Are All Red Algal Parasites Cut from the Same Cloth?

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Are all red algal parasites cut from the same cloth?

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Abstract

Parasitism is a common life strategy throughout the eukaryotic tree of life. Many devastating human pathogens, including the causative agents of malaria and toxoplasmosis, have evolved from a photosynthetic ancestor. However, how an organism transitions from a photosynthetic to a parasitic life history strategy remains mostly unknown. This is largely because few systems present the opportunity to make meaningful comparisons between a parasite and a close free-living relative. Parasites have independently evolved dozens of times throughout the Florideophyceae (Rhodophyta), and often infect close relatives. The accepted evolutionary paradigm proposes that red algal parasites arise by first infecting a close relative and over time diversify and infect more distantly related species. This provides a natural evolutionary gradient of relationships between hosts and parasites that share a photosynthetic common ancestor. Elegant microscopic work in the late 20th century provided detailed insight into the infection cycle of red algal parasites and the cellular interactions between parasites and their hosts. Those studies led to the use of molecular work to further investigate the origins of the parasite organelles and reveal the evolutionary relationships between hosts and their parasites. Here we synthesize the research detailing the infection methods and cellular interactions between red algal parasites and their hosts. We offer an alternative hypothesis to the current dogma of red algal parasite evolution and propose that red algae can adopt a parasitic life strategy through multiple evolutionary pathways, including direct infection of distant relatives. Furthermore, we highlight potential directions for future research to further evaluate parasite evolution in red algae.

Keywords: Rhodophyta; parasite evolution; pit connections; Florideophyceae, organelles

Introduction

Parasitism has evolved innumerable times throughout the eukaryotic tree of life [1]. Some of the more virulent parasites have transitioned from a once photosynthetic ancestor, including the causative agents of malaria and related mammalian diseases [2,3]. Therefore, understanding the evolutionary trajectory between photosynthesis and abandoning autotrophy for a parasitic strategy, is of particular importance. Red algal parasites are uniquely valuable to study this path because they have independently evolved many times, providing literally dozens of discrete events to compare [4–7]. This system may provide novel insights into the evolution of parasitism, especially with regard to the early stages of transitioning from a photosynthetic past.

Red algal parasites exclusively infect other red algae, typically ones with which they share a recent common ancestor [5–8]. The relationship between host and parasite was first recognized using morphological similarities in the life-cycles of parasites and their hosts [9]. More recently, molecular data have confirmed this hypothesis [4–6,10]. Traditionally red algal parasites have been placed into two different groups, based on their phylogenetic relationships with their hosts [6]. Adelphoparasites (adelpho is Greek for “kin”) are closely related to their host and often infect only one host, whereas allopasites are more divergent from their host(s) [4,6]. Currently, adelphoparasites are believed to make up roughly 90% of all red algal parasites [6].

Among the Florideophyceae, parasites belonging to at least 66 different red algal genera have evolved independently over 100 times (Tab. 1) [11]. The accepted evolutionary paradigm proposes that adelphoparasitism is the initial state, followed by parasite diversification, which leads to the development of allopasites (Fig. 1). These “older” parasites can infect more distantly related taxa, and make up roughly 10% of red algal parasites [5,7]. Due to their rarity, allopasites are relatively unstudied, with the exceptions of Choreocolax polysiphoniae and Harveyella mirabilis.

The importance of red algal pit connections

One of the defining characteristics of the florideophycean red algae is the ability of cells to form connections with their adjacent cells [12]. There are two distinct forms of these “pit connections” formed by red algae. Primary pit connections...
Red algal parasites often evolve from a recent common ancestor with their host. These ‘adelphoparasites’ (purple branch) are usually host-specific. However, parasites that have diversified into more than one species and/or infect distantly-related hosts, are known as ‘alloparasites’ (blue branches).

Spore germination and host infection

Rhodophytes lack flagella in all stages of their life cycle, making the initial stages of locating a host a passive process. Once a parasite spore lands upon a susceptible host, the parasite carpospore (2N) or tetraspore (1N) will germinate and undergo an initial cell division [21]. Adelphoparasite cells will divide between 1 and 3 more times before one of the cells forms a rhizoid that penetrates the surface of the host, growing into the wall of a host epidermal cell [21]. The tip of the rhizoid swells isolating a single parasite nucleus along with its organelles into a conjunctor cell which divides from the infection rhizoid [21,22]. This conjunctor cell then fuses, via a secondary pit connection, with the adjacent host cell (Fig. 2a). The contents of the conjunctor cell, which include the parasite nucleus and organelles, are deposited into the host cell, thus forming a heterokaryotic cell (containing both parasite and host nuclei) [8,17,21]. This connection between the parasite infection rhizoid and the transformed host cell is sealed by a pit plug that was formed previously during the initial fusion between the conjunctor cell and the parasite infection rhizoid [8,21].

The differences between adelpho- and alloparasite infection cycles

Differences in adelphoparasite and alloparasite infection cycles

Fig. 1 Red algal parasites often evolve from a recent common ancestor with their host. These ‘adelphoparasites’ (purple branch) are usually host-specific. However, parasites that have diversified into more than one species and/or infect distantly-related hosts, are known as ‘alloparasites’ (blue branches).
network of multicellular filaments between the host cells [8,23,24]. These filaments enable the parasite to spread numerous cells deep into the host away from the initial site of infection (Fig. 2b). Each alloparasite cell in these filaments contains a single nucleus and can form a conjunctor cell and secondary pit connection through which the parasite deposits its cellular contents into the host, creating a heterokaryotic cell [8,23,24].

Inside the heterokaryon
After the host cell becomes heterokaryotic, both adelpho- and alloparasites take control of the host cellular machinery [8,21]. Almost immediately upon infection, the hosts’ central vacuole tonoplast is lysed, allowing cytoplasm to spread throughout the space previously occupied by the vacuole [4,25]. Subsequently, the number of organelles including plastids, mitochondria, and ribosomes increases throughout the cytoplasm causing it to appear denser [8,21,23,25]. Along with the increase in cytoplasmic organelles comes an increase in cell size (hypertrophy), a process in which the cell can grow to 40 times its original size [8,22,26]. In addition to the increased organelles, either the parasite or host nuclei also increase in size and/or number [8,23,24].

Goff and Coleman used 4',6-diamidino-2-phenylindole (DAPI) staining and microspectrofluorometry to examine the interactions between the alloparasite, Choreocolax polysiphoniae and its host Vertebrata lanosa [8]. Their study showed that infected V. lanosa central cells will become enlarged and the nuclei will undergo DNA synthesis but not nuclear division resulting in polyploid host nuclei [8]. Alternatively, in infected V. lanosa pericentral cells, the host nuclei will either increase in size, increase in number, or some combination of both [8]. An increase in the number of host nuclei is the most common response [8]. Host cells that are adjacent to infected cells and connected by pit connections will not show any cytological transformation [8,23]. Conversely, no DNA synthesis or nuclear division has been observed from the host nucleus after infection by the adelphoparasite Janczewskia gardneri [24]. Instead, the adelphoparasite nucleus rapidly undergoes DNA synthesis, generating numerous parasite nuclei inside a single host cell (Fig. 2) [24]. The adelphoparasite subsequently spreads to...
additional host cells through the formation of conjunctor cells that can infect adjacent host cells [21]. Adelphoparasites can also form rhizoidal infection cells, which are multinucleate and contain large numbers of mitochondria, ribosomes, and dedifferentiated host-derived proplastids and can fuse with more distant host cells [21].

Alloparasites are capable of mitotic divisions to create the multicellular filaments that spread between host cells [23,24]. However, the alloparasite nucleus does not undergo DNA synthesis inside the host cell [8,23,24]. Therefore, parasite nuclei remain at a 1:1 ratio with the number of secondary pit connections between parasite and host cells [8,23,24]. Once inside a heterokaryon, the adelphoparasite continues spreading to adjacent host cells via pit connections, while utilizing the host to progress through its lifecycle and reproduce [21].

**Formation of reproductive structures**

As the adelphoparasite spreads throughout the host, a gall or “erumpent pustule” begins to form as host cells continuously expand upon infection by the parasite. Eventually the adelphoparasite will start to form reproductive structures [21]. If the original infecting spore was haploid the parasite will form carposporangia that can be fertilized by a spermatozoid from another parasite forming a diplodiploid carposporophyte that will eventually release carpospores [21,27]. If the original infection was from a diplodiploid carpospore, the parasite will undergo meiosis forming haploid tetraspores that will be released from the erumpent pustule [21,27].

An alloparasite does not spread through the host like the adelphoparasite. Rather than forming a gall from invaded cells, a host pericentral cell containing a parasite nuclei and many host nuclei will form a protuberance [8]. This protuberance will become isolated from the original host cell and undergo mitotic divisions, which produces the mature parasite pustule containing reproductive cells similar to that of adelphoparasites [8]. After the reproductive cells are released, the former host tissue that made the erumpent pustule becomes necrotic [8]. While the fate of future adelphoparasites lies in the released spores, alloparasites are able to continue their infection of the same host as parasite filaments continue to grow into uninfected areas [8].

**Organelles**

Studies of cellular organelles have yielded particularly interesting findings during investigations of red algal parasite biology. Early studies established the role of secondary pit connections between the parasite and host cells and demonstrated their role in transferring the parasite nucleus to the host cell [8,17,21]. However, it was unclear whether the parasite maintained its own mitochondrion and plastid or if it utilized the host organelles once the parasite nucleus was transferred into the host cell. Cytoplasmic organelles support many major metabolic pathways as well as play major roles in cellular energy and carbohydrate production. It has been well established that purifying selection is relaxed on parasite organellar genes that become unnecessary, leading to genome reduction in parasites as they increasingly rely on a host for energy and carbohydrates [28–32]. Therefore, it seems likely that some red algal parasite mitochondrion and plastid genes would be truncated or even lost over time. The origin and roles of mitochondria and plastids in the parasite-host interaction may reveal key information regarding red algal parasite biology and their ability to infect and control the host cellular machinery.

First using the alloparasite *Choreocolax polysiphoniae*, and later the adelphoparasites *Gracilariophila oryzoides* and *Gardneriella tuberifera*, researchers observed that in addition to the parasite nuclei, organelles are also transferred to the host cell via the conjunctor cell upon infection [21,24]. Once molecular tools became more widely available, Goff and Coleman utilized restriction fragment length polymorphisms (RFLPs) to investigate the origin of mitochondria in the adelphoparasites *Plocamiocolax pulvinata*, *Gracilariophila oryzoides*, and *Gardneriella tuberifera* and their respective hosts, *Plocamium cartilagineum*, *Gracilariopsis lemaneiformis*, and *Sarcodiotheca gaudichaudii* [22]. This work revealed that *P. pulvinata* and *G. oryzoides* maintain a genetically unique mitochondrial genome and that both the parasite and host mitochondria are present within the heterokaryotic cells [22]. The study was unable to conclusively demonstrate that the mitochondrial genome from *Gardneriella tuberifera* is unique from that of *Sarcodiotheca gaudichaudii*, due to the extremely close relationship between the two species [22].

The mitochondrial genomes of the adelphoparasites *Plocamiocolax pulvinata* and *Gracilariophila oryzoides*, as well as its host *Gracilariopsis andersonii*, were recently sequenced. These data paved the way for a new level of fine-scaled investigations of red algal parasites, elucidating details of the organellar genome architecture that was previously unattainable [33]. When comparing the mitochondrial genome sequences of the parasites with the free-living host, the *atp8* and *sdhC* genes from *G. oryzoides* were determined to be pseudogenes [33]. Furthermore, *atp8* was determined to be absent from *P. pulvinata*. However, the authors noted that according to sequenced cDNA libraries, the genes were still transcribed [33]. Recent second generation sequencing of additional samples of these species has revealed that the “missing” genes are all present and lack frameshift mutations (Salomaki and Lane, unpublished). These data suggest that purifying selection is maintained on red algal parasite mitochondria and that even though much of the parasite life cycle exists inside a host cell, red algal parasites still require their own mitochondrion for their survival.

While evident that parasites maintain their native mitochondrial genome, microscopy and molecular studies have demonstrated that red algal parasites do not maintain their own plastid [21,22]. Microscopy shows that the spores of adelphoparasites *Gracilariophila oryzoides*, and *Gardneriella tuberifera* contain proplastids lacking photosynthetic pigments, phycobilisomes, and thylakoids [21]. Once the parasite injects its nuclei and organelles into a host cell, the host plastids transform and their light harvesting phycobilisomes disappear from the thylakoids [21]. After rapid dedifferentiation, simple proplastids that are similar to the infecting parasite plastid bud off the host plastid [21]. As the parasite nuclei, mitochondrion, and host derived proplastids spread to adjacent cells through pit connections, plastids from the newly infected host cells also rapidly dedifferentiate.
into proplastids [21]. Eventually cells emerge from the heterokaryotic host cell containing only parasite nuclei, parasite mitochondrion and a host-derived proplastid [21]. RFLP analysis was utilized to investigate whether this plastid was a genetically unique parasite plastid, or instead, the parasite was incorporating a host-derived proplastid [22]. This study revealed that adelphoparasites Placamiocolax pulvinata, Gracilariophila oryzoides, and Gardneriella tuberifera and their hosts had identical banding patterns [22]. Subsequent DNA sequencing of the variable plastid rbcL-rbcS spacer region revealed that the plastid from both hosts and parasites were genetically identical, confirming that the parasite plastid is a dedifferentiated host plastid [22].

Interestingly, two studies suggest that the plastid may be capable of differentiating again into a photosynthetic plastid. While investigating the photosynthetic rates and C¹⁴ transfer from Polysiphonia (=Vertebrata) lanosa to the alloparsite Choreocolax polysiphoniae, Callow et al. examined the alloparsite pustules after dissection from their host [34]. The authors note that many of the parasite pustules had a pinkish hue and incorporated radioactively labeled C¹⁴ into their thallus [34]. Furthermore, the carbon fixation rate increased over time (up to 66 hours) leading the authors to conclude that C. polysiphoniae is capable of photosynthesis on its own. However, the source of photosynthetic activity in dissected C. polysiphoniae pustules may be from host cells that have been incorporated into the pustule as observed in that study, and independently, by Kugrens and West, and Goff examining Janczewskia gardneri [21,26,34]. Additionally, the status of J. gardneri as a parasite or obligate epiphyte has been debated due to its pigmentation [24,35,36]. Most recently, it was noted that during the early stages of the interaction between J. gardneri and its host, Laurencia spectabilis, J. gardneri exists as colorless cells and “infects” host cells in the same manner as other adelphoparasites. As J. gardneri cells erupt from the host they remain colorless but the cells become pigmented once the adelphoparasite becomes reproductively mature [24]. Whether this pigmentation originates from host cells in the pustule matrix, or if the plastid differentiates back into a photosynthetic plastid remains unknown.

**Nutrient transfer**

With the exception of a few adelphoparasites that gain pigmentation upon reproductive maturity, red algal parasites are not capable of photosynthesis on their own and must obtain carbohydrates and other nutrients from a host. After parasite infection, the host (now heterokaryotic) cell loses the ability to photosynthesize as a result of plastid dedifferentiation [21]. This leads to a differential gradient of carbon between the heterokaryotic cell and the adjacent normally functioning host cells [21,22,25]. To account for the loss of carbon fixation, uninfected host cells directly photosynthesize to heterokaryon and parasite cells that they are connected to via pit connections [24,37].

The first studies investigating carbon transfer between a red algal host and its parasite found three products of photosynthesis (floridoside, isofloridoside, and manitol) were transferred from the host to its parasite via a concentration gradient [34,38]. Later five different sugar species were identified to be assimilated by the host Rhodomela confervoides and translocated to its parasite Harveyella mirabilis [39]. Investigations into carbon translocation in H. mirabilis demonstrated the localization of carbon, from being fixed by the photosynthetic host through its movement into the parasite cells and revealed that heterokaryon cells incorporated more C¹⁴ than neighboring uninfected host cells [37]. Furthermore, it was determined that starch was not distributed evenly throughout the parasite cells as might be expected, but instead was being directed preferentially to parasite reproductive cells [8,37]. Given the capabilities of parasites for obtaining carbon from the host, the role of the maintained proplastid in parasite cells remains in question.

**Host specificity and parasite resistance**

Red algal parasites are known to be extremely host specific, usually infecting one to a few, closely related host species [7,40,41]. A study using the adelphoparsite Janczewskia morimotii tested its ability to infect 15 other species including close relatives of its natural host, Laurencia nipponica, as well as members of different genera [42]. While J. morimotii was capable of infecting two close relatives of its natural host, the more distantly related potential hosts prevented parasite infections [42]. Additionally, the host specificity of Leachiella pacifica was assessed through culture studies attempting to use parasites isolated from Polysiphonia paniculata to infect Pterocladia bipinnata and vice-versa [41]. Parasites isolated from P. paniculata could infect other populations of the same species as well as some other Polysiphonia species, however they could not infect Pt. bipinnata populations that were susceptible to parasites isolated from other Pt. bipinnata specimens [41]. These L. pacifica isolates showed strong genus-level host specificity. However, due to the greatly reduced morphology of red algal parasites, it cannot be ruled out that parasites isolated from different genera are, in fact, different host-specific species. Revisiting this study with molecular data would strengthen our understanding of host specificity and potentially reveal cryptic parasite species.

Dawsoniocolax bostrychiae and Bostrychiocolax australis are parasites that infect Bostrychia radicans [40]. A study on host range and specificity of these parasites on a variety of potential hosts, yielded similar results to the J. morimotii study: the genetic distance between parasite and host has a strong negative correlation with susceptibility to parasite penetration and infection [40]. The authors note that they encountered hosts that are resistant to parasite infection, including some host populations that contained resistant and susceptible specimens [40]. In several cases the parasite was capable of forming an initial infection in a resistant host, however the host cell or cells adjacent to the infected cell died off, preventing the parasite from spreading further into the host [40]. However, subsequent molecular studies revealed phenotypic plasticity and cryptic diversity in B. radicans [43]. Therefore, the possibility remains that resistant and susceptible hosts from the host resistance study were actually different species. These findings emphasize the need
for ongoing taxonomic evaluation of red algal parasites and their hosts. Without the taxonomic framework, questions about whether or not the host is actually resisting parasite infection cannot be answered conclusively.

Many questions remain

Why does the parasite maintain a copy of the host plastid as it is forming its own reproductive cells and spores? Other parasites that have evolved from a plastid bearing ancestor, including the apicomplexans *Eimeria tenella* and *Plasmodium falciparum*, the parasitic plant *Epifagus virginiana* and many others, maintain a reduced plastid for cellular functions other than photosynthesis, such as fatty acid biosynthesis [2,30,31]. However, none of these plastid-bearing parasites steal a plastid from their host like the red algal adeloph- parasites. Are adelophparasites genetically similar enough to their hosts that they can target nuclear-encoded proteins to the host-derived plastid and utilize those products for fatty acid biosynthesis? Genomic analyses of signaling and targeting peptides for plastid targeted nuclear genes in red algal parasites, combined with transcriptomic and proteomic approaches, will provide valuable insight into the role of the plastids in the infection mechanism and parasite life cycle. The use of additional molecular tools including in-situ hybridization would enable researchers to localize parasite nuclear-encoded proteins in the heterokaryotic cell.

Furthermore, the taxonomic range and multiple independent origins of red algal parasites makes it difficult to make generalizations based on a few observations. Thus far, the origin of red algal parasite plastids has only been investigated in adelophparasites and the origin of the allop-algal plastid remains unknown. The assumption is that allop-parasites first progress through an adelophparasite stage and also maintain a co-opted host plastid. However, there are distinct developmental differences between adelph- and allop-parasites, including the initial steps of infection and allop-parasites inability to synthesize DNA in heterokaryon cells (Fig. 2). Therefore, it seems plausible to propose an alternative hypothesis that, rather than passing through an adelophparasite stage, allop-parasites are capable of directly evolving infection mechanisms to parasitize distantly related hosts. In the proposed scenario, allop-parasites would presumably maintain their own plastid, as they are likely incapable of utilizing such a genetically distant host plastid. Preliminary genomic data from *C. polysiphoniae* indicates this may, in fact, be the case (Salomaki and Lane, unpublished).

Future research investigating red algal parasite evolution will provide unique insight into the effects of transitioning from a free-living to a parasitic life strategy. Molecular data has supported morphological observations that red algal parasites share a recent common ancestor with their hosts [4–6,10]. However, further use of molecular tools is essential to provide a robust taxonomic framework of red algal parasites and their hosts. Only then can meaningful observations be made about host specificity and parasite resistance. With the technological advances of the past few decades and continually decreasing costs of DNA sequencing, information about the relationships between parasites and their hosts, unraveling the roles of parasite and host interactions, and the origins and function of organelles is within our grasp.

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The following declarations about authors’ contributions to the research have been made: conceived of the topic for this review and wrote the initial draft: EDS; provided editorial feedback, conceptual guidance and figures have been made: conceived of the topic for this review and wrote the initial

Competing interests

No competing interests have been declared.

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