A METHOD FOR IDENTIFYING A *GANODERMA*-INFECTED PALM TREE

FIELD OF THE INVENTION

The present invention relates to a method for identifying a *Ganoderma*-infected palm tree. More particularly, the present invention relates to a method for identifying a *Ganoderma*-infected palm tree using sample derived from leaves of a palm tree and applying difference gel electrophoresis (DIGE) technique to the sample.

BACKGROUND OF THE INVENTION

Proteomics is the study of the protein complement of the genome. It can be defined as the large-scale study of proteins in terms of their expression levels, post-translational modifications and interactions with other molecules to obtain a global view of cellular processes at the protein level.

The field of plant proteomics is just at the very beginning and lags several years as compared to proteomics of unicellular prokaryotes and mammalian eukaryotes. There is no doubt that the understanding of protein expression in plants will contribute to crop improvement.

Basal stem rot (BSR), which is caused by *Ganoderma* sp, is the most serious disease which affects mature palm trees. *Ganoderma* come from the fungi kingdom and are basidiomycetes which cause the rotting of hardwoods of palm trees by decomposing lignin, as well as cellulose and related polysaccharides. *Ganoderma* species which cause stem rot (or butt rot) disease include, but are not limited to, *Ganoderma boninense, Ganoderma lucidium* (prominent in temperate region), *Ganoderma miniatocinctum, Ganoderma zonatum and Ganoderma tornatum.* Of particular interest is *Ganoderma boninense*, which is a main threat to palm trees, such as oil palms in the Southeast Asia region. The disease involves degradation in the base or butt of the palm trees. All palm trees are susceptible to *Ganoderma* basal stem rot. Currently, no palm trees are resistant to this disease.

The abovementioned problem has been known for generations as search for solutions has been considerably hindered by natural restrictions. These restrictions include slow disease progress where the disease does not show any visual or physical symptoms until the oil palms are at least 7 to 15 years old. Though many researches on *Ganoderma* infection have been carried out over the years, basic understanding at the molecular level of *Ganoderma* infection has not been studied. Most of the studies looked at the problem from an applied point of view and this has had limited results. Some studies looked at detecting *Ganoderma* disease using roots of palm tree. This method however requires digging into the soil to harvest the roots for analysis. This method can cause adverse harm to the palm tree especially if digging is not carried out with care.

Consequently, there is a need to provide a method that seeks to detect *Ganoderma*-infected palm trees at an early stage without causing any adverse harm to the palm trees or to address at least one of the problems described hereinabove, or at least to provide an alternative.

SUMMARY OF THE INVENTION

The above and other problems are solved and an advance in the art is made by providing a method for identifying a *Ganoderma*-infected palm tree in accordance with this invention. It is an advantage that the method in accordance with this invention allows early detection of *Ganoderma* disease in a palm tree without causing any adverse harm to the palm tree. A second advantage of this invention is that with the early detection, actions can be taken early to prevent basal stem rot disease in palm tree or to cure the palm tree of the disease.

In accordance with an embodiment of this invention, a method for identifying a *Ganoderma*-infected palm tree is provided. The method comprises the steps of 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 gel electrophoresis on a 2-dimensional gel; and comparing the protein profile of the sample to protein profile obtainable from a normal non-*Ganoderma*-infected palm tree, wherein a difference in protein profile of the sample as compared to the protein profile

of the normal non-*Ganoderma*-infected palm tree indicates that the palm tree is infected with *Ganoderma* disease.

In accordance with some embodiments of this invention, the palm tree is selected from the group comprising oil palm, coconut palm, date palm, sago palm, nipa palm betelnut (*Acreca catechu*) and ornamental palms. In accordance with an embodiment of this invention, the palm tree is an oil palm.

In accordance with some embodiments of this invention, the sample comprises a palm tree extract or a palm tree fraction obtainable from the leaves of the palm tree.

BRIEF DESCRIPTION OF THE DRAWINGS

The above and other features and advantages of the present invention will more clearly understood from the following detailed description taken in conjunction with the accompanying drawings:

Figure 1 illustrates how artificial infection is carried out to obtain *Ganoderma*-infected seedlings.

Figure 2 shows images of a 2-dimensional gel electrophoresis separation of proteins in Gel_1 containing samples H2 (not infected with *Ganoderma* at month 2), M2 (infected with *Ganoderma boninense* PER71 at month 2) and an overlay image of both samples.

Figure 3 shows images of a 2-dimensional gel electrophoresis separation of proteins in Gel_2 containing samples H3 (not infected with *Ganoderma* at month 3), M3 (infected with *Ganoderma boninense* PER71 at month 3) and an overelay image of both samples.

Figure 4 shows images of a 2-dimensional gel electrophoresis separation of proteins in Gel_3 containing samples H4 (not infected with *Ganoderma* at month 4), M4 (infected with *Ganoderma boninense* PER71 at month 4) and an internal overlay image of both samples.

Figure 5 shows images of a 2-dimensional gel electrophoresis separation of proteins in Gel_4 containing samples H5 (not infected with *Ganoderma* at month 5), M5 (infected with *Ganoderma boninense* PER71 at month 5) and an overlay image of both samples.

Figure 6 shows images of a 2-dimensional gel electrophoresis separation of proteins in Gel_5 containing samples H6 (not infected with *Ganoderma* at month 6), M6 (infected with *Ganoderma boninense* PER71 at month 6) and an overlay image of both samples.

Figure 7 shows images of a 2-dimensional gel electrophoresis separation of proteins in Gel_6 containing samples H7 (not infected with *Ganoderma* at month 7), M7 (infected with *Ganoderma boninense* PER71 at month 7) and an overelay image of both samples.

Figure 8 shows images of a 2-dimensional gel electrophoresis separation of proteins in Gel_7 containing samples E2 (infected with *Ganoderma boninense* SDG55 at month 2), E3 (infected with *Ganoderma boninense* SDG55 at month 3) and an overlay image of both samples.

Figure 9 shows images of a 2-dimensional gel electrophoresis separation of proteins in Gel_8 containing samples E4 (infected with *Ganoderma boninense* SDG55 at month 4), E5 (infected with *Ganoderma boninense* SDG55 at month 5) and an overlay image of both samples.

Figure 10 shows images of a 2-dimensional gel electrophoresis separation of proteins in Gel_9 containing samples E6 (infected with *Ganoderma boninense* SDG55 at month 6), E7 (infected with *Ganoderma boninense* SDG55 at month 7) and an overlay image of both samples.

Figure 11 is an exploded image of an overlay of samples H2/M2 for Gel_1.

Figure 12 is an exploded image of an overlay of samples H3/M3 for Gel_2.

Figure 13 is an exploded image of an overlay of samples H4/M4 for Gel_3.

Figure 14 is an exploded image of an overlay of samples H5/M5 for Gel_4.

Figure 15 is an exploded image of an overlay of samples H6/M6 for Gel_5.

Figure 16 is an exploded image of an overlay of samples H7/M7 for Gel_6.

Figure 17 is an exploded image of an overlay of samples E2/E3 for Gel_7.

Figure 18 is an exploded image of an overlay of samples E4/E5 for Gel_8.

Figure 19 is an exploded image of an overlay of samples E6/E7 for Gel_9.

Figure 20 shows a representative image of a 2-dimensional DIGE gel produced using sample H6 vs M6 (where H6 is a non-*Ganoderma* infected sample at month 6; M6 is a *Ganoderma* PER71 infected sample at month 6). The DIGE gel image shown in Figure 20 has been cropped to illustrate only protein spots from pH 4 to 9. The numbers shown on the image correspond to the spot numbers listed in Table 1

Figure 21 is a pie chart showing the functions of the differentially expressed proteins during *Ganoderma* infection.

DESCRIPTION OF THE INVENTION

The present invention relates to a method for identifying a *Ganoderma*-infected palm tree. More particularly, the present invention relates to a method for identifying a *Ganoderma*-infected palm tree using sample derived from leaves of the palm tree and applying difference gel electrophoresis (DIGE) technique to the sample.

The method comprises first isolating proteins from a sample derived from leaves of the palm tree. The proteins from the sample can be isolated by a known method described in Wang *et al.* (2006), "A universal and rapid protocol for protein extraction

from recalcitrant plant tissues for proteomic analysis", Electrophoresis 27:2782-2786 or using any suitable method known in the art.

After the proteins are isolated from the sample, the proteins are subjected to gel electrophoresis on a 2-dimensional gel to determine the protein profile of the sample. The protein profile of the sample is then compared with the protein profile of a normal non-*Ganoderma*-infected palm tree. A difference in the protein profiles of the sample and that of the normal non-*Ganoderma*-infected palm tree indicates that the palm tree is infected with *Ganoderma* disease.

The *Ganoderma* species which causes the *Ganoderma* disease may include, but is not limited to, *Ganoderma boninense*, *Ganoderma lucidium* (prominent in temperate region), *Ganoderma miniatocinctum*, *Ganoderma zonatum* and *Ganoderma tornatum*. In one embodiment of the present invention, the *Ganoderma* species that causes the *Ganoderma* disease is *Ganoderma boninense*.

Palm tree as herein referred to includes, but is not limited to, oil palm, coconut palm, date palm, sago palm, nipa palm, betelnut (*Acreca catechu*) and ornamental palms. In some embodiments of the present invention, the sample may comprise a palm tree extract or a palm tree fraction obtainable from the leaves of a palm tree.

In the present invention, key plant proteins which are related to fungal infection responses in palm tree can be identified by analyzing proteomes at various infection stages. For example, proteins can be isolated from samples derived from palm tree and analyzed across several time points, such as in a monthly or bimonthly manner.

A palm tree is determined to be infected with *Ganoderma* disease when the protein profile of the sample from the palm tree includes two or more proteins selected from the group consisting of the proteins as shown in Table 1 below.

Table 1

No.	Spot #	Protein Identification	Accession no.	Category of Function	Functions
1	221	24 kDa seed maturation protein [*Elaeis guineensis*]	gi|192910858	Metabolism	growth + development
2	379	40S ribosomal protein S5	gi|192910844	Metabolism	protein synthesis

		[*Elaeis guineensis*]			
3	218,224, 225	60S ribosomal protein L7-like protein [*Elaeis guineensis*]	gi|192912978	Metabolism	protein synthesis
4	334	ABC transporter B family member 15 OS=*Arabidopsis thaliana* GN=ABCB15 PE=1 SV=1	AB15B_ARATH	Metabolism	integral membrane proteins involved in diverse cellular processes
5	56	ABC transporter C family member 2 OS=*Arabidopsis thaliana* GN=ABCC2 PE=1 SV=2	AB2C_ARATH	Metabolism	integral membrane proteins involved in diverse cellular processes
6	267	abscisic stress ripening [*Musa* ABB Group]	gi|270064305	Stress response	over-expressed under water/salt stress
7	57, 78	acetyl-CoA carboxylase [*Elaeis guineensis*]	gi|209168853	Metabolism	biosynthesis of fatty acids
8	170, 172	actine [*Elaeis guineensis*]	gi|48527433	Cell structure	housekeeping
9	203, 206,207	AGAMOUS-like MADS box transcription factor [*Elaeis guineensis*]	gi|73852969	Metabolism	metabolic pathway/KEGG
10	220	aldo/keto reductase family protein [*Arabidopsis lyrata* subsp. *lyrata*]	gi|297848944	Metabolism	catalyse mainly the reduction of carbonyl groups or carbon–carbon double bonds of a wide variety of substrates including steroids
11	290, 292, 293	ascorbate peroxidase, cytosolic [*Elaeis guineensis*]	gi|192912966	Disease /defense	reactive oxygen gene network; cellular signaling; PR-9
12	136, 312, 335	ATP synthase beta subunit [*Elaeis guineensis*]	gi|192910868	Energy	energy - electron transport
13	28, 36	ATP-dependent clp protease [*Cucumis melo* subsp.]	gi|307136002	Energy	chloroplast function
14	301, 307, 308, 316, 317, 320, 321	carbonic anhydrase 3 [*Flaveria vaginata*] & carbonic anhydrase [*Triticum turgidum* subsp. *durum* x *Secale cereale*]	gi|326582932, gi|290875537	Energy	carbohydrate metabolism
15	302	CBL-interacting protein kinase 4 OS=*Oryza sativa* subsp. *japonica* GN=CIPK4 PE=2 SV=2	CIPK4_ORYSJ	Disease/defense	signaling
16	287	chlorophyll A/B binding protein, putative [*Ricinus communis*]	gi|255557387	Energy	light-harvesting
17	260	chloroplast manganese stabilizing protein [*Solanum tuberosum*]	gi|313586398	Energy	PS II
18	357	cyclophilin [*Elaeis guineensis*]	gi|192910744	Housekeeping, disease/ defense	catalyze the isomerization of peptidyl–prolyl bonds, play a variety of important roles in infection, including facilitating host penetration and colonization and activating pathogen effector proteins within the host cytoplasm
19	277, 337, 370	cytochrome c oxidase subunit II PS17, putative	gi|109892850	Energy	electron transport chain; transmembrane protein complex
20	96, 98	disulfide isomerase 2 precursor	gi|192912964	Cell structure	protein folding

		[*Elaeis guineensis*]			
21	55	E3 ubiquitin-protein ligase SINA-like 6, putative [OS=*Arabidopsis thaliana* GN=At5g37870 PE=3 SV=1]	SINL6_ARATH	Metabolism	nodulation, PTM (protein ubiquitination)
22	179	elongation factor Tu, predicted similar to, (chloroplastic) [*Vitis vinifera*]	gi|225456880	Metabolism	mediates the entry of the aminoacyl-tRNA into a free site of the ribosome
23	349	endoglucanase 18 OS=*Oryza sativa* subsp. *japonica* GN=Os06g0715300 PE=2 SV=1	GUN18_ORYSJ	Disease/ defense	PR-2
24	367	endoribonuclease Dicer homolog 1 OS=*Oryza sativa* subsp. *japonica* GN=DCL1 PE=3 SV=1	DCL1_ORYSJ	Disease/ defense	PR-10
25	48, 295, 363	F-box/kelch-repeat protein [*Arabidopsis thaliana*]	gi|15230186	Cell structure	cell division; actin-binding protein
26	242, 243, 245, 246, 249	ferredoxin--NADP reductase, putative [*Ricinus communis*]	gi|255538962	Energy	electron transport, PS I
27	6	fiber protein Fb2 [*Elaeis guineensis*]	gi|192910804	Cell structure	support
28	201, 214, 226	fructose-bisphosphate aldolase	gi|255557204, gi|300681519	Metabolism	energy
29	326	Geminivirus Rep-interacting motor protein OS=*Arabidopsis thaliana* GN=GRIMP PE=1 SV=1	GRIMP_ARATH	Metabolism	for viral DNA replication, transcriptional regulator
30	271	ginkbilobin-1 (Fragment) OS=*Ginkgo biloba* GN=GNK1 PE=1 SV=1, (antifungal protein)	GNK1_GINBI	Disease/defense	protective function against fungal infection
31	178	glutamine synthetase, cytosolic [*Cucumis melo*]	gi|113171384	Metabolism	nitrogen metabolism
32	151, 192, 197, 210, 212, 219, 228	glyceraldehyde 3-phosphate dehydrogenase [*Elaeis guineensis*]	gi|82400215	Energy	energy metabolism
33	40, 43, 66, 81, 82, 85, 92, 95	heat shock protein 70 or 90	gi|238054071, gi|255570990, gi|2827002, gi|6969976, gi|108862740	Stress	protein destination/storage
34	266	hypothetical protein [*Micromonas pusilla* CCMP1545]	gi|303275936	Unknown	
35	167	hypothetical protein [*Oryza sativa Japonica* Group]	gi|22202781	Unknown	
36	22	hypothetical protein [*Physcomitrella patens* subsp. *patens*]	gi|168034023	Unknown	up-regulated in canola treated with an ACC deaminase-containing plant-growth-promoting bacterium, essential for cell division and growth, involve in plant nutrition up take
37	274	hypothetical protein [*Populus trichocarpa*]	gi|224140861	Unknown	
38	230	hypothetical protein	gi|225466832	Unknown	

		[*Vitis vinifera*]			
39	318	hypothetical protein LOC100216776 [*Zea mays*]	gi|219363037	Unknown	
40	248	hypothetical protein SELMODRAFT_422914 [*Selaginella moellendorffii*]	gi|302803987	Unknown	
41	381	hypothetical protein VITISV_010874 [*Vitis vinifera*]	gi|147843505	Unknown	
42	336	hypothetical protein VITISV_023080 [*Vitis vinifera*]	gi|147766924	Unknown	
43	17, 374	IAA type protein [*Elaeis guineensis*]	gi|50404477	Metabolism	growth + development
44	237	isoflavone reductase, putative [*Ricinus communis*]	gi|255543713	Disease/ defense	biosynthesis of plant defense metabolites
45	247, 250	isopentenyl-diphosphate Delta-isomerase I OS=*Camptotheca acuminata* GN=IPI1 PE=2 SV=1	IDI1_CAMAC	Metabolism	catalyzes precursors for terpenoid (plant natural products) biosynthesis
46	255	LOC100284083 [*Zea mays*]	gi|226530191	Unknown	
47	263	NADH-cytochrome b5 reductase-like protein OS=*Arabidopsis thaliana* GN=At5g20080 PE=1 SV=2	NCB5R_ARATH	Energy	flavoprotein, electron transport
48	204	Os04g0234600 [*Oryza sativa Japonica* Group]	gi|115457386	Unknown	
49	369	Os07g0544800 [*Oryza sativa Japonica* Group]	gi|115472625	Unknown	
50	252, 253, 254, 257, 258, 261, 262, 272	oxygen evolving enhancer protein 1 [*Litchi chinensis*]	gi|326467059	Energy	Defense signaling
51	305, 306, 309, 315, 324, 325	oxygen evolving enhancer protein 2	gi|8131593, gi|297826499, gi|11134035,	Energy	Defense signaling
52	364, 366	oxygen-evolving enhancer protein 3-1 [*Zea mays*]	gi|195633817	Energy	Defense signaling
53	12	P1B-ATPase heavy-metal transporter [*Oryza sativa Japonica* Group]	gi|315623028	Metabolism	transport heavy metals across biological membranes
54	88, 373	pentatricopeptide, putative, expressed [*Oryza sativa Japonica* Group]/Pentatricopeptide repeat-containing protein At4g38010 OS=*Arabidopsis thaliana* GN=PCMP-E45 PE=2 SV=1	At4g38010, gi|108864632	Metabolism	PTM fo RNA; coordinators of nuclear and mitochondrial genes expression
55	346, 347, 350, 353, 354	peptidyl-prolyl cis-trans isomerase, putative [*Ricinus communis*]	gi|255547634	Metabolism	catalyse protein folding by accelerating the slow step of cis-trans isomerisation of peptidyl-prolyl bonds
56	359	peroxiredoxin [*Elaeis guineensis*]	gi|192910922	Disease/ defense	antioxidant defense, redox signaling

57	195	peroxisomal glycolate oxidase [*Glycine max*]	gi|167962794	Energy	Glycolate oxidase (Ferredoxin-containing form); flavoprotein
58	268, 279	peroxisome type ascorbate peroxidase [*Elaeis guineensis*]	gi|192910808	Disease/ defense	PR-9
59	360	phosphoenolpyruvate carboxylase [*Anthoceros punctatus*]	gi|7768089	Energy	nitrogen response genes; photosynthesis; catalyzes the addition of bicarbonate to phosphoenolpyruvate (PEP) to form the four-carbon compound oxaloacetate
60	173, 177	phosphoglycerate kinase	gi|226530482, gi|332591479	Stress response	Signaling
61	11	phospholipase D zeta OS=*Arabidopsis thaliana* GN=PLDZETA PE=2 SV=1	PLDZ1_ARATH	Metabolism	hydrolyzes lipids to fatty acids
62	352	phosphoribosylaminoimidazole carboxylase, chloroplastic (Fragment) OS=*Vigna aconitifolia* GN=PURKE PE=2 SV=1	PUR6_VIGAC	Metabolism	nucleotide biosynthesis; fusion protein
63	356	Photosystem I reaction center subunit II, chloroplast	gi|255551453	Energy	light-induced electron transfer
64	361	Photosystem I reaction center subunit IV, chloroplastic; Short=PSI-E; AltName: Full=P	gi|131176	Energy	photosynthesis
65	311, 313, 314	Photosystem II 23 kDa polypeptide [*Nicotiana tabacum*]	gi|19898	Energy	membrane protein complex
66	222	plastidic aldolase [*Nicotiana tabacum*]	gi|294440432	Metabolism	converts glucose into energy
67	264, 284	porin, outer plastidial membrane protein OS=*Pisum sativum* GN=POR1 PE=1 SV=2	VDAC_PEA	Transport	voltage-gated diffusion pores; transmembrane protein; are beta barrel proteins that cross a cellular membrane and act as a pore through which molecules can diffuse
68	232	protochlorophyllide reductase A,chloroplastic; Short=PCR A; AltName: Full=NADPH-prot	gi|129708	Energy	light independent photosynthesis
69	323	PsbP [*Xerophyta humilis*]	gi|25992740	Energy	Photosystem II
70	236	pterocarpan reductase-like protein [*Linum corymbulosum*]	gi|169639232	Disease/defense	phytoalexins
71	31, 54, 240	Ras-related protein RIC1 [*Elaeis guineensis*]	gi|192910784	Signal transduction	cell growth, survival, differentiation
72	1, 2, 5, 14, 19, 30, 52, 53, 59, 60, 63, 75, 77, 80, 90, 91, 97, 100, 101, 103, 107, 117,	ribulose-1,5-bisphosphate carboxylase/oxygenase (large & small subunit, large subunit-binding protein subunit beta and activase B)	gi|11558717, gi|76574195 gi|134104, gi|7960277	Energy	carbon fixation/photosynthesis; carbohydrate metabolism

	118, 134, 138, 139, 141, 143, 144, 155, 161, 181, 183, 193, 196, 276, 281, 297, 339, 341, 343, 348, 371, 375, 377, 380,				
73	168	serine-glyoxylate aminotransferase, putative [*Fritillaria agrestis*]	gi|2754849	Metabolism	transferase; participates in glycine, serine and threonine metabolism
74	186	stearoyl-Acyl-carrier protein desaturase [*Elaeis guineensis*]	gi|1785862	Metabolism	fatty acid biosynthesis
75	328, 329, 330, 331, 332	thioredoxin peroxidase [*Elaeis guineensis*]	gi|192910848	Disease/ defense	PR-9
76	185, 188, 189	T-protein of the glycine decarboxylase complex [*Pisum sativum*]	gi|407475	Metabolism	phosphorespiratory pathway
77	64, 70, 72, 73	transketolase	gi|14787119, gi|75140229	Metabolism	reductive and oxidative pentose phosphate pathways - synthesis of sugar phosphate intermediates
78	44	translation elongation factor G, putative [*Ricinus communis*]	gi|255537029	Cell structure	protein synthesis; peptide elongation
79	286, 288	triose phosphate isomerase cytosolic isoform [*Elaeis guineensis*]	gi|192910674	Metabolism	carbohydrate metabolism, balance of metabolic fluxes in plant primary metabolism
80	49	vitamin-b12 independent methionine synthase, 5-methyltetrahydropteroyltriglutamate-homocysteine [*Populus trichocarpa*]	gi|224131686	Metabolism	photosysnthesis and respiration; methylation

There are several advantages in using leaves or leaf tissues of palm tree to determine if a palm tree is infected with *Ganoderma* disease in the method of the present invention. First of all, the present invention relies on the systemic responses, in terms of protein profiles, of palm trees in determining if the palm trees are infected

with the *Ganoderma* disease. Regardless of which root branch is infected with the *Ganoderma* disease, infection can easily be detected from the leaves of the palm tree by applying DIGE technique to proteins isolated from samples derived from the leaves of the palm tree to determine the protein profile of the palm tree. A difference in the protein profile of the samples and that of a normal non-*Ganoderma*-infected palm tree indicates that the palm tree is infected with the *Ganoderma* disease. One may not accurately detect that the palm tree is infected with the *Ganoderma* disease if root tissues are used as the root that is used for the detection may not be the one that is infected with the disease.

Another advantage of the present invention is that leaves grow on the aerial part of palm tree and they are therefore easily accessible. Collecting samples from leaves of palm tree for analysis will not cause any adverse harm or injury to the palm tree. Roots of palm tree, on the other hand, are hidden underground, in the soil. To harvest roots for analysis, one needs to dig into the soil to harvest the roots. Digging into the soil can sometimes cause adverse harm or injury to the roots especially if digging is not carried out with care.

Leaves of palm tree are present in abundance. Samples from leaves of palm tree can therefore easily be obtained and this allows regular inspection of the palm tree to be carried to determine if the palm tree is infected with the *Ganoderma* disease. This in turn allows early detection of the *Ganoderma* disease.

Furthermore, roots are often contaminated with soil and microbes which may hinder accurate determination of the disease. Leaves, on the other hand, are relatively clean and this allows more accurate analysis to take place. The use of leaves allows easy-to-use diagnostic kits to be developed for the detection of *Ganoderma* disease.

The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

Ganoderma strain isolation and identification

To infect oil palm seedlings with *Ganoderma* disease, two strains of *Ganoderma boninense* were used as inocula. They were PER71 (a strain originated from United Plantations, Perak and is obtainable from the Pathology Lab, Malaysian Palm Oil Board) and SDG55 (a strain isolated by Plant Protection Unit, Sime Darby R&D Centre).

Inoculum cubes were prepared by culturing the fungal pathogen on surfaces of 6 x 6 x 6 cm rubber wood cubes based on the method described in Idris *et al.* (2006), "Technique for inoculation of oil palm geminated seeds with *Ganoderma*", MPOB Information Series No. 321, pp. 4, June 2006. The cubes of dried rubber wood were washed and put into polypropylene bags containing 60 ml of 5.6% malt extract agar. The bags were sealed prior to autoclaving for 1 hour at 121°C. Upon cooling down, the cubes were inoculated with *Ganoderma boninense* and then placed in the dark at room temperature for 60 days. Fully colonized cubes were used as inoculum cubes.

Preparation of Non-*Ganoderma* infected and infected samples of oil palms

Germinated seeds of oil palm used in this example were of commercial DxP standard cross, obtained from Sime Darby Seeds & Agricultural Services Sdn. Bhd., Banting, Malaysia.

Ganoderma-infected seedlings were produced by artificial infection (see Figure 1). Here, the inoculum cubes, fully colonized by the pathogen, were placed in the middle of a 30 x 38 cm black polythene bag filled with unsterilized top soil. Germinated seeds were then planted 4 to 5 cm above the inoculum cubes. For control where non-*Ganoderma* infected seedlings were needed, the seeds were planted as described but with the absence of inoculum cubes. All the seedlings were maintained with regular watering and manuring as prescribed by Sime Darby Good Agriculture Practice (Sime Darby Plantation, 2001), but with no application of any fungicide or pesticide throughout the whole period of growing the seedlings. To minimize pest attack, netting was put up as a physical barrier around and above the nursery where the oil palms were kept.

Leaf samples from the seedlings were collected monthly, beginning from the second month to the seventh month after the seeds were planted, for analysis. It is believed that infection, via the roots, has taken place by the second month under this mode of artificial infection; supported by the presence of disease symptom like foliar yellowing and browning, as described in Idris *et al.* (2006).

In this Example, leaves of 10 different seedlings per treatment were pooled and their protein extracted for Difference Gel Electrophoresis (DIGE) analysis.

2-Dimensional DIGE experiment

A modified protein extraction method published by Wang *et al.* (2006) was used to isolate total leaf protein. Subsequently, the extracted protein samples were re-suspended in a 2-dimensional cell lysis buffer (30 mM Tris-HCl, pH 8.8, containing 7 M urea, 2 M thiourea and 4% CHAPS). The mixture was sonicated at 4°C, followed by shaking for 30 minutes at room temperature. The samples were then centrifuged for 30 minutes at 14,000 *rpm* and the resulting supernatant was collected. Protein concentration of the supernatant fraction was measured using Bio-Rad protein assay method as described in Bradford M.M. (1976), "A dye-binding method for the determination of microgram quantities of protein", Anal. Biochem, 72:248-54.

To aid downstream analysis, an internal standard (IS) was prepared, by mixing equal amount of protein from each sample. Each internal standard prepared was included in the 2-dimensional DIGE experiment.

CyDye labelling

For each sample, 30 µg of protein was mixed with 1.0 µl of diluted CyDye, and the mixture was kept in the dark on ice for 30 minutes. Samples from each pair (e.g. not infected and infected samples) were labelled as Cy3 and Cy5 respectively, while the internal standard was labelled as Cy2. The labelling reaction was carrying out by adding 1.0 µl of 10 mM Lysine to each sample, and incubating each sample in the dark on ice for additional 15 minutes. The 3 labelled samples were then mixed together. Two times of the 2-D sample buffer (8 M urea, 4% CHAPS, 20 mg/ml DTT, 2% pharmalytes and trace amount of bromophenol blue), 100 µl of Destreak solution

and rehydration buffer (7 M urea, 2 M thiourea, 4% CHAPS, 20 mg/ml DTT, 1% pharmalytes and trace amount of bromophenol blue) were added to the labelling mix to make a total volume of 250 µl. The resulting mixture was thoroughly mixed and spun down prior to loading the labelled samples onto immobilized pH gradient gel (IPG) strips housed in a strip holder.

Setup of 2-dimensional DIGE analytical gels

DIGE gels were designed to contain the appropriate sample pairings in order to facilitate gel analysis in the later part of the experiment. A total of 9 DIGE gels were produced with the sample pairings indicated below:

Gel 1: H2, M2, IS
Gel 2: H3, M3, IS
Gel 3: H4, M4, IS
Gel 4: H5, M5, IS
Gel 5: H6, M6, IS
Gel 6: H7, M7, IS
Gel 7: E2, E3, IS
Gel 8: E4, E5, IS
Gel 9: E6, E7, IS

wherein,

H represents non-*Ganoderma* infected samples (control);
M represents samples infected with *Ganoderma boninense* PER71;
E represents samples infected with *Ganoderma boninense* SDG55; and
IS represents the internal standard which was made up of a pool of all the 18 samples included in this analysis. The numbers indicate months after seed planting.

Internal Standard (IS)

Internal Standard (IS) is used to match and normalize protein patterns across different DIGE gels, thereby negating the problem of inter-gel variation. The IS allows

accurate quantification of differences between samples with an associated statistical significance. Quantitative comparisons of protein between samples are made on the relative change of each protein spot to its own in-gel internal standard.

IEF (isoelectric focusing) and SDS-PAGE (polyacrylamide gel electrophoresis)

The labelled samples prepared above were then loaded onto pH 3 to 10 IPG strips. Isoelectric focusing (IEF) was run following the protocol provided by Amersham BioSciences in GE Healthcare (2004), "2-D electrophoresis: principle and methods, pp. 43-72. Upon finishing the IEF, the IPG strips were incubated in a freshly prepared equilibration buffer 1 (50 mM Tris-HCl, pH 8.8, containing 6 M urea, 30% glycerol, 2% SDS, trace amount of bromophenol blue and 10 mg/ml DTT) for 15 minutes with gentle shaking. The strips were then rinsed in another freshly prepared equilibration buffer 2 (50 mM Tris-HCl, pH 8.8, containing 6 M urea, 30% glycerol, 2% SDS, trace amount of bromophenol blue and 45 mg/ml DTT) for 10 minutes with gentle shaking. Following that, the IPG strips were rinsed in a SDS-gel running buffer before the strips were transferred into 12% SDS-gels. The SDS-gels were run at 15°C until the dye front of the strips ran out of the gels.

Image scan and data analysis

Gel images were scanned immediately following the SDS-PAGE using Typhoon TRIO (Amersham BioSciences). The scanned images were then analyzed by Image Quant software (version 6.0, Amersham BioSciences), followed by DeCyder™ 2D software version 6.5 (Amersham BioSciences).

The gel images of the 9 analytical gels were as shown in Figures 2 to 10 respectively.

RESULTS

2-Dimensional DIGE Analytical Gels results

The 9 analytical gels, produced from 18 samples, were analyzed to detect the differential expression of the proteins in following pairs:

(1) M2 vs. H2
(2) M3 vs. H3
(3) M5 vs. H5
(4) M6 vs. H6
(5) M7 vs. H7
(6) E2 vs. H2
(7) E3 vs. H3
(8) E4 vs. H4
(9) E5 vs. H5
(10) E6 vs. H6
(11) E7 vs. H7

Figure 20 is a representative image of a 2-dimensional DIGE gel produced using sample H6 vs M6 (where H6 is a non-*Ganoderma* infected sample at month 6; M6 is a *Ganoderma* PER71 infected sample at month 6). The DIGE gel image shown in Figure 20 has been cropped to illustrate only protein spots from pH 4 to 9.

Collectively, the number of differentially expressed proteins found in these pair-wise analyses was 382, after being narrowed down to those with expression ratio greater than 1.5 folds change (see Table I below). Sequentially, the corresponding protein spots in their respective gels were cross-checked by eye to ensure they were of good quality/resolution spots with no artificial streaks or not an artifact. All were not found to be artifacts. Of the screened spots, 210 were subsequently selected for identification via mass spectrometry.

The spot selection criteria for mass spectrometric identification practiced in this example were based on (i) the visibility of the spots on the DIGE gels; (ii) the protein expression ratio greater than 1.5 folds change; and (iii) the occurrence of protein isoform. Candidate spots that were not clearly visible on the DIGE gel (and having lower than 1.5 folds change in expression), as well as being redundant (its isoform has already been chosen), were excluded for identification work.

2-dimensional DIGE preparative gels for spot picking

Gels used for spot picking are termed as preparative gels. The preparative gel was run after differentially abundant spots were identified from analytical gels. For spot identification work, Gel 5 (with H6, M6, IS samples) was reproduced as preparative DIGE gel for spot picking as it contains all the 382 differentially expressed spots.

To have sufficient protein sample for identification purposes, 3 preparative DIGE gels were prepared for spot picking and the spots pooled. These gels were used for spot-picking all the 210 protein spots of interest. The spots picked were sent for mass spectrometry identification via MALDI-ToF/ToF.

Identification assignment of differentially expressed protein spots

Of the 210 spots sent for mass spectrometric identification, 200 spots were positively matched based on peptide mass finger-printing spectra to existing proteins from public domains (NCBI non-redundant database) while 10 were matches of no confidence (protein score C.I. (confident index) % lower than 80% is regarded as no confidence). From the 200 positive matched ID's, repetitive identities assigned to different spots for 120 proteins were removed, leaving behind 80 unique protein matches or ID's (see Tables 1 and 2). Of the 40 proteins with repetitive assignments, majority were of photosynthesis related proteins like ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit and oxygen evolving enhancer proteins.

In the present invention, 80 protein leads (see Table 1) have been identified to be associated to the occurrence of ganodermatosis in oil palm seedlings.

The 80 proteins identified were grouped based on their molecular functions (see Table 1). Of these, 11 proteins were found to be uncharacterized. The annotated proteins were found to be involved in photosynthesis, protein modifications, transport, energy, signal transduction, metabolisms, stress responses and defenses (Figure 20).

Apart from the 80 proteins detected, more differentially expressed proteins are expected, knowing that disease manifestation is a complex interaction between the pathogen and its host, possibly involving multiple intermediary metabolic pathways.

In this example, protein samples were focused on broad pH range IEF strips, i.e. between pH 3 and 10. Therefore, resolution of some proteins could be compromised and the protein spots could possibly be masked by proteins of higher abundance.

Of the 80 proteins detected, ginkbilobin is of particular interest because of its antifungal property (Wang *et. al.* (2000), "Ginkbilobin, a novel antifungal protein from *Ginkgo biloba* seeds with sequence similarity to embryo-abundant protein", Biochemical and Biophysical Research Communications 279:407-11).

In this study, ginkbilobin was up-regulated 1.9 folds in seedlings 6 months after the inoculation of *Ganoderma* (see expression profile of Spot 271 in Table 2). Although the up-regulation observed was not greater than 2 folds, the significance of this protein in oil palm defense against *Ganoderma* still warrants a further investigation.

In this study, cyclophilin, a ubiquitous housekeeping protein, was expressed 2.8 folds higher in infected seedlings at month 5 post infection (see Spot 357 in Table 2). Godoy *et al.* (2000). "Expression of a *Solanum tuberosum* cyclophilin gene is regulated by fungal infection and abiotic stress conditions", Plant Sci. 152:123-34 observed a higher cyclophilin RNA transcripts in tuber tissues (compared to other tissues) of *Solanum tuberosum* during the infection of fungus *Fusarium solani.* Cylophilin, which catalyzes the isomerization of peptidyl–prolyl bonds, known to accelerate folding of certain proteins and can function as a chaperone (Freskgard *et al.* (1992), "Isomerase and chaperone activity of prolyl isomerase in the folding of carbonic anhydrase", Science 258: 466-68; Gething *et al.* (1992), "Protein folding in the cell", Nature 355:33-35; Schmid *et al.* (1993), "Prolyl isomerases: role in protein folding", Adv. Protein Chem. 44: 25-66). It has also been indicated to play a variety of important roles in infection, including facilitating host penetration, as well as host colonization (Gan *et al.* (2009), "Characterization of cyclophilin-encoding genes in *Phytophthora*", Mol. Genet. Genomics 281: 565–78). Furthermore, the activation of pathogen effector proteins within the host cytoplasm is attributed to this protein (Gan *et al.*, 2009). Taking all these together, the up-regulation of oil palm cyclophilin during infection is intriguing, as if the host is encouraging the invading pathogen.

The differential regulation of proteins in non-infected and infected oil palm alluded to the possibility of using non-pathogen related proteins as markers in differentiating a

diseased palm from a healthy one. Building on this thought, antibodies for the proteins identified are obtained for further validation work via immuno-detection in a larger sample size, including samples from the fields.

The protein leads identified in the present invention can also be used as markers in screening for oil palms which are resistant or tolerant to *Ganoderma*. As plant infection takes place, it would onset a mechanism called as systemic acquired resistance (Colditz *et al.* (2007), "Plant proteomics upon fungal attack", Plant Proteomics, Samaj, J. and Thelen, J. (eds.). pp. 283-309. Springer). During this mechanism, plants would up-regulated defense related to biochemical compounds, may it be in the form of metabolites or polypeptides, to counter the invading pathogen systemically. Proteins found differentially expressed in this study, especially the up-regulated ones, would probably have an important role in systemic acquired resistance; making them a potential markers for selecting tolerant palms. The capability in identifying disease tolerant palms would be invaluable to oil palm breeding program and industry.

Table 2

Spot #	Appearance	Protein Expression Ratios												Name	Accession number
		M2 / H2	E2 / H2	M3 / H3	E3 / H3	M4 / H4	E4 / H4	M5 / H5	E5 / H5	M6 / H6	E6 / H6	M7 / H7	E7 / H7	(blank = spot not selected for MS identification)	
1	21 (27)	2.0	2.0	2.2	1.1	1.2				1.6	12.7	1.0	-3.4	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
2	18 (27)					1.1	2.0			1.3	3.8	2.0	1.0	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
3	21 (27)			1.4	-1.0	1.2		-1.3		1.0	4.5	1.4	-1.3		
4	21 (27)					-1.4	-1.1	1.1	-1.0	-1.6	1.4	1.9	-1.3		
5	27 (27)	1.1	-1.5	1.3	1.7	-1.4	-2.7	1.2	1.1	-4.2	-1.9	2.4	1.3	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
6	24 (27)			-1.6	-2.1	1.8	1.5	1.9	-1.1	1.7	6.0	-1.1	1.2	fiber protein Fb2 [*Elaeis guineensis*]	gi|192910804
7	15 (27)	1.2	2.3							1.1	2.8	-1.2	-1.6		
8	27 (27)	-1.4	1.1	1.3	10.2	1.8	-2.2	1.2	-1.0	-2.7	-1.6	1.0	1.2		
9	21 (27)			1.1	-2.8			1.5	1.0	-1.2	1.7	1.2	-1.2		
10	24 (27)	1.2		-1.2		1.6	1.6	-1.0	1.1	1.8	3.4	1.1	1.3		
11	27 (27)	1.1	1.2	-1.1	-1.3	1.7	1.4	1.2	-1.0	2.0	4.1	-1.1	-1.0	Phospholipase D zeta OS=*Arabidopsis thaliana* GN=PLDZETA PE=2 SV=1	PLDZ1_ARATH
12	27 (27)	1.1	1.4	1.1	-1.5	1.4	1.4	-1.1	-1.2	-1.1	2.0	1.1	1.1	P1B-ATPase heavy-metal transporter [*Oryza sativa Japonica* Group]	gi|315623028
13	15 (27)	1.0				1.7	1.7			1.0	2.1				
14	24 (27)	1.2	1.3	1.2	-1.1			1.2	1.4	3.4	4.1	-1.9	-1.6	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
15	27 (27)	1.2	1.2	1.5	-1.0	2.0	-4.0	-1.1	1.3	3.3	3.2	-1.5	1.0		
16	27 (27)	1.1	-1.0	1.4	1.1	1.5	-5.4	-1.1	1.1	2.2	1.7	-1.3	1.2		
17	27 (27)	-1.0	-1.1	1.1	1.8	1.2	-9.4	-1.3	-1.1	1.2	-1.4	-1.2	1.3	IAA type protein [*Elaeis guineensis*]	gi|50404477
18	27 (27)	-1.1	-1.4	1.4	6.7	-1.0	-8.6	-1.5	-1.2	-1.8	-3.3	-1.0	1.4		
19	21 (27)	-1.1	1.7	1.3	1.6			1.1		1.4	1.8	-1.2	-1.4	ribulose-1,5-bisphosphate	gi|11558717

														carboxylase/oxygenase large subunit [*Elaeis guineensis*]	
20	27 (27)	-1.1	-1.4	1.1	3.9	1.1	-16.8	-1.1	-1.2	-2.8	-4.9	-1.1	1.4		
21	21 (27)			-1.1	1.3	1.7	1.2			1.7	2.9	-1.5	-1.4		
22	27 (27)	1.0	1.6	1.2	2.2	2.2	1.9	-1.1	-1.3	2.1	2.6	-1.1	1.2	predicted protein [*Physcomitrella patens* subsp. *patens*]	gi|168034023
23	18 (27)			1.1		1.2	-2.5	1.2	-1.0			1.3	1.5		
24	27 (27)	-1.0	1.2	1.1	-1.9	1.1	-1.1	1.1	1.1	-1.2	1.1	1.1	1.1		
25	27 (27)	-1.2	-1.8	1.1	5.6	-1.1	-4.0	-1.4	-1.0	-3.2	-4.3	-1.1	1.3	S-ribonuclease binding protein-like [*Elaeis guineensis*]	gi|32250937
26	27 (27)	1.2	1.5	1.1	-1.6	1.3	-1.6	-1.1	-1.1	-1.3	1.2	1.2	1.2		
27	24 (27)	-1.2	-1.1	2.1	2.1			1.2	1.0	1.0	-1.3	-1.0	-1.1		
28	27 (27)	1.1	1.2	1.3	1.3	1.4	-4.9	-1.0	1.1	1.7	2.5	-1.1	-1.1	ATP-dependent clp protease, putative [*Ricinus communis*]	gi|255540075
29	27 (27)	1.2	-1.2	1.1	2.3	1.1	-15.4	-1.0	1.4	-1.4	-1.7	1.3	1.5		
30	27 (27)	1.2	-1.1	1.3	3.9	1.1	-32.5	1.0	1.4	-1.8	-2.0	1.2	1.7	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit *[Elaeis guineensis]*	gi|11558717
31	24 (27)	1.2	1.2			-1.1	-1.9	1.3	1.3	-4.2	-4.0	-1.1	-1.1	Ras-related protein RIC1 [*Elaeis guineensis*]	gi|192910784
32	27 (27)	1.2	-1.0	1.4	-1.7	1.6	-3.4	-1.0	1.2	2.3	4.5	1.1	1.0		
33	24 (27)	1.3	1.4	1.6	-2.9			-1.3	1.1	1.5	4.5	1.1	-1.0		
34	27 (27)	1.2	1.1	1.4	-2.5	1.7	-1.6	-1.3	1.2	3.5	9.4	1.1	1.1	Eukaryotic initiation factor 4A-3 OS=*Nicotiana*	IF4A3_NICPL
35	24 (27)	1.4	1.5	1.3	-1.5	3.2	2.4			-1.1	3.6	-1.2	-1.3		
36	24 (27)	1.4	1.7	1.3	-4.2	2.1	1.6	-1.7	-1.1	1.6	7.5			ATP-dependent clp protease [*Cucumis melo* subsp.	gi|307136002
37	27 (27)	1.3	1.5	1.5	-3.0	1.9	1.3	-2.3	-1.1	1.2	5.9	-1.1	-1.1		
38	27 (27)	1.4	1.8	1.2	-4.5	2.6	2.1	-1.3	-1.2	1.3	4.8	-1.2	-1.2		
39	15 (27)			-1.8				-1.0		-1.3	-1.4	-1.3	1.0		
40	27 (27)	1.1	1.7	-1.2	-3.0	2.3	-1.2	1.2	1.3	1.0	3.0	1.3	2.0	heat shock protein 90 [*Ipomoea nil*]	gi|260505494
41	24 (27)	-1.0	1.8	-1.0	-1.3	2.5	-1.1	1.5	1.4			-1.7	-1.5		
42	24 (27)	-1.0	2.5	-1.1	-1.5	1.7		1.6		2.0	3.1	-1.3	1.1		
43	18 (27)	1.3	1.8					1.3	1.1			1.1	1.3	Hsp90 protein, expressed [*Oryza sativa Japonica* Group]	gi|108862740
44	27 (27)	-1.1	-1.2	1.1	-1.2	1.2	-1.0	-1.6	-1.0	1.2	1.6	1.0	1.5	translation elongation factor G, putative [*Ricinus communis*]	gi|255537029

45	27 (27)	1.1	1.0	1.1	-1.7	-1.0	1.4	1.3	-1.0	1.5	1.9	-1.3	-1.4		
46	24 (27)	1.0	1.1	1.1	-2.5	-1.1	1.5			1.6	1.7	-1.3	-1.3		
47	27 (27)	1.1	1.2	1.1	-1.2	1.0	1.2	1.4	1.0	1.5	2.0	-1.4	-1.4		
48	27 (27)	1.2	1.0	1.2	-1.4	-1.1	1.9	1.4	-1.1	1.3	1.4	-1.3	-1.5	F-box/kelch-repeat protein At3g24760 OS=*Arabidopsis thaliana* GN=At3g24760 PE=2 SV=1	FBK69_ARATH
49	27 (27)	1.0	1.2	1.2	1.0	1.2	-1.2	1.3	1.1	1.8	1.7	-1.3	-1.1	vitamin-b12 independent methionine synthase, 5-methyltetrahydropteroyltriglutamate-homocysteine [*Populus trichocarpa*]	gi|224131686
50	27 (27)	1.0	1.0	1.3	2.6	1.3	-4.1	-1.6	-1.0	-1.2	-1.3	-1.1	1.2		
51	24 (27)	-1.0	1.2	1.2	-1.1			-1.2	1.3	1.5	1.7	-1.2	1.0		
52	27 (27)	-1.0	1.2	1.0	-1.1	1.2	-1.7	-1.1	1.2	1.4	1.9	-1.2	1.1	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
53	27 (27)	-1.0	-1.0	1.1	1.5	1.2	-2.4	-1.4	1.0	1.1	-1.0	-1.1	1.1	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Elaeis guineensis]	gi|11558717
54	21 (27)	1.2	1.2	1.2	-2.3	-1.1	1.7			1.4	1.8			Ras-related protein RIC1 [*Elaeis guineensis*]	gi|192910784
55	27 (27)	1.3	1.3	1.2	-2.1	-1.2	1.5	1.2	-1.1	1.5	2.2	-1.2	-1.5	Putative E3 ubiquitin-protein ligase SINA-like 6 OS=*Arabidopsis thaliana* GN=At5g37870 PE=3 SV=1	SINL6_ARATH
56	27 (27)	1.2	1.1	1.3	-1.6	-1.2	1.4	1.2	-1.2	1.5	2.1	-1.3	-1.5	ABC transporter C family member 2 OS=*Arabidopsis thaliana* GN=ABCC2 PE=1 SV=2	AB2C_ARATH
57	27 (27)	1.1	1.1	1.3	2.1	1.3	-4.0	-1.5	-1.1	-1.2	-1.4	1.0	1.2	acetyl-CoA carboxylase [*Elaeis guineensis*]	gi|209168853
58	24 (27)	1.2	1.2	1.5	4.9	1.1	-2.8			-1.6	-1.6	-1.0	1.3		
59	27 (27)	1.1	-1.2	1.2	3.4	1.5	-1.6	-1.2	-1.1	-1.8	-1.6	-1.2	1.2	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
60	27 (27)	1.1	-1.1	1.1	3.5	1.3	-2.3	-1.2	1.1	-2.1	-1.7	-1.4	1.4	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
61	27 (27)	-1.0	-1.1	1.3	3.0	1.4	-2.7	-1.3	-1.2	-2.1	-1.7	-1.3	1.4		
62	27 (27)	1.1	1.0	1.1	2.7	1.3	-2.7	1.1	1.1	-2.3	-2.3	-1.2	1.1		
63	27 (27)	-1.0	-1.2	1.4	5.9	1.7	-3.0	1.0	-1.1	-2.9	-2.7	-1.2	-1.1	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis*	gi|11558717

														guineensis]	
64	27 (27)	1.1	1.6	1.1	2.3	3.8	2.6	-1.1	1.1	-3.8	-1.2	-1.2	-1.9	transketolase [*Polygonum tinctorium*]	gi|14787119
65	24 (27)	1.1	2.0	1.3	1.5	3.6		-1.5		-1.2	2.7	-1.3	-2.0		
66	27 (27)	1.2	1.3	-1.1	-2.5	-1.2	1.1	-1.1	1.1	2.9	3.2	-1.1	1.1	heat shock protein, putative [*Ricinus communis*]	gi|255570990
67	21 (27)	1.3	1.9	1.5	-1.0	2.6	1.4			1.5	6.0				
68	27 (27)	1.4	1.7	1.4	-1.6	2.0	-1.1	-1.1	1.1	2.2	7.0	-1.2	-1.3		
69	27 (27)	1.2	1.3	1.5	-1.7	1.7	-1.5	-1.1	-1.0	2.5	6.5	-1.1	-1.1		
70	27 (27)	1.1	1.1	1.4	-1.4	1.4	-2.0	-1.1	-1.0	2.9	5.9	-1.1	1.0	Transketolase, chloroplastic; Short=TK	gi|75140229
71	24 (27)	1.1	1.2	1.3	-1.5			-1.1	-1.0	2.6	4.3	1.0	1.2		
72	27 (27)	-1.0	1.0	1.2	1.1	1.3	-2.3	-1.0	-1.1	1.5	2.2	1.1	1.3	transketolase [*Polygonum tinctorium*]	gi|14787119
73	27 (27)	-1.2	-1.1	1.1	1.7	1.1	-3.3	1.1	-1.0	1.1	1.2	1.1	1.4	transketolase [*Polygonum tinctorium*]	gi|14787119
74	27 (27)	-1.2	-1.2	-1.1	2.1	-1.0	-4.4	1.2	1.0	-1.4	-1.5	1.1	1.4		
75	27 (27)	-1.2	-1.3	-1.1	3.2	-1.2	-5.8	1.3	1.1	-2.2	-2.6	1.2	1.5	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
76	27 (27)	-1.1	-1.4	-1.2	3.9	-1.2	-7.4	1.4	1.1	-2.7	-3.8	1.1	1.6		
77	27 (27)	1.2	-1.1	1.2	2.2	-1.1	-1.8	1.2	1.1	-2.6	-2.2	-1.1	1.0	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
78	27 (27)	-1.3	-1.3	-1.2	5.3	-1.3	-6.4	1.5	1.2	-3.3	-4.6	1.0	1.3	acetyl-CoA carboxylase [*Elaeis guineensis*]	gi|209168853
79	27 (27)	-1.1	-1.3	-1.4	4.6	-1.3	-3.5	1.3	1.1	-3.3	-5.1	-1.1	-1.2		
80	27 (27)	-1.0	1.1	1.0	-1.2	1.0	-1.1	1.1	-1.4	-1.3	-2.0	-1.0	-1.1	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
81	27 (27)	1.2	1.4	1.2	2.8	1.5	-3.2	1.2	1.2	-1.4	1.2	-1.2	1.1	heat shock protein, putative [*Ricinus communis*]	gi|255570990
82	18 (27)	1.2				1.8		-1.1		1.2	1.8	-1.0	1.4	heat shock protein, putative [*Ricinus communis*]	gi|255570990
83	24 (27)	1.2	1.1	1.1	2.6	1.4	-3.9			1.5	1.5	1.1	1.6		
84	24 (27)	1.0	-1.3	1.4	8.4	1.3	-5.1			-1.4	-2.5	1.3	1.8		
85	15 (27)			1.0	12.5					-1.9	-4.0			high molecular weight heat shock protein [*Malus x domestica*]	gi|6969976
86	18 (27)	1.0	1.9	1.0	17.9							1.2	1.8		
87	24 (27)	1.2	-1.3	1.4	4.6			-1.3	-1.7	-1.4	-2.6	-1.3	1.1	predicted protein [*Micromonas* sp. RCC299]	gi|255074859
88	27 (27)	1.0	-2.0	1.3	7.5	1.1	-4.9	-1.3	-2.4	-1.9	-6.9	-1.1	-1.2	Pentatricopeptide repeat-containing protein At4g38010 OS=*Arabidopsis thaliana* GN=PCMP-E45 PE=2 SV=1	PP355_ARATH

89	24 (27)	1.1	-1.3	1.3	2.1			-1.1	1.1	-1.0	-1.9	-1.1	-1.1	oil palm profilin-like allergen PF2 [*Elaeis guineensis*]	gi|34223519
90	27 (27)	1.8	1.8	1.1	-1.8	1.7	1.1	-1.1	1.5	2.8	3.9	-1.6	1.0	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
91	27 (27)	1.1	1.3	1.1	1.2	1.0	-1.4	1.0	1.2	1.6	1.4	-1.2	-1.1	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
92	24 (27)	1.3	1.2	1.1	-1.6	1.0	-1.6			-2.1	-2.7	1.2	1.4	heat shock protein 70 [*Pellia endiviifolia* (species B)]	gi|238054071
93	21 (27)			1.3		-1.1	-1.6	1.1	1.0	-2.7	-2.9	1.3	-1.1		
94	24 (27)	1.2	1.2	1.2	-4.7			1.1	1.0	-2.3	-2.1	1.2	1.3		
95	24 (27)	1.2	-1.1	1.0	-2.1	1.2	-1.1			-3.0	-2.0	1.2	1.4	HSP70 [*Triticum aestivum*]	gi|2827002
96	24 (27)	-1.3	1.2			2.4	1.6	-1.3	-1.1	1.8	2.5	-1.2	1.2	protein disulfide isomerase 2 precursor [*Elaeis guineensis*]	gi|192912964
97	27 (27)	1.1	1.2	1.1	-2.2	-1.1	-1.0	1.1	1.0	1.9	2.1	1.2	1.3	RuBisCO large subunit-binding protein subunit beta, chloroplastic; AltName: Full=60 k	gi|134104
98	27 (27)	1.1	1.2	1.0	-4.3	1.2	2.2	-1.1	1.0	1.5	2.5	-1.0	1.1	protein disulfide isomerase 2 precursor [*Elaeis guineensis*]	gi|192912964
99	27 (27)	1.1	1.3	1.1	-2.9	1.0	1.4	1.2	1.2	1.4	2.3	1.0	1.1		
100	27 (27)	1.0	-1.0	1.1	-1.5	-1.5	-1.6	1.4	1.3	1.3	1.0	1.3	1.4	RuBisCO large subunit-binding protein subunit beta, chloroplastic; AltName: Full=60 k	gi|134104
101	27 (27)	-1.0	-1.3	1.2	1.4	-1.8	-2.4	1.3	1.5	-1.3	-1.6	1.4	1.6	RuBisCO large subunit-binding protein subunit beta, chloroplastic; AltName: Full=60 k	gi|134104
102	27 (27)	1.0	1.1	1.1	1.1	1.1	-1.1	1.3	1.0	-2.0	-1.4	-1.1	-1.3		
103	21 (27)	1.1	1.3	1.3	1.4	1.9				-2.4	-1.1	1.0	-1.3	RuBisCO large subunit-binding protein subunit beta, chloroplastic; AltName: Full=60 k	*gi*|134104
104	27 (27)	1.0	1.4	1.3	-3.5	1.1	1.3	-1.1	-1.0	1.4	4.4	-1.0	-1.2		
105	27 (27)	-1.1	-1.4	1.3	-1.5	1.1	1.3	-1.1	-1.3	-1.1	1.9	1.1	-1.1		
106	27 (27)	-1.0	1.1	1.3	-3.0	1.2	2.1	-1.1	-1.3	1.7	4.2	1.1	-1.1		
107	27 (27)	-1.0	1.2	1.4	-4.6	1.5	2.4	-1.2	-1.2	3.4	9.1	1.0	-1.1	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
108	27 (27)	-1.0	-1.1	1.2	-1.7	-1.1	2.4	1.1	-1.5	1.3	2.8	-1.2	-1.5		
109	27 (27)	1.2	1.4	1.1	-2.8	1.2	1.8	-1.0	-1.2	1.4	3.7	-1.1	-1.2		
110	27 (27)	-1.2	-1.3	1.1	2.3	-1.1	-3.0	1.6	1.1	-2.5	-3.6	-1.0	1.2		

111	27 (27)	-1.3	-1.3	1.2	1.8	1.0	-1.8	1.5	1.1	-2.9	-2.6	1.1	1.1		
112	15 (27)					-1.6	-3.4			-1.6	-1.1	1.0	1.1		
113	24 (27)	-1.1		1.1		-1.4	-2.9	1.4	1.2	-1.9	-1.6	1.0	1.2		
114	27 (27)	-1.0	-1.0	1.2	2.4	-1.3	-1.8	1.3	1.0	-1.5	-1.3	-1.1	-1.0		
115	27 (27)	-1.2	-1.1	1.2	2.7	-1.3	-2.4	1.2	-1.0	-1.4	-1.5	-1.1	1.1		
116	27 (27)	-1.1	-1.2	1.2	3.9	-1.4	-6.4	1.3	-1.2	-2.3	-3.6	-1.1	-1.2		
117	18 (27)			1.2	6.7	-1.1	-7.4			-2.5	-3.6			ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
118	24 (27)	-1.0	1.0			1.4	-1.5	1.0	1.1	-1.0	2.5	-1.3	-1.1	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
119	27 (27)	-1.1	-1.0	1.2	3.9	-1.1	-4.8	1.2	-1.1	-2.0	-2.1	-1.2	1.1		
120	27 (27)	-1.2	-1.2	1.2	3.3	-1.3	-3.7	1.2	-1.1	-1.5	-1.9	-1.0	1.2		
121	27 (27)	-1.2	-1.2	1.2	3.0	-1.4	-4.8	1.3	-1.0	-2.1	-3.7	1.0	-1.1		
122	24 (27)	-1.2	-1.6	1.1	5.4	-1.3	-3.8			-2.2	-2.5	-1.1	1.1		
123	27 (27)	-1.0	1.0	1.2	1.3	1.4	-1.5	1.1	1.1	1.0	2.4	-1.3	-1.2		
124	24 (27)	-1.0	1.2	1.1	1.5	1.3	-1.8	-1.1	1.0			-1.2	-1.0		
125	18 (27)	1.1	1.5							1.7	4.5	-1.6	-1.3		
126	27 (27)	-1.1	-1.1	1.2	3.7	-1.2	-5.5	1.3	-1.1	-1.9	-1.9	1.0	1.1		
127	27 (27)	-1.1	-1.2	1.2	3.5	-1.2	-3.1	1.3	1.0	-1.9	-2.3	1.1	1.3		
128	27 (27)	1.2	1.4	1.1	-1.8	1.4	1.6	-1.0	-1.0	1.6	3.0	-1.2	-1.1		
129	24 (27)	1.2		1.1		1.4	1.8	-1.1	-1.1	1.9	3.4	-1.2	1.0		
130	18 (27)	-1.2		1.1		-1.3		1.2		-2.3	-2.6				
131	27 (27)	1.2	1.3	1.2	-2.9	1.3	1.7	-1.3	-1.1	2.1	3.7	-1.1	1.0		
132	27 (27)	1.0	1.5	1.2	-2.4	1.4	1.1	1.2	1.2	1.3	4.3	-1.7	-1.4		
133	24 (27)	-1.0	1.2	1.3	1.1	1.6		-1.1		1.4	4.5	-1.2	1.0		
134	27 (27)	1.0	1.5	1.3	-3.2	1.8	1.2	1.1	1.3	2.6	12.3	-1.7	-1.5	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
135	27 (27)	-1.1	-1.0	1.2	2.8	1.1	-3.8	1.0	1.0	-1.6	-1.1	1.0	1.2		
136	27 (27)	1.1	1.2	1.2	-3.6	1.2	1.4	-1.1	-1.2	2.1	3.4	1.0	1.0	ATP synthase beta subunit [*Elaeis guineensis*]	gi|192910868
137	27 (27)	1.0	1.4	1.3	-2.2	1.7	-1.2	1.1	1.2	2.3	9.2	-1.6	-1.4		
138	27 (27)	-1.2	-1.1	1.1	3.2	-1.2	-5.3	1.2	1.1	-2.3	-1.8	1.1	1.2	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis*	gi|11558717

														guineensis]	
139	27 (27)	-1.2	-1.2	1.1	4.4	-1.3	-8.5	1.3	1.2	-3.3	-3.2	1.1	1.2	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
140	15 (27)	-1.0	1.5					1.0		-2.8	-2.9				
141	27 (27)	-1.3	-1.3	1.0	7.2	-1.4	-12.5	1.6	1.3	-3.8	-4.7	-1.1	1.2	ribulose-1,5-bisphosphate carboxylase/oxygenase large	gi|11558717
142	21 (27)	1.1	1.1	1.2	-3.6					1.6	2.4	1.0	1.1		
143	27 (27)	-1.3	-1.2	1.1	7.4	-1.4	-11.6	1.6	1.2	-4.4	-8.0	-1.2	-1.2	ribulose-1,5-bisphosphate carboxylase/oxygenase large	gi|11558717
144	27 (27)	-1.2	-1.2	1.1	6.8	-1.3	-6.1	1.4	1.1	-4.6	-6.9	-1.2	-1.1	ribulose-1,5-bisphosphate carboxylase/oxygenase large	gi|11558717
145	27 (27)	1.0	1.4	1.3	-1.5	1.9	-1.7	-1.1	-1.0	2.2	7.0	-1.4	-1.2		
146	24 (27)	1.0	1.2	1.1	-2.6			-1.0	1.1	1.3	1.9	1.0	1.1		
147	27 (27)	-1.1	1.0	1.3	1.6	1.3	-2.4	-1.2	-1.1	-1.1	2.1	-1.1	1.0		
148	21 (27)			1.0	1.6	3.2	-2.7	1.1	1.6	-1.1	2.2				
149	27 (27)	-1.2	-1.2	1.2	4.0	-1.2	-9.0	-1.0	1.2	-1.8	-2.3	-1.0	1.1		
150	27 (27)	-1.2	1.2	1.3	8.9	-1.2	-6.0	2.2	2.7	-3.4	-4.3	-1.3	-1.1		
151	24 (27)	1.3	1.4	-1.1	1.6	1.1	1.7	1.3	1.6	-1.7	-1.2			Glyceraldehyde-3-phosphate dehydrogenase B, chloroplastic; AltName: Full=NADP-depende	gi|120663
152	24 (27)	1.1	1.3	1.1	-1.6	1.3	1.1	-1.1	1.1	2.2	2.5				
153	27 (27)	-1.0	1.1	1.1	1.4	-1.0	-1.6	-1.2	-1.0	-1.0	-1.3	-1.1	-1.0		
154	27 (27)	1.0	1.1	1.2	-1.2	1.1	-1.0	-1.3	-1.1	2.7	2.4	-1.2	-1.2		
155	27 (27)	-1.0	1.0	1.2	1.2	-1.1	-1.2	-1.3	-1.2	2.3	1.7	-1.1	-1.1	ribulose bisphosphate carboxylase activase B [*Triticum aestivum*]	gi|7960277
156	27 (27)	-1.1	-1.0	1.2	1.7	-1.3	-1.6	-1.2	-1.2	1.4	-1.4	-1.0	-1.0		
157	27 (27)	-1.1	-1.1	1.1	2.1	-1.5	-2.1	-1.0	-1.1	-1.1	-2.4	1.0	1.1		
158	27 (27)	-1.2	-1.1	1.1	2.3	-1.7	-2.5	1.2	1.0	-1.4	-2.7	-1.0	1.1		
159	18 (27)	1.4	1.5	1.1	3.3							1.1	-1.1		
160	21 (27)	1.3	1.2	1.0	-1.4					1.6	1.1	-1.0	-1.1		
161	27 (27)	-1.1	-1.1	1.0	2.2	-1.9	-2.2	1.3	1.0	-2.0	-3.6	-1.0	-1.0	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
162	27 (27)	-1.3	1.0	1.0	2.7	-1.7	-1.4	1.4	1.2	-2.7	-3.4	-1.2	-1.1		
163	27 (27)	-1.1	1.1	1.4	2.7	-1.2	-1.7	1.3	1.2	-2.3	-1.7	-1.1	-1.1		

164	24 (27)	1.1	-1.2	1.2	4.6			1.2	1.3	-1.6	-2.0	-1.1	-1.1		
165	27 (27)	1.2	1.0	1.2	2.6	-1.2	-1.4	1.3	-1.1	-1.3	-1.3	1.2	-1.0		
166	24 (27)	1.2	1.4	1.1	-1.3	-1.3	-2.1			1.9	1.1	1.0	1.0		
167	15 (27)	-1.1	1.1			-1.2				-1.5	-1.7			hypothetical protein [*Oryza sativa Japonica* Group]	gi|22202781
168	24 (27)	1.1	-1.3	1.3	3.4	-1.1	-1.6	1.1	1.4			1.1	1.1	putative serine-glyoxylate aminotransferase [*Fritillaria agrestis*]	gi|2754849
169	27 (27)	1.1	1.1	1.3	1.2	-1.0	-2.1	1.0	1.2	1.2	1.4	-1.0	1.2		
170	27 (27)	1.1	1.0	1.4	2.2	1.0	-2.7	-1.2	-1.2	-1.2	1.1	1.0	1.2	actine [*Elaeis guineensis*]	gi|48527433
171	21 (27)	-1.1	-1.1	1.5	4.8	-1.1	-2.7	1.0	-1.0						
172	27 (27)	1.1	1.1	1.3	-2.2	1.2	1.7	-1.1	1.1	1.6	1.7	-1.2	-1.1	actine [*Elaeis guineensis*]	gi|48527433
173	27 (27)	1.1	1.1	1.6	1.1	1.2	-2.3	-1.1	1.1	1.0	1.4	1.2	1.2	phosphoglycerate kinase [*Zea mays*]	gi|226530482
174	27 (27)	1.1	1.3	1.4	-3.6	1.2	1.4	-1.2	-1.0	1.6	1.8	-1.1	1.2		
175	27 (27)	-1.0	1.1	1.5	-1.4	1.2	-1.9	1.1	1.2	1.3	2.2	1.0	-1.0		
176	27 (27)	1.0	1.1	1.4	-2.3	1.2	-1.5	1.2	1.3	1.3	2.5	-1.0	-1.0		
177	27 (27)	-1.1	-1.2	1.5	1.3	1.2	-1.4	1.2	1.1	-1.4	-1.0	1.2	1.1	phosphoglycerate kinase 1 [*Pinus pinaster*]	gi|332591479
178	27 (27)	1.1	1.2	1.4	-1.5	-1.0	-1.3	1.0	1.2	1.1	1.5	1.0	-1.1	cytosolic glutamine synthetase [*Cucumis melo*]	gi|113171384
179	27 (27)	1.1	1.1	1.2	-1.8	1.0	-1.2	1.1	1.1	1.0	1.3	-1.1	-1.0	PREDICTED: similar to Elongation factor Tu, chloroplastic [*Vitis vinifera*]	gi|225456880
180	24 (27)	1.2	1.4	1.3	-2.8	1.0	1.2	-1.2	1.1	3.7	4.7				
181	27 (27)	1.1	1.1	1.3	-3.4	1.1	1.5	-1.2	1.1	3.2	3.5	-1.1	-1.0	ribulose bisphosphate carboxylase activase B [*Triticum aestivum*]	gi|7960277
182	27 (27)	1.0	1.1	1.4	-2.1	-1.1	1.4	-1.2	-1.1	2.5	2.3	-1.1	-1.2		
183	27 (27)	1.0	1.1	1.3	-1.2	-1.2	1.0	-1.2	-1.4	1.9	1.5	1.0	-1.0	ribulose bisphosphate carboxylase activase B [*Triticum aestivum*]	gi|7960277
184	27 (27)	1.1	1.3	-1.0	-1.3	1.3	-3.7	1.4	1.1	1.8	1.6	-1.3	1.3		
185	27 (27)	1.1	1.2	-1.2	1.0	1.5	-1.8	1.4	1.4	2.3	2.4	-1.4	-1.1	T-protein of the glycine decarboxylase complex [*Pisum sativum*]	gi|407475
186	27 (27)	1.1	-1.2	1.3	2.4	-1.0	-2.7	-1.1	1.0	1.3	1.2	-1.2	1.1	stearoyl-Acyl-carrier protein desaturase [*Elaeis guineensis*]	gi|1785862
187	24 (27)	-1.0	-1.1	1.1	1.0	-1.4	-1.1			1.6	1.1	-1.0	-1.2		
188	27 (27)	-1.0	-1.2	1.1	2.4	-1.2	-3.4	-1.1	1.0	1.4	-1.5	-1.1	1.1	T-protein of the glycine decarboxylase complex [*Pisum sativum*]	gi|407475
189	24 (27)	-1.0	-1.1	1.3	2.8	-1.2	-2.9			-1.2	-1.4	-1.2	-1.1	T-protein of the glycine decarboxylase complex [*Pisum sativum*]	gi|407475
190	15 (27)	-1.1		1.2						-1.1	-1.6	1.1	1.2		

191	18 (27)	-1.0		-1.1				-1.1		-1.5	-1.7	-1.2	1.1		
192	27 (27)	1.1	1.1	1.2	1.2	1.1	-1.0	1.1	-1.0	-1.2	1.8	1.1	1.1	glyceraldehyde 3-phosphate dehydrogenase [*Elaeis guineensis*]	gi|82400215
193	24 (27)	-1.0	1.1	1.2	-1.8	-1.0	-1.2	-1.0	1.2	2.0	2.0			putative rubisco activase [*Vigna unguiculata*]	gi|149941206
194	27 (27)	1.0	-1.1	1.3	2.7	-1.1	-3.9	1.0	-1.7	-1.7	-2.5	1.2	1.3		
195	15 (27)	-1.0	1.1			-1.1	-3.2							peroxisomal glycolate oxidase [*Glycine max*]	gi|167962794
196	27 (27)	1.1	-1.2	1.0	1.6	-1.4	-1.7	-1.4	1.3	-1.4	-2.5	1.2	1.2	ribulose bisphosphate carboxylase activase B [*Triticum aestivum*]	gi|7960277
197	18 (27)			1.4		-1.2	-3.3			-1.9	-2.2	1.3	1.2	glyceraldehyde 3-phosphate dehydrogenase [*Elaeis guineensis*]	gi|82400215
198	27 (27)	1.1	-1.2	1.3	2.4	1.4	-1.4	-1.3	-1.3	-1.2	-1.4	1.1	1.2		
199	27 (27)	1.2	1.0	1.2	1.4	-1.2	-1.7	-1.3	-1.2	1.1	-1.1	1.2	1.2		
200	27 (27)	1.1	1.2	1.4	-1.3	1.2	1.1	-1.0	1.3	1.6	2.7	1.3	1.1		
201	18 (27)	1.0	-1.1			-1.2	-2.5			-1.6	-2.0			fructose-bisphosphate aldolase, putative [*Ricinus communis*]	gi|255557204
202	27 (27)	1.1	-1.2	-1.0	2.6	-1.3	-2.9	-1.2	-1.3	-1.9	-2.7	1.3	1.2		
203	27 (27)	1.3	1.1	1.1	-1.7	1.1	1.6	-1.1	1.1	1.9	2.4	-1.1	1.0	AGAMOUS-like MADS box transcription factor [*Elaeis guineensis*]	gi|73852969
204	27 (27)	1.2	-1.0	1.1	-1.3	1.1	1.2	-1.1	-1.1	1.8	1.9	-1.1	1.0	Os04g0234600 [*Oryza sativa Japonica* Group]	gi|115457386
205	18 (27)			1.1	1.0	1.2				1.8	4.1	-1.3	-1.1		
206	27 (27)	1.2	1.2	1.2	-1.2	-1.1	1.1	1.0	-1.2	1.6	1.5	1.1	1.0	AGAMOUS-like MADS box transcription factor [*Elaeis guineensis*]	gi|73852969
207	27 (27)	1.2	1.1	1.6	-1.0	-1.1	1.3	1.1	-1.1	1.3	1.5	1.0	-1.1	AGAMOUS-like MADS box transcription factor [*Elaeis guineensis*]	gi|73852969
208	27 (27)	-1.1	1.1	1.2	1.5	-1.1	-1.8	1.6	1.6	-1.4	1.6	-1.1	-1.1		
209	27 (27)	1.1	1.3	1.2	-1.1	1.2	-2.5	1.6	1.8	-1.1	2.6	-1.1	1.1		
210	24 (27)	1.1	1.0	1.2	6.2	1.5	-5.1	-1.4	-1.4	-3.1	-2.8			glyceraldehyde 3-phosphate dehydrogenase [*Elaeis guineensis*]	gi|82400215
211	27 (27)	-1.1	1.0	1.6	2.8	1.2	-4.6	1.2	1.2	1.3	2.1	-1.1	-1.0		
212	27 (27)	1.1	-1.1	1.1	2.3	1.6	-2.4	-1.2	-1.1	-1.8	-1.2	1.1	1.4	glyceraldehyde 3-phosphate dehydrogenase A subunit [*Arabidopsis thaliana*]	gi|166702
213	27 (27)	1.1	1.2	1.1	-2.2	-1.2	1.6	1.1	-1.3	1.4	1.5	1.2	-1.1		
214	27 (27)	-1.2	-1.2	-1.1	1.9	1.1	-5.7	-1.5	-1.2	-3.1	-3.7	1.0	-1.0	fructose-bisphosphate aldolase, putative [*Ricinus communis*]	gi|255557204
215	27 (27)	1.1	1.0	1.3	1.3	-1.0	-1.7	-1.0	-1.0	1.2	1.6	1.1	1.2		
216	27 (27)	1.1	1.3	1.2	-1.9	-1.4	1.0	1.2	1.2	1.6	2.1	-1.0	-1.0		

217	27 (27)	1.3	1.2	1.2	-1.7	-1.3	1.1	1.5	1.2	1.7	2.7	1.1	1.1		
218	21 (27)	-1.0		1.2		-1.3	-2.1			-1.4	-1.0	1.3	1.4	60S ribosomal protein L7-like protein [*Elaeis guineensis*]	gi|192912978
219	21 (27)	1.2	1.1	1.1	1.8			1.1	-1.2	-1.5	-1.7			glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [*Arabidopsis thaliana*]	gi|145323880
220	24 (27)	1.3	1.1	1.1	1.9	-1.2	-1.6	1.1	-1.4			-1.0	1.1	aldo/keto reductase family protein [*Arabidopsis lyrata* subsp. *lyrata*]	gi|297848944
221	27 (27)	1.1	1.1	1.4	-1.6	1.0	-1.3	1.2	-1.0	1.9	2.8	1.1	-1.1	24 kDa seed maturation protein [*Elaeis guineensis*]	gi|192910858
222	27 (27)	1.2	1.1	1.3	-1.1	-1.1	-1.6	1.0	1.1	1.3	1.5	1.3	1.1	plastidic aldolase [*Nicotiana tabacum*]	gi|294440432
223	27 (27)	1.0	1.1	1.3	-1.4	-1.0	-1.4	1.1	1.1	1.6	2.0	1.1	-1.0		
224	27 (27)	1.0	-1.2	1.2	2.0	-1.1	-2.6	-1.1	-1.1	-1.3	-1.4	1.3	1.3	60S ribosomal protein L7-like protein [*Elaeis guineensis*]	gi|192912978
225	27 (27)	1.2	1.1	1.2	-2.1	1.1	-1.1	1.1	1.3	2.7	3.7	-1.1	1.1	60S ribosomal protein L7-like protein [*Elaeis guineensis*]	gi|192912978
226	27 (27)	1.0	-1.1	1.2	2.8	-1.3	-2.2	1.2	1.0	-1.8	-2.1	1.4	1.5	fructose-bisphosphate aldolase, chloroplast precursor, expressed [*Triticum aestivum*]	gi|300681519
227	27 (27)	-1.0	1.1	1.4	1.5	-1.5	-2.6	1.2	1.2	1.0	1.8	1.2	1.1		
228	27 (27)	1.1	1.0	1.2	2.4	-1.2	-2.0	1.1	1.1	-1.4	-1.7	1.1	1.1	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [*Arabidopsis thaliana*]	gi|145323880
229	27 (27)	1.2	1.1	1.2	-3.9	-1.5	1.4	1.2	1.3	1.4	1.8	1.1	1.0		
230	27 (27)	1.0	1.0	1.1	1.8	-1.2	-1.9	1.2	1.3	-1.3	-1.3	1.1	1.0	PREDICTED: hypothetical protein [*Vitis vinifera*]	gi|225466832
231	15 (27)					-1.1	-1.5	1.4	1.3						
232	15 (27)			1.2		1.0				1.1	-1.7	1.0	1.2	Protochlorophyllide reductase A,chloroplastic; Short=PCR A; AltName: Full=NADPH-protochlorophyllide oxidoreductase A	gi|129708
233	18 (27)			1.1		1.1	3.5			1.6	1.2	-1.3	-2.3		
234	24 (27)	1.6	1.4	-1.1	1.1	-1.1	-4.1	-1.4	-1.4	1.3	-1.4				
235	24 (27)	1.5	1.1	-2.1	1.0	-3.8	-4.9	-1.4	-1.6	-1.0	-1.5				
236	27 (27)	-1.7	-1.3	1.2	-1.4	-1.0	-1.3	-1.0	-1.0	1.3	1.0	-1.0	-1.1	pterocarpan reductase-like protein [*Linum corymbulosum*]	gi|169639232
237	27 (27)	-1.3	-1.0	1.1	-2.5	1.6	1.8	-1.2	1.0	1.6	1.4	-1.3	-1.6	Isoflavone reductase, putative [*Ricinus communis*]	gi|255543713
238	27 (27)	-1.1	1.1	1.3	1.2	1.2	-1.7	1.0	1.3	2.5	2.6	-1.1	-1.2		
239	27 (27)	-1.1	-1.0	1.0	1.1	1.2	-1.6	-1.1	1.0	1.6	1.5	-1.0	-1.1		
240	27 (27)	-1.0	1.3	1.3	-1.9	1.3	-1.2	1.1	1.5	3.3	4.2	-1.2	-1.3	Ras-related protein RIC1 [*Elaeis guineensis*]	gi|192910784

241	27 (27)	1.1	1.2	1.2	-1.9	1.3	1.3	1.3	1.3	2.2	2.8	-1.1	-1.2		
242	27 (27)	1.0	-1.1	1.2	2.1	-1.2	-2.0	-1.0	-1.1	1.7	1.2	-1.0	-1.2	ferredoxin--NADP reductase, putative [*Ricinus communis*]	gi|255538962
243	27 (27)	-1.2	-1.0	1.2	2.6	-1.1	-1.7	-1.2	-1.2	1.6	1.4	-1.0	1.1	ferredoxin--NADP reductase, putative [*Ricinus communis*]	gi|255538962
244	27 (27)	-1.0	1.1	-1.1	-2.0	1.1	1.5	1.2	1.1	1.6	1.6	-1.0	-1.2		
245	27 (27)	-1.1	-1.1	1.2	4.4	-1.4	-2.7	-1.0	-1.2	1.1	-1.4	1.1	1.0	ferredoxin--NADP reductase, putative [*Ricinus communis*]	gi|255538962
246	27 (27)	-1.2	-1.1	1.2	4.9	-1.2	-2.8	-1.2	-1.4	1.1	-1.1	1.1	1.0	ferredoxin--NADP reductase, putative [*Ricinus communis*]	gi|255538962
247	27 (27)	-1.1	1.1	1.5	24.3	-1.1	-14.2	-1.1	-1.1	-2.3	-4.1	-1.0	1.0	Isopentenyl-diphosphate Delta-isomerase IOS=*Camptotheca acuminata* GN=IPI1 PE=2 SV=1	IDI1_CAMAC
248	27 (27)	-1.1	-1.0	1.1	11.0	-1.9	-9.4	-1.2	-1.4	-2.0	-3.3	1.1	1.2	hypothetical protein SELMODRAFT_422914 [*Selaginella moellendorffii*]	gi|302803987
249	18 (27)	-1.1	-1.1	1.1	9.6	-1.2				-1.4	-3.0			ferredoxin--NADP reductase, putative [*Ricinus communis*]	gi|255538962
250	15 (27)	-1.0	-1.2	1.2	4.4			-1.2						Isopentenyl-diphosphate Delta-isomerase I OS=*Camptotheca acuminata* GN=IPI1 PE=2 SV=1	IDI1_CAMAC
251	24 (27)	-1.2		1.2		-1.2	-6.0	-1.3	-1.6	-1.5	-2.6	1.1	1.1		
252	27 (27)	1.4	1.1	-1.1	-3.6	1.3	2.2	-1.3	1.0	3.0	3.2	1.0	1.1	oxygen evolving enhancer protein 1 [*Litchi chinensis*]	gi|326467059
253	24 (27)	1.4		-1.1		1.3	2.4	-1.2	-1.2	2.8	2.3	-1.0	-1.0	oxygen evolving enhancer protein 1 [*Litchi chinensis*]	gi|326467059
254	27 (27)	1.3	1.0	-1.1	-2.5	-1.0	2.9	-1.2	-1.3	2.6	1.8	-1.0	-1.0	oxygen evolving enhancer protein 1 [*Litchi chinensis*]	gi|326467059
255	27 (27)	1.3	-1.0	-1.1	-2.1	-1.0	2.9	-1.2	-1.1	1.4	1.6	-1.0	1.6	LOC100284083 [*Zea mays*]	gi|226530191
256	27 (27)	1.4	-1.1	-1.1	-1.3	1.0	2.7	-1.1	-1.1	-1.4	-1.2	-1.1	1.2		
257	27 (27)	1.2	-1.0	-1.1	-1.4	-1.2	2.0	-1.3	-1.2	2.0	1.3	1.0	1.0	oxygen evolving enhancer protein 1 [*Litchi chinensis*]	gi|326467059
258	15 (27)			-1.1	1.5	-1.6						1.1	-1.0	oxygen evolving enhancer protein 1 [*Litchi chinensis*]	gi|326467059
259	18 (27)	1.2		-1.1				1.0	-1.1	1.1	-2.1				
260	27 (27)	-1.3	1.1	-1.1	3.3	-1.5	-2.1	1.4	-1.0	-1.8	-2.5	1.0	-1.5	chloroplast manganese stabilizing protein [*Solanum tuberosum*]	gi|313586398
261	27 (27)	1.1	-1.1	-1.2	2.3	-1.9	-1.4	1.2	1.2	-1.3	-3.6	1.1	1.0	oxygen evolving enhancer protein 1 [*Litchi*	gi|326467059

														chinensis]	
262	27 (27)	-1.0	1.0	-1.3	2.5	-2.0	-1.4	1.5	1.2	-1.5	-3.4	-1.1	-1.2	oxygen evolving enhancer protein 1 [*Litchi chinensis*]	gi|326467059
263	24 (27)	1.1	-1.1	-1.1	1.0	-1.3		1.1		1.0	-1.7	1.6	1.8	NADH-cytochrome b5 reductase-like protein OS=*Arabidopsis thaliana* GN=At5g20080 PE=1 SV=2	NCB5R_ARATH
264	27 (27)	1.1	-1.0	1.1	-1.5	1.1	-1.2	-1.1	-1.1	-1.2	-1.4	1.1	1.3	Outer plastidial membrane protein porin OS=*Pisum sativum* GN=POR1 PE=1 SV=2	VDAC_PEA
265	24 (27)	1.1	1.1	1.3	1.8	1.0	-1.1	-1.1	1.3	-1.4	-1.6				
266	24 (27)	1.2	-1.0	1.2	2.1			1.1	1.5	-1.6	-1.9	1.2	1.0	predicted protein [*Micromonas pusilla* CCMP1545]	gi|303275936
267	27 (27)	-1.0	-1.4	1.5	-1.1	6.3	2.4	-1.1	1.2	2.0	-2.2	1.4	1.2	abscisic stress ripening [*Musa* ABB Group]	gi|270064305
268	27 (27)	1.0	1.1	1.3	1.0	-1.2	-2.3	1.2	1.3	1.6	-1.0	1.1	1.2	peroxisome type ascorbate peroxidase [*Elaeis guineensis*]	gi|192910808
269	27 (27)	-1.2	-1.1	1.0	-1.5	1.2	1.2	-1.6	-1.3	1.4	1.2	1.0	1.2		
270	24 (27)	-1.1	1.1			-1.1	-1.8	1.1	1.0	-1.0	-1.1	1.1	1.2	oxidoreductase [*Micromonas pusilla* CCMP1545]	gi|303276240
271	27 (27)	-1.1	-1.2	1.4	-1.1	1.7	1.3	-1.1	1.2	1.5	1.9	1.3	1.3	Antifungal protein ginkbilobin-1 (Fragment) OS=*Ginkgo biloba* GN=GNK1 PE=1 SV=1	GNK1_GINBI
272	21 (27)			1.1	-2.7	1.1	-1.4			-1.4	-1.3	-1.1	1.1	oxygen evolving enhancer protein 1 [*Litchi chinensis*]	gi|326467059
273	27 (27)	1.1	1.5	1.1	2.0	1.2	-1.7	-1.3	-1.2	-1.0	-1.3	1.1	1.3		
274	27 (27)	1.2	-1.1	1.1	-1.4	1.0	1.3	-1.0	1.0	1.5	-1.1	1.2	1.3	predicted protein [*Populus trichocarpa*]	gi|224140861
275	27 (27)	1.1	-1.3	1.0	1.2	2.1	1.2	-1.3	1.0	-1.4	-1.2	1.3	1.4		
276	24 (27)	1.1	1.1	1.1	2.2	1.2	-1.9			-2.0	-2.4	1.3	1.3	small subunit of ribulose-1,5-bisphosphate carboxylase [*Oryza sativa Japonica* Group]	gi|218210
277	27 (27)	1.1	-1.1	-1.0	1.3	-1.0	1.0	-1.2	-1.2	1.1	-1.8	1.3	1.4	Putative cytochrome c oxidase subunit II PS17	gi|109892850
278	21 (27)	1.1	1.0	-1.1	-1.8	1.2				1.9	-1.1	1.1	1.1		
279	24 (27)	1.1	-1.1	1.1	2.7	1.2	-1.2			-1.7	-3.1	1.3	-1.2	peroxisome type ascorbate peroxidase [*Elaeis guineensis*]	gi|192910808
280	21 (27)	1.3	-1.0	1.1	1.8	1.6				-1.1	-1.3	1.2	1.6		
281	27 (27)	1.1	-1.2	1.0	2.0	-1.0	-1.4	-1.2	-1.3	-1.4	-3.4	1.3	1.3	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|290586530
282	27 (27)	1.3	1.0	1.5	2.1	1.2	-1.4	1.0	1.2	-1.8	-1.7	1.6	1.4	Pyruvate, phosphate dikinase 1, chloroplastic OS=*Arabidopsis thaliana* GN=PPDK PE=1 SV=2	PPDK1_ARATH
283	27 (27)	1.2	-1.1	1.3	2.1	1.5	-1.2	1.1	-1.0	-1.7	-1.7	1.3	1.1		

284	24 (27)			1.1	1.5	1.1	1.2	-1.4	1.4	-1.6	-1.6	-1.1	-1.4	Outer plastidial membrane protein porin OS=*Pisum sativum* GN=POR1 PE=1 SV=2	VDAC_PEA
285	18 (27)			1.0	1.1	1.6	-1.7					1.1	1.5		
286	27 (27)	-1.1	1.1	1.1	-1.2	1.2	1.4	-1.1	-1.2	-1.0	3.9	1.2	-1.1	triose phosphate isomerase cytosolic isoform [*Elaeis guineensis*]	gi|192910674
287	27 (27)	-1.4	-1.1	-1.1	-2.4	-1.0	1.8	-1.1	-1.2	1.4	3.4	1.1	-1.3	chlorophyll A/B binding protein, putative [*Ricinus communis*]	gi|255557387
288	27 (27)	-1.3	-1.1	1.2	-1.7	1.1	1.6	-1.0	-1.1	1.2	3.8	1.1	-1.1	triose phosphate isomerase cytosolic isoform [*Elaeis guineensis*]	gi|192910674
289	27 (27)	1.1	1.1	1.1	1.1	1.1	1.2	-1.1	-1.3	-1.2	1.9	1.2	-1.2		
290	27 (27)	1.0	1.1	1.3	1.2	1.5	-1.8	-1.1	-1.2	1.3	1.7	1.3	1.0	cytosolic ascorbate peroxidase [*Elaeis guineensis*]	gi|192912966
291	27 (27)	-1.1	1.3	1.4	2.3	1.5	1.1	-1.1	-1.0	2.0	2.9	1.1	-1.1		
292	27 (27)	-1.1	1.5	-1.2	2.4	1.1	-1.5	-1.2	-1.3	1.6	1.5	-1.1	1.1	cytosolic ascorbate peroxidase [*Elaeis guineensis*]	gi|192912966
293	27 (27)	-1.1	1.1	1.4	1.4	1.1	-1.7	-1.3	-1.1	1.2	1.1	1.0	1.1	cytosolic ascorbate peroxidase [*Elaeis guineensis*]	gi|192912966
294	27 (27)	-1.1	1.0	-1.1	1.1	-1.7	-2.7	1.3	1.4	-1.2	-1.4	1.1	1.1		
295	18 (27)	-1.1		-1.6				-1.4	-1.3			-1.2	1.2	F-box/kelch-repeat protein At3g24760 OS=*Arabidopsis thaliana* GN=At3g24760 PE=2 SV=1	FBK69_ARATH
296	15 (27)	1.6		-1.0		-5.7	3.2								
297	24 (27)			-1.0	-1.7	-2.0	-1.3	1.2	-1.0	-1.2	-2.0	1.1	-1.1	small subunit of ribulose-1,5-bisphosphate carboxylase [*Oryza sativa Japonica* Group]	gi|218210
298	24 (27)	-1.2	-1.2	-1.1	1.7	-1.4	-1.6	1.2	-1.1			-1.1	-1.3		
299	27 (27)	-1.1	-1.4	-1.1	-1.2	-1.4	-1.2	1.2	-1.2	-1.3	-2.3	-1.0	-1.3		
300	18 (27)	-1.1	-1.1			-1.7	-1.3	1.3	1.1						
301	27 (27)	-1.5	-1.0	1.2	-2.2	-1.1	1.1	-1.1	-1.1	1.8	1.4	-1.1	-1.5	carbonic anhydrase 3 [*Flaveria vaginata*]	gi|326582932
302	21 (27)			1.1	-1.4			1.2	-1.5	-1.1	-1.9	1.2	-1.3	CBL-interacting protein kinase 4 OS=*Oryza sativa* subsp. *japonica* GN=CIPK4 PE=2 SV=2	CIPK4_ORYSJ
303	24 (27)	1.5	1.4	-1.2	1.1			-1.1	-1.3	1.6	-1.0	1.4	-1.1		
304	27 (27)	1.1	-1.0	1.0	1.0	-1.4	1.2	1.1	1.3	-1.1	-1.5	1.1	-1.2		
305	27 (27)	1.3	1.3	1.0	-1.1	-1.4	1.7	1.2	-1.0	2.5	1.7	1.2	1.1	oxygen evolving enhancer protein 2 [*Bruguiera gymnorhiza*]	gi|8131593
306	27 (27)	1.3	1.1	1.1	-1.5	-1.0	1.8	1.2	-1.0	2.7	2.1	1.2	1.1	Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2; AltName: Full=23 kDa	gi|11134035

														s	
307	27 (27)	-1.1	-1.3	-1.0	1.6	1.0	-3.3	1.1	1.1	-1.1	-1.6	-1.1	-1.2	putative carbonic anhydrase [*Triticum turgidum* subsp. *durum* x *Secale cereale*]	gi|290875537
308	27 (27)	-1.0	-1.1	1.1	1.4	1.3	-2.7	-1.0	1.0	1.2	1.1	-1.2	-1.2	putative carbonic anhydrase [*Triticum turgidum* subsp. *durum* x *Secale cereale*]	gi|290875537
309	27 (27)	1.6	1.5	1.0	-2.1	-1.1	2.0	1.0	1.1	2.5	1.3	1.0	-1.1	oxygen-evolving enhancer protein 2 [*Arabidopsis lyrata* subsp. *lyrata*]	gi|297826499
310	21 (27)	1.3	1.1			-1.2	1.7	-1.0	1.1	1.5	1.7				
311	24 (27)	1.0	-1.1			1.1	-3.3	1.1	1.1	1.6	1.3	-1.2	-1.4	photosystem II 23 kDa polypeptide [*Nicotiana tabacum*]	gi|19898
312	21 (27)					-1.7	-1.7	1.3	-1.0	-1.9	-2.3	1.1	-1.1	ATP synthase beta subunit [*Dictyoloma vandellianum*]	gi|4206614
313	27 (27)	1.3	-1.1	1.1	3.1	-1.2	-2.1	-1.2	-1.3	-1.2	-2.3	1.1	1.1	photosystem II 23 kDa polypeptide [*Nicotiana tabacum*]	gi|19898
314	27 (27)	1.4	1.1	-1.2	1.1	1.2	-1.1	-1.0	1.1	1.1	1.9	1.1	-1.1	photosystem II 23 kDa polypeptide [*Nicotiana tabacum*]	gi|19898
315	27 (27)	1.2	-1.5	1.0	4.1	-1.8	-4.0	-1.1	-1.2	-1.4	-3.1	-1.1	-1.4	Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2; AltName: Full=23 kDa s	gi|11133884
316	27 (27)	-1.2	-1.7	-1.0	2.0	-1.3	-6.8	1.7	1.7	-1.7	-3.8	-1.1	-1.0	putative carbonic anhydrase [*Triticum turgidum* subsp. *durum* x *Secale cereale*]	gi|290875537
317	27 (27)	-1.2	-1.2	-1.1	1.9	-1.2	-3.5	1.2	1.1	-1.4	-2.5	-1.1	-1.0	putative carbonic anhydrase [*Triticum turgidum* subsp. *durum* x *Secale cereale*]	gi|290875537
318	27 (27)	-1.2	-1.4	-1.1	2.8	-1.6	-3.7	1.6	1.2	-2.2	-3.6	1.1	-1.2	hypothetical protein LOC100216776 [*Zea mays*]	gi|219363037
319	21 (27)	-1.1	-1.6	1.0	5.1	-1.3	-3.8					-1.0	-1.1		
320	24 (27)	-1.1	-1.1	-1.1	2.2	-1.3	-2.6			-1.7	-2.8	-1.4	-2.2	putative carbonic anhydrase [*Triticum turgidum* subsp. *durum* x *Secale cereale*]	gi|290875537
321	27 (27)	-1.0	-1.2	-1.1	3.6	-1.8	-3.2	1.4	-1.1	-2.4	-5.0	1.0	-1.1	putative carbonic anhydrase [*Triticum turgidum* subsp. *durum* x *Secale cereale*]	gi|290875537
322	15 (27)			-1.1	1.6	-1.7						1.1	1.2		
323	27 (27)	1.2	1.0	-1.1	-1.8	-1.4	2.4	-1.4	-1.3	1.6	1.1	-1.1	-1.1	PsbP [*Xerophyta humilis*]	gi|25992740
324	27 (27)	1.1	-1.1	-1.2	-1.8	-1.2	2.2	-1.3	-1.4	1.1	-1.6	-1.2	-1.2	Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2; AltName: Full=23 kDa s	gi|11134035
325	27 (27)	1.3	-1.1	1.1	-1.1	-1.4	-1.3	-1.1	-1.5	1.1	-2.2	-1.3	-1.1	oxygen-evolving enhancer protein 2 [*Arabidopsis lyrata* subsp. *lyrata*]	gi|297826499
326	27 (27)	1.1	1.1	-1.2	-1.6	-1.1	1.7	-1.1	-1.1	1.1	-1.1	1.1	-1.0	Geminivirus Rep-interacting motor protein	

														OS=*Arabidopsis thaliana* GN=GRIMP PE=1 SV=1	GRIMP_ARATH
327	27 (27)	1.3	-1.0	-1.1	-1.1	-1.2	-1.0	-1.4	-1.3	1.1	-2.1	-1.1	-1.3		
328	27 (27)	-1.0	1.1	-1.2	-3.9	-1.2	2.7	-1.1	-1.2	1.4	1.8	-1.1	-1.1	thioredoxin peroxidase [*Elaeis guineensis*]	gi|192910848
329	27 (27)	-1.1	-1.0	-1.2	-2.3	-1.2	3.0	-1.1	-1.2	1.3	1.3	-1.1	-1.1	thioredoxin peroxidase [*Elaeis guineensis*]	gi|192910848
330	27 (27)	-1.0	-1.0	-1.1	-2.0	-1.3	2.3	1.1	-1.1	1.2	1.1	-1.0	-1.0	thioredoxin peroxidase [*Elaeis guineensis*]	gi|192910848
331	27 (27)	1.1	1.0	-1.1	-1.8	-1.5	1.6	-1.6	-1.2	1.1	-1.4	-1.4	-1.1	thioredoxin peroxidase [*Elaeis guineensis*]	gi|192910848
332	27 (27)	1.0	-1.0	-1.3	-2.0	-1.5	1.3	-1.3	-1.5	1.1	-1.8	-1.3	-1.2	thioredoxin peroxidase [*Elaeis guineensis*]	gi|192910848
333	27 (27)	1.1	1.0	-1.1	-1.5	-1.5	-1.2	-1.3	-1.6	-1.0	-2.3	-1.7	-1.2		
334	24 (27)	1.6	1.2	-1.3	-2.1	-1.4	2.3			1.3	-1.2	-1.4	-1.1	ABC transporter B family member 15 OS=*Arabidopsis thaliana* GN=ABCB15 PE=1 SV=1	AB15B_ARATH
335	27 (27)	1.5	1.4	-1.4	-3.5	-1.2	3.0	-1.2	-1.1	1.4	1.2	-1.3	-1.1	ATP synthase subunit b, chloroplastic OS=*Aneura mirabilis* GN=atpF PE=3 SV=1	ATPF_ANEMR
336	27 (27)	1.3	1.3	-1.5	-3.9	-1.1	3.5	-1.3	-1.2	1.3	1.4	-1.4	-1.4	hypothetical protein VITISV_023080 [*Vitis vinifera*]	gi|147766924
337	27 (27)	1.2	1.3	-1.2	-2.3	-1.5	1.2	-1.0	-1.3	1.0	-1.9	-1.6	-1.2	Putative cytochrome c oxidase subunit II PS17	gi|109892850
338	24 (27)	1.2		-1.2		-1.6	-1.1	-5.0	1.8	-1.1	-1.3	1.3	1.4	23 kDa polypeptide of water-oxidizing complex of photosystem II [*Nicotiana tabacum*]	gi|417604
339	27 (27)	-1.0	-1.1	-1.0	1.3	-1.2	1.7	1.5	1.3	1.3	-1.1	-1.0	1.1	large subunit of ribulose-1,5-bisphosphate carboxylase/oxygenase [*Trichomanes elegans*]	gi|29467126
340	27 (27)	1.2	1.1	1.2	-1.1	1.1	2.1	1.1	-1.1	1.5	1.0	1.1	1.0		
341	27 (27)	1.4	1.1	-1.1	-1.6	-1.4	1.7	1.0	-1.4	-1.2	-1.5	1.1	-1.0	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|11558717
342	27 (27)	1.3	1.2	-1.1	-2.3	-1.4	1.6	1.2	-1.1	1.4	-1.1	-1.3	-1.1		
343	24 (27)	1.3	-1.0	-1.2	-3.2	-1.5	1.9			1.4	-1.0	-1.1	-1.2	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [*Elaeis guineensis*]	gi|290586530
344	24 (27)	-1.3	1.5	1.2	-1.2	-2.4	-1.8	1.5	-1.3			1.1	1.2		
345	18 (27)					1.3	1.2			1.3	-1.3	-1.7	-1.9		
346	27 (27)	1.1	-1.0	1.0	-1.2	-1.1	-1.0	1.1	1.1	1.6	1.0	-1.1	1.0	peptidyl-prolyl cis-trans isomerase, putative [*Ricinus communis*]	gi|255547634
347	27 (27)	1.1	1.0	1.1	-1.8	-1.2	1.2	1.3	1.2	1.7	1.1	1.1	1.1	peptidyl-prolyl cis-trans isomerase, putative [*Ricinus communis*]	gi|255547634
348	15 (27)			-1.7		1.7	5.6	-3.5	-2.0					ribulose-1,5-bisphosphate	gi|11558717

														carboxylase/oxygenase large subunit [*Elaeis guineensis*]	
349	24 (27)			-1.3	-2.4	-1.3	2.1	-1.1	-1.5	1.4	1.1	-1.2	-1.5	Endoglucanase 18 OS=*Oryza sativa* subsp. *Japonica* GN=Os06g0715300 PE=2 SV=1	GUN18_ORYSJ
350	27 (27)	-1.0	-1.1	1.0	1.9	-1.0	-1.4	-1.5	-1.4	1.1	-1.6	-1.1	-1.0	peptidyl-prolyl cis-trans isomerase, putative [*Ricinus communis*]	gi|255547634
351	21 (27)	-1.0	-1.2	-1.0	2.6			1.1	-1.2	-1.1	-2.0				
352	27 (27)	-1.0	-1.0	-1.1	-4.3	-1.1	2.4	-1.5	-1.3	1.3	1.3	-1.1	-1.7	Phosphoribosylaminoimidazole carboxylase, chloroplastic (Fragment) OS=*Vigna aconitifolia* GN=PURKE PE=2 SV=1	PUR6_VIGAC
353	21 (27)	-1.2	-1.3	1.1	4.2					-1.5	-3.0	-1.1	-1.1	peptidyl-prolyl cis-trans isomerase, putative [*Ricinus communis*]	gi|255547634
354	27 (27)	-1.2	1.0	-1.4	-2.4	1.1	2.2	-1.5	-1.7	1.1	1.1	-1.2	-1.3	peptidyl-prolyl cis-trans isomerase, putative [*Ricinus communis*]	gi|255547634
355	24 (27)			-1.3	-1.5	1.1	1.7	1.1	1.0	-1.2	-1.6	-1.0	1.0		
356	21 (27)	-1.3	1.1	1.0	1.0	-1.0	1.0					-1.4	-1.5	Photosystem I reaction center subunit II, chloroplast	gi|255551453
357	27 (27)	1.1	1.2	1.0	1.4	1.1	-1.3	1.1	2.8	2.4	1.4	-1.1	1.1	cyclophilin [*Elaeis guineensis*]	gi|192910744
358	21 (27)	-1.2	-1.1			-1.1	-1.6	1.2	1.4	-1.0	-1.8				
359	24 (27)	-1.1	1.1	-1.1	-2.8			-1.3	-1.1	1.3	1.2	1.0	1.1	peroxiredoxin [*Elaeis guineensis*]	gi|192910922
360	27 (27)	-1.2	1.8	-1.8	-1.8	-1.3	2.6	1.6	1.3	1.0	-1.3	1.2	-1.4	phosphoenolpyruvate carboxylase [*Anthoceros punctatus*]	gi|7768089
361	27 (27)	-1.1	1.2	1.0	-1.2	-1.3	1.9	1.0	1.3	1.7	1.1	1.2	1.1	Photosystem I reaction center subunit IV, chloroplastic; Short=PSI-E; AltName: Full=P	gi|131176
362	21 (27)			-1.2	-1.8			-1.0	1.3	2.3	2.3	1.2	-1.1		
363	27 (27)	-1.1	-1.2	-1.7	1.6	-1.9	-1.7	1.3	-1.5	1.3	1.5	-1.1	1.1	F-box/kelch-repeat protein [Arabidopsis thaliana]	gi|15230186
364	24 (27)			-1.1	-1.8	-1.3	2.0	1.2	1.1	1.4	1.2	1.1	-1.0	oxygen-evolving enhancer protein 3-1 [*Zea mays*]	gi|195633817
365	15 (27)	-1.1				-1.3	2.9			1.2	2.0				
366	27 (27)	-1.2	1.5	1.1	-3.3	-1.1	2.5	1.0	-1.2	1.6	1.0	1.4	-1.2	oxygen-evolving enhancer protein 3-1 [*Zea mays*]	gi|195633817
367	27 (27)	-1.1	-1.1	-1.2	-2.9	-1.3	1.5	-1.0	-1.2	-1.1	-1.5	-1.1	-1.2	Endoribonuclease Dicer homolog 1 OS=*Oryza sativa* subsp. *japonica* GN=DCL1 PE=3 SV=1	DCL1_ORYSJ
368	15 (27)					-1.1	2.1	1.3	1.1			1.3	-1.2		
369	24 (27)	-1.0		-1.4		-1.0	1.8	1.1	1.3	1.2	1.7	-1.5	-1.6	Os07g0544800 [*Oryza sativa Japonica* Group]	gi|115472625
370	21 (27)			1.1	-6.2	1.1	2.3			1.3	2.1	1.2	1.2	Putative cytochrome c oxidase subunit II PS17	PS17_PINST

371	24 (27)			-1.3	-2.6	1.1	1.6	1.6	-1.0	1.5	1.6	-1.2	-1.3	(Fragments) OS=*Pinus strobus* PE=1 SV=1 *chloroplast ribulose-1,5-bisphosphate* carboxylase/oxygenase small subunit [*Musa* AAAB Group]	gi|76574203
372	27 (27)	-1.1	1.0	-1.2	-2.0	1.0	1.5	1.2	-1.1	1.1	1.3	1.0	1.3		
373	27 (27)	-1.0	-1.0	-1.2	-2.0	1.1	1.8	-1.1	-1.2	-1.1	1.2	-1.3	-1.1	pentatricopeptide, putative, expressed [*Oryza sativa Japonica* Group]	gi|108864632
374	27 (27)	1.0	-1.1	-1.2	2.7	1.5	-3.5	-1.1	1.1	1.1	-1.1	-1.2	-1.2	IAA type protein [*Elaeis guineensis*]	gi|50404477
375	27 (27)	-1.0	-1.1	-1.1	2.3	1.1	-4.2	1.1	1.4	-1.1	-1.7	-1.1	-1.1	chloroplast ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [*Musa balbisiana*]	gi|76574195
376	27 (27)	1.3	-1.1	-1.1	-1.0	1.1	-1.1	1.3	1.5	1.5	1.6	1.2	1.1		
377	27 (27)	-1.1	1.1	-1.2	-1.7	1.2	-1.9	1.9	2.3	1.3	1.4	-1.5	-1.5	chloroplast ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [*Musa balbisiana*]	gi|76574195
378	24 (27)	-1.2	-1.2	-1.3	1.3	1.2		1.2		1.1	-1.2	-1.4	-1.5		
379	27 (27)	-1.1	1.1	-1.2	1.1	1.3	-3.6	1.5	1.4	1.3	1.1	-1.4	-1.4	40S ribosomal protein S5 [*Elaeis guineensis*]	gi|192910844
380	21 (27)			-1.3	2.9	1.2	-5.3	-1.0	1.4			-1.2	-1.2	chloroplast ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [*Musa balbisiana*]	gi|76574195
381	18 (27)	-1.1	-1.1			-1.7		1.8		1.2	-1.3			hypothetical protein VITISV_010874 [*Vitis vinifera*]	gi|147843505
382	21 (27)			1.0	-1.5	-1.1	1.8			1.3	-1.4	-1.0	-1.3		

Appearance	# of gels the spots can be detected
P value	Student t test
Av. Ratio: M / H, E / H	Positive value means increased ratio
	Negative value means decreased ratio

The results above demonstrate that the technique of protein analysis using DIGE can effectively differentiate non-*Ganoderma* infected oil palm from *Ganoderma*-infected oil palm.

The above is a description of the subject matter the inventors regard as the invention and is believed that others can and will design alternative processes that include this invention based on the above disclosure.

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 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 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 group 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*.