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 ~~on a 2-dimensional gel~~; and

comparing the protein profile of the sample to a protein profile obtainable from a normal non-*Ganoderma*-infected palm tree~~, wherein a difference in the protein profile of the sample as compared to the protein profile of the 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.

2. 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 having an energy function~~, wherein the proteins~~ are selected from the group consisting of ATP synthase beta subunit (ID No. gi|192910868); ATP-dependent clp protease (ID No. gi|307136002); 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 ~~palm tree is infected with *Ganoderma* disease when the protein profile of the sample includes two or more~~ proteins having a metabolism function~~, wherein the proteins~~ are 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); transketolase (ID No. gi|14787119 and gi|75140229); 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 ~~palm tree is infected with *Ganoderma* disease when the protein profile of the sample includes two or more~~ proteins having a stress response function~~, wherein the proteins~~ are selected from the group consisting of abscisic stress ripening (ID No. gi|270064305); 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 ~~palm tree is infected with *Ganoderma* disease when the protein profile of the sample includes two or more~~ proteins having a disease/defense function~~, wherein the proteins~~ are 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); ginkbilobin-1 (ID No. GNK1_GINBI); 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); and cyclophilin (ID No. gi|192910744).

6. 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 having a cell structure function~~, wherein the proteins~~ are 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); fiber protein Fb2 (ID No. gi|192910804); and translation elongation factor G, putative (ID No. gi|255537029);.

7. 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 selected from the~~ groups of proteins further comprises ~~consisting of~~ *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, wherein the protein profile of the sample comprises ginkbilobin and cyclophilin.

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