGPRAGIVFYLYLVALTTYFSGFACLSFSGSTFLSGRKIIFACIPIILFISPIVTTFTGHDSAIYI
 AVIYVFIGALILGLRSVASKWVTWYQKLRKTDDEIRKWWYVETYGNGDEKVFGGSDPAVLKLSREALKDVTAEARNRWF
 FSRPTTKSTLVELLARDWEATNFFLEWYCRYADVPRPIPYSSGWNQTKVALESKAAQGRIRLHNAFIHWRQSSREIGC
 GMLYFIVALLDKWVELLSGGHLIGLSASLTITAYRMAVGFSLAYLIGAVLIDTKAQELHSLVGSHTPVPLKTAKDIRDQ
 KRDRVFRKRVYKTLGKYLMMHWSGLAFSTALVWTFQSHMEAMVMFLSYVAAYTGLLWYQYTKIFTGPHALKPLLVGSLV
 GLPLGIALKVCLPHFMYQSVVGLGAATWTVAFSLIPAKMGMPKRVDSPELVGKTFHAYTAPWDDPDWSQQELQTFYESI
 SLIPSDARLKLVPASHPGSEVKQMLISRRKEPRIEEAFPHSQELVDALKAWEAGEVLELVPLGSIQPNVHALSGSTSD
 HLKIAIAVGRGLDHRIDVSANQVIAETLLHVAESIMQIPHEQAVLAESLVAAGVTETTARQLREEADTPLVVRWAKKE
 LLRQLCLGFECDFHWEKLPRAVRKALLDRCLGQPCRLSEKHYRWLEESICQFDIKDLAVHIARSNLAAAAAIVSILDYANY
 GTGESATYKESETPAYIPYLPKQLPTVAYFIMKPLFSVYKVAIALKFVVVALVADPEFQREYNHVMSPYPAIIRVPATF
 ALSMWNYYAKIMQDLGLTFFLFHGRDNVQQLWDETKGMTINIKKSRYIVQSLDGTFTAFRHNQPDGGFKVYYTGTPKTE
 PQGTSKLSVCVSTYSKDLLLIRQEYKGGNIIVNEYHYDYRTPTKKGITLKLTDKVKPMGRRCVGRGNHLQSVQYNRKGLIE
 AGSYMKGDNLIRFKYHYRKNPQFGDELLRAEFALSHITCTVSWCAPLRHPEKVDRIWPHAKVTEATFVQGPVVEARWL
 YDHKFHPTJFTTLNGQKIQTPPMIEHDYLGVLAKPRLTSFVHDNPLFYCDLSLSSNIFTRILGLTRKRFVPSISRARSLLIW
 KAWKEKADFDTITVRWMDERLLRRDRTLSPYWRSDWDGLTSAKKYLELRADTIAASADLDDGISSWTPLAVKVSDFNF
 QPGGDVAVNTRSDNFGSDEKSLHVMADNGTWPNEGGSVSACRRDMINSLRTIKWHMICESANDFGVPKHQTEQNILSL
 KVJPLWGMDFLTPTHGLFRNKLDAEVESVTSANDMDIKMNFIPILTALVKGARAVHLSKADIRQATRALVNLNTFFQDSR
 HWTQIWNSEIVKESWRDLWLTQEMPNTMPSAEWFSTDLPTLGLTDLVALELWYRYLFIISIPPEKIPSVFQASHHSVSAS
 YGVVCKIKRNCTLQIWDHAIWRETNLCLSSALCKLSPFVRNALLQLMRVTSALTLYHADIIISPCADFFNPQWEVEIGTC
 QGTIEHRNIFRRKVDPVVNGITDMQKFAPVKEIKSERPTVTMLSHVWYAKDIKTALLAADIINQWKFDYHLDIYGAID
 KAPTYSTECQEIISKGLRGRVTLRGADPMKVLESTWLFNLSSLSEGLPLALGEAALTGAPVVCTDVGASLRVLSDDPD
 FSRFSAVVAPNDALALARAQISMLALLGEWSQYAEDETEPAPILPSSPTPEDVAKITQRMVDKSEHRRKLGMMTRKIVQKS
 FSGDRLREHEQMLWIGKSAKMMATRAPGLHEPADIATAIQOTLPIEEVITIPRSVHWSRSSAASGMSTLYTSYSTS
 TPFSLNPNNQPPTRSSYYAPAHTSASANLLTRPSSLYSAISNASTTDASSFLPLNTPLPVFAPRHSFALPSAPGANGG
 NGGGISRPLSPAQRSPFLTRARHSRSGSLSTGGREQLRGLQREDLQQRNSDVSTIMREDFQSSYIRGIEGGNNQV

Fig. 49

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus nidulans* gtb3 (Genbank accession No. AN2955)

[illegible]

Fig. 50

[illegible]

Fig. 51

CTGACGTGGGCGCCTCCCTTCGGCTCCTCAGCGACCCAGATGACTTCTCCGTTTCAGCGCGGTGTCGCCCCCAACGAC
GCACTGGCGCTCGCCAGGGCCAGATTTCCATGCTCGCCCTCCTCGGCGAATGGTCTCAGTACGCCGAAGACACCGAGCC
CGCCCTATTCTTCCATCATCAGCCAGCCCGAAGACGTGCGAAAGATCACCAGCGCATGTACGACAAGTCGGAGCACC
GCCGAAACTGGGAATGATGACCCGCAAGATCGTCCGAAAGTCTTTACGCGGTGACCGCTACCTCGCGAGCACGAGCAG
ATGCTCTGGATTGGCAAAGTCCGCGAAAATGATGGCCACGCGTGCCCGCGGCTCCACGAGCGGGCAGACATCGCAACAGC
CATCCAGCAGACCTCCCGATCGAAGAGGAAGTCATCACCATCCCGCGCAGCGCGGTACACTCCTGGCGCTCGTCCGCGG
CCTCTGGTATGTCCACCGCTGTACAGGAGGTACACTAGCTCCAGCACTCGCTTCTCCGACTTGAAGCGCAACAACCAACGA
CCCACCGCGCTCAAGCTATTACGCTCCTGCACACACATCCGCATCCGCCAACCTCCTCACC CGCCCATCCTCCTCTACTC
CGGCATCTCCAACGCTTCCACAACGGACGCTCCTCCTTCTCGCCGCTCCCAACACCCCCCTTCCGTTTTTGCCCCGC
GGCATCCTTCGCCCTTCCTCTGTCTCCGGTGCCAATGGCGGAAACGGAGGCGGGATTTCAGCCCCCTATCGCTGCA
GGTCGAAGGTCCCGCTTTCAGCGCGGCTCGCATTCGGCATCAGCTCCGTTAGTCTCTCTACGGGCGGGCGGAGCA
CTCCGCGGGCTACCAAGGAGGATCTGCGACGATTCGCAATTCCGACTTAGCACCATCATGAGGAGGACTTCTTCC
AGTCGAGTATCTACCGCGGATCGAGGGTGGAAATAACCAAGGTTTAA

Fig. 52

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus sojae* Uge3

MESLQGS DASTPVEPY SPECVDTPATQSSV LFDGNLEELLRNFP LDQYILVTGGLGFIGSH TLELLKANYNVIVIDNLS
 NAFQNVFDRIKLLASKHHEQQG TKMP EMHLHAHDYRDSVALRK LLEGYQIQSRWGT PKTKISGVIHFAAHKAVEESIRNP
 LKYYANNVGG LIDFATTLGEFGIKTFVFSSSATVYGT LATSGLPLKEELCVHKDEIFEDRDGSKKLM EPGCTGITNPYGR
 TKWICEAILADLAASDPEWTIVALRYFNPVGCDESGLLGEDPKQIPTNLLPVVVKVMTGQYKELQMF GTDWDTE DGTAVR
 DF IHVTDLARGHIAALSAANEGLKENFR TFNLTGTGHSVMEVVNTMESVSSKEIPRRAADRRAGDVGSCVAVATRSQE
 ELQWKTEKLTLDACASLCNFLTVSGLSS

BASE SEQUENCE (PUTATIVE) OF NUCLEIC ACID MOLECULE OF *Aspergillus sojae* uge3

ATGGAGAGCCTCCAACAGTCTGACGCAAGTACTCCCGTGGAGCCTTATTCTCCAGAATGCGTCGATACACCAGCGACGCA
 GTCATCCGTCTTTGTTGATGGAAATCTTGAAGAGTTGCTGCGCAACTTCCCCCTGGATCAATACATCCTCGTCACCGGCG
 GTCTCGGTTTCATTGGAAGTCACACAACATTGGAGCTACTCAAGGCCAATTATAACGTAATCGTCATTGACAACCTTAGC
 AATGCTTTCGAGAAGCTCTTCGATCGCATCAAACCTCGGCTTCCAAGCACCATGAGCAACAAGGAACCAAGATGCCGGA
 GATGCATCTGCATGCCATGATTACCGCGACAGTGTGCTCTTCGCAAGCTTCTTGAGCAATATCAAATCCAGTCCAGGT
 GGGGTACACCTAAGACCAAGATCTCCGGCGTCATTCACTTTGCTGCCACAAAGGCAGTTGAGGAGAGTATCAGGAATCCT
 TTGAAGTACTACGCAACAATGTGCGCGGCTCATCGACTTTGCCACGACGCTGGGTGAGTTTGGTATCAAGACCTTCGT
 CTTCTCGTCGTCCGCCACCGTATACGGAACCTTAGCAACTTCCGGTCTTCCCCTCAAGGAGGAGCTTTGTGTCCACAAGG
 ATGAGATCTTCGAAGACCGTGACGGGTCCAAGAAGCTCATGGAGCCTGGGTGCACAGGTATCACAACCCCTATGGCGCG
 ACAAATGGATCTGCGAAGCCATCTTAGCCGACCTCGCGGCTCCGATCCAGAGTGGACAATCGTGGCTCTACGATACTT
 CAACCCGTTGGATGCGATGAATCCGGCCTTCTCGGCGAAGATCCCAAGCAAATACCTACCAACCTTCTCCAGTTGTG
 TCAAGGTGATGACTGGGCAGTACAAGGAGCTGCAGATGTTTGAACCGACTGGGACACGGAAGATGGCACAGCTGTCCGT
 GACTTCATCCAGTACCGATCTGGCTCGAGGACATATCGCAGCCCTCAGTGCTGCCAACGAAGGGAAGCTCAAGGAGAA
 TTTCGGCACATTCAACCTCGGAACCGGTACAGGCCATTCCGTAATGGAGGTGGTGAACACTATGGAGAGTGTGTCTTCCA
 AAGAAATCCCGAGAAGAGCTGCTGACCGCCGCGCGGCGATGTGCGTTCTGCGTTGCTGTGCCACCAGGTACAGGAA
 GAGCTGCAGTGAAGACCGAGAAGACATTGACCGATGCCTGTGCCAGTCTGTGCAATTTCTGACTGTACGCGGACTGTG
 CTCTTAG

Fig. 53

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus sojae* Sph3

MGPDKHVSGRRCLQSRRSRIILGVFVFIAILAVVJPPAVVVTLRKKNSMGPKANIFVPLYVYPAGAWDPLEAEISSHPE
 ANFTVVINPASGPGPNALPDANYTREIPKLASYDNVRLGYPVTTWAKRNISAVRRDIATYAEPNTSSNPKLAVRGIFF
 DETPQQYDADALSYLQELTSFVKGLSGLGPDNFIHNPAGVPDSRYMSSADSTVVFEAAYDTFNERNGTKQFDVLPKSDR
 GRGQLCIVIHSPDEVEGSKLRELVKLRKTADEIFITHLSTDYYANFGDRWGEFVDWMAK

BASE SEQUENCE (PUTATIVE) OF NUCLEIC ACID MOLECULE OF *Aspergillus sojae* sph3

AATCCACTTTCTTGCCCTCCTTTGTTGCATACTCCGGAGTACTAAGGCATTACATTTTAATTGCCTCCCTAACGTGGG
 AACGATGGGGCCAGACAAACACGTGAGCGGTGCTGCTGCCGTGCAAAAGCCGACGTTCTCGAATCATTTTGGGGGTCTTTG
 TCTTTATTGCTATCCTCGCGGTGCTTATACCTCCCGCAGTCTGGTCAACCTACGCAAGAAGAACAGCATGGGCCCTAAA
 GCTAACATCTTCGTCCTCTCTATGTGTATCCTGCCCTGGCCTGGGATCCATTGGAAGCAGAGTATGTCTGAATATT
 TTTTATGCCTATTTGTATTTCTAATTCTTCCTTGCATTTACCCCACTACTTCCCTCACCCCAAAAGCCAGTAT
 GTTCTGGTCCCTGGTATATACATTGTACACGATAAGCAAGGTGAAAGCCAATTGCATGATGCATGCAAGTGGGAAGCTAT
 AATTTGGGGGAAAGTAAGCAAGCGCCACAGGATCTCTTACATCCGGAGGCCAACTTTACCGTTGTGATTAATCCTGCCA
 GCGGCCAGGGCCCAATGCCCTGCCGATGCCAATTATACTCGAGAGATTCCCAAGCTCGCCTCTTATGACAACGTGCGT
 CTCTTGGGTTATGTCCCTACAACCTGGGCCAAACGCAACATCTCGGCCGTGCGTCCGACATCGCAACCTACGCAGAATG
 GCGGACCAACAGTTCGAACCTAAGCTCGCGGTTCGGGGTATATTCTTTGATGAAAGCCCCAACAGTATGATGCCGATG
 CGTTGTCATATTTGCAAGAGCTCACCTCATTCTGTAAAGGCCTTTCTGGTCTTGGTCCAGACAACCTTTGTACGTGTGACC
 CTTCTCTTTACCCCTCTGTATTTGTATTACCGCTCGGTATTCATGGTAATTTACATGGGTACATACCTCATGCCCGG
 TACCTTCTCCACCCTCTGTGTACTTTTATGCTTTTCACTTTTGCCAATATGGTCCATACCTGCCCTTTTGTAGGTTT
 TATTACGGTTTTGACTGCAACTCCGACAACCTCATTGGGTCAATTTATCAACGATGATGCTAATAGTGGCTGTCTAGA
 TTGTCCATAACCCGGGAGCCGTTCCAGACTCTGTTACATGTCTTCAGCTGACTCGACTGTGCTATTGGAAGCGGCTTAT
 GACACCTTCAACGAGCGTAATGGCAGGAAGCAATTGACGTTCTTCCGAAGAGCGATCGCGGTGCGGTCAGCTCTGCAT
 TGTGATCCACTCCGTTCCGGATGAAGTTGAAGGTTGGAAGCTTCGTGAGCTCGTCAAGAAGCTTCGCAAGACCGCGGATG
 AGATTTTCATTACCCACCTGAGCACGGATTACTATGCCAAGCTTTGGGGATAGGTGGGGCGAATTTGTGATTGGATGGCT
 AAATAATCCCTACGGGGGGCGCTTTTTCGAGCATACCTGATGCAACATTGCTTATGATCAGGACCGGATTGGCGTCCACTG
 ATAATATATGCGCGGGCGCTTTGATGGATTGGATTGACTAATCAACTTACGACCTGTCTATACTGTATGAACGTCTATAT
 CCTGTATGGTTATTCTGCTGATAATATGCTATTTGACTTTGGCGTTGTGACTATCAAATGATACCTAGAAATTACGATAG
 AGTTTACGATCGTCAAGATTTCTTTTGTGTC

Fig. 54

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus sojae* Ega3

MAGIDEALPLKGGQAAASGWKTWSGKKRMLIIGAIALVIALAIGLVGLGVGLNKGGEDEGEVPPTTGGGVTTAKWQPA
 VGTKWQIELLYALNDTSVDADIYDIDLFNNNKSTINDLQKQGRKVICYFSAGSYENWRPDKDKFKDSMDMGNTLDGWPDEK
 WLDLNSKNVRSIMTSRLDMAVEKNCQDGVDPDNDVAYDNDNGLDMKKEDSANFMMWLANETHARNMSIGLKNAGAIIPAVI
 DNMQWSVNEQCAQYEECDTYAAFIDKNKPVFHI EYPKGGDTNNNDLVSTSQKKSACDFEGSSNFSTVIKNNMLDNIQTG

BASE SEQUENCE (PUTATIVE) OF NUCLEIC ACID MOLECULE OF *Aspergillus sojae* ega3

CCGCAGGTGACCTCGAAACAACAGCCACTGTGGCAGAGTCCATTGTTTGGACAGCGACTGCCGCAGTCTGTAAGGCATTG
 ACTTGCCCTTTAATTCGAACCCAGGGCAGGCGTCTCTGCATCCGATTCCCCGGACCACTCAACGCAATCTCTGAACAAGC
 CACTTCATAGTTTCAGTGTAACCGCGGAGAGAGGGGATTTCTTTGTCCTCTCCTAGCCTATACATTTAACGGTTGCCGTGT
 AACCCCTGTGGTTCTACTCCGGAATACGCCACTCTATTTGCTTCTTTATCTGATCGTTTGATCTTCATCTCAGGTCCTCT
 TTATATTTTCCCTTCTTACCCGCCACCCACCTTACCGCTGTGGTTTGTGAAAATCAAATCGCAGGTCGTACCTTTCTTTC
 TCAGAATTCCCTTCTTTGAACATTTCTTTCTTTAGCCCTTCATTTTATTGGAATTTTCTTTGTGAAATCTATTGTACTA
 TGCCGGGTATTGATGAAGCGCTGCCCTTGAAGGGCAAGGGACAAGCTGCGTCCGGCTGGAAGACTTGGTCTGGCAAGAAG
 CGTATGCTGATTATCGGCGCTATCGGTCTCGTGATCGCTCTCGCTATTGGTCTAGGAGTTGGCTTGGGAGTCGGTCTGAA
 TAAGGGCGGAGGGGAAGACGAAGGCGAGGTTCCGCCCACTACCGGAGGAGGCGTGACCACAGCCAAGTGGCAGCCGGCCG
 TAGGAACGAAATGGCAGATCGAGCTTCTGTACGGCGTCAACGACACTTCAGTAGACGCGGATATCTACGACATTGATCTC
 TTCAACAATAACAAGTCGACCATCAACGATCTGCAAAAGCAAGGCCGCAAGGTGATCTGCTACTTCTCCGCTGGGAGCTA
 CGAGAACTGGAGGCCCGACAAAGGACAAGTTCAAGGATTCGGACATGGGCAACACGCTGGATGGGTGGCCGGATGAGAAAT
 GGCTTGACCTCAACTCCAAGAACGTGCGGAGCATCATGACGTGCGTCTGGATATGGCGGTGAGAAAGAACTGCGATGGA
 GTTGACCCGGATAACGTGATGCCTACGACAACGACAATGGTCTCGATATGAAGAAGGAGGATTGGCGGAATTTTCATGAT
 GTGGCTCGCCAATGAAACGCATGCACGCAATATGTCCATTGGCTGAAAGAATGCCGGGGCAATCATCCCTGCAGTGATCG
 ACAACATGCAGTGGAGCGTGAACGAGCAATGCCGCAATATGAGGAGTGGGATACCTACGCCGCATTTCATCGATAAGAAC
 AAGCCCGTCTTCCACATCGAGTACCCAAAGGGCGACGACCAACAACAACGATTTGGTCAGCACGAGCCAGAAGAAGAG
 TGCTTGCGACTTTGAGGGATCCTCCAACCTTTTCGACGGTCATCAAGAACATGAATCTGGATAACTGGATCCAGACCTGCT
 AGTCGCACAATTGATCCGCATCTAGATACTCTGTTGATCAGCAAGGGCGCCGGAGTTTGAGATTGGGATTTCCACCAT
 CCGCTTACCATCTATATAGTTTGACTATGATGTAATCTGGCTCATTTAATTAACCTTTGACATTGCTCTTTCA

Fig. 55

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus sojae* Agd3

NVLPKLRITGCGYFLITGCDPGVWFEGEIPSVIAPVPPRSIGVTNSPQFISSTSLVTSSSSPPYVGGSSFVTITTLA
 SSTSTSTSLTSPSTLVSFVSPYASSTNLSIPSSSLIPSSSLPASPASYIANGVNAOGLNIAKDTAAANAYTSGLNG
 YGIPFTTILVPQSAETLPIVNTSGSNGFGLIVASEFVSIGAGGQSAITDQNNQYAYGLFYSVRMVQVQVDPVNGP
 GASAVGGGCGDSGVEQLVSFSDVDFKEAGLRKTAGVSTTGLWHYPASYNQDATKKEIRFAAANGNYGSETTAAVINNFN
 GQUAMFFSLPFTITWASNYLQAHNIATGLTGLYAGHRVNAITDQJDFMLEITDYPYNGTIFRITITADMGGSSMLPI
 INQKNGNNAFVFEVGHNGNYVIESATKQDADACNGGGEYDSPADTLEPKPLGTGDTLPPAKDQTEYNWTECTCLDD
 LFYWNRTTPANRDKFVGHISHTFHEEQNNATYNDVKREISFNQAWLRQSGFYDAKYFTNSGILPPAKITGLHNGDALWAYE
 NGTINCVDGNITPPLNGNANVDPYFTTSASDGGFNGVKNPWARTIYVQCFPLPACTQWLEJDTISAGSGDFSMLLATEA
 DTMRLHFLGDLHRDPYHGHANLRNVDVPEINGETSGWNSMGAAVEITMNGCFYRLVDYRIVITITHGEMSANFLDRYNRDQ
 TMSLYQYITGNKQITGVTLSAXDNTNAPIPVFSVPAPDTKGAFTTEQYGSGLTVMWGLSGSPVFTSLSTPIPI

BASE SEQUENCE (PUTATIVE) OF NUCLEIC ACID MOLECULE OF *Aspergillus sojae* agd3

ATGGTCTACCGTGGTTCGCGAAGACTGGTGTGTTACTTCGACCTATAAAGTTGCGACACTCCGCCAGGTGTTTGCCCTGA
 AGGATATCCCAAGATGATGATCGCTCTCTGCCCCTGCTGACACGCAATCTGGAGATCAGCAGCAACCTCCGCCGGTTACTTCGT
 GGATCGTCTGCTGACTCTTCTGTTCTGTCCTGCTGACCGGTGATCGTCTTTCGTAGATTAAGTACTAGCTTCGCT
 TCCTCCACATCCACTTCTACTTCAACCTCTCTACCTTCGTTTACTAGCACACTGCTTTCTGTGACACTCCGGTCAGTGC
 CTCGAGCAAGATGTGTAATTCCTCTGCTCTGCTGCTGAGTCTGATTCCTTCGCGACAGACTTCGCGCTCGGATGATGGCA
 ATGGTAATGTCGCGGTGAAGTCTGGTGATGTGGCAAGGACACCGGACGCTTAATGTGGCAACCTCGGCGCTCAATGGC
 TATGATATCTCTTTTACTACCTTGTCTGTTCCCGAGTCTGTGCTACTCTACGAGAGCTGAACGGGACCTCGGAGGAA
 CTTTGCGGATATCGTTGTGACGAGAGAGTCAGCTAGCAATATGGTGGCCAAAGGTCGACAGAGCTCTGACTACCGCCAC
 ATGCAATCAAGCTCTATGCTATCAGCTCGGATGAGTGTAGCATGTGATGACGAGCTGTACCGCGGACCGCAACTGAC
 GGTGCTTCGCGCCTGGGCGGGGATGCTGTGACTCGGATAGAGCAGCTTATTTCTTCTCAGAGCTCAGTGACTTTAA
 GGAAGCGCGGCTGAAGCCGATGGTGGGTGTCAGTACGACAGAGCTCTGGGACTACCGCAAGCTCGGTAATGATGATCTGTA
 CACCAAGCAAGTGTGCTGGTTGGCGGCCAAGGTAAGTACGGCGAGGACGACCTGCTGCAATGACCAACCTTATGT
 GGCAGACAGCAAAATGGTTCGTCTGTGCTTTGACACTACTGGAGTGAACCTGGAACCTGTCGACAGGCAATGGAT
 CAGATGTGCTACTCGGAGCTCTACGCTGGCCACCTGCGCTGCAAGCTGAACACCGAGATGATGATGTGTCGAA
 CTGATATCTACCTCCCAATGGAACAGCTTCGATTTACCGGAGTGAATGATGATGATCTGAGCTGGCTCCGCAAG
 ATGAAACGGCAAGATGAACCGCGTAGCTCATACTTTGTTCAGTCCGACACAAACGGTATGACGGTGTGTCGAACTCGGCTAC
 GGGAGAGATGACGAGTCTGCTGCAACGGAGGTGGCATGGAATACGACTACCGGCTGATCTGCTCTGGATGATGAGAGG
 CTCTGGGACAGCTGATGCACTTTGGCCGACAGGACGAGGATGCAAGTGGACTGATGAGTGCGCAAGTGTGAGCAAT
 CATTTCGTCTGGTGGACACCGCGGCTAAACCGGCAAGTTTGTGCATCTCTCACACTTCTCACTATGAAGAGAGAA
 CAATGGCAGCTACAACGACCTTAAGAAGGAGATCTCTTCAACAGGCTGGTTGGGACAGAGTGGTTTCTATGATGCCA
 AGTATTTCACATCAACGGTATGATCCCTCGGCCATCAAGTATGACATGACATGACAGCAGCTCTCGGGCTGGTATGCC
 AACGGCATCACCACACTGTCTGGTGATAACACTCTGTACACCGGCTCTCAACAGCAGCAGCGATATGGGCCCTACTTCAC
 TACCTCGCATCGGATGGATGGATGATGAGGTGAACCCCGCTGGGCGACTCGCATCTACTACCATGTGATAGCT
 CTGGCTGACAGCTTCAGGAATGGATGACACTCTCGCGGAGAGCGGCACTCAGCAACTGCTCGGACGGAAGAGGCC
 GACCAATGCGGCATCTCTTGGCTTCTACGCGACCGTTACATGTTCCACAGGCCAATCTTCGCAATGTGCGAGCTTGA
 CCGGCTTGAGATCAACGGGACAGCTGTGCAATGGCCATCTAGCGGCTGGGCGAAACATGGTGCAGAGATTCGTGGT
 CTCGTGGATGAGTGGGCCATCTGTGACATCTGCGCAGAGGAGTAGTCAAGGATCTTAGAAGATCTAGAACTCTCCCAACCGCC
 GCAATTGCTAATCAATCACCAGAGATGTCGGGCAACTTCTCGACGCTACAACAGTGATCAATGCAACTCTCGGTGCA
 GTACACGATCGGAACAAAGCAAGTAATGTCGGGTGACTTTAGCGGCAAGGACAGCTGCAATCGGCCATCGGCTGCTG
 TCTCCGTCTGCGGCCACGACACCAAGGGGCTACAGCAGCAAGTACGGGATGACCACTACGCTCTGGGTGGAG
 GGTCTGGGCTCCCGGTCACTTTCCGCTTCGACCTCTATTCCCTTGTAAATGGATTGACCACTAGTAATTATGGAG
 CTTGTTGAAAGGATCTCGGACCAATAATCTCTAATGTTAATGGGTTGGTGAGGATTCGAAATGGGAGAGATG
 AATGAATATTAGTACATACATAGATAGCTCATTTGCATCACTACTACATA

Fig. 56

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus sojae* Gtb3

MAEILHVSALGWDKMDHWWQVFIAILACVATGSLWLLYSGTKRLRNYIKTRPRSEKVPNPVSQRLVTLNKLSSVPN
 IGRRKPSSFGYYLGSFSPDRDQLRLNEWDLIVDPFQSGTAQAIRYVEGKQLLGRVDLDRILSKDESTLSAJEKTEN
 LLTGTFDSANFSGMVLANWEGKFPAPVFTKLVEVIDELGLAVYLETAPDFLKDHTSMQNPASIGVIVQNASILPEGGQR
 DYFQLVKMQPTIKAFVSEACVRFVVMWETIDDNASLSNAVQSRLOWCNFYSAIPWIGOKSALTNAALNVKISEPLSS
 FGWLKDAEIIKAHWRWSNLHLKDDASDTSAWNLTLPFFPTLEELLTSSEYGQPESELNLTTLKLRDPPPEWVAQVKSLGSPL
 SISMAGIEYNLSGCFPLGSEATALAFAEVLQSQLRLKSLGLLHPVPASKIQSIGLLKKFHESYLLPNATSSDPYVIPNA
 TSDQLATTIKELSNLATNGSLQVNLGLDSGLRKSVDVRFWAVYQMSDGFVEVFASKKAQGLAGTVLHTFLSAKGYPRHVC
 FEVETALAKWSKDLVNDTGLPRRFVEDIDMLSPEERLLLFQHLSTDSYSELSDTICAYIRRLIDAPSLAQLKELNTIS
 YLEGSASPEILVNTRIKWYREGGQHPSPSKCLALFYQDAAFTQILREHREGDLALISKGFCQLLQNDHIDAYTIDMAL
 ALFCAARKGAIDEITYETVORNPLFNNGSQAAAFSESFALGSRCEVYFDVQPSAFGKLLSDRFRREYNDEKLPDWINGA
 PEMATSYAGAIDVNPDDKVKPMGPYGRFTFLGVFAFPALIDTILLTIGRGLYLSAFMTHDELQSATIALMISLLLSGA
 IGTMIACGGPYLISMAFAASNMFVLIRLIAGVAFTIAAGLIGFIVISGVKSPQAGIFYLYLVALTIYLTTFATLASFS
 YPGTGFLSGRKVIFSCIPILFVSPITITWSGHDSAIFYLAVLYVFIGFLLGLRSVASKWVTWYQNIIRRTDDTEIRKWIIS
 TYGNNDKVFNGMSDPAVLKMSRDALFKDVLAEKSRSFFSKPTTDTLVRELARDWDSTNFFLDWYCRYADVPRPIPFSSS
 WNIQTKVGLDLVRNSQKGI RLHNAFIHWRQSSKEIGCGILYFIALLDKWVELLSGGQLVGLSTSLSDANRMVAGFGLAY
 YLIGAVLIDTKAQELHDLVGQHSVAVYGSKEIRPSQKRDVRFKRVYWKTFKFLMWLVWSLAIALATLWTFQAPVQAM
 IMFFAYVLSYTGLLWYQYTKIFTGPHALIPLMTGVVVGLPVGIALKVCLGNFLYSQVIGLGAATWTVAITLSLFTAKMG
 PKKVDSPVELGKTFHAYTAPWADPEWSQQLQTFEGVSVVPADARLKLVPQSHPGVEVKITILLSRKIEPRIEEAFPESE
 KLISMALGAWETGEISLELVPLGSLGPNIQALSCSMQHLQIACVGRGLDERIDVSANCCQIAETLLHAVAESNMRRMPH
 EYAVLSESLVTAGVTETTARQLREEDTPLVVRWSKKEILLRLCLGFEVDSHWEKLPENVRNMLLDRLGRPCLLSEGSQ
 QWLQTSCLRFDTSDLNVHVARCNLGAATAVSILDYANYGTGEAGAIKDPEIPIYIPEIPKLPMAISIIOKPLSYVYHSI
 GSGVKFFIAALLADSEFQREFDHVMSEHRTLIRVPLVFLNMVWLYFKTVQDIGLSFFLFHGRSNVKRLWNETKGITVSI
 KKSRLFVQSLEGTFATFRHNEPDGQFKVYYYSGEHKTEPEGMKLLKYVSTYSKDMLLLIRQEFKQGVLYNEYHYDYRAPT
 KKSFTLSKAWATRIPLGRRRCVRGQNNLQSVQYNRKGLIEAGSYMKGDLIRFKYHYRKNPRFGDELLRAEFSLTHITCTV
 SWCAPPLRHPEKVERWIPHSKVTEATFVQGDVYEARWLYDHKFHPTIFTTLNGQKVQTPPMIENDFIGVLAKPKQTSFV
 NDNPLLYCDSLSSNTVTRFLGLTTKRFVSTSRARSLLWKSWKDRVDFAIMVRWLDERLLRREKTLAPYWRARNRGDLA
 AAKKYLELRADAITASADLDNITSSWTLPAVKISDLFNFPGGDVYVHTRSKDFGSDTDKSMHVMAADNGTWPNEGGGVS
 ACRDRMINSRLRTVKWHMICESANDFGIPKHQTEQNVLSLKVVPLWGLDFTPTHGLFRNKLDSEVDNVTASDMDIKLNF
 IPILTALVKGARATHLSKADIHQATRALVNLNTYFGDSRHWTQIWNSDIVKESWRDLWLTQEMPNTVPSSQWFRTELPTL
 TSLDTALELWYRYLFIISPIPEKIPSVFQASHHSVSASYGVVCKMKRNCTLQIWDHAIISWRETNLCLSSALCKLSPFVR
 NALLGLMRITSALTLLHADIIILCADFFNPGEVEIGTCQGTIEHRNVFRKKVDPVYVNGITDMQKFAVPYKEIKSQRPTVT
 MLSHVWYAKDIKIALLAADIIINQWKFDYHLDIYGAIDKAPTYSTECQEIISKGLRGKVTLRGTADPMKVLENTWLFL
 NSSLSEGLPLALGEAALTGAPVVCDDVGASLRVLSDPDDFSRYSAVVPNDAAHALAKAQITMLGLLGEWSKYTDDEPAP
 VLTSSPTPEDVAKITRRMYEKSDYRRKLGMTRDIVQKFSGDRYLREHEQMLWIGKSAKIMANRVGGAITEPTDIATAM
 RQTLPIEEEVITIPRSVHWSRASAAGSMSTVYSEVSNFPMNGYHRPSSIRSGISQMSDTESEFLPLPSNASLPVFAPR
 QTLGYPSTPDGRLSPSGLSPLPNRNSGRRSMSTAGREQLRGLGREELNPYRNSDVSTIMRDEFLQSSIYKNIEGSNST
 PNMI

Fig. 57

BASE SEQUENCE (PUTATIVE) OF NUCLEIC ACID MOLECULE OF *Aspergillus sojae* gtb3

CCGACCTGTGAGGTTGGCTGCAATATCTAATCAGGATGGCGGAAATCGTCCAGCTCTCAGCCCTCGGCTGGGATAAAAT
 GAAAGATCATTGGTGGCAGTTTGTAAAGTAGTGATTGGATATACGTTTCAAATATCACTGACTAATGCTATGCTAGGTGT
 CATCGCTATCTTAATAGCTTGTGTAGCTACAGGATCGTTGTGGCTCGTGTACTCTGGGACGAGAGAGCTGGCGCACTACA
 TCAAGGTAGGGCTTCCTTGAATATGCTGTGAATGTATATCTGATCTGTGGCTACCGTGAATCAAAATCAIAGACAAGGCCA
 CGTTTCAGAGAAAGTGGCCCAATGTATCTCAACGGTTGGTTACTCTTCCAAACAAGTTGCTGAGTTGGCCAAACATTCA
 AAGAGCGCAAGCGGTCTTCTTTGGCGTCTATCTGGGTTCAATCAGTTGGCGGCCAGATCGGGATCAGCTTCGGCTCGTGA
 ATGAATGGGAGCTGTGATCGTTGACCGTTTTCAGTGGGGACGGGCCAAGGAATCGGTTATGTGGAGGGTAAAGCAGTTA
 TTGGGAAGAGTTGACCTTGATCGTATCGTCTCAAAAGGATGAGTCCACATTTGTCAGCAATTGAAAGATGAAAGCCTTGT
 CACCGGCACATTGATAGTGTAACTTCAGCGGTATGGTACTGGCCAACTGGGAAGGAAAGTTCCCGCCCGGTTTTCAT
 CTAAGCTTGTGTAGGTGATCGATGAGCTGGGTTTGGCAGTGTACCTGGAGACGGCACCCCGGACTTTCTAAAGGACCAC
 ACCTCCATGCAAAACCGCTGCAATTTCCGGAATCGTTATTCAAAATGCCAGTATACCTGGCAGAAGGCCAGAAAGCGGACTA
 TTTTCAAGTGGTGAAGATGCAAGCCAGCATCAAGGCGTTGCTCTCGAAGCTTGTGTGAGAGATTTCGTGGTATGGCGT
 GGGAGACAATCGATGACAAATGCTCATTAATGCTGTGTGTGCAAGAGATCTCGCAGTGGTGAACITTTACAGTGGC
 ATCCCATGGATTGGTCAGAGTGGCTCTCACAATGCCGCGCTTAATGTCAAGATCTCAGAGCTCTCTCCTCTTTTGG
 ATGGCTGAAAGATGCCGAATCATCAAAAGCCACGATCGCTGGCGCTCAAAATTTACATCTCAAGGATGATGCTATCGGATA
 CGAGCGCTTGGAAACACATTTGTGGCGTTTTCCTTACCCTAGAGAAATTTGCTTACCTCGTGGGAATATGTCAGGCTGAG
 AGCAACGAGTTGACGCAAAACTCGCGCATCCACCGGAGTGGGTAGCACAGGTAAATCTCTAGGGAGTCCACTTTCCAT
 ATCAATGGCGGGCATGATATAACTCTCTTGGTTGCTTCGCGCTTGGATCTGAGGCGACAGCACTTGTCTTTGGCCAGG
 TCCTTCAGTCTCAATTCGCGCTTAAATCCTGGCTTGTCTCAGCGGTTCTGCTTCAAGATTCAGAGCATCGGCTG
 CTCTTCAGAGAAATTTACGGAATCTTATTTGGTTCCGACGCAACGAGCTCAGATCTTACGTCAITCCAAACGCAACCTC
 GGGACCACTGGCGACTACGATCAAGGAATGTCGAACCTGGCACTAACGGCTCATTGCAAGTCAACCTTGGACTGGACT
 CAGGACTTCGTAAGACGCTCGAGTGGCTTTTGGCCAGTTTATCAGATGGACTCGGATGTTTGAAGTTTTCCTTCG
 AAAAGGCCGCAAGTTTAGCAGGAAGTGTACTGATACATTTTATCTGCAAAAGGATACCGCCGCGAGTTTGTGTA
 GGTAGAAACCGCTTTAGCGAAATGGTCTAAGGACCTCGTCAATGATACAGGACTTCTCGCGCTTTCTGCAAGACATCG
 ACATGCTGAGCCGAGAGAGCGACTGCTCTGTCTGAGCATCTCTCTTACCGAGTCTCTACAGTGAAGCTCTCGGATCT
 ATCTGTGATACATTGAGAGATGCTTATGATGCGGCTTCACTCGCTCAGCTGAAGGAGCTTAACAGGATCTCATATCT
 TGAAGGATCGGCTTCTCGCGAAATTTTGGTTAATACCGGCTCAAAATGGTACGGAACAGGATGCCAAGATCGGTCAC
 CATCCAAATGCTCGCATTATTCTACGAGCGGATGCGGCTTTTACTCAGATGCTAAGGGAGCATGCGGAGGGAGACCTT
 GCTTTGATATCAAAAGGGCTTCTGCGAGCTGCTTCAAAATGATGAGATCGATGCTATACATGATATCATGCGATTGGCACT
 TTTCTGCGCTGCGAGGAAGGAGCAATCGATGAGATTATCTGAAAGTACCGATCGTAACCGGTTGTTCAACAATCAAT
 CAGAGCAAGCGGCTGCTTCTCAGAAATCGTTTGGCTTAAAGGTACGTTTGAAGGTCTACTTTGATGTTACGCTAGCGCT
 TTTGGAAGGCTGCTCTGGGATGCTTTCAGAGGGGATACACGATGAGAAGCTGCGCGATTGATGAATGGCGCGCTGA
 GATGGCCACATCTTATGCGGGTGGCCAAATGACGTTAACCGGATGACAAGGTTAAACCGATGCTGCTACGAGCGAT
 TTAATTTCTGCGGTGTTTTCGATTGCCAGCATGATGAGCATGATTCTGCTCAGAAATATCGGCGGTGGTCTCTACCTT
 TCAGGCTTATGATCCCATGAGAGCTACAGATGCCACCATCGCTTTGATGATCTCGCTTCTCTATCTGCTGCAATCGG
 TACGATGATTGCTGTGGAGGACCTACTATGTCATTTGATGGCTTTCGCAAGCTTCAAAACATGTTTGTCTTATCGGAC
 TAATTTGCTGGTGTGGGTTTACAATTTGCTGCTGGTTAATGGGATTCATCGTTATGCTGCGGTGAAAAGGCCACAGGCT
 GGAATATCTTCTATCTGTACCTAGTGGCTTGAACATTTACCTGAGGAGCTTGGCTACGCTCGGTAGCTTTAGTTACCG
 TGGAAACGGTTTCTTGTCCGGGCGCAAGGTGATCTTCAGCTGCAATCGGATTTCTTCTGCTCACCTATCATCAGTACCT
 GGAAGCGCCACGATTCAGCTATTTACCTCGCTGTCTATATGCTTCTCATCGGTTTTCCTTCTCGGCTTGGCATCAGTT
 GCTCTAAATGGGTGACCTGGTATCAGAACATCAGGAGGACGGACGATACGGAATCCGGAATGGTATATTTCCACGTA
 CGGTAAATACGAGCGAAGGTGTTTGGAAACATGAGTGACCGGGCTGTCTTGAATATGCAAGAGATGCTCTCTTAAAGG
 ATGCTTGGCTGAGAGTCCCGAGCTTCTGCTAAGGCCACAACTGATACGCTGCTCGGAGGCTTCCAGGGGACTGG
 GATTCGAGAAATTTCTCTCGACTGGTACTGCGGTTATGCTGATGTGCTCGGCGGATTCGTTCAAGTTCTCTTGGAA
 TATCCAGACCAAGGTGGGCTAGAGCTTCTCGGAATTCGCAAGAAAGGAATCGGTTGCAATATGCTTTCATCCATTGGC
 GCGCAATCGAGCAAGAAATAGGCTGTGGAATTCGTACTTTATCATAGGCTGCTTGGCAAAATGGGTTGAGTTATGAGC
 GGTGGACAACCTGTTGCTCTCGAAGCTCGCTTCTGATGGCAATCGATGGCAGTGGGATTGGATTGGCTTACTACCT
 CATTTGGGCGCTTCTCATGATACCAAGGCCAGGAAGTCCATGATCTTGGGCGAGATTGCGCTGTTGCTGTGGAT

Fig. 58

[illegible]

Fig. 59

GTCACTTTCGGAAGGTCTGCCCTTAGCCCTAGGTGAAGCTGCTTTGACGGGTGCCCCCGTGTTTGTAACCGATGTCGGTG
CATCTCTTCGTGTTCTGAGCGACCCAGACGACTTCTCTCGTTACAGTGCCGTCGTGCGACCAATGACGCTCAGCGCCCTC
GCAAAAGCGCAGATACCATGCTTGGCCTTCTGGGAGAATGGAGCAAGTATACTGATGACACTGAGCGGGCACCTGTGCT
CACTTCATCTCCAACACGAGAGGACGTTGCCAAGATCACCGCCGCATGTATAGAAGAGCGATTACGCGCGCAAACTCG
GCATGATGACCCGCGATATCCTCCAGAAATCATTCAGTGCGCAGCGATACCTCCGTGAGCAGGAGCAGATGCTGTGGATC
GGCAAGTCTGCCAAGATCATGCGCAACCGTGTTGGAGGAGCCATCACTGAGCCCAAGACATCGCAACAGGCATGCGCCA
GACTCTCCGATTGAAGAAGAAAGTCATACCATCCCTCGCAGCGCCGTGCACTCGTGGCGTTCGTCTGCTGCATCGGGCA
TGTGACAGTATACAGTGAGGTTTCCAATTTCCAATGCTCAATGGCTACCACCGTCGATCCTCTATTGCTCAGGTATA
AGCGGTATGTCAACGGATACAGAGTCTTTCTTCTCTCCCGAGCAACGCCTCCCTCCCTGTCTTCGGCGCTCGTCAGAC
CCTGGGCTACCCGAGCAGCCCTGACGGTCTGCTCTCAGCTTCGGGGCGTCTCTCAGCGCTACCAAACCGAGGGAACAGTG
GCCGACGATCCATGTCAACCGCTGGCCGCGAGCAGCTACGTGGTCTCGGACCGGAAGAATTGAACCGTTACCGCAATTCC
GACGTCAGTACCATCATGAGAGACGAATTTCTTCAATCAAGCATCTACAAGAATATAGAAGGACGCAACAGCAGCCCCAA
CATGATCTAAAACGAAAAAGGAAAAAGAAAAAGAAAAATCCCATCTAGTTCTCTTGGTTTTGCATCTCGTTTTTAAATTT
AATTTTCAATTTTTTGCATACATATGACTGATTTTTGGTTTAACTCCGCGCCCTGGCAATAATTGCTAATCTGTCT
TGTGTATACCAACCATATACCCGAGATGATGAAGTGCTGTTGTAAATACCTGCATCTTGCATATACTTTCCGTTATTT
TGCATCTAAGTTTCATCATTA

Fig. 60

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus niger* Uge3

MESPRQSDASTPVEPCSPGCVDTPATQSSVLFQGNLEELLRNFPDQYILVTGGLGFIGSHTTLELLKAGYNVIVIDNLS
 NSFQSVFDRIRQLAAKYHDQEGTCMPSLQLHAHDFRDIAALRGLLEQYQIQSRWGTPKSRIGGVIFHAAYKAVEESIRNP
 LKYYANNVSGLIDFATTLGEFGIKTFIFSSSATVYGTLATSGPLKEELCVHKEEVYSDQDGLEQTVKPGCTGITNPYGR
 TKWICEAILADLAASDPEWTIVALRYFNPIGCDSEGLLGEDPRQTPTNLLPVVVKVMTGQYKELQMFQTDWDTEDGTAVR
 DFIVHTDLARGHIAALNAANGKLVENFRFTNLTGTRGHSVMEVVNTMEAVSSKPIPRKAAGRRAGDVGSCVAVATRSQD
 ELEWKTEKSLKDACVSLCNFLNVSGLSS

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus niger* uge3

GTTGCTCGTTTTGAGGAAAATATAAGATTTGGGAAACTCCTTTCCTTGGGTTATCCCGTCCAGAGTCAAGTCACTGCGG
 TCGTTAAATTCGTGTTGAGAATAAATCTTCTGCTCTTTCCTTGTGTTTTGTTTGTCCAAGTGATTCTGTCCGCATTGC
 CCCCCAACGGTGCTCATCCTTCGACCCATCAGTTATGGAGAGCCCTCGACAGTCCGATGCAAGCACTCCTGTGGAGCC
 TTGCTCCCTCGTTGCGTTGACACGCCGGCGACGCAATCTTCGCTGTTGTTTGATGGCAACCTTGAAGAGTTGCTGCGCA
 ACTTTCCCTCGATCAGTACATCCTCGTCACAGGGGGTCTCGGGTTCATCGGCAGTCACACAACATTGGAGCTACTCAAA
 GCCGGCTATAATGTAATTGTGATCGACAATCTCAGCAACTCTTCCAGAGCGTCTTCGACCGCATCAGACAACCTGGCCGC
 AAAGTACCATGACAGGAGGGGACATGCATGCCGTCAATGACGCTCCACGCCATGATTTCCGGGATATTGCTGCTCTTA
 GAGGCCCTTCTTGAGCAGTATCAGATCCAATCCAGATGGGGAACCTCCAAGTCCAGAATTGGTGGCGTCATCCACTTTGCT
 GCTTATAAGGCTGTGGAAGAGATATCAGGAACCCCTTGAAGTATTACGCGAACAATGTTAGTGGTCTTATCGACTTTGC
 CACAACCTTTGGGAGAATTTGGAATTAACATTCTTTTCTCCTCCTCGCCACGGTGTACGGAACCTTGGCAACTTCGG
 GTCTTCCCTTAAAGGAAGAACTCTGTGTCCATAAAGAAGAGGTCTACAGTGACCAAGACGGTCTGGAACAGACCGTTAAA
 CCTGGCTGCACGGGTATTACGAACCCGTATGGCGCACCAAAATGGATCTGCGAAGCCATATTAGCGGACCTTGGCGCTTC
 TGATCCAGAATGGACCATTGTAGCCCTACGCTATTTCAACCTATAGGATGTGACGAATCTGGCCTTTTGGGAGAGGATC
 CCAGGCAGACGCCACGAAACCTTCTCCGGTTGTGGTAAAAGTCATGACCGGACAATATAAGGAGCTGCAGATGTTTGGC
 ACGGACTGGGACACTGAGGATGGCACTGCAGTTCGCGATTTTCATCCATGTCACCGATCTTGCTAGGGGACATATTGCTGC
 GCTCAACGCCGCCAACGGTGGAAAGCTGGTTGAGAACTTTCTGACCTTCAACCTGGGCACCGGACGGGGTCACTCTGTGA
 TGGAGGTGGTCAACACAATGGAAGCAGTGTCTTCAAACCTATTCAGAAAAGCTGCAGGTCGTGCGCTGGAGATGTT
 GGCTCTTGGCTGCTGTGCGCCACAAGATCCAGGACGAGCTCGAATGGAAGACCGAAAAATCTCTGAAGGATGCTTGCCT
 GAGCCTATGCAATTTCTCAATGTGACGGGCTGTCTCTTAG

Fig. 61

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus niger* Sph3

MGQGEHVRDRRCLQSRRL ILAILVFIAL LAVVIPP AVVLTLHKFTMGPKASVFVPLYVYPAPGAWDPLEKVISSHPDV
 NFTVVVNP GSGPGPNALPDGNYTREIPKLASYGNVRL LGYVATTY GQRNFSLVRRDIETYAAWPTNSSNP NLAVRGIFFD
 ETPQQYESNTLAYLQDLTAVVKTTTGLGPDHFVVHNP GTIPDARYLPTADSTVVFEATYETFLERQGAQLFQEIPNSTRS
 QLCAVVHSVPDSVEGHKFRDLVKQVRKVADEIFITHLDTDYASFGGQWEEFVELMARS

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus niger* sph3

ATGGGGCAGGGTGAACACGTGAGAGACCGGCGCTGCCTGCAAAGCCGGCGCTCGCGACTCATTCTGGCAATCCTTGTATT
 CATTGCCCTTCTGCCGTCGTACATACCACCAAGCAGTAGTGTGACCCTACACAAATTCACCATGGGCCCTAAAGCATCAG
 TTTTCGTACCGCTCTACGTCTACCCTGCCCGGGAGCATGGGATCCCTTAGAAAAGGTGTAGGTGCTTTTTCTTTTGT
 TATCCCTTCTCCATATCTCAACAAGCCCTGCCAAATGTTAAGCCCTCCCTTCCCTTCCCGCCGCAACCACAT
 TGTACTCCAGTCCATGCCACGCTATCTGTACGCCACGGATGTCCCGCGGCACGATACAAGTAACCTGATGTACGAAG
 GACGCGCTGAACGCCACAGGATCTCTCTCATCCGACGTCAATTCACCGTCGTGGTCAATCCTGGTAGTGGTCCAGG
 GCCAACGCTTGCCGATGGAAATTACACAGGAGAGATACCAAGCTGGCGTCTTATGGCAACGTCCGCTCCTAGGCT
 ATGTTGCTACCACGTACGGGACGCGAACTTCTCGTTGCTGCGGCGGACATTGAGACCTATGCCGCGTGGCCGACCAAC
 AGTTCGAACCCCAATCTAGCGGTTCCGGGTATATTTTCGACGAAACCCCGAGCAATACGAAAGCAATACCTTGGCCTA
 CCTCCAAGATCTGACTGCTGTCTGAAGACAACACCGGCTGGGTCCGGACCATTTTGTACGTGCAGAAAGTCTCTCCG
 TATTTTCATTCTTTCTTACTAGGGGTAACGCCGGTAATTTACACCATTACCAATTTCCGCGAGCTGGCATTTCGCGCC
 ACTCGCTCATTGCCCTTTGCTGCCCTCAAACGCATGGTTCTTTTCTTTTCTTTTGGATGCTTCTGTTCTGGC
 TCCTGTTCTCGCGACAATCCTCATCCAGAGCGGTCGTTGGATCGCCCGGATAGATCTGGATGGACGCCACCATTTGGC
 CGGAGTTTACCATGCTAACGAGACTGTCTCAACTAGGTCGTCCATAATCCCGGACGATCCCTGATGCCCGTACTTGGC
 GACGGCTGATTGACTGTGCTTTGAGGCAACCTACGAGACGTTCTTGGAGCGTCAAGGGGCTAAGCTGTTTCAGGAAA
 TCCCGAACAGCACTCGCAGCCAGCTGTGCGCGTGGTCCACTCGGTGCCAGACAGCGTGGAAAGGBCACAAGTTCGAGAC
 CTGGTGAAGCAAGTGCAGCAAGTGCAGGATGAGATTTTCATCACTCATCTGGATACAGATTATTATCGGAGTTTTGGCGG
 CCAATGGGAGGAATTTGTGGAATAATGGCTCGATCGTGA

Fig. 62

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus niger* Ega3

MEPASEAALKGPPSRGWKTWTFKKKLIIGGIIGFIIALGIGLVGLVGLGGGGGGEEEGGGGETTPSSGNYTSAKW
 QPAVGTSWQIELLYPLNDTSVDVDVYDIDLNNKSVINDLQKAGRKVICYFSAGSYENWRPDKDFNSDDLGNLDGWP
 GEKWINISSPRIRKIMLTRDLAQNKSCDGVDPDNDVGYDNDNGLDLTEADSI SYMNWMAEHAHARNMSIGLKNAGSIIS
 SVIKNMQWSVNEQCSQYDECPTYAAFTAGKPVFHI EYPKGDDTNNDL SVTSSQKSKACNFTDSGNFSTVIKNMDLDNWI
 EMC

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus niger* ega3

GCAACGCCAAGGGTTATACACACCCCAAGTGGCATAGTCGAGTCGACGAGCTTGTCCTCTATCCAGGATCA
 CCGTGTTTCAAGCTGTTCACTAGCTCCGAAGCCGAGGTTCCATGGTTGGAGGTGGAGATGGCTCTGGTGTTCGAGCAT
 CGAACACCGTGGAAGCTCCTGAAGAAATCGCAATCTCTGGGTCCCTATTTTGTGGACTGAGCACGGTCGCATCTTAGCG
 ATCTCTGTTTATTTCCGCTTAAGTCTTTTGGTAAGCGACCCAAAGACTGAGTTAGACTGGAATCAGTCACTAAGGGCAT
 CGGGCCGAACCCGGTTTGCCACCAGTCGAGTGAAGCATCAAACGCCAAGTTGGTGAACGGACAAGACACCGGCGGCTT
 GGTGGTTTGAATCTTGGCCAGTTAGGCCCCGAATTTTGGCTCTTTGTCTTCCGGCGTTTCCCTCTCGTCACTACC
 CATTCAATTTAGGGCAGGTTGCACAGCTAATGAGCGTGCGGGAACGATTTGCAGGGTCCAGCTGGTTCCCTTCAGGGT
 CCGACTCTCTACCCACCTACCCACACTGCCTATCATCATCACTTGCAGCCCTTCAGTTTCGCTCATTGGCAAGC
 TGTTCGGACGGCGTGCTGCAATATGAACCGCAGATCCGTGTGACCAAGTGAAGCTTCTTTGACTTCGTCTTCAGGCAACT
 TCATTTCTCAAGCTGCAATCGCGTGCTTTTGACAGGCAAGTCCCGGTCTAGACTCAACTGGTGAAGTCTTTCTTTGCAT
 TGGCTCCACCTTTTATTCCTGAGCCCGGATCTTCTTGTTCGTGCGGAGGTTTGTCTTTTTCGGATTCTCTCT
 TTGCTCTCACTCGTGTGAAATCTGTTCTAGCGATGGAGCCTGCCAGTGAGGCCGCCCTCAAGGGCCCTCCCTCGCGGG
 ATGGAAGACATGGACATTCAGAAGAAGCTCATCATCTTGGAGGAATCATCGGTTTATCATCGCCCTGGGCATCGGTC
 TTGGAGTCGGACTGGGTGTTGGACTCGGCGGCGGAGGGGAGGAGAGGAAGAGGGAGGAGGCGGGGAGACGACGCCA
 CCCAGTTCAAGCAATTACACCTCAGCCAAATGGCAGCCCGCGTCGGCACCAAGTTGGCAGATCGAGTTGCTCTATCCTCT
 GAATGACACCTCCGTGAGGTGGATGTCTACGACATTGATCTGTTCAACAACAACAAGTCTGTAATCAACGATCTGCAAA
 AAGCAGGCCGTAAAGTCATTTGCTACTTCTCCGCCGGCAGCTACGAGAACTGGCGCCCGGACAAGGACAAATTCAACTCG
 GATGATCTGGGTAAGAACTGGACGGATGGCCCGGCGAGAAATGGATCAACATCAGCTCTCCTCGCATTGAAAGATCAT
 GCTACCCGCCCTGGACCTGGCTCAGAACAGAGCTGCGACGGGTGGACCCGGATAACGTCGACGTTACGACAATGATA
 AGGGCTGATCTGACAGAGGCCGATTGATCAGCTACATGAACTGGATGGCAATGAAGCGCATGCGCGCAACATGTCC
 ATCGGTCTGAAGAATGCGGGTTCCATCATCTCGTGGTTTATCAAGAATATGCAGTGGAGCGTCAACGAGCAATGCTCGCA
 GTACGACGAGTGGATACCTACGCTGCCTTACGGAGGCGAGGAAGCCAGTCTTCCACATCGAATACCCCAAGGGTGAAG
 ACACCAACAATGACTTGTGAGTGACCTCGAGTCAGAAGTCCAAGGCGTGCAACTTCACCGACTCGGGCAACTTCTCCAG
 GTGATCAAGAATGACCTGGACAATTGGATCGAGATGTGCTAG

Fig. 63

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus niger* Agd3

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MNSLKSSSITSLNGLFGITITGTPPGIPWKNPVLTSASATASVAEVRPTTPGTTSAVHSLSTTTTASLVFSLSSSTSS
AASLNYFIVSGVSPFTITVDSITSAQSASALSSSTITWMSVLSSSSVASSAPVAPPTSSSIAADILVIARDTASAGVAS
SGLNAYGIPFFTLTPVQSGSITPALNGTEGNGFGBIVYVASEVSYNYNGNAIGYOSALTDGQGNOLYAYOLAGVYRNVYVDO
YPGFSYGASAAAGBCCATGVEQLMSFTDITSDFFTSLGKLTAGVSTGTGLWHYPATVINTTTIKETARFAANSDDSSSTTAA
VWNFNNGREQMAGVISFDTWTSVSTYLOHAWIPWLTGRGLYAGVRVNLNITQDDMFLETDIYPKNGTFRITIPADLGI
ANWLPENIGKWNAGNYSFVSHVSHGNGNIIIEAAGVSDSEGTYTCEHGEYINSYPADTIRKPKPLGTGNLWPSPPSTYDW
STACTQDPLWLLWNTTNGOKFKHISHTTEDEQDATSYDVYKEISFNWAKLQVGIISPKHKTANGIIPPAITOLHN
GDLARFNGENITNGYCDNTPALLNODNNWYPTIENDSQFAGMGNVPFRATRIYNNCDITADDTTGTLETDISAGSGDF
DNLLATEKQEYMRHLFQDHHDPYMFHOANLNWADVTPITVNGVYAGYSIFOAWVETQVQEFVRLVWPLVTINHEDMAS
FLARYTRDACYNLSRYTISDHKITGATSVATDNTCNATIPVTFVPVNTTQSGFTIEQVGSPLTYWVGLSGSPVSTLST
PIALY

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BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus niger* agd3

A GAATTCGCCCAATCGTGTACACCGATCTCAACTGCTTTCTGGGCTTTATAACATGACCAACGCGCCCGGGGATTTG
GCTTAAGAACCCGACGCTGTCAACGACGGCATCTACTGCTCAGCTACTTCTGTGCTGAAGTACACGACGGGACGACCTC
CTGEGTACTCTTCAGTGTGCGATCTGTTGACGCTGACGAGCACTGCTCTCTGCTTTTGCTTCTGCTAGTACTAGTGTCT
GCGCGCTCCCACTTTGTGACCTCTGGTGGGCTCTCTACCAACATCTGTTGATACCTCTGCGAGTGGTCTGCCAACGCGCT
ACACGACGACGCTATCCACGCTGATCTGTGACGTCTGAGTCTAGGACATGTGGCGCTCTCTGCTGTGTCCGGCAG
CAGCGCGGCTCAGACGCGGCTGCTTATGCGCGGACATCTGCTGGTATGTCGACGCGACACTGCTCGGACGGCTGGCATC
TCGGGTCTCAATGGCTATGGCATTCGCTTCACCACTCTGATTTGCGCGGAGTCCGGCAGACGCTCCGGGCGCTGAACGG
ACGGAGGGGTCGCAACTTCGCGGCTATTTGTGGTGGCAACGAGCTCAGCTACCACTATGCCATATGCGACAGGGTACAGA
GTGGCTTAACGACGGACCAATGGAAACGAGCTTATAGCGCTACCAAGTGGGGTATGCGGGTGGCGATGTGGGATACGAGCT
TCTCGGGGCGGAGTTACGCGGCGACGCTCTGCGGGCGACGCGGCTCTGTGCGCCAGCGGGTCTGACAGATGTGATGTGGTCA
GATCATACGCGACTTTTCCCACTCTGCGGGCTGAAGACGCGGTGCGGGGTGAGACCACTGBCCTCTGGCATCTCTGCCA
CTGTACCAACACGACCCACCCACCAAGAAATCGCTCGTTTGGCGCACTCGGACTCGGCGACGAGACGACCCGCTGCC
GTGATCAACACTATGATGGCGCTGACAAATGGCTCTTCTGATCTCTCGATACGTAAGTACCTGACCGGCACTCGCATG
CTGTGACGACGCGATGGAATCTGCTGGCTACCGCGCGCTGTGACGGGGTGTACGCGCGGCTGAGCGTCCCAACGACGAT
ACGACATGTTCTGGAAACGACATCTACAAGCCAAATGGCACCTTTTCGCAATCAGCCCGGCGGAGCTGGACGGCAT
GCTAACTGGAGTCGCGGAAATTAACGCGAAGATGAACGCGCGGACGCAACTACTGCTGAAGTGGGCGACACGCGCACT
GCAATTTGAAGCGCGCGGGGCTCTGCGACGACGCGTACCGCACTGCAACGAGGGGCGATGAGTACCACTGACTCGGCG
CGCACTCTCCCTGGAATGAAGAAGAGCTCTGCGAACCGGCAACCACTCTGCGGCTCTCTCTCGCATCTGCACTACGACTGG
ACGACCGGCTGACACAGTGTGACCTCTCTCTCTGTGTTGGCAACCAACGACCAACGACGAGTCTGGTCCAGTCTCT
CGACAGCTCTGACGCAAGGCGGACGAGCAATGGCACTCTCTGATGTGACAGGAATCTGTTCAACGACGGCTGGC
TGAATAGTGGTGTGGCATCTCTCTCGCGCAAGCACTCTACCTCGCAACGCGCATATCGCTCCGCGCATCTACGCGGCTGCAAC
GGCGACGCTCTCGCGGCTGTGGGAACAAGGAATCACCACCTCGTGGGTGATACACCGCGGCTCGCTCTGACCA
CGAAGACGACATGTGGGCTCTGTGAGCAACGAAGAGCTCGACGGTCTTGGCGGTTATGCGAGTGAACCGCGGTTTGCGCA
CGCGCATCTGCTACCACTCGCATACGCGGAGCTGACGCGTCTGCGAGGTATGATCGACAGCTCCGCTCGCGGAGCTTT
GACCACTGCTGCTGCTGACGGAAGAAGGCGAGBETCATGCGTCACTTTGTGGTGTGCAACCATGACCGCTACATGTTGCATCA
GGCCAACTGCTGTAATGCGAGATGTACGCCCATACGGTCAACGGGCTACGCGGCGGATGCTCATCTTCCAGGCTGGG
TGGAGACCGGCTGGAGAGTGTGTGCGCTTGGTGTGTTGGCGGCTTTTACCATCAAGATGAAGATGTACGCAATAT
AGCGCGGCTTTATAGCATCTCAACTGACCAACCACTTATATGAATGCTAATAATGAATAGTGTGCGCGCTCTCTGGC
CGGCTACACCGCGGACGCTGCAACTACTCGCTGCGCTACCCATCTCGGACGCAAGATACGGGCGCGACGGTCTCGC
CGACGATACCACTGCACTGCTACCTACCTCGGCTTACCTTTCTGCTGGGCGCGGACGACGAGAGTCTACACGACGAG
CAGGTGGGAAGTGAACCTGTGACGTTGGGTGCACTTTGCGGGTGGCGGGTCACTTTACGCTGTGACGCGCAATGG
GCTGTAGAGAGCGGGGGAGTTTCTAGATGTTCAATAAATGTGTAATGGATATATAGATACTAGTCAAGTACGCTG
GTATGATATATGTGCTGTGATATATAGTATGTTAGTGCGATGGGATGAATACGGCTATGACATAAATACACAAAT
ACATGGGTATTAAGC

Fig. 64

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus niger* Gtb3

MVEILDVSPVGVFMKEFWQYVLIATILLASVVCGSYLTYSGTRRAIRWYKTRPRVEIVPAAVSQRLEKIANQQTLAA
 AHHTKRKPTSVGVYLGTFATPLDETHRQLLDRYDLLIVDPSKSGVVHALLHTDGKQVLRVDLALSSSQQDLTLAAIEQI
 DSALAGSFHGSFSGIVLANWEDKFKPKVLAKLAEATHGLGLAVYLETGPPTFLEDGQSLQTPAISGLVVRNASILPDGQ
 KRDFQLDKLRPTIKAFVSEACMRDFVLAWETVDDVTLSNAVVRSMQWCNFYSAIPWIGRKAALENAAINVKTPEPL
 SSFSWLKDAETMKAHDRWRNLDIARNYVAKASWDLRAYFPSVDDLFSSEHSPTIKNPPANKLREPPEWVAQVKSQGS
 PLSISMAGVEYKELGCFPLGSEATPVFAEIVHSQQRKSLNLLHPVPSSKLGNMGLLFRQFYENFALSSWMSDQLAAS
 IKELSNMAANDTLRVHLGLDSGLRKSADVRFWAVYQMDADGDFVASKNAQGLAGTVLHTFLSAKGYPRHVCFAEIALA
 RWSKDINEDIGLPRRIIQDIDALSPEERLLLQHLSLDAKGDSETMCAYIRRQLVDAPTLAQLKELNTVAYLEGSASP
 ELLIETRINWYKEGQCYPSAASSLALFYEAESVFTKVLRREREDLAQJSSGLGQLVODGPIDAYTDVLI.SLFGAARK
 GALDEIYAEVTDNRPLFNNQSDQAAFAESFALGSRCEAYFDVSPSAFGKLLSDRFRKSYNDEKLPDWHGAPDMATSYA
 GAQIDVDATHKVKPMRGYQRTFLSVFAFPALDIIILLTIIGRGLYLSAFMTAEEQQSATIALMISLLSGAIGTWIACG
 GPYYLISMAFAAANMFVIRLIAIAFTVAGGLIGFICISAAVSPRAGIIFYLYLIALTLFYSCFASLASFSYPGSTFLS
 GRKVIACVPILFVSPIVTFTGHDSAIYLAVIYAFIGLLLLGLRSVSKWVTWYQSIIRRTDDTEIRKWWYATYGNDEK
 VFGNLSDPAVLKLREALFKDVLAEKRWYQKPTDKLVLELAKDWEATNFLDWYCRYADVPRPIPFSSSWNIQTKVG
 LEVLRNSQKGIIRLHNAFIQWRQSSREIGCGVLYFLLALLDKWVELLTGGQMTGLAPSVTSSORMAVGGLAYYLJGAVLI
 DTKAQELHDLVYGKQTLAVPNAKDIRLAQKRDVKYKRMVYWRTLFKYLGWHVMSLALATALIWTQDTMEAMIFVAYIL
 AYTGLLWYQYKIFSGPHAFKTLIGCVVGLPVGIALKTRLPHFLYSEVIGLGSATWIVAILTFLKAKMGMPKKVSSPVE
 LGRVFHAYSSPWSDEPWSQQLQTFYEKLSLVPDARLSLSPQAHPGVEVKEILLSRKETRIEEAFPKSDDLNLALGA
 WGGKEISLELVPGSLGPGIHALSCCTSGQLHJATCVGRGLDQIDVSANCQVIAETLLHAVAESMLHMPHEHVAESEL
 VTAGVTETMARQLRAEPNTPVIRWAKKELLQQLCLGFCDSHWEKLPKDVRQALJNRCLGQPCQLSEASROWLEGRLCQ
 FDADTLDVHVARSNLGAASAVSILDYAHYGTGEAATFNDPETPEHPIYVYPKKLPSJIQMLAKPWNTIYYAFASVVKFIVV
 ALVADPEFQREFDHVJGQHHAIRVPATLALLWSYSRIMQNIIGLSFFLFHGRDNVQKLWNEAKGMTISIQKSRFIIQS
 LDGTFATFKHDETGGGFIYYYSQGHKTEPEGTKSLSYVCVYSKDVLLMVRQEFKGGKLLNEYHYDYRAPTKKAFGLSKS
 SQARIPMGRRICVRGDNHLQSVQYNRKGLIEAGSYXXXXXXXXXXXXXXXXXRYKNPRFGDELLRAEFALSHITCTVSWCAP
 PLRHPEKIDRWIPHSKVTEATFVQGDVYEAREWLVDHKKFHPTJFTTLNGQKVQTPPMMEHDYLGVI.AKPKHTSFVHDNPL
 LYCDSLSSIFSRRFGLTKKRFVSTSRARSLIWKAWKERVDFDQVIVRWMDERLLRRDKTLAPYWRSDRGDLASAKKY
 LDVRAADIITASADLDDNISSWTPLAVKISDLNFPGGDAVVNIRSKDFGADTEKSLHYMAADNGIWPNEGGSVACRRD
 MINSRLTIKWHMICESANDFGIPKHQTEQNILSLKVVPWLGLDFTPTHGLFRNKLDSEENVTSASEMDIKMNFIPILT
 ALVKGARAIHLSKADIQQATRALVNLNTYFQDSRHWTVQWDSEIVKESWRDLWLSQEMPNTVPSEWFTELPTLASLDI
 ALELWYRYLFIIFSIPJPEKIPNVFQASHHSVSASYGVCKVKRNCTLQIWDHAISWRETNLCLSSALCKLSPFVRNSLLG
 LMRVTSVLTLHHADIISPCADFFNPGEVEIGTCGGTIEHRNVFRKVDPPVNGITDMQKFAPVKEIKSQRPVTMLSHV
 WYAKDIEIALLAADIINQWKFDYHLDIYGAIDKAPTSTECQEIASKGLRGKVTLRGTADPMKVLNTWFLNSSL
 EGLPLALGEAALTGAPVVCVDVGASLRVLSDDPDSRFSAVVAPNDALAKAQITMLGLLGEWSKYAEDDAPPPVLTSS
 PTPDDVAKITRRMYEKSEHRRKLGMMTRKIVQKSFGDRYLREHEQMLWJGSAKIMANRPHVNLQEPDVALQQTLP
 IDEEVITIPRSVNSWRSSAASGNSTLYSSVSNFPLPTGNQRPSSIRSSLNNTSDASSFMRLPSSASLPVFAPRQTL
 FSGGPGGDLTHSPGRLSPVYSRGRHSRSQSISTAGREQLRGLQREDLHQYRNSDVSMIMREEFLQSSIFRGIEGSGGS
 NJV

Fig. 65
BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus niger* gtb3

ATGTTGGAAATCCTCGACGCTCACCCGTCGGGTGGTGTCATGAAAGAAATCTGGTGGCAATATGTACGTGACTGTGT
GTCTGCTCCTCGGAGAAACTGTGCTGGTGTAAACGCTGTACTGTTTGTAGGTCGTGTGCTTCATCTCTGGCAAGATGT
TGGTCTGTGGATGTTTATATCTTACTACTCTGCGACCGCGACAGATACGATGAGTAAGGTGGGTTCCCAACCCCA
ACATGATATGCTAAITGGAAACCGCTTAACTGATCACTGCTTTCAGACAGACGCGGTGTAGAAATGTGTCGCGCTGCT
GTCTCTCAACCGCTGGAAAGAGATGCGCAACCAACGACTTACCTAGACCGCGCGGCTACGACGAAGACGGAGAGCTATCAT
GCTGGGAGATCTACCTAGCAACTTTGCTACTGCTTGGATGAGAGCAAGTTCAAGCCCAAGGTTTCCGCGCAATTTGGCGAATCGTGTGA
TGTGGATCCTTCCAAGTCGCGGGTGTGTCATGCAATTTTGCATACCGACGGGAAGAGAGTTTGTGGCGSAGTGTGATCTG
AGCTCTAAAGTTTGTCCAGCAGGAGCTGACTGTGCGCGCGCTGAGACAGATCGACAGCGAGCTGTCTGGAAAGCTTTCACGG
GCGTGGCTTTTGTGGTATGTGTGGGCAATTTGGAGGACAGAGTTCAAGCCCAAGGTTTCCGCGCAATTTGGCGAATTTGGCGAATCGTGTGA
TCGACGGGTGTGGGTGTGGCTGTGATCTGTGAGACGTGTCGGCCCACTCTCTGGAGAGTGGTCAATGTGACCAACCCCGC
GCCATCTCGGTTTGTGTCGTGGAATGTGATGCTGTATCGTCAAGCCCGGACGGGCTGCTGCTCTTTAGTGGTGAAGATGGGGA
GCGCGCAACCATCAAGAGCTTTTGTGTGAGAGGCATGCATGAGAGACTTTTGGTGTGGGCTGGGAAACTGTGCGACGAGCG
ATGTTACGCTTTGGAATGAGTGTGCTCAATCGCTGTATGAGTGTGGTGTAACTTGTACAGCGCAATTCCTGGTGGTGGCGG
AAGGCGCTGTGAGACGCTGCGCATCAAGTGTCAAGTCAAGCTGAGAGGCAAGTCGGCTGTGCATCTGCGGCGGGGTGTG
GAGCATGAAGGCCACGATCGCTGCGCACCAACCTCGACATCGACGCAATTAATGTTGCCAAGGCTCTTGGGATACAC
TGGCGGCATATTTCCCTCTGTGGAGACAGCTGCTCTTTCTTCCBAAGACTTCCGCGACAAATCAAAACCCACGCGCAAC
AAGCTTTCGCGAGCTCGGAATGGGTGCTCAAGTCAAGTCAAGAGGCAAGTCGGCTGTGCATCTGCGGCGGGGTGTG
ATCAAGGGAACCTTGGTTGTTTCCGCTCGGCTGTGAGAGCAACACCGGCTGCTTTTGCAGAAATTTGTTCAATCCGACGACG
GTCTGAAGTCACTCAACCTGCTCATCGGTTCCGTCGTGGAATTCGACAGCAATGGGGTGGCTCTTCCGACAGCTTTAT
GAAATTTGCCGCTCTGACGATGGATGGCTCGGACCAACTGGCTGCTTATCAAGAGATTTGCAACATGGGACATCA
CGATACGCTGGGGTACACTCGGGCTGGATTTGTGCTGCGCAGAGAGTCTGATGTGCGGCTCTGGGCGGTGATACAG
TGCGACGGGATGGTTCGATGTCTTCCCTCTAAGAAATGCCAGGAGCTGGCTGGGACGATTTGCACAGCTTCTCTCCG
GCCAAAGGCTACCGCGCTCACTGTTTGTGAGAGCAAAATTCGTTTGGGAGATGTCAAAAGATTAAGGAGGAGATG
CGGTTTACCGGTGCTCATCTCAGGACGATTCAGCGCTTAAGTCCGAGGAGCAAGCTTTGCTGTTGCAGCATGTGTCA
TGACCGATGCCAAGGCGCAACTTCTGAACCACTGTTGTCTGATACGCGGACCAACTGTGGACGCGCAACTCGCTGG
CAGCTGAAGGAGCTCAACACGGTTCGCTACCTGGAGGGTGGCTTCCGCGAGCTCTTGTATCGAGACTCGGATCAACTG
GTCAAGGACGAGGCTGCAATATCGCTTCTGCTGGCTGTGCTTGGATGTTTGTACGAGAGGAGTGGCTGCTTACCA
AGTACCTGCGAGAGCGGAGAGGACGAGCTGCTGCTGATTCGAGTGGTGGCTGCGGACAGCTGCTTCAGBATTGGCTCT
GATGCTTAACTGACGTACTGGTCTGTGTTGTTCTGCGCGCAGGAAAGGGTGGCTTCGACAGAGATCTATGCCGAGGT
AAGTACCGCACTCGGTGTTTTCACCAACAGCTCCGACAGCGCGAGCTTTCCGCGAATGGTTGCTCTCGGATCGCGG
CGAGAACCTCATTCGATGTTTGCACCAAGTGGCTTTGGAAGAACTTCTGTCGAGTGTGTTCCGCAAAAGCTACAACATGA
AAGTCTCTGACTGGATCGACGGTGTTCGCGACATGGTACTTTATATGCGGCTGCCAGATTTATGTGCGATGGCATTCG
GAAGGTCAAGGCCATCGGTGGATTCAGCGCTTCACTTCTCTCATGTGTTGCGTTTGTGCTGCTGTGATGATATCATC
TGTTCAGCATCTGCTGCGCGAGTGTCTTCTGCTGCTTCAAGCGCGGAAGACAGCAAGAGTGGCATTTGCACTCT
ATGATTTCCGCTCTGCTCTCGGTTGCTATTCGAGCACTGGATGCTTGGGAGAGACCTTATCACTCATGTCGATGGCTT
CGCAGCTGGCAACATGTTTGTCTGTAGAGCTGATCTGCTGGCATCTGACAGTGGTGGTCTCATCGGTTTCA
TGTGATTTCCGCGCGGTGAGCGCGCGGCGGAGATGCTTCTACCTTACCTTACCTTGGCTGAGACTGATCTTCTGG
TGTTTCCGCTCGGTGGGAGTTTCAAGTACCTGCGGTCGACCTGCTCTCGGCGCGGAAGGTGATGCTTCGATGTGTGCCG
GATGTTATTTGTCTCGCCATTTGTACCACTTTCAACGGCTGATAGTGGGCACTACCTGTTGTGATCTATGTTT
TGGATTTGCTGCTGTTGTGCTGAGTGGGCTCTGTGCAATTTGGTGACTTGGTACCGAGATCTGGGSAACAGATGAT
ACCGAAATCCGAAGATGGAGATCTGCACTTACGCTTACGTTAAACGATGAGAGGATTTTGGAAATTTGGATGAGCCGCGG
CCTAAAGCATTCGAGAGAGCGGTTGTCAAGBATTCTTCGCGAGACTTAAAGCGTGGTTGTCCGAAAGAGCTTACCACG
ACAAGTTGGTGTGGAGTACCGAAGGATTTGGAGCGGCAACCACTTCTCTCGAGTGGTACTCGAGATATGGCGAGTA
CGCAGGCCAATCTGTTTCAGTTTCTGGGAACATCGAGACAGAAATTTGGACTGAGGTTGCTCGGAAGTCCGGAAGTCCGGAAGAGG
CATACGATGACAAATGCTTTCATCGATGGCGACATTCAGCAGAGAAATTCGATTCGCGTGGTCTGTGATCTTGTGAT
CCTGCTGTACAAGTGGGTGGAGCTACTCAACGGCGGCAAAATGACAGGCTTTCGCCCTTGGTTACCAAGTTCGACGCGGG
ATGGCCTCGGAATTTGGCTGGGATCACTTCACTAATCGCTGCGGCTCTCATCGACACAGGCTGAGGAGTCTGTGATGCT
TGTTGGAAGAGAGCAACGCTTGGCGTGGCAATGTGAAGATATTCGCTTGGCGGAGCAAGGCGSAGCTGAATACAAGA

Fig. 66

AATAAGGTTACTCGGSAACATTATTCAGATCTCGGGTGGCAGCTATGGAGTTTGGCCCTTGCACCGCGCTCTGATCTGG
 ACCTTCCAGGATACCAATGGAAAGCATGATCATCTTTGGCTGATTCATCTTGGCATACCCGCTCTCTTTTGGTACCAATG
 CACGAAGATCTTCTCCGGCCGCGATGATTCAGAGCCATCTACTTGGGTGTGTGCTTGGCTACGGTGTGGCTATCGCTC
 TCGACAGCCGCGCTGGCCAGCTCTTGTTATTCGGAAGCTCATTTGGCTCGGGTCTGCCATCAAGAGCTTCGCTATCTCCACA
 CTATTCCAGGCGAAGATGGGATCGGCGAAGAGGCTCTCATCTCGGTGTGGAGCTTGGAAAGGTTATCCACGATCATCTGCT
 TCGCTGTGTGAGTCCGGAATGTGCCAACAGGAGCTCGAAACGTTCTACGAGAGAGCTCTCGCTTGTTCGGTCCGACGCGC
 TGTGAGGCTGTGCTCCCAAGGACCTCCGCGTGTGGAAGTCAAGAGATCTACTTTCGGCGGAAGAGGAACAAAGTAAT
 GAAGAAGCATTCGCGAAGCTCGCAGCACTGTGAAGCTTGGCGTTAGGGCGTGGGGACAAGCGAATTTCCGCTGGAAGCT
 TGTTCGCTTGGCTCATGGCTCTGGCATTCACAGTCTGAGTTGAGTTGTGTAACGTCAAGCCCATGCAACATCGCCATCTGTG
 TAGGCCGCGGAGCTAGCCAAACGGATTGACCTGAGTCGGAAGCTCCGAGCTCATCGCAGAGACTCTGCTTCACGCTCTGGC
 AATACGATGCTGCAATGATCTGAGCTCATGAACAATGCTGATCTGCGGAGTTCGCTGATCGAGAGCTCTGCTGCTGCTG
 ACGTCAACTTCGCGCGGAGGCTTAATACACCGGTCGCTCATACGCTGGCCCAAGAGGAAGCTCTCTTCACGAGCTGTGGCTCG
 TGTGCTGACTGTGATTCTACTCGGGAAGAGCTGGCCAGGAAGAGCTTGGCATCAACCGGTCGCTTGGCCAGCCA
 TGCCAGCTCTCTGAGGCTGAGGACATGGCTCGGAAGAGAGCTTCAGCAGTTGCAATGCTGATCTGATACCTCTGATCTGCACT
 CGCCCGAAGCAATCTCGAGGCTGCTAGTGTCTGACAGTTCTGATATACGACAGCACTACGCTATGTGTAAGACAGCACTCT
 TCAACGACTCTTGAGACTCCAGAGACTATTCCATGTGCCGAAGAGCTCTCTGCACTATTCAAAAGTGTGCTGCAAGCCG
 TGGAAACCACTCATCTAGCTTCTCGCTCGAGTTGACAGTTGTTGAGTTGCTTGTGTTGCTGCTGCTGCGCGATCCGGAATTCGAGG
 AATGAAATCGATATGTTATGGGCAACACCATGCCATTATCCGCTACCGGCTACCGTGGCATTTGAGTGTGCTTGTGTTAT
 ATTCAGATCTGTGTGAGAAATTCTCGGCTCTCGCTCTTTTGTTCATGCTGCTGCAATAATGTGAAGAGCGCTCTGGCATTGAG
 GCCAAGGGAATGACCATCAGCATCCAAAGAGAGAGGTTTCACTATTCAAAGTCTGGATGGCATTCTACTGCTTCAAAGCA
 TGATGAAGAGCGTGAGGGCTCTCAAATCTATTACTACTCCGCGCAGCAGCAAGAGCTGTGAAGGACCAAGAGGCTCTCA
 GCTAGCTCTGTGTTTATGCTCAAAGATGTGTGCTGTATGTGTCGGGACAAGAGTCAAAGGTGGAAGAGTGTCTCAAGAGTAC
 CATTACGACTACCGCGCCCGCCAGCAAGAGGCTTTGCGTTATCCAAGTCTGCGCAAGCAGGAATCCCAATCGCGCGCGC
 TTGTTGTCGCGGAGACACCAATTTCGAGACTGTGCATACAGCCGGAAGGAGCTCATCGAGCGAGACTCTTACANNNNNNN
 NNN
 NNN
 NNN
 TGTGACGCTCTCATGTTGGCGGCTCTCTCTCGGCCATCCGGAAGAGATAGGACGTTGGATCTGCACTCCCAAGTCCAG
 AGGCAACTTTGCTTTCAGGGCGGCTGCTGTCTAGGAGGCACTTTGGCTCTACGATGACAGATTGCACTCCGATCTTCTGAGC
 AGCTCTGCGAGCAAGAAAGTTGACAGCGCCGCCATGATGGAACAGCACTACCTCGGAGTGTGCTGGCCAGCGCCAAACACAC
 CAGCTTTGTGTCATGCAACTACTCTTCTGCTGTGATGATTTGAACTGACAGCATCTCTACGCGGCTCTCTGCACTTCCAGCA
 AGAAGCGCTTCCCGTGTCAAAGTCTCGGCTCGCTGTTGATCTGGAAGGCGTGGAGGAACGCTGCGACTTTGATGCT
 GTGACTGTTGCTGGTGAATGAGTAAAGCACTTTGGCGCAGATGAAGACCTCTGCTCTGATCTGCGATATGCTGGGATCGCGG
 TGACCTTCTCTCGGCGAAGGATCTTGGATGTTCCGCGAGAACACCTCACAGCCAGCTGCGATCTGGACGACAAACATCT
 CTAGCTGGACCGCGCTTGGCTGAAGATCAGTGATCTTTCAACTTTGGCCCTGTGTGTGATGCACTGCTCAACACTCACT
 TCCAAAGCATCTTGGCTGTGATCCGGAAGAGAGGCTGATCATGTGCTGTGATGATGATTTGCTGGCAAGAGCAAGAGG
 TGGCGTTCTTGACGCTCGAGCGGATATGATCAAGCTCTCGAGGACTTCAAGTGGCATATGTTTGGGATCTGCGCAATCT
 ACTTTGGGATTCGCAAGACCGACAGGACAGCAAGCTTTGTTCTTGAAGGCTGTCCGCTCTGCGGCTGTGCACTTCTG
 CGCCCGACCGCGGCTCTCTCAGGAAGAGAGCTGAGTCTGGAAATCGAGAATTTGCTCTCGCCAGCTGAGATGGACATCCG
 GATGAACTCTGATCCCATCTTGAAGGCACTAGTCAAGGAGAGCTGCGCTATGCTATCTGATCGCAAGCGGATATTCAGAGAA
 CGACTCGAGGCTTGGTCAATCTCAACACTACTTCCAGATTCGCGGCACTGAGCCCAAGCTGTGGGACAGAGGATGATGTC
 AAGGAAGACTGGGCGGACGCTGTGGCTCAGTCAAGAAATGGCCCAACCGCTGCTTGTGTAAGTTGTGCTGCGCAGGAATCT
 CCGCAACGCTGGCTCTCTCGACATTGCACTGGAACCTTGATATGGTACTGTTGATCTTCTGATCTGCAATCCCGGAGA
 AGATCCCCAATGTCTTCAAAGATCGACACAGAGTATGATGTCATCTACGTTGTGCTGTCAAAGTGAAGAGAAAGCTG
 ACACCTCCGATCTTGGGACATGCGCATGTGCTGGGTGAGAACACCTCTGCTGTTCACTCGGCACTTGGCAAGCTCTGCTCG
 CTTGCTGGGCACTCCGTACTCGGCTCATGGCGTCAGCTGCTGCTTAAGCGTGCAGCAGCGGATATCATCTCCGCTC
 CGCGGCACTCTTCAAACCGGCTGGGAAGTCAGATCGGCACTCGCAGCGGCACTGAGAGAGCTCAAACTCTCTCCGCG
 CGGAAGGTGACCGCGCTGTCAAAGGACTCAGAGACTCGAGAAGTTTGGCCGCGCTCAAGAGAGATCAATTCGACGCGCGC
 AACGCTCAGCATCTTATCCAGCTCTGCTGACGCAAGAGCATGAAATCGCGCTCTGGCGCGGACATCATCTATCAAGAA
 AGTGGAAAGTTGCAAGCACTACCACCTTGACATCTCAGGAGCATCGCAAAAGCCCTCACTCTCCAGCGAATCTCAAAGA
 ATCATCGGCTCGAAGGGGCTCGGGGCAAGTCAACCTCGCGGCGACCGGCGACCGCTCAAGGCTTGAAGCTCTGGAGAACAGCTG

Fig. 67

GCTCTTCTCAACTCTTCCCTCTCCGAAGGTCTCCCTCGCCCTCGGCGAAGCCGCCCTAACCGCGCCCCGTGCTCTGCACGACGTCGGGGCCTCCCTCGCGCTCTCAGCGACCCAGATGACTTCTCCCGCTTCAGCGCCGTGCTGCGCCCCAACGACGCCCTCGCCCTCGCAAAGGCCCAAAATCACCATGCTCGCCCTCCTCGCGGAATGGAGCAAGTACGCCGAAGACGACGCTCCACCACCAAGTGCTTACCTCCTCCCGACCCCGACGACGTCGCCAAGATCACCCTGTCGATGTACGAGAAGACGACGACCGTCGCAAACTGGGAATGATGACCCGCAAGATCGTCCAGAAATCGTTACGCGGTGATCGCTACCTCCGTGAACATGAGCAAATGCTCTGGATCGGCAAAATCCGCTAAGATCATGGCAACCGTCGGCACGTC AACCTCCAAGAGCCCAAGGACGTCGCGCAGGGCGCTGCAGCAGACCTCCCCATGCAGCAAGAAAGTCATCACTATCCCGCGCAGCGCGGTCAACTCCTGGCGCTCGTCCGCTGCATCAGGCATGTCCACTCTCTACAGCTCCGTCTCGAACTTTCGATGCTGCCACCGGCAATCAACGTCCTTCGTCTATCCGGTCCAGTCTAAGTAATACCTCCACGGACGCGAGCTCCTTCATCGCCCTCCCGACGCGGCTTCCTCTCCCTGCTTTGCACCGCCGACAGACGCTGCTTTTCCGGTGGACAGGGGAGATACTATCTTCCCTGGTCGTTTGTGCGCGGTGGTGAGCCGCTCGGACGCTCAITTCGCGCTCTCAGTCTATTTCACCGCTGGAAGAGACGACGTCGCTGGCTGCAACGTCGAGGATCTGCATCAGTATGCAACTCAGATGTCAAGCATGATTATGAGAGAGGAGTTTCTGCAATCGAGCATTTTCAGGGGCATTGAAGGTGGCAGTGGTGGTAGCAACATCGTCTGA

Fig. 68

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus fumigatus* Uge3

MDSYQQSDASTPVEPCSPGCVDTPATQSSVLFQGHLDLLRHFPDQYILVTGGLGFIGSHTTLELLKANYNVIVIDNLS
 NSFQIVFDRIKLLASQYHERQGTKMPSLHLHAHDYRDTAALKELLEQHQTQTRWGTTKSKISGVIHFAAYKAVEESIRNP
 LKYYANNVSGLIDFATTLGDYGIKTFIFSSSATVYGTLATSGPLKEELCTHKEEIIYTDHDGSERIVQPGGTGITNPYGR
 TKWICEAILADLAASDPEWTIVALRYFNPIGCDSEGLLGEDPRQTPTNLLPVVVKVMTGEYRELQMFQTDWNTEDGTAVR
 DFIHVTDLARGHIAALSAANEGKLAENFRFTNLGTGRGHSVKEVVETMEEVSSKHIPRRAADRRAGDVGSCVAVATRSQ
 ELNWKTEKSLKDACVSLCNFLEVSGLST

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus fumigatus* uge3 (Genbank accession No.
 AFUA_3607910)

ATGGACAGCTACCAGCAATCCGACGCAAGCACTCCGGTGGAGCCTTGCTCCCCAGGCTGCGTGGACACGCCCGCAACGCA
 ATCGTCCGTCTTGTGTTGATGGTCATCTGGACGATCTCCTGCGCCACTTCCCTCTCGACCAATACATCCTTGTACGGGGCG
 GCCTCGGCTTCATTGGCAGTCACACAACATTGGAAGTGTCAAGGCCAATTATAATGTGATTGTGATCGACAATCTCAGC
 AACTCCTTTGAGATCGTCTTCGACCGCATCAAGCTGTTAGCCTCCCAATACCATGAGCGGCAGGGGACCAAGATGCCGTC
 GCTGCACCTGCATGCACACGACTATCGTGACACTGCTGCTCTCAAGGAACCTCTAGAACAGCACCAGACCCAGACCCGAT
 GGGGTACGACCAAGTCCAAGATCTCTGGTGTCACTTCCCTGCTACAAGGCAGTGGAGGAGAGCATCCGCAACCCA
 CTCAAGTACTATGCCAACAACGTCAGCGGCTCATCGACTTTGCCACGACCCCTGGGTGACTATGGCATCAAGACTTTTAT
 CTTCTCCTCGTGGGCCACAGTGTACGGCACCTTGGCAACCTCCGGTCTCCCTGAAAGGAAGAGCTGTGCACGCACAAGG
 AGGAGATCTATACCGACCACGACGGGAGTGAACGCATTGTCCAGCCCGGCTGTACAGGCATCACCAACCCCTATGGCCGT
 ACCAAATGGATCTCGGAGGCCATCCTGGCGGACCTCGCCGCTCCGACCCAGAATGGACTATCGTCGCTCTGCGGTACTT
 CAACCCCATCGGATGTGACGAGTCCGGCTCCTCGGAGAAGACCCAGACAGACTCCACAAACTTACTTCTGTCTGTCG
 TCAAAGTCATGACAGGCGAGTACCGGAGTTGCAGATGTTCCGGAAGTGAATGAGGACGGGACGGCCGTCCGG
 GACTTCATCCAGTCAACGACCTTGGCGCGGCCACATCGCGGCTCTCAGCGCAGCCAAAGGCAAACTGGCCGAGAA
 CTTCCGCACGTTCAACCTGGGAACCGGTGCGGACACTCCGTCAAGGAAGTGTGAGACCATGGAGGAAGTTTCTCCA
 AGCAGATCCCCGAAGGGCGGCTGATCGCGCGCGGGGATGTGGGCTCCTGCGTCGCGGTGGCCACCGCATCGCAGCAG
 GAGCTCAACTGGAAGACGGAAAAGTCACTCAAGGATGCTTGTGTGAGCTTGTGCAATTTCTGGAAGTCAGTGGGTTATC
 TACTTAG

Fig. 69

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus fumigatus* Sph3

MAEKHVSNNRCLQSRRSRILLAVFVLIAILAVVIPPVAVVTLHKKNDMGPKSKVFVPLYVYPAPGAWTPLEDVISKHPDV
 NFTVVINPGSGPGPNALPDGNYTREIPKLASYENVRLGYVATTYAKRNISLVRRDIETYAAWPTNSSNPALAVRGIFFD
 ETPQQYDEDALAYLQELTDVVKNTPLGLPDHYVVHNPGAIPDSRYLSTADSTVVFEATYDTFQERHGAKLFEAIPDSNRS
 QLCVAIHVSVPESVEGSALRSLVKQVRKVADEIFITHLDTDYASFGROWPEFVDLMGK

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus fumigatus* sph3 (Genbank accession No.
 AFUA_3607900)

ATGGCGGAAAAACAGTGAAGCAATCGACGGTGCCCTGCAAAGCCGGCGCTCTCGAATCCTCTTGCCCGTCTTTGTTCTTAT
 TGCTATTCTGGCTGTCTGATCCCTCCGGCGGTTGTGGTGACGCTGCACAAGAAGAAGACATGGGGCCTAAATCCAAGG
 TCTTTGTGCTCTCTATGTGTACCTGCACCCGGAGCCTGGACTCCGCTTGAAGATGTGTATGTTTTCCGCCACGTTCA
 CCTTGACCTTGGTCATCTTGGGCTAGCTGAATCATTTAGTCAGCATTGAGGACAACAGCTGACGCCACACCCACATATAC
 ACACACACAGGATCTCCAAACACCCAGACGTGAACCTTACCGTTGTGATCAACCCAGGGAGCGGACCTGGACCCAACGCA
 CTGCCGGATGGCAACTACACGGGTGAGATTCCCAAGCTGGCTTCGTACGAGAATGTGCGGCTGCTAGGCTATGTGGCGAC
 AACCTACGCGAAGCGCAATATCTCGCTGGTGGCGCGGACATCGAGACGTATGCAGCGTGGCCAACGAACTCTTCCAACC
 CGGCTCTAGCTGTTCCGGGGATCTTTTTCGACGAGACCCCTCAGCAGTATGATGAGGATGCCTTGGCGTATCTGCAGGAG
 TTGACCGACGTTGTGAAAAATACCCCTGGTTTGGGGCGGATCATTACGTACGTTTCCCTGGTAATTCATTATCATATTT
 GGTAATTTTTATTTCCATTTTTATTTATTTTTTTTATTTGTTTGGTTTTGTTTCTCGCTTGCCACCTTCCAGTGTATA
 TATCACTTTGTTTTTTTTTTTTTTTTCAGTCAAGCTGTCTGTACAGTTTGCAAGTGCTAAAATGCTCACTAATTACAG
 GTGGTTCACAATCCGGGCGGATCCCTGACTCTCGCTACCTGTGACTGCAGACTCGACTGTCGTGTTTCAAGCAACGTA
 CGACACCTTTTCAAGAACGCCATGGAGCCAAGCTGTTTCAAGGCGATCCCGGACAGCAACCGCAGCCAGCTCTGTGCGGTGA
 TCCACTCCGTCCTCCGAGAGTGTGAAAGGGTCTGCGCTCCGGAGTTTGGTGAAGCAGGTCCGCAAAGTTGCCGATGAGATC
 TTCATCACCCACTTGGATACGGATTACTATGCCAGTTTTGGGCGGCAAGTGGCCGGAGTTTGTGGATTTGATGGGAAAATA
 G

Fig. 70

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus fumigatus* Ega3 (Genbank accession No. AFUA_3607890)

MDSLGKGQSAGGWKSWTTRKKLFVLALVLLVIIALGVGLGVGLGIGLGGGGGEGEEGSGGETTPPEGNYTTAKWQPAVG
TKWQIELLYALNDTSVDAEIIYDIDLFINDKSTIAGLQRAGRKVICYFSAGSYENWRPDKDKFKDSDLGHDLDWPGKWL
NISSANVRQIMLDRLDMARDKGCDGVDPDNVDGYDNDNGLDLTQADSISFVNFLANAHAHARNMSIGLKNAGDIIPSVIKN
MQWSVNEQCAQYNECDTYAVFPQNGKPVFHI EYPKGDKTNNLSVTASQKNAACDFAGSANFSTVIKMNMLNNWVEYC

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus fumigatus* ega3 (Genbank accession No. AFUA_3607890)

ATGGATTCCCTTGAAAAAGGCCAGTCGGCCGGCGGCTGGAATCATGGACCACCAGGAAGAAGCTCTTCGTCTCGCGCT
CGTTCTCCTCGTCATCATCGCCCTGGGAGTCGGTCTCGGAGTTGGACTCGGCATCGGTCTGGGCGGCGGCGGCGGCGG
AAGGTGAAGAAGGCTCAGGCGGGGAGACCACCGCCAGAAGGCAACTACACCACGGCCAAGTGGCAGCCAGCGGTGGGA
ACCAAATGGCAGATCGAGCTGCTTTACGCGTTGAACGACACCTCCGTGGACGCTGAGATCTACGACATCGACCTGTTTAT
CAACGACAAGTCCACCATCGCAGGACTCCAACGAGCCGGCCGCAAGGTGATCTGCTACTTCTCGGCAGGCAGCTACGAGA
ACTGGCGACCGGACAAGGACAAGTTCAAGGACTCGGATCTGGGCCACGACCTGGACGACTGGCCGGGAGAGAAATGGCTG
AACATCAGCTCGGCAAAACGTACGCCAGATCATGCTGGACCGGTTGGACATGGCGCGCGACAAGGGCTGCGACGGGGTGGGA
CCCGGACAACGTGACGGGTACGACAATGACAACGGGCTGGACCTGACGCGAGGCGGACTCGATCAGCTTTGTGAACTTCC
TGGCGAATGCGGCGCATGCGCGGAACATGTCGATTGGCCTGAAGAACGCGGGGGACATCATCCCGTCGGTGATCAAAAAC
ATGCAGTGGAGTGTAACGAGCAGTGTGCGCAGTACAACGAGTGGGACACCTACGCGGTGTTTCCGCAGAATGGCAAGCC
GGTGTTCACATCGAGTATCCAAGGGGGATAAGACCAACAATGATCTGTCCGTACGGCCAGTCAGAAGAACGCGGCGT
GCGACTTTGCCGGCTCGGCGAATTTCTCCACTGTCATTAAGAATATGAATCTGAACAATTGGGTGGAATATTGTTAG

Fig. 71

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus fumigatus* Agd3 (Genbank accession No. AFUA_3607870)

[illegible]

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus fumigatus* agd3(Genbank accession No. AFUA_3607870)

[illegible]

Fig. 72

PUTATIVE AMINO ACID SEQUENCE OF *Aspergillus fumigatus* Gtb3 (Genbank accession No. AFUA_3607860)

MDQPGDAARMHGPAVHPLCQARRKRKLLLSALNRALLRGLLSLTRLVRDQMAATLLTPSFWSRIAGFSRLFLVRVHAGO
 PDVFSAVVTTPRRFHPGLGQKHTLLLSAILAQTGQTDGQQRSYFCLHQRALPRQTVLIGLLLGSVVIGCSYLLYAGLSRARK
 WYQVGIRSMSSVDALEEIADILQSRAGSAVVRNVLDRDLRSRQQLSLPNVQWAKKPSFGVYLGSDASPTRDQSRLL
 SQWDLIIVDPAQSGVVEALSRAERKQFLGRVDVGSQSGSTLAADRIESALSDFDGPFGMILLANWESSFNPAATRKLA
 EALHAFGLPVYLETAPPDFLQDHKTLQTDALAGLVIRNASIMPDGEKRDYFQMIKMQPTIKAFVSEACMRDFVVMWETV
 DDNAHLSNAVIQRSLQWCNFYSAITWIGRGAALHDSLVNKIPEPLSAFSLWKEAEIMKVHDIWRANLNQEEVGPDA
 WTALLQYFPTLSNVLTSSEREPPSHMDSATIAVRDPPPEWVAQVRSQGSPLSI SMAGVEYKEFGCFPLGSEATAVAFVEIL
 KSQQRKLSLGLLHPVPSDKIQKL GALLRRFHOKFAVSHWPDLPATIKDLANFASQDSLRLNLGLDSGLRKSADVRFW
 AVYQSDADGFEVFASKSAQGLAGTVLHTFLSARGFPRHVCFAETALAQWSKDVNEDIGLPRRLIQDQDALSPERLLLL
 QHLSLTDKSELSETICRYIRROLIDAPSLAQLKELNTVAYLDGSLPPEALIKSRIHWYRDQGRSPAPAAACALFQETD
 AVFTRILRRERESDLAQITNALCQLVQKDRIDVYADILTLSLFCAARKGAFDEIYMEVTDNRNLFNDQSDQAAAFESFA
 LGSRCAYFDLSPSAFGKLLSGRFRYYQDRELPDWINGAPQMATS YAGAIDVNPDDKVKPMRGYGRFTFLSVFAVPAL
 IDILLTLYGRGLYLSGHMPEEYMHASIALMISLLSGAAGTWIACGGSYLLISMAFAATNMVFVIRLIACFAFTIAGV
 LVGFIYMSAVKGPBGIVFYLYLIALTYFSIFASLACFSYPGSKFLSGRKAIFACIPVLFISPIVTNWSHHDVVIYLIY
 LYIFIGLLLSLSRVASKWVTWYQNIIRRTDDEIRKWWYSKYGNDEKCFGGRSDDPAVLKLSREALYRDVMAEVSRRGFS
 KPTTDQLVLELARDWEATNFLDWYCRYADVPRPIPFSSGWNITQKVGLDLNRNSQKGQRHLNFMHWRSSREIGCGVL
 YFVLALLDKWADLLTGGRMTGFLQMPNGDTRFAYGFLAYYLIGAVLIDTKAQELHDLIGGQTNQAVGTSKEIRPSQKRA
 VRFRKRYWRTFVKYLMWQVWSLALSTALLWTRSSVDAMAMFCAYVLSYTGLLWYQYTKIFAGPHALRPLLAGIVVGLP
 VGIIVLKTQVSGNFSNYGPVIGLGTATWTTAILLTLAKMGMPKKVDSVDLQKTFHAYTTPWADPEWSQQLQTFFERIS
 LVPSDTRLKLEPGAHPGMEVKSLLSRREEPRIEEAFKASEL IHRALQAWAGGEISIELVPLGSLGPGIRALSCHAADQ
 LKLVAVGRGLDQRIDVSGNCQVIAETLLHAVSESLRMPHEYAVLAESLVTAGVTETMARQLREEPNTPVVVRWAKKEL
 LRELCLGFECDTHEWELPKTIRKALLDRQVGP SHF SERDRQWLQEHLCRFDTSDLDVHVARNLGAATAVSILDYAHYG
 TGEEALGKDSETPLFIPYVSKKLPAALAFVKDPLHNFWYSVASAIKFI IIALIADPEQREFDHVMKQRARIIRVPCVFL
 LNLWYSYKIVQDVILSFFLHFGDRNVKRLWDET KGMTISIKKS RFMLQSLDGTFAFKHDEDDGGFKVYVYSGEHKTEP
 EGTKSLKYVSTYSKMDLLIRQEFKDGKALNEFHYYDRAPNKKSLRLTRGSDTRIPLGRRCI RGDShLQSVQYNRKGLIE
 AGSYNKDGNLIRFKYHYRKNPRFGDELLRAEVLSHITCTVSWCAPVVRHPEKVERWI PHSKVTEATFVQGDVYEARWL
 YDHKFHPTIFTTLNGGKIQTTPMIEHDFLGVLAKPKYTSFVHDNPLFYCDLS SNAITRFLGLSTKRFPVSTSRARSLVW
 KAWKDRVDFGIIYRWMDERLLRRDKTLAPYWRSDRGDLASAKKYLDLRADTVMASADLDDNISSWTPMAIKVSDLLNF
 GPGGDVAVNTRSKDFGSDTDKSLHVMAADGTWPNEGGSACRRDMINSLRTIKWHMIGESANDFGIPKHQTEQNVLSL
 KNIPLWGLDFLTPHGLFKNKLDSEVENVTSANDMDIKMNFIPILTALYKGARATIELSKADIHQATRALVNLNTYFQDSR
 HWTQVWNSDIVKESWRDLWLTQEMPNTIPSAQWFHTELP TLTGLDVALELWYRYLFI FSIPIEQIPSVFQASHHSVSAS
 YGVVCKIKRNGTLLQIWDHAISWRETNLCLSSALCKLSPFVRNALLGLMRITSVITLHHADII SPGADFFNPGWEVEIGTC
 QGTIEHRNIFRRKYDPVVNGITDMQKFAPVKEIKSQRPTVTMLSHVYAKDIKTALLAADII INQWKFDYHLDIYGAID
 KAPTYSYECQEITASKGLRGRVTLRGSADPMKVLENTWFLNSSLSEGLPLALGEAALTGAPVVC TDVGASLRVLSDDPD
 FSRFSAVVAPNDALALARAQITMLALLGEWAQYADDTEPAPVLTSSPTDDVAKITRRMYEKAHRRKLGMNTRNIVQKS
 FSGDRYLREHEQMLWIGKAVKTMAVRAAAGAPGTALGDPIDJADALQVADPIEEVITIPQSAVHSWRSSAASGMSTVYS
 TISGYPMLPLTRPASIRSSFSNFSTATDSQSFMLPSNASLPVAPRQTL SFDAGGAVIPTGRLSPSGRLSPAFGRHRHS
 HARSISTLGREQLRGLGREEPHYRNSDVSLHMRREEFLQSSIFKSIDGNAGGKS

Fig. 73

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Aspergillus fumigatus* gtb3 (Genbank accession No. AFUA_3607860)

ATGGACACACGACGAGTATGACAGCCAGGATGCGATGCTGCTGCTGATACATCCACTCTGCCAAAGCTCGGAGGAAACGCAAAAGT
GCTGCTGTCTGCTCTCAACCGGGCAGCTCTCCGTGGAGTGTCTTCCTTAACGAGGCTGTGTCCGGCATGGAATGGCTGCCA
GCTGTGTGACACGGCTGTTCTGTGTCAGAGAGATACGAGATGCTGACAGTACTCTTTAGTCCGGGTGCATGGCTGTGATCA
CCGACGATGTTCTCGGCTGTAGTGAATCAACGCGGGTTTATCCGCTTGGGCCAGAACACACCTCTTCTTATAGGCCCAT
CTTAGCGGACGACGAGACAGACGACAGACAGACAGACAGCAAGAGTATTTTTGTCTTCAGCGGTGATTCGGCGACAGAACGG
TCCATGAAGTAAGCAGTTGCTGGTTGGCTCGAGAAATTTCAAGTGTATGATATGGCGAAAACCGAATAAAGCCCGCTGCTATT
ACTTTCGCTGACCAAGTAGATTCTTCGAGGGGGCGCTATGATCTTCGCGCTCGAGCTAGGCTGGTGGTTTGAAGTCGGAGCGCGCT
GGTTGGCCATCGGACACGCGCTTTTCTGGTCTTTATGAAGCAACAGTCAAGTGTAGTCTATAGCGCTGTAGATGTACAT
GCTGGGTTTGCTGTGTGTGTGACATCTGGCTGCCAGCTCTTTGAGCTGGCTGTGTGGCTGGTCGATCGATCGATCGTCTGCT
TATCGTTTCTTTTGGCGCTGTGTGGCTGGCTGGTGGTTTCTTCAATGATCTCTCGATGATGATTTGCGTATGATCTCGCTGGCT
CGTTTATGCAAGAAATGGCGTCGGGGTCGATCGATCGCTGACTGGGTGTATGGTTTATAGAGGATGTGTCTGTCTGTGGT
GTGACATTTTGGGCTTCGGAGTCGGCTGGCTGGCTGGCTGGCTCTCGCTTTTGGACGCTTCTCGTGTTCATGTTCGCTGTCTGATCT
CTAAGCTTCTGATCTTAATCATACCACTAGGGTTTATCGTCGGCAGTACCCAGCATGATGATGATTTTCAAGAGGGCTC
TGGCGCTCGAGTGGGCGCATATGACAGATTTCTCGGTGGCAATTTGATAGGATCTTCTCTCAAGGCTCGTGGCTTTACTAA
CGAGATATAGGCTCTCATCGGGCTTGCTGTAGGTAGGCTAGTATGGATGTTCATAGCTCTCTCTACGAGAGAGTGTGTGAG
GAGCTCGCAAAATGGTACGAGTAGATATCCGCTCGATGTCTCGGCTCGATAGCTCGGCTCGAAGGATTTGCTACATTTTACAG
TCGGCGGCGCAATCGCAGTGGTGGCGCAAGTGTGTGTGATAGGCTGACGAGCATATCAAGGACGAGCTGTGCTTGGC
CAATGTCCGATGGGCAAGAAAGCGCTGTGCTGTCCGCGTCTACTTGGGCTCTTCGACCGATCCCGAACAGGAGTACGAT
CGAGACTCTGAGTCAATGGGATGTGCTGATGCTGATGTGACCCCGGCGAGTCGGGTGTGGTCCAGGCGCTCTTCGAGGCGAG
AGGAAAGCATTTCTGGCGGAGTAGACGTGGTTGGGCTCAGGCTGACCTTGGCGGCTATCGACCAATCGAGAGCGC
CTACGACAGAGTGTGATGGCGCGCGGTTTGGCGGCTGCTGCTGGCAGCTCGGAGAGCGAGCTTCAACCGGGCGCGCATCA
GGAAGTGGCGCAGCGCTCTCATGGCTTTAGCGCTCCGCGTGTATGTGAGACAGCCGCGGAGACTCTCTCGACAGACCAT
AGAGACTCTGACAGCATGAGTGGCATCGGCGGCTCTGCTGATCGCAATGCTTCATCATGCTGTGAGTGGCGAGAAACGCGCAT
TTCTTGAATGATCAAGATCGACGCCACCATCAAGGCTTCTGTGTGCGAGGCTGATCGAGCGGACTCTGTGCTCATGGCT
GGGAGAGCGTGGAGCGACAAGCGTACGCTGTGCAATGGGCTCGAGAGGCTCTGCGAGTGTGAGCAATCTTCAAGACGGC
ATCAACGTGATCGCGCGCGAGCGGCGGCTTGACAGATGGCTCTTGCAAGTCAGAAATTCGGAGCGGCTTCTCGGCTCTGT
TTGGGTCAGAGGAGAGCGAGATGATGAAGTGCAGCAATCTGGCGCGCAATCTGCAAGCTCAGGAGAGGAGGAGTGGCG
CGAGAGACGAGTGGACGGCTCTCGGCTGAGCTACTTTGGCAGCGTTTCCAGCAAGTGTCAAGTGTCTCGGATCGTGGAAAGAGAGAGCGCGC
TGCAGATGAGACAGCGCAGCATCGGCTTCTGATGCTGAGCGGAAATGGGCGCGAGTCAGTTCGAGAGGCGACAGCCGCT
GTCCATCTCCATGGCCGCGCTGGAATCGAGAGGATTTGGCTGTTTCCCGTGGGATCGAGAGGACCGCGCGCTGGCTCTT
TCGAGATGCTCAAGTCCCAACAGCGGCTGAAGTCTCTGGAGCTGCTGCAGCGGTTCCGTGGGCAAAATCCGAAAGCTG
GGCGCGCTCTCGGACGATTCACGATGAATTTGGCGTGTGCGACTGGCGGCGACTTGGCCAGTCTCGCGCGGACATCGAAC
GGACTCGGCAATTTTGGCTCGGAGATTTCCGTGGCATGACTTATGGGCTGACCTGCGGCTTCGGCAAGACGCGGACGAG
TCCGCTCTGGGCGCTTACCAATCGAGCGCGACAGGATTCAGAGTGTGTGGCTGAAAGCGCGCACAGGCTCTCGCGGCG
ACCGTGTCTGCACAGTCTCTCTCGCGCGAGGTTTCCCGCTCATGCTCTGTGCTGCAAGCGGACAGGCGCTTGGGCGAGT
TCCAGAGGAGCTGAAGCAAGACATCGAGCTGCCCGCGCTCATCAAGATGTGACAGCTCGCTGAGTCCGAGAGAGCAT
TGCTCTCGCTGACGACATCTTCTGTTGACCGAGCGCAAGATGAAGTGTCCGAGCTGAGTGTGCGGCTACCTTGGCGGCGCAG
CTGATGATGAGTGGCGCTCTCGTGGCGACTTCAAGAGCTCAACCGGCTGGCGTACCTCGAGCGATGCTCTCGCGCAGAGCG
CTGTATCAAGTCGGCATTCAGTGTGAGTCAAGAGTCAAGGTTGGCTTTCTGTGGCTCTGGCGGTGGCTGGCGGTTTGG
AGGAAAGGAGCGAGCTGTCTTCAGCGGCATCTCGCGAAGACCGCGAGAGGAGATCTGGCTGAGTACCAACAGCGCTTGTG
CAGCTGTGTCAGGAAGAGCGGATCGAGCTGTATGGCATATCTCGACGCTCTGGCTCTGTGTGGCGCGCGCAAAAGGCGC
CTTTGACGAGATGTACATGCAAGTCAAGGATGCGAACCGCGTTTGAACGAGGATCGGATCAAGCGGCGCGCTTGGCG
AGTGTGTTGGCTGTGGTGGCTGCGTGGGAGCTACTTGCAGCTCTCGCGCAGCGGCTTGGCGAGATTTGCTCTCGGCTGTG
TTCAGAGATCTACACAGAGCGGAGATTCGGCGAGTGGATCAAGCGGAGTTCGAGATTTGGAGCTCTGATCTGGCGGCG
ACAGATCGATGTCAACCGCGACGACAAAGTCAAGCCCATCGGGGTACCAAGCGCTTCAAGTTCTCTAGTGTCTTTCGCG
TGGCGCGCGCTGATCGACATCTGCTGCTGAGGCTTATGGCGCGGCTTACGCTTCTGGCGCGCTACCGGAGAGGCTG
ATCGACAGTGGTGTGATCGCGGTGATGATCTCTGCTGCTGTGCGGTGGCGGCGGACATGATCGCTGGCGGCGGCTG

Fig. 74

ATGACTACCTGATCTCCATGTGGTTTGGCGGCCAACCAATGTTTGTCTTTATCGCACTATCGCGCTTTTGCCTTCAGGA
 TCCGCTGCGGGCTGGTGGGATTCATCGCTGATCTCCGCGCTCAAAAGGCGCGGGCCGCGATCTCTTCACTCTCACTCG
 ATTCCGTCGACCGCTTCACTTCACATGCTTCGCTCGCTCGCGCTTTGTACAGTACCGGGCTCCAAGTTCCTCTCGGGCGCG
 CAAGGGCACTCTTCGCGTGCATCCCGGCTGCTGTCATCTCGCGCGATGTCAGCCACGGAGCGCTACAGGATGTGGTCACT
 ACGTCAATTGTCGTCATCACTTCTAGCGAGTGGTTCGTCGTGTCAGCGTCCGCGTGGCTCGCAATTCGAGTTACCTGTGTC
 AGGACATCCGACGCGACCGACACGAGATCGGCAAAATGATATGTTCGAAGTACGGGCAACAGCAGCAAGAGTGGTT
 CGTGCGGCGGAGCAATCCCGCGTGGTGAAGGTTGTCGAGGAGTGGTTCGAGTATCTGATGTCGAGGAGTGGTCCGCGG
 GCTGTTTTCGAAGCGCCAGACAGACAGCGTGGTCTGGAAGTGGCCCGGCGGAGCGGAGTACGATGCTTCTCTCGAC
 TGGTACTGCGGGTATGCGGAGCTGCGCGGGCGGATCGGCTTCAGCTCGGGCTGGAATATCGAGACCAAGTTCGGGCTGTA
 GTGTGTCGGCAATTCGCAAAAGGCGCAAGCTTGACAAATTCGGTTATCATGATTCGGCGCATTCGACCGCGGAGATCGGCT
 CGGGGGTGCTACTCTTTTCTTCTGCTCTGCTGATAATGGGCGGCACTTGCTGACGGGGGCGGAGATCGATGGTTTCTTA
 AGATGGCCCAATGGGACACGCGTTTTCGGTTTGGGTTGAGCTCGGCTTCGCGTTATTAACCTGATCGGCGGCTGCTCATCGAAC
 CAAGGCTCAGGAAGCTCATGATCTATCGGGGGGACAGCAAAATCAGCGGTCGGGACGCTCCATAGGAGATTCGCGGCTGCG
 AGAAGCGGGGCTCGAGGTTTCAGAGAAAGGTTGATCGAGGAGGCTTCGAGATATCTGATGTCGAGGCTTCGAGTCTTT
 GCGTTGTTCGACCGAGCTTGTCTTGACAGTTTCGGTGCTCGATGGATGCCATGGCCATGTTCTCGCGCTACGTGCTGTCGTA
 CACCGCGCTGCTGTGTATCAATCAAGCAAGATCTTCGTCGTTCGCGATGCCCTCGGACATTCGTCGCGGGATTCGTG
 TGGGCTGCGGCTCGGGATGCTCTCAAGCAATGTGTGTGGGCAATTTACGAATATCGCGCGGTGATGTGAGCTGGG
 ACGCGCACTTGACGACCGCGGATCTCACTCTGCTGCTGACGAAATGGAATTCGACGAGAAAGTGGAATCGGCTTCGTA
 CTTGGGCAAGAGCTTTCAGAGCTACACGACCGCTGGGCGATTCGGAATGGTCCGAGCAAGAGCTCGCAACCGTCTTCTG
 AGAAGATCTCTGTGGTCGCTCCGACACGGGACTCAAGCTGGAAGCGCGTGGGCTACCGGGATGGAAGTCAAGTCGCTG
 CTGCTCTTCGCGCGCGAGGAAGACGCGAATCGAGGAGGCTTCCGCAAGCAATCGGAGATGATACCGCGGCTCGGAGCG
 CTGGGGCAAGGAGGAGATTTGATCAAGCGGCTTCTCTTCGTGGTCGCTGGGCTCGCGGCTCTAGCTGCAATGT
 CGCGGCGACAGCTGAAACTGCTCTGCGGCTGGACGCGGACTGGACAGCGCATTCAGACTGGAGCGGCACTCGCAAGAT
 ATCGCGGAGACTTGCTTCTATCGGCTGTGGGATCGCGATCTGATCGGGATGCTCGACGATCGCGCTGCTCGGGAATCGCT
 CTGACGCGCGCGGCTCGAGGAGCATGCGCGCGGACGATTCGCGAAGAACCCACACCGCGGATGTCGTCGCGGGGCA
 GAGAGGAGTCTCTCGGGAGCTGTGTCTGGGTTGCAATGTGACACGCAATGGGAGAACTGGCCAAAGACGATTCGGAAG
 GCGTTGCTGGACGATGTGTGTCGCGAAGCTGCTGCGAGCGCGACCGAGCAATGGCTTCAGGAGCACTCTGCTCGG
 CTTTGATACGATGATGTGATGTGCATGTTGGCGGATGCAACTGGGCGGGGCGACCGGACTGAGCATCTGTGATGTAG
 CCGCACTACGGCACCGGCGAAGGAGCTTGGGCAAGGACTCCGAGACCGCGCTGCTGCTGATGATGTGCAAAAAGCTG
 CGCGCGGCGCTCGGTTTCGTAAGGACTCCCTGCGCAACTTGTGATCTGGTGGCTGCGGCTCGGCACTCAAGTTCACTCATCAT
 CGGCTTGATTGCGGATCGGGAATTCAGCGGAGAATTGAGCATGTGATGAACAGCGCGCGCGCATCATCGCGCTCGGCT
 GTGTGTTCTCTCAACCTGATCTGTGGTGTGATCGAAGATGCTGTCAGAGATGTATCTGTTCTCTCTCTCTCTCTGCTGCG
 CGGAGACGCTCAAGCGTCTTGGGAGGACGACGAGBACATGACCATGACATGAGTCAAGAGGCGGCTTATGCTGCTGAGAG
 CGTGACGCGCACCTTTATGGCGGTTCAAGACGACGACGAGAGAGCGCGGCTCAAGCTCTACTACTACGCGCGGAGACACA
 AGGACGAGCGCGGAGGCGCAAGCTGCTCAAGTACGTGACGAGCACTGCTCCGAGGACATGCTGCTCATCTCGGAGGGAG
 TGAACAAAGGCAAGAGGCCATCAAGAGTTTCAACATGACTACCGCGCTCGAAGAACAAAGAGAGCGCTCGGTTGACCGCGG
 CTGATACCGGCACTCCCTCTGGGCGGGCGGAGTGCATCGGCGGACGACGCATCTCGAGAGCTCGGATATACCGGCAAGG
 CTTCTCATCGAGCGCGCTTCTCATGTAAGATGACATGCTCGGTTCAAGTACCACTACCGAGAGAACCGCGGAGTGT
 GCGACAGCACTGCTCTCGCGGAGTTTGTGCTCTGCGACATTACTGTCACGCTCTGCTGATGGGCTCTCGGTCGGGCA
 TCGGCAAGGCTGCGAGCGCTGATCGGCACTCAAGGTCGACGAGGCGAGCTTGTGTCAGAGCGCGGCTGCTCATGAGG
 CTGCTGGTGTACGACGAGCAAGTTTCGCGCGGCACTCTACCAAGCACTACGCGGCGAGAGATGCAGAGCGCGGCTGCTG
 ATGAGCATGACTTCTCGGCGCTCTGGGCAAGGCCAAGTACACAGGCTTTGTGATGACAATCGGCTCTTCTACTGCGA
 CAGTCTCAGCTGCAAGCGCATACCGGCTCTCTGGGCTCTCCAGCAAGCGGTTTCGCTGCTGCGCTGCTCGGCGCGGCTGCT
 CGGTGGTGTGCAAGGCGGTGAAGACGCGGCTGAGCTTTGACGGGATCGGATGGTCCGCTGGATGAGACAGCGCGGCTGCTG
 CGGCAAGAGCGCTGGCCGCTACTGGCGGACCGGGGACCGGGCGATTCGGCTTCGGCGAAGAGTACCTGGAACCTGGC
 GCGGCAACGCGTCAATGGGATGTCGAGCTCTGACGACAGCAATCTCCAGCTGGACCGCACTGGGATCAAGTCAAGTCAAGCAT
 TCGTGAATTTTGGCGCGCGGCGGACTGGCTGTGTAACACCGGCTCCAAGGATTTCCGCTGGGACAGCGCGCAAGCTGGCTG
 CAGCTCATGGCGGCGGACACGGGCACTGGCGGACGACGAGCGGTGTGTGTGCGGCTGTGCGACGCGGCTCATCAACTCT
 TCTCGGCGGATCAAGTGGACATGATCTGCGGCTCGGCGCAAGCACTTTGGCATTCGCAAGCTCAGACGAGGACAGAGCG
 TGCTCTGTTGAAGATGTCCGCGTGTGGGCTGTGACTTTTGGCGCGACGAGTGGGCTCTTCAAGACAAAGTGGAGTAA

Fig. 75

TGGGAGGTGGAGAAGCTCAGCTCGGCCAACGACATGGACATCAAGATGAACTTCATCCCGATCCTGACAGCGCTGGTGAA
AGGCGCGCGGCCATCGAGCTGTCCAAGGCCGATATCCACGAGGCCACGCGGGCGCTGGTCAACCTCAACACGTACTTCC
AGGACTCGCGGCACCTGGACGCAGGCTCTGGAATAGCGACATCGTCAAGGAGAGCTGGCGCGACCTCTGGCTCACGCAGGAG
ATGCCCAACACGATCCCGTCGGCGCAGTGGTTCCACACCGAGCTCCCGACCTGGGGACGCTCGACGTGGCGCTGGAGCT
CTGGTACCGGTACCTGTTTCATCTTCTCGATCGCCATCCCGGAGCAGATCCCGAGCGTGTTCAGGGGTGGCATCACAGCG
TCAGCGCCTCGTACGGGGTCTGTCTGCAAGATCAAGCGGAAGTGCACCCCTGCAGATCTGGGACCAGCCATCAGCTGGCGC
GAAACCAACCTCTGCCTCTCTCGGCCCTGTGCAAGCTCTCGCGTTTGTCCGCAACGCCCTCCTGGGCCGTATGCGCAT
CACCTCCGTATCACCCCTCCACCATGCGGACATCATCTCGCGGTGTGCGGACTTCTTCAATCCCGGCTGGGAGGTGGAGA
TCGGCACCTGCCAGGCGACCATCGAGCACCGCCAACATCTTCGGCCGCAAGGTGACCCCGTCTGTAACGGCATCACGGAC
ATGCAAAAGTTCCGCCCCGTCAAGGAGATCAAGTCGCAGCGGCCACCGTCACCATGCTGTGCGACGTCTGGTACGCCAA
GGACATCAAGACGCCCTGCTGGCCGCGACATCATCAACAGTGGAAAGTTCGACGACTACCATCTCGACATCTACG
GCGCATCGACAAGGCCCGACCTACTCCACCGAGTGCAGGAGATCATCGCCTCCAAGGGCTCGCGGCGCGGTCACC
CTCGCGGCGAGCGCCGACCCCATGAAGGTCTCGAAAACACCTGGCTCTTCCTCAACTCCTCCCTCTCGGAAGGGCTCCC
GCTCGCCCTCGGCGAAGCGGCCCTACCGCGCGCGCGTCTGTGCACCGACGTGGTGGCTCCCTGCGCGTCTCAGCG
ACCGGAGCAGACTTCTCCCGTTTACGCGCGTCTGTCGCCCAACGACGCCCTCGCGCTCGCCCGCGCCAGATCACCATG
CTCGCCCTCTCTCGGCAATGGGCCAAGTACGCCGACGACACCGAGCCCGCCCGCTCTACCTCTCGCCACCCCGGA
CGACGTGCGCAAGATCACCGCGCGCATGTACGAGAAGGCCGAGCACCGCGCAAACTCGGCATGATGACCGCAACATCG
TCCAGAAGTCTTCTCGGGGACCGCTACCTGCGGCAACACGAGCAGATGCTCTGGATCGGCAAGGCCGTCAAGACCATG
GCCGTCCGGCGCGCGCGCGGCCCGCGGCCCGGACCGCCCTCGGGGACCCCATCGACATCGCCGACGCCCTCCAGGTGCGAGA
CCCCATCGAGGAAGAAGTCATCACCATCCCGCAGTCCGCCGTGCACTCCTGGCGCTGTCGCGCGCTCGGGCATGTCCA
CGGTCTACTCCACCATCTCGGGTACCCCATGCTCCCGCTGACCCGGCCCGCGTCCATCCGCTCCTCCTCAGTAACTTC
TCCACCGCGACCGACTCGGACTCCTTCATGGGCTGCGGAGCAACGCATCCCTGCCTGTCTTCGCGCGCGCGGAGACCT
CTCATTGATGCGGGCGGGGCGGTGACGCCACGGGTGGGTGTCCCGTCAAGGAGGCTGTGCGCGCGCTTTGGGCGGC
ACCGACACTCGCACGCGCGGTCCATCTCCACGCTGGGCGCGAGCAGTGGTGGTTTGCAGCGTGAGGAGCCTCATCCG
TACCGCAACTCGGATGTGATCTGCATATGCGCGAGGAGTTCCTGCAGTCGAGTATCTTCAAGTCTATCGACGGTAATGC
GGGGGGGAAATCCTGA

Fig. 76

PUTATIVE AMINO ACID SEQUENCE OF *Penicillium chrysogenum* AgsB (Genbank No. Pc16g06130)

MKWSLASGLVSLVTTVTAWPYDEAYLDYNINTNKTATNPADYWGTPGHEGKYFSPDNWRFPFYSMFLDRFVNGDPTN
 DNANGTTFEHDIHRIRHGGDVAGLVDLTDYLGGMGIKIYITGTSLLNMPWTS DGYGVVDITLLDAHFGTIQAWRDAIT
 EIHKRGMYVLFNDTIATMADLIGFEGHLNKSTPFSEKEWPALWKSERRYRDFDIKEGHYNASCDYPRFWYEDGYPVNESQ
 TAGLVGCYDSDFDQYGDIEAFGVWPDWKRQLAKFASVQDRLREWNPSVRERLIRHSCMIHSFDIDGFRYDKATQATVDA
 LGDMSAAYRECAREVGENFFITGEITGGNDFGTIYLGRGRQRNQYPENSAVTMNL TNTSSAQYFLREAGHEAIDSAAFH
 YSTYRALTRFLGMDGQLTAGFDAPVDWVEGWDMVKTNDLINANTGVFDPRHMFGATNQDVFRWPAIANGTHRQLLGTFFV
 GTLLPGIPLLLWGEEQNFIYLDASAENYIYGRQAMSPATAWMTHGCFQLDSSQYYKWPITAGREGCHDITVSYDHRDPS
 HPVRNVMRHMFMREHPVPLNDGYSLGSLTKQTEWVHYPGSNETATETGMWSVYRDVNAVLOEDLALNPDSIPVWLVTN
 LNDTMTYNFDCKSKNPNTLTAPFDAGTTVKNLFPYDEITLVEGAQKLGNGSKEMNGCTESMEMKAYEFRAVYVKNKH
 KSARPMITKFTPGHDFPLRSTVAPDLPEDVTVELYFSEEMNCDLVTDAITFNSSTEEKQVPTIDPKTVNCTTIPPLQSN
 WTAEIPSVWKWTANLTGVYNGVHKLTVNNATNTDKSDSTNAIDHFLFRVGGFDNPMVFITANYSSSLHRRENGDLFIQH
 HAAGADKYRYSTNWGSSFSWDRYKGGNDTIDKLPSWGTQDQEWGDEHVRVEYWSRLTGSSDYVQQGDLWNHPVTRRFP
 HAFNGPYNQYGYDAGLDNRIRLDTRTGVSYSYHFTSEWPAVGQLNIWGINPDGKPDQTWVLGDIDNDTILDRSPSSLSA
 TVINITAAPAKGYLSHKLYFDDGTLHFWDLPVGPQSTQIVMFIWFIIIPFITAVGCVYIFMKSFYKVKFNEVGYTEKQNI
 PLAIWNKIKPSRRDQSSNPLMRLANKSGFMQSTSALGGALASGKRRMVL IATMEYDIEDWAIKIKIGGLGVMAQLMGKTL
 GHQDLIWVVPVCGGVDPYDQVAEPMVTIILGSPYQVQVQYHVLNNITYVLLDAPVFRQQSKTEPYPARMDLDSAVVYS
 AWNQCIAEAIKRFIDTYHINDYHGS LAPLYLLPRTIPACLSLHNAEFQGLWPMRTIKEKQEVCSVFNLEEDIVRRYVQF
 GEVFNLLHAGASYLRVHQAGFGAVGVSKKYGKRSYARYPIFWGLHKVGNLPNPDPSDVGEWTKPTKEEDITVDPTYEAG
 RGELKRAQGEWAGLDQNPADLLVFVGRWSMQKGVDLIADALPAVIEARPNVQLICIGPVIDLYGKFAALKLDHMMKVYP
 GRVFSKPEFTALPPFIFSGAEFALIPSRDEPFLVAVEFGRKGALGIGARVGGLGQMPGWWYNVESVSTSHLLIQFKLAI
 EAALNSKTSVRAMMRARS AKQRFPAQWVEDLEILQNTAIQVHIKEASKTHSTNSTRPGTSSGFSTASAAMSPSMNQLGS
 PLPSPGINSPFTHSRESSYSFNQMNSLGTQKKVSYSDPDQEE TEKPKSGLSRSLSLGVRSGPGHAGRRRRRAAEGGIPES
 DENGATDVDENSDEEAHNAFDDDEYTLTPAQVEAGRRQAQAQRDRAQNLPSPSRRPSQDSLQPRFMVPLESPRSPGTPP
 AVDSL LLLPPQPF AESNRLSSASVSLDSVVGKTDYKLGKVDPFPTDQTGEYRIFDKKLDVLNGSNSESQLCIEEFLIK
 SEQEWDFRFRNARLGRNKSPTPSIRHSSRNTATPDTMFYNDOLASNVNSEDENHLQDDEFLGKDYVPPTGLKKWMQVKI
 GDWPIYSMFLALGQIIAANSYQITLLTGEVGQTAEKLYGIATTYAIASMCWWLVYRYFKSVVCLSTPWFLYATAFLIGS
 AHWEGDSFTRGWIQNVGTGFYAAASASGSIFFASNFGDEGGAPVKTWIFRACVIQGIQAYVIALWYWGSTMTKASSEGL
 LNPETNIANSWKMSAICYPICIFLCIVGVLLAMGLPNYYRQKPGKVP SFYKSLFRRKIVTWNFI AVILQNFFLSAPYGRN
 WSFLWTSIHTHAQIVILCIVFFGFVWCIFLFVVSRSKRHSWFLPVFACGLGAPRFIQIWWAVSGIGYYLPWAGGYTSG
 ALVSRSLWLWLGVLDSIQGLGFGIILLQTLTRVHMCFALIASQVIGSIATICARAFGPNNVGPPI SPDMTQGAHSLANG
 WFWVALFCQLLVCAAGFLFFRKEQLAKP

Fig. 77

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Penicillium chrysogenum* agsB (Genbank No. Pc16g06130)

ATGAAGTGGTCACTCGCTAGCGGGTGGTCTCACTTCTTGTGACGACCGTCACAGCTTGGCCCTACGATGAGGCTACCT
GGATTATAACATAAACACAAATAAGACGGCCACCAACCGCGCAGATTACTGGGGAACATGGCTGGTCACGAGGGGAAAT
ATTTGGCGTGGCGGATAACTGGGGTTGGGTTGTATTCTATGTTCTTGGATGGCTTGGTAATGGTGACCGTACCAAT
GACAAIGCAAACGGIACCACCTTCGAGCATGATATGAACAICGCAICGCAATGGTGGGAGTGGGCTGGCTTGTGGA
CACACTGGATTATCTCAAGGAATGGGAATCAAGGTTTGTCTCATCCGAATTTGTCTAATGGCAAGAAAATATATGCTCAC
AATGTCAGGGTATCTATATACGGGAACCTCCTTGGCTGAACATGGCGTGGACTTCAGACGGATATGGAGTTGTGGATAC
AAGCTTCTTGACGCCCATTTTGGCACAATTCAGGCTTGGCGAGACGCCATCAGGAAATACACAAGCGGGATGTAGG
TCTTTGTCGACAATACGATTGGGACGTAAGTTGTCTCTGTATGCAATGTAATAGAGCAAGCTAACCTAATTGTATAGA
ATGGCTGACTTGTATTGGGTTTGAAGGCCATCTCAACAATCCACCCATTCTCGGAGAAAGGAATGGCCAGCACTATGGAA
GAGTGAAGCGGCATACAGAGACTTCGACATTAAGAAGGTCACATAATGCCAGCTGTGACTACCGTGGATTCTGGTAGG
AAGAGGATACCGCGTAATGAATCGGAGACCGAGGTTTGGTTGGATGTTATGACAGCGACTTCGACGAGTATGGTGAT
ATTGAGGCTTTCGGTGTGGCCCGATTGGAGCGACAACCTGGCAAGTTCCGCTCCGTCCAGGATCGTCTACGTGAATG
GAACCGGAGTGTGGCGAAAGGTTGATCGGACACTCTGTATGATCATTCATTCTTCGACATCGATGGTTCCGCTATG
ATAAGGCGACCGAAGCTACTGTGGATGCCCTTGGGAGATGTCCGCTGGCTACAGAGAATGGCGCGGAGGTGGGAAAG
GAAACCTTCTTATCACTGGCGAAATCACGGGTGGAAATGACTTTGGTACTATTTACCTCGAAGGGATAGCGAGGAA
CGAATACCGTGAAGACTCGGCGGTCACAATGAACCTGACAAACACGCTCCTCTGCCAGTACTTCTTACGCGAAGCGGGC
ATGAAGCATTGATAGTGGCGGCTTCCACTACTCGACCTATCGTGCAATGACTCGGATTCCTGGGATGGAGGGAACACTC
ACGGCAGGCTTTGACCGGCTTTGACTGGGTTGAGGGCTGGGACTACATGGTGAAGCAATGACTTTGATCAATGCCAA
TACCGCGGCTTTCGACCGCTCGACACATGTTTGGTGGCACTAATCAAGACGCTTCCGCTGGCCAGCGATTGCGAAGCGCA
CGCATCGACATTTACTCGTACTTTTGTGGTACATTGCTGCTCCCGGAATCCGCTTCTCTTTGGGAGAAAGAGCAG
AATTTCTATATCTTGGATGGCGCGGAGAGACTACATTTACGGGCGACAGGCTATGTGCGCTGCAACTGCGTGGATGAC
CGATGGCTGCTTCAATTTGGACTCTCTCCAGTACTACAAGTGGCCCATCACGGCGGTAGAGAGGGCTGTCTATGATATA
CAGTTTCTTACGAGCCACCGGACCGCTCCGACCGCTGTCGAAATGTTATGAGGCATATGTTCCAGATGGCGAGCACTAC
CCAGTTCTCATGACGGGTAAGCTTGGCAGCTTGACAAAGCAACGGAGTGGGTTCACTACCGTGGTTCGAATGAAC
GGCCACGGAGACCGGAATGGTCTGTTTACCGGATGTCAACGGGCTCTGCAAGAAATGTTGGCTTGAATCTTGACA
GGATTGAGTCTGGCTGTTTACACAAGCTCAATGACACAATGACATAGAACTTCGACTGCAAGTCCAAAGAAATCCGAAC
AAGACACTGACAGCGGCTTTGATGCTGGCAGCACTGTCAAGAGCTTTTCTAGCGGTAGGATGAATCACACTGTAGGA
AGGAGCTCAAAAGCTTGGCTTGAATGGATCGAAGGAGATGAATGGCTGTACGGAAAGCATGGAGATGAAGGCATACGAGT
TCCGCGCATACCTCCATAAAATAAGCACAAATGAGCTCGGCGCATGATCACAAATTCACCTCGGCGCATGATTTCGA
CTACGCTCTACCGTGGCGCGGAGCTTCCGAGGATGTGACAGTTGAAGCTTTACTTCTCGGAAGAAATGAAGTGTGACTT
GGTGAAGTGAATACGTTCAATTCATCGACAGAAAGGGGCGGTCGCAAGCATAGACCCCAAGACTGTTAATTGCA
CAACCATCCCTCCCTTGGTCCAATCAATTTGAGCTGCTGAGATACCAAGCGTTTGGAAATGACAGCAAACTGACTGGA
GTTTATACGGAGTTCAAAAGTTGACTGTCAACAACGCAACCAACCGGACAAAGCGATTCTACCAACGCTATTGATCA
CTTCTCTTGGGTTGGGTCAGTTGATTAAGCGTATGGTATTGATCACTGCCAAGTACTGAGCGAGTCTACTCCAGAGAA
GAGAAATGGCGACCTTTTATCGAGCACCGCGGCTGGTGCAGACAAATACCGCTATCTACCAACTGGGATCGTGA
TTCTCTGACTGAGAGACTACAAAGTTGAAATGATACTATTGACAAGCTCCCATGGTGGGAGCCAAAGGATCAGGAGTG
GGATGGTGAGCATGCTGCTGCAATCTGGAGTGGCTTACCGGAAAGGAGGATACGTCGAGCAAGGAGCTTGAAGT
GGATACCGCACTCACAGGACGCTTCCCGATGCTTCTTCAACGGACGCTATAATCAATAGGATACGATCGGCGCTA
GATAACAGAAATCGGCTCGACAGGAGAACCGGGCTTGGTCTCTACCAATTCACCTCCGAATGGCTGCAAGTGGAGAGCT
CAACATCTGGGGAATTAATCCAGAGGGAAGCGGATCAAACTTGGGTTTGGGAGATATGACAAATGACACAATCTGG
ACCGAAGTCTCGGCTTCTCTGAGCGGCACTGTGATCAATATCACTGCAAGCGCGGCTAAAGGCTACCTCTCCGACAAG
CTATACTCGACGATGGAAGTCTCCATTTCTGGCTTGTCCGTTGGACCCAGTCCACAGAGATTGTCTATGTTTCAATCT
ATTCTGGATCATACCATCATCACTGCGGTGGGATGTGTATATCTTCAAGAGTCAATCTACAAAGTCAAGTTCAAAG
AGGTCGGTGTGACTGAGAAACAAACATCCCGCTCGCAATTTGGAACAAGATAAGCCCTCCGTAAGGATCAATCTCG
AAGCCAGTCTATCGGTTGGCGCAAAATCTGGCTTCAATGCAAGACCAAGTCCGCTAGGGCGGGGCTTGCATCTGGCAA
GGCGCGCATGGTTCTAATCGCCACTATGGAATACGACATTGAGGATTGGGCTATCAAAATCAAGATCGGTGGTCTGGTG
TCATGGCTCACTCATGGGTAAGACCTAGGTCACCAAGACCTAATCTGGGTCGTTCCATGGCTGGAGGTGTCGACTAC

Fig. 78

CCTGTGGACCAAGTCGCGGAGCCTATGACAGTCACTATTCTAGGCAGCCCTACCAAGTTCAGTGCAGTACCAGTCTT
 GAATAATATCACTATGTACTGTCTCGATGCTCCAGTGTCCCTCAACAGTCGAAGACCGAACCCTACCCCTGCTCGCATGG
 ATGATCTCGACAGTGCAGTGTACTATTGCGGATGGAACCAAGTGTATCGCTGAAGCTATCAAGCGATTCCCAATTGACACG
 TACCACATCAACGACTACCAAGGTTCTGTCGGCGCTCTTTACTTGTACCAAGAACCATGCCCGCTGTCTTTGATTGCA
 CAATGCTGAGTTCCAGGGTCTCTGGCCTATGCGCACCATCAAGAAAAACAGGAGGTTTGTCTGGTCTTTAAGCTTGAAG
 AAGATATCGTTGCTGCTTACGTGCAATTTGGTGAAGTGTCAACTTGTCTCCAGCCGGTGAAGCTATCTCGGTGTGCAC
 CAGGCGAGGATTCGGTGCCGTTGGTGTCTTAAGAAGTACGGCAACCGTCTTACGCTCGCTATCCTATCTTCTGGGGTTT
 GCATAAGGTTGGCAATCTACCTAACCTGATCCATCTGACGTCGGTGAATGGACAAAGGAGGCCACCAAGAGGAGACAC
 TGACTGTGGATGCAACTTACGAGGCTGGCGGTGGTAGGCTTAAGAGACAGGGCCAGGAATGGGCAAGGCTGACGAGAAT
 CCTGATGCCGACCTGTGTGTGTTGCTGGTGGTGTCTATGCAAAAGGGTGTGTATCTTATTGACAGACGACTGCTGCTG
 TGTATCGAAGCTCGACCTAACGTGCAAGTTGATCTGTATTGGTCCGTCATGATCTCTACGTTAAATTCGCTGCTCTCA
 AGCTTGACACATGATGAAGCTATCCGCGACGAGTTTCTCAAGCCTGAGTTCACTGCACTTCGCGCTTTATCTTT
 TCTGTTGCCGAGTTGCGCTTGTGCTCCGTCGGTGACGAGCCCTTCGGTCTGGTTGCCGAGAGTTTGGCGAAAAGGTTGC
 ATTGGGTATCGGAGCTCGTGTGGTGGTCTTGGCCAAATGCCAGGCTGGTGGTACAATGTGGAATCAGTCTCGACGTCGG
 ATCTCTCATTTCAATTCAAGCTGCAATTTAGGCTGCCCTCAACTCTAAGACATCCGTCGGTGGCATGATGCGTGGCAGA
 TCTGCGAAACAGGCTTTCCGCTGTGCTCAATGAGTTGAGGATCTTGAATCTCTGCAAAATACCTGCAATGCAAGTTGCAAT
 CAAGAAGGCTCGAAGACACATAGTACCAACAGCACTGACCTGGGCACTTCTTCTGGATTGACGACTGCGAGTGGCGCA
 TGTCACTTCCATGAACCAACTAGTAGCGCACTGCTTCAACCGGCATAAACTCTCCATTACGCAATTCAGAGAAAGC
 AGCTACTCTTCAACCAAAATGAACAGCCTTGGCAGCCAGAAAGCTCAGCTACAGGCGAGATCCAGACAGGAAGAAAC
 GGAGAAACCAAGTCCGAGCTGAGTCTGTTCCCTTTCCGTGGTGTCCGCTCAGGCCCGGTCATGCTGGACGTCGACAA
 GAGCAGCAGAGGTTGATTCGAGAGAGGATGAAGATGAAGCCACTGATGTCGACGAGAACAGCAGTGAAGAAAGCTGCT
 CACACAGGCTTTGACGATGAGGAATACACTCTCAGCCAGCCAGCTCAGGCGAGGACAGCTGCCAGGCTGCCGAAAG
 GGACCGGCTCAAAAGTTGGCTTCGCTCAAGCAGAGCGCCAGTCAAGATCTTTCAACCCAGTTTCACTGGTTCTCTTTGG
 AAAGCCGAGGAGTCCGGGAACGCCGCCCGGCGTAGACAGCTCTCTCTCCCTCCCAAGCATTTCGCGAGTCCAAAGCT
 CTCAGCAGCGCATCGCTTCTCTCTGATTCGCTGCTCGGAAACAGAGCTGACTACAGCTACAAAGGTTGATCTCTT
 CTTACGCGATCAGACTGGCGATCTACAGGATATTGACAGAAAGTTGGATGCTCTCAACGATCCAACTCTGAGTGGC
 AGCTCTGATCGAAGAGTTCTTGATTAGAGGGGAACAGAGTGGTTCGACAGGTTCCGTAATGCCAGACTGGGTGCAAC
 AAGTCTCCACTCCGTAATTGCCATTCTCAGAGAAACAGCCAGCCAGACACAATGTTCTACAATGATGACCTCGC
 CTCCAAGCTGAACAGCGACAGGAATAACCATCTCCAAGATGATGAGTTCTTCTCGGAAGGACTATGCTCCCTCCCACTG
 GGCTTAAGAAATGATGCAAGTCAAAATTTGAGACTGGCGATCTACTCCATGTTCTTGTCTGGGCGAGTCAATTGCC
 GCAAACTCTACAGATCACTCTACTCACAGGTGAAGTTGGTCAGACTGCGGAGAGTTGATGGAATTGCGACACATA
 TGGCATTGATCCATGTTGCTGGTGGTCTGTACCGATCTTCAAGTCTGTCTGCTTTCTACCCGTTGGTTCTGT
 ACGCTACTGCTTCTCTGTTGATGATGCTGCTCACTGGGAAGGAGATTCTTCAAGCGGGATGGATCCAGAAATGTCGGC
 ACCGGTTCTATGCGCGGCTCCGCAAGTGGATCCATTTCTTCCCTTCAAACTTTGGTGAAGAGGTTGGTCTCAAGT
 TAAACCTGAGATTTCCGCGCTGTGTTATTCAAGGTATTCAACAGGCATACGTTATTGCCCTCTGTAAGTGGGTTCCA
 CGATGACCAAGCTTCTGTCAGAGGCTCTCTGAAGCCTGAGACCAAGATTGCCAAGCTGGAAAAATGAGTAAATACAC
 CTGCCACCTATGCTGTAATTGTTTTTACTGACAGATTCAGTGAATCTGTTACCCATCTGCACTTCTCTGTGTA
 TTGTTGGTGTGTTGTTGGCTATGGGACTTCCCAACTACTACCGCAAAAGCCAGGCAAGGTGCCATCCTTCTACAAGTCC
 CTTTCCGAGAAAGATGCTCACTTGAAGCTTCTGCGCGTCTCTGCAAGACTTCTTCTGAGTGCACCATACGGTGG
 GAACGGAGCTGTGAAGTCCAATTCTCCGATTCCAATTTTTCATACCGACCAATACTAATACCTCCCGCTCCGAGTCTAT
 GGACCTCATACACAGCCAGCATGGCAGATCGTCACTCTGATGCTCTTCTTGGGCTTCTGCTGGTGCATCTTCTCTC
 TTTGCTGTAGCAGATTCTCAAGGCGACAGTTGGTTCTTCCCTCTTCCCTGCGGCTGGGCGCACCCGCTTCAT
 CCAAACTCTGTGGCTGTCTCCGCTGCTGGTACTACCTGCGCTGGGCGGAGGTTACACATCCGCGCGCTGCTCTCTC
 GCAATTTGTGGCTGTGGCTGGGCTGTTGGATTCCATCCAAGTCTTGGATTGGGTATCATCTTCTGCAAGCTCTCACT
 CGAGTCCACATGTTGTTGCTCTCATGCTGCTGAGTGAAGTTGATTGCGACTATCTGCGCGCGAGCTTGGTGG
 GAACAATGTGGGACTGCGCCAACTCTCTGACATGACCCAGGCGCCCATCTTGGCTAATGGCTGGTCTGGTGG
 CTTTGTCTGTCAAGTTGTTGGTCTGGTATGTTGATCTTGGCTTGTCTTGGTGGATGCTGCTGAAGCTTATGCTGG
 AGTGGCGGTTCTGCTGTTCTTCCGTAAGGAACAACCTGCCAAACGATAA

Fig. 79

PUTATIVE AMINO ACID SEQUENCE OF *Penicillium chrysogenum* Uge3 (Genbank No. Pc20g06140)

MIEPTSFSSSRSGSPQRSNDANSPVHSPIAVDTPSTEAGDPFDNLHDLLRRLPLQSHILVTGGLGFIGSHTTLELLKANYN
 VIVIDNLSNAFENVVGRISLLAKKHHEENGTKMPSLRRLHAHYRDEALQSLLEEQLPWRGTPKSRIAGVIHFAAYKA
 VEESJRKPLKYYSNNVSGLVDFATTLGDFGIKTFIFSSSATVYGLATSGPLKEELCVHKEELYTDHEGSQQFIQPGCT
 GITNPYGRWKWMCETILADLAASDPEWTIVALRYFNPVGGDSSGLLGEDPRQAPTNLPPVVVKVITGQYSELSMFGTDWE
 TEDGTAVRDFIHVSDLARGHIAALSSANEGKLTENFRTFNLGTGKNSVMDVVSTMESVTEKHIPRRAAPRREGDVGACV
 AVVDRSTEELQWKTEKSLKDACRDICNFDISGLSS

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Penicillium chrysogenum* uge3 (Genbank No. Pc20g06140)

ATGATTGAGCCAACATCATTTTCTCTTCAAGGTCGGGCGAGCCCTCAAAGGTCGGATGCGAACAGTCCTGTGCACTCTCG
 TATCGCTGTGGACACACCGTCAACAGAGGCTGGAGAGCCATTGACAATCTCCATGACTTGTGGCGAGACTCCCTTTGC
 AGAGTCACATTCTTGTCACTGGCGGCTCGGTTTCATTGGTAGTCACACCACGCTTGAGTTGCTCAAGGCAAACTATAAC
 GTCATTGTGATCGACAATCTCAGCAATGCATTGAGAGATGTTGTGCGGCGTATCAGTCTCTTGGCCAAAAAGCATCACGA
 GGAGAACGGGACGAAGATGCCATCTCTGCGGTTGCATGCACATGACTATCGCGACACCGAAGCTCTTCAATCACTGCTCG
 AAGAATACCAGCTTCCATCCCGGTGGGGAACCTCCAAATCGAGAATCGCGGAGTCATCCACTTTGCAGCTTATAAAGCC
 GTGGAGGAGAGCATTGGGAAGCCACTGAAATATTACTCTAACAATGTGAGCGGCTGGTGGACTTTGCCACAACACTTGG
 TGACTTGGGATCAAGACCTTCATCTTCTCGTCTTCCGCCACAGTATACGGGTCCCTCGCAACCTCGGGTCTTCCATTGA
 AAGAGGAAGTGTGTGTTACAAGGAAGAGTTGTACACAGACCATGAAGGCTCACAGCAATTCATCCAACCTGGATGCACC
 GGAATCACCAACCCGTACGGAGCGACGAAATGGATGTGTGAAACCATCTAGCTGACCTCGCCGCATCAGACCCCGAATG
 GACCATTGTTGCACTCCGCTATTTCAACCCGTTGGCTGTGATTCTTCCGGTCTTTTGGGCGAAGACCCAAAGACAGGCAC
 CAACAAACCTGCTTCCGTCGTTGTCAAAGTCATTACCGGCCAGTATTCAGAACTTTCGATGTTTGGGACAGATTGGGAA
 ACCGAAGATGGCACTGCCGTCCGTGACTTCATCCACGTTAGTGATCTGGCTCGTGGACATATTGCCGCGCTTAGTTCGGC
 CAACGAGGGCAAGCTGACAGAGAATTTCCGCACATTCAACCTCGGAAGTGGAAAAGGGAATTGGGTGATGGATGTGGTCA
 GCACTATGGAGTCTGTTACTGAGAAGCACATTCTAGGCGTGCCGCACACGTCGCGAAGGTGACGTTGGAGCCTGCGTT
 GCGGTAGTCGATCGGTGACGGAAGAGCTTCAGTGAAGACAGAAAAGAGCTTAAAGGATGCTTGCCGGGACATCTGCAA
 CTTCTTGGATATCAGTGGGCTGTCTTCGTAG

Fig. 80

PUTATIVE AMINO ACID SEQUENCE OF *Penicillium chrysogenum* Sph3 (Genbank No. Pc20g06130)

MSDSEKHVSKRTCLKSKRSRFILATVALIVIAAVVPSVVVTTLKKNSMGPKAKVFVPLYIYPAPEAWAPLENVISTHPN
VNFVTVINPGNGPGPDSLPGNYTREIPKLTAYDNVRVLGYVHTSYGKRNFSAVRKDIQTYADWPTNSSNPNAVLRGIFF
DETQQYDAQLTLYLQGLTDFAKNLKGLGPDQFVVHNPGLPDSRYLATADSTVFEAAYSTFQEREGAKLFNSIADSNR
TQLCAIVHSVPESVEGKHLRGLVKQVRKVAEEVYITHLSTDYYSFQAKWTEFVDLMAA

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Penicillium chrysogenum* sph3 (Genbank No. Pc20g06130)

ATGATTGCTGCCCAAGTCTGGGCTTTGAAGGTCGGTTGCTACTACGCCCTTTATAACATGCGACACTGCCCGCGGCTTTG
GCCGTGAGAAAGACGCCGACTGTCATCACCCTACCCCTCCAGTCTCGACTCCCTCTAGTACTCCTACTAGTCTGCTGGAG
TGAATTCACCCACGGTCGCTACTTCTACACACTCTTTCAGTCTCTCTTTGTCCTCTACCCCTGTTACGAGTTCGCCIAAG
ACGAGCACTACTTCTGTAACATCAACCTTCGTTACTTTACCTCGTCGGGTTCAAATCTCGTCCGACTGTTTCAGAGTCT
CGTAATCGTCACTGTCCCATCTGGTACCTCCAGCGTCCCTACCGAGAGTGGGACATTGCTCTGTTTCATCCAGCTCATCCG
CTATTCCGAGCAGCTGGTCTCTTCGTCAGTCTGTTCTTCTCGGCTGTTTCGACTGCACTGTTTCCACAAGTCTTCT
GTGACTACTCGTAGAATGTGCTGCCACAGCTATCTCAATCTCGGCTTCTCGCTCTGCCAGCTCGCTCAACGACGCTACTGT
TGCAGCTGACATTCTTGTCAATGCTAGAGATGCTGCCGCTGCAGGTTGCGCCAGCTCTGGGCTCAATGGATACGGTATCC
CATTTAGCACTCTGCTGTTTCCCTCTGCTGGTGTGCTCTTCCGACCTCAATGGCAGCGCTGGAGGAAACTTTGGTGGT
ATTGCTGTTGCCCTCTGAAGTCACTATGAGTATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
CCAGCTATATGCTTATCAGCTTGAATACGGTGTCCGCTATGGTCCAATATGATGTCTACCCGGGTCGCAAGTTCGGTACAT
CTGCTCTCGGTGGATGTTGTGATGACGCGATCGAGCAGCTTGTCTCATTCACTGATATTAGCGATTTCCCGACATCTGGC
TTAAAGCACTGGTGACAGGTGTGAGCACCAGTGGTCTGTGGCACTATCCGCGCACTATCAAGTAACACGACCTCTACCAAGCA
AATCGCTCTGTTTGGCCCCACTACAGGTTCACTACTGAGAGCGCTGCTGGTGTGATCAACAACCTTCGATGGCGCTCAGC
AGATGGCGCTTCTTCAATGGTTTCGACACTAATTGAGTGTACATCCAGCTACCTGCAGCAGCATGGATCACCTGGATC
ACCGCGGTCTGTACGCGCGGTACCGCGGTGTCAACCTGAACACCCAGATTGATGACATGTTCTCGAGACTGAAATTTA
CTCGCGCGGTGTGAAACTTCCGTATCCGCGCGCAAGATATGATCAATATTGCCAGTTGGACGGATGAGATCAACGCCA
AGATGCCCGCGCGCACTTCTTACTTTGTGAGGTCGGCCATAACGGTAATGGAACATCGAGAACTCTTCTGATACATCG
GATGCTGGCTGGGATCTTGGCGATCTGCTATTGAATATGACTCGGCTCCTGACACTGAGCGCGAATGGATGAAACCGCT
TGGTACTGGCACTGACCTGTGGCGCGCGCGCTTACTGCTTATGACTGGACTAATAGTTGCACTGGCATGGATGAACTCC
TGACCTGGTGGACACCCGAAAGCAACCTCAACAAGTTGCGTCAATGTTTCCGACACCTTCTCACAGAGGAGCAGAATAAT
GCTACCTACAGCATGTCTACAAGGAGATCAGTTTCAACCAAGCTTGGCTAAAAGCGCTCGGTATCGATAAGGCCACCAA
GTTCACTTCCACGGTATCATTCTCTGCGATTACCGGCTCTGCAATGGCATGCCCTTGGCGCTGGTGGGAGAACG
GCATCACTAACTGTGTGGGCGACAACACCGCGCTGCTCTTCTGAACAAGGAGAAAGACATGTGGCTCTCTTCCAACT
ATTGGCGCAACAATTTGACGGCATGCAGATCAACCTCGCTGGGCGACTCGCATCTACTATAACTGCGACACTCCTGC
CTGTACCGTTCGAGAATGGATCGGCACCTCTGCTGGTGGCGGTACCTTCGAGGACCTCTCTGCCATTGAGAAAGGCTGAGA
CCATGCGGCATCTGTTGCGGCTCTACCATGATGTTATATGTTCCACCAAGGCCAAGCTGCGCAACATTGATGTTACCGCA
ATTACCATCAACGGTGTGTCTGAGAGTACTCCATTATGCAAGCTTGGGTGGAGGTCCAGGTCAGGAGTTCTGCGGCT
GGCTGAATGGCGCATCATCACTCACACACAGGAGGTAGGATGAACCCCATCTAACATGTTACAACGCTCATTCACT
CGCTAACTCGTCATAGATGTCCGCTTCTTCTTGGCGGTTTCAACCGTGAGAAAGTGGGCTACTCTCTGAGCTACGCGA
CTAGCAACGAGAGATACCGCTGTCACTGTCTCTGCCACTGGCAATACCTGCAGTGAACCGATTCCGGTGAACCTTCCCA
GTTGGTCTACCAAGCACCAGGGCTTCCGCACTGAGCAGCTAGGTGCTGACCCACTGACCGTCTGGGTTAAGCTCACTGG
ATCCGCTGTCACTTCACTCTCTGCACTGCCATTTTCTTTAA

Fig. 81

PUTATIVE AMINO ACID SEQUENCE OF *Penicillium chrysogenum* Ega3 (Genbank No. Pc20g06110)

MGEPPSSKAGWWAWSTRKKVLIFGTVALVIALGVGLGVGLGISAKNGGDDDDNNNEGTGSNTTPTNTTVRWQPPVGA
 WKIILKSEDEPISTSVNAPIYDIDLFDNNKTFISNLQKMDRVICYFSAGSFENWRDDAGDFNDADKGGDLGWPGEKWL
 NVKSTNVRKIMQTRLDIAVEKGCDDGVDPDNIDGYDNANGLDLTKAEADYVNWLAQSHSRGLSIGLKNAGIIDSVIDN
 MQWCVNEQCAEFDECDTYAPFIEADKPVFHIEYPKGGNTNNDKSVSASQAKSACTANSSGNFSTVIKNMDDLNWVEYCP

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Penicillium chrysogenum* ega3 (Genbank No. Pc20g06110)

ATGGGTGAACCATCATCCAAGCGGGCTGGTGGGCTTGGTCGACCAAGGAAGAAGTTCTTATCTTCGGAACCGTCGCCCT
 TGTCACTATTGCTCTAGGTGTCCGACTAGGTGTCCGACTGGGATTAGCGCCAAGAATGGCGGAGACGACGATAACGATA
 ATAACAACGAGGGCACCAGTTCTAATACAACAACCAACCAACAACCGTGAGATGGCAGCCACCTGTTGGCGCCAAG
 TGGCAGATCATCCTGAAGTCCGAGGACGAACCGATATCCACCTCAGTGAACGCACCAATCTACGACATCGATCTTTTGA
 CAACAACAAGACCTTCTATTCAAATCTCCAGAAAATGGATCGCAAAGTGATCTGCTACTTCTCTGCCGGCTCGTTGAGA
 ACTGGCGGATGACGCCGGCGATTTCACGACGACGATAAGGGCGACGATCTCGACGGATGGCCCGGCGAGAAATGGTTG
 AACGTCAAAGTCCACAAACGTGGGCAAAATCATGCAGACGCGTCTCGATATTGCCGTAGAGAAGGGCTGCGACGGCGTGA
 CCCTGATAACATCGACGGGTACGATAACGCGAACGGGCTGGATCTCACTAAGGCTGAGGCTATCGACTACGTGAACCTGGC
 TTGCTGCCAGTCCCACAGCGTGGTCTCTCAATTGGACTGAAGAATGGCGCTGGCATTATCGACTCTGTCAATTGATAAC
 ATGCAGTGGTGTCAATGAGCAGTGCCTGAGTTGATGAGTGTGATACCTATGCGCCCTTCATCGAAGCGGACAAAGCC
 TGTCTTCCATATCGAGTACCCCAAGGGTGGTAATACGAACAATGACAAATCTGTGTCGGCCAGCCAGGCGAAATCCGCTT
 GTACGGCCAACAGCTCTGGCAACTTCTCAACTGTCATCAAAAACATGGACTTGGATAACTGGGTTGAATACTGCCCGTGA

Fig. 82

PUTATIVE AMINO ACID SEQUENCE OF *Penicillium chrysogenum* Agd3 (Genbank No. Pc20g06090)

MIAAPVWALKVGCYYAFITCDTAPGVWPEKPTVITYHPPVSTPSSTPTSSAGVSSTTVATSTHSFTSSLSSTPVTSSPS
 TSTTSVTSTFVFTTSSGSISSDSVSESIVTVPSGTSSVPTQSGTSLVSSSSSAIPSSLVSSSVSSSAVSTAPVSTSAS
 VTTPRMSSTAISISASPSATSLNHATVAADILVIARDAAGVASSGLNGYGIPFTLLVPSAGVALPDLNGTAGGNFGG
 IVVASEVSYEYGGDVGFQALTTDQWNQLYAYQLEYGVRMVQYDVYPGPKFGTSALGGCCDDGIEQLVSFTDISDFPTSG
 LKTGAGVSTSGLWHYPATISNTTSTKQIASFGPTTGFTTESAAGVINNFDRQMAFFIGFDTNWSATSSYLQHAWITWI
 TRGLYAGYRRVNLNTQIDDMFLETEIYSPAGENFRIRAQDMINIASWTDEINAKMPAGSSYFVEVGHNGNGNIENSSDTS
 DAGWDSGSAIEYDSPDTEPEWMKPLGTGDLWPAAPTAYDWTNTCTAMDELLTWWTTESNLNKFHVSHTFSHEEQNN
 ATYSVYKEISFNQAWLKAVGIDKATKFTSNGIIPPAITGLHNGDALRAWWENGITNCVGDNTRPALLNKENDMWPLFTT
 IAANNFDGMQINPRWATRIYNCOTPACTVAEWIATSAGAGTFQDLAIEKAETMRHLFGLYHDGYMFHQANLRNIDVTP
 ITINGVSEKYSIMQAWVEVQVQEFVRLAEWPIITLTHQEMSASFARFNDRKCGYLSYATSNQKITAVTVSATGNTCTE
 PIPVTFPVGPTSTQGFATEQLGADPLTVWVKLTGSPVFTLSTPIFL

Fig. 83

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Penicillium chrysogenum* agd3 (Genbank No. Pc20g06090)

ATGATTGCTGCCCAAGTCTGGGCTTTGAAAGGTGGTTGCTACTACGCCCTTTATAACATGCCGACACTGCCCGCGGGCTTTG
 GCCTGAGAAGACGCCGACTGTATCACCCTATCACCCTCCAGTCTCGACTCCTTCTAGTACTCCTACTAGTTCTGCTGGAG
 TGAGTTCCACGACGGTGGTACTTCTACACACTCTTTCACCTTCTCTTTGTCTCTACCCCTGTTACGAGTTCCGCTAGC
 ACGAGCACTACTTCTGTAACATCAACCTTCGTTACTTTTACCTCGTCGGGTTCAATCTCGTCCGACTCTGTTTCAGAGTC
 CGTAATCGTCACTGTCCCATCTGGTACCTCCAGCGTCCCTACCCAGAGTGGGACATTGTCTGTTTCATCCAGCTCATCGG
 CTATTCCGAGCAGCTGGTCTCTTCGTCAAGTCGTTTCTTCTCGGCTGTTTCGACTGCACCTGTTTCCACAAGTGGTCT
 GTGACTACTCCTAGAATGTCTGCCACAGCTATCTCAATCTCGGCTTCTCCCTCTGCCACCTCGCTCAACCACGCTACTGT
 TGCAGCTGACATTCTTGTATTGCTAGAGATGCTGCCGCTGCAGGTGTGGCCAGCTCTGGGCTCAATGGATACGGTATCC
 CATTACCCTCTGCTTGTTCCTCTGCTGGTGTGCTCTTCCCGACCTCAATGGCAGCGCTGGAGGAACTTTGGTGGT
 ATTGTGTTGCTCTGAAGTCAGCTATGAGTATGGTGGTACGTTGGCTTCCAGAGTCCCTGACCACGGATCAGTGGAA
 CCAGCTATATGCTTATCAGCTTGAATACGGTGTCCGCATGGTCCAATATGATGTCTACCCGGGTCCCAAGTTCCGATCAT
 CTGCTCTCGGTGGATGTTGTGATGACGGCATCGAGCAGCTTGTCTATTCACTGATATTAGCGATTTCGCCACATCTGGC
 TTAAGACTGGTGCAGGTGTCAACACAGTGGTCTGTGGCACTATCCCGGCACTATCAGTAACACCAGCTCTACCAAGCA
 AATCGCCTCGTTTGGCCCACTACAGGGTTCACTACTGAGAGCGCTGCTGGTGTGATCAACAACCTTCGATGGCCGTGAGC
 AGATGGCCTTCTTATTGGTTTCGACACTAATTGGAGTGTACATCCAGCTACCTGCAGCAGCATGGATCACCTGGATC
 ACCCGCGGTCTGTACGCCGGGTACGCCGCTGTCAACCTGAACACCCAGATTGATGACATGTTCTCGAGACTGAAATTTA
 CTGCGCCGCTGGTGAACACTTCGCTATCCGCGCCAGGATATGATCAATATTGCCAGTTGGACGGATGAGATCAACGCCA
 AGATGCCCGCGGGCAGTTCTTACTTTGTGAGGTGCGGCCATAACGGTAATGGAAACATCGAGAAGTCTTCTGATACATCG
 GATGCTGGCTGGGATTCTTGGGATCTGCTATTGAATATGACTCGCCTCTGACACTGAGCCCGAATGGATGAACCGCT
 TGGTACTGGCACTGACCTGTGGCCCGCCGCCCTACTGCTTATGACTGGACTAATACTTGCAGTGGCATGGAATGAACTCC
 TGACCTGGTGGACACCGAAAGCAACCTCAACAAGTTCGGTCATGTTTCCACACCTTCTCACACGAGGAGCAGAATAAT
 GCTACCTACAGCGATGTCTACAAGGAGATCAGTTTCAACCAGGCTTGGCTAAAAAGCCGTGCTATCGATAAGGCCACCAA
 GTTCACTTCCAACGGTATCATTCTCTGCTGCTTACCGGTCTGCACAATGGCGATGCCCTTCGCGCTGCTGGGAGAACG
 GCATCACTAACTGTGTGGGCGACAACACCCGCCCTGCTCTTCTGAACAAGGAGAATGACATGTGGCTCTCTTCACAACT
 ATTGCCGCCAACAATTTCCGACGGCATGCAGATCAACCTCGCTGGGCCACTCGCATCTACTATAACTGCGACACTCCTGC
 CTGTACCGTTGCAGAATGGATCGCCACCTCTGCTGGTGGCGGTACCTTCCAGGACCTCCTCGCCATTGAGAAGGCTGAGA
 CCATGCGCCATCTGTTCCGCCCTTACCATGATGGTTATATGTTCCACGAGGCCAACCTGCACAACATTGATGTTACCCCA
 ATTACCATCAACGGTGTGCTGTGAGAAGTACTCCATTATGCAAGCTTGGGTGGAGGTCCAGGTCCAGGAGTTGCTCCGCT
 GGCTGAATGGCCCATCATCACACTCACACACGAGGAGGTAAGGATGAACCCCATCTAACATGTTACAACGCCCTCATTCACT
 CGCTAACTCGTCATAGATGTCCGCTTCTTCTTGGCCGTTTCAACCGTGACAAGTGGGGTACTCTCTGAGCTACGCCA
 CTAGCAACCAGAAGATCACCGCTGTCACTGTCTCTGCCACTGGCAATACCTGCACTGAACCCATTCCGGTGACCTTCCCA
 GTTGGTCTACAGCACCCAGGGCTTCGCCACTGAGCAGCTAGGTGCTGACCCACTGACCGTCTGGGTTAAGCTCACTGG
 ATCCCTGTCACTTCACTCTCTCCACTCCCATTTTCTTTAA

Fig. 84

PUTATIVE AMINO ACID SEQUENCE OF *Penicillium chrysogenum* Gtb3 (Genbank No. Pc20g06080)

MNGVESLPSRPHLOWDAMKEHWWQFVFIGVLLFTVTTGSLSIISGVKSLIKYKSRPLPQNVPSAVSKRLAKLANREL
 NLIDRRPCKGKPVSFQVYLGSEFNPTASQERLLGEWDILVDPFQTGYAKAISRHRSQVIGRVDFGKFLPPKASALTV
 TEKIEELLAIGFNDTAFSGVLLANWEDVLRPTARRKLLLETISLGLAVYLESEPPHFLKDRKAVQSDAVAGLVIRNASIM
 PQGEKRDYFQLAELQATIKAFVSESCMRDFVVMWETVDDNVTVSNAIVRRSIQWCGFYSAITWIGPEAALRDADLNVTT
 LEPLPAFGWLKEAEIMKAHDIWRANLNLPSPTKAGWDILKPIFPAIDALLDSSEYDPKAPDSPTARLRDPPEWVAQVK
 SQGSPLSISMSGMAYNSLGCFLGSDSNPLAFAEIVQSQRRLKSLNLLHPVPTSKIQSIGLLLRQFYDSLDFSGDDEHLA
 NTIKDLANWASDILLHVNLCLDSGLRKSSDLRFWAVFOMEHDGIEIYVSKNAQGLAGTVLHTFLSAKGFRHVCFEAEAT
 FATWSQNVSHDTGLPRRLIQDIDALSPEERLLLLQHLSTGSHSELKVICTYIRKQLVDAPSFAQLKALNTVGYLEKST
 SPEELIRSRINWYMDQGCNPSLEVCLGLFNQADSFLFDVLRYYRREDDLAITSGLCALLQGGSDAYVDMMALALFCAA
 RRGAFDEIYAEVTDNRNPLFNHNTDQAAFAESFALGSRCEAYFDVAPSVFGKLLSDRFRAYYGDHQPNNVNGAPQLATS
 YAGAQIDVNPDEQPKTMPGYQRTFLSVFAIPALIDITLLTMVGRGLYLSAAMSHDEQDSATMALMISLLSGAIGTWIA
 CGGPYYLISMAFAANMFVLRILAGIAFTVAGGLIGFVAISGVRGPAGIIFYLYLIALTIFYSTFASLASFSYPGSTF
 LSGRKSIIIMCIPILFLSPIITAWTGHSADVLTVIYIFIGVLLLSLRSVTSKWVTWYQSVRRTDDEIRKWIYISAHGKND
 EKVYFANMSDPAALKLAREALSKEVLAETTRGIFSKASKDKMVVELARDWESTNFLDWCYADVPRPIPFSSGWNIOQTK
 VALDTRLNSQKGLHLHNAFVHWRQSSKEMGCGVLYFVIALLDKWAQLLSGDRMLAFLPAENDANRMVGFALAYLIGAV
 LIDTKAQELHDALGSKPPLSVRSKDIRLVQKQEVQLRRKYVRVLFRLWHVWSLALATALIWTFGSMVEGMTIFFSY
 VLAYTGLIWIYQYTKIFTOPHALKPLIIGICIGLPVGIARVSLPDKYSQIIGLGAATWTVAILSMWNAKMGMPPNKVDSP
 VELGRTHAFTTPWSDPEWSQQLQTFEESYLLPSDSRFRNLNPGVHPGVEIKSVMLSRREELRIEEAFPCSKNIVNTAI
 TSWEKGDIVIELVSPGSLGPGIRALSCSTGNQLKLAIAVGGLDERLDISANCOVIAETLLHAATELMMGVPHEYASLAG
 SIVSGGVTHMARQLREEANTTTVVRWAKKELLRQLCLGFEPDLHWDKLPTEVRDVLKRCLEGEQCSLSNSQREWLQONL
 CTFTDIDLNVHVARCNLGAATAVSVLDYAHWGTGETALPKEPETSKEYISYIPRKLPMALSLVRSPASYIYHKLGLSVKFF
 VVALVADPEFQREFNHVTQTLPTVVRVPIVFLNVMVYYSKIVQNLGLSFFVFHGRKNVKQLWEETKGMTIHIKKNRVIV
 QSLEGTFTTFRHHEIDGGFKVYHYSGEHNTEPKEVKSLEYVSTYSSEMLLVKQEFKDGKVVNEYHYDYQAPTCKGFKLT
 KSSNRIPLRRCVSGANHLQSYQYNRKGLIESGSYMKDGNLIRFKYHYRKNPRFGDELLRAEFVLSHISCTVSWCAPRR
 HPEKVERWIPHSKYTEASFVQGADVYESRWLYDHKFHPTIFTTNGQKMOTPPMIEHDYLGVLAKPKYTSFVHDNPFVYC
 DSLQSNILTRALGLTKKRFVYSTSQARSLMNAWKADRVDFDAIIVRWMDRILRRDKVLSPYWRSRDWGNLTSAKKYMDL
 RADAIMASADLDDNVSSWTPLAVKLTDLLSFGSGGDSVVNTRSKNFGTDTKTLHVMAADNGTWPNEGGSVACRRDMIN
 SLSTIKWHMIGESANDFGVPKHQTEQNIQSLKIIPLWGMDFLTPHGLFHNKLD AEVDNVTSAEFDIKMNFIPILTALV
 KGARAVHLKSDIHQATRALVNLNTYFQESRHWTQVWNSEMYKQSWRDLWLTQEMPNTIPSSQWFDTELPTLGSLDIALE
 LWYRYLFISSIPVEKIPSTFQASHHSVSASYGVVCKIKRNLCTLQIWDHAIWRETNLCLSSALCKLSPFVRNALLGLMR
 ITSVLTLHHADIILPCADFFNPGWEVEIGTCQGTIEHRNTFRRKIDPVVNGITDMQKFSVPKEIKSERPTVTMLSHVWYA
 KDIKTALLAADIIINQWKFEYHLDIYGAIDKAPTYSTECQEIASKGLRGRVTLCGTADPMKVLENTWFLNSSLSEGL
 PLALGEAALTGAPVCTDVGASLRVLSDPDDFSRFSAVVAPNDALALAKAQIGMLAMLGEWSKHSDDASPAPVLTSSPTP
 EEVAAITRRMYEKSEHRRKLGMTRKIVQKSFSGDRYLREHEQMLWIGKSAKMMASRAAGDPIEPADVAAALETGYDEEI
 IAIIPRGVVHSSRAQSGISTIYSSASQIPGRGGLHRPASDISAMSMMSNVSTDTESFGRLPVFAPRPTVLPNGGSPGN
 MSPMWTSHRLSALNAGPHSRPQSYSRSVSTAGREQLRGLQREDFLPYRNSDISVANRDDFLRAGGLDPSQAS

Fig. 85

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Penicillium chrysogenum* gtb3 (Genbank No. F020g06080)

ATGAATGGAGTAGAATCACTCCCATCGAGGCGACATCCTGTTGGTTGGGATGCCATGAAAGAACATTGGTGGCAATTTGT
 ATGTTGACCTGGCTCTCTTTACAACTTGACGTTTGGCACTCTCGTCCCAACGCGAGAGCAGGAAGATTTCGTGACTATT
 TTCCCTAGGTATTCAATGGAGGTGTGCTATTACAGTGCAGCACTGGGTCTTTGTCAATCATATATTCTGGTGTAAAAAGT
 CTTATCAAGTACTATAAGGTATGATATAGCGGTCACCGACAGCTGTTCTCTCTAGTCTGAATATTAATCCAGTCTAT
 TTTTAGTCGAGACCGCTGCCAGATAATGTACCTCGGCTGTGTCCAAACGCTGTGGCCAAAGTATGCCAACCGAGAGCTCAA
 CTTGATTGACAGGCGTCCATGCCAAGGAAAGCGGCTGAGCTTCGGAGTCTATCTG66AAGTTTGGAAACCGCAGGCTG
 CCTCTCAAGAAAGACTTTTCCAAAGATGGGATATCTTGGTCTGGATCCCTTCCAGACAAGTCTGGCCAAAGCTATTTCG
 AGACGACGCGCGAGCGAAATAGGACGTGTGATTTTGGGAAATTCCTTCCGCAAGGCAATCGGCTGTGACCGTGAT
 CGAAAGAGTCGAGGAATTGCTTGCATTTGGAATTAACGATACCGGCTTTTCCGCTGTCTCTCGCGAATTGGGAAGATG
 TGCTCGGCTCTACCGCTCGAAGAAAGCTTCTCGAGACCATCAGCAGGCTCGGCTGGCAGTATATCTCGAGTCTGAGCGCT
 CCTGATTTCTTGAAGGATGAAAGGCGCTGCGAGGCGATGCGCTGGCGGCTTTGGTCTATTGAAACGCTAGCATCATGCC
 TCAAGGCGAAAGCGGATTTATTTCCAACTGGCGCACTGCAAGCAACAATCAAGGCTTTGTTCTGAGTCTTGATGA
 GAGCTTTGTTGTAATGGCTGGGAAACCGTCGACGACAAATGTCACCTGTTCCCAATGCCATAGTCCGCGATCTATTGAG
 TGGTGGGCTTTTACAGCGCAATTACCTGGATCGGCTTGAAGCTGCTCTCGCGATCGGATCTTAAATGTCACGACTCT
 CGAAGCTCTCCCGGCTTTGGTTGGCTGAAGGAAGCAGAAATTAAGAGGCCACGACATCTGGCTGGCAACCTGAACA
 TATTGCTTCCGCGGATACCAAGGCTGGCTGGGACATTCTCAAGCGGATTTCCCTGGGATGATGCGCTAGTGGATTGG
 TCGAATAACGACCGCCAAAGGCGCCGATAGCCCAACTGCTCGACTGCGTGTCTCCAGATAGGCTCGCAGAGTCAAAGT
 ACAGGCGAGCGCTCTCTGATCTCCATGTCAGGATGGCATACAATTCGCTTGGTGGCTCCCTCTCGGCTCTGACTCGA
 ACCCACTGGCTTTGCGAGGATTTCCAATCTCAACGAGCGCTTAAGCTCTTAATCTTCTCATCCGCTCCCGACATCC
 AAAATACAAAGCATTTGGACTCCTTCTACGTCAATTCTATGACTCTGGATTTCTCGGAGATGACGAGCATTTGGCCAA
 CACAATCAAGGATTTGGCAATTTGGGATCGGACGATTTGTTGCTGTAATCTTTGCTCGACTGCTGGTCTCGCGAAGA
 GCTCTGATCTCGGCTTTTGGGCGGTTTTGATATGGAACATGATGGTATGAGATCTATGATCCAAAGATGCAACAAGGC
 CTGGCTGGAGCTGTTCTGACAGCTTCTCTCAGCAAGGCGGTTTCCAGCGCATGTTTGGTTGAGGCGAGAGGCAAGCTT
 CGGACCTGGTCTCAGAAATGTGTCCACGATAGTGGCTTACCTCGTGGACTGATTAAGATATGATGCTCTCGAGCGCTG
 AAGAAGCTCTGCTTCTCTTGGAGCAGCTCTCTGACTGGTTGACATAGCGAGCTATCCAAAGGTCATCTGACATACAT
 GGGCAAGCAACTGGTGGATGCCCGCTTTTGGCTGAGTTGAAAGCGCTGAACAGGTTGGGTATCTTGAGAAGTCCACCTC
 TCGTGAGGAACTGATCAGGCTCGTATCAACTGGTATATGATCAAGGATGCAACTACCCATCTCTCGAAGTCTGTCTTG
 GTCTTTTCAATCAGGCGCGACAGGCTACTGTTGATGTTTTGAGGTATCGCGGCGAGGATGACCTTGGCGGCTTACTAGC
 GGTCTGTGCGGCTTCTCAAGGCGGCTCTGTTGATGATATGTGACATGATGGCTCTTGGGCTTTTCTGGCTGCAAG
 ACGGGAGGCTTCTGATGAGATTACGCGAGGTTACGGATCGGAATCCCTTTTTTAAACAACATACCGATCAGGCTGCCG
 CCTTCCGAGAGTGATTTGGCCTGGGATCTCGATGTAGGCTTACTTGGATGTGGCTCGGAGTGTTTTGGGAAAGTTGCTA
 TCGGACCGATTGAGAGCTATTATGAGAGCCATCAGCGCGCGAAGTGGGTGAACGAGGCTCGGAGCTTGTACATCTA
 CGCGGAGCTCAGATGATGTCAAGCTGATGAACAGCTTAAGACTATGGCTGGATACCAAGGATTCACATCTTGAAGCG
 TCTTCCGCAATTCGAGCTGTGATGATATTATCTTGGCTTACGATGTTGGCGTGCGGCTTATCTCTCTGCTGCCATGTCT
 CATGATGACAGGACAGTGCACAAATGCGCTGATGATCTCCCTGCTGCTTTCCGCTGCAATTTGGTACCTGGATTGATG
 TGGCGGCTCTTACTACCTCATTTGATGGGCTTTGGCGAGCGAACAATGTTGCTTCTCATTTGCTCTAATGCAAGTATTG
 CTTTCACTGTGGCGGCTGGCTGATGCGCTTTGTTGCCATTTGAGGTGTTGAGGCGCTCGGCTGGTATCATCTTCTAC
 CTCTACCTGATCGCTCTGACAATCTACTTCTCGACTTTCCGCTCGCTTCCAGGCTTCAGTTATCGCGGCTCGAGCTTCTT
 GTGAGGTGCTAAGTCAATGATTATGTGCAATTCGATCCTCTCTTGTGCGGATCATCACGCGCTGGAATGGCGAGGCT
 CGGCTGTCTATCTCAGGCTTATCTATATCTTATTGGTGTGCTCTTCTCTCCCTTCGTTGCGTTACCTCCAAGTGGGT
 ACTTGGTACCAATCGGTGCGAGCAGTATGATACCGAGATCGGCAAGTGGTATATCTCTGCCACGGAAGAAATGACGA
 GAAAGTGTTTGGGAACATGAGTGTGCGGCTGGCTCAAGCTGGCGAGAGAAAGCGCTATCGAAGGAAGTCTTGGCTGAAA
 CGACGCGAGGATTTTTCAAAGGCTATTAAGACAAATGGTCTTGAAGTTGCCCGGAGCTGGAGTCTACCAATTTTC
 CTCTCGACTGGTACTGTCGCTATGAGATGTTCCGAGGCGGATTCGCTTTAGTTCTGGTTGGAATATCCAAACCAAGGT
 CGCACTTGACACCTACGCACTCGCAGAAAGGCTTCACTGCGACAATGATTCGTTCACTGGCGTCACTCAAGCAAGG
 AGATGGAGTGGTGTCTCTACTTTGATGCGCTTCTGACAAATGGCGCAAGCTGTTGAGTGGTGTATGATGCTGCT
 CCTTTTCTCTCGCGAAGATGATGCTAATCGAATGGCGCTTGGCTTGGCTTGGCTACTATTGATGCGAGCGGCTCT
 CATTTGATACCAAGCGGAGGAGCTGATGCTGCTTGGCGCAAGCTGCTCTTTCCGTGAGATGCGGAAAGACATTC

Fig. 86

ATACGCTACAGAAACAGGAGGTACAACTCCGGCGCAAGTATACCTGGCGTGTCTTTTCAGATTCTCTTGTGGCATGTCT
 TGGAGCACTTGGCGTCGGTACTCCCTCATTTTGGACCTTCCAGTATATGTCAGAAAGTATGCAATTTCTTCTCTCACTACGT
 TCTCGCCATACACAGCTTGATCTGTGGTACCAATACCAAGAGATCTTACGGGTCTCATGCACTGAAGCGTCTCATGATTT
 GTATTGTGATCGGATTCGGACGTCGTTTGGCGTCAGAGTCTCTCGGCAAGTAAAGCAATCCGAGATCATGTGGACTCT
 GGGCGTGGCCACTTG6ACAGCTTGGCATCTG6ATGTG6AATGG6AATGG6TACG6AACAAATGG6ATCCAGCGGT
 GGAAGTCTGGCGGACGTTTCGATGGTTTACGAGCGCTTGGTGG6ATCGCTGAAATGGTCCGAGCAAGAGCTTCAGACTTCT
 TCGAAGAGATATTCGCTGCTCTCTCGCATATCCGCAATTCAGGCTTCTCTGATGAGTCTGCTGATATCAGGCGAAATGTGAC
 GTTATCTGCTGAACATCTGCTTCACTGTCGCAACAGATATATGATGGTGTCTCATGATACGCACTGCTGG6AGGGTCT
 AATCGTCTCGGTTGG6TAATCACTACACAAATGGCTCG6ACAGCTTCGG6AGAGG6CAACCAAGCACTACGGTGTATACGCTGG6
 TATAGGAAG6AAGCTTGTTCGGACGTTTGTCTGTGTTTCGAGAGCGCTCTCCATTGG6GCAAGCTTGGCTCAAGCAATCTTCG
 GATGTGCTGTATAACCGTTGTGTGGGTAGCAATCAGCGCTCTCCATATAGCAAGCGGAAATGGCTCCAGCAAAATCTTCG
 CAGATTCGATACCGATCAGCTCAATGTCCGATGTCCGCGTGGCAAGCTTGG6AGCTTGG6AGCTGGCATGCAATTAGCGTCTGTATT
 ATGCTCATCTGG6GAACTGG6AAGAACTGCTCTTCCCAAGAGGCGAGCACTTGAAGTAAATCTTCCATCAAGCTTCGGAAG
 CTCCCGATGGCATTTCTGCTAGTCCGATCACCAGCTAGCTACATTTACCACAAGCTGG6ATCATGGTCAAGTTCTCGT
 GATGGTTTGTGTCGAGATACCGGAATTCGAGAGGAGTTCATACGCTCAGCTACGAGCGCTTCG6AGGTTCTGCGTGGT
 CATCGTATTCTGCTATTGAAATTTAGGTTGG6TATGTTTGAAGATCTTCAAAATTTGG6TGTGATCTTTGTCTTGGAT
 GGCGGTAAAAAGCTCAAAAGCTGTGG6AAGAGACCAAGGGCATGCAATCCATATCAAGAAGAACGGGTCAATTGTCCA
 GAGTCTGG6AGGGCACTTTACCAATATCAGACAGCAAGATTTAGTGGTGGTTCAGAGTCTACCAACTCATCTGTGGAGC
 ATATACAGGCGCAACGAAGAATCAAGTCTTGAAGTACGTCAGCACTATTAGG6ATGAGATTTGCTCTG6TGAAGCA
 GAGTTCAAG6AGGCGAAAGTGTGACAGCAATCCGCTACGACTACGAGCCGCGCATATGAAG6GTTTCAAATCTTCCAA
 ATCATCAAGCGGATTTGCACTGG6AGCAAGTCCGCTTCAGGG6CAACCACTTCCAAAGCGTGGCATCAAGCGGAGGAG
 GTCTTATGAATCAGGTTCTGATAGAAG6ATGGCAAGTATCGTTTCAAGTAAAGCTTCG6AAGAACCGCGTTCT
 GGCGATGAGTGTCTCGAGCGGAGTGTCTTTATCCCAATACAGCTGCACTGTGTCTGGTGG6CGCTCCG6GAGGCA
 TCCG6AGGAGTGTG6AGCGTGAATTCGACTCCCAAGTCAAGCAAGCGGCACTTTTGG6AGGCGCGAGCTTCAGAA
 GCTGTTGGCTGTAGATCAGAAATTCATCCGACATCTTCAACGAGCATTTGG6GAGAGAGTGCAGACTCCGCGATCT
 ATAGAACAGGATATCTGG6GTGCTG6GCAAGCGGAGTATCCGACTTGTGATGATACACCGCTTTGTCTCATGCGCA
 CAGTGCAGTCAAACTCTTGTACCG6GCACTGG6GCTTACGAAAGAGCGGCTTTGTGTGATCACTTCCGAGCGCTGG
 CTTGTGATGG6AGGCGTGG6AAGGATCGTTTGACTTGGATGCAATTATCGTTGGCTGGATGG6AGCCGATATTCTGGCG
 CGGATAGGAGTTCTTCCGCTTCTGCG6GACCGGTCAGTGG6GCAATCTTCATATCGCAAGGATATATGATCTCGC
 CAGATTCG6ATCATGG6CACTGG6AGTCGAGATCGAG6GACAGCTTTCCAGCTGG6ACCGGCTCGCTGTGAAGCTACCGGAT
 TGCTCAGGCTTTGGTTCTGGTGG6TATTCGTTGTTAAGCGCGCTTCCAAAAGCTTGG6CACTGATACG6AAGAGCACTT
 CATGTTATGGCGG6GAGAGGATGCTGG6CTTAATCAAGGCTGGTGGTGTCTGCTGGCTGTG6AGGAGATATGATCAACTCT
 CTGTGAGCAGCATCAAGTGG6CACTGTTTGG6GATCGAGCAAGCAATTTTGGTGTTCGCAAGCATCAAGCGCAAGCA
 TCCGAGTCTCAGAGATCATCCGCTTTGG6GATG6ACTCTGCTCATGCAACTCAGGTTTGTGTTCAACAGCTAGAT
 GCGAGCTGG6CAAGCTTACATCCGCGAGCGAGTTCGACATCAGAGTGAATCTTCGATATGACGACCTTTGGTTAT
 GGGTGG6GCTGGAGTACATCTCTCAAGTGTGATATCCAGACAGCGACTCGGGGCTTGTAGACTGAGACACTTCTCG
 AGGATCGCGGCTCATCGACTCAGGTTGG6AAGCACTAAATGGTCAAGCAAGCTCGG6GAGTTTGTGGCTGG6AGCGAG
 ATGG6AAGCAACCGTCTGAGTATCCGAGTGGTTCGAGATGAGCTTGTGAGGTTCTGTCGACTTGG6GATCGGCTCAGAGCT
 CTGGTACCGCTATCTCTCATCTCTCAATCCGGGTTCGTGAAGAGTTCTTCAAGGTTTCCAAAGCTCAGATCAGATCAGG
 TCAAGTGGCTTTACG6GTGTGTATGCAAGATCAAGGCGCAACTGTACCTTGCAGATTGG6GACAGGCACTGCTGTGG6CT
 GAAACAGATCTGTGTGTGATGTGCTGG6CTTGG6AGGCTTGG6GATTTGTG6AAGAGCGACTGCTGGATTTGATGG6AAT
 AACCTCG6TCTTGAAGCTTTCACACGCGAGACATCATCCTTGGCTTGGCAGACTTCTTCAACCGGCTTGG6GAGCTGAGA
 TTTGGATCTGCG6AGG6AGCATTTGAGCAGCG6AAGCACTTTCCG6GCAAGAGTCGATCTGTGCTCAGAGTATCAGCGAT
 ATGCAAGATTTTCTCGACTCAAGGAATCAAACTCAGGCGGCGAGTGTAGCAATTTATCCGAGCTTTGGTGTGCGAA
 G6ACATCAAATG6CCCTTCTGCTGCG6ATTCATCATCAAGCAAGTGG6AAGTTCAGAGGATACCACTGG6ACATGTGAG
 GTGGCATTGATAGG6GCGGCACTTACTCTACCGGATGTCAAGGCTCAGAGTCAAGGGTCTTCTGG6GACAGTCAAG
 CTGTGTGG6AGTGG6GCGG6GATGAAG6GCTGG6AAGACAGTGGCTTTCTGTAAGCTCATCTGCTGCTGAGGCTGTGCG

Fig. 87

TCTCGCCCTAGGAGAGGGCTGCTCTGACCGGAGCCCCGTCGTCGTGCACGGACGTCGGTGCTTCCCTCCGAGTCTCTCAGCG
ACCCAGATGACTTCTCCGCTTCAGTGCTGTCGTGGCACCGAATGACGCCCTCGCCCTAGCAAAGGCCCAAAATTGGCATG
CTTGCCATGCTCGCGGAATGGAGCAAAACACAGCGACGACGCATCGCCCGCGCCAGTCTGACCTCTCCCCACACCGGA
GGAAGTAGCAGCCATAACCCGCGCATGTACGAGAAAGAGCGAGACCGCCGCAAACTCGGCATTGATGACCCGCAAAATTG
TCCAGAAGTCTTTCAGCGGTGACCGGTACCTCCGCGAGCACGAGCAGATGTTGTGGATTGGCAAGTCCGCCAAGATGATG
GCCAGCGCGCGAGCTGGCGACCCAAATCGAGCCTGCCGAGCTGGCAGCGCCATCGAGACTGGCGTCGATGAAGAGATCAT
CGGCATCCGCGCGGCGTGGTAGACTCTGGCGCTCATCTGCCAGTCCGGTATCTCGACAATCTACAGTTCTGCGTCCC
AGATTCTGTGTCGCGCGGCGCTCCACCCTCCCGCATCTGATATTTACGCTATGAGCATGAGCATGAGCAATGTCTCTACG
GATACCGAGTCTTCTCGTGCTCTGCCGCTTTTGCGCAAAGCCATACGCTGTTGCCCAATGGCGGCTCCCGGGGAATAT
GTACCCCATGTGAGACTCCAAACCATCGGTTGTTCGCGCGTAAATGCCGGTCTCACTCTCGCCCTCAGTGCTACTCGCGCT
CGCTCTCAACTGCTGGTTCGGGAACAGCTGCGTGCGTTGCAACGTGAAGACTTCTCCGATCGAAACTCGGATATTAGT
GTGCGTAACAGAGACGACTTCTTCGGGCTGGCGGACTTGATCTAGTCAGGCGTCTTGA

Fig. 83

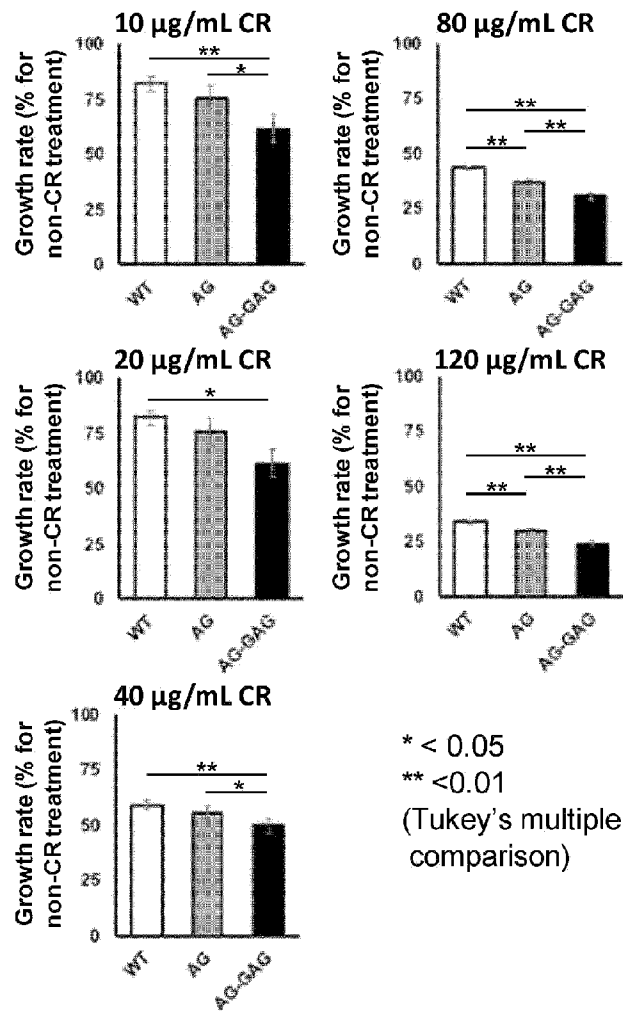


Fig. 89

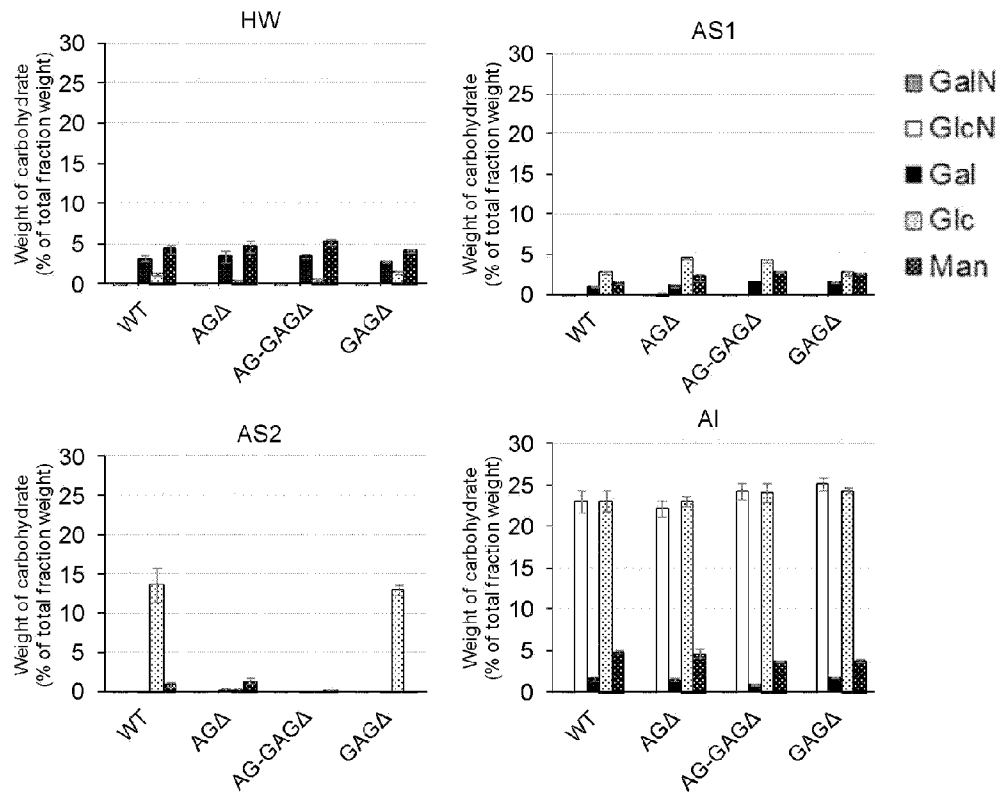


Fig. 90

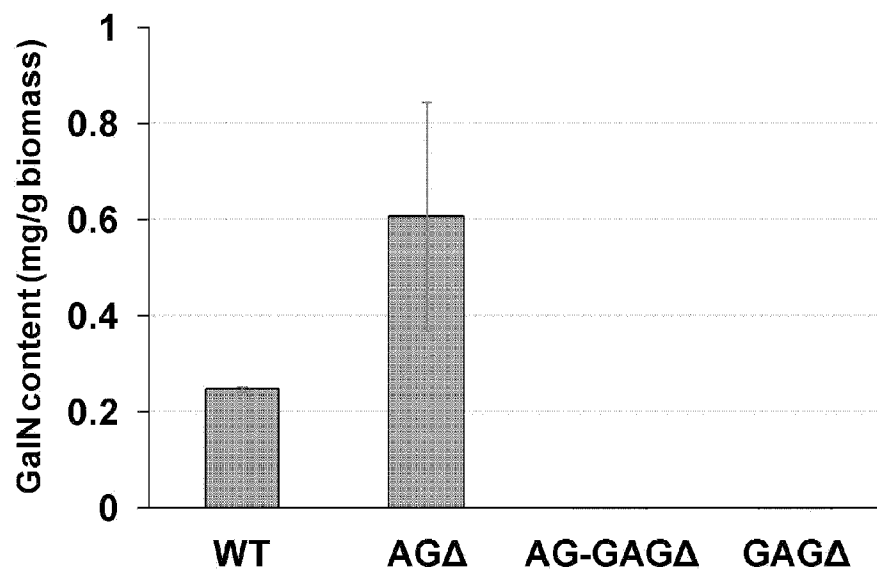
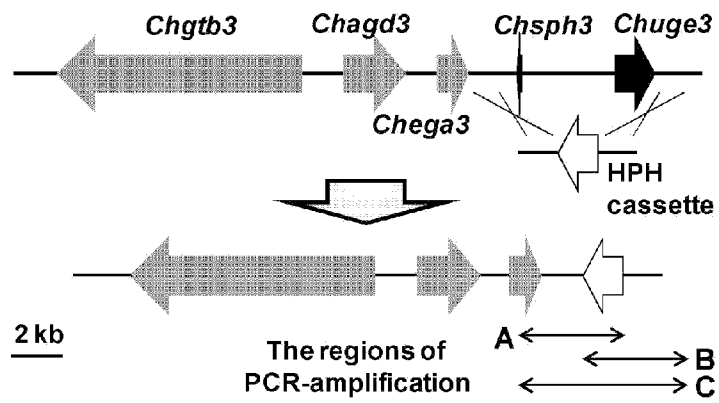


Fig. 91

(A)



(B)

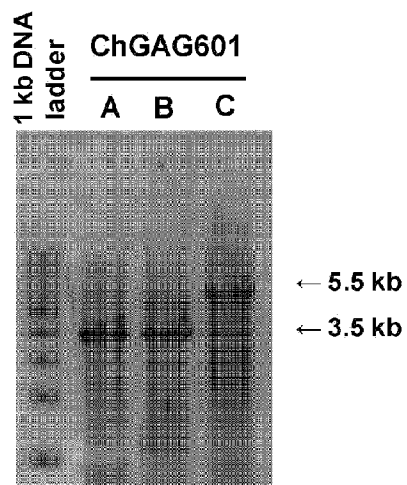
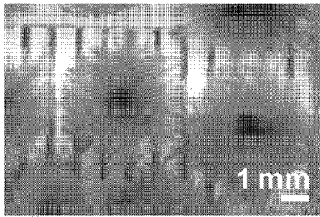
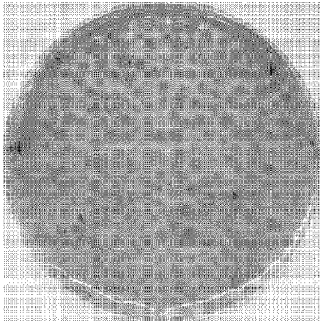


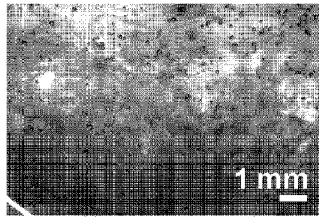
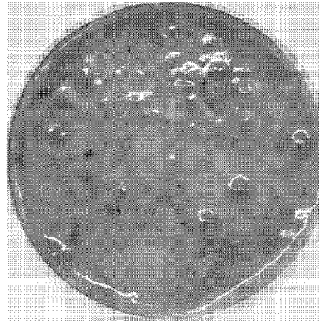
Fig. 92

(A)



C. heterostrophus
Wild-type

(B)



C. heterostrophus
GAG601

Fig. 93

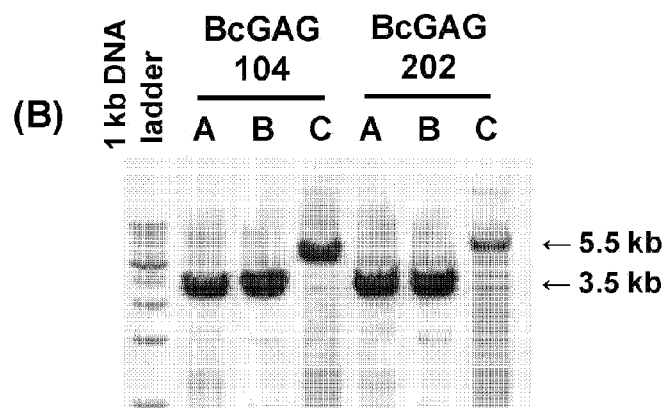
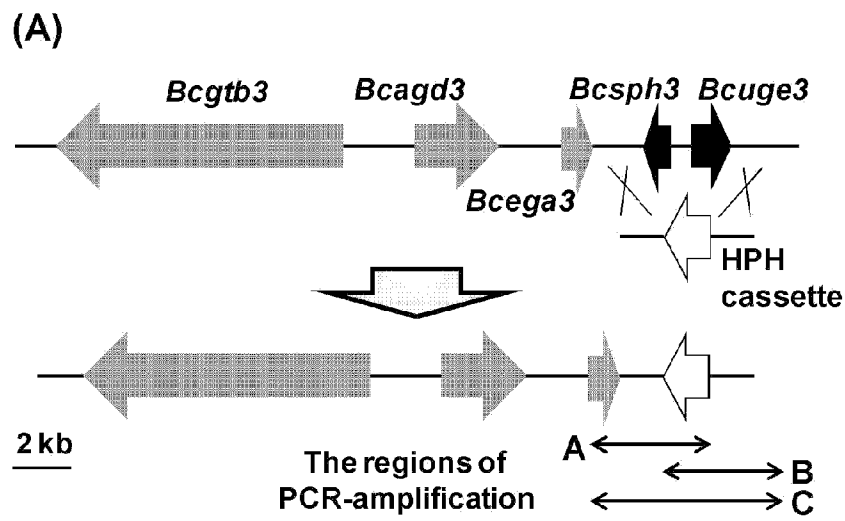
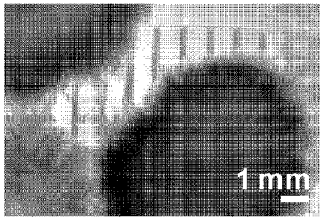
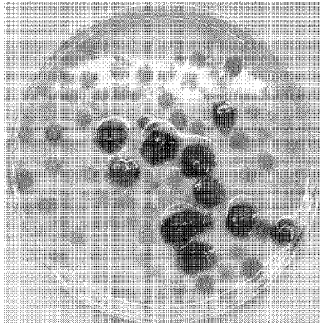


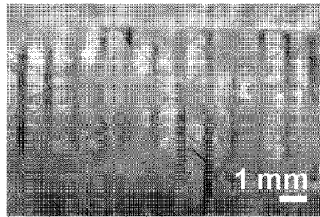
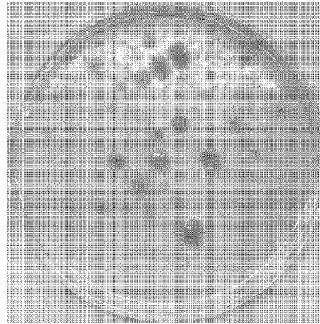
Fig. 94

(A)



B. fuckeliana
Wild-type

(B)



B. fuckeliana
GAG Δ 104

Fig. 95

PUTATIVE AMINO ACID SEQUENCE OF *Bipolaris maydis* uge3 (Gene ID: COCHEDRAFT_1185586)
 MSACSSQFSVSPSATPEMVSTPATQSSVLFDDDDVAADPLDIEGVGSSFIMVVGGLGYIGSHTTLELLKEGYNNVLVIDDLS
 NSYQNVLDRLVKFLAEFCREQRRRLPALHFQQLDYRSPQMKIVLANYSYSVSSKPVSAARRFPYTNLQRTDSGIEMET
 DDRQEPVIERRSRITGVIFHAAYKSVEESIRTPLRYSNNVCGLVDFLGLIEQFGIKNFVFSSSATVYGEQANGGVPLRE
 ELCVHHPETFYDGEGRERQVLPVGLGLTSPYGRSKFMCESILADLAVADPTWSITALRYFNPVGCHEGILGEDPRQKPS
 NLIPVIAVTMTGARPVLDIFGTDWNTPDGTAVRDFIHVVDLARGHIAALAASAAGRTKAPFRTYNLGTGNHGTVREVLHS
 LEEVSQRKIPAREVGRRAQDVGFCAEVQRAETELQWKAERNLRDCAQDVWNFTKGRCPDVQEVSDAQG

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Bipolaris maydis* uge3 (Gene ID: COCHEDRAFT_1185586)
 ATGTCTGCATGCTCCTCACAGTTCTCGGTTGTCGCCATCCGCGACACAGAGATGGTCAGCACACACGCGACACAAAAGCTC
 TGTGCTTTTCGACGACGAGTACGAGCGGATCCATTGGACATTGAGGGCGTCGGCTCTTCCTTCATCATGGTTGTTGGCG
 GATTGGGTACATTGGCTCCACACACAACACTGGAGCTGCTCAAAGAAAGGATACAATGTCCTTGTAATCGACGACCTCAGC
 AACTCTTACCAAAATGTCCTGGACAGGGTCAAATTCCTTGCCGAGGAGTTCTGCAGGGAACAAGGACGACGACTGCTGC
 ACTTCAGTTTCAGCAATTGGATTATCGAAATCCGACAGATGAAGATCGTACTGGCCAATTACTCTTCGTATTCGCTCAGCA
 GCAAACAGTATCAGCATTAGCCCGTCGCTTCCCGTATACGAATCTGCAGCGAACAGATTCCGGCATCGAAATGGAGACG
 GATGATCGCCAGGAGCGGTGATCGAGCGTCGATCCGGGATAACGGGTGTTATCCACTTTGCCCGCTACAAATCTGTGGA
 AGAAAGCATTGCGACGCCACTGAGGTACTACAGCAACAACGTTTGGGGTCTAGTTGATTTCTGGGCTTGATCGAGCAAT
 TCGGCATCAAGAACTTTGCTTCTCGTCTCGGCTACAGTATATGGTGAGGGTGCCAATTGTGGTGTGCTCTACGGGAG
 GAGCTATGCGTGCATCATCCAGAGACTTTTGTGCGAGGTGAGGGACGGAGCGTCAGGTGTTACCGGGTGTCTTGGGTCT
 CACTTCGCTTACGGACGTTCAAAATTCATGTGCGAATCCATCCTTGACAGATCTTGCTGTGGCGGATCCGACATGGTCCA
 TCACTGCTCTGAGATACTTCAACCCAGTAAGCCCTCATTCAAGTGACTTTTCAAACGAGAAATGCTAACGGGAACAAGGTC
 GGCTGCCATGAATCGGGAATACTAGGTGAAGATCCACGACAGAAACCAAGCAACCTCATCCAGTCATTGCCACAGTCAT
 GACGGGAGCCAGGCGGTGCTGGATATTTTCGGTACCGACTGGAACACTCCTGATGGAACCGCTGTGCGTGACTTCATCC
 ATGTGCTGCACTTGGCTCGTGGTCATATCGCGGCTTTGGCTGCTTCAGCAGCTGGTCGCACAAAGGCTCCATTCCGAACC
 TACAACCTGGGTAAAGTGCATTTTGCCTACAGCCGCGCCCTCTAGATGTGGTTGGTAACTCTTTCTAGGCACTGGCAAC
 GGACACACGGTTCTGTAAGTGCTTCACAGCCTGGAGGAGGTGCTCAACGGAGATCCAGCACGGGAAGTCGGACGAAG
 GCGGGGAGATGTTGGTTTTGTGTGCTGAAAGTGCAGCGAGCAGAGACTGAGCTGCAGTGGAAAGGCTGAGAGGAATCTCA
 GGGATTGCGCTGGAGATGTGTGGAACCTTACCAAGGGTGGGTGTCGGATGTGCAAGAAGTTAGTGACGGCGAGTGC

PUTATIVE AMINO ACID SEQUENCE OF *Bipolaris maydis* sph3 (Gene ID: COCHEDRAFT_1023805)
 MEAFHTPVLQALLASHHPLTSFPAKSMGGRHVLNDWTSVYLSITKVCTMPLIP

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Bipolaris maydis* sph3 (Gene ID: COCHEDRAFT_1023805)
 ATGGAAGCTTTTCACACACCAAGTGTGTCAGGCCTTGGCTGGCTAGCCATCACCCCTCACTTCGTTTCCCAAAGCGAGCAT
 GGGTGGGAGGCATGTGCTGAACGATTGGACGAGCGTCTACTTGTCCATAACCAAGGTTTGCACAATGCCATTAATCCCTT
 AA

Fig. 96

PUTATIVE AMINO ACID SEQUENCE OF *Bipolaris maydis* *ega3*

(Gene ID: COCHEDRAFT_1023806)

MDVKPTATTSRRRKILCIVLPLVIVIVLALALGLGLGLNSGGDDDDNNNGGSTPLPSPNNLTWTPSVASTWQIIL
 NHPPDVSSNNALTPNVSVYDIDLFDTPKSTIDTLHAQGI RVLGYFSAGSYEDWRTDAKDFKDTDLGKPLDGWAGERWIDL
 KSDNVRAIMKTRIQLAKEKGCDGVDPDNDVGYNQDNLGLTPADSLAFMQYLSNITAPLNALGLKNAGDIVTTVLPVVH
 FSVNEEGVKYSECAEFAPFIDAGKPVFHI EYPDGAGAAQGLRANVLTDYCAKSGKGAGSDRFSTVLKKIELDGWVEYCDG
 SVDVTNVSEAVGGGRNNSSS

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Bipolaris maydis* *ega3* (Gene ID: COCHEDRAFT_1023806)

ATGGACGTCAAACCCACAGCGACAACGCGGTGCGCGCGCGCAAGATCCTCTGCATCGTGCTCCCGCTCGTCATTGTCAT
 TGTCTCGCCCTCGCCCTCGGTCTAGGACTAGGACTAGGCTCAACTCTGGCGGCGACGACGACGATAATAACAACAACG
 GTGGCAGCACGCTCTCCCTCCCAACAATACCGTTACGTGGACCCCTCGGTGCGCTCAACCTGGCAAATCATCCTC
 AACCAACCCACAGAGCTCTCTCCAAACAACGCGCTCAACCCCAACGTGAGCGTCTATGACATCGACCTCTTCGACACGCC
 CAAATCCACAATCGACAGCTGCACGCTCAGGGAATCAGAGTGCTGTGCTACTTCAGCGCTGGCAGTTACGAGGACTGGC
 GCACCGACGCCAAGGACTTCAAAGATACCGATCTAGGCAAGCCCTTGATGGGTGGGCGGTTGAAAGATGGATTGACCTC
 AAGAGCGACAATGTGCGGGCTATCATGAAGACGAGGATACAGTTGGCCAAGGAAAAAGGGTGTGACGGGGTAGATCCCGA
 TAACGTGATGGTTATGTGAGTTTTTTTTTTTTTATTCTCTCTTTTCTCTACCTCACAACCACCACTTCTTTACCATGTT
 ACCAAGCCACACAAAAAAAAGTTGGAAGGGTGCTACAAGGGGGGGGGGGGGGAAACGAGTATGACTACAAAAATTGCT
 AACGGAGAAATTTAAAAAAAAGCAAAACGACAACGGCGCTCGGTCTCACCCCGCGGACTCGATCGCCTTCATGCAATACC
 TATCCAACATCACGGCGCCGCTGAACCTCGCACTCGGCTCAAGAACGCGCGCGACATCGTCACCACGGTACTCCCGTT
 GTGCACTTCTCGGTCAACGAAGAGTGCGTCAATACAGCGAGTGCGCCGAATTGCGCGCCCTTCATCGATGCGGGGAAACG
 CGTATTCACATCGAGTATCCGGATGGCGCGGGTGCTGCGCAGGGATTGCGCGCAACGTGCTGACCGACTACTGTGCAA
 AGAGTGGCAAAGGCGCGGGCAGCGACAAGTTTAGCACCGTCCTAAAGAAGATCGAGCTCGATGGCTGGGTGCGAGTATTGC
 GATGGCAGTGTGATGTTACTAATGTCAGTGAGGCCGTGGGTGGCGGCCGGAATAATTCTTCAAGCTGA

PUTATIVE AMINO ACID SEQUENCE OF *Bipolaris maydis* *agd3*

(Gene ID: COCHEDRAFT_1146217)

MSSYSRSLLRACLVSLSFVLQPVSAFVGSATVSSVTLVIARDATSALNSASLGLQGYGIPYETLLVPQAGIANLPLLNA
 SATNGNYGGIVVVGEVSYNNDYQSALTTAQWNQLYAYQTNFGVRMVRLDVFPTEFGVVSTGGSLDDQPVFTNTSAF
 PSANLKTGVPISIASIYHPANITNSSIAWEFASFNAGTAAVINQIGARQMAWFLPFALDWAPSSNILQHAWITWITR
 GLFLGFRRIYLNLTQVDDMFLETSLYRPEGQDFRVTTPQDLTAHVITWQAALNARLPAGSEFFIEIGHNGNGDIEASAYDLG
 QTRCSPARAIEYADQPDGSPYEYTKPIGTGVNIWPTTPTSYSWLSLQCAQIDPLENWFVTSNRDSFAHISHTFSHMDLTNA
 TYADTSKEISFNRAWLKQVGLDAAQRWSTKGLIPPAITGLFNGDAIKAWMDNGIANVVGDNTRPRLRNQSSFWPLATTT
 SFNGYAGLNIMPRWATLIYYNCDLPACTTQEWIDTSAGAGTFDDLNDNARDTAIRNLFGLHWDPMFQANMRVADVPTT
 TINGKTGQFSLMSWLEVVTSMTLTTWPMKTLKHDDMAQQFLNRQTRDLCRPSMTWKTSANGASIESVSVFTAGGNTC
 GTTIPITVPGSVADSTGATREQLGSDPLTLWVSMGASRTYRLSSALPL

Fig. 97

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Bipolaris maydis* agd3 (Gene ID: COCHEDRAFT_1146217)

ATGTCGTCCTATTCTCGCTCGTTATTGCGGGCATGCTTAGTCTCCTCTCTTTCTTTCTGCTGCTGCAACCAAGTGTACAGCGTT
 TGTGGGAAGCGCAACGGTCTCAAGCACCGTTTTGGTCATCGCTCGCGATGCAACTCCGCGCTTAACAGCGCCTCAGTTG
 GTCTTCAAGGCTATGGCATACCGTATGAGACCGTACTTGTGCCCCAGGCTGGTATCGCCAATCTTCCGCTTCTCAATGCC
 TCTGCAACAAATGGCAACTACGGTGGTATCGTTGTCTGCGGGCAAGTCAAGTACAACGACTCGTACCAAGCGC
 ACTTACAACCGCTCAATGGAACCAAGTTGTACGCTTATCAGACCAACTTTGGTGTGAGGATGGTCCGCTTGGACGCTCTTC
 CTACCACTGAATTTGGTGTGTTAGCACTGGTGGCAGCTTGGACGATCAACCAAGTCACTTTACCAACACAAGTGCCTTC
 CCTTCAGCCAATCTCAAGACGTAAGTGCAAAACGACCCCTTTACCCAATTGCAACAATTTGCAACGATGCCTGCTCAGC
 TTCCACAAGCGCGCTGGTGGCAACGTTGATAGCCGAAACAGGATACACACAGGACTAATCATGATGACAGGGGTG
 TGCCGATAAGCATTGCTAGCATCTACCATACTCCGGCCAACATCACAACTCTTCAATTGCATGGGAATTTGCTAGTTTT
 TCCAATGCCGGTACTGCTGCAGTCAATCAACAGATTGGCGCACGCCAGCAGATGGCATGGTTTCTTCCATTTGCGCTAGA
 TTGGGGCCATCCAGCAACATTCTGCAACAGCGGTGGATCACTTGGATCACCAGGGGCTCTTCTTGGTTTCAGGAGAA
 TCTACCTCAACACGCAAGTTGACGACATGTTCTGGAGACAGGCTTGTACCGTCCAGAAGGCCAAGACTTCCGCGTCACG
 CCACAGGATCTCACGGCCACGTTGACATGGCAGGCTGCGCTCAACGCAAGGCTGCCCGCGGGATCCGAGTTCTTCATTGA
 GATTGGCCACAACGGTAACGGTGACATTGAAGCATCTGCATACAGGACCTAGGCCAGACAGCTGCAGCCCTGCCCGGG
 CTATTGAGTACGCTGATCAGCCTGACGGCAGCCCGGAATACACCAAGCCCATTTGGTACCGGCGTGAACATTTGGCCTACG
 ACACCCACTTCATACACCTGGAGTCTTCAGTGTGCCAGATTGATCCACTTGAGAACTGGTTTGCAGTGACATCGAACCG
 CGACTCTTTTGTCTATATTTCCACACATTGTAGGTGTACAATTGCTACTAAGACCCTGGCCACTGCTGACAAGACGCTA
 GCTCACACATGGACTTGACCAATGCCACCTATGCGGACACATCAAAAGAAATTTCTTCAACAGGGCCTGGCTGAAGCAA
 GTCGGACTCGACGCTGCTCAGCGATGGAGTACCAAGGCTCTCATTCCACCTGCCATCACTGGTCTGTTCAACGGCGACGC
 CATCAAGGCATGGATGGACAATGGTATTGCCAATGTTGTTGGCGACAACACCCGCCACGCTCCGCAACAACAGAGCT
 CGTTCTGGCCATTGGCCACGACGAGCTCGTTCAATGGGTACGCTGGGCTGAACATCATGCCACGTTGGGCTACTCTGATT
 TACTACAACGCGATCTCCCTGCCTGCACTACGCAGGAATGGATTGATACGTCTGCTGGCGCTGGTACATTGACGATCT
 ATTGGACAATGCCCGGGATACTGCTATACGCAATCTTTTTGGGCTGCACTGGGATCCGTGAGTTCTCCGCTCGTGTCCGC
 TTGGAGAAAGTTTACTGAGACATCACGCAGGTACATGTTCCACCAGGCTAACATGCCGGTTGCTGACGTGCCAACGACGA
 CTATTAATGGCAAGACTGGCCAATTCTCGCTACTCATGTCTGCTCGAGGTTGTGACCAGTGAGATGACACGCTTGTAC
 GTCAATCATGGCGGCTTTCGATTAAGCAATGCTGACACACCTCTCTAGGACGACCTGGCCCATGAAGACGCTTAAGCATG
 ACGACATGGCCAGCAATTCCTGAACCGGCAGACGCGCGATCTGTGAGGGCCAGCATGACCTGGAAGACATCGGCCAAT
 GCGCGAAGCATCGAGTCTGTGAGCGTGTTCAGGGCAGGCGGCAACAGTGCGGTACAACATTTCCAATCACGGTGCAGG
 GTCGGTAGCAGACTCAACTGGCGCAACCAAGGAGCAGCTAGGCAAGTATCCCTTGACGCTGTGGGTGTCTATGAGTGGTG
 CGAGCAGGACGTACAGGCTCTCTTCCGCTTGCCTCTCTAG

Fig. 98

PUTATIVE AMINO ACID SEQUENCE OF *Bipolaris maydis* gtb3 (Gene ID: COCHEDRAFT_1146218)

MAKPDVLGIEAFKDGTRIRDWWDWTLIAITAASGFVGLVALVWSTYRSLRKVLKEDDEETALPRSVQERIHLLSNSSSVV
 RVTHALPAKPSSFGVYLGAALQTPVPEEAQVLSQWEALVLDYROTGLEAVSNDVPMGPYIIARLDLSHVITSAYKGTE
 LDLSQATYLLSCTIEQNLRPDQKRYFTGVLIAEWRNRVPIALLHGLTKLLSAHGLDSYLEIGAPDFLDGVKKLDLSLFA
 GVVVRNGTIKSNQFRRDFFDMDKMKITTRSFVSQACQSFVTMMWDIVDDNAELSHAVLRRAHMWCSYHGAVPYFPRQCA
 LTNIDVSSQEEPLAFAQWLKTRKVMVDVHDKYRTARTISPGFSSLFDDYVPLQEIFPLADTLAQLDGMPPNDDSSSTL
 TLTVPEYPEVDENGVLVPEPSSPTSLGLDWTMAVEKHNDNPLSCSFQDGSFYSSLGCFPIGIDASKADFDRVLKSRHLRD
 LKLLSRLPVEQFSATAETLSRYASSSSHFLNLVPTMREAILALVEALDHAVEDGADPYRFQAYSALDSGFHTPNGASFNG
 VWELDPRTKAIITYVSKSVQDVKVLHTYLSMMGFSTRYQCFLAEYGLSEFAAGSFSPERLPDRLVODLQLSSSELLNY
 LQHIRYSEWEEFCSLPAIRERCKELLIDVPTYHQFKQLSNVDYIGEKVTDEELVNAKLKWYRLSRVPTLDEAQLQLFR
 HINEVFTSILWNRDHQKLDITISAITDITSRGLDSAADFVLCIFCAARKAGFEVYIEVSDRNPFLNQYSDQSAFAE
 LFALGSRCEAYFDIKPSDMGILLSEKHAYYNOEEHQPPMWIFNAPSFASAYAAAQTDIDPEQKASVMPAYRRFTFLSVF
 AIPALVDIVLLSTTGHLGLYSVRMTEDDRYYATLALMCSLLLSGAIGTWISIGGTYYLISMAFSAANMFVLRVGGALF
 TLAGCLLGFIVISAVSGPGHGAFFFFYLFGLTITVLAFLSTYQIPGSSFLNGRKIIMVITPLVISPLTIFIGMKGH
 DIYLYGLVLYIFVTLILGTRRATQWVTWYHNKTLNDSIDKNWYMKLHSEREQEATLKNRQSKGPAISTVAGGSLV
 ASSEGSFSEPDIFQGMSEPAIALCRNALHEAVLKEHGRHFWQKSTKDSFVKLAGCWDSTLFLDHYARITDTRPIPY
 SSTWNLEQVALESQQSQKQIRLHNSFIHWRTAGDEIYCGILYFLVALMDRWLDILNGGQIVDMPGADSPVQLSAGLGL
 AYDFAGEMDIALRLSYGFLAYYLIGAVLLDYKAQHLHTLSEQMAPISIENTQIQKAKANDLKFRHLYFNTLCRFIGV
 HVWALAFCTALIWIFNSSSIGLTLFLSYVGAYIGLLLYQYNKIFSGPHALMPLLAUVVGLIVGNVLLAVFPGLYDRII
 ALAASWTAAALSFRTAKLGMPEALDFSKWVSEFSQAKRSKKAANTVNAQPDGTESPMSDKFHAYNSGNSDSEYSQSE
 LRAYCNMIRAAKENRYRVNPGQPGDQIVALLLSCDHSLSRQALGAFFPAMPSTIQRIVSAWRNGQIDVFIPLQAVVN
 FNNDLRAISHFADGHLTLYITSDAKGPGFGQTNVSSNCTAIAETLLHACMETFLETPHSQAEIAESILACRENDGGEQYAI
 SECNRRSMPALVAGQDALSYGACRRELLRNLCGLGDCETQWDSLPLDIRRFFRRCLGIRAPYTNKELSWIHENIRTEE
 SCALSVIARYDLGAYLAVVKYSYFRNRGQDLSNKEYRQVTADIQAYHPVLNRSAYSMFSLFTEYIRLPVAYVYHCAG
 TWVKFFVLACMADEPYQRELNGLLHKPWIVAKPTIFLLTGLWIYSRRANSIALPFFLYHRRKDIAGLAGTVKGSLLIQR
 KNRLVQSAGETETAFVHPDKDGGFKLIFYSGALKTEPTWGGQIRVSHYDKEMRIKLQEWKNGSVTNEFTYEYETNQTS
 KIKISKVRSTKIPLSRICGKGENDGAKVLYNHKGHIESGSYISHNNLVRFKYHYRKNKYDDELLRAEFVLPHMSANVSW
 CAPPVRAEKTERWIPTPRVHEATFVQGDVYECTWFYDHFHPTITTKLNGIMVDTPDMIRHDWLGVKKKPTRCTFADE
 NPLLAFTKPTSNFLGRFLRRNIKQOEISTSRARSHLWKAWKKRNDLDGVVIRWVDEELIRKEALLRPYWRRRDRGSLVKA
 EDYLALHADAIMASSDLTSDISAWTPLAIRMSDLFSFGGGGDAVVFTRTKALORDTNSLHVIAVDGTGWPNEGGSVAC
 RRDLINNLRTIKWMMVVESANDFGLPKHQTEENVESLKIPLWGLDFMHPNHGMFINKLDSEVDHLVKAATLTDIETNFI
 PTLTALVRGARATTMSADVKQATRALVNLNTYFQDSRHWEVWTSIDVKDSWRKLWLTDDMPNAQPAKDWHLFIIFSIP
 IPDKIPHVFQASHHSVSASYGIVCKLKRNTLQIWDHATSWRETNLYLSSAMCTLPPFIRNSLLGLMKLTSCLILHHAQ
 ILPCADFFNPGEIEIGSAKGQLTHRNVFKRVDPIVNGITDMTKFAPVTEIKAKTPTVTMLSHVWFADIKTALLAADI
 ITNEWGFKDYKLDIYGALNKSPVYSECQEIACKGLGQNVMTMRGTADPANVLANTWFLNSSVSEGLPLALGEAALTGA
 PVVCTDVGASLRVLTDPDDGKRYSEVVAPNDAYGLARAQINLLAMLDEWAQYAEDEGPGVAAPVLPKPTPKDVEIITRM
 YEKSDHRRKLGMWARNIVQKSFGGERYLREHEQMLWIGKSFYEMLDFEKQTPPPRNPARMLSLGRTRTPQRDTMDTSS
 SIFDQPMKMMHPRRPFQAHRASAATSFSSVYIDDEDDSGPSSRYSPDLWESEAWDTQPGSAGASTKYATSESEWALP
 VIPRPTRTYSGTHIAPMRTPSSSVAPAKGRPMQFYAGSMAREDTGNGLDPRRDVLAQSWAPNSGRSSLRRSHLNEM
 ELA

Fig. 99

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Bipolaris maydis* gtb3 (Gene ID: COCHEDRAFT_1146218)

ATGGCAAGCCGACGCTTCTAGTATCGAAGCCTTCAAGGATGGCAGCGGAATCCGGGACTGGTGGGATTGGACTCTCAT
 TGGCATCATTGCTGCCAGCGGATTTGTGGGCTTGTGGCTCTCGTTTGGTCGACTTATCGTTCTCTTCGAAAAGTGCTCA
 AGGTATGAAAAGCTGTCTGCACCGACATGGGCCCAAACTGACAAATCCTGCAGGAGGATGAAGACGAAACTGGCTTGGCAC
 GGTCTGTACAGAGGCGCATTCATCTCGTGTCAACAGCTCAAGCGTGGTTCTGTATTACGCACGGCTCGCGGCAAACTT
 TCATCTTTTGGCGTCTACCTTGGCGATTGCAAAAGCCAGTCTCAGAGGAGGCGCGAGTTCTATCGCAATGGGAAGC
 GCTGTCTTGGATTACGGGCGAGCTGGTATCCTGGAGGCGGTCAAGCAATGATGGTGTTCGATGGGCGCTTACATTATCG
 GCGAGCTGGATATCCCATGTTATCACTTCGGCGGTAAAGGCGACTGAGTTGGACCTGTACAAAGCAATATATCTCTTG
 TCTTCGCAATCGAAGAGAACTTGGACGGCGAGACGAGAGGCGATCTTCACTGGTGTCTCTATTGCGCAATGGCGAA
 CGCGGTTGCCATCGCTTTGCTGCATGGCTCACAAGACTTCTTTCAGGCCATGGCTTGGATAGTATCTGGAGATCGGTG
 CTCGCGACTTCTTGGATGGTGAAGAAACTCGACCTCTCGCTCTTTCGGCGCGTATGGTTCGCAATGGTACGATCAAG
 TCGAATGGCGAGGCTCGGATTTCTTGGACATGGACAAAGATGAAGAGCAACCGAGGTCAATTTGTTCCCAAGCTTGGCA
 ACGTTCATTTGTCAAGATGATGTGGATACAGTGGATGATTAATGGCAACTGTGGCATGCTGTTCTAGGAGAGCGGACA
 TBTGTGAGATTATCACGGCGCAGTGGCTTCTTCCACGGCAGTGGCGCTTACCAACATCTACGATGTCAAGCTCTGCG
 GAGGAGCGCTTGGCGGCTTCCCAATGGTTGAAGACTCGAAAGGTCATGGATGTTCTATGACAAATACCGAACTGCTCGTAC
 GATTTCCGCTGGATTTTCCAGCTCTTTTGCAGACTACGTGGCGCTACAAGAAATTTTCCCTCTCTTGGCTGACACGCTCG
 CGGGCTTGGTGGAGACATGCTTACGACGACGACTCATCGACTACCTTACACTTACTGTGGAGTATCCGAGGTTGAT
 GACAAATGGAGTGTGTGGTTCCGCAAGAACGCTCATCAGCCAGGAGTTTGGGGCTCGACTGGACATGGCAGTGGAAAGCA
 CAGCGACAAACGACTTTCATGTTCTTTTCAGCGGATCACCATAATTCATCTTAGGGTGGTTTCCAAATGGTATTGATGCTT
 CGAAAGCAGATTTGGATCGGCTCTCAAGTCACAGCGGCTATGGCGGATCTCAAGTTCGTTAGCGGTCTCGCTGTGGAA
 CAGTTCAGTGGCACTGTGAGACACTCAGCGGCTACGCTTTCAGCAGCATCACTTTCTGAACCTTGTCCCTACTATGAG
 AGAGGCTATATTAGCTCTTGTAGAGGATTTGGACCATGCTGTTCAGGATGGTGGCGAGCTTACGGATTCGAAGCATATT
 CTGCACTTGTATCAGGATTTTCATCTCCCAAGCGCGCTCATTTTGGGGAGTGTGGGAACTAGACCTCGGACTAAAGCT
 ATCATCATATATGTGTCCAAATCTGTAGAGGATGTCAAAGGACTGTGTCTTACACATACCTGAGTATGATGGGCTTTTC
 TAGGTACCGAGTGTTCCTTGGGGAATACGGTCTTAGCGAATTTGGTGGCGGATCAATTTCCAGAGAACGACTACGGGATC
 GGGTATTCAGGATCTGGATCTTCTTTCTGCTCCTCAGAGCTTCTAAATTACCTGCGACATATTGTTATTCGAATGGGAA
 GAGGAATGCTCGCTGCTCGCTGCGATTCGCGAACGCTGTAAAGAGTGTGTGATTGATGTACCTACGATATCATGAGTTAA
 GCAACTGAGCAAGTACAGTACATTTGGCGAAAAGTCAAGGAGTGTAGTGAAGCGGAACTCAAAATGGTATCGAC
 TCTCGCGGCTCGCGACTCTTGTATGAGCGGCAAGCTTTACAACCTCTTCAGACACATCAATGAGGTGTTTACCAGCATACTA
 TGGTGGAGGATCAGCAGAGCTTGTATACCATCACTTCAGCCATCAGAGACATCAGCGCGGGGAGACACTCGACTCGGC
 GGTGACTTTGTCTTTCTGTATCTTCTGTGAGCCAGGAAAGCGGATTCGAAGAGTCTACATTTAGGCTCTCAGACA
 GGAACCGACTCTTCAACGATTTGGATCAGAGTGGCGCATTCGCGAAGCTGTTTGGGTAAGGATCTCGATGTGAAGGT
 TATTTGGATATCAAGGCTAGCGACATGGGATCTTGTCTATCGCGAAGACATAGGGGCTACTACAAGCAAGAAACAGCA
 GCGTCCGATGTGGATCTTCAATGCGGCTTCAATTTGCTTCCGCTTATGCTCGAGCCAGACAGATATCGAGCGTGAAGCA
 AGGCGTCCGTCATGCTGCTGCTATGCTGCTTTACTTTGCTCAGTGTCTTCCCAATTCCTGGCGTGTGATATTGTGCTT
 CTCTCCACTACGGGCGACGGCTTTACCTCAGTGTGAGGATGACTGAAGACGACAGGACTATGCTACGCTGGCATTTGAT
 GTGCTCATTTGCTGCTCTGCGGCTATAGGAAGTGGATCTCTATTGGTGGCACAATACTACCTCATTTCCATGGCATTTGT
 CGCGAGCGCAACATGTTTGTCTCAGCGATTGGTGGTGGCGTGGCTTTTACTCTTGGTGGATGTCTTCTTGGATTATC
 GTCAATTTGGGCTGTATCAGGAGCGGTCAGCGCGCGCTCTCTCTTCTACCTCTTTGGACTGACTACATACCTGAGCGT
 CCTGGCTGTGCTTTCCACGATATCAGATTCTTGGATCCAGGTTCTCAAGGGCGGAAAAATCATCATATGGTCAATTCGAA
 CCTTGGTGTATCTCCCTATTTCTGACCATCTTCAATGGGATGAAGGGCGATGACATTTATCTCTATCTGGGTTTGTGAT
 ATCTCTGTTACGCTTTTGTATTCTTGGCAGCAGACGGTGGCAAGCGAATGGTAAGCTGGTATCACAACATCAAGACACT
 CAAGGATTGGATATCAAGAACTGGTATATCAAAATTCAGCTCTGAAAGGGAGGAGGAAAGCGCGGCTCAAAAACAGAG
 GTCAAAGCAAGGCTCCAGCTATATCAACTGTGGGGGGGGATCCCTCGTTGCTGCTCGGAGGGGCTTTTATGTAGGCCA
 GATATCTTCCAGGGCATGAGCGAACCGCATTCGGCATTTGGCGGAAAGCTCTTCAATGAAGCGGCTCTTAAAGAACAA
 TGGAGGTCAATTTCTGGCAGAGTCCACAAAAGATAGCTTCGTGAAGCAACTCGCTGGCTGGTGGATTGCACTTTGTTT
 TGTGGATTGGTACGCTCGCATACAGACAGCAAGCGACCAATTCGCTACAGTTGCACTTGAAGCTCGAAACCGCAAGTC
 GCTTGGAGGATATGCAACAATCGCAGAAACGAAATTCGCTCGCAATTCCTTCACTTGGCAACAGAGGTGATGA
 AATCTACTGCGGATCTTACTTCTTGGTGGACTCATGGACGTTGGTTGGACATATTGAAGGGGGCGAGATGTTG

Fig. 100

[illegible]

Fig. 101

CCATGTGCAGGTACGTATATATATCCCTTGAGTTTGTGCTCTCAACTAACTCCTTTCTCTCAGACTTCTTCAACCCAGG
ATGGGAGATTGAAATTGGAAGCGCAAAAGGACAGCTCAGACATCGCAACGTCTTCAAGCGCAAGGTGGATCCTATTGTCA
ACGGTATCACTGATATGACAAAGTTCGCTCCAAGTACAGGAGATCAAGGCAAAAGACACCAACTGTGACCATGTTGTCCAC
GTCTGGTTTGCCAAGGACATCAAGACGGCTCTGCTGGCCGCCGACATTATTACAAACGAGTGGGGTTTCAAAGACTATAA
GCTTGACATTTACGGTGCTCTCAACAAATCTCCTGTCTACTCTTCCGAGTGTCAAGAGATTCTCGCCTGTAAGGGTCTGG
GCCAGAACGTACCATGCGCGGTACAAGCGATCCAGCAATGGTTCTTGCAAACACCTGGCTGTTCTCAACTCATCGGTT
TCCGAAGGTCTGCCTCTCGCACTTGGAGAAGCTGCGTTGACTGGAGCCCTGTTGTCTGCACTGATGTGGGTGCGTCTTT
GCGCGTGCTCACCGATCCCGATGATGGAACGTTACAGCGAAGTTGTTGCTCCAAACGATGCATACGGCCTGGCTCGCG
CCCAGATCAATCTCCTCGCCATGCTAGACGAATGGGCACAGTATGCCGAAGACGGCCCTGGTGTGCTGCTCCAGTCTC
CCCCACAAGCCACACCCAAAGACGTCGAAATCATCAGCCGCCGATGTACGAGAAATCCGACCACGGCCGAAACTCGG
CATGATGGCCGTAACATTGTCCAAAAGTCGTTTGGCGGCGAGCGCTACCTCCGCGAGCACGAGCAATGCTCTGGATTG
GCAAGTCTTCTACGAAATGCTCGACTTTGAAAAGCAAACCCCTCCGCCCGAAACCCAGCGCGCATGTTGTGCTTGGC
CGCACCCGACCGTGCCGCGAGCGGACACCATGGACACAACCTCGAGCGAGCATCTTCGATCCGCAATGGAAAAGATGAT
GCATCCCCGTCGTCCTTTTGTCAACATCGCGCTTCGGCTGCTACGTCCTTTTTCGTCCGTCTACATTGACGACGAAGATG
ACTCGGGCCCTTCATCCCGTACTCGCCCGACCTTCCTGCGGAATCTGAAGCCTGGGACACGCGAGCCCGCTCGGCTGGC
GCAAGCACAAAGTACGCTACCTCTGAGAGCGACGAGTGGGCTCTCCCTGTTATCCGCGCCCGACTCGAACGTACTCTGG
CACGACATTGCGCCGATGGGTACACCGTCGTGCTGGTGGCTCCCGCCAAAGGGCAAGCGCCCATGCAGTTCAGTACG
CGGGCTCCATGGCTAGAGAGGACACTGGTAATGGCATGTTGGATCCCGCCGCGATGTCTGGCAGGACAGAGCTGGGCG
CCTAATAGTGGACGGAGTAGTTTGAGGAGGAGTCATTTGAATGAGATGGAACTCGCCTAA

Fig. 102

PUTATIVE AMINO ACID SEQUENCE OF *Botrytis cinerea* ags1 (Gene ID: Bcin08g02140.1)

MLARTFVALCSVLLSTQVDALRYEEFVGYNLNTNQATATSPFDYYGKWEDHEFFQSPDNWRFPFYSFFLDKFVNGDPTND
 DINGTKFETDFMQTLRHGGDLQGLIDSLDYIQGMGIKGIYIAGSPMINAPWGADQYSPLDFSLLDQHFGDIDLWRKTTT
 AIHDRGMYVMLDNTMGTMGDLIAFKGYENSSTPFTLTEHEVLWRNDNRQYLDIFSFGSKYNETCNYPFRWLDGTGTVKEDV
 TDLMNGCYDSEFDQYGDTEAFGVFPD#QRQLSKFASVQDRLEWVPSVRTKIEIFTGMIQQQLDIDGLRVDKATQITVDA
 LGSFSHAIRECARDVNKTNFMVTGEITGNTFGSIYLGRGRQPDMLPSSMADAVKLTSNSSLAYFIRDHDQNALDSAAFH
 YSVYRTLTRFLGMDGNLASGYDPTN#VDAWNEMLVTNDFVNPNTGVFDPRHMYGVSNDQVFRWPAIQNGTKQKQLGFFI
 TTTHMPGIPLLLWGEEQAFYVLDNTADNYLFGRQAMSPSQAWQTHGCYALGSGTYQFPNDSCTRGCNDDWNSRDHRDPS
 HPVRNIVKAMYQMRDNPVLTGDAFLRQLSNQTEIILLPGSNGTATETGMWSTMRGQYDGIQDLSKAGGQANQSVWVYH
 NNYDTVTYSFDCSSNETSLVAPFLDGVTVKNLFYPYEEVTLKAGPFQLGIANQTGFNGCLDSLTLVPYEEKAYVPKKS
 WVGPSPMITSFSPGHDARLVSTVAPGEQETIEIEFGFSAEMKCSDLISKMVITSATEDGQVATLANATGEYSCITLLPSAVNV
 TEFVGSIPTMTWTFKGNLTNVSNGVHSITLANITSNSGNSSTGATDTFLFRVGGVQDNPIAFPGSANFTRELLHKYDNGTLY
 VSHKAAGADRFKYSLNWGSSSEWLPYVGGNTTLEPQAWTGTSKQKWDGDHVIHQYWSKLTGSSDVVQHADLETNKWSRR
 LPHLFANGPYNGYGYDTGIDNGFTLNKKDSLWEYKFMTEWPAVMQVNVWGMNPDGQPDETIVLGDIDNDNILDORMPPSSL
 STALINITRVPPSPYLGYKIAIDDGNYRYQIPYGNRSYQMLMVVLFWIVPVLSSGLSIWLFMKSFYAVKLSVGVKEAK
 NYIPLALRRKLKREKKEDPSEKEMTVMGGLHSMFHENATQLGLQADVAATGRRTVLATMEYDIEDWAIKIKIGGLGVMA
 QLMGKNLGHQDLIWWVPCVGGIDYPIHQAEPMQDVTILGNSYTVQVQYHTLRNITYVLLDAPVFRAQSKSEPPARMDDL
 DSAVYSAWNQCIALTIKRFPVDLYHNDYHGAVAPVHLLPETIPGCLSLHNAEFQGLWPMRNQKERSEVCQVYNIPEEV
 AIKYVQFGDVFNLHAGSSYLRIHQKGFAGVGVSKKYGKRSWARYPIFWGLSKIGNLPNPDPSDTGDWNGTQDSTGKTIV
 NQDFESQRADLKRQAQEWAGLEQNPKAELLVFVGRWSMQKGIDLIADVMPAVLEENPNVQLICVGPVIDLYGKFAALKLD
 VMMTKYKGRVFSKPEFTALPPFIFSGAEFALIPSRDEPFGLVAVEFGRKGALGIGARVGGLGQMPGWWFTVESTTTTHML
 HQFKQAIKEALASKLETRQIMRARSQKQRFPAQWVNDLEILQSKAIKIHDKKEAKHSGRPRSRRGRDGGNIFYSSAKRLS
 SFGTSFASTSQLDVAITGGSTRPSSPTRVEQPPAGGGLSRKLSLGYRAGPGHRVTKNRFNGSNAPGAGIKNDEGLTDVD
 EDSDDEDARIRDDIYDEYVLTPEELEAQRQQEQWRGQAESPAAGGAFLAPQPGFLDSPRRSPSANTGSLHINDSELSPR
 LKDGSNITYSTHSPGSPGLESPGTPGAHDSLLPPPSIFGAGGDNANRASMLSSSVIGDKTDFKLQKVDPFFTDQTGEYY
 QQFARNLDNLDGKNSEGQLCIEEYLKSEKKWFRDRDAKLGRNSVAPSFSAALGSGRRSHDSRGRSNSRDSFTNDTITHS
 RQNSSQDNMALTTGGSTANDQFLLGKDYKPPTGLRLVMQYRFFDWPVYSFLLAFGQIIAANSYQITLLTGTVGQSAEKLYI
 TATIYLVTSIMWWEVFSFFKSIYVLSIPFIFYGLAFFLLGMAPFVDGADGRGWVQNVATGLYAVAASSGSIFFALNFGDE
 GGSPVKAWVFRACIIQGTQQAYVVLWFWGSYLNRRQADGLTSFTSASPMSAVVLPVAVLMWAVGLITFLGLPEYYRQ
 APGKVPSEFYASLFRRKIVMWFVTVLIQNFFLSTLYGRNWL YLFSSNHAPTWAIIILLIIFFFGLWAGFLWFFAILSKDH
 SWVLPIFAIGLGAPRWQMLWCTPIGQYVPWVGGGLASAFSRSLWLWLGMLDALQGVGFGLLLQTLTRVHIAFTLIA
 AQVLGSIATMVARACAPNKIGPGTVFPDFSDGAAGLGNWFWIGLILQLVICGGFFTFRKEQLSKP

Fig. 103

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Botrytis cinerea* ags1 (Gene ID: Bcin08g02140.1)

[illegible]

Fig. 104

ATGGATGTACAAATTGTTGGAAATTCCTACAGTGTCAAGTTCAATACCATAGTCTACGAAACATCACTTACGTTCTTCT
 CCAATGCCACATTTTCAAGACACAATCTAAGTCTGAGCCATACCCAGCTCCTATGGATGATTTAGACTCBBCCGTTTACT
 ACAGTGGCTTGGAAATGAATGATCCTGTTACCATCAAGCGTTTCCCGGTGGATTGTATCAGATCAACGATTAGCAGCGA
 GCCGTTGGACAGTCCATCTCTTCCAGAAACGATTCCATGTTGTTTGTCCCTCCACACCGCGAGTTCCAAAGGTTATG
 GCCCATGGTAACCAAGAAAGAGAGAGTGAAGTCTGTCAAGTCTACAACATTCAGAAAGAAAGTCCGCATCAATACGTTT
 AATTCCGAGATGTGTTCAATTTCTCCACCGCGGAAGTCTTATCTTGGTATTCATCAAAAGGTTTCCGTCCTGTTGGT
 GTCAGTAGAAATACGGAAAGCGCTTCTGGGCAAGATATCCTATTTTCTGGGGATTGAGCAAGATCGGCAATCTTCTGTA
 TCTGTATCTTCTGATCTGAGACTGGAATGGTACTCAAGATCAACGGGCAAGACAATTTGTTAAACAGGATTTTGAAA
 GTCAAAAGAGCGAGCTCAAAAGACAAGCACAGGAATGGGCGGTCTCGAACAAAATCCTAAAGCGAACTTTTGGTTTTT
 GTCGTTGATGTTGATGCAAAAGGATTTGATTTGATTTGATGTTATGCTGCTGTTTGGAGGAGAAATCCAAATGT
 TCAACTTATTTGCTTGGTCTGTTATTTGATCTTTATGGAAATTCGCGCTCTCAAACTCGATGTCATGATGACAAAAT
 ACAGGGCGGTGTTCTTCAATAGCTGAGTTTCACTGCTCTTCCACCATTCATTTTCTCGGAGCGCAATTCGCTTGAAT
 CCAATCTAGAGATGAACCTTTCGCTCTTCTGCTGTAGAGTTTGGTAGAAAAGGAGCTTTGGGATTTGGTCTGTTGG
 TGGTCTTGGTCAATGCTGTTGGTGGTTCACGTGCAATCTACTACGACAAACCATATGCTTCAATTCAAACAAG
 CCATTAGGAGAGCTTGGCTCCAAATTTGAAACTCGTCAAAATATGAGAGCAGATCTGCAAGCAACGTTTCCGAGTC
 GCTCAATGGGTCAATGATCTTGAATATTGCAAGTAAGCAATCAAGATTCACGATAAGGAAGAGGCCAAACATTTCTGG
 TAGACCAAGATCTAGAGCAAGAGATGGAGGAATATTTCTATTCTTCCGCTAAGAGATTATCGAGTTTGGTACCAATT
 TTGCTAGTACCTGACAACCTTGAATGTTGCCAGTACCATTTGGTGGCTTACGAGACCATCATCGGCAACTCGTGTGAACAG
 CCACCGCGAGGAGGTGACTGAGCGGAAAGCTTTCTTTGGGATACAGAGCTGCCCGGACATCGGTAACGAAAAATAG
 ATTCATGGCAGTAATGACCGGGTGTGGAAATCAAAAATGACGAAGGACTTACCGATGTGGATGAGGACAGCGATGATG
 AAGATGGCGGAATTCGTGACGACATATACGATGAATACGTACTCAACCTGAAGAACTAGAAGCAGAGACACAAGAG
 CAATGGAGAGGACAAAGTGAAGTCCCGCAGCAGGAGGCGCATTCCTCGCACACAACAGGATTTCTGGATTCTCCAGC
 CAGAAATCCAAAGTCCCAATCTGTTAGTTTGCATATCAACGATTCCGAACTGTGTTGCCACGCTCAAGGATGGCTCAA
 ATATTTATTCACCCACTCGATACCTGGCTCTCTGGTTTGAAGTCACTCGAACTCCGGAGCAGCAGGATTTCTTTGCTT
 CCTCTCATCAATCTTTGGAGCGGTGGTGGACACGCAACAGAGCTTCCATGCTTATGTTTGAATTCGGTTATCGGAGA
 CAAGACAGATTTCAAACCTTCAAAAGGTGATCCATTCTTCACTGATACTCAAGGAGAATACTATCAACAATTTGCCAGGA
 ATCTTGATAATCTGGATGGAAGAACAGTGAAGGACAATTTGATATCGAGGAATATCTGATCAAAATCTGAAAAAATGG
 TTTGACAGGTTCCGTGATGCAAAATTTGGAGAGAACTCAGTTGCACTTCTGTTCTGCGCTTGGAGTGGACGAAGATC
 TCACGATAGCGGTGGACGATCCAACAGTCCGGATAGCTTTACCAACGATACCATACCCACTCAAGGCAAAATCTAGTC
 AAGATAACATGGCACTCACTGGCGGATCTACTGCCAATGATCAATTTCTTACTTGGCAAGATTATAAACCACTACTGGT
 CTTGCTGCTGATGCAATACCGCTTCTTTGATTGGCTGTCTACTATTCTTACTGCGCTTGGGCAAAATCATCGAGC
 TAAATCTTATCAATCACTCTTCTTACCGGTACTGTGGTCAAAGTGCAGAGAACTTTACATCAGACGCAACGATCTATC
 TTGTTACCTCGATCATGTGGTGGGAAGCTTTTCTCTTCAAATCAATCTACGTCTCAGTATTCGATTCATCTTTTAC
 GGATTGGCTTTTTCTCTCTCGCATGGCTCCTTTCTGATAGCGGTGCTGATGGAAGGGGTTGGTCCAGACGATAGCTAC
 TGGTTTGTATGCTGTTGCCGCTCATCGGTTAGTATTTCTTCTGCTTGAATTTCCGAGATGAAGGAGATCTCTGTGA
 AAGCTGGTTTTTCCGCGCTGCATCATTTCAAGGAACACACAAGCTTATGTCGTCATTCTCTGGTTCTGGGGATCTTAT
 CTCACAGACGCTCAAGCTGATGGTCTTGGAACTTCTTCAATCTGCTAGTCCCAAAATGCTGCAATGCTTCTTCTAT
 TGGCTACTCATGTGGCGGTGTTGCTCATCACTTTCTCGGATTGCCAGAAATATATCAGACAAGCGCTGGAAGATAC
 CATCTTTCTAGCGCTCGCTTTCAGAGCTAAGATTGTCATGTGGTTTTTGGTCACTGTTTTGATTGAGAATCTTCTCTC
 TCGACGCTCATGTGCTGAATGCTTATCTATTCTCTCTAACCAGTGGCTCATATGGGCAATCATCTTCTCATCAT
 CTCTCTCTTGGATTCTTATGGCAGGCTTCTCTGGTTCTTCCGAATCTTGAATAAGATCACAGTTGGGTTCTACCAA
 TTTTCCGCTTGGTCTCGAGCTCCTAGATGGTGTCAAATGCTGTGGTCTTGCACACCGATAGGACAATACGTACCATGG
 GTTGGCGGTGGGCTTCCAGTGGCTTCTCTCTGATCATTTGGGCTTTGGCTCGGATGCTCGATGCACTTCAAGGTGT
 GGGATTGGTATGCTGTTGCTTCAAACCTTACTGCTGTTCATATTGCTTTCACTCTCATCGGCGCTCAAGTTTGGGTT
 CAATAGCTACTATGTAAGCAGAGCATGTGCACCAAAATAAATGGACCTGGAAGTGTCTTCCCTGATTTTATGACCGG
 GCGGCTGCACTTGAATAAGGTGGTGGTTTGGATCGGTTGATTTTACAACCTGTTATTTGGCGTGGATTTTTCACATCTT
 CAGAAAAAGCAACTTAGCAAGCTTAG

Fig. 105

PUTATIVE AMINO ACID SEQUENCE OF *Botrytis cinerea* uge3 (Gene ID: Bcin01p05750.1)
 MPGSTNSSSDSASTPERLSFDNENS AVGTPLTEKSL LFDVDDIDFAVRNAVREAVNDQWILVYGG LGFISHTVWELAK
 AGYNVAI IDNLSNSFFTVFEKLGIMVDDHYSA PRKNHRPL LKFHDADF RDMNKMTAILEKYDYPGVMSFDSSTVLCNG
 ORSSISQVIHFAAYKAVEESIQHPLKYYSNNVGG LVDFCALLQFGIKMVFSSSATVYQTVADTGVPLREEYVVGSGCS
 GLTNPYQRTKWMGEAILSDLANSDDWEITALRYFNPIGCDSEGLLEDPRAAATNMPVVLRLTGALPALNWYGSQYD
 THDGTAVRDYIHVTDLARGHLAALSNRPSGGFKVYNLTGGOYSVLDVVNAMEKATQTKIPTNI VGRRGDGVGKCV ALAN
 KAEELNWKTEKSLDCNDLWRFLEGTITKAGAC

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Botrytis cinerea* uge3 (Gene ID: Bcin01p05750.1)
 ATGCTCTGGCTCGACAAATTCCTCTCAGATTCGGGAGCTTCCACTCCTGAACGACTCTCCTTTGACAAACGAAAACAGTGC
 TGTGGAACTCCGTTGACCGAAAAATCCTTATTATTCGACGTCGACGATATCGATTTTCAGATTAGAAATGCACTTAGAG
 AAGCAGTTAACGATCAATGGATATTGGTCGTCGGTGGTTTGGGATTCATAGGTAGTCACACAGTCTGGGAAC TAGCCAAA
 GCTGGGTACAATGATATACACCCACAAATTCGCGGTAATCGCTAACAAATTGTTATAGGTGCCATAATCGACAAAC
 CTCAGCAATTCGTTTTTACCGTCTTCGAAAAGCTCCAGTTGATGGTCGATCAGCATTACAGTGCTCCGCGCAAAAATGG
 ACACCGACCATTTACTCAAATTTACGATCGCGATTTTCAGAGACATGAACAAATGACAGCGATACTCGAAAAATATGACT
 ATCCCGGGGTGATGAGTTTCGATTCGAGTTCGCTTACTCTTTGCAATGGTCAGAGATCAAGCATATCCGGCTCATACAC
 TTCGCGCGGTACAAAGCGCTCGAAGAGAGCATACAACACCCCGCTCAATACTATTCAAACAAATGTTGGCGGGCTGGTCGA
 TTTCTGCGCTCTGCTGCAGCAATTTGGGATCAAGAAGATGGTGTTCAGTTCTTCTGCGACCGTTTATGGAAACCGTTGCGAG
 ATACTGGGGTCCACTTCGCGAAGAAATATGGTGGGGTCAGGATGCTCGGGTCTCACAAATCCCTACGGACGCAAAAG
 TGGATGTGCGAAGCAATCTTGAGCGATCTCGCCAATTCGATCCGGATTGGGAGATCAGTGCCTGCGCTACTTCAACCG
 GATCGGATCGGATGAATCGGGCTTCGCTGGGCGAAGACCTCGGGCTGCGCGACAAATCTGATCCCGTCTGCTTTCGCGG
 TGCTTACGGCGGTTTGGCTGCGCTAAAGGTGATGGAAGTATTATGATACCGCAGATGGCAGCGCGTGGGAGACTAC
 ATCCAGCTTACCGATCTTCGCGCGGGCATCTGGCAGCTCTCAGCAATCGGCCAAGCGGTGGCTTCAAGGCTATAACCT
 GGGTACTGGCCAGGATACTCGGCTCTGGACGCTGTAACGCAATGGAGAAGGCCACTCAAGCAAAAATCCGACCAATA
 TTTGTTGGCAGGAGAGGAGGATGTGGCAAGTGTGTAGCACTGGCGAACAGGCGGAGGAGGATTAATGTGGAAGACG
 GAGAAAACTCGAAGATGTTGTTAATGATCTGTGGCGTTTCTTAGAAGGCACCTCAATCAGCAAAAGCACAAAGCATGTTG
 A

PUTATIVE AMINO ACID SEQUENCE OF *Botrytis cinerea* sph3 (Gene ID: Bcin01p05740.1)
 MFFKKASVIPAKSKVLVFLYIYSPGAISTYGLFIVVNPNGPQGLLDSNYRREIQTLNSYPNVTVVGYVSTAYAT
 RQYSSVLEDVITYATWRLEDAGLVGRGIFFDETPSQWSASNASFLANINAAYKNSGLGAELV IHNPGTI PHKKLISGP
 CLPDINVVFEATHKTYRENACEKALTOLKMDPGR LACLMHSPDLSMSTHSDVVS ETQKLRSIVGTLYITSQATELYTDL
 GEHNEQFIHAVSL

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Botrytis cinerea* sph3 (Gene ID: Bcin01p05740.1)
 ATGTTCTTCAAGAAAGGCGCTCAGTGATACCTGCCAAATCCAAAGTTCTCGTCCCGCTCTACATTTACCGTTCCCGTGG
 TGCCTGGGACGGTTACTTCAAGGCAAGTCGGGGAGAGCGACGGGATGTTTGGGAATATTGATCATGGGTCTGACTGAA
 CAACAGCATCTCTAGGATCCGGGCTCGAATTCATCGTCGTGGTTAATCCTCACAATGGCGCTGGACAATTACTTGATA
 GTAAGTACCGAAGAGAGATCCAAACATTGAAGCTCATACGCTAATGTTAGAGTTGTGGTTATGTCTACTGCATATGCA
 ACCAGGCAATTTCCAGTGTCTAGAAAGATGTGACAACCTTACGCCACTTGGAGGCTCGAAGATGCTGGGCTCGGCGTTGG
 AGGCATATTTTCGATGAAACTCGGAGCAATGGTCGGGTCAAAGCGTTCAATTTTGGCAATATTAAAGCTGCAGTAA
 AAGGCAATTCGTGCTAGGAGCAGAGCCCTCTTGTGCTGCATTTCCCAATAIGTTCTATTACTACTGACTGATGTGTC
 ATCGAGGAGGTCAATCACAATCCAGGAACAATTCCTCACAAGAAATTGATATGTGGTCCATGTTTACGAGATATCAATGT
 GGTGTTTGAAGCAACTCACAAGACATATCGTGAACCGCTTGGGAGAAAGCTCTCAGGATCTCAAGATGGACCCAGGGC
 GTTTGGGCTGCTTGATGCACTCTGACGGGATCTCTGATGTCCAGCATTCGGACGTTGATCCGAGACACAGAAAGCTG
 AGATCGATTGTGGGACATTATATATCACTAGTCAGGCAACAGAACTTTATACCGATTTGGGGAGCATTTGGGAACAATT
 CATCGATGCTGTAGTCTCTAA

Fig. 106

PUTATIVE AMINO ACID SEQUENCE OF *Botrytis cinerea* ega3 (Gene ID: Bcin01p05730.1)

MSSGGIFKTPLTSSSEIAINTPPMASKEQKPVNPHKIFTRKCNIIILGLIALFLLAIALALGLTFGLRHHHSSPPASTPTTT
 PSNPYPPTNASYWTPLNLSASNTWNIELLAALDPANIYANTTIYDIDLFLAANTTPPIIRTLHSQSHKVICYFSAGTIETY
 RPDNTNRFPSDYGKQLPDWPNEYWANISSPNVRSIMQTRLDLAVNQSCDAVDPDNDGYSNDNGLKLTEDDSIDYMQWLA
 AEAHGRGLGIGLKNAGEIIDRVLDNVGFVNEQCVQYQECDTWQAFIDNGKPVFNIEYPKADPKVSEAEKTRVCDGSDIH
 ADGFFTIIKKMELDDWVERC

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Botrytis cinerea* ega3 (Gene ID: Bcin01p05730.1)

ATGTCCTCAGGAGGAATATTCAAAACACCTCTCAGGAGCAGCGAGATCGCCATCAACACACCACCCATGGCTTCCAAAGA
 ACAGAAACCTGTTAATCCACACAAGATTTTCACCAGGAAATGCAACATCATTCTTGGTCTGATCGCGCTCTTTCTCCTGG
 CAATAGCCTTGGCTCTGGGTCTGACATTGGTCTACGACATCACCATTCTCCCTCCAGCATCCACTCCTACTACTACA
 CCATCGAACCCGTACCCTCCTACCAACGCCTCATATTGGACCCCAATCTCAACGCTTCCAATACATGGAACATCGAGTT
 ATTAGCGGCGCTCGATCCCGCCAACATCTATGCGAATACAACAATCTATGACATCGATCTCTTCTTGGCGCCAATACCA
 CCCCCCTATAATCCGTACCTTACATTGCGAATCCCAAAAGTAATTTGTTATTTTTCAGCGGGCACCATCGAAACATAC
 CGTCTGACACGAATCGCTTCTTCTTCCGATTATGGCAAGCAGCTTCCGACTGGCCAAACGAATATTGGGCTAATC
 TTCTCACCAAAATGTGCGATCCATCATGCAACACGCTTGGATTGCGGTTCAATCAATCATGCGATGCGGTCGATCCCG
 ACAACGTTGATGGGTATTCCAATGACAACGGGCTCAAACAAACAGAAAGATGACTCTATTGATTATATGCAGTGGTTGGCG
 GCTGAGGCCCATGGACGGGGTTTAGGGATTGGTCTGAAGAATGCTGGCGAGATTATCGATCGTGTATTGGACAACGTGCA
 GTTTGCTGTCAACGAGCAGTGGGTGACGTACCAGGAGTGTGACACCTGGCAGGCATTATTGACAATGGTAAGCCCGTAT
 TCAATATCGAGTACCCAAAAGATGCACCGAAGGTTAGTGAAGCGGAAAAACAAGAGTTTGTGATGGCTCAGACATACAT
 GCGGATGGCTTTTTCACCATCATCAAAAAGATGGAGCTGGATGACTGGGTAGAGCGCTGCTGA

PUTATIVE AMINO ACID SEQUENCE OF *Botrytis cinerea* agd3 (Gene ID: Bcin01p05720.1)

MVLLYHLVTHILPLSLFLDAALGHRHRRNPAAEDNLPQSESVAVTNPQAIMTSTVPAAPLATVSIQTLAVLANTTVATP
 PLAELIATDAVDTVSSKVLVIARDSVSAYSASWGLNDRGIPYETLIVPAAGVALPTLNSSETHGNYGLIVMSELSYSYP
 DLGYQSAITADQWQAIYNYQTAFRVRLVRLDSYPSAAFGEALGACCNDGVEQLVHISDNFAFPKAGLKTGATMSTKGIY
 HYPTQITNSTLAKEFLQLGASSDGGFTTASTAGVINNINGREQMVFYVPFSTDWAVTSVWLQHAWIDWGRSLYTGYYRA
 LLSTQIDDMFLESDIYSPAGSTYRIGTADLAQHITFMGSVNSKLNAGSNWFIEVGHNGNGNVEKSDEINASESVCSGPI
 EYGEQIDTPLEWVKPLGTGTDIWPKTSVLYPNYTTACLSDDSLLTWWITPSNLNAFAHISHTFTHEQNNATYADVYREM
 TWNQAWLTATGFANAEEKFSPQGLIPPAITGLHNGDALRAWADSGITHAVGDNTRAALLNTENEHWPLFTTVEANGYAGIQ
 VTPRWATNIYYNCDMPDCTVLEWINTSAGSGDINTLLEVEKQTNVRHLLGLHDAFMVDWPLITHKHDDLAEIFVNRMT
 DSCGASLSYQLDTSSTITGFTLSANGNTCSPLPVTLPGSVTDTQGATVEQIGNDPTTLWVTLSGAPVSFTLTTPIT
 SS

Fig. 107

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Botrytis cinerea* agd3 (Gene ID: Bcin01p05720.1)

ATGGTGTATTGTACCACCTCGTTACCCATATTCTCCCTCTGAGCTTGTTCCTAGATGCAGCTCTTGGCCATCGGGCTCA
TCGCCGAAATCCCGCTGAGGCGGATAATCTCCCTCAATCAGAATCAGTTGCGGTTACCAACCCTCAGGCTATTATGACCT
CGACAGTTTCTTGGCGCACCTCTCGCTACGGTATCCATTGGAAACGCTAGCTGTCTTGGCAATACTACTGTTGCTACCGCC
CCTCTAGCAGAGCTTATTGCTACTGATGCAGTTGATACTGTCAGCAGTAAAGTTCTTGTTCATTGCACGAGATTCACTCTC
CGCATACTCTGCTTGGAGTGGGCTCAATGATCGAGGAATCCCATATGAAACCTTGATCGTCCCTGCAGCTGGTGTAGCAC
TACCAACCTTGAACAGTTGAGAAACCCACGGAATTATGGACTCATTGTTGTTATGTCAGAACTGAGTTACTCCTACCT
GACTTGGGATATCAAAGTGAATTACAGCGGACCAATGGCAAGCAATCTACAATTATCAAACCGCCTTTGCGGTTGATT
GGTGAGACTTGATTCTTATCCATCCGCTGCATTGGGTACAGAGGCACTAGGAGCTTGTTCATGATGGTGTGAGCAGC
TTGTTACATTTCGACAACTCAGCCTTCCCTAAGGCGGGACTCAAGACCGGTGCGACCATGAGTACCAAGGGCATATAC
CACTATCCTACTCAAATCACAACCTCGACGCTGGCAAGGAGTTTCTACAACCTAGGAGCCTCTTCTGATGCCCCAATTAC
TACCGCAAGTACAGCAGGTGTAATCAATAATTAATGGCAGAGAACAAATGGTGTCTTACGTTCCATTTTCCACAGATT
GGGCTGTACACTCTGTATGGTGGCAACATGCTTGGATCGACTGGGGTACAAGAAGTCTCTACACTGGATACAGAAGAGCA
CTACTCAGCACACAGATTGACGATATGTTCTTGGAGTCAGATATTTATTCACCTGCTGGGTCGACTTACCGCATTGGCAC
GGCCGACTTGGCTCAGCATATTACATTCATGGGTTGCGTTAACTCTAAATTGAATGCTGGAAGTAACTGGTTCAATTGAAG
TTGGACATAATGGTAATGGAATGTGCAAAATCCGATGAAATCAACGCAAGCGAAAGTGTATGTACTCCTTTGATCATG
TGACCCTTACTTCAITCTCTCCGCTTTTGGGTCGCTTTCGGTTCCTTTCAGCCCAATAGATGAGCAAACTAACTTT
TGACTTCAGGCTGTCTCTCTGGAGCCATTGAGATGCGGAACAATCGATACACCATGGAGTGGGTCAAGCCCTTGG
AACCAGAACCGATATCTGGCCCAAAACATCGGTTCTTTACCCCAATTATACCACCGCATGCTTAAGCGACGATTCTCTAC
TCACGTGGTGGATCACCCCTCTAATCTTAATGCCCTTTGCACACATTTCTCACACGTTTACACACGAGGATCAAAACAAT
GCGACTTACGCGGATGTATATCGAGAGATGACCTGGAATCAAGCCTGGCTTACTGCGACCGGATTTGCCAATGCAGAAAA
GTTCACTCCACAGGGACTTATTCACCTGCCATCAGGGGCTTCAATGGTGTATGCGCTTAGGGCTGGGCTGACAGCG
GTATCAGCGATGAGTTGGAGACAATACCAGAGCGGCTCTCTTGAATACCGTAAGTGTGCTGCGTGGCGTGTCTTGGGA
AAACCCCTCTTCTCTTGTGTCACAAACCTTTTCCACACAATTTGCTTAATGTGAACACAGGAAAAATGAGCATTGGCC
TTTGTTCACAACAGTTGAGGCCAACGGCTATGCTGGTATCCAAGTGAAGTCCAAGATGGGCAACCAACATTTACTACAATG
TAAGTTGAGCTTGATCGAGTAGAATCGCTAAATCTGACACAATTAGTGCAGCATGCGCTGATTGTACCCTGTTGGAAATGG
ATCAACACCAAGTCCCGGATCCGGTGATATAAACACTCTCCTTGAAGTTGAGAAACAGACAATGTACAGACATTTGTTGGG
TCTTCACCATGATGCGTTTATGTTAGTGCCACATTCGCTCTTCTCTCCATGAGTGTGTTGCTAATTTTGAATAGGTT
CCATCAAGCCAAATTTGAAGTTATGGCCCTCCTGTTGATTCTTCTCACCACGATTGCGTTGATGTGGTATCCAAACAGG
CCACCATGATAAGCAGTTACTAATTCATTAATGATGTAGTGGCTACACAGGAGCGGCAACGTACACTATCAATGGAGTG
ACAGCGCAACTTTGCTGCTCATGGCATGGGTTGAGACCGTGAAGTCAAGAAATCGTCCGATTGTGAGTTTTGTTTCTGCG
ATGTTTTTCATCCGTAAGTACCGAGTATAGGGTTGATTGGGCTCTTATCACCACAAACATGACGACGTAAGTCTAAAGG
TCCTGTTAACTGTATATCTTCAACCGGTATCAGCTTGTCTGCTATATTTGCAATCGAATGACACGAGATTCTTGTGGA
GCTAGCTTGTATATCAACTCGATACTACAGCTCATCGATCACAGGCTTACACTCTCTGCAATGGCAACACCTGCTC
GACACCGCTCCCGGTCACTCTCCAGGTTCAAGTCACTGATACCGAAGGGGCACTGTGAGCAGATTGGTAACGACGCTA
CAACACTGTGGGTCACTTTGCTGGCGCGCTGTCACTTCACTTTAACCACAGCAATCCCATACGAGCAGCTAA

Fig. 108

PUTATIVE AMINO ACID SEQUENCE OF *Botrytis cinerea* gtb3 (Gene ID: Bcin01p05710.1)

MAQITGLEAASWGDLTKDWWQFIIAFILASVGLGLSFISYLAFOSSIEAYRKWKSAAKQSVASIKKYLVKTLSEL SHYK
 VVAYEKKPESFGVYLLGGFNHTPTSEDLGVLAAQWDLVVDADFQENVIHVLSGLYKPPQVLARLDISLVVPPQCKGSAAL
 EGATIAWVTKLLASSTASGSDCRFSGILISNWDQLPSPMLIEFIFIHKLGFQTYLETSSPGFLRDPKLAELNEVAGLI
 RNGTISNGDERDAFQNGENRPTIKAFYSQAQLRPFVCLWETLDDGVNANAIVRRSYQWSKFYSALSPWIGSNSDLTS
 TSHGIDQKEPLGAFSWLKEPGVMEAHKKWRNLNHTIANEYIPEMTDLAENILGALSIEVDLQPEKSNQLSFADVDLEMP
 ATPQVLLDIPRNSSDVNLPGFSSRSLTPAESLLSIHAPNRRFSDGPYSYLNQSPGNPISASPGSSNDFLGCFPLGVHAS
 RKSFDEILQSGKKLKSLLDLDIDNNVLKEIGGKLSQFCNQHGMMVLSAWHAAIQELANQLCALADDSAPTDFIRVYKGL
 DSGLYQONESRYWAVFAFEERTKLDIFMSRNVQDLSGTILHTFLSSRGCPRHESFEAEKGFQWSTQSDSYLPPRLNDI
 SSLSPSELLRFLQTLQLSSVKGNGDLIDSIIFACERELLSDTFIQMKDACSVMGLGNQKSPQDLIALRSKWHVDNNSQH
 PSEENALYVFNQINDAITIVLKERRNLTLQAITKALIEIMEAKKIDARYDIICLALFSVFRKHAFDEAYVEVDRNTLFN
 DQSDQAAFAELFATGARGESYFDMTPSCFGKLLSDRYRTCHHQPGREPIWTDADPSTPSAYAAKIDIGDFKAKGLSG
 TMRFTFLSVFAIPALLDILLTSTGKGLYLSGNMSRTAQHSATLALMISLLISGMCGTWITCGGSYYLISMAFSAMNQFI
 ATRIVGGVAFSLAAGLIGLIGLIGKDGIVAGLVFFLYLFALSTYLILLATLANFSYPGTTFGSGRPVJLMILPVLFVSP
 TTFVPGYDIYIYLSVLYYFIFLLALGRHTASKWTTWHQNTJEKISDKELKEWYIKTHKGDDRAFDGMTDPAALKISRT
 AMIEEIRKVRSGFRHNCQDPTVKSIVSDSYDATIFLLKWSYSGSGTLPMPYSSTWNMQIKVALDTLKQMTGLRLHNAFI
 HWRQAGDEVGCSLLYFIVALLDKWNSLLAGGRLLGLSAQNTRYRMPVGFALAYYIIGAVLLDLNAAKLHMTAESQNM
 IGDVSSIPDAYDAGVKARRHLYWSMLGRYSLFHVWSLAVASSLLWVFDSTEATLLFIAYVGAYTGLLFYQYTKIFAGPRS
 LKPLL IATCGVLPSSGQILRHFLPQFEYGDVVALAAATWTAAFSLYYAGIRAKPVDTMDSEGRWNKISQDRSFHEFTSP
 GRELLLSQDELRTMFENLDALNDDEKYEVDPMTHPGLIEKISILHHAVGIFEEIKGSSVDSIPNFALSAFPEVKALLDETI
 TAFESGKIYVEGVAMSMFSEDFKDLKAIIGCDSSNIMRIIGCETMDAMDQNSSISLFCGATAEILLHIAAETFGQVSHED
 AILLESLLSSVSPSGLLEQLTYPQGLRNFLNFSNPSKADAENVATCFDDEILRHTAIGCNPNIDWEGLPTEIRELILDRG
 TGQVDALTTDQHSWVRANKLKGPIATFLARRNFGAFVATEKKRYTLEFAKTAPVESSDKHEKSNIMNLFQKTQTRRLTA
 DLITKQLKWPFSKVYHTIGHCLKLFAIAFVAEPELQRELNYTMKSTPKYMRISVMFLITGIWSYANFLOGILMPIFLLHQ
 RKNVETLWKQIRGTTVSLKRQIRIMIDSTGGSSTAFVRVPDASITGSHIINNREGAEAIQESLLSNGICELRGYGGVLK
 QEPADSAKLERISISYKDLALLRREDYVKGKANVYEYEDLEKISKQNVMTTTRRRYPISRRCEGSGNQFEQVLFNKQGL
 VQSGSYILDGNLVRFNCHYRONSFEDELLRAEFVLPHMFCMVSWAAPPKRDQKLDTWIPHSQVIEATFVIGPDVYESQ
 WSYDHKYHPTIYITLNGEPVDTPALIEWDHLGVLLKPTNFAFRHDDHMI GFKSLRSHALPRWLG MNTHQNPVSTSKARSR
 LWQAWKNNSAYDGVIMRWLDERLLRREPMLRPYRRRDHGNLRLAEEYLHENADAIMAVIDLKSISGWAPLAFQIADLY
 AFGGGGSANARTSAPDFKSDHLVLTDSGTWPNEGGSVACRRDMVNLLKAAKWYIMISEANDFGVPKHQTEQENVQTL
 KVIPIWGLDFMTPTHGIFRDRDSEVIAHVRDATKLDIQKNFVPIKALKVKGARTSQYNSNDILQSTRALVNLNAYFSQG
 KHWTVGNNSRIVKNAWRNLWISQDLVSPTPSEGWFQTEIPTIAQLDAALDLWFRYLFIFSLPMPIPAIFQASHHSVSA
 SYG[VCKITRGSTLQIWDHAISWRETNLYSSDLCSLPPFVRNSLLGLMKLTSQTLHHADIILPCADFFNPGEIEIGS
 HQGKLEHRNIFKRKIDPVVNGIPPADISKFSPIKETTSPLPTVTMLSHVWYAKDIKTATLAADIIVNVWGFQDYRLDIYG
 AIDKAPQYSTDCFEILASKSLPGYVNLGCTASPTDVLKKTWVFLNSSISEGLPLALGEAALTGAPVVCTDVGASLRVLT
 FNTGDCFSAYVAPNDAQSLARAQINMLGLLDEWAPYANDPQGYKPPSII DKPSAEVAIITKRNYEKKGELRALGMRRE
 IVQSFQGNRYLREHEQMLWIGKSRDYIKFPSKQRPRTLRLPALPSLAVASNMWQASIPSAIQRPMRPSIFRQSSPSIM
 ARSMQAASTVVPSTLERPTSIMGYGSGVKGYQNIINDYFAGYRPGDSNASTPDQLFLTPPGIHTPGGNSVRSQSPMRKGA
 STRLTMLSRGTSYDTRSESSSLIVPSKRLPGEDSLRDLDTALGRV

Fig. 109

BASE SEQUENCE OF NUCLEIC ACID MOLECULE OF *Botrytis cinerea* gtb3 (Gene ID: Bcin01p05710.1)

ATGGCTCAAAATCACAGGCTTGAAGCTGCTCTTGGGGGACTTAACAAAGATGGTGGCAGTTTGTAACTTTCCCAT
 GCGTCTGGCTGGCTGTTTCCCGTGTAAATTTTGAACAGATTCTGATTGCAATTTATCCTTGGTCTGTGTGCTTGGCTT
 GAGCTTCATATGCTTATCTTGGCTTCCAGAGCTCAATAGAGGCTTATCGAGTAAGTAAAAATAGCAAGAATATCTTCATAT
 CTTATCGCAGACCTGAAAGGTTCAATGTGATAAAGCTTCACTGGCTGTCAACATCTATAGCTAACCTTCTGTGTATGAGA
 AATGGAAATCTGCAAAAGCAATCTGTCCCGGCTCCATCAAGAAGTATCTTGTCAAGACTCTTTCTGAAGTATCACATTAT
 AAAGTCGTGGCTGTGAGAAAGAACCCGAAAGCTTTGGAGTATAGTTAGGTGGGTTCATATAGGCAACAAAGTGAAGA
 CCTGCAAGTGTATAGCAATGGGACCTTCTTGTGTGATGCTTTTCAGGAGAAATGTAATGCATGTTGTATCATCCGGGG
 TTACTACAAACCGCCACAGGCTCTGGCAAGACTTGATATAAGCCTTGTGTGCGGAGCAATGCAAAAGTTCAAGCGGG
 CTGAAAGGTGCTATTGGCTGGGTACCAAGCTATTAGCTTCATCAACAGCGTCAGGTAGCGATTGGCGTTTCTGGGAT
 TTTAATTAGCAATTTGTATGATCAACTACCAAGTCCAATGCTCATCGAATTCATTACCTTCAATCAAACTTGGATTCC
 AGACCTATCTGAAACATCATCTCTGGATTTTACGGATCTCAAAATGGCAGAACTGAATGAAGTAGCTGGCTGATA
 ATAAGAAATGGCAATATCATCAATGGGACGAAACGGGATGCAATTCAGATGCAAGAGATGAGGCCAGCATCAAAAGC
 TTTTGTCTTCAAGCTGCTCTCGGCCATTCTGTGTCTGTATTAGGGAGCTCTGGATGATGGGTAATTCAGCAAAAGC
 CCATTGTGCAAGATCTTACCAATGGTCAMAGTTCTATAGCGCGCTATCCCATGGATGGTTGGTTCAAAATCTGATTAACT
 TCAACATCTCATGGCATAGACAAAGAAAGCCGTTGGGAGCTTTTCATGGCTCAAGGAGCTTGGATCATGGAGGCACA
 TAAAGATGGCGCTGAACCATAGTGAAGCAGATCATCAATATAGCACTCTATCTGTGATCAGCATCAAAATTTAG
 TCGTTGGCATCGACACCAAACTTTACTAACGCTGGTTCAAGATTGCTAATGAATATATACGGAAATGACGGACCTAGCT
 GAGAACATCTGGGAGCGCTCTCATTTGAAGTCGACCTCCAGCCATCGGAGAAATCTAACGAGCTCTCATTTGGCGATGT
 AGACCTTGAATGCCCTCTGCCACTCCTCAAGTCTTTTGGACCTACCAAGAAATTCATCTGATGTAACTACCGGAT
 TTTGCAGTAGATCTCTGACGCGGCGAAGTCACTTTATCCATCGACGACCGAAACGATAGATTCTCGGATGGTCATAT
 TGGTATCTCAATCAATCAGCTGGGAATCCCATATCAGCGCTCTCGTGGTGGTCAATCCAAAGCTTCCTTGGATGCTTGC
 ACTTGGGTTTCATGCTTCGAGAAATCGTTTGTATGAATCTCCAAATCACAAAGAACTCAAAATCCCTTGTATCTTCTG
 ATCCGATGCAATAAATATGTGTGAAGAAATTTGGTGGCAATTAAGCGAATTTGTAACTGAGGAGGAAATGGTGGAGCTT
 TCAGCGTGGCATGCAAGGATACAAAGAACTTGGGAATCAGCTTTTGGCTTAGCTGATGATTCTGCGCCACAGACTTCAT
 CAGAGTGTACAAAGGCTTGAATCGGATTTGAGTACCAAAATGAAGTCGCTAGTGGGAGTGTTTGGCTTGAAGAGC
 GGCATAAGCTTGACATTTTGTATGCAAGAAATGTTCAAGATCTCAAGTGAACAAATCTTGCATACATCTTATCAAGTGGT
 GCGTGTCTCGCCAGCAATCATTTGAGGCGAGAGAAAGGATTTTGGCAGTGGTGGACAGCAATCAGATTGATACCTACCTCG
 ACCATTGGTCAATGACATAAGCTCTCTCTCGCCATCAGAGCTGCTTAGATTCTTCAAGACATTGCAAGTTATCTTCCGTCA
 AGGGCAAGCGGGATTTGATCGATTGATAAATTTGCAATGCGAAAGAGAAATTAAGACTCCAGAGACTTTATCCAGATG
 AAAGATGCTGTGTGTGGTTACCTAGGGAATCAAAATCTCCCAAGATCTCATAGCATTAGATCAAAATGGCAGCT
 GGACAAATTAAGTCGAGCATCTTCTGAGGAGAAATGCTCTCTACGCTTCAACCAATCAATGATGCAATCACTATTGTAT
 TAAAGAAAGAAAGATTGAACACACTTCAGGCTATCAGCAAGGCTCTGATTGAGATTATGGAGGCAAAAGATTTAGCGCC
 CGTGTGATATTATTATTTGCTTGTCTTTATTTTCTGTTTTTGGAGGAGCTTTTGTAGAGGCTATGTTGAAGTCACTGA
 TAGAAAGACCTTGTCAATGATCAGAGCGACAGGCGGCTGCAATTTGGGAGCTTTTGGCAAGGAGGCGCGATGCGAGT
 CTTACTTTGACATGACCCCTAGTTGTTTCCGCAAAATTAATCTGGATGCTTATCGGACTTGTCTATCAACCTGGCGG
 GAGGCTCCAAATCTGGACCGATGCTGATCTTCAACTCCCTCAGCTATGCAAGTGAAGATTTGATCTGGAGATTITAA
 AGCCAAGGCTCTTTGCGGCAATGAGATTACTTTCTTGAAGTGTCTTCCGATACGAGGCTTTTGGATATCTGCTAT
 TAACAAGGCTGGAAGAGGCTCTACTTGAAGTGAATATGAGTGGGAGGCTCAGGATCTGCTAGCTTGGCTTGAAG
 AITTCCTTTTAAATATCAGGCAATGTGTGGCAGATGGATAACATGGGCGGCTTCTTACTATCTCAATTCATGGGCTTTTC
 CGCAATGAACAAATTCATAGCAGGAAATCGTTGGCGGTGTGCTTTCTCACTTGGCGCTGGCTTGAATGGCTTGAATG
 GTCTTGGATCAAAAGATGGTATGTTGGAGGCTAGTATCTTTTGTACTTGTTCACCTAAGGCACTATTTGATAGCTG
 CTTGCAACTCTGGGCAATTTTCTATCCAGGTACGACTTTCCAAATCGGAGCTCAGTTATCTCATGATTTTACCTGT
 CTTATTTGTTTCCAAATCAGACAAATTTTGTCTGCTGTTATGATATCTATATCTATTGAGTGTCTTGTATGTCTTTA
 TATTTCTTCTCGCTTTGGGAATCGACACAGGATCTAAATGGACTACATGGCATCAAAATATGAAAAGATTAGTGAC
 AAGGAATGAAAGAAATGGTATATTAGACTCACAAGGAGCGGATGAGGCTGCAATTCGATGGAATGAGCGATCGGCAAGC
 CTTGAAAATTTCAAGAACTGCAATGATTGAAGAAATAGAAAGTACGAGTGGCTTTGAGCATCACTGTCAAGATCCAA
 CTGTCAAAATCGTTGGTGGACAGCTATGACGCAACAAATTTCTATTGAATGGTACTGGGGTACTCGGSAACGGCACTA
 CCAATGCCATATTGATCACTTGAAGATGCAAAATTAAGGTTGCTCTGGATGCTCAAGCAATGCAACAGGCTTAG

Fig. 110

GTTGCAGCAATGCTTTATCCATTGGCGTCAGGCTGGTGTAGGTGAGTAATTTCTTTCCACATATAATTATTAAATG
 CGAAATGAATACTAAAATAAGGCAGGTTGGTTGTAGTCTTCTACTTTATCGTAGCACCTTCTCGACAAATGGAACCTCA
 CTTCTTCCCGGTGGACGTCTCCTCGGCTATCGGCGCAGAAATACAAATACCGGATGCCCTGTGGCTTTGGCTTTGGCTTA
 TACCTAATTTGGTGCAGTCTTCTAGATCTCAATGCCGCAAGGCTTCATACCATGACAGCTGAAAGTCAGAAATATGCTGA
 TTGGCGACGCTGCTTCAATTCCAGACGCAAGTCGACGCAAGGTGTCAAGGCGACGGAGACACCTTTATTGGAGTATGCTGGGA
 CGGTACTGATTTATTCATGTTTGGAGTTTGGCTGTAGGCTCTAGTCTTCTGTGGGTATTGACAGCACAGAGGCTTCAAC
 CCGTCTTTTATTTGCTTATGTTGGAGGCTTACAGGTAAGGACCAATTCCTAATGATTTGAAACGTTTGTAAATGATATCC
 ACAGGTTTACTATTCTATCAGGTACATTTCCCTTGTCAAGAACCTTGACAAAAATTTTAAATCTACATCAGCTAAACTCT
 CATCTAGTACACAAAAATTTTGGCGGCGCTCGAAGTCTCAAGGCTCTTCTCATAGCCAGTTGGCTTGGCTTGGCTCTG
 GACAAATACTTAGACATTTTCTTCTCAATTCAGTACTGTGATGTGGTAGGCTTGGCGGACGCAACATGAGCTGACGCA
 TTCTCTCTCTATATTACGGCGGCAATAGAGCAAAACAGTTGATACGATGGACTCGAAGGTCGCAATTTGGAATAAGAT
 ATCACAAGATAGATCATTTCCAGCAATTCACAAGTCCGGGCTGTGAGTTATTACTATCTCAAGACGAGCTCCGATGACTT
 TCGAGAATCTGGATGCCCTTAACGATGACGAAAAATATGAAGTGGATCCTATGACACATCCCGGTTTGGAAATTAAGTCG
 ATTCTACATCATGCTGTGGAAATTTTGAAGAGATCAAGGCGAGCTCGGTTGATTCAATCCCAATTTTGGCTGTAGTGC
 ATTTCCGGAAGTAAAGGCTATTGGATGAGACCATCACAGCTTTTGAAGGTGGAAGATTTGGTGTGAAATGCTGCTGCTA
 TGTCTATGTTCTCTGTGATGAATTCAGGACCTAAAGCAATTGGCTGCGATTCCAGTAATCTAATGAGGATCATCATTTGGT
 TGGGAAACATGGATGCGATGAGCCGAAATTCAGCATCAGTCTTTTGGCCAGCGTAAGTGAATTTTCTCTATTGGC
 GCGCAGGATGTCAGATTCCTTACTGGAGTCATTCTATAGCCGACCATTTTGTGCTACCTGCTACAGGACTGCGGAA
 ATAGTGTTCAGATTGCGAGCGGAAAGCTTTTCAAGGCTTTTGGCAGGAGAGGCTATAGTCTGGAATCATTTGCTGTCTG
 CGTTTCAGCGCTAGGCTTATTGGAGCAAAACCTTGTACCTCAGGAGCTACGAAACTTCTTGAATTTCTCAAAACCTCAA
 AAGCGATGCGAAAAATGTTGGCAGCTGTTTGTATGCGAAATCTTAGACATACAGCTATCGGATGCAACCCCAACAT
 GATTGGAAGGACTTCTTACAGAGATTCGAGAGCTCATTTCCGACAGATGACGCGGACAAATGATGATGACAGCTGGA
 CGAGCATAGTTGGGTACGAGCGAAGCTCAAGGCGCTACCCATCGGCTTCTTATAGCTCGCGCAATTTTGGTGGCT
 TGGTGGCAGTGAAGAAAGAGGTCAGACATTTGGAATTTGCGAAGACTGCTCGGATGAGAGTTGCGATAAGCATGAAAG
 TGTAAACATAATGAACCTTATTGGAAAGACACAAACACGAGATTGACAGCAGATTAAATCACAACACAGCTGAAATGGCG
 ATTCAAGTAAGGTTTATCATACGATTGGGCTTGGCTGAAGTTATTGCGCATAGCATTTGTGGCAGAGCGAGGTTGCAAA
 GAGAGCTCAATTTATACCATGAAGTCAACTCCAAAGTACATGCGATCGATTGTCTGTTGATACTGGAATATGCTCA
 TAGCGCAATTTTTGCGAGGATTTTGTATGCGCAATTTTGTGCTCCATGGTAGAAAGATGTAGAAACTCTCTGGAAACA
 AATACGTGGTACGAGAGTGTCTATTAAAGCGCTCAAGGATAATGATAGACAGCACTGGAGGCTCTTCCGACAGCATTTGTC
 GAGTCCCGGATACAGCCAGCATTAAGTGGTATGCGCATATCATTAACAATGATAGGGAAGGTCGTGAAGCCATACAAGAGTCG
 TTAGTCAGCAATGGCATGTGGAGCTCCGACAAATAGTGGTGTCTCTCAAGCAAGAGCGAGCCGATTGAGCCAGGCTGA
 GCGCATTAGCATTTACAGCAAGGATCTTCTCTTTTACGCAAGAGAGCTATGTCAAAGGCTGAAAGGCAACGTTTATG
 AATATGAATACGACTTGGAAAGATTTCAAAACAGAAATGTCATGACACAGCTCGCGCTATCCGATTTCCGAGCATGT
 GTGGAAAGGAGTAACCAATTTGAACAAGTGTGTTCAATAAACAAGGCTTGTGTTCAAGTGGGTCCTACATTCTGATGG
 AAATCTCGTGGCTTCAATTGCCATTATAGACAAAAACAGCAATTTGAAGATGAGTTGTTGAGAGCAGAGTTGTATTGC
 CGCATATGTTTTCATGTTTTCATGGGCGCTCTCTCTGTAACGTCAGACAAAGCTGGACACATGATACCCCATTCG
 CAAAGTATCGAGGCCACCTTTGTCATCGGCGCGATGTATATGATCAGTGGTCATATGATCATAAATATCATCCAAC
 CATATACACAACATTTGAATGGCGAGCTGTGACACAGCTGGCTGATAGAATGGGATCATCTCGAGTCTCTCAAAAAGC
 CCACCAACTTTGCAATTTGGCCATGATGATCAGATGATTGGCTTTAAATCATTAGGCTCAGATGCTTTGGCCAGATGGCTA
 GGCATGAATACCCATCAAAATCCAGTCTCCACTTCGAAAGCTAGGTCGAGGCTATGGCAAGCATGGAAGAAACATTTGGG
 GTATGATGGTGTATCATGATGAGATGGCTTGAAGAAAGACTTCTTGGACGGGAACCAATGTTGGGCGCATATTATCGAAGAC
 GTGATCAGCGCAACCTCAGGCTGGCTGAAGAAATTTGATGAGAAATGCAAGACCAATTATGGCGTTATCGATCTTGAT
 AAATCAATTTGGGATGGGACGACTGCTATTGAGATTGAGATTGTACGCAATTTGGACAGGGGGTTCTGCCAATGC
 TCGCACGAGGTCGCGCCAGATTTCAAAAGCGACGAGCTTCTATGTTCTTGGCACAGACTCCGGAACCTTGGGCGAATGAAG
 GAGGTGGGGTGTCTGATGTGGAAGAGACATGTTAAACAATCTTAAAGCAGCGAAATGTTCAATGATTTCAGAAATCAGCG
 AATGACTTTGGAGTGGCTAAACATCAACACAGAGAACGTCCTCAACACTGAAAGTCATTCGAATTTGGGAGCTGATTT
 CATGACACCGACCCATGGAATTTCAAGAGATCGATTAGATTCAAGAGGTCATTGATGCTGTAGAGATGCGACAAATTAG
 ACATTCAGAGAAATTTTGTTCGAATTCGAAAGCTGTGGTGAAGGGGCTAGAAACGAGTCAATATTGCAACAGTGAATG
 CTCCAATCAACCGGAGCTTTGGTCAACCTAAAGCGCTATTCTCCCAAGGAAACATTTGGACGGGTGTCTGGAACAGTAG
 AATCGTTAAGAAATGCTGGCGGAACCTATGGAATCTGACAGAGAGCTTGTGAGGCCAAGCTGCTGAGAGGGTGGTTTCAAG

Fig. 111

CTGAGATACCTACAATAGCTCAACTCGACGCCGCACTCGATCTCTGGTTTCGCTACTTGTTTATATTCTCTCTTCCCATG
CCTGAGAGGATTCCGGCGATTTTCCAAGCGTCACATCATTCCGTCAGTGCTTCGTATGGAATTGTGTGCAAGATTACTAG
GGGCAGCACATTGCAAAATCTGGGATCACGCTATTAGTTGGCGCGAAACAAATCTCTACCTGTCTTCAGATCTTTGCTCTC
TACCACCATTTGTGAGAACTCGTTACTTGGTCTCATGAAGCTCACCAGTCAACTGACACTTCACCACGCCGATATCATT
CTACCTTGGCGCGACTTCTTCAATCCTGGATGGGAAATCGAAATTGGATCACACCAAGGCAAACTCGAGCACCGAAACAT
TTTCAAGCGCAAGATTGATCCTGTCTGTTAATGGTATCCGACCTGCAGATATCTCTAAATTCAGTCCAATCAAGGAGACAA
CTTCACCTTTGCCAACAGTCACCATGCTTTCTCATGTTTGGTATGCCAAGGATATCAAGACTGCCATTTTAGCTGCTGAT
ATCATTGTAAATGTATGGGGATTTAAAGACTATCGCCTCGATATCTACGGTGCAATTGACAAAGCACCACAATACTCAAC
AGACTGTTTCGAAATATTAGCCTCCAAATCCTTACCAGGCTATGTCAACTTGTGCGGAAGTCAAGGCCAACTGATGTGC
TCAAGAAAACCTGGGTCTTCTTAATTCCTTATCTCCGAGGGGCTTCCCTTAGCATTGGGCGAAGCAGCTTTGACTGGC
GCGCCTGTTGTATGTACAGATGTTGGGGCTTCCCTTCGGGTTCTTACAGATTTCAACACCGGCGACTGCTTCAGTGCTGT
GGTTGCCCCCAATGATGCACAAAGTCTTGCAAGAGCGCAGATCAATATGCTTGGTCTTTTGGACGAATGGGCTCCTTATG
CGAATGACCCTCAAGGTTACAAGCCTCCTTCTATCATCGATAAGCCTTCTGCAGAAGAAGTTGCGATTATTACCAAGAGA
ATGTATGAGAAGAAAGGCGAAGCTTCGAGCCCTTGAATGCGAAGTCGAGAAATTGTTCAAAAATCTTTGGAGGGCAACAG
GTATCTCAGAGAGCATGAGCAGATGCTCTGGATTGGAAGTCTCGCTACGACATAAAATTCCTTCAAAAACAACCAAGAC
CCACATTAAGACCTGCACTACCATCACTCGCAGTAGCAAGTAACATGTGGGGACAAGCATCTATACCTCTGCTATCCAG
ACTCGACCTATGCGACCATGCATCTTCCGGGGATCCAGTCTAGCATAATGGCAGGATCCATGCAAGCAGCTTCAACCGT
TGTTCCATCCCCACTCTCGAAAGACCTACTTCCATCATGGGTTACGGCAGTGGTGTCAAGGGTTATCAAAATATCAACG
ATTACTTCGCCGGCTACCGACCTGGCGATAGTAACGCCTCTACTCCGATCTCCAATTCCTCACGCCTCCTGGTATCCAC
ACGCCGGTGGTAATTCTGTTAGAAGCCAGTCACCGATGAGGAAAGGGGCATCTACAGTCTTACGATGCTCTAGAGG
CAGCACTAGTTACGATACTAGATCTGAGAGTTCCTCATTAATCGTACCCTCTAAACGATTACCTGGAGAGGATTCAATCC
TTCGTGATCTGGACACCGCTCTTGGACGCGTGTA

Fig. 112

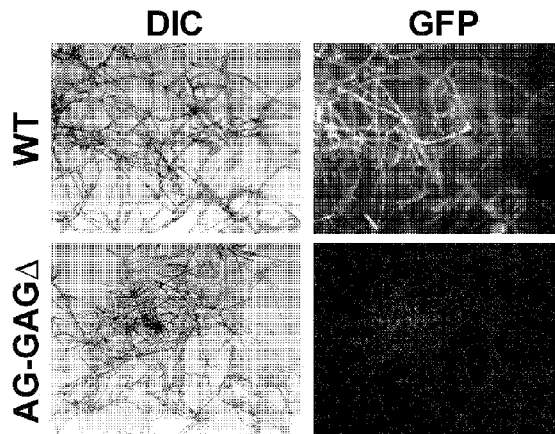
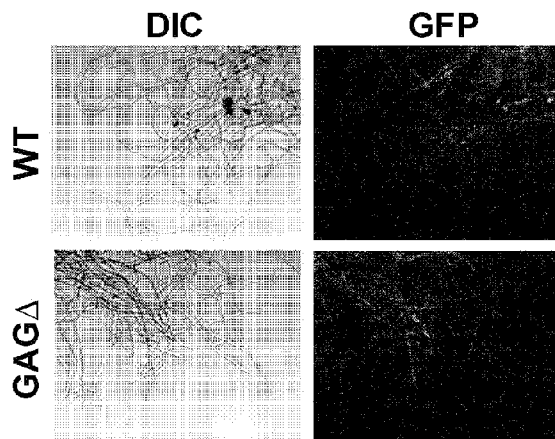
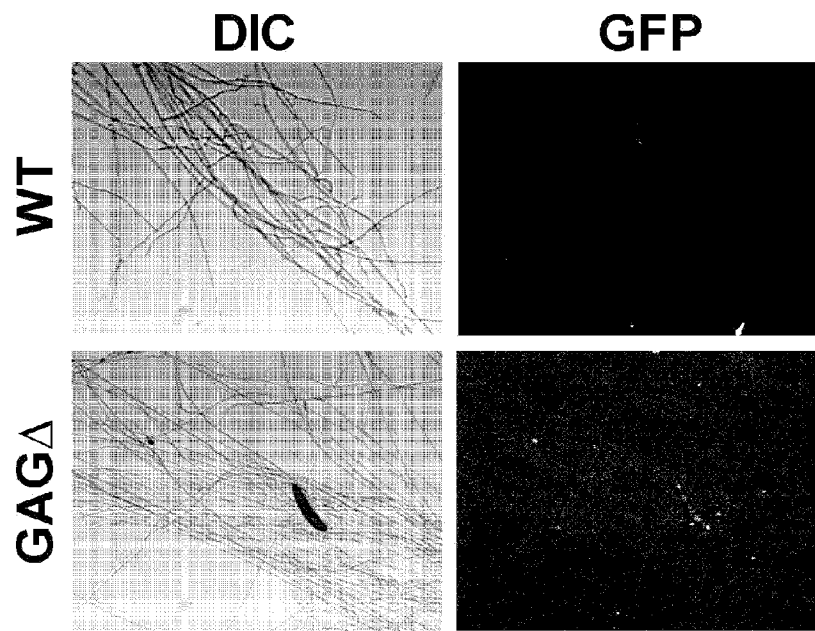
Aspergillus oryzae***Botrytis cinerea***

Fig. 113

Cochliobolus heterostrophus

SEKVENSLISTE

Sekvenslisten er udeladt af skriftet og kan hentes fra det Europæiske Patent Register.

The Sequence Listing was omitted from the document and can be downloaded from the European Patent Register.

