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Biochemical and genetic analyses of the oomycete *Pythium insidiosum* provide new insights into clinical identification and urease-based evolution of metabolismrelated traits

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ABSTRACT

The oomycete microorganism, Pythium insidiosum, causes the life-threatening infectious condition, pythiosis, in humans and animals worldwide. Affected individuals typically endure surgical removal of the infected organ(s). Detection of P. insidiosum by the established microbiological, immunological, or molecular methods is not feasible in non-reference laboratories, resulting in delayed diagnosis. Biochemical assays have been used to characterize P. insidiosum, some of which could aid in the clinical identification of this organism. Although hydrolysis of maltose and sucrose has been proposed as the key biochemical feature useful in discriminating P. insidiosum from other oomycetes and fungi, this technique requires a more rigorous evaluation involving a wider selection of P. insidiosum strains. Here, we evaluated 10 routinely available biochemical assays for characterization of 26 P. insidiosum strains, isolated from different hosts and geographic origins. Initial assessment revealed diverse biochemical characteristics across the P. insidiosum strains tested. Failure to hydrolyze sugars is observed, especially in slow-growing strains. Because hydrolysis of maltose and sucrose varied among different strains, use of the biochemical assays for identification of P. insidiosum should be cautioned. The ability of P. insidiosum to hydrolyze urea is our focus, because this metabolic process relies on the enzyme urease, an important virulence factor of other pathogens. The ability to hydrolyze urea varied among P. insidiosum strains and was not associated with growth rates. Genome analyses demonstrated that urease- and urease accessory protein-encoding genes are present in both urea-hydrolyzing and non-urea-hydrolyzing strains of P. insidiosum. Urease genes are phylogenetically conserved in *P. insidiosum* and related oomycetes, while the presence of urease accessory protein-encoding genes is markedly diverse

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in these organisms. In summary, we dissected biochemical characteristics and drew new insights into clinical identification and urease-related evolution of *P. insidiosum*.

Subjects Biochemistry, Mycology, Infectious Diseases

Keywords Pythiosis, *Pythium insidiosum*, Biochemical feature, Urease, Evolution, Identification, Biochemical test

INTRODUCTION

Infectious diseases pose a greater threat to humans, animals, and plants as drug-resistant varieties emerge. Among these is pythiosis (the infectious condition caused by the funguslike, highly invasive, oomycete microorganism Pythium insidiosum), which has been increasingly reported in tropical and subtropical countries (Thianprasit, Chaiprasett & Imwidthaya, 1996; Krajaejun et al., 2006b; Gaastra et al., 2010). Many healthcare personnel are not familiar with pythiosis. The use of anti-fungal drugs to control this pathogen has generally been ineffective (Lerksuthirat et al., 2017). Affected individuals often undergo surgical removal of the infected organ, and many succumb to the progressive disease (Krajaejun et al., 2004, 2006b). Early and accurate diagnosis is necessary to ensure prompt and proper treatment, and thus an improved clinical outcome for patients. Isolation of the pathogen from infected tissues by the standard microbiological procedure is timeconsuming and requires experience (*Chaiprasert et al.*, 1990). A number of detection tools such as serological tests (Pracharktam et al., 1991; Krajaejun et al., 2002, 2006a, 2009; Grooters et al., 2002; Jindayok et al., 2009; Supabandhu et al., 2009; Chareonsirisuthigul et al., 2013; Keeratijarut et al., 2013; Intaramat et al., 2016), immunostaining assays (Keeratijarut et al., 2009; Inkomlue et al., 2016), and molecular biology methods (Grooters & Gee, 2002; Botton et al., 2011; Keeratijarut et al., 2014, 2015; Rujirawat et al., 2017), have been successfully developed for P. insidiosum infection. However, such tools are not generally available in non-reference clinical laboratories, resulting in missed or delayed diagnosis of pythiosis.

Biochemical assays may be used to characterize *P. insidiosum* and could aid in the clinical identification of this organism. Different patterns of enzymatic activities in phosphatases, esterases, lipases, glucosidases, and proteases have been observed among strains of *P. insidiosum* (*Davis et al., 2006; Zanette et al., 2013*). Recently, Vilela and co-workers adopted an array of biochemical assays (hydrolysis of sugars, citrate, urea, esculin, etc.) to differentiate the pathogenic oomycetes, including six strains of *P. insidiosum* (*Vilela, Viswanathan & Mendoza, 2015*). They proposed that an ability to hydrolyze maltose and sucrose is a key biochemical feature to discriminate *P. insidiosum* from other mammalian-pathogenic oomycetes (i.e., *Lagenidium* species) and morphologically similar fungi. Although the use of these biochemical assays in the clinical identification of *P. insidiosum* is promising, it requires further evaluation with a more extensive selection of *P. insidiosum* strains.

In the current study, we evaluated 10 routinely available biochemical assays for characterization of 26 phylogenetically defined strains of *P. insidiosum*. The strains tested

had different geographic origins (i.e., Clade-I strains from Americas, Clade-II strains from Asia and Australia, and Clade-III mostly from Thailand) and were isolated from different hosts (i.e., humans and horses) (*Schurko et al., 2003; Chaiprasert et al., 2009; Rujirawat et al., 2017*). Initial assessment revealed strain to strain variation amongst the strains of *P. insidiosum* tested. The capacity to hydrolyze urea became our focus because this metabolic process relies on the enzyme urease, an important virulence factor of *Helicobacter pylori* and *Cryptococcus neoformans* (*Cox et al., 2000; Rutherford, 2014; Mora* & *Arioli, 2014*). Since the genome of *P. insidiosum* is publically available (*Rujirawat et al., 2015*), we were able to explore the genetic and evolutionary details of the urease gene in *P. insidiosum* and related oomycetes.

MATERIALS AND METHODS

Ethics statement

This study was approved by the Committee on Human Rights Related to Research Involving Human Subjects, at the Faculty of Medicine, Ramathibodi Hospital, Mahidol University (approval number ID 05-60-77).

Microorganisms and growths

Twenty-six strains of *P. insidiosum* isolated from humans (n = 14) or equines (n = 10) with pythiosis and from the environment (n = 2), were available for this study (Table 1). Identity and genotyping (i.e., Clade-I, II, and III) of *P. insidiosum* were confirmed through culture identification, single nucleotide polymorphism-based multiplex PCR, and rDNA sequence analysis (*Chaiprasert et al., 1990, 2009; Badenoch et al., 2001; Rujirawat et al., 2017*). Because *P. insidiosum* has been classified as a Biosafety Level 2 organism (https://www.atcc.org), Biosafety Level 2 precautions were followed throughout this study (https://www.cdc.gov/biosafety). All of the organisms were retrieved from stock cultures, and maintained on Sabouraud dextrose (SD) agar at 37 °C for at least three passages. SD agar plugs (5 mm in diameter) from one-week-old, actively growing cultures of *P. insidiosum* were then prepared (*Krajaejun et al., 2010; Lerksuthirat et al., 2017*) for biochemical assays. Radial growth rate (mm/day) of *P. insidiosum* was evaluated, using the previously described method (*Krajaejun et al., 2010; Lerksuthirat et al., 2017*). Strains with growth rates ≥ 5 mm/day were defined as fast-growing strains, while the rest were defined as slow-growing strains.

Biochemical assays

To set up biochemical assays, 10 different routinely available agars were each prepared in test tubes (except the DNase assay agar, which was prepared in a Petri dish), using ingredients purchased from BD Difco and BBL (if not stated otherwise), and the recommended protocols of the manufacturers. These agars included: urea agar (urease assay), Simmons'citrate agar (citrate hydrolysis assay), bile esculin agar (esculin hydrolysis assay), DNA agar (DNase assay), and purple agar base (sugar hydrolysis assay) with 2% (wt/v) dextrose, lactose, maltose, sucrose (Merck, Darmstadt, Germany), trehalose

Strain ID Rel str str Pi08 CB Pi03 CB ATCC38351 AT	ference	Source														
Pi08 CB Pi03 CB ATCC78751 AT	ain ID	2000	Country	Phylogenetic clade	Growth rate (mm/day)	Fast/slow growth	Urease (Sitrate	Bile esculin	Dextose	Lactose	Maltose	Sucrose	Trehalose	Xylose	DNase
Pi03 CB	S580.85	Equine	Costa Rica	I	10.6	Fast	+	· ·	+	+	<u> </u>	+	+	+	<u> </u>	+
ATCC28251 AT	S577.85	Equine	Costa Rica	Ι	10.1	Fast	+	·	+	+	<u> </u>	+	(-)	+	(+
	CC28251	Equine	Papua New Guinea	Π	9.5	Fast)	T	+	+	<u> </u>	+	+	+	<u> </u>	+
Pi10 AT	CC200269	Human	USA	I	9.0	Fast	+	· T	+	+	<u> </u>	+	+	+	<u> </u>	+
Pi02 CB	S579.85	Equine	Costa Rica	Ι	8.4	Fast	+	·	+	+	<u> </u>	+	+	+	(+
Pi26 N/.	A	Human	Thailand	Π	8.3	Fast	+	· ·	+	+	(-)	+	+	+	<u> </u>	+
Pi36 AT	CC64221	Equine	Australia	Π	7.9	Fast	+	·	+	+	<u> </u>	+	+	+	()	+
Pi35 Pi-	S	Human	Thailand	Π	7.4	Fast	+	·	+	+	(-)	+	+	+	(-)	+
Pi42 CR	02	Environment	Thailand	Π	7.3	Fast	+	·	+	+	<u> </u>	+	+	+	()	+
Pi23 N/.	Α	Human	Thailand	Π	7.2	Fast) (-)		+	+	(-)	+	+	+	(-)	+
Pi05 CB	S575.85	Equine	Costa Rica	Ι	7.0	Fast	+	·	+	+	-	+	+	+	(-)	+
Pi09 CB	S101555	Equine	Brazil	Ι	6.6	Fast	+	·	+	+	(-)	+	+	+	(-)	+
Pi51 N/.	Α	Environment	Thailand	III	6.2	Fast)	·	+	+	-	+	+	+	(-)	+
Pi49 N/.	А	Human	Thailand	III	5.7	Fast) (-)	·	+	+	-	+	+	+	(-)	+
Pi11 N/.	Α	Human	Thailand	II	5.2	Fast	+	·	+	+	(-)	+	+	+	(-)	+
Pi19 N/.	А	Human	Thailand	Π	5.1	Fast	+	·	+	+	(-)	+	+	+	(-)	+
Pi45 MG	CC13	Human	Thailand	III	5.0	Fast) (-)	·	+	+	<u> </u>	+	+	+	(+
Pi20 CB	S119455	Human	Thailand	Π	4.6	Slow	+	·	+	+	(-)	+	(-)	+	(-)	+
Pi50 AT	CC90586	Human	USA	III	4.2	Slow)	·	+	+	<u> </u>	+	+	+	(+
Pi07 CB	S573.85	Equine	Costa Rica	Ι	3.7	Slow	+	·	+	+	-	+	+	+	(-)	+
Pi04 CB	S576.85	Equine	Costa Rica	Ι	3.7	Slow	+	·	+	+	<u> </u>	+	(-)	+	(+
Pi46 N/.	Α	Human	Thailand	III	2.6	Slow	+	·	+	(-)	(-)	()	(-)	(-)	(-)	<u> </u>
Pi47 N/.	A	Human	Thailand	III	2.4	Slow)	·	+	<u> </u>	<u> </u>	(-)	+	() 	<u> </u>	<u> </u>
Pi44 CB	S119454	Human	Thailand	III	2.1	Slow	+	·	+	(-)	-	(-)	(-)	(-)	(-)	+
Pi48 N/.	А	Human	Thailand	III	1.8	Slow	+	·	+	+	<u> </u>	+	+	+	(+
CBS574.85 CB	S574.85	Equine	Costa Rica	Ι	0.7	Slow	+	·	+	(-)	-	(-)	(-)	(-)	(-)	(-)
% Positive read ((n = 26)						73.1 0	0.0	100.0	84.6	0.0	84.6	76.9	84.6	0.0	88.5

The symbol "+" and "(-)" indicate positive and negative biochemical reaction, respectively. Fast (>5 mm/day) and slow (<5 mm/day) growths are determined based on mean radial growth rate. The strains Pi07, Pi35, and Pi45 have their genome sequences available. The strains CBS574.85 and ATCC28251 are included in this and other biochemical studies (*Vilela, Viswanathan & Mendoza, 2015*).



Figure 1 The Oomycete Gene Table demonstrating the identified gene clusters containing the urease- and urease accessory protein-encoding genes presented in the genomes of *P. insidiosum* (arrow head), 19 related oomycetes, and two diatoms (asterisks). Cluster identification numbers (Cluster ID), function annotations, and identities of the genomes are shown in the table header. The arrow head indicates the genome of *P. insidiosum*. A gray box represents a similar sequence is identified, while a black box represents no similar sequence is found, in any given genome. Colored boxes refer to gene copy number. Full-size DOI: 10.7717/peerj.4821/fig-1

(Sigma-Aldrich, St. Louis, MO, USA), or xylose. A 5 mm diameter agar plug of an actively growing colony of each *P. insidiosum* strain was placed upon each type of agar and incubated at 37 °C for two days before biochemical reactions were read. Each biochemical assay was interpreted as "negative" if the agar color remained unchanged, and interpreted as "positive" when the agar color changed: (i) from yellow to pink (urease assay); (ii) from brown to black (esculin hydrolysis assay); (iii) from green to blue (citrate hydrolysis assay); (iv) from dark blue to yellow (all sugar hydrolysis assay); and (v) from blue to colorless (DNase assay). All biochemical assays were performed in duplicate.

Identification of urease- and urease accessory protein-encoding genes

The Oomycete Gene Table is an online comparative genomic analysis tool, derived from sequence similarity based gene grouping of the genome sequences of *P. insidiosum*, 19 related oomycetes, and two diatoms (Table S1) (*Kittichotirat et al., 2011*; *Rujirawat et al., 2018*). In the current study, the Oomycete Gene Table shows identification of putative urease- and urease accessory protein-encoding genes in the genomes of the oomycetes and diatoms (Fig. 1). Predicted urease protein sequences of the oomycetes and diatoms were aligned using MUSCLE (*Edgar, 2004; Dereeper et al., 2008, 2010*), and assessed for sequence identity and similarity using NCBI BLAST (https://blast.ncbi.nlm.nih.gov/).

The urease and urease accessory protein sequences of the plant *Arabidopsis thaliana* (accession numbers: NP_176922 (urease structure protein, URE); NP_850239 (urease accessory protein D, URED); NP_173602 (urease accessory protein F, UREF);

and NP_180994 (urease accessory protein G, UREG)) (*Witte, Rosso & Romeis, 2005*) were retrieved from the NCBI database. To assess the presence of the orthologs in *P. insidiosum*, all of these *Arabidopsis* proteins were TBLASTN searched against the genome of the *P. insidiosum* strain Pi35 (also known as Pi-S), and two Illumina-derived genomes of the *P. insidiosum* strains Pi07 (also known as CBS 573.85) and Pi45 (*Rujirawat et al., 2015*; *Kittichotirat et al., 2017*; *Patumcharoenpol et al., 2018*), using the locally installed blast 2.2.28+ program (http://www.ncbi.nlm.nih.gov/) and the cut-off *E*-value $\leq 10^{-6}$.

Phylogenetic analysis

Phylogenetic analysis of 24 urease-encoding sequences from *P. insidiosum* (strains Pi07, Pi35, and Pi45), related oomycetes, and diatoms (outgroup) (Table S1) was executed online at www.phylogeny.fr (*Dereeper et al., 2008*). In brief, the sequence alignment was performed by MUSCLE (*Edgar, 2004*). Poorly aligned positions or gaps were eliminated by Gblocks (*Castresana, 2000*). Phylogenetic relationships were calculated by PhyML, using the maximum-likelihood algorithm and the branch-assessing aLRT test (*Anisimova & Gascuel, 2006; Guindon et al., 2010*). The phylogenetic tree was reconstructed using TreeDyn (*Chevenet et al., 2006*).

Sequence accession numbers

Sequences of the putative urease genes of *P. insidiosum* identified in the genomes of *P. insidiosum* strains Pi35 (accession number, LC317047 for *Ure*1), Pi07 (accession number LC325168 for *Ure*1), and Pi45 (LC325169 for *Ure*1A, and LC325170 for *Ure*1B) have been submitted to the DDBJ database.

RESULTS

Growth and biochemical characteristics of P. insidiosum

Twenty-six strains of *P. insidiosum* included in the current study were derived from different sources (humans, n = 14; animals, n = 10; and the environment, n = 2) and geographic origins (Asia, n = 15; Americas, n = 10; and Australia, n = 1). Based on the growth rates, *P. insidiosum* can be divided into two groups: (i) fast-growing strains (growth rate ≥ 5 mm/day; n = 17; 65% of all strains), and (ii) slow-growing strains (growth rate <5 mm/day; n = 9; 35% of all strains) (Table 1). Each group contained representatives from all phylogenetically distinct Clades (-I, -II, and -III), and from both humans and animals. Both environmental strains belonged to the fast-growing group.

As summarized in Table 1, all strains of *P. insidiosum* hydrolyzed esculin in the presence of bile but failed to breakdown citrate and two sugars (i.e., lactose and xylose). The majority of the strains can hydrolyze dextrose (n = 22; 85% of all strains), maltose (n = 22; 85%), sucrose (n = 20; 77%), trehalose (n = 22; 85%), and DNA (n = 23; 89%), while those that cannot utilize these substrates were almost all slow-growing. Unlike the other fast-growing strains, Pi03 did not hydrolyze sucrose. With regard to the urease assay, 71% (n = 12) of the fast-growing and 78% (n = 7) of the slow-growing strains could



of inoculation (Day#0; the colors of all agars remain unchanged), and strains Pi02 (B), ATCC 28251 (C), and CBS 574.85 (D) at two days post-inoculation (Day#2; biochemical results are read). Ten routinely available biochemical agars are included in this study: urea agar (Ure), Simmons'citrate agar (Cit), Bile esculin agar (Bil), DNA agar (DNA), and purple agar base with dextrose (Dex), lactose (Lac), maltose (Mal), sucrose (Suc), trehalose (Tre), or xylose (Xyl). The symbols "+" and "(–)" indicate positive and negative biochemical reaction, respectively. Photographs by Teerat Kanpanleuk. Full-size DOI: 10.7717/peerj.4821/fig-2

catabolize urea. Biochemical characteristics of some representative strains at day 0 (all agar colors remained unchanged) and day 2 post-inoculation (all biochemical reactions were read) were displayed in Fig. 2.

Ureases and urease accessory proteins of *P. insidiosum* and related oomycetes

Urease requires a number of urease accessory proteins to mediate enzymatic activity. Genes annotated as "urease" or "urease accessory protein" were searched using the Oomycete Gene Table (*Rujirawat et al., 2018*). All oomycetes and diatoms harbored a single copy of urease-encoding sequence (Gene cluster ID, #057948; average protein length: 849 amino acids; range: 761–1,345 amino acids), except the oomycete *A. invadans*, which contained three copies of this gene (Fig. 1; Table S1). Protein sequence alignment showed a high degree of identity (59–81%) and similarity (72–88%) between the ureases of oomycetes and diatoms (Fig. 3; Table S1).

A total of eight clusters of urease accessory protein-encoding genes were differentially presented in the genomes of 20 oomycetes (Fig. 1). These gene clusters included Cluster IDs: #051204 (found in 19 species), #291367 (17 species), #181024 (16 species), #152345 (15 species), #205644 (13 species), #213938 (12 species), #122775 (10 species), and #007410 (five species). Each oomycete genus possessed a different number of urease accessory gene clusters, for example: seven to eight clusters in *Phytophthora*, five to eight in *Pythium*, seven in *Phytopythium*, four in *Saprolegnia*, one to three in *Aphanomyces*, and one each in *Albugo* and *Hyaloperonospora*. None of these urease accessory gene clusters was identified in the diatom genomes.

TBLASTN search of the function-verified urease URE and urease accessory proteins URED, UREF, and UREG of the plant *A. thaliana* showed significant matches (*E*-value \leq -6) in the genomes of three representative *P. insidiosum* strains (Table 2): Pi07 (Clade-I strain), Pi35 (Clade-II strain), and Pi45 (Clade-III strain). One exception is UREF, which failed to find match in the genome of strain Pi07.

Urease-based phylogenetic relationships

A set of 24 urease-encoding sequences identified in the genomes of *P. insidiosum*, related oomycetes, and diatoms (Fig. 1; Table S1), were subjected to reconstruction of a maximum likelihood-based phylogenetic tree. As expected, phylogenetic locations of the ureases of the diatoms (serving as an outgroup) were separated from that of the oomycetes. The oomycete ureases were allocated into three phylogenetically distinct clades (Fig. 4): (i) the clade of *Pythium*, *Phytophthora*, *Phytopythium*, and *Hyaloperonospora* species; (ii) the clade of *Aphanomyces* and *Saprolegnia* species; and (iii) the clade of *Albugo* species. Most of the organisms contain one copy of the urease-encoding gene, except *A. invadans* (three copies) and *P. insidiosum* strain Pi45 (two copies). Four urease-encoding sequences from the *P. insidiosum* strains Pi07, Pi35, and Pi45 were grouped together, and placed more proximally to non-*insidiosum Pythium*, *Phytophthora*, *Phytopythium*, and *Hyaloperonospora* species than to other oomycete species.

DISCUSSION

A capacity to hydrolyze esculin, but not citrate, lactose and xylose, was the shared biochemical characteristic found in all 26 strains of *P. insidiosum* (Table 1), consistent with

Al_lai	MyairvlEscLMrslthstlrKndsqtkndaYMtchtvfeT	LELIRDGK-SVAELMaLGSQMLGrl	. lllnrtcicfdsirsRRQVlrGVAdMLDEVQVEGFFPDGTKLVTIHfPIvlLDGDmeLALYGSFLPiPSiDiFsq-PSiddrdayLVdHpPGeIITpDED-transformed and the state of	-111
Sa_dec	MhLSPREEDHLrLHQAGVLAQKRLARGLRLNYVEaIALIAT	QmLELIRDGK-SVAELMsLGkt1LG		-VVL
An ast	MRLSPREBOHLGLHOAGTLAOKRLARGLRLNIVECTALIAT	-OCLELIEDGR-UVAELMSLGKUILG-	IQVIDGVEAMIAGVDIGTEPBGTRUVTVBGDIGVGDUALALIGGELPFGDAGG_VYADVAKGLTPhilipi	GTeT.
Ap inv3	MRLSPREveHLgLHQAGVvAQKRLARsLRLNYVEtVALiAs	QcLELIRDGr-SVAEiMsLGkaMLG		GIeL
Ap inv1	MRLSPREveHLqLHQAGVvAQKRLARsLRLNYVEtVALiAs	QcLELIRDGr-SVAEiMsLGkaMLG	lRQVMDGVsAMLhdVQVEGTFPDGTKLVTvHNPICRvDGDmSLALYGSFfPVPSLEsFGPAepsvdLnkqIIvvDDeN	GIeL
Ap_inv2	MRLSPREveHLqLHQAGVvAQKRLARsLRLNYVEtVALiAs	QcLELIRDGr-SVAEiMsLGkaMLG	lRQVMDGVsAMLhdVQVEGTFPDGTKLVTvHNPICRvDGDmSLALYGSFfPVPSLEsFGPAepsvdLnkqIIvvDDeN	GIeL
Py_ins	PREEDHLVLHaAGVLAQKRLARGLRLNYtEScs	ssfaMak <mark>SVAELM</mark> a <mark>LG</mark> tQl <mark>LG</mark>	RRhV1DGVAeMLDEVQVEGTFPDGTKLVTvHhPIatMDGnLeLALYGSFLPVPSaDcFP1pasvaVtrLaeAPGAVLTaDEe-	-lVL
Hy_ara	MtglPRicknLsylYnfLLcs		RRQWMDGVASiLDEVQVEGTFPDGTKLVTIHNPIAnSGCDLALALVGSFLEVPGLkVFG-AAVSKptVAPGAItTqDaD-	-IVL
Py_irr Py_iwa	MRESPREEDHEVEHAAGVEAQKREARGERENITEAVALLAT			
Ph_iwa Ph_vex	MRLSPREEDHLVLHaAGaLAOKRLARGLRLNYsEaVALLAagyrlr	IdovLevIRDGK-tVAELMTLGAOMLG		-1VL
Ph inf	MRLSPREEeHLMLHtAGaLAQKRLARGLRLNYSESVALLAT	QVLELIRDGK-tVAELMTLGAQMLG	RROVMEGVASILDEVOVEGTFPDGTKLVTIHNPISALDGDLSLALYGSFLPVPKLEVFG-aAATttaIAPGAlITgDtD-	-IVL
Ph par	MRLSPREEeHLMLHtAGaLAQKRLARGLRLNYSESVALLAT	QVLELIRDGK-tVAELMTLGAQMLG	PRQVMeGVASiLDEVQVEGTFPDGTKLVTIHNPISnLDGDLSLALYGSFLPVPkLEvFGaAATvtaIAPGAlITqDtD-	-IVL
Ph_ram	MRLSPREEDHLMLHtAGaLAQKRLARGLRLNYtESVALLAT	QVLEfIRDGK-tVAELMTLGAQMLG	PRQVMeGVASiLDEVQVEGTFPDGTKLVTIHNPISnLDGDLSLALYGSFLPVPkLEvFGspATttaVAPGAlITqDtD-	-IVL
Ph_cin			MeGVASiLDEVQVEGTFPDGTKLVTIHNPISsLDGDLSLALYGSFLPVPkLEvFGPAATtpvVAPGAlITqDaD-	-IVL
Ph_soj	MRLSPREEDHLMLHsAGfLAQKRLARGLRLNYtESVALLAT	QVLEfIRDGK-tVAELMTLGAQMLG	RRQVMeGVASiLDEVQVEGTFPDGTKLVTIHNPISsLDGDLSLALYGSFLPVPkLEvFGPAATtpaVAPGAlITqDsD-	-IVf
Py_arr	MRLSPREEDHLVLHAAGALAQKRLARGLRLNYTESVALLAT	QVLELIRDGK-SIAaLMTLGtQMLG	RRNVIDGVAGMLDEVQVEGTFPDGTKLVTIHNPIALVGDGDSLALVGSFLEVPSpDIF	TAT
Ph_tri⇒	hLSPREacHLgLHOVGrLAOVRLARGURLNVVEaVAL ism	OmmEkIRDGadSVAdLMTmGasliG	- ROUM CVALWIG VOVEATED GTKLITTINED SANGAL CHARGE HEVEN SI FLAGACHUM PGUTTAGDA	-T+i
Th pse*		OmmEMyRnGggtVsdLMsiGtOlLG	RnOVIDGVAALVTdVOVEaTFPDGTKLITVHdPIGReDGDLeLALeGSFLPVPdLsvFr-gvmvsptLpPieInavssD-	ac
Allai	NeaRKosliktTNISDRDUOUGSHYHLTECNDVLEMDRURAYCERL	AT A SCTA I REEPODEKTUST I PLOCKOVI		
Sa dec	NAGREMBLEVTNLSDRPTOVGSHTHLIECNFILEMDRGRAVGGRL	NIPSGTAVRFEPGDsk1VctVPIGGbRII	Soong in sour - Draw and a source - quadaugi is indicate source in the formation in the source is source in the source of the so	
Sa par	NAGREmRhLRvTNLSDRPIQVGSHfHLIETNP1LEMDRgRAYGqRL	NIPSGTAVRFEPGDsKlVctVPIGGhRIJ	sGGNNLAsGpV-DDSRIDAIVAslVqKGFHHaPmqliPptpptPCRMsRrnYAhTfGPTTGDIlRLGDsELliriEKDyTVYGDEC	
Ap_ast	NAGRviqrLvvkNLgDRPIQVGSHYHLIEsNPiLdMDRRlAYGHRLM	NIPaGTAVRFEPGDvKTVSIVPIrGNRII	sGGNNLAsGvV-DmksVDsIVAalVAqGFlHtPLvpSvdsvhpppCiMsRqtYArTYGPTTGDrIRLGDtaLvVhVEKDLTVYGDEC	
Ap_inv3	NgGRvpqrLvvkNmgDRPIQVGSHfHLIETNPiLdMDRRAYGHRLM	NIPAGTAVRFEPGDvKTV <mark>SI</mark> VPIGGhRVI	:sGGNNvATGpV-DQasIDgIvstlvgrGFlHtPiDptdeelqsrpPpCiMsRqtYArTYGPTTGDrIRLGDtsLvVhVEmDfTVYGDECtvlqttrmr	whfy
Ap_inv1	NgGRvpqrLvvkNmgDRPIQVGSHfHLIETNPiLdMDRRRAYGHRLM	NIPaGTAVRFEPGDvKTVSIVPIGGhRVI	sGGNNvATGpV-DQasIDgIVstlVgrGFlHtPiDptdeelqsrpPpCiMsRqtYArTYGPTTGDrIRLGDtsLvVhVEmDfTVYGDEC	
Ap_inv2	NgGRvpqrLvvkNmgDRPIQVGSHfHLIETNPiLdMDRRRAYGHRL	11PaGTAVRFEPGDvKTVSIVPIGGhRVI	sGGNNvATGpV-DQasIDgIVstlVgrGFIHtPiDptdeelgsrpPpCIMsRqtYArTYGPTTGDrIRLGDtsLvVhVEmDfTVYGDEC	
Py_ins	NGSRUPRALEITNLTDRPIQVGSHIHLIEANPILEMDRKRAIGYRL	MIPSGTAVRFEPGDRKTVSTVPIGGNRVI	TGGNNLASGVU-DVaaadAlvAKAVeKGFHAPMVVSSeedarnalam-VCKMPKSVIAQTIGPTIGDVNLGDMELVULIEDMTVIGDEC	
Py irr	NAGREAGALOTTNLTDRPTOVGSHYHLTETNPYLEMDRK AVGHRL	NIPSGTAVRFEPGDOKTVSTVPIGGkgTI	TGGNNLATGV-DESKVDATVASAVVKGFHKPLDVS11Pany11PaFnTCKMPRSVAOTfGPTGDVRLGDMELFVSVEKDMTVGDEC	
Py_iwa	NAnRtaqvLQvTNLtDRPIQVGSHYHLIETNPYLEMDRKRAYGHRL	NIPSGTAVRFEPGDQKTVSIVPIGGkaVI	TGGNNLATGKV-DtSKVDAIVAGAVeKGFHHKPLDvS11Psnv11PsFnVCKMPRSVYAQTfGPTTGDVVRLGDMELFVsVEKDLTVYGDEC	
Ph_vex	NAGREpRvLQITNLtDRPIQVGSHYHLIETNPYLEMDRK1AYGHRL	NIASGTAVRFEPGDQKTVSIVPIAGkkIJ	TGGNNLASGVV-DESKVDAIVAKAVSqGFHHKPLDlaalpasakqagFGICKiPRSVYAQTYGPTTGDVIRLGDMELFVaVEKDMTVYGDEC	
Ph_inf	NeGRKaRvLQITNLSDRPIQVGSHYHLIEaNPYLEMDRKlAYGHRLM	NIaaGTAVRFEPGDQKTVSIVPIAGNKVI	TGGNNLATGvV-DESKVDAIVAKAVAeGFHHReLelStlPrhvtkPeFGVCKMPRSVYAQTYGPTTGDVVRLGDMELYVaVEKDMTVYGDEC	
Ph_par	NeGRKaRvLQITNLSDRPIQVGSHYHLIEaNPYLEMDRK1AYGHRLM	MIaaGTAVRFEPGDQKTVSIVPIaGNkVI	TGGNNLATGvV-DESKVDAIVAKAVAeGFHHReLelStlPrhvtkPeFGVCKMPRSVYAQTYGPTTGDVVRLGDMELYVaVEKDMTVYGDEC	
Ph_ram	NAGREERVLQITNLSDRPIQVGSHYHLIEANPYLEMDRKVAYGHRLM	ALASGTAVKTEPGDQKTVSIVPIAGNKVI	TGGNNLATGKY-DETKVVAIVAKAVAGGHHKVLDIAKIPSNVLJPGGICKMPRSVAQTGGPTCGVVRLGOMELZVAVEKOMTVGGDC	
Ph_Cin	NAGRKARVLQITNLSDRPIQVGSHYHLIETNPYLEMDRKIAYGHRLM	MIASGTAVRFEPGDQKTVSIVPIAGNKVI	I GUNNERBOY V DE DRYVAI V LAVAGOF HIRGEDI I SKI PSINT GYCHEGI CKMPRSVIAGT I GUTTGUVKIGDMEL I VAVEKUMTVY GDEC	
Pv arr	DITNLSDRPIOVGSHYHLIETNPYLEMDRyRAYGmRL	NIASGTAVRFEPGDCKTVGVVPIGGkgVI	TGGNNLATGY-DBARVDATVAKAVAKGFHIKPmDdalggslrs-altVCKMPRSVAOTYGPTGDrVRIGDMaIVV+VEKDfTVYGPEC	
Py aph	NAdRDisvLQITNLSDRPIQVGSHYHLIETNPYLEMDRKRAYGVRL	NIPSGTAVRFEPGDpKTVSVVPIGGkqII	sGGNqLATGqV-DqSKaDAvVsaAVAKGFrHKPmDdalqqslra-avtkCtMPRSVYAQTYGPTTGDVlRLGDMELYvtVEKDfTVYGDEC	
Ph_tri*	NAnRElieLsvTNtgDRPIQVGSHYafvETNkaLsfDRsasiGkRLM	NvPSGasVRFEPGeRKTVtlcalGGigrv	vvsGNrLtdGdarDpaRhaAIleRvtSqGFqHEPvDpadiPkgrayvMeRSsYAdmYGPTvGDrIaLGDtgLvVrVErDyTVYGDEC	
Th_pse*	peGphlveipvTNtgDRPIQVGSHYpflETNaaLvfDRKaAlGrRLM	NvPSGasVRFEPGetKTVtlVnlGGkRnv	vvcGNgLtaGva-DgdRwgeIekRmeeKG-gfgnvssakvPegkpyvltRSaYsdaYGPTTGDrVRLGDtsLiariqaDhThYGDEC	
Al_lai	KFGGGKVLREGMGQnTGtgADeaLeTIITNALvlD-YTGIYK	ADIG1KDGrIvGIGKGGNPDVMDGVg	aNI IVGVsTEVIAGEGLILTAGGvDAHVHFICPQLCvEALASGLTTLIGGGTGPATGTKATTCTPGPNHiKMMLQATDTIPINIGLTGKGNsshPl-	GLQn
Sa_dec	KFGGGKVLREGMGQATGrcAadVLDTvITNvvIVD-YsGIYK/	ADvGIKhGrISaIGKaGNPDVMDGVd	PNMviGVNTEalAGrdLlLTAGGvDtHVHFICPQLCeEALASGLTTLVGGGTGPATGTkATTCTPhPdHlqsMLrATDgiPiNvGLTGKGNsAsht-	GLQD
Sa_par	KFGGGKVLREGMGQATGrcANdVLDTvITNvvIVD-YsGIYKA	ADvGIKhGrIwaIGKaGNPDVMDGVd	$- \verb"PNMviGVNTEalAGrdLlLTAGGvDtHVHFICPQveyhgdErshSGLTTLVGGGTGPATGTkATTCTPhPdHlrsMLrATDgiPiNvGLTGKGNsAsht-$	GLQD
Ap_ast	KFGGGKVLREGMGQATGrnAlQVLDTvITNAvIID-YTGvYK	ADIGIKhGVIwaIGKaGNPDVMDGVh	-dNMIVGVNTEVIAGEGLvvTAGGvbtHVHFICPQLCdEAisSGLTsLVGGGTGPATGTKATTCTPhPdHvrTMLQATDTFPINIGLTGKGNSAsPv-	GLQD
Ap_inv3	ISVGKFGGGKVLREGMGQATGChADQVLDTVITNAVIVD-YTGVYK	ADIGIKNGVIWAIGKAGNPDVMDGVQ	- addwydynteu i Aceglywfagdul Hyfric Pol fabai ssol fflygg Gfepargi xaffraff rffran fran yw can berne yw can a can	GLQD
Ap inv2	KFGGGKVLREGMGQATGChADQVLDTV1TNAVIVD-YTGVK	ADIGIKIGVIWAIGKAGNPDVMDGVQ	- ddwydynreu aceciwraego chwr i cryw - fdeai seciwr weder ar charffor ar chwr ar chwr ar chwr ar can a carffer ar car a carffer a carffer a carffer ar carffer a	GLOD
Py ins	KxGGGKVLREGMGQASGlaAgOVLDTIITNALID-YTGIYK	ADIGIKDGLIAGIGKGGNPDVMDGV1	- PNMIVGVNTEVIAGEGLIVTAGGEDAWHFICPOLCTEALASGLTTLVGGGTGPATGTNATCTPGPAHMKLM.OATDVIPINIGITGKGNTSmPE	GLOD
Hy_ara	KFGGGKaiREGMGQAsGktsDQVvDTIITNALIVD-cTGIYK	ADvGIKndLIvsIGKGGNPDVlaGVt	Pdl ivgvnteviagegliltaggfdahvhficpol CTEALASGLTTLVGGGTGPATGTkATTCTPGPNHvKLMLQATDviPMNigLTcKGNTAlpo-	GLQD
Py_irr	KFGGGKVLREGMGQvsGvgsDkVLDTIITNALIVD-YTGIYK/	ADIGIKDGLIAGIGKGGNPDVMnGVm	dNMvVGVNTEVIAGEGLIvTAGGFDAHVHFICPQLCTEALASGLTTLVGGGTGPATGTNATTCTPGPNHMKLMLQATDSfPMNIGLTGKGNTAmPE-	GLQD
Py_iwa	KFGGGKVLREGMGQAsGvgsEgVLDTIITNALIID-YsGIYK/	ADIGIKDGLIAGIGKGGNPDVMDGVm		GLQD
Ph_vex	KFGGGKVLREGMGQAsGvgskQVLDTIITNALIVD-YTGIYKA	ADvGmKDGLIAGIGKGGNPDVMeGVm		GLQD
Ph_inf	KFGGGKVLREGMGQAsGrnsaQVvDTIITNALIVD-YTGIYK	ADVGIKDGLIAGIGKGGNPDVMeGV1	-PdlIVGVNTEVIAGEGLILTAGGFDAHVHFICPQLCTEALSGLTTLVGGGTGPATGTNATTCTPGPNHIKMMLQATDStPMNIGLTSKGNTSIPE-	GLQD
Ph_par Ph_ram	KFGGGKVLREGMGQASGFHSaQVVDTIITNALIVD-ITGIIKA	ADVGINDGLIAGIGKGGNPDVMeGVI	- PGLIVGVIDVIAGGGLIFFAGGPDARVNFICPQLCIDALSGGLIFFAGINATICIPGPNILMALQATDSCPMNIGLISAGANSIF DNI TUGVIDVIAGGLIFFAGGPDARVNFICPQLCADALSGGLAFTUGGGTGPAGINATTCIPGPNILMALQATDSCPMNIGLISAGAN	GLOD
Ph cin	KFGGGKVLREGMGQASGKtSaQVVDTIITNALVVD-YTGIYK/	ADVGIKDGLIAGIGKGGNPDVMeGVV	-PNITVGVNTEVIAGEGLILTAGGEDAHVHFICPOLCTEALASGLTTLVGGGTGPATGTNATTCTPGPNHMKLMLOATDSSPMNIGLTSKGNTAIPE-	GLOD
Ph soj	KFGGGKVLREGMGQAsGktsaQVvDTIITNALvVD-YTGIYK	ADVGIKDGLIAGIGKGGNPDVMeGVm		GLQD
Py_arr	KFGGGKVLREGMGQtTGrvADQVLDTIITNALIVD-YTGIYK	ADIG1KnGLItGIGKGGNPDVMDGVm		GLQD
Pv aph			PNMIVGVNTEVIAGEGLIVTAGGFDAHVHFICPOL aTEALASGLTTLVGGGTGPATGTNATTCTPGPNHMKMMLOATDS i PinvGLTGKGNTASPE-	
- 1	KFGGGKVLREGMGQATGlfAhQVLDTIITNALIID-YsGIYK	ADIGIKnGIIAGIGKGGNPDVMDGVm		GLQD
Ph_tri*	KFGGGKVLREGMGQATG1fAhQVLDTIITNALIID-YsGIYK KFGGGKtLREGMGQATGptsDdaLDvvITNALIIDpciGIvK	ADIGIKnG <mark>IIAG</mark> IGK <mark>G</mark> GNPDVMDGVm ADVGIKgtsIVGIGKaGNPDmMDGVt	$- PNMIVGntdVIAGEkLILTAGGIDtHVHyICPQqieEAisSGvTTmfGGGTGPsaGs\texttt{NATTCTPaPsqveIMLkATDkyPlNfGfsGKGNTsdtKPNMIVGntdVIAGEkLILTAGGIDtHVHyICPQqieEAisSGvTTmfGGGTGPsaGs\texttt{NATTCTPaPsqveIMLkATDkyPlNfGfsGKGNTsdtKPNMIVGntdVIAGEkLILTAGGIDtHVHyICPQqieEAisSGvTTmfGGGTGPsaGs\texttt{NATTCTPaPsqveIMLkATDkyPlNfGfsGKGNTsdtK$	GLQD aLen
Ph_tri* Th_pse*	KFGGGKVLREGMGQATG1fAhQVLDTIITNALIID-YSGIYK KFGGGKtLREGMGQATGptsDdaLDvvITNALIIDpciGIvK KFGGGKsLREGMGQmTsvsAslaLDcvITNAmIIDaklGIiK	ADIGIKnG <mark>IIAG</mark> IGKGGNPDVMDGVm ADvGIKgtsIv <mark>G</mark> IGKaGNPDmMDGVt ADIGIKgnkIhnIGKaGNPDtMnGVtltp	PNNIVGntTdVIAGEkLILTAGGIDtHVHyICPQqieEAisSGvTTmfGGGTGPsaGsNATTCTPaPsqveIMLkATDkyPlNfGfsGKGNTsdtK- gkeMIVGatTdVIAGEkmIvTAGGvDtHiHFICPQqCdEAi <mark>a</mark> SGvTTmfGGGTGPsaGTsATTCTPGPgHve <mark>M</mark> MLrATDdlPlNfGfs <mark>G</mark> KGNTsdPnt	GLQD aLen siiD
Ph_tri* Th_pse*	KFGGGKULREGMGQATGJfAhQVLDTITTNALIID-YsGIYK. KFGGGKLLREGMGQATGptsDdaLDvvITNALIIDpciGIVKI KFGGGKSLREGMGQmTsvsAslaLDcvITNAmIIDaklGIKJ	ADIGIKnGIIAGIGKGGNPDVMDGVm ADVGIKgtsIv <mark>GIGKaGNPDmMDGVt ADIGIKgnkIhnIGKaGNPDtMnGVtltp</mark>	PNMIVGntTdVIAGEkLILTAGGIDtHVHyICPQqieEAisSGvTTmfGGGTGPsaGsNATTCTPaPsqveIMLkATDkyPlNfGfsGKGNTsdtK- gkeMIVGatTdVIAGEkmIvTAGGvDtHiHFICPQqCdEAiASGvTTmfGGGTGPsaGTsATTCTPGPgHveMMLrATDdlPlNfGfsGKGNTsdPnt	GLQD aLen siiD
Ph_tri* Th_pse* Al_lai	KFGGKVLREGMGQATGIFADULDTIITNALIID-YGGIYK 	ADIGIKNGIIAGIGKGGNPDVMDGVm ADVGIKgtsIVGIGKAGNPDmMDGVt ADIGIKgnkIhnIGKAGNPDtMnGVtltp YCVEHTIAAFKGRTIHTYHSEGAGGGHAP	PNMIVGntTdVIAGEkLILTAGGIDtHVHYICPQqieEAisSGvTTmfGGGTGPsaGSNATTCTPaPsqveIMLkATDkyPlNfGfsGKGNTsdtK- gkeHIVGatTdVIAGEkmIvTAGGvDtHiHFICPQqCdEAiASGvTTmfGGGTGPsaGTsATTCTPGPgHveMMLrATDdlPlNfGfsGKGNTsdPnt PDIIsVCGEsNiLPSSTNPTRPfTvNTIDEHVDMLMVCHHLDrNIAEDVAFAESRIRaETIAAEDvLHDMGAISIISSDSQAMGRIGEVITRTWQTADKMKG	GLQD aLen siiD
Ph_tri* Th_pse* Al_lai Sa_dec	KFGGKVLREGMGQATGIFADULDTIITNALILD-YGGIYK KFGGKVLREGMGQATGIFADALDVITNALILD-YGGIYK KFGGKSLREGMGQMTSVSÅSIALDCVITNAMIIDAkIGIKU VVDAGAVGIKLHEDVGTTPALIDqCLUVAENDIQVTIHTDTLNESS IIDAGAVGIKLHEDVGTTPALIDALEVAEINDVQVTIHTDTLNESS	ADIGIKnGIIAGIGKGGNPDVMDGVm ADVGIKgtsIVGIGKAGNPDmMDGVt ADIGIKgnkIhnIGKaGNPDtMnGVtltp ICVEHTIAAFKGRTIHTYHSEGAGGGHAP	PNMIVGntTdvIAGEkLILTAGGIDtHVHyICPQqieEAisSGvTTmfGGGTGPsaGSNATTCTPaPsqveIMLkATDkyPlNfGfsGKGNTsdtk- gkeMIVGatTdVIAGEkmIvTAGGvDtHiHFICPQqCdEAiASGvTTmfGGGTGPsaGTsATTCTPGPgHveMMLrATDdlPlNfGfsGKGNTsdPnt vDIIsVCGEsNiLPSSTNPTRPfTvNTIDEHVDMLMVCHHLDrNIAEDVAFAESRIRGETIAAEDvLHDMGAISIISSDSQAMGRIGEVITRTWQTADKMK vDIITVCGEINVLPSSTNPTRPfTKNTIEHVDMLMVCHHLDKNIAEDVAFAESRIRGETIAAEDiLHDMGAISIISSDaQAMGRIGEVITRTWQTADKMK	GLQD aLen siiD (ERGC QRGP
Ph_tri* Th_pse* Al_lai Sa_dec Sa_par Ap_ast	KFGGKVLREGMGQATGIFAhQUDTIITNADIID-YGGIYK, KFGGKLREGMGQATGIFADGLOVITNADIIDaklGIKU KFGGKSLREGMGQmTsvsäslalDcvITNADIIDaklGIKU vvDAGAVGIKLHEDWGTTPATIAGLCLVAdENDIQVTIHTDTLNESS iIDAGAVGIKLHEDWGTTPATIAGLEVAENDVQVTIHTDTLNESS iDAGAVGIKLHEDWGTTPATIAGLEVAENDVQVTIHTDTLNESS	ADICIENCIIACIENCONPOYNDOWD- ADVGIKgsSIVGIGKAGNPDmhDGVL ADVGIKgnklniGKaGNPDtMnGVlt; SCVEHTIAFKGRTIHTYHSEGAGGGHAP SCVEHTIAFGRTIHTYHSEGAGGGHAP SCVEHTIAFKGRTIHTYHSEGAGGGHAP	PMIVGntTdVIAGELLIITAGGIDHUHYICPQiGEAISSGYTTMIGGGGGBAGENATTCTPBPGUVENLAATDKYBINGISGKGGBAG NgkeMIVGatTdVIAGEkmIvTAGGVDHIHFICPQCGEAIASGVTTMIGGGGBSAGTSATTCTFGGPUVENLAATDKYBINGISGKGGNTAGTA PDIISVCGENILPSSTNPTRFTVNTIGEHUDHUVCHHLDVAFASRIRAETIAAEDVLHDMGAISIISSDSQAMGRIGEVITRTWOTADKMK PDIITVCGELNUPSSTNPTRFTRNTIGEHUDHLWVCHHLDNIAEDVAFASRIRGETIAAEDLLHDMGAISIISSDSQAMGRIGEVITRTWOTADKMK PDIITVCGGLNUPSSTNPTRFTRNTIGEHUDHLWVCHHLDNIAEDVAFASRIRGETIAAEDLLHDMGAISIISDSQAMGRIGEVITRTWOTADKMK PDIITVCGGLNUPSSTNPTRFTRNTIGEHUDHLWVCHHLDNIAEDVAFASRIRGETIAAEDLLHDMGAISIISSDSQAMGRIGEVITRTWOTADKMK	GLQD aLen siiD (ERGc QRGp QRGp
Ph_tri* Th_pse* Al_lai Sa_dec Sa_par Ap_ast Ap_inv3		ADIGIKnGIIAGIGKOGNPDWDGVm ADVGIKgtsIVGIGKAGNPDmWDGVL ADIGIKgnkInnIGKAGNPDMMGVLLT SCVEHTIAFKGTIHTYHSEGAGGGHAP SCVEHTIAFgnRTIHTYHSEGAGGGHAP SCVEHTIAFgnRTIHTYHSEGAGGGHAP SCVEHTIAFGNRTIHTYHSEGAGGGHAP	PNMIVGntTdVIAGEkLILTAGGIDtHVHyTCPQqieEAisSGvTTmfGGGTGPsaGSNATTCTPaPsqveIMLkATDkyPlNfGfsGKGNTsdtK- gckHIVGatTdVIAGEkLILTAGGIDtHUHJTCPQqCGBAISGCVTmfGGGTGPsaGTsATTCTFGGHveMMLrTDdIPlNff5GKGNTsdTh DIIsVCGESNILPSSTNPTRFTwTIDEHVDMLMVCHHLDTNIAEDVAFAESRIRGETIAAEDLHDMGAISIISSDSQAMGRIGEVITRTWQTADKMK DIIIVCGELMUPSSTNPTRFTRMTiGEHVDMLWCHHLDRNIAEDVAFAESRIRGETIAAEDLLDMGAISIISSDSQAMGRIGEVITRTWQTADKMK DIIIVCGELMUPSSTNPTRFTRMTiGEHVDMLWCHHLDRNIAEDVAFAESRIRGETIAAEDLLDMGAISIISSDSQAMGRIGEVITRTWQTADKMK DIIIVCCGELMUPSSTNPTRFTRMTiGEHVDMLWCHHLDKSIAEDVAFAESRIRGETIAAEDLLDMGAISIISSDSQAMGRIGEVITRTWQTADKMK DIIIVCCGELMUPSSTNPTRFTRMTiGEHVDMLWCHHLDKSIAEDVAFAESRIRGETIAAEDLLDMGAISIISSDSQAMGRIGEVITRTWQTADKMK DIIIVCCGELMUPSSTNPTRFTRMTIGEHVDMLWCHHLDKSIAEDVAFAESRIRGETIAAEDLLDMGAISIISSDSQAMGRIGEVITRTWQTADKMK	GLQD aLen ssiiD (ERGC QRGp QRGp QRGf QRGf
Ph_tri* Th_pse* Al_lai Sa_dec Sa_par Ap_ast Ap_inv3 Ap_inv1		ADICIENCIIAGICKONPONNDCVM ADVGIKGLEIVGIGKAGNPDMNDGVU ADVGIKGLEINGKAGNPDMNDVLUE SCVEHTIAAFGRIHTYHSEGAGGGHAF SCVEHTIAAFGRIHTYHSEGAGGGHAF SCVEHTIAAFGRIHTYHSEGAGGGHAF ICVEGTIAAFGRIHTYHSEGAGGGGHAF	PNMIVGntTdVIAGEkLILTAGGIDtHVHyICPQqieEAisSGvTTmfGGGTGPsaGSNATTCTPaPsqveIMLkATDkyPlNfGfsGKGNTsdtk- gkeHIVGatTdVIAGEkmIvTAGGvDtHiHFICPQqCdEAiASGvTmfGGGTGPsaGTsATTCTPGPgHveMMLrATDdlPlNfGfsGKGNTsdtk- PDIISVCGEhVLPSSTNPTRPfTvNTIDEHVDMLMVCHHLDrNIAEDVAFAESRIRGETIAAEDLLHDMGAISIISSDSQAMGRIGEVITRTWGTADKMK PDIITVCGELNUPSSTNPTRFTKNTiEHVDMLMVCHHLDKNIAEDVAFAESRIRGETIAAEDLLHDMGAISIISSDSQAMGRIGEVITRTWGTADKMK PDIITVCGELNUPSSTNPTRFTKNTiEHVDMLMVCHHLDKSIAEDVAFAESRIRGETIAAEDLLHDMGAISIISSDSQAMGRIGEVITRTWGTADKMK PDIITVCGELNUPSSTNPTRFTKNTiEHVDMLMVCHHLDKSIAEDVAFAESRIRGETIAAEDLLHDMGAISIISSDSQAMGRIGEVITRTWGTADKMK PDIITVCGELNUPSSTNPTRFTKNTiEHVDMLMVCHHLDKSIAEDVAFAESRIRGETIAAEDLLHDMGAISIISSDSQAMGRIGEVITRTWGTADKMK PDIITVCGELNUPSSTNPTRFTNTIEHVDMLMVCHHLDKSIAEDVAFAESRIRGETIAAEDLLHDMGAISIISSDSQAMGRIGEVITRTWGTADKMK PDIITVCGELNUPSSTNPTRFTvNTIEHVDMLMVCHHLDKSIAEDVAFAESRIRGETIAAEDLLHDGAISIISSDSQAMGRIGEVITRTWGTADKMK	GLQD aLen siiD (ERGC QRGp QRGp QRGf QRGf QRGf
Al_lai Sa_dec Sa_par Ap_ast Ap_inv3 Ap_inv1 Ap_inv2		ADIGIENGIIAGIKOGUNPOWNDOWn ADVGIEGSIVGIGEAGNPOWNDGV SOUGHENATHAIGEAGNEPUNGVILU SOUGHENAAFGRTIHTYHSEGAGGGHAF SOUGHENAAFGRTIHTYHSEGAGGGHAF SOUGHENAAFGRTIHTYHSEGAGGGHAF SOUGHIAAFGRTIHTYHSEGAGGGHAF SOUGTIAAFGRTIHTYHSEGAGGGHAF	PMIYUQnETQVIACEKLIIFAGGIDEHUHYICPQqiGEAISSGVTTmfGGGTGBSGESMATTCTPBPGUPEMLATDKYBIHfGfSGKGNTSdtE sgkeMIYGGLTAVIAGEkmIvTAGGVDEHIHFICPQqCGEAIASGVTTmfGGGTGBSGTSATTCTFGGPHveMmLaTDdlPlhfGfSGKGNTSdEn DIISVCGENILPSSTNPTRFTVNTIGEHUMLHVCHHLDRNIAEDVAFAESRIRGETIAAEDLHDWGAISIISSDSQAMGRIGEVITRTWQTADKHK DIITVCGELMULPSSTNPTRFTKNTIGEHUMLHVCHHLDRNIAEDVAFAESRIRGETIAAEDLHDWGAISIISSDSQAMGRIGEVITRTWQTADKHK DIITVCGELMULPSSTNPTRFTKNTIGEHUMLHVCHHLDRNIAEDVAFAESRIRGETIAAEDLHDWGAISIISSDSQAMGRIGEVITRTWQTADKHK DIITVCGELMULPSSTNPTRFTNNTIGEHUMLHVCHHLDRNIAEDVAFAESRIRGETIAAEDLHDWGAISIISSDSQAMGRIGEVITRTWQTADKHK DIITVCGELMVLPSSTNPTRFTNNTIGEHUMLHVCHHLDRSIAEDVAFAESRIRGETIAAEDLHDWGAISIISSDSQAMGRIGEVITRTWQTADKHK DIITVCGELMVLPSSTNPTRFTNTIGEHUMLHVCHHLDRSIAEDVAFAESRIRGETIAAEDLHDUGAISIISSDSQAMGRIGEVITRTWQTADKHK DIITVCGELMVLPSSTNPTRFTNTIGEHUMLHVCHHLDRSIAEDVAFAESRIRGETIAAEDLHDUGAISIISSDSQAMGRIGEVITRTWQTADKHK DIITVCGELMVLPSSTNPTRFTVNTIGEHUMLHVCHHLDRSIAEDVAFAESRIRGETIAAEDLHDUGAISIISSDSQAMGRIGEVITRTWQTADKHK DIITVCGELMVLPSSTNPTRFTVNTIGEHUMLHVCHHLDRSIAEDVAFAESRIRGETIAAEDLHDUGAISIISSDSQAMGRIGEVITRTWQTADKHK	GLQD aLen siiD (ERGC QRGp QRGf QRGf QRGf QRGf QRGf
Al_lai Sa_dec Sa_par Ap_ast Ap_inv3 Ap_inv1 Ap_inv2 Py_ins		ADATOLINGTIAGISKONPDYNDCYm ADIGIKGUSKONPDYNDCYL ADIGIKGNLINIGKAGNPDHNGYLL SCVEHTIARFGRTIHTYHSEGAGGGHAF SCVEHTIARFGRTIHTYHSEGAGGGHAF SCVEHTIARFGRTIHTYHSEGAGGGHAF SCVEGTIARGNRTIHTYHSEGAGGGHAF SCVEGTIARGNRTIHTYHSEGAGGGHAF SCVEGTIARGNRTIHTYHSEGAGGGHAF SCVEGTIARGRNTIHTYHSEGAGGGHAF	PMHIVGntTdVIAGEkLILTAGGIDtHVHyTCPQqieEAisGGvTfmfGGGrGPsaGsNATTCTPaPsqveTMLkATDkyPlNfGfsGKGNTsdtK- ggkHIVGatTdVIAGEkLILTAGGIDtHUHJTCPQqCGRAigGGvTmfGGGrGPsaGsNATTCTPaPsqveTMLkATDkyPlNfGfsGKGNTsdtK- DIIsVGGENLPSSTNPTRPfTWTIDHVDNLNVCHHLDRNIAEDVAFAESRIRGETIAAEDLHDMGAISIISSDGAMGRIGGVITRTWQTADKNK DDIITVCGELNUPSSTNPTRPfTWTIGHUDNLNVCHHLDRNIAEDVAFAESRIRGETIAAEDLLDMGAISIISSDGAMGRIGGVITRTWQTADKNK DDIITVCGELNUPSSTNPTRPfTWTIGHUDNLNVCHHLDRNIAEDVAFAESRIRGETIAAEDLLDMGAISIISSDGAMGRIGGVITRTWQTADKNK DDIITVCGELNUPSSTNPTRPfTWTIGHUDNLNVCHHLDRNIAEDVAFAESRIRGETIAAEDLLDMGAISIISSDGAMGRIGGVITRTWQTADKNK DDIITVCGELNUPSSTNPTRPfTWTIGHUDNLNVCHHLDRNIAEDVAFAESRIRGETIAAEDLLDMGAISIISSDGAMGRIGGVITRTWQTADKNK DDIITVCGELNUPSSTNPTRPfTWTIGHUDNLAVCHHLDRNIAEDVAFAESRIRGETIAAEDLLDIGAISIISSDGAMGRIGGVITRTWQTADKNK DDIITVCGELNUPSSTNPTRFTWTIGHUDNLAVCHHLDRNIAEDVAFAESRIRGETIAAEDLLDIGAISIISSDGAMGRIGGVITRTWQTADKNK DDIITVCGELNUPSSTNPTRFTWTIGHUDNLAVCHHLDRNIAEDVAFAESRIRGETIAAEDLLDIGAISIISSDGAMGRIGGVITRTWQTADKNK DDIITVCGELNUPSSTNPTRFTWTIGHUDNLAVCHHLDRNIAEDVAFAESRIRGETIAAEDLLDIGAISIISSDGAMGRIGGVUTRTWQTADKNK DDIITVCGELNUPSSTNPTRFTWTIGHUDNLAVCHHLDRNIAEDVAFAESRIRGETIAAEDLLDIGAISIISSDGAMGRIGGVUTRTWQTADKNK DDIITVCGELNUPSSTNPTRFTWTIGHUDNLAVCHHLDRNIAEDVAFAESRIRGETIAAEDLLDIGAISIISSDGAMGRIGGVUTRTWQTADKNK DDIITVCGELNUPSSTNPTRFTWTIGHUDNLAVCHHLDRNIAEDVAFAESRIRGETIAAEDLLDIGAISIISSDGAMGRIGVUTRTWQTADKKK	GLQD aLen siiD (ERGc QRGp QRGp QRGf QRGf QRGf QRGf ERGp
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Ph_tri* Th_pse* Al_lai Sa_dec Sa_par Ap_st Ap_inv2 Py_ins Hy_ara Ph_var Ph_var Ph_var Ph_par Ph_ram Ph_cin Ph_soj Py_art Ph_tri* Th_pse* Al_lai Sa_dec Sa_par	KFGGGKULREGMGQATGIFAhQUDFIITMADIID-YSGIYK KFGGGKULREGMGQATGIFAHQUDFIITMADIID-YSGIYK 	ADICIENCITACIGNOPUNDOVM ADICIESCONTONIC CARGANDPUNDOVL ADICIESCONTACESCONTONIC CARGANDUNDOVL ADICIESCONTACESCONTONIC CARGANDIA SCVENTIARENTINYISSECAGGGHAI SCVENTIARENTIARENTINYISSECAGGGHAI SCVENTIARENTIARENTINYISSECAGGGHAI SCVENTARENTIARENTINYISSECAGGGHAI SCVENTARENTIARENTINYISSECAGGGHAI SCVENTARENTIARENTIARENTINYISSECAGGGHAI SCVENTARENTIARENTARENTIARENTIARENTIARENTIARENTARENTIARENTIARENTIARENTIARENTIARENTIARENTIARENTIARENTIARENTIARENTIARENTIARENTIARENTIARENTIARENTARENTIARENTIARENTIARENTARENTARENTIARENTIARENTARENTARENTARENTARENTARENTARENTARENT	PMIYUQnETQVIAGEKLIIFAGGIOHUHYICOPQGEAISSGVTTMEGGGGBSGENATTCTPB9QHVEMLATDKYIHEGESGKGNSdEK gkeMIYGGLTQVIAGEKUIVTAGGVDHIHFICPQGEAISSGVTTMEGGGGBSGGTAATTCTFG9QHVEMLTATDdIPINEGFSGKGNSdER DIISVGGENLDESSTNPTRFTSWTIEHUHVCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DDIIVGGELNUESSTNPTRFTSWTIEHUHVLMUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIIVGGELNUESSTNPTRFTSWTIEHUHVLMUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIIVGGELNUESSTNPTRFTSWTIEHUHVLMUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIIVGGELNUESSTNPTRFTSWTIEHUHVLMUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIIVGGELNUESSTNPTRFTSWTIEHUHVLMUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIIVGGELNUESSTNPTRFTSWTIEHUHVLMUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIIVGGELNUESSTNPTRFTSWTIEHUHVLMUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIIVGGELNUESSTNPTRFTSWTIEHUHVLMUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIIVGGENUESSTNPTRFTSWTIENTIDHUVMLWUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIVVGGENUESSTNPTRFTSWTIENTIDHUVMLWUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIVVGGENUESSTNPTRFTSNTIDHUVMLWUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIVVGGENUESSTNPTRFTSNTIDHUVMLWUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIVVGGENVLPSSTNPTRFTSNTIDHUVMLWUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIVVGGENVLPSSTNPTRFTSNTIDHUVMLWUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIVVGGENVLPSSTNPTRFTSNTIDHUVMLWUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIVVGGENVLPSSTNPTRFTSNTIDHUVMLWUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIVVGGENVLPSSTNPTRFTRNTIDHUVMLWUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIIVUGGENVLPSSTNPTRFTRNTIDHUVMLWUCHHLDRVIAEVAFASSNIRGETIAAEDLIADGAISIISSDSQAMGRIGSVTRTWQTAAKKK DIIVUGGENVLPSSTNPTRFTRNTIDHUVMLWUCHHLDRVIAEV	GLQD aaLen aaLen aaLen QRGp QRGp QRGf QRGf QRGf QRGf QRGf LERGt LIYG1 EIG1 EIG1 EIG1 EIG1 EIG1 EIG1 EIG1 EI
Ph_tri* Th_pse* Al_lai Sa_dec Sa_par Ap_ast Ap_inv1 Ap_inv2 Py_iva Py_iva Ph_inf Ph_ar Ph_inf Ph_ar Ph_rar Ph_soi Py_ar Py_arr Py_ar Py_ar Py_ar Ph_se* Al_lai Sa_dec Sa_par		ADICIENCITACIGNEDVENDEVM- ADICIENCIENCIENCE ADICIENCIENCIENCE SCVEHTIAAFKGRTIHTYHSEGAGGGHAI SCVEHTIAAFGNTIHTYHSEGAGGGHAI SCVEHTIAAFGNTIHTYHSEGAGGGHAI SCVEHTIAAFGNTIHTYHSEGAGGGHAI SCVENTIAAFGNTIHTYHSEGAGGGHAI SCVENTIAFGNTIHTYHSEGAGGGHAI SCVENTIAFKGRTHYHYHSEGAGGGHAI SCVENTIAFKGRTHYHYHSEGAGGGHAI SCVENTIAFKGRTHYHYHSEGAGGGHAI SCVENTIAFKGRTHYHYHSEGAGGGHAI SCVENTIAFKGRTHYHYHFUN SCUENTAFKGRTHYHYHFUN SCUENTAFKGRTHYHYHFUN SCUENTAFKGRTHYHYHFUN SCUENTAFKGRTHYHYHFUN SCUENTAFKGRTHYHYHFUN SCUENTAFKGRTHYHYHFUN SCUENTAFKGRTHYHYHFUN SCUENTAFKGRTHYHYHFUN SCUENTAFKGRTHYHYHFUN SCUENTAFKGRTHYHYHFUN SCUENTAFKGRTHYHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHFUN SCUENTAFKGRTHYHF	PMIYQntTqVIACELLIFAGGUPHW9YCCPQGEAISSGVTTMEGGGGPSaGSNATTCTPB9QWFMLATDV9HEGESGKGNSdtg gkeMIYGatTdVIAGEkulIFAGGVDtHIHFICPQqGEAISSGVTTMEGGGGPSaGSNATTCTFGPgHveMLrATDdHPHEGFSGKGNSdtPh DIISVGEBNILPSSTNPTRFTVNTIDHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIIVCGELNUPSSTNPTRFTVNTIGHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIIVCGELNUPSSTNPTRFTVNTIGHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIIVCGELNUPSSTNPTRFTVNTIGHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIIVCGELNUPSSTNPTRFTVNTIGHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIIVCGELNUPSSTNPTRFTVNTIGHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIIVCGELNUPSSTNPTRFTVNTIGHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIIVCGELNUPSSTNPTRFTVNTIGHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIIVCGELNUPSSTNPTRFTVNTIDHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIIVCGELNUPSSTNPTRFTVNTIDHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIIVCCELNUPSSTNPTRFTVNTIDHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIVVCCELNUPSSTNPTRFTNTDIDHVDHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIVVCCELNUPSSTNPTRFTRNTDHUDHUWHLHDLNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKHK DDIVVCCELNUPSSTNPTRFTRNTDHUDHUWHLHDLNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKKK DDIVVCCELNUPSSTNPTRFTRNTDHUDHUWHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKKK DDIVVCCELNUPSSTNPTRFTRNTDHUDHUWHLWCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKKK DDIVVCCELNUPSSTNPTRFTRNTDHUNHWUCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKKK DDIVVCCELNUPSSTNPTRFTRNTDHUDHUMUKUCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKKK DDIVVCCELNUPSSTNPTRFTRNTDHUDHUMUKUCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISIISDSQAMGRIGEVTRTWGTADKKK DDIVVCCELNUPSSTNPTRFTRNTDHUDHUMUKUCHHLDNIAEUAPAESRIRGETIAAEDLHDWGAISISSDAMGRIGEVVPRTW	GLQD aLen aLen SilD CRGp QRGp QRGf QRGf QRGf LRGP QRGf LRGP QRGf LRGP QRGf LEG LEG LEG LEG LEG LEG LEG LEG LEG LEG
Ph_tri* Th_pse* Al_lai Sa_dec Sa_par Ap_ant Ap_ant Py_int Py_int Py_int Py_irt Py_irt Py_irt Py_irt Ph_inf Ph_par Ph_oin Ph_oin Ph_oin Ph_oin Ph_oin Ph_se* Al_lai Sa_dec Sa_pat Ap_int Ap_ant Ap_Ant		ADICIENCIIACIGNEDWLDOWD- ADVGINGLSIVGINGKONPDWLDOWD- ADVGINGLSIVGINGKONPDWLDOWD- ADVGINGLSIVGINGKONPDWLDOWD- SCVEHTIAAFQRTIHTYHSEGAGGGHAI SCVEHTIAAFQRTIHTYHSEGAGGGHAI SCVEHTIAAFQRTIHTYHSEGAGGGHAI SCVEHTIAAFQRTIHTYHSEGAGGGHAI SCVEQTIAAFGRTIHTYHSEGAGGGHAI SCVENTIAFKGRTIHTYHSEGAGGHAI SCVENTIAFKGRTIHTYHSEGAGHAI SCVENTIAFKGRTIHTYHSEGAGHAI SCVENTIAFKGRTIHTYHSEGAGHAI SCVENTIAFKGRTIHTYHSEGAGHAI SCVENTIAFKGRTIHTYHSEGAGHAI SCVENTIAFKGRTIHTYHSEGAGHAI SCVENTIAFKGRTIHTYHSEGAGHAI SCVENTIAFKGRTIHTYHSEGAGHAI SCVENTIAFKGRTIHTYHSEGAGHAI SCVENTIAFKGRTIHTYHSEGAGHAI		GLQD GLQD GLQC GLQC GLQC GLQC GLQC GLQC GLQC GLQC
Ph_tri* Th_pse* Al_lai Sa_dec Sa_dec Sa_bar Ap_inv2 Ap_inv2 Py_ins Hy_ara Py_irr Py_irr Ph_vex Ph_or Ph_par Ph_or Ph_par Ph_soi Py_aph Ph_tri* Al_lai Sa_dec Sa_par Ap_inv2 Ap_inv2 Py_inv2 Py_inv2		ADICIENCITACIGNOPUNDOVM ADICIESCONTRACTOR AND		GLQD GLQC GRGp QRGp QRGp QRGf QRGf ERGt QRGf ERGt EIG 11yG1 11yG1 11yG1 11yG1 EIG1 EIG1 EIG1 EIG1 EIG1 EIG1 EIG1 EI
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Figure 3 Sequence alignment of full-length deduced urease proteins from *P. insidiosum*, related oomycetes, and diatoms. Initials of the genus and species names of each organism (Table S1) are listed on the left. The open box indicates *P. insidiosum*. The asterisks represent the diatoms. The symbol "-" indicates an absent amino acid in any given sequence. Cyan and gray colors highlight the identical and similar amino acids, respectively. Full-size 🖾 DOI: 10.7717/peerj.4821/fig-3

(cut-off <i>E</i> -value \leq -6) in the genomes of <i>P. insidiosum</i> strains Pi07, Pi35, and Pi45.							
Strain	Pi07	Pi35	Pi45				
Phylogenetic clade	Ι	II	III				
Growth rate (mm/day)	3.7	7.4	5.0				
Fast/slow growth	Slow	Fast	Fast				
Urease test	+	+	(-)				
Gene copy	Copy-1	Copy-1	Copy-1	Copy-2			
URE							
<i>E</i> -value	0.0	0.0	0.0	0.0			
Identity (%)	64	63	64	64			
Similarity (%)	75	73	75	76			
URED							
<i>E</i> -value	3E-19	2E-16	5E-26	2E-18			
Identity (%)	42	42	31	47			
Similarity (%)	60	58	52	67			
UREF							
<i>E</i> -value	-	1E-53	3E-54	6E-52			
Identity (%)	-	42	42	40			
Similarity (%)	-	61	61	59			
UREG							
<i>E</i> -value	6E-86	6E-60	5E-39	2E-33			
Identity (%)	53	73	74	56			
Similarity (%)	64	87	89	64			

Table 2 Urease and urease accessory protein orthologous sequences identified by TBLASTN search

Notes:

The query sequences are the plant *A. thaliana* urease (URE; accession number, NP_176922) and urease accessory proteins D (URED; NP_850239), F (UREF; NP_850239), and G (UREG; NP_850239). Information on phylogenetic clades, growths, urease test results, gene copy, and TBLASTN search output (i.e., *E*-values, identity, and similarity) of *P. insidiosum* is summarized in the table.

the observations of *Vilela, Viswanathan & Mendoza (2015)*. The enzymatic components necessary to hydrolyze urea and certain sugars (i.e., dextrose, maltose, sucrose, and trehalose) were found in some strains but were not ubiquitous (Table 1). This finding contrasts with reports by Vilela et al., who showed all six *P. insidiosum* strains tested (including the strains CBS 574.85 and ATCC 28251 of the current study) could utilize urea and these sugars. This is especially important considering maltose and sucrose are two key sugars that were thought to differentiate *P. insidosum* from other pathogenic oomycetes and fungi (*Vilela, Viswanathan & Mendoza, 2015*). Failure to breakdown these sugars, in some strains, was markedly associated with slow-growth (growth rate, <5 mm/day) in *P. insidiosum* (Table 1). Because the biochemical characteristics varied among different strains (and even between different cultures of the same strain), caution is



Figure 4 Maximum-likelihood phylogenetic tree reconstructed from a set of 24 urease-encoding sequences identified in the genomes of *P. insidiosum*, related oomycetes, and diatoms (outgroup; as indicated by asterisks). The oomycete ureases can be allocated in three phylogenetically distinct clades: (i) the clade of *Pythium*, *Phytophthora*, *Phytopythium*, and *Hyaloperonospora* species; (ii) the clade of *Aphanomyces* and *Saprolegnia* species; and (iii) the clade of *Albugo* species. Most of the organisms contain one copy of the urease-encoding gene, except *A. invadans* (three copies) and *P. insidiosum* strain Pi45 (two copies). The red box encompasses the urease sequences from three representative strains of *P. insidiosum*. Only branch support values \geq 70% are shown at the nodes. The bottom bar reveals nucleotide substitution per site. Full-size DOI: 10.7717/peerj.4821/fig-4

advised for the use of tests for the hydrolysis of maltose and sucrose in the clinical identification of *P. insidiosum* (especially for slow-growing strains).

Unlike the hydrolysis of sugars and DNA, the ability to utilize urea was not associated with growth rate in *P. insidiosum*. Efficient breakdown of urea can be observed in many slow-growing strains (i.e., Pi04, Pi07, Pi20, Pi44, Pi46, Pi48, and CBS 574.85), and not in all fast-growing strains (i.e., Pi23, Pi45, Pi49, Pi51, and ATCC 28251) (Table 1). The inability to utilize urea in a number of *P. insidiosum* strains could correspond to the lack of the urease-encoding gene, *Ure*1, in their genomes. We investigated the presence of *Ure*1 in the genomes of three representative strains of *P. insidiosum*, which included: (i) the urea-hydrolyzing, slow-growing, Clade-I strain Pi07; (ii) the urea-hydrolyzing, fast-growing, Clade-II strain Pi35; and (iii) the non-urea-hydrolyzing, fast-growing, Clade-III strain Pi45. All three strains contain *Ure*1 orthologous sequence, which significantly

matched the plant *Arabidopsis* urease (URE) (algorithm, TBLASTN; *E*-value, 0.0; identity, 63–64%; similarity, 73–76%; Table 2). Surprisingly, the non-urea-hydrolyzing strain Pi45 harbors two copies of *Ure1* (designated as *Ure1*A and *Ure1*B), suggesting that the presence of *Ure1* genes in the genome is not necessarily associated with the ability to hydrolyze urea in *P. insidiosum*.

In plants and microbes, urease accessory proteins (i.e., UreE, UreF, UreG, and UreD (orthologous to UreH)) are necessary for maturation and activation of the nickelcontaining metalloenzyme urease (*Witte, Rosso & Romeis, 2005*; *Fong et al., 2013*). The urease structure protein (URE) and several accessory proteins (URED, UREF, and UREG) are required for enzymatic activity of the *Arabidopsis* urease (*Witte, Rosso & Romeis, 2005*). In addition to urease, we also sought evidence of urease accessory protein-encoding genes in *P. insidiosum*. TBLASTN search showed the URED, UREF, and UREG orthologs in the genomes of *P. insidiosum* strains Pi07, Pi35, and Pi45, as summarized in Table 2. A UREF ortholog was not found in the urea-hydrolyzing strain Pi07 (this may be due to the incompleteness of its genome), but URED and UREG orthologs were. Unlike the other strains, the non-urea-hydrolyzing strain Pi45 has two copies of both urease and urease accessory genes (Table 2). Since *P. insidiosum* generally contains a complete set of urease- and accessory protein-coding sequences, failure to utilize urea in some strains (Table 1) may be due to limited expression and/or down-regulation of these genes.

Genome analyses demonstrated that urease- and accessory protein-encoding genes are conserved in *P. insidiosum* from all three phylogenetically distinct clades, although gene duplication could occur in some strains (Table 2). We used the identified urease-encoding genes to further investigate metabolism-related evolution in *P. insidiosum*, non-human-pathogenic oomycetes, and diatoms (outgroup) (Table S1). The ureases are highly conserved in all organisms (Fig. 3), and their phylogenetic relationships are allocated as expected in the reconstructed tree (Fig. 4). However, the presence of urease accessory protein-encoding genes is diverse in these organisms (Fig. 1), ranging from: (i) harboring a wide variety of these genes in the genera *Phytophthora*, *Pythium*, and *Phytopythium*; to (ii) containing just a few genes in the genera *Hyaloperonospora*, *Albugo*, *Aphanomyces*, and *Saprolegnia*.

CONCLUSIONS

No unique biochemical characteristic is observed among different strains of *P. insidiosum*, cautioning the use of related biochemical assays for pathogen identification. Unlike the hydrolysis of sugars, the ability to hydrolyze urea was not associated with *P. insidiosum* growth, as many slow-growing strains, and not all fast-growing strains, can utilize urea, even though the urease- and accessory protein-encoding genes are present and highly conserved in both urea-hydrolyzing and non-hydrolyzing strains of *P. insidiosum*. Future investigations on expression and regulation of the urease and accessory protein-encoding genes could elaborate the urea metabolism and its potential role in pathogenicity in *P. insidiosum*. Gain and loss of urease and accessory protein-encoding genes occurred in

the genomes of oomycetes and diatoms as their evolutions diverged. In the current study, we dissected several biochemical characteristics, and provided new insights into urease-based evolution of *P. insidiosum*.

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ADDITIONAL INFORMATION AND DECLARATIONS

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Competing Interests

The authors declare that they have no competing interests.

Author Contributions

- Theerapong Krajaejun conceived and designed the experiments, performed the experiments, analyzed the data, contributed reagents/materials/analysis tools, prepared figures and/or tables, authored or reviewed drafts of the paper, approved the final draft.
- Thidarat Rujirawat performed the experiments, analyzed the data, prepared figures and/or tables, authored or reviewed drafts of the paper, approved the final draft.
- Teerat Kanpanleuk performed the experiments, prepared figures and/or tables, approved the final draft.
- Pitak Santanirand conceived and designed the experiments, contributed reagents/ materials/analysis tools, approved the final draft.
- Tassanee Lohnoo performed the experiments, approved the final draft.
- Wanta Yingyong performed the experiments, approved the final draft.
- Yothin Kumsang performed the experiments, approved the final draft.
- Pattarana Sae-Chew performed the experiments, approved the final draft.
- Weerayuth Kittichotirat performed the experiments, analyzed the data, contributed reagents/materials/analysis tools, approved the final draft.
- Preecha Patumcharoenpol performed the experiments, approved the final draft.

Ethics

The following information was supplied relating to ethical approvals (i.e., approving body and any reference numbers):

This study was approved by the Committee on Human Rights Related to Research Involving Human Subjects, at the Faculty of Medicine, Ramathibodi Hospital, Mahidol University (approval number ID 05-60-77).

DNA Deposition

The following information was supplied regarding the deposition of DNA sequences:

Sequences of the putative urease genes of *P. insidiosum* identified in the genomes of *P. insidiosum* strains Pi-S (accession number, LC317047 for *Ure*1), Pi07 (accession number LC325168 for *Ure*1), and Pi45 (LC325169 for *Ure*1A, and LC325170 for *Ure*1B) have been submitted to the DDBJ database.

Data Availability

The following information was supplied regarding data availability:

The raw data are included in the 'Results' section as well as in the tables and figures in the article.

Supplemental Information

Supplemental information for this article can be found online at http://dx.doi.org/ 10.7717/peerj.4821#supplemental-information.

REFERENCES

- Anisimova M, Gascuel O. 2006. Approximate likelihood-ratio test for branches: a fast, accurate, and powerful alternative. *Systematic Biology* 55(4):539–552 DOI 10.1080/10635150600755453.
- Badenoch PR, Coster DJ, Wetherall BL, Brettig HT, Rozenbilds MA, Drenth A, Wagels G. 2001. Pythium insidiosum keratitis confirmed by DNA sequence analysis. British Journal of Ophthalmology 85(4):502–503 DOI 10.1136/bjo.85.4.496g.
- Botton SA, Pereira DIB, Costa MM, Azevedo MI, Argenta JS, Jesus FPK, Alves SH, Santurio JM. 2011. Identification of *Pythium insidiosum* by nested PCR in cutaneous lesions of Brazilian horses and rabbits. *Current Microbiology* 62(4):1225–1229 DOI 10.1007/s00284-010-9781-4.
- **Castresana J. 2000.** Selection of conserved blocks from multiple alignments for their use in phylogenetic analysis. *Molecular Biology and Evolution* **17(4)**:540–552 DOI 10.1093/oxfordjournals.molbev.a026334.
- Chaiprasert A, Krajaejun T, Pannanusorn S, Prariyachatigul C, Wanachiwanawin W,
 Sathapatayavongs B, Juthayothin T, Smittipat N, Vanittanakom N, Chindamporn A.
 2009. Pythium insidiosum Thai isolates: molecular phylogenetic analysis. Asian Biomedicine 3:623–633.
- Chaiprasert A, Samerpitak K, Wanachiwanawin W, Thasnakorn P. 1990. Induction of zoospore formation in Thai isolates of *Pythium insidiosum*. *Mycoses* 33(6):317–323 DOI 10.1111/myc.1990.33.6.317.
- Chareonsirisuthigul T, Khositnithikul R, Intaramat A, Inkomlue R, Sriwanichrak K, Piromsontikorn S, Kitiwanwanich S, Lowhnoo T, Yingyong W, Chaiprasert A, Banyong R, Ratanabanangkoon K, Brandhorst TT, Krajaejun T. 2013. Performance comparison of

immunodiffusion, enzyme-linked immunosorbent assay, immunochromatography and hemagglutination for serodiagnosis of human pythiosis. *Diagnostic Microbiology and Infectious Disease* **76**(1):42–45 DOI 10.1016/j.diagmicrobio.2013.02.025.

- **Chevenet F, Brun C, Bañuls A-L, Jacq B, Christen R. 2006.** TreeDyn: towards dynamic graphics and annotations for analyses of trees. *BMC Bioinformatics* **7**:439 DOI 10.1186/1471-2105-7-439.
- **Cox GM, Mukherjee J, Cole GT, Casadevall A, Perfect JR. 2000.** Urease as a virulence factor in experimental cryptococcosis. *Infection and Immunity* **68**(**2**):443–448 DOI 10.1128/iai.68.2.443-448.2000.
- Davis DJ, Lanter K, Makselan S, Bonati C, Asbrock P, Ravishankar JP, Money NP. 2006. Relationship between temperature optima and secreted protease activities of three Pythium species and pathogenicity toward plant and animal hosts. *Mycological Research* 110(1):96–103 DOI 10.1016/j.mycres.2005.08.009.
- Dereeper A, Audic S, Claverie JM, Blanc G. 2010. BLAST-EXPLORER helps you building datasets for phylogenetic analysis. *BMC Evolutionary Biology* 10(1):8 DOI 10.1186/1471-2148-10-8.
- Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard J-F, Guindon S, Lefort V, Lescot M, Claverie J-M, Gascuel O. 2008. Phylogeny.fr: robust phylogenetic analysis for the non-specialist. *Nucleic Acids Research* 36:W465–W469 DOI 10.1093/nar/gkn180.
- Edgar RC. 2004. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research* 32(5):1792–1797 DOI 10.1093/nar/gkh340.
- **Fong YH, Wong HC, Yuen MH, Lau PH, Chen YW, Wong KB. 2013.** Structure of UreG/UreF/ UreH complex reveals how urease accessory proteins facilitate maturation of *Helicobacter pylori* urease. *PLOS Biology* **11(10)**:e1001678 DOI 10.1371/journal.pbio.1001678.
- Gaastra W, Lipman LJA, De Cock AWAM, Exel TK, Pegge RBG, Scheurwater J, Vilela R, Mendoza L. 2010. *Pythium insidiosum*: an overview. *Veterinary Microbiology* 146(1–2):1–16 DOI 10.1016/j.vetmic.2010.07.019.
- Grooters AM, Gee MK. 2002. Development of a nested polymerase chain reaction assay for the detection and identification of *Pythium insidiosum*. *Journal of Veterinary Internal Medicine* 16(2):147–152 DOI 10.1892/0891-6640(2002)0162.3.co;2.
- Grooters AM, Leise BS, Lopez MK, Gee MK, O'Reilly KL. 2002. Development and evaluation of an enzyme-linked immunosorbent assay for the serodiagnosis of pythiosis in dogs. *Journal of Veterinary Internal Medicine* 16(2):142–146 DOI 10.1892/0891-6640(2002)0162.3.co;2.
- Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O. 2010. New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. *Systematic Biology* **59**(3):307–321 DOI 10.1093/sysbio/syq010.
- Inkomlue R, Larbcharoensub N, Karnsombut P, Lerksuthirat T, Aroonroch R, Lohnoo T, Yingyong W, Santanirand P, Sansopha L, Krajaejun T. 2016. Development of an anti-elicitin antibody-based immunohistochemical assay for diagnosis of pythiosis. *Journal of Clinical Microbiology* 54(1):43–48 DOI 10.1128/JCM.02113-15.
- Intaramat A, Sornprachum T, Chantrathonkul B, Chaisuriya P, Lohnoo T, Yingyong W, Jongruja N, Kumsang Y, Sandee A, Chaiprasert A, Banyong R, Santurio JM, Grooters AM, Ratanabanangkoon K, Krajaejun T. 2016. Protein A/G-based immunochromatographic test for serodiagnosis of pythiosis in human and animal subjects from Asia and Americas. *Medical Mycology* 54(6):641–647 DOI 10.1093/mmy/myw018.
- Jindayok T, Piromsontikorn S, Srimuang S, Khupulsup K, Krajaejun T. 2009. Hemagglutination test for rapid serodiagnosis of human pythiosis. *Clinical and Vaccine Immunology* **16**(7):1047–1051 DOI 10.1128/CVI.00113-09.

- Keeratijarut A, Karnsombut P, Aroonroch R, Srimuang S, Sangruchi T, Sansopha L, Mootsikapun P, Larbcharoensub N, Krajaejun T. 2009. Evaluation of an in-house immunoperoxidase staining assay for histodiagnosis of human pythiosis. *Southeast Asian Journal of Tropical Medicine and Public Health* **40**:1298–1305.
- Keeratijarut A, Lohnoo T, Yingyong W, Nampoon U, Lerksuthirat T, Onpaew P, Chongtrakool P, Krajaejun T. 2014. PCR amplification of a putative gene for exo-1, 3-beta-glucanase to identify the pathogenic oomycete *Pythium insidiosum*. *Asian Biomedicine* **8**(5):637–644 DOI 10.5372/1905-7415.0805.338.
- Keeratijarut A, Lohnoo T, Yingyong W, Sriwanichrak K, Krajaejun T. 2013. A peptide ELISA to detect antibodies against *Pythium insidiosum* based on predicted antigenic determinants of exo-1,3-beta-glucanase. *Southeast Asian Journal of Tropical Medicine and Public Health* **44**(4):672–680.
- Keeratijarut A, Yingyong W, Chongtrakool P, Srichunrusami C, Krajaejun T, Lohnoo T, Onpeaw P, Rujirawat T, Brandhorst TT. 2015. Detection of the oomycete *Pythium insidiosum* by real-time PCR targeting the gene coding for exo-1,3-β-glucanase. *Journal of Medical Microbiology* 64(9):971–977 DOI 10.1099/jmm.0.000117.
- Kittichotirat W, Bumgarner RE, Asikainen S, Chen C. 2011. Identification of the pangenome and its components in 14 distinct Aggregatibacter actinomycetemcomitans strains by comparative genomic analysis. *PLOS ONE* 6(7):e22420 DOI 10.1371/journal.pone.0022420.
- Kittichotirat W, Patumcharoenpol P, Rujirawat T, Lohnoo T, Yingyong W, Krajaejun T. 2017. Draft genome and sequence variant data of the oomycete *Pythium insidiosum* strain Pi45 from the phylogenetically-distinct Clade-III. *Data in Brief* 15:896–900 DOI 10.1016/j.dib.2017.10.047.
- Krajaejun T, Chongtrakool P, Angkananukul K, Brandhorst TT. 2010. Effect of temperature on growth of the pathogenic oomycete *Pythium insidiosum*. Southeast Asian Journal of Tropical Medicine and Public Health 41:1462–1466.
- Krajaejun T, Imkhieo S, Intaramat A, Ratanabanangkoon K. 2009. Development of an immunochromatographic test for rapid serodiagnosis of human pythiosis. *Clinical and Vaccine Immunology* 16(4):506–509 DOI 10.1128/CVI.00276-08.
- Krajaejun T, Kunakorn M, Niemhom S, Chongtrakool P, Pracharktam R. 2002. Development and evaluation of an in-house enzyme-linked immunosorbent assay for early diagnosis and monitoring of human pythiosis. *Clinical and Diagnostic Laboratory Immunology* 9(2):378–382 DOI 10.1128/cdli.9.2.378-382.2002.
- Krajaejun T, Kunakorn M, Pracharktam R, Chongtrakool P, Sathapatayavongs B, Chaiprasert A, Vanittanakom N, Chindamporn A, Mootsikapun P. 2006a. Identification of a novel 74-kiloDalton immunodominant antigen of *Pythium insidiosum* recognized by sera from human patients with pythiosis. *Journal of Clinical Microbiology* **44**(5):1674–1680 DOI 10.1128/JCM.44.5.1674-1680.2006.
- Krajaejun T, Pracharktam R, Wongwaisayawan S, Rochanawutinon M, Kunakorn M, Kunavisarut S. 2004. Ocular pythiosis: is it under-diagnosed? *American Journal of Ophthalmology* 137(2):370–372 DOI 10.1016/S0002-9394(03)00908-5.
- Krajaejun T, Sathapatayavongs B, Pracharktam R, Nitiyanant P, Leelachaikul P,
 Wanachiwanawin W, Chaiprasert A, Assanasen P, Saipetch M, Mootsikapun P,
 Chetchotisakd P, Lekhakula A, Mitarnun W, Kalnauwakul S, Supparatpinyo K,
 Chaiwarith R, Chiewchanvit S, Tananuvat N, Srisiri S, Suankratay C, Kulwichit W,
 Wongsaisuwan M, Somkaew S. 2006b. Clinical and epidemiological analyses of human
 pythiosis in Thailand. *Clinical Infectious Diseases* 43(5):569–576 DOI 10.1086/506353.

- Lerksuthirat T, Sangcakul A, Lohnoo T, Yingyong W, Rujirawat T, Krajaejun T. 2017. Evolution of the sterol biosynthetic pathway of *Pythium insidiosum* and related oomycetes contributes to antifungal drug resistance. *Antimicrobial Agents and Chemotherapy* **61**(**4**):e02352-16 DOI 10.1128/AAC.02352-16.
- Mora D, Arioli S. 2014. Microbial urease in health and disease. *PLOS Pathogens* 10(12):e1004472 DOI 10.1371/journal.ppat.1004472.
- Patumcharoenpol P, Rujirawat T, Lohnoo T, Yingyong W, Vanittanakom N, Kittichotirat W, Krajaejun T. 2018. Draft genome sequences of the oomycete *Pythium insidiosum* strain CBS 573.85 from a horse with pythiosis and strain CR02 from the environment. *Data in Brief* 16:47–50 DOI 10.1016/j.dib.2017.11.002.
- Pracharktam R, Changtrakool P, Sathapatayavongs B, Jayanetra P, Ajello L. 1991. Immunodiffusion test for diagnosis and monitoring of human pythiosis insidiosi. *Journal of Clinical Microbiology* 29:2661–2662.
- Rujirawat T, Patumcharoenpol P, Lohnoo T, Yingyong W, Kumsang Y, Payattikul P, Tangphatsornruang S, Suriyaphol P, Reamtong O, Garg G, Kittichotirat W, Krajaejun T.
 2018. Probing the phylogenomics and putative pathogenicity genes of *Pythium insidiosum* by oomycete genome analyses. *Scientific Reports* 8(1):4135 DOI 10.1038/s41598-018-22540-1.
- Rujirawat T, Patumcharoenpol P, Lohnoo T, Yingyong W, Lerksuthirat T, Tangphatsornruang S, Suriyaphol P, Grenville-Briggs LJ, Garg G, Kittichotirat W, Krajaejun T. 2015. Draft genome sequence of the pathogenic oomycete *Pythium insidiosum* strain Pi-S, isolated from a patient with pythiosis. *Genome Announcements* **3**(3):e00574-15 DOI 10.1128/genomeA.00574-15.
- Rujirawat T, Sridapan T, Lohnoo T, Yingyong W, Kumsang Y, Sae-Chew P, Tonpitak W, Krajaejun T. 2017. Single nucleotide polymorphism-based multiplex PCR for identification and genotyping of the oomycete *Pythium insidiosum* from humans, animals and the environment. *Infection Genetics and Evolution* 54:429–436 DOI 10.1016/j.meegid.2017.08.004.
- Rutherford JC. 2014. The emerging role of urease as a general microbial virulence factor. *PLOS Pathogens* 10(5):e1004062 DOI 10.1371/journal.ppat.1004062.
- Schurko AM, Mendoza L, Lévesque CA, Désaulniers NL, De Cock AWAM, Klassen GR. 2003. A molecular phylogeny of *Pythium insidiosum*. *Mycological Research* **107**(5):537–544 DOI 10.1017/s0953756203007718.
- Supabandhu J, Vanittanakom P, Laohapensang K, Vanittanakom N. 2009. Application of immunoblot assay for rapid diagnosis of human pythiosis. *Journal of the Medical Association of Thailand* 92:1063–1071.
- Thianprasit M, Chaiprasert A, Imwidthaya P. 1996. Human pythiosis. Current Topics in Medical Mycology 7:43–54.
- Vilela R, Viswanathan P, Mendoza LA. 2015. A biochemical screening approach to putatively differentiate mammalian pathogenic Oomycota species in the clinical laboratory. *Journal of Medical Microbiology* 64(8):862–868 DOI 10.1099/jmm.0.000111.
- Witte CP, Rosso MG, Romeis T. 2005. Identification of three urease accessory proteins that are required for urease activation in Arabidopsis. *Plant Physiology* **139(3)**:1155–1162 DOI 10.1104/pp.105.070292.
- Zanette RA, Ferreiro L, Alves SH, Jesus FPK, Lautert C, Spanamberg A, Santurio JM. 2013. Enzymatic variability among Brazilian *Pythium insidiosum* isolates. *Revista Iberoamericana De Micología* 30:264–266 DOI 10.1016/j.riam.2012.12.005.