

Clonal Genotype of *Geomyces destructans* among Bats with White Nose Syndrome, New York, USA

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The dispersal mechanism of *Geomyces destructans*, which causes geomycosis (white nose syndrome) in hibernating bats, remains unknown. Multiple gene genealogic analyses were conducted on 16 fungal isolates from diverse sites in New York during 2008–2010. The results are consistent with the clonal dispersal of a single *G. destructans* genotype.

Geomycosis, or white nose syndrome, is a newly recognized fungal infection of hibernating bats. The etiologic agent, the psychrophilic fungus *Geomyces destructans*, was first recognized in caves and mines around Albany, New York, USA (1,2). The disease has spread rapidly in New York and other states in the northeastern United States. At least 1 affected bat species is predicted to face regional extinction in the near future (3). Much remains unknown about this fungus, including its ecology and geographic distribution. For example, although hibernacula are high on the list of suspected sites, where the bats acquire this infection is not known. Similarly, although strongly suspected, the role of humans and other animals in the dispersal of *G. destructans* and the effect of such dispersals in bat infections have not been confirmed. We recently showed that 6 *G. destructans* strains from sites near Albany were genetically similar (2), raising the possibility of a common source for the spread of this infection. Corollary to this observation and other opinions (3,4), the US Fish & Wildlife Service has made an administrative decision to bar human access to caves as a precautionary measure

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(www.fws.gov/whitenosesyndrome/pdf/NWRS_WNS_Guidance_Final1.pdf). Thus, an understanding of the dispersal mechanism of *G. destructans* is urgently needed to formulate effective strategies to control bat geomycosis.

The Study

We applied multiple gene genealogic analyses in studying *G. destructans* isolates; this approach yields robust results that are easily reproduced by other laboratories (5). Sixteen *G. destructans* isolates recovered from infected bats during 2008–2010 were analyzed. These isolates originated from 7 counties in New York and an adjoining county in Vermont, all within a 500-mile radius (Table 1). The details of isolation and identification of *G. destructans* from bat samples have been described (2). One isolate of a closely related fungus *G. pannorum* M1372 (University of Alberta Mold Herbarium, Edmonton, Alberta, Canada) was included as a reference control. To generate molecular markers, 1 isolate, *G. destructans* (M1379), was grown in yeast extract peptone dextrose broth at 15°C, and high molecular weight genomic DNA was prepared according to Moller et al. (6). A cosmid DNA library was constructed by using pWEB kit (Epicenter Biotechnologies, Madison, WI, USA) by following protocols described elsewhere (7). One hundred cosmid clones, each with ≈40-Kb DNA insert, were partially sequenced in both directions by using primers M13 and T7. The nucleotide sequences were assembled with Sequencher 4.6 (Gene Codes Corp., Ann Arbor, MI, USA) and BLAST (www.ncbi.nlm.nih.gov/BLAST) homology searches identified 37 putative genes. Sequences of 10 genes, including open reading frames, 3' and/or 5' untranslated regions, and introns, were evaluated as potential markers for analyzing *G. pannorum* and *G. destructans*. Our screening approach indicated that 8 gene

Table 1. *Geomyces destructans* isolates studied, New York, USA

Isolate	Date obtained	Site, county*
M1379†	2008 Mar 28	Williams Hotel Mine, Ulster
M1380†	2008 Mar 28	Williams Hotel Mine, Ulster
M1381†	2008 Mar 28	Williams Hotel Mine, Ulster
M1383†	2008 Apr 11	Graphite Mine, Warren
M2325	2010 Jan 25	Westchester
M2327	2010 Feb 2	Dewitt, Onondaga
M2330	2009 Mar 5	Lancaster, Erie
M2331	2009 Mar 9	White Plains, Westchester
M2332	2009 Mar 11	Dannemora, Clinton
M2333	2009 Mar 11	Dannemora, Clinton
M2334	2009 Mar 12	Newstead, Erie
M2335	2009 Mar 16	Ithaca, Tompkins
M2336	2009 Oct 6	Bridgewater Mine, Windsor, VT
M2337	2010 Feb 9	Akron Mine, Erie
M2338	2010 Mar 4	Hailes Cave, Albany
M2339	2010 Mar 11	Letchworth Tunnel, Livingston

*All locations in New York state except Bridgewater Mine, Windsor, Vermont.

†Previously analyzed by randomly amplified polymorphic DNA typing.

targets could be amplified from both *G. destructans* and *G. pannorum* by PCR (Table 2).

To obtain DNA sequences from 1 *G. pannorum* and 16 *G. destructans* isolates, we prepared genomic DNA from mycelia grown in yeast extract peptone dextrose broth through conventional glass bead treatment and phenol-chloroform extraction and then ethanol precipitation (7). AccuTaq LA DNA Polymerase (Sigma-Aldrich, St. Louis, MO, USA) was used for PCR: 3 min initial denaturation at 94°C, 35 amplification cycles with a 15-sec denaturation at 94°C, 30-sec annealing at 55°C, and 1-min extension at 68°C and a 5-min final extension at 68°C. PCR products were treated with ExoSAP-IT (USB Corp., Cleveland, OH, USA) before sequencing. Both strands of amplicons were sequenced by the same primers used for PCR amplification (Table 2). A database was created by using Microsoft Access (Microsoft, Redmond, WA, USA) to deposit and analyze the sequences. Nucleotide sequences were aligned with ClustalW version 1.4 (www.clustal.org) and edited with MacVector 7.1.1 software (Accelrys, San Diego, CA, USA). Phylogenetic analyses were done by using PAUP 4.0 (8) and MEGA 4 (9).

We cloned and sequenced ≈200 Kb of the *G. destructans* genome and identified genes involved in a variety of cellular processes and metabolic pathways (Table 2). DNA sequence typing by using 8 gene fragments showed that all 16 *G. destructans* isolates had identical nucleotide sequences at all 8 sequenced gene fragments but were distinct from *G. pannorum* sequences. A maximum-parsimony tree generated from the 8 concatenated gene fragments indicated a single, clonal genotype for the 16 *G.*

destructans strains (Figure 1). This consensus tree included 4,470 aligned nucleotides from all targeted gene sequences with 545 variable sites that separate the *G. destructans* clonal genotype from *G. pannorum*. Further analyses of the same concatenated gene fragments with exclusion of 50 insertions and deletions between *G. destructans* and *G. pannorum* yielded a tree with a shorter length (495 steps instead of 545 steps) but an identical topology (online Technical Appendix Figure 1, www.cdc.gov/EID/content/17/7/1273-Techapp.pdf). This pattern remained unchanged when different phylogenetics models were used for analysis (online Technical Appendix Figure 2). The lack of polymorphism among the 16 *G. destructans* isolates was unlikely because of evolutionary constraint at the sequenced gene fragments. We found many synonymous and nonsynonymous substitutions in target genes among a diversity of fungal species, including between *G. destructans* and *G. pannorum* (10) (online Technical Appendix Figure 3).

Conclusions

Our finding of a single clonal genotype in *G. destructans* population fits well with the rapid spread of geomycosis in New York (Figure 2). Our sampling population covered both spatial and temporal dimensions, and the numbers of isolates analyzed were adequate in view of difficulties encountered in obtaining pure isolations of *G. destructans* (11). Although the affected New York sites are separated by sizable distances and include geographic barriers, a role for the natural dissemination of the fungus through air, soil, and water cannot be ruled out. Indeed, several fungi with

Table 2. *Geomyces destructans* and *G. pannorum* target gene fragments used for multiple gene genealogic analyses, New York, USA

Gene*	Homology (GenBank accession no.)	Amplicon size/sequence used for comparison, bp	Primer sequence, 5' → 3'	<i>G. destructans</i> / <i>G. pannorum</i> GenBank accession nos.
<i>ALR</i>	<i>Penicillium marneffeii</i> (XP_002152078.1)	654/534	V1905 (f): CGGAGTGAGATTTATGACGGC V1904 (r): CGTCCATCCCAGACGTTTCATC	HQ834314– HQ834329/HQ834330
<i>Bpntase</i>	<i>Glomerella graminicola</i> (EFQ33509.1)	921/745	V1869 (f): TCAGACGGACTCGGAGGGCAAG V1926 (r): TCGGTTACAGAGCCTCAGTCG	HQ834331– HQ834346/HQ834347
<i>DHC1</i>	<i>Sordaria macrospora</i> (CBI53717.1)	597/418	V1906 (f): GGATGATTCCGGTACCAACAG V1907 (r): ACAGCAAACACAGCGCTGCAAG	HQ834348– HQ834363/HQ834364
<i>GPHN</i>	<i>Ajellomyces capsulatus</i> (EEH06836.1)	659/525	V1918 (f): CACTATTACATCGCCAGGCTC V1919 (r): CTAAACGCAGGCACTGCCTC	HQ834365– HQ834380/HQ834381
<i>PCS</i>	<i>A. capsulatus</i> (EEH08767.1)	920/749	V1929 (f): AGGTCGCGATTGCTGAGTGC V1873 (r): CCTTATCCAGCTTTCTTGCTC	HQ834382– HQ834397/HQ834398
<i>POB3</i>	<i>Pyrenophora tritici-repentis</i> (XP_001937502.1)	653/417	V1908 (f): CACAGTGGAGCAAGGCATCC V1909 (r): ACATACCTAGGCGTCAAGTGC	HQ834399– HQ834414/HQ834415
<i>SRP72</i>	<i>A. dermatitidis</i> (EEQ90678.1)	941/640	V1927 (f): AAGGGAAGTTGGAGAGACTC V1895 (r): CAAGCAGCATTGTACGCCGTC	HQ834416– HQ834431/HQ834432
<i>VPS13</i>	<i>Verticillium albo-atrum</i> (XP_003001174.1)	665/545	V1922 (f): GAGACAACGCTTGTGCAAGG V1923 (r): ACATGCGTCTTCCAAGATCTG	HQ834433– HQ834448/HQ834449

*Genes: *ALR*, α-L-rhamnosidase; *Bpntase*, 3'(2'),5'-bisphosphate nucleotidase; *DHC1*, Dynein heavy chain; *GPHN*, Gephyrin, molybdenum cofactor biosynthesis protein; *PCS*, peroxisomal-coenzyme A synthetase; *POB3*, FACT complex subunit; *SRP72*, signal recognition particle protein 72; *VPS13*, vacuolar protein sorting-associated protein.
ff, forward; r, reverse.



Figure 1. Consensus maximum-parsimony tree derived from analyzing 8 concatenated gene fragments including a total of 4,470 aligned nucleotides by using PAUP* 4.0 (8). The number 545 on the branch indicates the total number of variable nucleotide positions (out of the 4,470 nt) separating *Geomyces pannorum* M1372 from the clonal genotype of *G. destructans* identified here. Fifty of the 545 variable sites correspond to insertions and deletions. Scale bar indicates number of nucleotide substitutions per site.

geographic distributions similar to that in our study have shown major genetic variation among strains (12,13). It is also possible that humans and/or animals contributed to the rapid clonal dispersal. In such a scenario, the diseased or asymptomatic bats might act as carriers of the fungus by their migration into new hibernation sites where new animals get infected and the dissemination cycle continues (4). Similarly, the likely roles played by humans and/or other animals in the transfer of the fungal propagules from an affected site to a clean one cannot be ruled out from our data.

Virulent clones of human and plant pathogenic fungi that spread rapidly among affected populations have been recognized with increasing frequency in recent years (12,14). However, other pathogens, such as the frog-killing fungus *Batrachochytrium dendrobatidis*, have emerged with both clonal and recombining populations (13). Our data do not eliminate the possibility that the *G. destructans* population undergoes recombination in nature. This process to generate genetic variability would require some form of sexual reproduction, which remains unknown in *G. destructans*. In addition, the fungus might have both asexual and sexual modes in its saprobic life elsewhere in nature, but it exists only in asexual mode on bats (15).

In conclusion, our data suggest that a single clonal genotype of *G. destructans* has spread among affected bats in New York. This finding might be helpful for the professionals involved in devising control measures. Many outstanding questions remain about the origin of *G. destructans*, its migration, and reproduction, all of which will require concerted efforts if we are to save bats from predicted extinction (3).

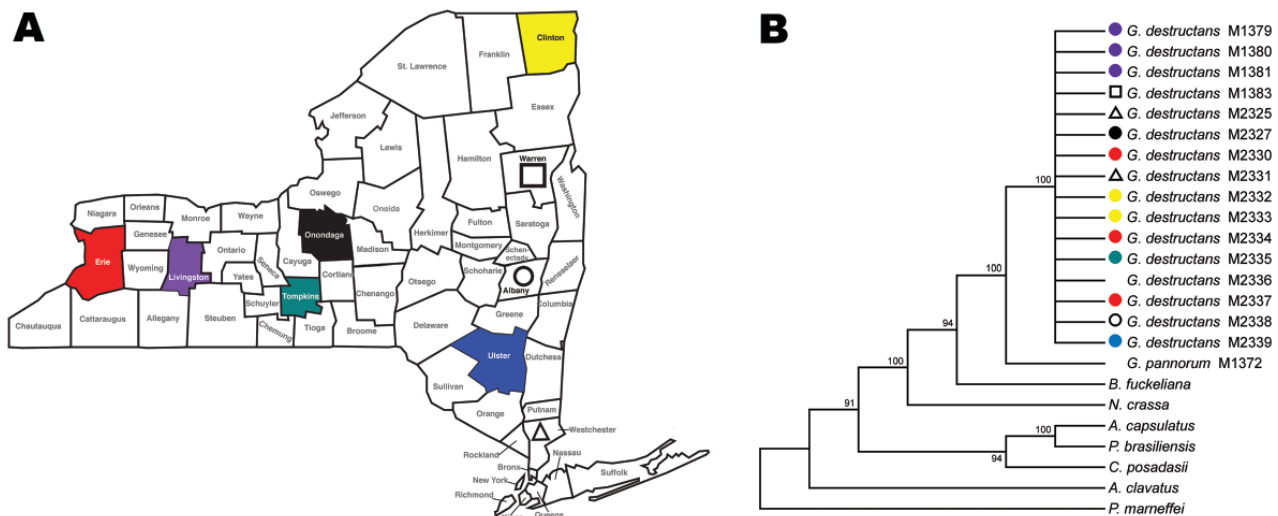


Figure 2. Collection sites in New York counties (A) are color-matched with respective *Geomyces destructans* isolates in maximum-parsimony tree based on nucleotide sequence of the VPS13 gene (B). The tree was constructed with MEGA4 (9) by using 450 nt and bootstrap test with 500 replicates. In addition to *G. destructans* and *G. pannorum*, fungi analyzed were *Ajellomyces capsulatus* (AAJ101000550.1), *Aspergillus clavatus* NRRL 1 (AAKD03000035.1), *Botryotinia fuckeliana* B05.10 (AAID01002173.1), *Coccidioides posadasii* C735 delta SOWgp (ACFW01000049.1), *Neurospora crassa* OR74A (AABX02000023.1), *Paracoccidioides brasiliensis* Pb01 (ABKH01000209.1), and *Penicillium maffei* ATCC 18224 (ABAR01000009.1).

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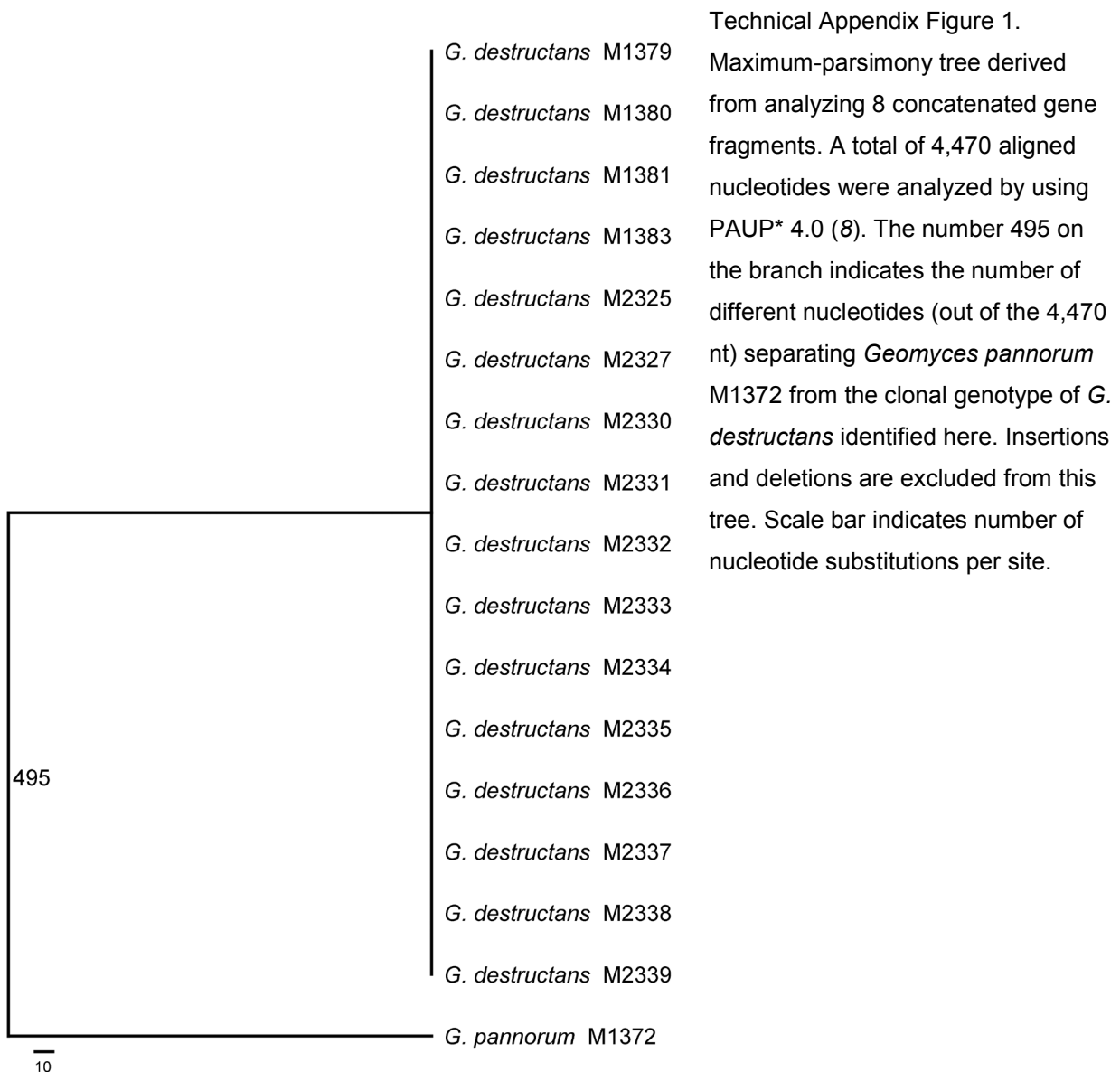
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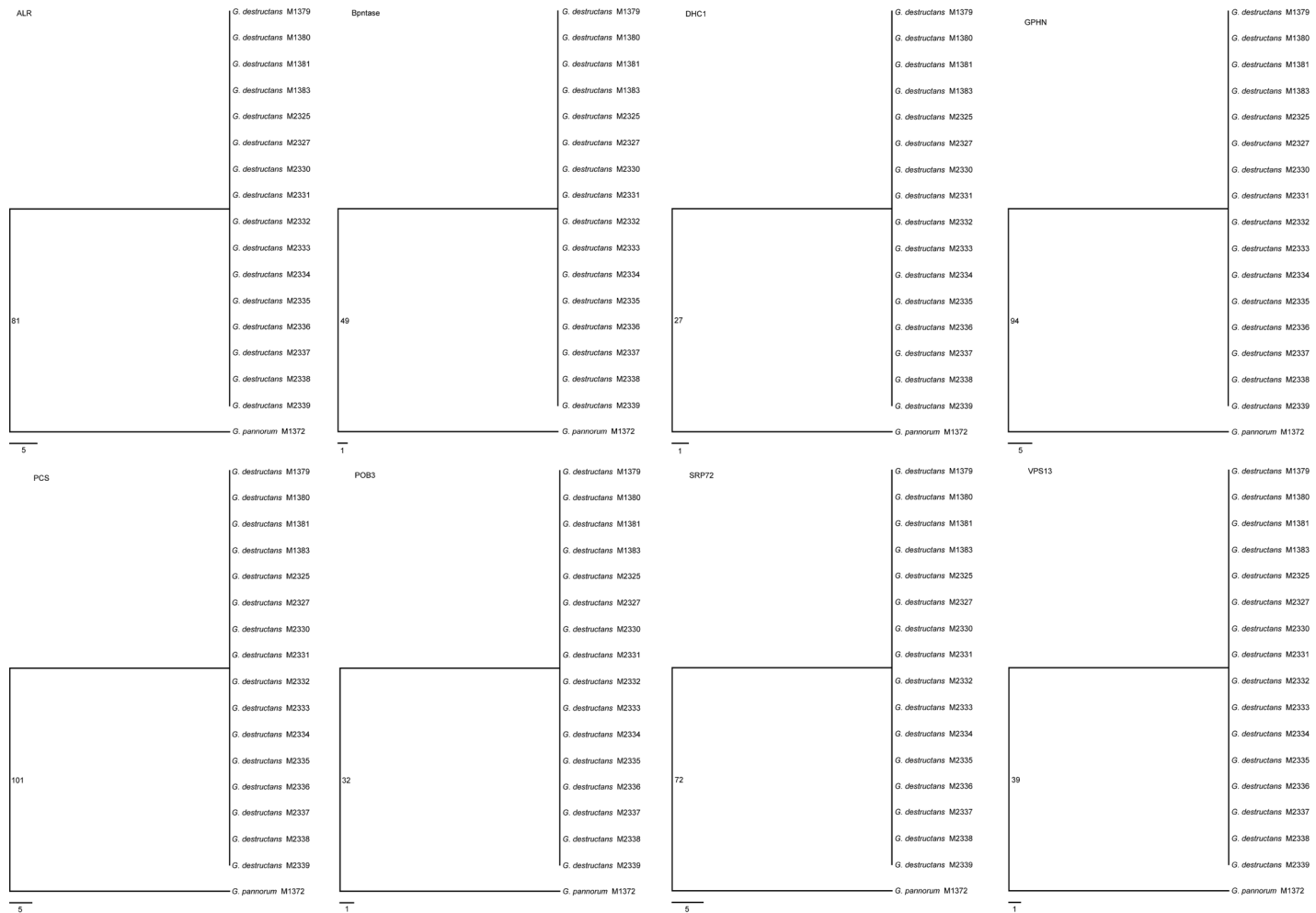
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Clonal Genotype of *Geomyces destructans* among Bats with White Nose Syndrome, New York, USA

Technical Appendix





Technical Appendix Figure 2. Maximum parsimony trees derived from individual target sequences. Alpha-L-rhamnosidase (*ALR*), 530 aligned nucleotides with 81 nt difference between *Geomyces destructans* and *G. pannorum*; 3'(2'),5'-bisphosphate nucleotidase (*Bpntase*), 667 nt/49

nucleotide difference; dynein (*DHC1*), 417 nt /27 difference; gephyrin molybdenum cofactor biosynthesis protein (*GPHN*), 522 nt/94 nt difference; peroxisomal-coenzyme A synthetase (*PCS*), 719 nt/101 nt difference; FACT complex subunit (*POB3*), 413 nt/32 nt difference; signal recognition particle protein 72 (*SRP72*), 613 nt/72 nt difference; vacuolar protein sorting-associated protein (*VPS13*), 527 nt/39 nt difference. The tree topologies were identical when neighbor-joining methods were used for analysis. Scale bars indicate number of nucleotide substitutions per site.

Technical Appendix Figure 3 (below). Multiple alignments of 8 target gene fragments. Synonymous substitutions are shaded light gray while nonsynonymous substitution are dark gray and amino acid changes are highlighted in red. A smaller fragment of nucleotides used in phylogenetics construct was used in this comparison. Putative amino acid sequences for *Geomyces destructans* and *G. pannorum* were deduced by using EMBOSS Transeq (EMBL-EBI, Cambridgeshire, UK). Homologous sequences from either *Ajellomyces dermatitidis*, *Arthroderma otae*, *Aspergillus nidulans*, *Aspergillus clavatus*, *Botryotinia fuckeliana*, *Glomerella graminicola*, *Nectria hematococca*, *Sclerotinia sclerotiorum*, and *Verticillium albo-atrum* were included in this comparison.

ALR (Alpha-L-rhamnosidase): 450 bases aligned (Gd = *Geomyces destructans*, Gp = *Geomyces pannorum*
An = *Aspergillus nidulans*, Va = *Verticillium albo-atrum*)

Gd-DNA	CTC	TCT	ACA	AAA	CTC	TTG	GCA	CCG	GAT	GCG	CCG	CCC	GTT	ACG	GTC					
Gp-DNA	CTC	TCT	ACA	AAA	CTC	ATC	GCT	CCA	GAT	GCG	CCA	CCC	GTC	ACT	GTG					
An-DNA	CCA	GAG	ACG	CAG	CTG	GTG	GCG	CCA	AAC	GCG	CCA	CCA	GTG	CGA	GTG					
Va-DNA	GAT	ACC	GTC	CAG	CTC	CAT	GCG	GGT	GAC	GCC	GAG	CCT	GTT	CGA	CGC					
Gd-PRO				K	L	L	A	P	D	A	P	P	V	T	V					
Gp-PRO				K	L	I	A	P	D	A	P	P	V	T	V					
An-PRO				Q	L	V	A	P	N	A	P	P	V	R	V					
Va-PRO				Q	L	H	A	G	D	A	E	P	V	R	R					
Gd-DNA	ACA	GAA	GAG	GTC	AAC	CCA	GTC	GAT	ATT	ATC	AAG	ACA	AAG	TCC	GGG	AAA	ACA	GTC	ATT	GAT
Gp-DNA	ACA	GAA	GAG	CTG	AGC	CCA	ACT	GAG	ATT	ATC	AAG	ACA	AAG	TCC	GGC	AAA	ACG	GTC	ATT	GAC
An-DNA	ACC	GAA	GTG	GTC	AAT	CCA	GTT	GAA	ATC	ATT	CGC	ACG	CCG	TCC	GGC	AAA	GTA	ATC	ATT	GAT
Va-DNA	CTC	GAA	ATC	GTC	AAG	CCC	ATC	GAA	AAG	ATC	ACG	ACC	CCC	TCC	GGA	AAG	ACG	GTG	CTT	GAC
Gd-PRO	T	E	E	V	N	P	V	D	I	I	K	T	K	S	G	K	T	V	I	D
Gp-PRO	T	E	E	L	S	P	T	E	I	I	K	T	K	S	G	K	T	V	I	D

An-PRO	T	E	V	V	N	P	V	E	I	I	R	T	P	S	G	K	V	I	I	D
Va-PRO	L	E	I	V	K	P	I	E	K	I	T	T	P	S	G	K	T	V	L	D

Gd-DNA	TTT	GGG	CAG	AAC	CTG	GTA	GGC	AAG	CTT	CGT	GTC	AGC	TCC	GTC	CGA	CTC	CCC	GCG	GGT	CA
Gp-DNA	TTT	GGG	CAG	AAC	CTC	GTA	GGG	AAA	CTT	CGT	GTC	AAC	TCC	GTC	CGA	CTC	CCT	GCC	GGT	GA
An-DNA	TTT	GGG	CAA	AAC	CTC	GTT	GGC	CGT	GTC	CGG	ATC	CGC	TCC	GTA	AAG	AAG	ACC	GTG	GGC	CA
Va-DNA	TTT	GGG	CAG	AAC	CTC	GTA	GGC	TAC	CTT	CGG	GTC	AAC	AAA	GTC	AGG	GGT	CCC	CGC	GGC	CA
Gd-PRO	F	G	Q	N	L	V	G	K	L	R	V	S	S	V	R	L	P	A	G	Q
Gp-PRO	F	G	Q	N	L	V	G	K	L	R	V	N	S	V	R	L	P	A	G	E
An-PRO	F	G	Q	N	L	V	G	R	V	R	I	R	S	V	K	K	T	V	G	H
Va-PRO	F	G	Q	N	L	V	G	Y	L	R	V	N	K	V	R	G	P	R	G	H

Gd-DNA	G	AAG	ATC	TCA	TTT	ACA	CAT	GTC	GAA	GTG	CTC	GAG	AAT	GGC	GAA	ATC	GGC	ACA	CGT	CCG	CT
Gp-DNA	G	AAA	ATC	ACA	TTT	ACA	CAC	GTC	GAG	GTA	CTC	GAG	AAT	GGC	GAA	ATT	AGC	ACC	CGA	CCG	CT
An-DNA	C	TCT	ATC	ATT	CTC	AAG	CAT	GCG	GAA	GTG	CTC	GAG	AAT	AGC	GAA	CTT	GGA	ACG	CGT	CCG	CT
Va-DNA	T	AAA	ATC	ACC	CTG	CTG	CAC	GCC	GAG	GTT	CTC	GAG	AAG	GGC	GAG	CTT	GGC	ATC	CGG	CCG	CT
Gd-PRO	K	I	S	F	T	H	V	E	V	L	E	N	G	E	I	G	T	R	P	L	
Gp-PRO	K	I	T	F	T	H	V	E	V	L	E	N	G	E	I	S	T	R	P	L	
An-PRO	S	I	I	L	K	H	A	E	V	L	E	N	S	E	L	G	T	R	P	L	
Va-PRO	K	I	T	L	L	H	A	E	V	L	E	K	G	E	L	G	I	R	P	L	

Gd-DNA	T	CGA	GGA	GCA	GTC	TGC	GTT	GAT	ACT	ATT	GTC	TTT	TCT	GAA	AAG	GAG	CTC	CGC	GGC	--
Gp-DNA	T	CGA	GAA	GCA	GTA	CCC	GTC	GAT	ACT	GTC	ATC	TTT	TCT	GAT	AAC	GAG	CTC	CTG	AAC	--
An-DNA	G	CGA	GTG	GCC	AAG	GCC	CAG	GAC	GAG	ATC	ATC	TCA	GCA	GGA	CAG	GAG	ATT	TGT	GAC	--
Va-DNA	G	CGT	GAC	TGC	AAG	GCC	CGG	GAC	ATC	TAC	ACC	CTC	TGT	GGT	GAT	GAG	GCT	GGC	GAA	TC
Gd-PRO	R	G	A	V	C	V	D	T	I	V	F	S	E	K	E	L	R	G	-	
Gp-PRO	R	E	A	V	P	V	D	T	V	I	F	S	D	N	E	L	L	N	-	
An-PRO	R	V	A	K	A	Q	D	E	I	I	S	A	G	Q	E	I	C	D	-	
Va-PRO	R	D	C	K	A	R	D	I	Y	T	L	C	G	D	E	A	G	E	S	

Gd-DNA	-	TGG	TCG	CCG	AAA	TTC	ACA	TTC	CAC	GGC	TTC	CAG	TAC	GTG	CAG	GTT	GAA	GGG	TGG	CCA	GC
Gp-DNA	-	TGG	TCC	CCA	AAA	TTC	ACA	TTT	CAT	GGT	TTC	CAG	TAC	GTG	CAA	GTT	GAT	GGG	TGG	CCA	GC
An-DNA	-	TGG	GCT	CCT	AGC	TTT	ACT	TTC	CAT	GGC	TTC	CGG	TAT	GTT	CAG	GTT	GAT	GGA	TGG	AGC	--
Va-DNA	G	TAC	GAG	CCT	CGC	TTC	ACC	TTC	CAC	GGC	TTT	CGC	TAT	GCC	CAG	GTC	GAC	GAC	TGG	CCA	--
Gd-PRO	W	S	P	K	F	T	F	H	G	F	Q	Y	V	Q	V	E	G	W	P	A	
Gp-PRO	W	S	P	K	F	T	F	H	G	F	Q	Y	V	Q	V	D	G	W	P	A	
An-PRO	W	A	P	S	F	T	F	H	G	F	R	Y	V	Q	V	D	G	W	S	-	
Va-PRO	Y	E	P	R	F	T	F	H	G	F	R	Y	A	Q	V	D	D	W	P	-	

Gd-DNA	A	ACT	GCG	GAT	GCT	GAA	CTC	CCT	---	TAT	AAG	TCT	GAC	TTT	ACT	GCG	CTA	GTC	ATG	CAT	445
Gp-DNA	A	ACT	GCG	GAT	GCT	GAA	CTC	CCA	---	TCT	TTG	TCT	GAC	TTC	ACT	GCA	CTA	GTC	ATG	CAT	452
An-DNA	-	CCT	GAA	GAC	GCC	GAC	ACC	CCT	CTT	ACT	CTA	CAA	AGC	CTG	ACC	GCC	GAA	GTC	ATG	CAT	444
Va-DNA	-	TCC	GCA	GAT	ATT	GAC	---	---	---	ATC	CTG	GAC	TCA	CTC	GAG	GCT	GTG	GTC	TGC	AAT	459
Gd-PRO		T	A	D	A	E	L	P	-	Y	K	S	D	F	T	A	L	V	M	H	
Gp-PRO		T	A	D	A	E	L	P	-	S	L	S	D	F	T	A	L	V	M	H	
An-PRO		P	E	D	A	D	T	P	L	T	L	Q	S	L	T	A	E	V	M	H	
Va-PRO		S	A	D	I	D	-	-	-	I	L	D	S	L	E	A	V	V	C	N	

BPntase (3'(2'),5'-bisphosphate nucleotidase): ~750 bases aligned; Alignment shows 3' region of the protein and the 3' UTR (Ss = *Sclerotinia sclerotiorum*; Af = *Aspergillus fumigatus*)

Gd-DNA										AG	AGC	CAG	CCG	ATC	CGC	ATG	AGC	GAG	AAG	A
Gp-DNA										AG	AGC	CAG	CCA	ATC	CGC	ATG	AGC	GAG	AAG	A
Ss-DNA										AG	GGT	CAA	TCT	ATT	CAA	ATG	AAG	CCA	GTT	A
Af-DNA										AG	AGC	AAG	CCC	ATC	TCG	ATG	CGT	CCC	GTT	C
Gd-PRO										S	Q	P	I	R	M	S	E	K		
Gp-PRO										S	Q	P	I	R	M	S	E	K		
Ss-PRO										G	Q	S	I	Q	M	K	P	V		
Af-PRO										S	K	P	I	S	M	R	P	V		

Gd-DNA	AG	GAC	ATC	ACC	GAT	GCC	ACT	TTC	TGC	GAG	AGT	GTT	GAG	GCT	GGC	CAC	TCA	TCT	CAC	GAC	G
Gp-DNA	AG	GAT	ATC	ACC	GAT	GCC	ACT	TTC	TGC	GAG	AGT	GTT	GAG	GCT	GGC	CAC	TCG	TCG	CAT	GAC	G
Ss-DNA	CG	GAT	TTA	AGT	CAA	GCT	ACA	TTC	TGT	GAG	AGT	GTT	GAG	GCA	GGT	CAC	TCT	TCC	CAT	GGC	G
Af-DNA	CG	GAT	ATA	AAA	CAG	GCT	GTC	TTC	TGT	GAA	GGA	GTT	GAG	GCT	GCC	CAC	TCT	GCT	CAA	GGC	G
Gd-PRO	K	D	I	T	D	A	T	F	C	E	S	V	E	A	G	H	S	S	H	D	
Gp-PRO	K	D	I	T	D	A	T	F	C	E	S	V	E	A	G	H	S	S	H	D	
Ss-PRO	T	D	L	S	Q	A	T	F	C	E	S	V	E	A	G	H	S	S	H	G	
Af-PRO	P	D	I	K	Q	A	V	F	C	E	G	V	E	A	A	H	S	A	Q	G	

Gd-DNA	AC	CAA	TCT	CAG	ATC	GCC	CAG	AAG	CTG	CAG	ATC	AGC	AAG	CCG	AGC	GTG	CGG	ATG	GAT	TCG	C
Gp-DNA	AC	CAG	TCT	CAG	ATC	GCA	CAG	AAG	CTG	CAG	ATT	AGC	AAG	CCA	AGC	GTG	CGA	ATG	GAT	TCG	C
Ss-DNA	AT	CAA	CAT	GCC	ATT	GCT	ACC	AAA	TTG	GGT	GTT	ACC	AAG	GCT	AGT	GTC	CGA	ATG	GAT	TCG	C
Af-DNA	AC	AAC	GCT	GCC	GTC	GCT	CAG	CTC	CTG	GGT	ATC	ACC	TCC	CCC	AGC	GTG	CGA	CTC	GAC	TCG	C
Gd-PRO	D	Q	S	Q	I	A	Q	K	L	Q	I	S	K	P	S	V	R	M	D	S	
Gp-PRO	D	Q	S	Q	I	A	Q	K	L	Q	I	S	K	P	S	V	R	M	D	S	

Ss-PRO	D	Q	H	A	I	A	T	K	L	G	V	T	K	A	S	V	R	M	D	S	
Af-PRO	D	N	A	A	V	A	Q	L	L	G	I	T	S	P	S	V	R	L	D	S	
Gd-DNA	AG	GCC	AAG	TAT	GCC	TCG	ATC	GCC	CGT	GGC	GCT	GGG	GAT	ATT	TAC	CTG	AGA	CTT	CCA	ACC	A
Gp-DNA	AG	GCA	AAG	TAT	GCC	TCG	ATC	GCT	CGT	GGT	GCG	GGG	GAT	ATT	TAC	CTC	AGA	CTT	CCA	ACC	A
Ss-DNA	AA	GCT	AAA	TAT	GGA	TCG	ATC	GCG	AGA	GGT	GCT	GGA	GAC	ATT	TAC	CTT	AGA	CTT	CCC	GTT	A
Af-DNA	AG	GCC	AAG	TAC	TGC	TCA	ATT	GCT	AGA	GGC	GCA	GGC	GAT	ATC	TAC	CTA	CGG	CTA	CCT	GTC	A
Gd-PRO	Q	A	K	Y	A	S	I	A	R	G	A	G	D	I	Y	L	R	L	P	T	
Gp-PRO	Q	A	K	Y	A	S	I	A	R	G	A	G	D	I	Y	L	R	L	P	T	
Ss-PRO	Q	A	K	Y	G	S	I	A	R	G	A	G	D	I	Y	L	R	L	P	V	
Af-PRO	Q	A	K	Y	C	S	I	A	R	G	A	G	D	I	Y	L	R	L	P	V	
Gd-DNA	GC	GCA	ACG	TAC	CAA	GAG	AAG	ATC	TGG	GAT	CAC	GCT	GCT	GGA	GAC	CTG	ATT	GTT	CGA	GAG	G
Gp-DNA	GC	GCA	ACG	TAC	CAG	GAG	AAG	ATC	TGG	GAT	CAC	GCT	GCT	GGA	GAC	CTG	ATT	GTT	AGG	GAG	G
Ss-DNA	GC	GCG	ACT	TAC	CAA	GAG	AAG	ATT	TGG	GAT	CAT	GCT	GCT	GGA	GAT	CTT	ATT	GTA	AGA	GAG	G
Af-DNA	GA	AAG	GAC	TAC	CAG	GAG	AAG	ATC	TGG	GAT	CAT	GCG	GCT	GGC	GAT	CTC	ATT	GTC	CGC	GAG	G
Gd-PRO	S	A	T	Y	Q	E	K	I	W	D	H	A	A	G	D	L	I	V	R	E	
Gp-PRO	S	A	T	Y	Q	E	K	I	W	D	H	A	A	G	D	L	I	V	R	E	
Ss-PRO	S	A	T	Y	Q	E	K	I	W	D	H	A	A	G	D	L	I	V	R	E	
Af-PRO	R	K	D	Y	Q	E	K	I	W	D	H	A	A	G	D	L	I	V	R	E	
Gd-DNA	CG	GGA	GGA	CAG	GTT	ACG	GAT	TCA	CTA	GGC	AGA	CGT	CTG	GAT	TTC	AGC	AAG	GGT	AGA	ACT	T
Gp-DNA	CA	GGA	GGA	CAG	GTT	ACG	GAT	TCA	CTG	GGC	AGA	CGT	CTG	GAT	TTC	AGC	AAG	GGT	AGA	ACC	T
Ss-DNA	CA	GGT	GGA	CAG	GTT	ACT	GAT	TCT	CTC	GGA	CGA	AGA	TTG	GAT	TTC	AGC	AAG	GGA	AGA	ACT	T
Af-DNA	CT	GGT	GGA	CAA	GTG	ACC	GAT	ATC	TAT	GGC	CAG	CGC	TTG	GAT	TTC	AGC	AAG	GGA	CGC	ACT	T
Gd-PRO	A	G	G	Q	V	T	D	S	L	G	R	R	L	D	F	S	K	G	R	T	
Gp-PRO	A	G	G	Q	V	T	D	S	L	G	R	R	L	D	F	S	K	G	R	T	
Ss-PRO	A	G	G	Q	V	T	D	S	L	G	R	R	L	D	F	S	K	G	R	T	
Af-PRO	A	G	G	Q	V	T	D	I	Y	G	Q	R	L	D	F	S	K	G	R	T	
Gd-DNA	TG	GCT	GAG	AAT	AAG	GGT	GTC	GTT	GCC	GCA	CCA	CAG	GCT	CTA	CAC	GCA	CGA	GTC	CTT	GAG	G
Gp-DNA	TG	GCT	GAG	AAT	AAG	GGT	GTC	GTT	GCC	GCA	CCA	CAG	GCT	CTA	CAT	GCA	CGA	GTC	CTT	GAG	G
Ss-DNA	TG	GCT	GAA	AAC	AAG	GGT	GTC	GTT	GCA	GCT	CCC	GCA	GCC	ATT	CAC	GAC	CAC	GTT	TTG	GAG	G
Af-DNA	TG	GCT	GCC	AAC	AAG	GGA	GTC	GTC	GCC	GCT	CCA	GAG	GCC	ATC	CAG	GAC	CAG	GTT	ATT	AGT	G
Gd-PRO	L	A	E	N	K	G	V	V	A	A	P	Q	A	L	H	A	R	V	L	E	
Gp-PRO	L	A	E	N	K	G	V	V	A	A	P	Q	A	L	H	A	R	V	L	E	
Ss-PRO	L	A	E	N	K	G	V	V	A	A	P	A	A	I	H	D	H	V	L	E	
Af-PRO	L	A	A	N	K	G	V	V	A	A	P	E	A	I	Q	D	Q	V	I	S	

Gd-DNA	TT	GTC	AAG	GAG	GTC	CTT	GGC	AAG	AAG	GGA	AAC	CTA	TAG	-----CAGATATGA
Gp-DNA	TT	GTC	AAA	GAA	GTC	CTG	GGC	AAG	AAA	GGA	AAC	CTA	TAG	-----TAGATATGA
Ss-DNA	TG	GTT	AAG	GAG	GTT	TTG	GGG	CCC	AAG	AAA	TAA	---	ATTGTT	CATATATTCGTCACAA
Af-DNA	CC	GTC	AAG	ACG	GTC	CTG	AAG	CTA	TGA	AGGATGACGCGAACG	ACCAACTGTTGTATCGA			
Gd-PRO	V	V	K	E	V	L	G	K	K	G	N	L	*	
Gp-PRO	V	V	K	E	V	L	G	K	K	G	N	L	*	
Ss-PRO	V	V	K	E	V	L	G	P	K	K	*			
Af-PRO	A	V	K	I	V	L	K	L	*					

Gd-DNA	ACAATTGAAATAGATTCTA---	CATATCGTATAACT-ATCCGCTTGG-GACCCTCCAATT
Gp-DNA	ACAGCTG---TAGATTCTA---	CATATCGTATAACT-ATCCGCTTGA-GACTCCACAATT
Ss-DNA	ATAAAAGCCATGATACCTTGATCCACTTGTACATCG-ACACCATAGATATATCTACAATA	
Af-DNA	ATCACTAAACCCGTTCTAA--ACCTTTGTTAGATCCTGCACGCTTGATGCGCCTAAAAGT	

Gd-DNA	CTATGACA-----ATATAAG---	AGCAATATAATAC-ATGGACG--AATCGTCTATTT
Gp-DNA	CTATGACA-----ATATAAG---	AACAATATAATAC-ATGGACG--AATCGTCTATTT
Ss-DNA	CCTACAAATG-----ACATTAT---	CTCTAGAGATTAT-TTGGATATTCATCCACTACTT
Af-DNA	ACATGAGATAGATACCAATTGGGAAAACAGGAGACTCTGCTGGAAT--ATACATGTACAG	

Gd-DNA	GATCTTCTTGGCCTTCAACCTGATCGTCTCACCGTTGACGAAAATTCCCTTCCCCT--TG
Gp-DNA	GATCTTCTTGCCTTTCAGCTTGATCGTCTCGCCATTGACGAAGATTCCCTTCCCCT--TA
Ss-DNA	AATCTTCTTATTCTTCAACTTAATCTCCTCTCCATTGACAAAAGATTCCCTTCCCCT--TA
Af-DNA	AAACAGCCCCAGACCCTGTTCCAAGAAAATGCCAAAGTAAAATAGAAACCACCCAGATC

Gd-DNA	TATGGCTCAGGCTTCCCTCCACTGGCGGATTTCCGCAGCAAAGTGCAGAACCCTT---CC
Gp-DNA	TATGGCTCAGGCTTCCCTCCATTACGAATTTCCGCAGCGAACTGGAGAACAACCT---CC
Ss-DNA	TACGGTTCTGGAAGTCTCCACTTTCTAATTTGCGCAGCGAAAAGTAATACAACCTT---CC
Af-DNA	ACCGAATCTT-CTTGGCCTTCAGTCTGATTGTCTCTCCGTTACAAAAATACCCTTGCCC

Gd-DNA	TTCTCCGGGCCCT-CCAGCAATATTCTCGTTGGCTGCGGTGTGCTGGCCGTCATGCCCTT
Gp-DNA	TTCTCTGGGCCCT-CCAGCAATATTCTCGTTGGCTGCGGTGTGCTAGCCGTCATGCCCTT
Ss-DNA	TTCTCTGGTCCTT-CTAACAATATACGTGTAGGTTGTGGTGTGCTCGCTTTCACAAATCT
Af-DNA	TTGTAAGGCTCTGGCTTCCGCCATTCTC-TGATTTCCGCCGCGAATTGTGTACAAACGTT

Gd-DNA	CGGCACTGGCAACTCGA-TAGGATGTGAGTAG	744
Gp-DNA	CGGCACTGGCAACTCGA-TTGGATGTGAGTAC	741

Ss-DNA TGGAACGGGTAATTTCGA-TAGGATGAGAGTAC 759
 Af-DNA TTTGTCTGACTCCCTCAAGCAGAATACGAGTAG 775

DHC1 (Cytoplasmic dynein heavy chain): 418 bases aligned (Ss = *Sclerotinia sclerotiorum*, Bf = *Botryotinia fuckeliana*)

Ss-DNA	GAT	GCT	GAA	TAC	CTA	GAT	CCA	ATC	CTT	AAC	CAC	GTT	CTT	AAC	AAA	GAG	TAT	CAA	AAG	ACT	60
Bf-DNA	GAT	GCC	GAA	TAC	CTG	GAC	CCA	ATT	CTT	AAC	CAC	GTT	CTC	AAC	AAA	GAG	TAC	CAA	AAG	ACT	60
Gd-DNA	GAT	GCC	GAG	CAT	TTG	GAT	CCA	ATC	CTT	AAC	CAC	GTC	CTC	AAC	AAG	GAA	TAC	CAA	AAG	ACT	60
Gp-DNA	GAT	GCC	GAG	CAT	TTG	GAT	CCG	ATC	CTT	AAT	CAT	GTC	CTC	AAC	AAG	GAG	TAC	CAA	AAG	ACT	60
Ss-PRO	D	A	E	Y	L	D	P	I	L	N	H	V	L	N	K	E	Y	Q	K	T	
Bf-PRO	D	A	E	Y	L	D	P	I	L	N	H	V	L	N	K	E	Y	Q	K	T	
Gd-PRO	D	A	E	H	L	D	P	I	L	N	H	V	L	N	K	E	Y	Q	K	T	
Gp-PRO	D	A	E	H	L	D	P	I	L	N	H	V	L	N	K	E	Y	Q	K	T	

Ss-DNA	GGT	GGA	CGT	GTT	CTT	ATT	CAG	CTT	GGT	AAG	CAA	GAA	ATT	GAC	TTT	TCG	CCC	GCA	TTT	AAG	120
Bf-DNA	GGT	GGG	CGT	GTT	CTC	ATC	CAG	CTT	GGG	AAG	CAA	GAA	ATC	GAT	TTC	TCG	CCC	GCA	TTC	AAG	120
Gd-DNA	GGT	GGA	CGT	GTC	CTC	ATC	CAG	CTC	GGT	AAA	CAA	GAG	ATC	GAT	TTC	TCC	CCA	GCC	TTC	AAG	120
Gp-DNA	GGC	GGG	CGT	GTT	CTC	ATC	CAG	CTT	GGC	AAA	CAA	GAA	ATC	GAT	TTC	TCC	CCA	GCC	TTC	AAG	120
Ss-PRO	G	G	R	V	L	I	Q	L	G	K	Q	E	I	D	F	S	P	A	F	K	
Bf-PRO	G	G	R	V	L	I	Q	L	G	K	Q	E	I	D	F	S	P	A	F	K	
Gd-PRO	G	G	R	V	L	I	Q	L	G	K	Q	E	I	D	F	S	P	A	F	K	
Gp-PRO	G	G	R	V	L	I	Q	L	G	K	Q	E	I	D	F	S	P	A	F	K	

Ss-DNA	ATC	TAC	CTT	TCC	ACT	AGA	GAT	CCA	TCT	GCA	ACA	TTC	GCA	CCG	GAT	ATT	TGC	AGT	CGG	ACA	180
Bf-DNA	ATT	TAC	CTT	TCC	ACC	AGA	GAT	CCA	TCT	GCA	ACA	TTC	GCA	CCG	GAC	ATT	TGC	AGT	CGC	ACA	180
Gd-DNA	ATC	TAC	CTC	TCG	ACC	AGA	GAT	CCA	TCT	GCT	ACG	TTT	GCA	CCA	GAC	ATA	TGC	AGT	CGC	ACA	180
Gp-DNA	ATC	TAT	CTC	TCA	ACC	AGA	GAT	CCA	TCT	GCT	ACA	TTT	GCA	CCA	GAT	GTA	TGC	AGT	CGC	ACA	180
Ss-PRO	I	Y	L	S	T	R	D	P	S	A	T	F	A	P	D	I	C	S	R	T	
Bf-PRO	I	Y	L	S	T	R	D	P	S	A	T	F	A	P	D	I	C	S	R	T	
Gd-PRO	I	Y	L	S	T	R	D	P	S	A	T	F	A	P	D	I	C	S	R	T	
Gp-PRO	I	Y	L	S	T	R	D	P	S	A	T	F	A	P	D	V	C	S	R	T	

Ss-DNA	ACG	TTT	GTC	AAT	TTC	ACT	GTC	ACA	CAA	AGC	AGT	TTA	CAA	ACA	CAG	TCA	CTT	AAT	GAC	GTC	240
Bf-DNA	ACA	TTT	GTT	AAT	TTC	ACA	GTC	ACA	CAG	AGT	AGT	TTG	CAA	ACA	CAG	TCA	CTC	AAT	GAC	GTT	240

Gd-DNA	ACT	TTC	GTC	AAT	TTC	ACC	GTC	ACC	CAG	AGC	AGT	CTC	CAA	ACG	CAA	TCA	TTG	AAC	GAA	GTC	240
Gp-DNA	ACC	TTC	GTG	AAT	TTC	ACT	GTC	ACC	CAG	AGC	AGT	CTC	CAA	ACA	CAA	TCA	TTG	AAC	GAA	GTC	240
Ss-PRO	T	F	V	N	F	T	V	T	Q	S	S	L	Q	T	Q	S	L	N	D	V	
Bf-PRO	T	F	V	N	F	T	V	T	Q	S	S	L	Q	T	Q	S	L	N	D	V	
Gd-PRO	T	F	V	N	F	T	V	T	Q	S	S	L	Q	T	Q	S	L	N	E	V	
Gp-PRO	T	F	V	N	F	T	V	T	Q	S	S	L	Q	T	Q	S	L	N	E	V	
Ss-DNA	CTC	AAA	TCT	GAG	CGA	CCT	GAT	GTG	GAT	GAG	AGG	CGC	TCA	AAT	CTC	ATC	AAA	TTA	CAG	GGT	300
Bf-DNA	CTC	AAA	TCC	GAA	CGA	CCT	GAT	GTG	GAC	GAG	AGA	CGC	TCT	AAT	CTC	ATC	AAG	TTA	CAA	GGC	300
Gd-DNA	CTG	AAA	TCT	GAG	CGA	CCT	GAC	GTG	GAT	GAG	CGA	AGA	TCC	AAC	CTG	ATC	AAA	TTA	CAG	GGA	300
Gp-DNA	CTG	AAA	TCT	GAG	CGA	CCT	GAC	GTG	GAT	GAA	CGA	AGA	TCC	AAC	CTG	ATC	AAA	TTG	CAG	GGA	300
Ss-PRO	L	K	S	E	R	P	D	V	D	E	R	R	S	N	L	I	K	L	Q	G	
Bf-PRO	L	K	S	E	R	P	D	V	D	E	R	R	S	N	L	I	K	L	Q	G	
Gd-PRO	L	K	S	E	R	P	D	V	D	E	R	R	S	N	L	I	K	L	Q	G	
Gp-PRO	L	K	S	E	R	P	D	V	D	E	R	R	S	N	L	I	K	L	Q	G	
Ss-DNA	GAA	TTC	AAA	GTT	CAT	CTT	AGA	CAG	CTC	GAG	AAA	CGC	TTG	TTG	CAA	GCA	TTG	AAC	GAA	TCA	360
Bf-DNA	GAA	TTC	AAA	GTT	CAC	CTC	AGG	CAG	CTC	GAG	AAG	CGC	TTG	CTG	CAA	GCC	CTG	AAC	GAA	TCA	360
Gd-DNA	GAA	TTC	AAG	GTC	CAT	CTT	CGC	CAA	TTG	GAG	AAG	CGT	CTT	TTG	CAA	GCT	TTG	AAC	GAG	TCC	360
Gp-DNA	GAA	TTC	AAG	GTC	CAC	CTT	CGC	CAA	TTG	GAG	AAG	CGT	CTT	TTG	CAG	GCT	TTG	AAC	GAG	TCC	360
Ss-PRO	E	F	K	V	H	L	R	Q	L	E	K	R	L	L	Q	A	L	N	E	S	
Bf-PRO	E	F	K	V	H	L	R	Q	L	E	K	R	L	L	Q	A	L	N	E	S	
Gd-PRO	E	F	K	V	H	L	R	Q	L	E	K	R	L	L	Q	A	L	N	E	S	
Gp-PRO	E	F	K	V	H	L	R	Q	L	E	K	R	L	L	Q	A	L	N	E	S	
Ss-DNA	CGT	GGC	AAT	ATT	CTC	GAT	GAT	GAT	AAC	GTC	ATT	GAA	ACT	CTC	GAA	ACT	TTG	AAG	AAG	G	418
Bf-DNA	CGT	GGC	AAT	ATT	CTT	GAT	GAT	GAC	AAC	GTC	ATT	GAA	ACT	CTT	GAG	ACT	TTG	AAG	AAG	G	418
Gd-DNA	CGT	GGC	AAT	ATC	TTG	GAT	GAT	GAC	AAC	GTC	ATT	GAG	ACT	CTC	GAG	ACG	TTG	AAG	AAG	G	418
Gp-DNA	CGT	GGT	AAT	ATC	TTG	GAT	GAT	GAC	AAC	GTT	ATT	GAA	ACT	CTC	GAA	ACG	TTG	AAG	AAG	G	418
Ss-PRO	R	G	N	I	L	D	D	D	N	V	I	E	T	L	E	T	L	K	K		
Bf-PRO	R	G	N	I	L	D	D	D	N	V	I	E	T	L	E	T	L	K	K		
Gd-PRO	R	G	N	I	L	D	D	D	N	V	I	E	T	L	E	T	L	K	K		
Gp-PRO	R	G	N	I	L	D	D	D	N	V	I	E	T	L	E	T	L	K	K		

GPHN (Gephyrin): ~300 bases aligned; the alignment starts with non-coding miscellaneous feature

Gd-DNA	TA	AGC	TCT	AGC	GGA	TCT	CAC	GCT	GGC	CAT	CAC	GGC	TAT	GGT	CAC	GGT	CAC	GAC	CA	303
Gp-DNA	TA	GGC	TCT	GGT	GGA	GCT	CAT	GCT	GGA	CAT	CAT	GGC	CAC	AGC	CAT	GGT	CAC	GGC	CA	318
Nh-DNA	TA	TCA	GGT	GGA	AAG	CCC	CAA	CCT	GCT	GCC	AGC	CAC	AGT	CAC	GGA	TGC	CAC	AGA	CA	324
Ac-DNA	TA	GCC	CCC	AAT	GAT	CCG	CGC	TCG	GAA	AGT	CAA	GGA	CAG	CAG	CAT	GAT	CAC	CAT	CA	354
Gd-PRO	I	S	S	S	G	S	H	A	G	H	H	G	Y	G	H	G	H	D		
Gp-PRO	I	G	S	G	G	A	H	A	G	H	H	G	H	S	H	G	H	G		
Nh-PRO	L	S	G	G	K	P	Q	P	A	A	S	H	S	H	G	C	H	H		
Ac-PRO	V	A	P	N	D	P	R	S	E	S	Q	G	Q	Q	H	D	H	H		

PCS (Peroxisomal-coenzyme A synthetase): ~480 bases aligned; Alignment shows the exonic region and a predicted intronic region (Ac = *Aspergillus clavatus*; Ao = *Arthroderma otae*)

Gd-DNA										GTA	CCC	TTG	ACA	CAC	A
Gp-DNA										GTG	CCC	TTG	ACA	CAC	A
Ac-DNA										GTT	CCC	CTG	ACG	CAC	A
Ao-DNA										GTA	CCG	CTC	TCA	CAT	A
Gd-PRO										V	P	L	T	H	
Gp-PRO										V	P	L	T	H	
Ac-PRO										V	P	L	T	H	
Ao-PRO										V	P	L	S	H	

Gd-DNA	GG	AAT	TTG	ACG	AGG	ACA	ATG	AGTATGCA--AGCCCCGCTAGTGGCTAGTGGGAGATTCTCA
Gp-DNA	GG	AAT	TTG	ACA	AGG	ACT	ATG	AGTATGTA--AATCCGCCCGTGG-----GAGATTTCCA
Ac-DNA	AG	AAC	CTG	ACC	ACT	AGC	ATG	AGTGAGTAC--AACATCCCTGTGT-----GATGTAACTG
Ao-DNA	AA	AAC	CTG	ACC	AGG	ACA	ATG	AGTGGGTGTTGGCTAGTTTTGTTG-----GAGATTTTTTA
Gd-PRO	R	N	L	T	R	T	M	
Gp-PRO	R	N	L	T	R	T	M	
Ac-PRO	K	N	L	T	T	S	M	
Ao-PRO	K	N	L	T	R	T	M	

Gd-DNA	----	ATTGCTAA-CA--ATT-GACA-GAG	AAC	ATC	CAG	GCA	ACA	TAT	GAG	TTG	AGC	CCT	G
Gp-DNA	----	ATTGCTAA-CA--ATTTGGCA-GAG	AAC	ATA	CAG	GCA	ACA	TAT	GAG	CTG	AGC	CCT	G
Ac-DNA		GAAGACCACTGA-CGCGGTATCACAAGAC	AAC	ATC	CGG	GCT	ACA	TAT	AAG	TTG	ACC	CCC	G
Ao-DNA		TTGTCATGCTAAATACATTCTCGTTAGGA	AAC	ATC	CAA	GCT	ACA	TAC	TCT	CTG	ACG	GGT	A
Gd-PRO			N	I	Q	A	T	Y	E	L	S	P	
Gp-PRO			N	I	Q	A	T	Y	E	L	S	P	

Ac-PRO
Ao-PRO

N I R A T Y K L T P
N I Q A T Y S L T C

Gd-DNA CT GAC CGA ACC ATG CTT GTC ATG CCT CTT TTC CAC GTC CAC GGC CTT CTC GCC GGG CTC
Gp-DNA CT GAC CGA ACC ATG CTC GTC ATG CCT CTT TTC CAC GTC CAC GGC CTT CTT GCC GGG TTC
Ac-DNA AG GAT CGC ACC TAC TTG GTG ATG CCT CTA TTC CAC GTC CAC GGC CTG TTG GCC GGA TTC
Ao-DNA AT GAC CGA ACT TAT CTT GTT ATG CCG CTC TTC CAC GTC CAC GGC CTT CTC GCC GCT TTC
Gd-PRO A D R T M L V M P L F H V H G L L A G L
Gp-PRO A D R T M L V M P L F H V H G L L A G F
Ac-PRO E D R T Y L V M P L F H V H G L L A G F
Ao-PRO N D R T Y L V M P L F H V H G L L A A F

Gd-DNA CTC GCC CCT CTT CTT TCC GGA GGC TCT GTC GTT GTC CCT GCC AAG TTC AGC GCC ACT ACC
Gp-DNA CTT GCC CCT CTA CTT TCC GGA GGG TCC GTC GTT GTC CCT GCC AAG TTC AGC GCC ACT ACT
Ac-DNA CTC GCC CCC CTT TTG TCT GGA GGC TCC GTA ATT GTG CCT CCC AGA TTC TCC GCA TCG GAG
Ao-DNA CTC GCC CCG TTA CAG TCT GGA GGG TCC GTC GTT GTG CCT CCC AAG TTC TCT GCT ACC GAT
Gd-PRO L A P L L S G G S V V V P A K F S A T T
Gp-PRO L A P L L S G G S V V V P A K F S A T T
Ac-PRO L A P L L S G G S V T V P P R F S A S E
Ao-PRO L A P L Q S G G S V V V P P K F S A T D

Gd-DNA TTC TGG GAG GAT TTC ATC ACG CAT AAA GCC AAC TGG TAC ACT GCT GTG CCC ACC ATC CAC
Gp-DNA TTC TGG GAA GAC TTT ATC AAT TAT AAA GCT AAC TGG TAC ACT GCT GTG CCC ACC ATC CAC
Ac-DNA TTC TGG GCG GAT TTC GTT GGA TTC CAC GCG AAC TGG TAC ACA GCT GTG CCT ACG ATC CAT
Ao-DNA TTC TGG TCG GAT TTC ATC ACG TAC AAG GCC AAC TGG TAT ACG GCG GTG CCG ACC ATA CAC
Gd-PRO F W E D F I T H K A N W Y T A V P T I H
Gp-PRO F W E D F I N Y K A N W Y T A V P T I H
Ac-PRO F W A D F V G F H A N W Y T A V P T I H
Ao-PRO F W S D F I T Y K A N W Y T A V P T I H

Gd-DNA CAG ATT CTC CTC AGA AAC CCT CCT CCG TCC ACC AAG CCC AAC ATT CGA TTC ATT CGC TCT
Gp-DNA CAG ATC CTT CTC AGA AAC CCA CCC CCG TCA GCC AAA CCT AAC ATT CGA TTT ATC CGG TCC
Ac-DNA CAG ATC CTC CTT AAG ACA CCG CTG CCG AAC CCC ATT CCC AAG ATC CGG TTC ATT CGC TCA
Ao-DNA CAG ATC CTA CTC AAG CAT CCA TTC CCA TCT CCC ATG CCA AAG ATC CGT TTC GTC CGC TCT
Gd-PRO Q I L L R N P P P S T K P N I R F I R S
Gp-PRO Q I L L R N P P P S A K P N I R F I R S
Ac-PRO Q I L L K T P L P N P T P K I R F I R S
Ao-PRO Q I L L K H P F P S P M P K I R F V R S

Gd-DNA	TGC	TCG	TCG	CCT	CTT	TCG	CCA	ACA	ACC	TTC	CAC	CAG	CTT	GAG	GAG	CAG	TAC	AAT	GCC	CCT
Gp-DNA	TGC	TCG	TCT	CCT	TTA	TCG	CCA	ACA	ACC	TTT	TAC	CAA	CTC	CAG	GAG	CAG	TAC	AAT	GCT	CCT
Ac-DNA	TGC	TCA	TCG	CCG	CTG	TCG	CCA	AAG	ACT	TTC	GAG	GAT	CTG	GAA	AAG	ACG	TTC	AAG	GCC	CCC
Ao-DNA	TGC	TCG	TCA	CCG	CTG	TCT	CCC	AAG	ACA	TTC	CAC	GAA	ATA	GAA	CGT	GCA	TTC	AAT	GCT	CCG
Gd-PRO	C	S	S	P	L	S	P	T	T	F	H	Q	L	E	E	Q	Y	N	A	P
Gp-PRO	C	S	S	P	L	S	P	T	T	F	Y	Q	L	Q	E	Q	Y	N	A	P
Ac-PRO	C	S	S	P	L	S	P	K	T	F	E	D	L	E	K	T	F	K	A	P
Ao-PRO	C	S	S	P	L	S	P	K	T	F	H	E	I	E	R	A	F	N	A	P

Gd-DNA	GTT	CTC	GAG	GCA	TAT	GCC	ATG	ACT	GAA	GCC	GCC	CAT	CAA	ATG	ACA	TCC	AGC	CCT	CTC	CCA	484
Gp-DNA	GTC	CTC	GAG	GCA	TAT	GCC	ATG	ACG	GAA	GCT	GCC	CAC	CAA	ATG	ACC	TCC	AAC	CCA	CTT	CCA	478
Ac-DNA	GTC	CTG	GAA	GCG	TAC	GCG	ATG	ACC	GAG	GCT	TCG	CAC	CAG	ATG	ACC	AGC	AAC	CCT	CTC	CCG	486
Ao-DNA	GTT	CTC	GAA	GCA	TAT	GCC	ATG	ACC	GAA	GCC	TCA	CAT	CAA	ATG	ACA	AGC	AAC	CCT	CTA	CCG	488
Gd-PRO	V	L	E	A	Y	A	M	T	E	A	A	H	Q	M	T	S	S	P	L	P	
Gp-PRO	V	L	E	A	Y	A	M	T	E	A	A	H	Q	M	T	S	N	P	L	P	
Ac-PRO	V	L	E	A	Y	A	M	T	E	A	S	H	Q	M	T	S	N	P	L	P	
Ao-PRO	V	L	E	A	Y	A	M	T	E	A	S	H	Q	M	T	S	N	P	L	P	

POB3 (FACT complex subunit): ~400 bases aligned; The alignment starts with non-coding miscellaneous feature (Va = *Verticillium albo-atrum*, Gg = *Glomerella graminicola*)

Gd-DNA	--CAATTGGCGCA-----CCCTCTAACCT-ATG-----TA	CAG	GAC	---	TTC	GAC	CG
Gp-DNA	--CGATTGGCGCA-----CCTTCTAACGT-ATG-----TA	CAG	GAC	---	TTC	GAC	CG
Va-DNA	CGCGACACCCGCA-----TCATCCAGCTCGACGGCTTCC-CG	CAG	GAC	GAG	TTC	GAG	CG
Gg-DNA	CCCAGTAAGTGGGGGAAGCCGAGCTAATTGAACACCCGGCGTG	CAG	GAC	---	TAC	GAG	CG
Gd-PRO		Q	D	-	F	D	R
Gp-PRO		Q	D	-	F	D	R
Va-PRO		Q	D	E	F	E	R
Gg-PRO		Q	D	-	Y	E	R

Gd-DNA	C	CTG	ACG	AAA	GTA	TTC	AAG	AAC	TGG	TAC	AGC	ACG	AAC	CTC	GAG	ACG	AAG	GAG	CAC	GCA	TT
Gp-DNA	C	CTG	ACG	AAA	GTG	TTC	AAG	AAC	TGG	TAC	AGC	ACG	AAC	CTC	GAG	ACG	AAG	GAA	CAC	GCA	TT
Va-DNA	C	CTG	TCG	AAG	CTC	TTC	AAA	AAC	TGG	TAC	AGC	ACG	ACC	CTC	GAG	AAC	AAG	GAG	CAC	GCC	CT
Gg-DNA	C	CTC	GCA	AAG	ATT	TTC	AAG	AAT	TGG	TAC	AGC	ACC	GCC	CTC	GAG	AAT	AAG	GAG	CAC	GCC	CT
Gd-PRO		L	T	K	V	F	K	N	W	Y	S	T	N	L	E	T	K	E	H	A	L

Gp-PRO	L	T	K	V	F	K	N	W	Y	S	T	N	L	E	T	K	E	H	A	L
Va-PRO	L	S	K	L	F	K	N	W	Y	S	T	T	L	E	N	K	E	H	A	L
Gg-PRO	L	A	K	I	F	K	N	W	Y	S	T	A	L	E	N	K	E	H	A	L

Gd-DNA	A	CGA	GGA	TGG	AAC	TGG	GGC	AAG	GCG	GAA	TTC	GGA	AAG	GCG	GAA	TTG	GCA	TTC	AAC	GTG	CA
Gp-DNA	A	CGA	GGA	TGG	AAC	TGG	GGG	AAA	GCG	GAG	TTC	GGA	AAG	GCG	GAG	CTG	GCA	TTC	AAT	GTG	CA
Va-DNA	G	CGC	GGC	TGG	AAC	TGG	GGC	AAG	GCG	GAG	TTC	GGC	AAG	GCT	GAG	CTG	TCC	TTC	AAC	GTG	CA
Gg-DNA	G	AGA	GGA	TGG	AAC	TGG	GGC	AAG	GCC	GAA	TTC	GGA	AAG	GCC	GAG	CTT	TCC	TTC	AAC	GTC	CA
Gd-PRO	R	G	W	N	W	G	K	A	E	F	G	K	A	E	L	A	F	N	V	Q	
Gp-PRO	R	G	W	N	W	G	K	A	E	F	G	K	A	E	L	A	F	N	V	Q	
Va-PRO	R	G	W	N	W	G	K	A	E	F	G	K	A	E	L	S	F	N	V	Q	
Gg-PRO	R	G	W	N	W	G	K	A	E	F	G	K	A	E	L	S	F	N	V	Q	

Gd-DNA	G	AAC	AGA	CCT	GCG	TTT	GAG	ATC	CCC	TAC	TCG	GAG	ATC	TCG	AAT	ACG	AAT	TTG	GCT	GGG	AA
Gp-DNA	G	AAC	AGA	CCT	GCG	TTT	GAA	ATT	CCT	TAC	TCG	GAG	ATC	TCG	AAT	ACG	AAT	TTG	GCT	GGA	AA
Va-DNA	G	AAT	CGT	CCG	GCC	TTT	GAG	GTG	CCC	TAC	TCG	GAA	ATC	TCC	AAC	ACC	AAC	CTC	GCT	GGC	CG
Gg-DNA	G	AAC	CGA	CCT	GCT	TTT	GAA	ATC	CCT	TAC	TCC	GAG	ATC	TCA	AAT	ACC	AAC	CTG	GCA	GGT	CG
Gd-PRO	N	R	P	A	F	E	I	P	Y	S	E	I	S	N	T	N	L	A	G	K	
Gp-PRO	N	R	P	A	F	E	I	P	Y	S	E	I	S	N	T	N	L	A	G	K	
Va-PRO	N	R	P	A	F	E	V	P	Y	S	E	I	S	N	T	N	L	A	G	R	
Gg-PRO	N	R	P	A	F	E	I	P	Y	S	E	I	S	N	T	N	L	A	G	R	

Gd-DNA	G	AAC	GAG	GTG	GCG	GTT	GAG	TTC	TCG	TTG	CCG	GCT	GGT	---	GGC	GAT	GAG	GGC	GCA	AAC	G
Gp-DNA	G	AAC	GAG	GTG	GCA	GTC	GAG	TTT	TCG	TTG	CCG	GCG	GGT	---	GGC	GAC	GAG	GGC	GCA	AAC	G
Va-DNA	C	AAC	GAG	GTC	GCC	GTC	GAG	TTT	GCC	GCC	CCC	ACC	GAC	GAG	AAC	GAC	ACA	GGC	ACC	AAC	G
Gg-DNA	C	AAC	GAA	GTC	GCC	GTC	GAA	TTC	TCT	GCC	CCG	ACG	GAC	CAG	AAC	GAT	ACC	GGC	ACG	AAT	G
Gd-PRO	N	E	V	A	V	E	F	S	L	P	A	G	-	G	D	E	G	A	N		
Gp-PRO	N	E	V	A	V	E	F	S	L	P	A	G	-	G	D	E	G	A	N		
Va-PRO	N	E	V	A	V	E	F	A	A	P	T	D	E	N	D	T	G	T	N		
Gg-PRO	N	E	V	A	V	E	F	S	A	P	T	D	Q	N	D	T	G	T	N		

Gd-DNA	GA	AGC	TTG	GGT	GGT	GCG	AAG	GGG	AAG	GGG	AAG	AAG	GCT	GGC	GCG	GGG	AAG	GAT	CAG	TTG	G	359
Gp-DNA	GA	AGC	TTG	GGC	GGT	GCG	AAG	GGG	AAG	GGC	AAG	AAG	GCC	GGC	GCA	GGG	AAG	GAT	CAA	TTA	G	393
Va-DNA	GG	ACT	CTC	GAC	GGT	GCG	CGT	GGC	AAG	GGC	AAG	AAG	GCG	GGT	GCT	GGC	AAG	GAC	CAG	CTC	G	459
Gg-DNA	GC	CAC	TTG	GGC	GGC	GCG	CGA	GGA	AAG	GGC	AAG	AAG	GCC	GGA	GCC	GGC	AAA	GAT	CAG	CTC	G	465
Gd-PRO	G	S	L	G	G	A	K	G	K	G	K	K	A	G	A	G	K	D	Q	L		
Gp-PRO	G	S	L	G	G	A	K	G	K	G	K	K	A	G	A	G	K	D	Q	L		
Va-PRO	G	T	L	D	G	A	R	G	K	G	K	K	A	G	A	G	K	D	Q	L		

Gg-PRO G **H** L G G A R G K G K K A G A G K D Q L

SRP72 (Signal recognition particle protein 72): ~400 bases aligned; Region shown include 5' UTR and 5' region of the protein (Ss = *Sclerotinia sclerotiorum*, Ad = *Ajellomyces dermatiditis*)

Gd-DNA CTAAATATACATATACATGGAATGAAACATATGCCGCGCATATAATACATATGATATCAGCTTACTCAAGTGCGCCCAAT
 Ss-DNA GCCGCGCTAGCTCAGCAGTTGATCGCTTTTTGACACCATCTCCATATCGCATGGCTACAGTAAATAGGAACCCATCGCCCTA
 Gp-DNA GGAGATATACATACACATGGACTGAAATATATATGGCCTCGCATATAATCAACATATCAGTTTACTCAAGTGCGCCTAATA
 Ad-DNA TTATTCCGCAACCTTCTTTCTTTTTTATTTCTTTAAACAATCCTTTTTCGGGAGCCAGTGCGGCGCCTGAACAGCCCTTGAA

Gd-DNA CTC GCT AGC ATG GCG TCC AAC CCC ACC GCT ACG TTG AGC AAA CTA CTC GGC TCA GCA ACT A
 Ss-DNA GAG TTT AAA ATG GCC --- GAT CAA ACA GCA ACG CTC AGC GCC CTC CTT CGT AAT TCT TCA A
 Gp-DNA CTC GCT AGC ATG GCG TCC AAC CCC ACC GCT ACC TTG AGC AAA CTC CTC GGC TCA GCA ACT A
 Ad-DNA CTT CTC CGT ATG GCG --- --- --- ACC CAG AGC ATC AGT GCG TTG GTT CAG CGA AGC ACA A
 Gd-PRO M A S N P T A T L S K L L G S A T
 Ss-PRO M A - D Q T A T L S **A** L L **R** **N** **S** **S**
 Gp-PRO M A S N P T A T L S K L L G S A T
 Ad-PRO M A - - - T **Q** **S** I S **A** L **V** **Q** **R** **S** T

Gd-DNA TG GAG GAC CAT GAG GAG ATT CTG AGA GCC GCC AAT GCC GTT CTC AAG AAG TCG AAA ACA A
 Ss-DNA TT **ACA** GAC CAT GAA GAG ATC CTC **AAA** GCT **ACA** AAT GAC GTA TTA AAG ACT TCT AAA **CTC** G
 Gp-DNA TC GAT GAC CAC GAG GAG GTT CTG AGA GCC GCC AAT GCT ATT CTC AAG AAG TCG AAA ACA G
 Ad-DNA TC GAC GAC CAT GAA GAA GTC ATC **AAA** GCT **TGC** AAT GCG GTA CTG AAA **ACG** TCC AAA **AAC** G
 Gd-PRO **M** **E** D H E E I L R A A N A V L K K S K T
 Ss-PRO I **T** D H E E I L **K** A **T** N **D** V L K **T** S K **L**
 Gp-PRO I D D H E E **V** L R A A N A **I** L K K S K T
 Ad-PRO I D D H E E **V** **I** K A **C** N A V L K **T** S K **N**

Gd-DNA AC CAG GAT GCG CTG CGT ACT CGC GTT ATT GCA CTC CTC AAG CTA GAC CGC TAC GCA GAT G
 Ss-DNA AC **CCC** GAT GCC TTG **CAT** ACC CGC **GCT** ATT GCT CTC CTC **AAA** CTT GAT CGA **TTC** **GAC** GAT G
 Gp-DNA AC CAG GAT GCG CTA CGT ACT CGT GTC ATT GCG CTG CTT AAG CTA GAC CGC TAC GCA GAT G
 Ad-DNA **AT** **CTC** **AAT** GCC CTC **CAT** **GTA** **AAA** **ACT** **GTT** GCC CTG **GTC** **AAA** **TTG** GAC CGT **TTC** **GAA** GAT G
 Gd-PRO **N** Q D A L R T R V I A L L K L D R Y A D
 Ss-PRO D **P** D A L **H** T R **A** I A L L K L D R **F** **D** D
 Gp-PRO D Q D A L R T R V I A L L K L D R Y A D
 Ad-PRO D **L** **N** A L **H** **V** **K** **T** **V** A L **V** K L D R **F** **E** D

Gd-DNA	CC	CTC	CGC	GCC	CTC	GAC	GAC	GGG	GGC	GAA	GCT	CTC	AGC	GAA	AGC	TGC	CAC	GTT
Ss-DNA	CA	CTA	AAA	GCC	CTC	GAC	GAA	GGT	GGA	GAT	AAA	TTG	GCT	TCT	CAA	TGT	ATT	CTC
Gp-DNA	CT	CTC	CGC	GCC	CTC	GAC	GAC	GGG	GGA	GAT	GCT	CTC	AGC	GAA	ATC	TGC	CAC	GTT
Ad-DNA	CG	ATT	CGA	GTG	ATC	GAG	GAT	GGC	GGG	GAT	GCG	CTG	AAA	AAG	AAA	GTC	CCT	CTG
Gd-PRO	A	L	R	A	L	D	D	G	G	E	A	L	S	E	S	C	H	V
Ss-PRO	A	L	K	A	L	D	E	G	G	D	K	L	A	S	Q	C	I	L
Gp-PRO	A	L	R	A	L	D	D	G	G	D	A	L	S	E	I	C	H	V
Ad-PRO	A	I	R	V	I	E	D	G	G	D	A	L	K	K	K	V	P	L

Gd-DNA	GAG	AAG	TCG	TAC	GCC	CTT	TAC	AAA	ACA	GGC	CAG	CTC	GAG	GCC	GCA	CAG	AAG	ATT	TTC	G
Ss-DNA	GAA	CGC	GCT	TAT	GCT	CTC	TAC	AAG	ACA	GGG	AAA	CTG	GCA	GAT	GCG	GCG	AAA	GTA	TGT	G
Gp-DNA	GAG	AAA	TCG	TAC	GCG	CTT	TAC	AAA	ACA	GGC	CAA	CTC	GAG	GCC	GCA	CAG	AAA	ATT	TTC	G
Ad-DNA	GAA	TGG	TCT	TAC	GCT	TTA	TAT	AAG	GTC	GGG	CAA	TTA	GAA	GAT	GCG	ATA	AAA	CTG	GCC	G
Gd-PRO	E	K	S	Y	A	L	Y	K	T	G	Q	L	E	A	A	Q	K	I	F	
Ss-PRO	E	R	A	Y	A	L	Y	K	T	G	K	L	A	D	A	A	K	V	C	
Gp-PRO	E	K	S	Y	A	L	Y	K	T	G	Q	L	E	A	A	Q	K	I	F	
Ad-PRO	E	W	S	Y	A	L	Y	K	V	G	Q	L	E	D	A	I	K	L	A	

VPS13 (Vacuolar protein sorting-associated protein): ~545 bases aligned (Ss = *Sclerotinia sclerotiorum*, Bf = *Botryotinia fuckeliana*)

Gd-DNA	GG	ATC	CCA	GAT	AGT	GGT	GGA	GCG	TTT	AGA	CTC	ACG	ATT	TAC	AGT	CCT	TAC	ATC	ATT	TTG	A
Gp-DNA	GA	ATC	CCA	GAC	GGC	GGT	GGA	GCG	TTT	AGA	CTC	ACA	ATT	TAC	AGT	CCT	TAT	GTC	ATT	TTG	A
Ss-DNA	AG	ATT	CCA	GAT	AGT	GGA	GGA	GCA	TTT	AGA	GTA	ACT	GTC	TAC	AGT	CCT	TAC	GTT	ATC	CTA	A
Bf-DNA	AG	ATT	CCA	GAT	AGT	GGT	GGA	GCT	TTT	AGA	GTC	ACC	GTA	TAC	AGT	CCT	TAT	GTA	ATC	CTA	A
Gd-PRO		I	P	D	S	G	G	A	F	R	L	T	I	Y	S	P	Y	I	I	L	
Gp-PRO		I	P	D	G	G	A	F	R	L	T	I	Y	S	P	Y	V	I	I	L	
Ss-PRO		I	P	D	S	G	G	A	F	R	V	T	V	Y	S	P	Y	V	I	L	
Bf-PRO		I	P	D	S	G	G	A	F	R	V	T	V	Y	S	P	Y	V	I	L	

Gd-DNA	AT	AAA	ACT	GGC	CTG	GAT	ATC	AAT	ATC	AAG	GCC	AAG	TCG	TTA	CTG	CAG	CAA	GCA	CGG	ACG	G
Gp-DNA	AT	AAA	ACA	GGC	CTG	GAT	ATC	AAC	ATC	AAG	GCG	AAG	TCG	TTA	CTG	CAG	CAA	GCG	CGG	ACT	G
Ss-DNA	AT	AAA	ACC	GGA	CTG	GAG	ATC	AAC	ATC	AAA	CAG	AAG	TCA	TTG	TTG	CAG	CAA	GCA	AAG	ACG	G
Bf-DNA	AT	AAG	ACT	GGC	CTA	GAG	ATC	AAC	ATC	AAA	CAA	AAA	TCG	CTA	TTG	CAG	CAA	GCA	AAG	ACG	G
Gd-PRO	N	K	T	G	L	D	I	N	I	K	A	K	S	L	L	Q	Q	A	R	T	
Gp-PRO	N	K	T	G	L	D	I	N	I	K	A	K	S	L	L	Q	Q	A	R	T	

Ss-PRO	N	K	T	G	L	E	I	N	I	K	Q	K	S	L	L	Q	Q	A	K	T	
Bf-PRO	N	K	T	G	L	E	I	N	I	K	Q	K	S	L	L	Q	Q	A	K	T	
Gd-DNA	CG	GCT	GGC	CAG	AAG	GTA	GTG	CGC	GAT	CTC	CTT	GGG	GAT	GAC	GAA	CAG	AAG	GCG	CTG	CCT	C
Gp-DNA	CA	GCT	GGA	CAG	AAG	GTC	GTG	CGC	GAT	CTC	CTC	AGC	GAT	GAC	GAG	CAG	AAG	GCG	CTG	CCT	T
Ss-DNA	CG	GCC	GGT	CAA	GGG	TTT	CGT	ACA	GAT	TCG	GCT	GAT	TCA	GAA	CGG	CGT	AAG	GCA	CTA	CCT	T
Bf-DNA	CA	GCA	GGT	CAA	GGG	TTC	CAT	ACT	GAC	TCA	GTC	GAT	TCT	GAA	CGG	CGC	AAA	GCA	CTA	CCA	T
Gd-PRO	A	A	G	Q	K	V	V	R	D	L	L	G	D	D	E	Q	K	A	L	P	
Gp-PRO	A	A	G	Q	K	V	V	R	D	L	L	S	D	D	E	Q	K	A	L	P	
Ss-PRO	A	A	G	Q	G	F	R	T	D	S	A	D	S	E	R	R	K	A	L	P	
Bf-PRO	A	A	G	Q	G	F	H	T	D	S	V	D	S	E	R	R	K	A	L	P	
Gd-DNA	TG	ATG	TTT	GCG	TTC	AGT	GGC	GAC	GAC	CAG	CGC	AAC	CGC	GTC	ATC	CTC	AAA	GTC	GGC	GAG	T
Gp-DNA	TG	ATG	TTT	GCG	TTC	AGT	GGC	GAC	GAC	CAG	CGT	AAC	CGC	GTC	ATC	CTC	AAA	GTT	GGC	GAG	T
Ss-DNA	AT	ATG	TTT	GCA	TAT	GGC	GGA	GAT	GAT	CAA	AGG	AAT	CGT	GCT	ATA	TTG	AAG	GTT	GGC	GAC	T
Bf-DNA	AC	ATG	TTT	GCG	TAT	GGC	GGA	GAT	GAT	CAA	CGA	AAT	CGT	GCT	TTA	ATG	AAG	GTC	GGT	GAC	T
Gd-PRO	L	M	F	A	F	S	G	D	D	Q	R	N	R	V	I	L	K	V	G	E	
Gp-PRO	L	M	F	A	F	S	G	D	D	Q	R	N	R	V	I	L	K	V	G	E	
Ss-PRO	Y	M	F	A	Y	G	G	D	D	Q	R	N	R	A	I	L	K	V	G	D	
Bf-PRO	Y	M	F	A	Y	G	G	D	D	Q	R	N	R	A	L	M	K	V	G	D	
Gd-DNA	CG	AAC	TGG	AGT	AAA	CCG	CAG	AGT	TTC	GAC	GCC	ATT	GGC	AGC	ACA	ATC	GAT	GTG	GTT	CTA	C
Gp-DNA	CG	AAC	TGG	AGT	AAA	CCG	CAG	AGT	TTC	GAC	GCC	ATT	GGC	AGC	ACG	ATT	GAT	GTT	GTT	CTA	C
Ss-DNA	CG	AAT	TGG	AGT	AAA	CCA	CAA	AGT	CTG	GAT	GCC	ATC	GGT	AGT	AAT	GTC	GAT	GTT	GTT	TTA	T
Bf-DNA	CC	AAC	TGG	AGT	AAA	CCG	CAA	AGT	TTG	GAT	GCT	ATC	GGC	AGC	AAT	GTA	GAT	GTC	ATA	TTG	C
Gd-PRO	S	N	W	S	K	P	Q	S	F	D	A	I	G	S	T	I	D	V	V	L	
Gp-PRO	S	N	W	S	K	P	Q	S	F	D	A	I	G	S	T	I	D	V	V	L	
Ss-PRO	S	N	W	S	K	P	Q	S	L	D	A	I	G	S	N	V	D	V	V	L	
Bf-PRO	S	N	W	S	K	P	Q	S	L	D	A	I	G	S	N	V	D	V	I	L	
Gd-DNA	CG	TCA	GCA	ACT	CAG	AAT	ACT	GAG	ATC	CAT	GTT	GGA	ATC	AGC	ATC	GAG	AAT	GGA	GAC	GGG	A
Gp-DNA	CC	TCG	GCA	ACT	CAG	AAT	ACC	GAG	ATA	CAC	GTT	GGA	ATC	AGT	ATC	GAG	AAC	GGG	GAC	GGG	A
Ss-DNA	CT	TCT	TCT	AAA	AAC	AAC	ACC	GAG	ATA	CAC	GTG	GGC	ATC	AAT	GTT	GAA	TCA	GGA	GAG	GGC	A
Bf-DNA	CT	TCC	TCA	AAG	AAC	AAT	ACC	GAA	ATT	CAT	GTA	GGT	ATC	AGT	GTC	GAA	GCA	GGA	GAG	GGT	A
Gd-PRO	P	S	A	T	Q	N	T	E	I	H	V	G	I	S	I	E	N	G	D	G	
Gp-PRO	P	S	A	T	Q	N	T	E	I	H	V	G	I	S	I	E	N	G	D	G	
Ss-PRO	S	S	S	K	N	N	T	E	I	H	V	G	I	N	V	E	S	G	E	G	

Bf-PRO	P	S	S	K	N	N	T	E	I	H	V	G	I	S	V	E	A	G	E	G	
Gd-DNA	AA	TAC	AAG	ATG	ACC	AAG	GTC	GTT	ACG	CTT	GCG	CCG	AGA	TTT	GTG	CTG	AAG	AAT	CGC	ATG	A
Gp-DNA	AA	TAC	AAG	ATG	ACC	AAG	GTC	GTT	ACG	CTT	GCA	CCG	AGA	TTT	GTG	CTG	AAG	AAT	CGC	ATG	A
Ss-DNA	AA	TAC	AAA	ATG	ACG	AAG	GTA	GTC	ACT	CTT	GCT	CCC	CGC	TTT	GTT	CTG	AAG	AAT	CAG	ATG	A
Bf-DNA	AA	TAT	AAG	ATG	ACG	AAG	GTT	GTC	ACA	CTT	GCT	CCT	CGC	TTT	GTT	TTA	AAG	AAT	CAA	ATG	A
Gd-PRO	K	Y	K	M	T	K	V	V	T	L	A	P	R	F	V	L	K	N	R	M	
Gp-PRO	K	Y	K	M	T	K	V	V	T	L	A	P	R	F	V	L	K	N	R	M	
Ss-PRO	K	Y	K	M	T	K	V	V	T	L	A	P	R	F	V	L	K	N	Q	M	
Bf-PRO	K	Y	K	M	T	K	V	V	T	L	A	P	R	F	V	L	K	N	Q	M	
Gd-DNA	GC	GAG	GAA	ATC	AGC	GCC	AGG	GAA	CCT	GGA	TCG	TCG	GAG	CTT	ATG	ACT	TTG	AAG	CGG	GGA	G
Gp-DNA	GT	GAG	GAA	ATC	AGC	GCC	AGG	GAA	CCT	GGA	TCG	TCG	GAG	CTC	ATG	ACT	TTG	AAG	CCG	GGA	G
Ss-DNA	AC	GAG	GAA	ATA	AAT	GTC	AGG	GAA	CCC	GGG	TCG	TCT	GAA	CTC	TGG	ACT	TTG	AAG	CCA	CAG	G
Bf-DNA	GC	GAA	GAA	CTA	AAC	GTT	AGA	GAG	CCT	GGG	TCA	TCT	GAA	CTT	TGG	ACT	TTG	AAG	CCA	CAA	G
Gd-PRO	S	E	E	I	S	A	R	E	P	G	S	S	E	L	M	T	L	K	R	G	
Gp-PRO	S	E	E	I	S	A	R	E	P	G	S	S	E	L	M	T	L	K	P	G	
Ss-PRO	N	E	E	I	N	V	R	E	P	G	S	S	E	L	W	T	L	K	P	Q	
Bf-PRO	S	E	E	L	N	V	R	E	P	G	S	S	E	L	W	T	L	K	P	Q	
Gd-DNA	AA	CTG	AAG	GCT	CTT	CAC	TTC	CTT	CAA	AAG	TCG	GCG	GTT	AAG	CAA	CTG	TGC	CTT	TGC	TTC	C
Gp-DNA	AA	CTG	AAA	GCT	CTT	CAC	TTC	CTT	CAA	AAG	TCG	GCG	GTG	AAG	CAA	CTG	TGC	CTT	TGC	TTC	C
Ss-DNA	CC	CTA	GAA	CCT	CTT	CAT	TTC	CTC	CAG	AAG	AGT	CCC	GTC	AAG	CAA	CTT	ACG	CTA	TGC	TTC	C
Bf-DNA	CT	TTA	GAG	CCT	CTT	CAT	TTC	CTT	CAG	AAG	AGT	CAT	GTA	AAA	CAA	CTC	ACG	ATG	TGC	TTC	C
Gd-PRO	E	L	K	A	L	H	F	L	Q	K	S	A	V	K	Q	L	C	L	C	F	
Gp-PRO	E	L	K	A	L	H	F	L	Q	K	S	A	V	K	Q	L	C	L	C	F	
Ss-PRO	A	L	E	P	L	H	F	L	Q	K	S	P	V	K	Q	L	T	L	C	F	
Bf-PRO	A	L	E	P	L	H	F	L	Q	K	S	H	V	K	Q	L	T	M	C	F	
Gd-DNA	CC	GGC																			
Gp-DNA	CG	GGC																			
Ss-DNA	CT	GGA																			
Bf-DNA	CA	GGA																			
Gd-PRO	P	G																			
Gp-PRO	P	G																			
Ss-PRO	P	G																			
Bf-PRO	P	G																			