Review

Not in your usual Top 10: protists that infect plants and algae

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SUMMARY

Fungi, nematodes and oomycetes belong to the most prominent eukaryotic plant pathogenic organisms. unicellular organisms from other eukaryotic lineages, commonly addressed as protists, also infect plants. This review provides an introduction to plant pathogenic protists, including algae infecting oomycetes, and their current state of research.

Keywords: algae, protist, plant pathogens, plasmodiophorids, stramenopiles, phytomonas, phytomyxae.

INTRODUCTION

Molecular Plant Pathology has published a series of the Top 10 most important plant-pathogenic viruses (Scholthof et al., 2011), fungi (Dean et al., 2012), bacteria (Mansfield et al., 2012), nematodes (Jones et al., 2013) and oomycetes (Kamoun et al., 2015). The reviews of these major groups of plant pathogens do not cover a selection of protists that infect plants and algae leading to economically important diseases. These ‘non-standard’ plant pathogens are dispersed across the eukaryotic phylogenetic tree (Fig. 1), often in taxa unfamiliar to many plant pathologists as they are usually not associated with plant infections. In this review, we would like to introduce and raise awareness of such phylogenetically diverse eukaryotic plant pathogens.

We describe diseases caused by these organisms, and the current state of research, especially with respect to their molecular biology and host interactions. We start with Phytomonas, plant pathogens in the trypanosomatids in the Excavata supergroup, a group better known as human and animal pathogens. They are followed by Phytomyxea, which are part of the Rhizaria supergroup and include agriculturally important plant pathogens, vectors of phytoviruses and species that infect marine plants and algae (Bulman and Braselton, 2014). Next, Labyrinthula are described, plant pathogens in the Stramenopiles, which are phylogenetic basal to oomycetes. Our review also includes marine oomycete parasites of red and brown algae, which impact on the fast growing aquaculture sector (Gachon et al., 2010). Advancing research in this field will benefit aquacultural sustainability and our understanding of higher oomycetes because of their basal phylogenetic position inside the oomycetes (Beakes et al., 2012).

Whole-genome or in-depth transcriptomic data for the species presented here are rare, with the exception of the Phytomyxea and Phytomonas. The organisms outlined reflect existing molecular knowledge; nevertheless, we emphasize that there are further important ‘unusual’ pathogens, especially on cultivated algae.

EXCAVATA – KINETOPLASTEA

TRYPANOSOMATIDAE – PHYTOMONAS

Trypanosomatids are a species-rich monophyletic group of obligate parasitic flagellates that are usually transmitted by insects. They are best known as agents of human and livestock diseases,
such as sleeping sickness, Chagas disease and leishmaniosis, caused by *Trypanosoma brucei*, *T. cruzi* and *Leishmania* spp., respectively (Luke et al., 2014). Trypanosomatids also include the monophyletic genus *Phytomonas* (Fig. 2), which contains all known plant-dwelling trypanosomatids, some of which are pathogenic (Seward et al., 2016). The ancestral monoxenous lifestyle (development restricted to one host species) of trypanosomatids evolved at least three times independently into a dixenous strategy (Maslov et al., 2013) in *Trypanosoma*, *Leishmania* and *Phytomonas* (Luke et al., 2014). *Phytomonas* spp. are adapted to sap-sucking insects as primary hosts and plants as secondary hosts (Jaskowska et al., 2015). *Phytomonas* spp. were first described from the latex of Mediterranean spurge (*Euphorbia pilulifera*) (Lafont, 1909). Currently, the genus *Phytomonas* includes more than 200 species that colonize over 20 plant families (Camargo, 1999; Jaskowska et al., 2015).

*Phytomonas* spp. can be separated into four ecological subgroups based on whether they inhabit the latex ducts, fruits, phloem or flowers of their host plants (Camargo, 1999). Most commonly, *Phytomonas* spp. reside in latex ducts, yet the most pathogenic species are phloem dwelling, such as *P. leptovasorum* and *P. staheli*, which cause coffee phloem necrosis (CPN) and palm wilts, respectively (Jaskowska et al., 2015). *Phytomonas leptovasorum* infection triggers multiple divisions of the sieve tubes in coffee roots, leading to CPN. The disease is a potential threat to Brazil as the world’s largest coffee exporter, from which CPN has been reported, but never spread (Camargo, 1999). This disease occurs either acutely (plants wither and die within 2 months) or chronically (plants gradually die within a year) (Stahel, 1931).

*Phytomonas staheli* causes wilts of coconut (*Cocos nucifera*) and oil palms (*Elaeis guineensis*) (McGhee and McGhee, 1979).

Both deadly wilts, ‘hartrot’ of coconut palms and ‘marchitez sorpresa’ of oil palms, are characterized by progressive leaf browning, followed by rapid rotting of fruits, spears and roots (Kastelein, 1987; Lopez, 1975). Slow wilt of oil palms (‘marchitez lenta’) manifests as additional chlorosis (Di Lucca et al., 2013). Symptomless plants and wild hosts can harbour *Phytomonas* flagellates (Di Lucca et al., 2013). Potential disease outbreaks constantly threaten palm cultivation in South and Central America. In one Surinamese district, *Phytomonas* destroyed half of the coconut population (Kastelein, 1987). The latex-inhabiting *P. francai* is linked to empty roots disease (‘chochamento de raizes’) of the Unha cassava (*Manihot esculenta*) variety, although its pathogenicity remains unclear (Jaskowska et al., 2015; Kitajima et al., 1986).

The first *Phytomonas* draft genome came from the tomato fruit-inhabiting *P. serpens* (Korený et al., 2012), which produces no significant systemic disease, but causes yellow spots on fruit (Camargo, 1999). The genomes of the pathogenic phloem-specific *Phytomonas* strain HART1 from Guyanan coconut and the non-symptomatic latex-specific strain EM1 from *Euphorbia* were generated shortly after (Porcel et al., 2014). Recently, the genome of the cassava latex-inhabiting *P. francai* has been announced (Butler et al., 2017), which will enable comparative genomics of *Phytomonas* spp. with different host and ecological lifestyles in the future.

The *Phytomonas* genomes are compact, consisting of single-copy genes, and are almost free of transposable elements and repeats. Therefore they are smaller (≥18 Mb) than most trypanosomatid genomes (26–33 Mb). *Phytomonas* spp. contain only about 6400 protein-coding genes versus approximately 10 400 found typically in trypanosomatids.

As in other biotrophs, *Phytomonas* metabolism is highly adapted to parasitic lifestyles. These plant pathogens contain...
fewer genes involved in amino acid synthesis and energy metabolism and fewer protein kinases than the related Leishmania and Trypanosoma spp. Fatty acids (FAs) are synthesized via elongases instead of de novo, as FA synthases are missing (Porcel et al., 2014). Phytomonas spp. have the unique capacity amongst trypanosomatids to live in the total absence of haem, although they might be able to scavenge it (Kořený et al., 2012). In addition, they have lost several cytochrome subunits of respiratory complexes. For energy production, Phytomonas may depend solely on glycolysis, whereas other trypanosomatids (at least in part of their life cycle) rely on mitochondrial amino acid metabolism as their main energy source (Jaskowska et al., 2015; Porcel et al., 2014). As their insect vector(s) feed on carbohydrate-rich plant juices, Phytomonas might not require a switch from carbohydrate to amino acid metabolism. Phytomonas spp. contain complete sets of glycolytic enzymes and large numbers of glycosomes, into which glycolysis is compartmentalized (Hannaert et al., 2003; Porcel et al., 2014). Also unique amongst trypanosomatids, Phytomonas spp. possess the capacity to feed on plant polysaccharides using glucoamylase and α-glucosidase enzymes. In addition, an α,α-trehalose phosphorylase, acquired by horizontal gene transfer, enables feeding on trehalose, a common sugar in the plant and insect hosts of Phytomonas (Porcel et al., 2014).

The Phytomonas HART1 and EM1 isolates share a majority of genes. However, only the phloem-restricted pathogenic HART1 encodes invertase genes for the degradation of sucrose (Porcel et al., 2014), probably as an adaptation to the abundance of sucrose in the phloem. For both the HART1 and EM1 isolates, 282 secreted proteins were predicted. Their secretomes contain no plant cell wall-degrading enzymes, which reflects the feeding of

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Fig. 2 Phytomonas sp. and palm infections. (A, B) Scanning electron micrographs of Phytomonas serpens cells in culture (scale bars, 10 and 1 µm). (Courtesy of Martina Tesárová.) (C) Transmission electron micrographs of Phytomonas sp. flagellates in the phloem of coconut palms affected by hartrot. C, companion cell; F, fibre; M, immature metaxylem; P, phloem parenchyma cell; S, sieve elements free of flagellates. (a) Transverse section of a differentiating vascular bundle, showing recently matured sieve elements filled with flagellates (scale bar, 10 µm). (b) Transverse section of the phloem in palm with advanced symptoms (scale bar, 5 µm). (c) Transverse section of a dividing flagellate (scale bar, 0.5 µm). (d) Longitudinal section of a sieve element filled with flagellates. Arrows indicate the kinetoplast DNA (scale bar, 1 µm). (Reproduced from Parthasarathy et al., 1976.) (D) Coconut palms with symptoms of hartrot. (Photograph: Monica L. Elliott, Professor, Plant Pathology, University of Florida, Institute of Food and Agricultural Sciences (UF/IFAS), Gainesville, FL, USA.)
the pathogens on extracellular plant fluids. It is unknown whether Phytomonas spp. secrete protein effectors, which modulate host plant immune responses. However, several aspartyl proteases that are absent from the genomes of Leishmania and Trypanosoma are secreted in both Phytomonas strains (Porcel et al., 2014). These proteases may be involved in Phytomonas–host interactions, as seen for oomycete and fungal plant pathogens (Jashni et al., 2015). The pathogenic HART1 strain carries five copies of a cathepsin-like aspartyl protease, derived from duplication events, whereas EM1 has only a single copy. This implies that these enzymes are potential virulence factors (Porcel et al., 2014). The gene family of major surface proteases, which are involved in the pathogenicity of Leishmania, underwent an expansion in the genus Phytomonas (Jackson, 2015). The surface glycoprotein 63 subfamily is present in 20 copies in HART1 and only twice in EM1, a putative adaptation of HART1 to the phloem environment (Jaskowska et al., 2015; Porcel et al., 2014).

Although the procyclic stage of Phytomonas spp. can be easily cultivated, an experimental system including their plant host is not available. Hence, our understanding of how these plant-dwelling or plant-parasitizing flagellates interact with their plant hosts is only at an early stage.

Currently, there is no treatment or prevention of the diseases caused by Phytomonas, except for the simple extermination of infected plants (Jaskowska et al., 2015). However, it has been observed that the tomato (Solanum lycopersicum) is relatively resistant to P. serpens, as the parasite only causes yellow spots on its fruits, resulting in their lower commercial value. Interestingly, the tomato defensive alkaloids tomatine and tomatidine, surface-active saponin-like compounds, induce permeabilization and vacuolation of the parasite (Medina et al., 2015). Both alkaloids inhibit the growth of P. serpens and therefore represent potential therapeutic agents against these phytopathogens (Medina et al., 2015).

RHIZARIA

Phytomyxea – plasmodiophorids

The obligate biotrophic Plasmodiophorida (plasmodiophorids) belong to the Phytomyxea (phytomyxids) in the eukaryotic supergroup Rhizaria (Fig. 1) (Adl et al., 2012; Burki and Keeling, 2014; Burki et al., 2010). These organisms infect a wide variety of hosts, including oomycetes and brown algae (Neuhauser et al., 2014). Plasmodiophorids cause substantial damage to crops, including brassicas (Plasmodiophora brassicae), potatoes (Spongospora subterranea) and as vectors of viruses to beets, peanut and monocots (e.g. maize, rice, sugarcane, wheat, sorghum) (Polymyxa spp.) and potatoes (S. subterranea).

The plasmodiophorid life cycle consists of two phases: a sporangial stage leading to short-lived zoospores, and a sporogenic stage leading to the formation of persistent resting spores (Figs 3–5). Resting spores give rise to biflagellate primary zoospores which inject their cellular contents into host cells via a ‘Rohr und Stachel’ (Aist and Williams, 1971) (Fig. 3), initiating the sporangial life cycle stage. Multinucleate plasmodia develop and produce (mitotic) secondary zoospores, which can infect host cells and develop sporogenic multinucleate plasmodia that mature into resting spores. In the sporogenic stage, gall-causing plasmodiophorids induce division and massive enlargement of host cells (for greater detail, see Bulman and Braselton, 2014).

The durability of resting spores and inconsistent chemical control make the management of plasmodiophorid diseases difficult, and biological control efforts are only beginning (Ludwig-Müller, 2016; O’Brien and Milroy, 2017). Current management mostly relies on the use of resistant host varieties and crop rotation (Bitara et al., 2016; Ludwig-Müller, 2016). Pathogen detection and quantification in soil and in planta are important. Sequences of
the ribosomal operon [i.e. 18S, 28S and internal transcribed spacer (ITS) ribosomal DNA (rDNA)] are widely used for these purposes (Bulman and Marshall, 1998; Faggian and Strelkov, 2009; van de Graaf et al., 2007; Vaianopoulos et al., 2007; Ward et al., 2004, 2005). Comparison of ITS and rDNA sequences has revealed various degrees of interspecific and intraspecific variation in plasmodiophorid species (Gau et al., 2013; van de Graaf et al., 2007; Qu and Christ, 2004; Schwelm et al., 2016).

**Plasmodiophora brassicae**

*Plasmodiophora brassicae* causes clubroot, a disease that leads to significant losses of *Brassica* oilseed and vegetable crop production worldwide (Dixon, 2009). Rapeseed cultivation for the production of biofuels, vegetable oils, industrial lubricants and rapeseed meal is of great economic importance, with a worldwide production of 27 million tonnes in 2012 (Carré and Pouzet, 2014). Clubroot has long been a major constraint for *Brassica* cultivation. A severe outbreak in 1872 in Russia led to the discovery of *P. brassicae* (Woronin, 1877). Clubroot causes crop losses of approximately 10% worldwide, but local losses are often greater (Dixon, 2009). Best practices for control are long crop rotation periods (although resting spores remain infective for decades), liming or cultivation of tolerant *Brassica* crops (Diederichsen et al., 2009; Ludwig-Müller, 2016). Clubroot resistance genes have been identified in *Brassica* genomes (Hatakeyama et al., 2013). However, resistance mechanisms are unclear and breakdown of ‘resistance’ has been repeatedly observed (Diederichsen et al., 2009; Strelkov et al., 2016; Zamani-Noor, 2017). Breeding for clubroot resistance is complicated as several pathotypes of *P. brassicae* exist. Genetic differences exist between *P. brassicae* strains, even within individual root galls, and chromosome polymorphism between strains has been suggested (Fäuling et al., 2003; Graf et al., 2004; Klewer et al., 2001). However, molecular markers for *P. brassicae* pathotypes have yet to be established.

The genome of a European *P. brassicae* single-spore isolate has been generated recently (Schwelm et al., 2015), followed...
shortly after by genomic data for isolates from Canada and China (Bi et al., 2016; Rolfe et al., 2016). The Pl. brassicae genome is small (24.2–25.5 Mb), as a result of a high gene density and few repetitive elements (2%–5%) (Rolfe et al., 2016; Schwelm et al., 2015). The first single-nucleotide polymorphism (SNP) cluster analyses of the available Pl. brassicae genomes indicated relationships between SNPs, host ranges and regional origins (Rolfe et al., 2016). Additional genome sequencing of Pl. brassicae isolates should shed light on Pl. brassicae genomic diversity and pathotype-specific features.

The Pl. brassicae genomes show similar features to those of other biotrophic plant pathogens. Host dependence is evident, i.e. from a reduced number of biosynthesis genes for thiamine and certain amino acids (Rolfe et al., 2016; Schwelm et al., 2015). Transporter proteins may aid nutrient acquisition from the hosts (Rolfe et al., 2016). The Pl. brassicae genome encodes few carbohydrate-active enzymes (CAZymes). Genes encoding for plant cell wall-degrading enzymes are also rare, possibly a consequence of the mechanical penetration strategy via a ‘Rohr und Stachel’. However, chitin-related enzymes are enriched (Rolfe et al., 2016; Schwelm et al., 2015), which are probably involved in building the chitinous resting spore cell walls (Moxham and Buczacki, 1983).

In root galls, different life cycle stages of Pl. brassicae occur simultaneously (Fig. 3), making time course experiments difficult. The transcriptomics of isolated plasmodia show a highly active metabolism, i.e. the high expression of glyoxylate cycle-related genes should shed light on Pl. brassicae genomic diversity and pathotype-specific features.

Depending on the strain sequenced, 553–590 secreted Pl. brassicae proteins were predicted. Effector candidates including the amino acid motif RxLR, known from Phytophthora effectors (Kamoun et al., 2015), are rare in Pl. brassicae (Rolfe et al., 2016; Schwelm et al., 2015). Crinkler (CRN)-related proteins were found in Pl. brassicae (Zhang et al., 2016a), but their functions are unknown. No effector candidates containing the chitin-binding LysM-motif, known to interfere with chitin detection in fungal-plant interactions (Kombrik and Thomma, 2013), were detected in Pl. brassicae.

Plasmodiophora brassicae infection results in a heavily altered host metabolism (Jubault et al., 2013): transcriptional and proteomic changes occur in pathways involved in lipid, flavonoid and plant hormone metabolism, defence responses, and carbohydrate and cell wall synthesis of the Brassica hosts (Agarwal et al., 2011; Chen et al., 2015; Ludwig-Müller et al., 2009; Pääsöld et al., 2010; Siemens et al., 2009; Zhang et al., 2016b). In Arabidopsis, gall formation results from increased host vascular cambium activity combined with significant reduction of xylem development (Malinowski et al., 2012). Conversely, higher activity of lignification-related genes occurs in less susceptible plants (Chen et al., 2015; Song et al., 2016).

On inoculation, amino acid transport and metabolism vary between tolerant and susceptible hosts, i.e. arginine and proline metabolism are less active in less susceptible B. rapa than in susceptible genotypes (Chen et al., 2015; Jubault et al., 2008; Song et al., 2016). Arginine and proline biosynthesis in Pl. brassicae also seems to be incomplete (Rolfe et al., 2016; Schwelm et al., 2015). Similar to other gall-forming plant diseases, galled roots also provoke hypoxic responses (Gravot et al., 2016). Infections by Pl. brassicae and morphogenic changes within roots leading to gall formation are accompanied by changes in phytohormone homeostasis of auxin, cytokinin and brassinosteroids (Aguwak et al., 2011; Ludwig-Müller et al., 2009; Schuller et al., 2014), but the exact mechanisms are not yet known. The contributions of plant hormones in clubroot have been addressed using Arabidopsis mutants altered in phytohormone biosynthesis, metabolism and signalling (Ludwig-Müller et al., 2017). In Arabidopsis, elevated cytokinins are associated with increased cell division early during infection. When galls are formed, the expression of host cytokinin biosynthetic genes is repressed, as is the expression of host cytokinin oxidases and dehydrogenases (Devos et al., 2006; Siemens et al., 2006). Plasmodiophora brassicae-produced cytokinins probably play a minor role in cytokinin homeostasis in infected tissues (Malinowski et al., 2016). Arabidopsis mutants of auxin conjugate synthesis, as well as auxin receptors, were more susceptible to the pathogen (Jahn et al., 2013), whereas nitrilase mutants were more tolerant (Grsic-Rausch et al., 2000). A Pl. brassicae protein can conjugate auxin and jasmonic acid to amino acids in vitro (Schwelm et al., 2015), but whether it manipulates host hormones in clubroots is unknown.

Effector-triggered immunity is likely to be important in host resistance to Pl. brassicae. During infection, resistance (R) genes and pathogen-related (PR) genes are expressed more strongly in tolerant than in susceptible plants, whereas the pathogen-associated molecular pattern (PAMP)-triggered immune response appears to be similar in both host types (Chen et al., 2015; Zhang et al., 2016b).

One Pl. brassicae effector candidate is a predicted secreted methyltransferase, PbBSMT. Biochemical expression assays have shown that this protein can mediate the methylation of salicylic acid (SA) (Ludwig-Müller et al., 2015). PbBSMT might interfere with SA signalling in infected root tissue. SA-mediated pathways are involved in resistance to Pl. brassicae (Aguwak et al., 2011; Lemarié et al., 2015; Lovelock et al., 2013). Accordingly, SA-responsive gene expression is increased in tolerant hosts (Chen et al., 2015; Song et al., 2016) and higher SA levels during early infection correlate with resistance (Chen et al., 2015; Zhang et al., 2016b).
**Spongospora subterranea**

*Spongospora subterranea* causes powdery scab of potato tubers (*Solanum tuberosum*) (Fig. 4A), an important blemish disease in most major potato-growing regions worldwide. This disease can result in the rejection of whole seed potato lots. The pathogen also causes root galling (Fig. 4B) and is the vector for the *Potato mop top virus* (PMTV, Pomovirus, Virgaviiridae) (Merz and Falloon, 2009; Tamada and Kondo, 2013). Root membrane dysfunction, which reduces water uptake and plant growth, has also been attributed to *S. subterranea* (Falloon et al., 2016). All of these diseases devalue potato crops, causing potato tuber yield losses of >20% in severely diseased crops (Johnson and Cummings, 2015; Merz and Falloon, 2009; Shah et al., 2012). Mature tuber lesions and root galls are filled with clusters of resting spores (sporosori; Fig. 4D), each containing a primary zoospore. Root infection results in the development of zoosporangia (Fig. 4C) producing secondary zoospores. Both types of zoospore infect the host tuber, root epidermis cells and root hairs, and can transmit PMTV.

Disease management is mainly preventative through the use of disease-free seed tubers and non-contaminated fields. Powdery scab and root galling susceptibility differ across potato cultivars of disease-free seed tubers and non-contaminated fields. *Powderydermis cells and root hairs, and can transmit PMTV.*

**Polymyxa spp**

The genus *Polymyxa* includes two morphologically indistinguishable agriculturally important species: *Polymyxa graminis* (Fig. 5) and *Polymyxa betae*. Both differ in their rDNA sequences and host ranges. The host range of *P. betae* is restricted to Chenopodiaceae and related plants, whereas *P. graminis* infects mainly graminaceous plants (Legreve et al., 2000, 2002). Infection by these obligate root endoparasites is asymptomatic (Desoignies, 2012). Unlike *Pl. brassicae* and *S. subterranea, Polymyxa spp.* do not cause root galls on infected hosts, but indirectly cause damage as vectors of plant viruses. *Polymyxa graminis* transmits viruses belonging to *Benyvirus, Bymovirus, Furovirus* and *Pecluvirus*. They include economically important viruses of different grain crops, such as *Barley yellow mosaic virus* (BaYMV) and *Soil-borne wheat mosaic virus* (SBWMV), and also cause virus diseases on other cereals, sugar cane and peanuts [Peauteen leaf clump virus (PCV)] (Diercky et al., 2011; Tamada and Kondo, 2013). *Polymyxa betae* transmits *Beet necrotic yellow vein virus* (BNYVV), causing ‘rhizomania’ in sugar beet (McGrann et al., 2009).

*Polymyxa betae* is a well-defined species, whereas, in *P. graminis*, five *formae specialiaes* or six ribotypes exist, with sub-type classifications based on ecological, molecular and biological characteristics, including specificity in virus transmission (Cox et al., 2014; Diercky et al., 2011; Kanyuka et al., 2003; Legreve et al., 2002; Smith et al., 2013; Vaianopoulos et al., 2007; Ward et al., 2005; Ziegler et al., 2016).

Obtaining genomic data from *Polymyxa spp.* is more difficult than for the gall-forming plasmodiophorids as high-density infections with substantial amounts of parasite DNA cannot be identified. *Polymyxa betae* cultures on sugar beet hairy roots (Desoignies and Legreve, 2011) and in its non-natural host *A. thaliana* (Desoignies and Legreve, 2011; Smith et al., 2011) were tested, but were difficult to maintain. A suppression subtractive hybridization experiment identified most currently known *Polymyxa* gene models (Desoignies et al., 2014), including 76 *P. betae* and 120 sugar beet expressed sequence tags (ESTs) putatively involved in the early stages of the host–parasite interaction. The *P. betae* ESTs included chitin synthase, polysaccharide deacetylases, ankyrins and galactose lectin domain-encoding transcripts, proteins which are also enriched in *Pl. brassicae* and *S. subterranea* (Bulman et al., 2011; Desoignies et al., 2014; Schwelm et al., 2015). Genes encoding for profilin and a von
Willebrand factor domain-containing protein were also highly expressed. The sugar beet response to *P. betae* infection, especially during the plasmodial stage, includes the over-expression of some defence genes, including those that encode PR proteins or lectins (Desoignies et al., 2014).

**Other Phytomyxea**

Other phytomyxids infect freshwater and marine organisms (Neuhauser et al., 2011). *Maullinia ectocarpii* (Fig. 3) and *M. brasseltonii* are plasmodiophorids infecting brown algae. *Plasmodiophora diplantherea*, *Pl. bicaudata*, *Pl. halophile* and *Tetramyxa parasitica* cause galls on seagrasses, and, in the case of *T. parasitica*, also other estuarine plants (Bulman and Braselton, 2014; Neuhauser et al., 2010). *Spongospora nasturtii* causes crook root on watercress and transmits the *Watercress yellow spot virus* (Walsh et al., 1989), impacting watercress cultivation.

**Stramenopiles – Labyrinthula**

*Labyrinthula* spp. are protists in the Labyrinthulida (Stramenopila), and are phylogenetically basal to oomycetes (Pan et al., 2017; Tsui et al., 2009). High-throughput environmental DNA sampling, ITS and ribosomal sequences suggest that *Labyrinthula* spp. are highly diverse, and globally distributed (Bockelmann et al., 2013; Collado-Mercado et al., 2010; Martin et al., 2016; Pan et al., 2017). These organisms are saline tolerant, and can be saprobic, coral inhabitants, endosymbionts of amoebae or endophytic facultative parasites of marine and terrestrial plants (Amon, 1978; Bigelow et al., 2005; Pan et al., 2017; Sullivan et al., 2013).

Marine *Labyrinthula*, such as *L. zosterae*, which causes seagrass wasting disease (SWD) (Sullivan et al., 2013), are usually associated with mangrove, macroalgal and seagrass ecosystems (Lindholm et al., 2016; Pan et al., 2017). Rapid blight disease (RBD) in turfgrasses is caused by the terrestrial species *L. terrestris* in high-salinity environments, such as salt lakes and golf course turf (Douhan et al., 2009; Kerrigan et al., 2012). This pathogen may have become important in specialized turfgrass because of increased salinity in irrigation or the use of reclaimed water, causing increased turf salification (Olsen, 2007; Stowell et al., 2005).

Both *L. zosterae* and *L. terrestris* vary greatly in virulence to their hosts (Chitrampalam et al., 2015; Douhan et al., 2009; Martin et al., 2016). Although the exact mechanism is uncertain, SWD and RBD manifest through the penetration of host leaf epidermis cells of individual *Labyrinthula* cells.

After infection, *Labyrinthula* spp. destroy the host chloroplasts and advance to neighbouring cells. This creates lesions, sometimes killing entire leaves or plants through interruption of photosynthesis (Fig. 6). These pathogens are therefore found on the edges of progressing infections rather than within the host lesions (Muehlstein, 1992; Olsen, 2007; Sullivan et al., 2016). They can be isolated from infected leaf tissues as they emerge from tissues plated onto serum seawater agar solutions (Fig. 6). The individual spindle- to oval-shaped *Labyrinthula* cells move through colonies of self-generated ectoplasmic networks or ‘slimeways’, a net-like tube within which *Labyrinthula* are able to move. (C) Symptoms of the seagrass wasting disease 4 days following the artificial infection of seagrass blades.

**Fig. 6** *Labyrinthula* and disease symptoms. (A) Single fusiform cells of the unicellular Labyrinthomycota *Labyrinthula* protist. (B) *Labyrinthula* cells emerging from a seagrass leaf on serum seawater agar. Cells move through colonies of self-generated ectoplasmic networks or ‘slimeways’, a net-like tube within which *Labyrinthula* are able to move. (C) Symptoms of the seagrass wasting disease 4 days following the artificial infection of seagrass blades.
(Preston and King, 2005). The slimeways are also thought to aid nutrient absorption (Vishniac, 1955). *Labyrinthula* cells contain two vacuoles, thought to serve as excretory organs in the cell and may also regulate osmotic pressure, as their presence depends on the environmental salinity (Young, 1943).

The seagrass-*Labyrinthula* pathosystem is the best-studied relationship for this group. Quantitative polymerase chain reaction (PCR) has shown that *Labyrinthula* spp. occur in most marine eelgrass populations in Europe, but pathogenic species may only cause disease when infection is coupled with host stress (Bockelmann et al., 2013; Brakel et al., 2014). However, the potential impact of SWD was observed in the 1930s, when *Labyrinthula* killed up to 90% of *Zostera marina*, the most abundant Northern Hemisphere seagrass (reviewed in Muellein, 1989; Sullivan et al., 2013). Seagrass meadows are ecologically rich and productive marine ecosystems, and important carbon sinks (Christianen et al., 2013; Fourquean et al., 2012). They support commercial fish nurseries (Jackson et al., 2001) and influence bacterial pathogen populations (Lamb et al., 2017). Despite the important ecological and economic roles of their hosts, and widespread evidence of their cause of severe disease, research in *Labyrinthula* pathology is still under development.

*Labyrinthula* spp. tolerate high temperatures up to 28 °C, but, in tropical and subtropical seagrasses, increased temperature results in reduced virulence (Olsen and Duarte, 2015). Low salinity also inhibits *Labyrinthula* growth (Muehlenstein et al., 1988), and so seagrass meadows in high-salinity waters may have an advantage compared with those in truly marine locations (Vergeer et al., 1995). The transcriptomic host response to a *Labyrinthula* infection of seagrasses includes the down-regulation of genes related to reactive oxygen species (ROS) and chitinases, whereas a phenolic acid synthesis gene is highly expressed (Brakel et al., 2014). Phenolic metabolites may produce ‘synergistic’ host benefits. Resistance to *Labyrinthula* is density dependent, and diseased leaves have enhanced phenolic metabolite concentrations and these may reduce host susceptibility to *Labyrinthula* (Groner et al., 2016; McKone and Tanner, 2009; Trevathan-Tackett et al., 2015). The first seagrass genome (of *Z. marina*) has been published recently (Olsen et al., 2016). As a host for *Labyrinthula*, this expands the ability to investigate the genetic and molecular interactions between *Labyrinthula* and seagrass, and to improve our understanding of this potentially devastating pathogen.

**Stramenopiles – oomycetes as algal parasites**

Oomycetes cause considerable damage in aquatic crops, including red (Rhodophyta) and brown (Phaeophyceae) algae. Worldwide algal industries have increased dramatically (Loureiro et al., 2015). In 2012, global macroalgal production was more than 23 million tonnes (dry weight), with a market value greater than six billion US$ (FAO, 2014). Most of this production (approximately 80%) is used for human consumption, and the remainder for fertilizers, animal feed additives and in medical and biotechnological applications, including biofuel production (Loureiro et al., 2015; Stengel and Connan, 2015). Seaweed farming is also often integrated into fish and shellfish aquaculture (Loureiro et al., 2015). The total market value for red seaweed reached 3.8 billion US$ (FAO, 2014). Best known in the form of Nori (sushi wrap), *Pyropia* (formerly *Porphyra*) spp. are the most common cultivated red algae. Brown algae are often the predominant primary producers in temperate and cold marine coastal ecosystems (Rodgers and Shears, 2016), and are phylogenetically distant from plants, green and red algae. They differ from red and green algae in cell wall composition (Michel et al., 2010), halogen metabolism (La Barre et al., 2010), oxylipin synthesis (Ritter et al., 2008) and life cycles (Coelho et al., 2011). Brown algae include edible seaweeds (e.g. kombu – *Undaria pinnatifida*, wakame – *Saccharina japonica* and sugar kelp – *Saccharina latissima*), and some species are commercially used to produce alginate. Collectively, red and brown algae are affected by many diseases (reviewed in Gachon et al., 2010). Because of the economic importance of *Pyropia* cultivation, and the growing economic burden of diseases for this crop (up to 50% of farm costs are spent on disease management: Kim et al., 2014), this review focuses on *Pythium porphyrae* and *Olpidiopsis* sp., the two main oomycetes that cause diseases on this crop.

*Olpidiopsis* diseases (previously ‘chytrid rot’) caused Korean Nori farms to lose nearly 25% of their resale value in 2012–2013 (Kim et al., 2014), but local losses can be greater (Klochkova et al., 2012; Loureiro et al., 2015). Environmental factors, such as temperature and seasonality, affect the severity of disease outbreaks.

*Pythium porphyrae* causes red rot disease, which is one of the most damaging diseases affecting *Pyropia* farming (Fig. 7) with production losses being greater than 20% (Kawamura et al., 2005). Distinct bleached patches on the algal blades characterize the initial infections. The diversity of *Olpidiopsis* is beginning to be described using molecular tools, with the recognition of new species, such as *O. pyropiae* from Korean farms (Klochkova et al., 2016; Sekimoto et al., 2008), in addition to the Japanese *O. porphyrae*.

*Olpidiopsis* spp

*Olpidiopsis* pathogens are obligate intracellular pathogens with biotrophic lifestyles. During the off-season of algal cultivation, *Olpidiopsis* may survive in alternative red algal hosts (e.g. *Heterosiphonia* sp.) or as dormant cysts (Klochkova et al., 2012, 2016). Germinating zoospores form germ tubes which penetrate algal cell walls. Within the cells, multinucleate walled thalli form, which quickly develop into sporangia, which release zoospores. With advancing infection, host cells break down and lesions in the blades become prominent.
The establishment of *Olpidiopsis* sp. and *Pyropia* pathosystems for research is difficult as the infected host disintegrates in a matter of days. However, with alternative hosts, such as *Heterosiphoenia japonica*, stable dual cultures can be achieved (Klochkova et al., 2012). *Olpidiopsis* infection in this system is cell type specific, and occurs on the extended rhizoid-like apical cells. This specificity has been attributed to α(+) mannose in host cell walls, indicating a specific lectin–carbohydrate interaction during host–parasite recognition, necessary for zoospore attachment to host cells (Klochkova et al., 2012). Until recently, the only available treatment for these diseases was to wash algal blades with acid, a practice now banned because of environmental concerns (Kim et al., 2014).

*Pythium porphyrae*

Red rot disease, caused by *Py. porphyrae*, was first described by Arasaki (1947). The disease spreads via zoospores and starts with distinct, small, red patches on the host blades in which the zoospores germinate. The pathogen develops extensive cell-to-cell spreading mycelium. Dead host cells change colour to violet–red and green before they degenerate, generating holes that finally destroy entire blades (Fig. 7). Red rot disease management is only effective during the early stages of infection, and PCR methods are important to detect the pathogen early during the algal cultivation period (Park et al., 2001, 2006). Disease control involves immersion of cultivation nets into organic acid, freezing of infected cultures and the application of fungicides (Amano et al., 1995; Hwang et al., 2009; Park et al., 2006). These treatments have significant costs and environmental impacts (Park and Hwang, 2015). Disease-resistant host cultivars are an alternative control strategy. Partially resistant *Pyropia yezoensis* cultivars, generated from living cells in lesions of infected tissue, have altered cell wall polysaccharide contents (Park and Hwang, 2015). Sulfated galactans (e.g. porphyran) of the algal cell walls may be essential for cyst attachment and infection of *Py. porphyrae*, although the attraction and contact of zoospores are independent of host exudates (Uppalapati and Fujita, 2000). On resistant *Pyropia* sp., cysts with germ tubes frequently grow on the host thallus surfaces without penetration, and show no or delayed induction of appressoria (Uppalapati and Fujita, 2001). Although *Py. porphyrae* zoospores attach and encyst on a number of red algal species, red rot disease only develops on *Pyropia yezoensis* and *Bangia atropurpurea* (Uppalapati and Fujita, 2000).

*Pythium porphyrae* grows best in low-salinity water, possibly explaining why red rot occurs in farms near river banks (Klochkova et al., 2017). The pathogen can also infect and grow on land plants, including Chinese cabbage and rice. *Pythium porphyrae* carried from the land into coastal waters may increase damage in seaweed farms close to river inlets (Klochkova et al., 2017). This could enable molecular research on *Py. porphyrae* using the model hosts rice and *A. thaliana*. Genomic data are already available for *Pyropia* hosts (http://dbdata.rutgers.edu/nori/index.php).
and are currently being generated for Py. porphyrae and Olpidiopsis sp.

Eurychasma dicksonii

The most frequently recorded eukaryotic pathogen of brown algae is the biotrophic oomycete Eurychasma dicksonii. This phylogenetically basal oomycete (Beakes et al., 2012) is geographically widespread, tolerates a broad temperature range (4–23 °C) and infects at least 45 different species of brown algae in laboratory cultures (Müller et al., 1999). Similar to Olpidiopsis spp., Eu. dicksonii is a holocarpic endoparasite (Sekimoto et al. 2008). Zoospores attach, encyst and build adhesorium-like structures at the host surfaces. The parasite cytoplasm is transferred into the host via a needle-like structure which is associated with the formation of the adhesorium chamber at the host–spore contact point (Tsirigoti et al., 2015), similar to the plasmodiophorid 'Rohr und Stachel'. After penetration, multinucleate non-walled immature thalli, with double membrane envelopes of host and parasite (Sekimoto et al., 2008), develop and expand in the infected host cells, until each cell is almost filled. The plasmodial thallus develops into a sporangium with peripheral primary cysts (Fig. 8), which release biflagellate zoospores through apical exit tubes. The empty cyst walls form a net-like sporangium, which is a distinctive morphological feature of this pathogen (Petersen, 1905).

Eurychasma dicksonii can be cultured in Ectocarpus siliculosus, the first brown alga to be genomically sequenced (Cock et al., 2010), explaining why the Eurychasma–Ectocarpus pathosystem is the most thoroughly investigated parasitic interaction in brown algae. A cDNA analysis of Ec. siliculosus infected with Eu. dicksonii identified 3086 unigenes of oomycete origin. The dataset of Eu. dicksonii included 351 proteins predicted to be secreted, but contained no CRN or RxLR effector candidates (Grenville-Briggs et al., 2011). The Eu. dicksonii genes included glucanases and a potential alginate lyase, for which no homologues in land plant-infecting oomycetes have been identified. Alginates and glucans are key components of brown algal cell walls. Similar to higher oomycetes, which secrete cell wall-degrading enzymes involved in host penetration, this lyase is probably an adaptation to the marine host. In brown algae, β-1,3-glucans are usually not part of the cell walls, but are storage polysaccharides. Cell wall modification is a putative host defence mechanism against Eu. dicksonii. On infection, cell wall thickening and increased amounts of β-1,3-glucans at the penetration site may build physical barriers to pathogen invasion. Large amounts of β-1,3-glucan occur at cell surfaces of partially resistant Ectocarpus strains (Tsirigoti et al., 2015).

Although the infection mechanisms remain largely unexplored, molecular data exist on the host response to infection by Eu. dicksonii. Host genes differentially expressed during infection include those encoding for proteins involved in the detoxification of ROS and halogen metabolism (Strittmatter et al., 2016). The host genome includes candidate immune receptors of the leucine-rich and tetratricopeptide repeat families, which quickly evolve via an original exon shuffling mechanism (Zambounis et al., 2012).

Fig. 8 Life cycle of Eurychasma dicksonii in its brown algal host Ectocarpus siliculosus. (A) A spore (arrow) attaches to the algal surface and injects its content into the host. (B) Within the algal cytoplasm, the Eu. dicksonii thallus (arrow) develops which, at the early stage of infection, is unwalled. (C) Later, the pathogen thallus (arrow) has a cell wall and causes hypertrophic expansion of the algal host cell. (D) At the final stage, the complete thallus differentiates into a sporangium from which motile zoospores (arrow) are produced, completing the life cycle of the pathogen. (Figure reproduced from Strittmatter et al. 2016.)
Different hosts display different levels of susceptibility to Eurychasma (Gachon et al., 2009), and the resistance mechanisms are currently being investigated using cytological and molecular approaches. A targeted movement of host nuclei to pathogen penetration sites has been observed (Grenville-Briggs et al., 2011), and microtubule disorganization in the host occurs only when zosporogenesis of the pathogen begins (Tsirigoti et al., 2015).

OUTLOOK

Our understanding of eukaryotic plant pathogens is built on studies of fungi, animals (both opisthokonts) and oomycetes (stramenopiles). For the plant pathogens introduced here, the biochemical interactions with their plant hosts are just beginning to be unravelled through the introduction of study systems (e.g. the Eu. dicksonii–brown algae interaction) or the generation of reference genomes (Pl. brassicae, Phytomonas spp.). This will allow the presented pathogens to take a more prominent place in the molecular plant pathology field in the coming years, create deeper insights into how these pathogens interact with their hosts and how they have evolved. This should finally lead to new strategies for the control of these pathogens.

AUTHOR CONTRIBUTIONS

A.S. and S.N. initiated and organized the manuscript, and the other authors are listed alphabetically. Section contributions are as follows: Phytomonas (J.L., A.N., A.S.), plasmodiophorids (A.S., S.N., S.B., R.E.F., U.M., N.D., A.L.), Labyrinthula (S.N., B.K.S.), oomycetes (C.M.M.G., M.A., S.N., J.B., M.E.). All the authors read the manuscript and agreed to publication.

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