CLAIMS

1. A method for identifying a *Ganoderma*-infected palm tree, comprising:

isolating proteins from a sample derived from leaves of a palm tree;

determining protein profile of the sample by subjecting the proteins from the sample to 2-dimensional gel electrophoresis; and

comparing the protein profile of the sample to a protein profile obtainable from a normal non-*Ganoderma*-infected palm tree to determine whether the palm tree is infected with *Ganoderma* disease, wherein protein profile of the sample including two or more proteins selected from one of the groups consisting of proteins having an energy function, proteins having a metabolism function, proteins having a stress response function, proteins having a disease/defense function and proteins having a cell structure function indicates that the palm tree is infected with *Ganoderma* disease, wherein the proteins having a

i. disease/defense function are selected from the group consisting of ginkbilobin-1 (ID No. GNK1_GINBI) and cyclophilin (ID No. gi|192910744);
ii. energy function are selected from the group consisting of ATP-dependent clp protease (ID No. gi|307136002);
iii. metabolism function are selected from the group consisting of transketolase (ID No. gi|14787119 and gi|75140229);
iv. stress response function are selected from the group consisting of abscisic stress ripening (ID No. gi|270064305); and
v. cell structure function are selected from the group consisting of fiber protein Fb2 (ID No. gi|192910804).

2. The method according to claim 1, wherein the proteins having an energy function are further selected from the group consisting of ATP synthase beta subunit (ID No. gi|192910868); carbonic anhydrase 3 and carbonic anhydrase (ID No. gi|326582932 and, gi|290875537); chlorophyll A/B binding protein, putative (ID No. gi|255557387); chloroplast manganese stabilizing protein (ID No. gi|313586398); cytochrome c oxidase subunit II PS17, putative (ID No. gi|109892850); ferredoxin-NADP reductase, putative (ID No. gi|255538962); glyceraldehyde 3-phosphate dehydrogenase (ID No. gi|82400215); NADH-cytochrome b5 reductase-like protein OS=*Arabidopsis thaliana* GN=At5g20080 PE=1 SV=2 (ID No. NCB5R_ARATH); oxygen evolving enhancer protein 1 [*Litchi chinensis*] (ID No. gi|326467059); oxygen

evolving enhancer protein 2 (ID No. gi|8131593, gi|297826499 and gi|11134035); oxygen-evolving enhancer protein 3-1 [Zea mays] (ID No. gi|195633817); peroxisomal glycolate oxidase (ID No. gi|167962794); phosphoenolpyruvate carboxylase (ID No. gi|7768089); Photosystem I reaction center subunit II, chloroplast (ID No. gi|255551453); Photosystem I reaction center subunit IV, chloroplastic, Short=PSI-E; AltName: Full=P (ID No. gi|131176); Photosystem II 23 kDa polypeptide (ID No. gi|19898); protochlorophyllide reductase A,chloroplastic; Short=PCR A; AltName: Full=NADPH-protochlorophyllide oxidoreductase A (ID No. gi|129708); PsbP (ID No. gi|25992740); and ribulose-1,5-bisphosphate carboxylase/oxygenase (ID No. gi|11558717, gi|76574195 gi|134104 and gi|7960277).

3. The method according to claim 1, wherein the proteins having a metabolism function are further selected from the group consisting of 24 kDa seed maturation protein (ID No. gi|192910858); 40S ribosomal protein S5 (ID No. gi|192910844); 60S ribosomal protein L7-like protein (ID No. gi|192912978); ABC transporter B family member 15 OS=*Arabidopsis thaliana* GN=ABCB15 PE=1 SV=1 (ID No. AB15B_ARATH); ABC transporter C family member 2 OS=*Arabidopsis thaliana* GN=ABCC2 PE=1 SV=2 (ID No. AB2C_ARATH); cetyl-CoA carboxylase (ID No. gi|209168853); AGAMOUS-like MADS box transcription factor (ID No. gi|73852969); aldo/keto reductase family protein (ID No. gi|297848944); E3 ubiquitin-protein ligase SINA-like 6, putative (ID No. SINL6_ARATH); elongation factor Tu (ID No. gi|225456880); fructose-bisphosphate aldolase (ID No. gi|255557204 and gi|300681519); Geminivirus Rep-interacting motor protein OS=*Arabidopsis thaliana* GN=GRIMP PE=1 SV=1 (ID No. GRIMP_ARATH); glutamine synthetase, cytosolic (ID No. gi|113171384); IAA type protein (ID No. gi|50404477); isopentenyl-diphosphate Delta-isomerase I OS=*Camptotheca acuminata* GN=IPI1 PE=2 SV=1 (ID No. IDI1_CAMAC); P1B-ATPase heavy-metal transporter [*Oryza sativa Japonica* Group] (ID No. gi|315623028); pentatricopeptide, putative, expressed [*Oryza sativa Japonica* Group] / Pentatricopeptide repeat-containing protein At4g38010 OS=*Arabidopsis thaliana* GN=PCMP-E45 PE=2 SV=1 (ID No. At4g38010 and gi|108864632); peptidyl-prolyl cis-trans isomerase, putative (ID No. gi|255547634); phospholipase D zeta OS=*Arabidopsis thaliana* GN=PLDZETA PE=2 SV=1 (ID No. PLDZ1_ARATH); phosphoribosylaminoimidazole carboxylase, chloroplastic (Fragment) OS=*Vigna aconitifolia* GN=PURKE PE=2 SV=1 (ID No. PUR6_VIGAC); plastidic aldolase (ID No. gi|294440432); serine-glyoxylate aminotransferase, putative (ID No. gi|2754849);

stearoyl-Acyl-carrier protein desaturase (ID No. gi|1785862); T-protein of the glycine decarboxylase complex (ID No. gi|407475); triose phosphate isomerase cytosolic isoform (ID No. gi|192910674); and vitamin-b12 independent methionine synthase, 5-methyltetrahydropteroyltriglutamate-homocysteine (ID No. gi|224131686).

4. The method according to claim 1, wherein the proteins having a stress response function are further selected from the group consisting of heat shock protein 70 or 90 (ID No. gi|238054071, gi|255570990, gi|2827002, gi|6969976 and gi|108862740); and phosphoglycerate kinase (ID No. gi|226530482 and gi|332591479).

5. The method according to claim 1, wherein the proteins having a disease/defense function are further selected from the group consisting of ascorbate peroxidase, cytosolic (ID No. gi|192912966); CBL-interacting protein kinase 4 OS=*Oryza sativa subsp. japonica* GN=CIPK4 PE=2 SV=2 (ID No. CIPK4_ORYSJ); endoglucanase 18 OS=*Oryza sativa subsp. Japonica* GN=Os06g0715300 PE=2 SV=1 (ID No. GUN18_ORYSJ); endoribonuclease Dicer homolog 1 OS=*Oryza sativa subsp. japonica* GN=DCL1 PE=3 SV=1 (ID No. DCL1_ORYSJ); isoflavone reductase, putative (ID No. gi|255543713); peroxiredoxin (ID No. gi|192910922); peroxisome type ascorbate peroxidase (ID No. gi|192910808); pterocarpan reductase-like protein (ID No. gi|169639232); thioredoxin peroxidase (ID No. gi|192910848).

6. The method according to claim 1, wherein the proteins having a cell structure function are further selected from the group consisting of actine (ID No. gi|48527433); disulfide isomerase 2 precursor (ID No. gi|192912964); F-box/kelch-repeat protein (ID No. gi|15230186); and translation elongation factor G, putative (ID No. gi|255537029);.

7. The method according to claim 1, wherein the groups of proteins further comprises *Micromonas pusilla* CCMP1545 (ID No. gi|303275936); *Oryza sativa Japonica Group* (ID No. gi|22202781); *Physcomitrella patens* subsp. *patens* (ID No. gi|168034023); *Populus trichocarpa* (ID No. gi|224140861); *Vitis vinifera* (ID No. gi|225466832); *Zea mays* (ID No. gi|219363037); *Selaginella moellendorffii* (ID No. gi|302803987); VITISV_010874 (ID No. gi|147843505); VITISV_023080 (ID No. gi|147766924); LOC100284083 (ID No. gi|226530191); Os04g0234600 (ID No. gi|115457386); Os07g0544800 (ID No. gi|115472625); porin, outer plastidial

membrane protein OS=*Pisum sativum* GN=POR1 PE=1 SV=2 (ID No. VDAC_PEA); and Ras-related protein RIC1 (ID No. gi|192910784).

8. The method according to claim 1, wherein the palm tree is infected with *Ganoderma* disease when the protein profile of the sample includes two or more proteins as claimed in any of claims 2 to 7.

9. The method according to claim 1, wherein the palm tree is selected from the group consisting of oil palm, coconut palm, date palm, sago palm, nipa palm, betelnut (*Acreca catechu*) and ornamental palms.

10. The method according to claim 9, wherein the palm tree is an oil palm.

11. The method according to claim 1 or 9, wherein the sample comprises a palm tree extract or a palm tree fraction obtainable from the leaves of the palm tree.

12. The method according to claim 1 or 10, wherein the *Ganoderma* disease is caused by presence of *Ganoderma boninense*.