

## Parasite transmission through suspension feeding

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### Abstract

Suspension-feeding bivalve molluscs are confronted with a wide range of materials in the benthic marine environment. These materials include various sized plankton and the organic material derived from it, macroalgae, detritus and a diversity of microbial parasites that have adapted life stages to survive in the water column. For bivalve parasites to infect hosts though, they must first survive and remain infectious in the water column to make initial contact with hosts, and once in contact, enter and overcome elaborate pathways for particle sorting and selection. Even past these defenses, bivalve parasites are challenged with efficient systems of mechanical and chemical digestion and highly evolved systems of innate immunity. Here we review how bivalve parasites evade these hurdles to complete their life cycles and establish within bivalve hosts. We broadly cover significant viral, bacterial, and protozoan parasites of marine bivalve molluscs, and illustrate the emergent properties of these host-parasite systems where parasite transmission occurs through suspension feeding.

### 1. Introduction

A typical liter of seawater collected from the surface waters of coastal seas can contain millions of algal cells, billions of bacteria and microbial eukaryotes, and up to 100 billion viruses (Pedrós-Alió, 2006; Suttle, 2007; Amend et al., 2012; Breitbart, 2012). This abundance of microbial life suspended in the water column has created a niche for suspension feeding, a trophic strategy that only rarely occurs on land. Suspension

feeders have adapted numerous mechanisms for sorting and capturing food particles that are often aggregated with other microbes, mineral grains, detritus, and various other incidental particles (Rubenstein and Koehl, 1977; Shimeta and Jumars, 1991; Kach and Ward, 2008). The importance of this feeding strategy is apparent in the bivalve molluscs, which have evolved distinct morphological structures capable of efficiently exploiting suspended particles as a source of food (Jorgensen, 1996; Ward, 1996). Owing to this efficiency, bivalves simultaneously sort, select, process, reject, ingest and transport food items (Shumway, 1985; Riisgard and Larsen, 1995; Ward and Shumway, 2004). These bulk-feeding activities contribute significantly the flux of organic material and nutrients from the water column to the benthos and back (Dame et al., 1984; Prins et al., 1998; Chauvaud et al., 2000; Ward and Shumway, 2004), and also confront these mostly sedentary and sessile generalist consumers with a diverse range of materials, including the many pathogenic microparasites that have adapted free-living stages capable of surviving adrift in the water column (Thompson et al., 2005).

Parasites with free-living stages often function as prey for generalist consumers (Johnson et al., 2010; Thieltges et al., 2013) such as bivalve molluscs (Thieltges et al., 2008). The consumption of parasites is neither rare nor limited to bivalves. Lafferty et al. (2006), for example, estimated that almost half of the trophic links in an estuarine food web involved predation on parasites. Although consumption by non-focal hosts is common (Mouritsen and Poulin, 2002; Lafferty et al., 2006; Thieltges et al., 2008; Johnson and Thieltges, 2010), the ubiquity of free-living stages of viruses, bacteria, and protozoans in coastal waters (Poulin and Morand, 2000; Thompson et al., 2005) suggests that consumption is a major pathway for parasite transmission in marine bivalves. The question of how bivalve molluscs survive in parasite-rich environments without adaptive immunity has been of fundamental interest to physiologists and immunologists (Martin et al., 2006), and a considerable body of work has identified sophisticated systems of innate immunity in bivalves (Kiss, 2010; Zhang et al., 2014, 2015) including highly developed processes for cellular internalization of parasites (Hine, 1999; Canesi et al., 2002; de Freitas Rebelo et al., 2013). Despite progress understanding the processes that allow bivalve parasites to avoid these cellular and molecular defense factors and proliferate in host tissues (Hervio et al., 1991; Wright et al., 2002; Ahmed et al., 2003; Brown and Reece, 2003; Munoz et al., 2003; Schott and Vasta, 2003; Kim et al., 2008; Flye-Sainte-Marie et al., 2009; Soudant et al., 2013), our understanding of parasite transmission remains limited by our knowledge of (1) the fate of free-living parasite stages in the environment, (2) processes of initial dissemination in host tissues, and (3) parasite life cycles, including interactions with secondary or intermediate hosts.

Here, we review mechanisms of parasite transmission and spread in suspension feeding marine bivalves. We first begin with a brief review of parasites of marine and estuarine bivalve molluscs, focusing on microparasites that are encountered through suspension feeding processes. We review the present understanding of their transmissive stages in the water column and dispersal from hosts, and then focus on the selection of particulate matter by bivalve molluscs, emphasizing behaviors of bivalve parasites to evade digestion and host defenses to successfully establish within host tissues. We conclude by integrating interactions between parasites and bivalve hosts to describe the life and reproductive cycles of bivalve parasites. Our intention is not to exhaustively describe all parasites of marine bivalves. Rather, we aim to direct new perspectives for integrative research by highlighting and connecting emergent properties from systems where bivalve hosts encounter parasites through feeding.

## 2. Parasites of bivalve molluscs

Bivalve molluscs, including oysters, clams, quahogs, scallops, cockles, and mussels, play host to a wide range of parasites (Table 1). These can include many agents of human disease, such as polio (Lees, 2000), Norwalk (Morse et al., 1986; Baker et al., 2011) and hepatitis (Mele et al., 1989) viruses, Listeria (de Simon et al., 1992), Salmonella (Greenwood et al., 1998), Shigella (Iwamoto et al., 2010) and Vibrio (Iwamoto et al., 2010; Audemard et al., 2011; Powell et al., 2013; Thongchan et al., 2013) species of bacteria, and protozoan parasites such as Cryptosporidium spp., Giardia duodenalis and Toxoplasma gondii (Fayer et al., 2004; Robertson, 2007) that are free-living in coastal waters and incidentally concentrate in bivalve tissues through particle-feeding processes (Meyers, 1984; Rippey, 1994). The role of bivalves as transient reservoirs of parasites of humans and other vertebrates is well documented (Potasman et al., 2002; Daniels, 2011; Sandifer and Sutton-Grier, 2014). Generally, these disease agents cause little to no ill effects in bivalve hosts but are transmitted to their definitive vertebrate hosts through the consumption of raw or undercooked shellfish (Rippey, 1994; Bellou et al., 2013).

There are numerous examples of parasites targeting bivalve molluscs as definitive hosts (Sindermann and Rosenfield, 1967; Bower et al., 1994; Elston, 1997; Paillard et al., 2004; Renault and Novoa, 2004; Soudant et al., 2013; Table 1), and disease outbreaks are increasingly recognized as a significant constraint to aquaculture production and the sustainability of wild shellfisheries (Harvell et al., 1999; Mann and Powell, 2007; Mann et al., 2009). Marine protists, among the most abundant eukaryotes on Earth (Baldauf, 2003; Tsui et al., 2009; Raghukumar and Damare, 2011), are also among the most commonly reported agents of bivalve diseases (Fig. 1). Among the most destructive are the intracellular parasites of the genera Bonamia, Haplosporidium, Marteilia, and Perkinsus, including Bonamia exitiosa, Bonamia ostreae, Marteilia refringens, Perkinsus marinus, and Perkinsus olseni (Grizel et al., 1988; Ragone Calvo et al., 2003;

Carnegie and Cochenne-Laureau, 2004; Villalba et al., 2004; Fernández Robledo et al., 2014; Soudant et al., 2013). These protozoan parasites are under surveillance by the World Organization for Animal Health (OIE; <http://www.oie.int/>; Aquatic Animal Health Code, Section 11: Diseases of Molluscs) due to their cosmopolitan distribution and severe impacts on harvests of wild and farmed bivalves. Groundbreaking progress on methods of parasite purification and cell culture, parasite virulence factors, and molecular tools have advanced both mechanistic studies of transmission and reporting of these and other protozoan parasites. This wealth of information has elevated protozoan parasites as models for basic and translational research on the emergence and spread of marine diseases (Grizel et al., 1988; Carnegie and Burreson, 2011; Burge et al., 2014; Fernández Robledo et al., 2014).

Viruses are by far the most abundant and genetically diverse life form in the oceans (Cochlan et al., 1993; Maranger and Bird, 1995; Wommack and Colwell, 2000; Suttle, 2005, 2007; Breitbart, 2012) (Fig. 1). The sheer abundance and narrow host range of most viruses suggests that viral infections place significant controls on the abundance and composition of planktonic communities (Wommack and Colwell, 2000).

Methodological constraints, such as the lack of continuous bivalve cell lines, have impeded the discovery, detection, and classification of most viral infections in marine bivalves (Elston, 1997; Renault and Novoa, 2004), and bivalve virology remains an emerging research frontier. Viruses are likely responsible for many of the cryptic mortality events observed both in bivalve hatcheries and wild stocks (Renault and Novoa, 2004) and virus-like infections have been identified and associated with mortalities of wild and cultured bivalves since the late 1960s (Farley, 1972; Elston, 1997; Renault and Novoa, 2004). Many proliferative diseases of commercially important marine bivalves, such as disseminated neoplasia, are of likely but unconfirmed viral etiology (Elston et al., 1992; Barber, 2004; Romalde et al., 2007). The initial classification of bivalve viruses is most often based on observations of morphology determined from histopathology and electron microscopy, making the definitive identification of viral taxonomy tenuous. However, viral infections have been interpreted as putative members from a diversity of viral taxa, including DNA viruses such as Herpesviridae (Farley, 1972; Comps and Cochenne, 1993; Hine et al., 1998; Arzul et al., 2001a,b,c; Renault et al., 2001; Renault and Arzul, 2001; Friedman et al., 2005; Burge et al., 2006) and Papovaviridae (Choi et al., 2004), RNA viruses such as Reoviridae (Meyers, 1979), Iridoviridae (Elston and Wilkinson, 1985), and Picornaviridae (Jones et al., 1996; Novoa and Figueras, 2000; Carballal, 2003), and retroviruses (Oprandy et al., 1981). As with many viruses infecting vertebrate hosts, most bivalve viruses are host-specific (Davison et al., 2005; Suttle, 2007), although this is not always the case (Arzul et al., 2001b,c). Herpes-like viruses infecting oysters have been classified as a member of the Herpesviridae family under the name Ostreid herpesvirus-1 (OsHV-1; Davison et al., 2005; Savin et al., 2010; Jouaux et al., 2013). The apparent lack of host specificity of OsHV-1 is unique among the Herpesviridae, and this herpesvirus has been found to infect

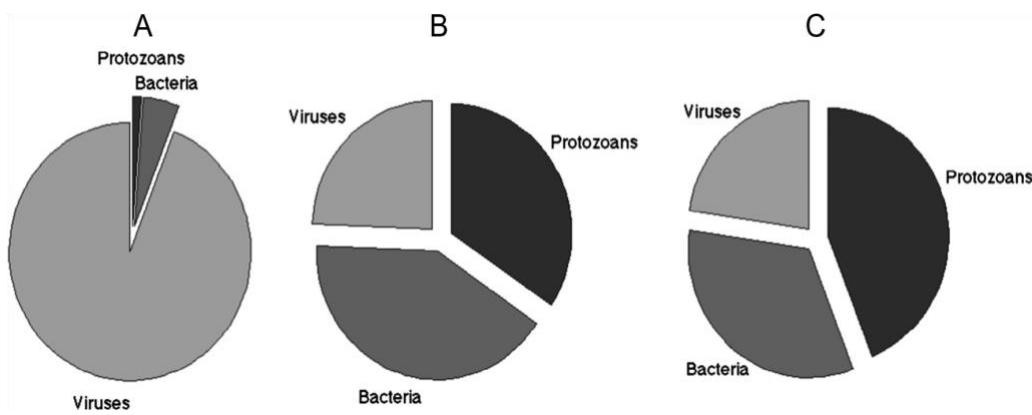
at least seven bivalve species across four genera (Arzul et al., 2001b,c) where putative hosts include *Crassostrea gigas*, *Crassostrea angulata*, *Crassostrea ariakensis*, *Ostrea edulis*, *Ruditapes philippinarum*, *Ruditapes decussatus*, and *Pecten maximus* (Renault et al., 2001; Arzul et al., 2001a,b; Lynch et al., 2012). In the case of OsHV-1, it is suspected that the virus uses common, conserved systems among bivalves to enter and establish within this diverse host community, having emerged as a consequence of selection arising from intensive aquaculture of multiple bivalve species (Arzul et al., 2001b,c). Further studies seem to indicate that OsHV-1 has the capacity to evolve rapidly, and an increase in mortalities of *C. gigas* linked with OsHV-1 infection along French coasts since 2008 has been associated with the detection of a virulent OsHV-1 variant, designated OsHV-1 Ivar (Segarra et al., 2010; Martenot et al., 2011). Continued observations of additional, new forms reinforce the possibility of the emergence of different and potentially virulent OsHV-1 variants (Martenot et al., 2011, 2012).

**Table 1.** Parasites that have impacted bivalve molluscs, by host species, mode of transmission, and key references selected by the author.

Parasite	Host species	Mode of transmission	Reproduction outside hosts?	Key references
<i>DNA viruses</i>				
Herpes-like viruses	<i>Crassostrea virginica</i> <i>Ostrea angasi</i> <i>Tiostrea chilensis</i>	Direct	No	Farley (1972) Hine et al. (1998)
Ostreid herpesvirus 1 (OsHV-1)	<i>Crassostrea gigas</i> <i>Crassostrea angulata</i> <i>Crassostrea ariakensis</i> <i>Ostrea edulis</i> <i>Ruditapes philippinarum</i> <i>Pecten maximus</i>	Direct	No	Renault et al. (2001) Arzul et al. (2001a) Arzul et al. (2001b)
Papova-like viruses	<i>Crassostrea gigas</i>	Direct	No	Choi et al. (2004)
<i>RNA viruses</i>				
Reo-like viruses	<i>Crassostrea virginica</i>	Direct	No	Meyers (1979)
Irido-like viruses	<i>Crassostrea gigas</i>	Direct	No	Elston and Wilkinson (1985)
Picorna-like viruses	<i>Mytilus edulis</i> <i>Perna canaliculus</i> <i>Ruditapes decussatus</i>	Direct	No	Jones et al. (1996) Novoa and Figueras (2000)
<i>Retroviruses</i>				
Retro-like viruses	<i>Mya arenaria</i>	Direct	No	Oprandy et al. (1981)
<i>Bacteria</i>				
<i>Vibrio tapetis</i>	<i>Ruditapes philippinarum</i>	Direct	Yes	Paillard et al. (1994) Borrego et al. (1996) Allam et al. (2000)
<i>Vibrio pectenicida</i> <i>Vibrio tubiashii</i>	<i>Pecten maximum</i> <i>Crassostrea gigas</i> <i>Ostrea edulis</i> <i>Crassostrea sikamea</i> <i>Panope abrupta</i>	Direct Direct	Yes Yes	Lambert et al. (2001) Hada et al. (1984) Elston et al. (2008)
<i>Vibrio aestuarianus</i> <i>Vibrio splendidus</i> <i>Vibrio harveyi</i>	<i>Crassostrea gigas</i>	Direct	Yes	Lacoste et al. (2001) Labreuche et al. (2006)
Roseovarian crassostreae	<i>Crassostrea virginica</i>	Direct	Unknown but likely	Ford and Borrero (2001) Maloy et al. (2007a,b)
Nocardia crassostreae	<i>Crassostrea gigas</i> <i>Ostrea edulis</i> <i>Mytilus galloprovincialis</i>	Direct	Unknown but likely	Friedman et al. (1998) Carella et al. (2013)
<i>Protozoans</i>				
<i>Perkinsus chesapeaki</i>	<i>Cerastoderma edule</i> <i>Tagelus plebeius</i> <i>Mya arenaria</i> <i>Macoma baltica</i>	Direct	No	Burreson et al. (2005) Bushek et al. (2008)
<i>Perkinsus marinus</i>	<i>Crassostrea virginica</i>	Direct	No	Perkins (1988) Perkins (1996)
<i>Perkinsus qugwadi</i>	<i>Patinopecten yessoensis</i>	Direct	Unknown but likely	Blackbourn et al. (1998)
<i>Perkinsus olseni</i>	<i>Austrovenus stutchburyi</i> <i>Venerupis pullstra</i> <i>Venerupis aurea</i> <i>Ruditapes decussatus</i> <i>Ruditapes philippinarum</i> <i>Paphies australis</i> <i>Crassostrea gigas</i> <i>Crassostrea ariakensis</i>	Direct	No	Goggin et al. (1989) Auzoux-Bordenave et al. (1995) Casas et al. (2002)
<i>Perkinsus mediterraneus</i>	<i>Ostrea edulis</i>	Direct	Unknown	Casas et al. (2004)
<i>Bonamia exitiosa</i>	<i>Ostrea angasi</i>	Direct	Unknown	Berthe and Hine (2003)
<i>Bonamia ostreae</i>	<i>Ostrea chilensis</i> <i>Ostrea edulis</i> <i>Ostrea angasi</i> <i>Ostrea puelchana</i> <i>Ostrea chilensis</i> <i>Ostrea denselammellosa</i> <i>Crassostrea ariakensis</i>	Direct	Unknown	Montes et al. (1994)
<i>Bonamia roughleyi</i>	<i>Saccostrea commercialis</i>	Direct	Unknown	Farley et al. (1988)
<i>Bonamia perspora</i>	<i>Ostreola equestris</i>	Unknown	Unknown	Carnegie et al. (2006)

**Table 1** (continued)

Parasite	Host species	Mode of transmission	Reproduction outside hosts?	Key references
<i>Mikrocytos mackini</i>	<i>Crassostrea gigas</i> <i>Crassostrea virginica</i> <i>Ostrea edulis</i> <i>Ostreola conchaphila</i>	Direct	Unknown	Bower et al. (1997)
<i>Marteilia sydneyi</i>	<i>Saccostrea commercialis</i>	Intermediate host likely	Unknown but unlikely	Roubal et al. (1989)
<i>Marteilia refringens</i>	<i>Ostrea edulis</i> <i>Ostrea angasi</i> <i>Ostrea puelchana</i> <i>Ostrea chilensis</i> <i>Mytilus edulis</i> <i>Mytilus galloprovincialis</i>	Intermediate host	Unknown but unlikely	Figuera and Montes (1988)
<i>Marteilia maurini</i>	<i>Mytilus galloprovincialis</i> <i>Mytilus edulis</i>	Intermediate host likely	Unknown but unlikely	Le Roux et al. (2001)
<i>Marteilia conchillia</i>	<i>Cerastoderma edule</i>	Intermediate host likely	Unknown but unlikely	Carrasco et al. (2013)
<i>Haplosporidium nelsoni</i>	<i>Crassostrea virginica</i> <i>Crassostrea gigas</i>	Intermediate host likely	Unknown but unlikely	Haskin (1966)
<i>Haplosporidium costale</i>	<i>Crassostrea virginica</i>	Intermediate host likely	Unknown but likely	Wood and Andrews (1962)
QPX	<i>Mercenaria mercenaria</i>	Direct	Yes	Stokes et al. (2002)



**Fig. 1.** (A) Relative abundance of bacteria, protozoans, and viruses in coastal oceans (data from Cochlan et al. (1993), Maranger and Bird, 1995 and Suttle (2007)). (B) Relative reporting of bacterial, protozoan, and viral parasites of bivalve molluscs from a search of the SCOPUS database (<http://www.info.sciverse.com/scopus/>) of peer-reviewed articles published between 1950 until 2014 with titles or abstracts containing parasite and host string names presented in Table S1 (16,846 records). (C)

Relative reporting of bacterial, protozoan, and viral parasites of bivalve molluscs (same as above) but removing parasites infectious to human hosts from the search results (11,229 records).

Bacterial parasites, although only rarely reported to be the primary cause of disease in adult bivalves (Bower et al., 1994; Lane and Birkbeck, 2000), are commonly described in bivalve larval stages and often associated with high mortalities in shellfish hatcheries (Paillard et al., 2004; Sainz-Hernandez and Maeda-Martinez, 2005). For many bivalve species, bacteria can provide some component of carbon and nitrogen requirements (Birkbeck and McHenry, 1982; Langdon and Newell, 1990; Paillard, 2004). At the same time, bivalves provide habitat for diverse communities of commensal bacterial microbiota, including various members of *Vibrio*, *Pseudomonas*, *Acinetobacter*, *Photobacterium*, *Moraxella*, *Aeromonas*, *Micrococcus*, and *Bacillus* (Pujalte et al., 1999; Romero et al., 2002; Beaz-Hidalgo et al., 2010). Nevertheless, major disease outbreaks in cultured larval and juvenile bivalves have been attributed to a number of bacterial parasites, particularly when environmental parameters such as water temperature and salinity influence bacterial diversity and the physiological state of bivalve hosts (Beaz-Hidalgo et al., 2010). These parasites include *Roseovarius crassostreae*, the etiological agent of Roseovarius Oyster Disease in *Crassostrea virginica* (Ford and Borrero, 2001; Boettcher et al., 2005; Maloy et al., 2007a,b), *Nocardia crassostreae*, the causal agent of Pacific Oyster Nocardiosis (Friedman and Hedrick, 1991; Friedman et al., 1998; Bower et al., 2005), and *Vibrio pectenicida* and *Vibrio tubiashii*, significant parasites of *P. maximus* and *C. gigas* larvae in hatcheries (Hada et al., 1984; Lambert et al., 2001). Brown Ring Disease, caused by *Vibrio tapetis* (Borrego et al., 1996), is a noteworthy exception to the observation that bacterial parasites principally target larval bivalves. This disease occurs in both wild and cultured *R. philippinarum* in France, England, Ireland, Spain and Italy (Allam et al., 2000; Paillard, 2004). Signs of the characteristic brown deposit on the inner surface of the valve caused by colonization of *V. tapetis* have also been detected in a number of bivalves, including *R. decussatus*, *Venerupis aurea*, *Dosinia exoleta* and *P. maximus* (Paillard, 2004), although resistance to infection and signs of disease vary significantly by species (Allam and Ford, 2006). In the case of Brown Ring Disease, *V. tapetis* acts initially as an external microparasite and does not directly enter host tissues (Allam et al., 2001, 2002). Rather, this bacterial parasite adheres to the surface of the host's mantle edge, which provides the substrate for initial colonization and subsequent spread throughout host tissues (Allam and Ford, 2006).

### 3. Parasite interactions in the environment

There is much to learn about the biological, morphological, and behavioral diversity of parasites in the sea and its consequences on modes of parasite transmission. Viruses are the most abundant members of marine microbial communities. In the water column, free-living but non-replicating viral particles exist as a protein coat or capsid, enclosing the DNA or RNA that code for the virus elements. Viral capsids can themselves be enclosed within a membrane, and many viruses, including the Herpesviridae and Retroviridae, have a supplementary phospholipid and protein bilayer, known as a viral envelope, covering their protective protein capsids (Brum et al., 2013). The viral envelope interacts with receptors on target cells to mediate virus entry, fusing viral and host cell membranes while evading host defenses (Wyatt and Sodroski, 1998; Poranen et al., 2002). This latter property is suggested to be associated with persistent infections (Forns et al., 2000). The phospholipid bilayer of the viral envelope also makes these viral particles sensitive to both desiccation and sunlight, suggesting that these viruses have limited survival outside host environments (Poranen et al., 2002).

Most of the virus inactivation in clear oceanic waters exposed to full sunlight can be attributed to solar radiation (Heldal and Bratbak, 1991; Suttle and Chen, 1992). However, the most mutagenic and lethal effects of solar radiation, in particular DNA photoproducts such as pyrimidine dimers, are often repaired by host-cell mechanisms such as photoreactivation and the majority of viral particles in the water column are thought to remain infective despite high rates of DNA damage (Wilhelm et al., 1998; Wommack and Colwell, 2000; Suttle, 2005). In addition, the lethal effects of solar radiation diminish at high latitude and in productive coastal waters, particularly at depth. In these regions, the most prevalent finding among studies of natural virus inactivation is that the presence of natural bacterial communities is critical to the rate of viral inactivation and decomposition (Wommack and Colwell, 2000; Simon et al., 2002; Weinbauer et al., 2009; Breitbart, 2012). This conclusion is supported by laboratory manipulations, where removal of bacterioplankton by filtration or autoclaving greatly improves virus survival (Wommack and Colwell, 2000). Temperature is an important interacting factor as well, as observations of increased viral inactivation at higher incubation temperatures can often be attributed to temperature-mediated enhancement of bacterial activity in seawater (Mathias et al., 1995; Garza and Suttle, 1998). The inactivating effects of bacterioplankton may be offset by the protective effect of viral adsorption to particulates suspended in the water column (Bitton, 1975). However, suspended particulates are more likely to further enhance viral decomposition. Suspended marine aggregates, sometimes referred to as marine snow, are heavily colonized by bacteria and other heterotrophic microbes (Lyons et al., 2010) and have been identified as hotspots of microbial decomposition of organic material. The abundance of heterotrophic bacterial production suggests that marine aggregates are more likely to serve as a sink rather than a source of suspended viral particles.

(Simon et al., 2002). The relative importance of aggregates on the decay and decomposition of suspended parasites is therefore likely to be variable (Kramer et al., 2013), ultimately depending on specific characteristics of the parasites themselves. For example, bacterial parasites such as *Vibrio* spp. and protozoan parasites such as QPX have been observed on marine aggregates (Lyons et al., 2005, 2007a,b). Whittington et al. (2015a) observed that mortality of *C. gigas* associated with the microvariant genotype of OsHV-1 was prevented when seawater pumped through an upwelling nursery system holding oysters was filtered to 5 lm. Since individual viral particles can certainly pass through a filter of this size, this observation supports the hypothesis that OsHV-1 is also associated with marine aggregates. It remains unknown whether suspended aggregates serve as a refuge or even abiotic reservoir for viral, bacterial and protozoan parasites though. Concentrations of aggregate-associated parasites may simply reflect ambient concentrations of these parasites in coastal marine ecosystems.

Many bacterial parasites of bivalves, such as *Vibrio* spp., *N. crassostreae*, and *R. crassostreae*, are common, though inconspicuous, members of coastal marine ecosystems (González and Moran, 1997; Paillard et al., 2004; Wagner-Dobler and Biebl, 2006; Beaz-Hidalgo et al., 2010). Though these parasites cause disease and mortalities in bivalves, most are not strictly intracellular and have adapted to alternate between growth within hosts and prolonged free-living survival and reproduction in the environment (González and Moran, 1997; Yildiz and Visick, 2009). This distinction is important, as bivalves most often serve only as incidental hosts for these facultative parasites. Many of the *Vibrio* species play an additional, larger role in nearshore marine ecosystems through the decomposition of organic material and cycling of nutrients (Benitez-Nelson, 2000; Fischer et al., 2014). Many bacterial parasites have also been identified in association with marine aggregates (Lyons et al., 2005, 2007a,b), and a key factor for their survival in the environment, in particular for the *Vibrio* species, is their ability to form biofilms on various surfaces, including benthic sediments and hard substrate in addition to the constituent particles of marine aggregates (Nyholm et al., 2000; Yildiz and Visick, 2009). The biofilm forming capacity of vibrios enhances their growth and survival in the environment by providing these bacteria both access to nutrients and protection from predators and antimicrobial compounds (Costerton and Stewart, 1999; Donlan and Costerton, 2002), and may even be linked with the pathogenicity of some species within hosts (Rodrigues et al., 2014). As a consequence, studies concerning the transmission and decay of bacterial parasites in coastal waters have focused on identifying the timing of, and environmental conditions associated with, periods of their abundance in the water column (Paillard et al., 2004, 2014; Elston et al., 2008; Beaz-Hidalgo et al., 2010), rather than the effects of these variables on the inactivation and infectivity of free-living bacteria.

Protozoan parasites differ from many bacterial parasites in that most, but not all, require primary and sometimes secondary hosts to complete their life cycles. Although most protozoan parasites cannot

reproduce in the water column, experimental studies have demonstrated that infective stages for many of these parasites, including *P. marinus*, *P. olseni*, *Marteilia sydneyi*, and *B. ostreeae* can survive for days, weeks, and even months in the water column, and remain infective when they enter a new host (Auzoux-Bordenave et al., 1995; Chu, 1996; Wesche et al., 1999; Chu and Lund, 2006; Arzul et al., 2009). Some parasite stages, such as hypnospores of *Perkinsis* spp., formed in decaying tissues of moribund hosts, can survive for months under environmental conditions that prevent further proliferation (i.e. zoosporulation) (Auzoux-Bordenave et al., 1995; Casas et al., 2002). The free-living and metabolically active meront stage of *P. marinus* has demonstrated the ability to survive for at least two weeks in seawater (Chu et al., 2002; Chu and Lund, 2006). The longevity of meront stages in seawater has been partially attributed to the ability of cells to synthesize a range of saturated and unsaturated fatty acids, including the essential fatty acid, arachidonic acid (AA), while maintained in seawater (Soudant and Chu, 2001; Lund et al., 2004; Chu and Lund, 2006). This capability is novel, as no other protozoan parasites have been reported to demonstrate such a capability, instead relying entirely on their hosts for essential lipids. Lipids play a vital role in both the long-term survival and the completion of the life cycle of all endogenous parasites (Soudant and Chu, 2001). In the case of *P. marinus*, lipids may facilitate disease transmission processes by serving as energy reserves for growth and survival during times of limited or nonexistent nutrient supply (Lund et al., 2004; Chu and Lund, 2006).

The capability of *P. marinus* to synthesize essential fatty acids for growth is unique to this parasite, but other protozoan parasites may be capable of long-term survival and growth outside hosts. QPX is a member of the phylum Labyrinthulomycota (Kleinschuster et al., 1998; Ragan et al., 2000; Stokes et al., 2002). Members of this phylum are ubiquitous epibionts of marine vascular plants, macroalgae, and detritus (Raghukumar and Damare, 2011). A distinguishing feature of the labyrinthulomycetes is their ectoplasmic net, an external cytoplasmic network that attaches the cell to its substrate and secretes digestive enzymes for absorptive nutrition (Tsui et al., 2009). This structure enables these microbes to live as mutualists, commensals, saprobes, and less frequently parasites (Muehlstein and Porter, 1988; Raghukumar and Damare, 2011). Laboratory experiments and field sampling have demonstrated that, although QPX does not appear to grow isolated in seawater, the parasite is capable of long-term survival outside quahog hosts when associated with marine aggregates. QPX can even grow outside its host if provided live or decaying macroalgae homogenates as a source of nutrients (Lyons et al., 2005; Buggé and Allam, 2007; Gast et al., 2008). The species of macroalgae is important however, as QPX growth can be limited and even inhibited depending on the taxonomy and transience of macroalgal media (Buggé and Allam, 2007). The specificity of QPX growth is most likely a consequence of species-specific plant antimicrobials present (Raghukumar and Damare, 2011). Consequently, QPX appears to be an opportunist, adapting to parasitism when

conditions are favorable (Ford et al., 2002; Dahl and Allam, 2007; Dahl et al., 2008). This apparently facultative parasite can be present throughout the year, and environmental sampling has confirmed that QPX is regularly present in samples of seawater, marine aggregates, detritus, sediments, live macroalgae and marine vascular plants, and various invertebrates (Lyons et al., 2005; Buggé and Allam, 2007; Gast et al., 2008).

Even in the absence of adequate sources of nutrition, free-living stages of protozoan parasites of the genera *Perkinsus*, *Bonamia*, and *Marteilia* have demonstrated the ability to survive for weeks or more in the water column (Grizel et al., 1988; Auzoux-Bordenave et al., 1995; Wesche et al., 1999; Casas et al., 2002; Chu and Lund, 2006; Arzul et al., 2009). A number of physical factors can influence the decay and inactivation of free-living stages of protozoan parasites, and extensive research has identified temperature and salinity as the most important environmental factors affecting the rate of cell inactivation outside hosts (La Peyre et al., 2006, 2008, 2010a,b; Arzul et al., 2009; Perrigault et al., 2010). A fairly precise range of optimal environmental conditions has been defined for the in vitro and in vivo growth and proliferation of many of these parasites. For example, optimal temperatures supporting the proliferation of *P. marinus* range from 28 to 32 C and optimal salinity ranges from 24 to 36 ppt (Dungan and Hamilton, 1995; Gauthier and Vasta, 1995; La Peyre et al., 2010a,b). Cellular and humoral parameters measured from quahogs challenged with QPX have demonstrated little difference compared to uninoculated control groups at 27 C, whereas different responses have been observed at 13 C and 21 C (Perrigault et al., 2011). This result supports observations of QPX disease occurring only in the cooler waters characterizing the region from Maritime Canada through New England to Virginia. Zoosporulation of *P. olseni* in seawater is abruptly reduced at salinities lower than 25 ppt, and zoospores have demonstrated the ability to survive for up to 14 and 22 days at 10 C and 28 C respectively (Casas et al., 2002). Contrary to observations of increased survival with increasing temperature in *P. olseni*, *B. ostreae* has demonstrated significantly lower survival at 25 C, compared to 4 C and 15 C (Arzul et al., 2009). The viability of *M. sydneyi* spores also appears to increase with decreasing temperature (Wesche et al., 1999). In addition, the survival of purified *B. ostreae* has been observed to increase at salinities greater than 35 ppt (Arzul et al., 2009). The survival of QPX in seawater is also higher at 15 C, relative to 20 C and 23 C, but in contrast to the observed survival of *B. ostreae*, increases with decreasing salinity (Perrigault et al., 2010). These studies suggest that the environmental conditions favoring the survival of free-living and metabolically active parasite stages are species-specific. In the cases of *B. ostreae* and QPX, relatively cool temperatures could decrease the metabolic rates of free-living parasites, delaying the onset of mortality and augmenting the parasites' ability to disperse throughout nearshore marine ecosystems.

Dispersal to new hosts begins with the release of parasite stages into the water column. Given the small size and limited swimming ability of most viral, bacterial, and protozoan parasites of bivalves, it is assumed that dispersal is passive, and driven by physical processes such as winds, tides, bathymetry, and river runoff (MacCready and Geyer, 2010). The relative contribution of these mechanisms varies, and ultimately defines the scale of parasite dispersal. For example, the short dispersal lengths of oyster larvae generally seen in the lower Delaware Bay, a semi-enclosed embayment characterized by high particle retention time, have been associated with an extensive recirculation that is maintained by the area's topography (Narváez et al., 2012). Suspended parasites are often retained by this recirculation, reducing their transport to other areas of Delaware Bay. Broad transport of particles throughout Delaware Bay has been demonstrated to occur though, often in association with high river runoff (Narváez et al., 2012). Below average flows, on the other hand, allow particles to move further into upstream regions (Narváez et al., 2012). Short term changes in river flows can therefore be crucial for the transmission of parasites that remain infective in the water column often for weeks or more.

Other physical mechanisms, such as tides and winds, are equally important. Dispersion by tides is dependent on the size of the estuary relative to the tidal excursion length. In small bays and estuaries, or areas with abrupt changes in topography, the consequences of tidal dispersion can be significant (Geyer and Signell, 1992). In mid-latitude regions, ebb and flood tide velocities can range between 0.5 and 1 m s<sup>1</sup> potentially transporting particles up to 4 km per hour (Valle Levinson and Wong, 2000). This estimate is supported somewhat by observations of new infections with *P. marinus* in disease-free oyster cohorts as early as ten days after placement in disease-enzootic waters of Chesapeake Bay. These new *P. marinus* infections occurred despite approximately 5 km of separation from naturally infected oyster reefs (McCollough et al., 2007). Wind patterns can also exert significant controls on estuary circulation, having both local and remote effects (Wong and Garvine, 1984). Local winds have an immediate effect on local circulation, but remote winds can also result in an elevation or depression of regional sea level, with cascading consequences on local circulation in estuaries (Wong, 1994). Furthermore, vertical mixing by winds can be important in the redistribution of particles in the water column, exposing displaced particles to different and often opposing currents. The consequences of these interacting physical mechanisms are difficult to interpret, imposing complexity to the prediction of parasite dispersal in nearshore marine systems.

#### **4. Suspension feeding and portals of entry**

Suspension feeding bivalve molluscs are confronted with a wide range of materials in the seston and benthic environment, including various sized plankton and the organic material derived from it, benthic

microalgae, detritus, microorganisms, fecal and pseudofecal pellets, and parasites that have adapted to survive in the water column. Suspension feeding processes and the mechanisms of particle selection have become a major area of marine biological inquiry (Shimeta and Jumars, 1991; Chauvaud et al., 2000; Ward and Shumway, 2004). Combined with studies of nutrient assimilation and biodeposition (Newell, 2004; Kellogg et al., 2013; Smyth et al., 2012), advances in research on the processes of suspension feeding have provided a robust mechanistic understanding of role of bivalves in the regulation of water column processes and the flux of organic material and nutrients from the water column to the benthos (reviewed by Dame (2011)). It has also become clear that particle-feeding bivalves rarely just encounter and consume particulate matter. Rather, particles are rapidly sorted, ingested, and assimilated based on a number of chemical, physical, and biological factors (reviewed by Ward and Shumway (2004)). Bivalves have evolved morphological structures and behaviors to exploit a diet of dilute, heterogeneous particles contained within the seawater matrix. Suspended particles are captured by ciliated feeding structures that sweep selected material toward the labial palps and mouth and into the stomach. Rejected material is diverted away from the mouth. Particle selection can occur either before capture or following capture but prior to ingestion (Shimeta and Jumars, 1991; Ward and Shumway, 2004).

Post-capture selection occurs by the differential transport of material along feeding structures, the end result of which is the collection of materials that are periodically expelled as pseudofeces (Shumway, 1985; Ward et al., 1998). In the stomach, selected and ingested cells and particulates are mechanically broken up and mixed with digestive enzymes. Bivalves may also post-ingestively discriminate among particles based on attributes such as size, density, and chemical properties through sorting in the gut lumen and preferential transport of selected particles to the digestive diverticula, the site of primary intracellular digestion (Brillant and MacDonald, 2000, 2003; Ward and Shumway, 2004). Intracellular digestion also occurs in the gut lumen and digestive diverticula by circulating hemocytes, and phagocytized materials are then transported across the gut lining to other tissues for assimilation (Hine, 1999; Canesi et al., 2002; Wootton et al., 2003). In addition to this digestive function, hemocytes encapsulate and phagocytize foreign materials, including any parasites present in the gut or within the hemolymph (Hine, 1999). Elimination of microbes results from the coordinated action of these phagocytic processes with humoral defense factors such as agglutinins, lysosomal enzymes, toxic oxygen intermediates, and various antimicrobial peptides (Chu, 1988; La Peyre et al., 1995; Hine, 1999; Canesi et al., 2002; Canesi et al., 2013; de Freitas Rebelo et al., 2013). Microbial defense is not restricted to the digestive tract either. Due to the open circulatory system of molluscs, hemocytes remain present in sinuses throughout all soft tissues (Hine, 1999) and even outside the external epithelium in extrapallial fluids (Allam and Paillard, 1998). For bivalve parasites to enter and infect hosts, they must first enter and overcome these elaborate pathways for particle sorting and selection, and once

within host tissues, are faced with highly diverse systems of innate immunity (Chu, 1988; Bayne, 1990; Hine, 1999; Canesi et al., 2002; Zhang et al., 2014, 2015). How bivalve parasites evade these behavioral, physical, chemical, humoral, and molecular defenses to infect and establish within hosts is remarkable, and bivalve parasites have demonstrated numerous adaptive strategies to evade particle sorting and immune defense processes to establish and proliferate within hosts.

The entry of viruses into bivalve hosts, when compared to the entry of bacterial and protozoan parasites, is perhaps most associated with normal feeding activities. It remains open how small virus particles (<50 nm) enter bivalve hosts (Provost et al., 2011), as the ciliated structures of gills can often be spaced as far as 500–600 nm apart. It has been suggested that viral particles can both become electrostatically bound to sulfates on the mucopolysaccharides of shellfish mucus (Di Girolamo et al., 1977) and become entrapped in feeding structures when associated with larger marine aggregates, plankton, and organic and inorganic particles large enough to be captured by the gill (Gentry et al., 2009; Whittington et al., 2015a). Both of these mechanisms of entry may occur simultaneously, and both lead to the rapid entry of viral particles into digestive organs. In fact, many viruses, including those of human health concern such as hepatitis A, murine norovirus, and poliovirus, have been observed to readily bioaccumulate within the lumen and cells of digestive tract tissues (Le Guyader et al., 2006; McLeod et al., 2009; Richards et al., 2010). Once there, circulating hemocytes may encapsulate and traffic viral particles across the gut lining and throughout bivalve tissues (Provost et al., 2011). The extent to which phagocytic and humoral processes can inactivate viral particles within bivalves remains open, as direct studies comparing the abilities of viruses to persist within hemocytes have been limited (Renault and Novoa, 2004; Provost et al., 2011). Studies of the persistence of enteric viruses infecting humans contaminating bivalve tissues suggest that certain acid-tolerant viruses can survive and remain infectious within bivalve hemocytes for extended periods, while other viruses decline more rapidly (Ueki et al., 2007; McLeod et al., 2009; Provost et al., 2011). Viruses have demonstrated the capacity to be retained by bivalve hemocytes for significantly longer periods of time than bacterial indicators such as *Escherichia coli* and fecal coliforms (Power and Collins, 1989, 1990).

Studies of human enteric viruses in bivalve tissues suggest that digestive organs and circulating hemocytes are the primary sites of virus entry and persistence (Richards et al., 2010; Provost et al., 2011). The direct and rapid penetration of viruses into digestive tissues and hemolytic systems, due to the open circulatory system of bivalves, suggests that these may be primary sites for virus replication as well. The targeting of hemocytes for virus entry and persistence is supported by the likely viral etiology of disseminated neoplasia, a progressive and lethal condition of bivalve hemolytic systems (Elston et al., 1992; Barber, 2004; Romalde et al., 2007) as well as the diversity of observations of hemocyte-infecting viruses, including iridio-like viruses associated with widespread mortality outbreaks of *C. angulata* in France in the

early 1970s (Elston, 1997) and picornavirus-like particles interpreted as granulocytomas localized in hemolymph spaces in *M. edulis* from Denmark. More recent evidence from the dynamics of OsHV-1 infections within *C. gigas* suggests that hemocytes, though not necessarily the site of viral replication, play an important role in the dissemination of virus particles to target tissues (Schikorski et al., 2011). OsHV-1 viral particles presumptively contact hosts through feeding activities, entering the digestive tract and the hemolymphatic system. Viruses are then transported by hemocytes to the target organs (Schikorski et al., 2011), thought to be the gills and mantle (Arzul et al., 2001b; Sauvage et al., 2009; Segarra et al., 2014a). Once there, viral particles begin intense replication and can spread rapidly throughout host tissues, explaining observations that only a short duration of exposure to OsHV-1 is sufficient for transmission in the field and laboratory (Arzul et al., 2001b; Burge and Friedman, 2012; Schikorski et al., 2011; Segarra et al., 2014a,b). The mechanisms underlying interactions between viruses and components of hemolymphatic systems remain mostly unresolved, but observations of the kinetics of viral infections in bivalve hosts suggest that hemocytes play an important role in the replication and dissemination of viral particles within bivalve hosts.

Digestive processes appear to be a strong barrier against the initial colonization by non-viral parasites in healthy bivalve hosts. Bacteria are encountered by many bivalve species as a food source (Birkbeck and McHenry, 1982; Langdon and Newell, 1990), and can be assimilated efficiently into bivalve tissues through digestive and phagocytic processes. Although the relative contribution of bacteria to the energy and nutrient demands of most bivalves is likely small compared to the contribution of phytoplankton (Lucas et al., 1987), the utilization of bacteria varies by bivalve species (Silverman et al., 1995) and with respect to the relative abundance of bacteria in the water column. Nevertheless, bivalves have demonstrated the ability to efficiently clear natural bacterioplankton assemblages in experimental systems (Lucas et al., 1987). *Mytilus edulis*, for example, have demonstrated the capacity to degrade bacteria at rates up to  $10^9$  cells h<sup>-1</sup> (Birkbeck and McHenry, 1982). Lysozymes, in particular, play a central role in the digestion and defense against bacterial parasites due to the ability of these humoral defense factors to break down bacterial cell walls (McHenry et al., 1986; Bachali et al., 2002). The susceptibility of bacterial parasites to elimination is a product of the sensitivity of bacteria to humoral defense factors and the capability of hemocytes to bind to and encapsulate different bacteria, reflecting both the ability for bacteria to evade hemocytes as well as the sensitivity of bacteria to intracellular elimination (Chu, 1988; Allam et al., 2002; Bachali et al., 2002; Canesi et al., 2002). As a consequence, the pathogenicity of bacterial parasites is often directly associated with the capacity for these parasites to evade and avoid host defense factors (Allam et al., 2002; Canesi et al., 2002; Pruzzo et al., 2005). For example, the persistence of pathogenic vibrios in hemolymph depends largely on their sensitivity to the bactericidal activity of circulating hemocytes and soluble humoral factors

(reviewed by Pruzzo et al. (2005)). The pathogenic effects of *Vibrio splendidus*, the likely cause of summer mortalities of juvenile *C. gigas* in Brittany, has shown to result from the capacity for some strains to interfere with the signaling pathways involved in hemocyte function (Lacoste et al., 2001; Labreuche et al., 2006). *V. tapetis* avoids phagocytic encapsulation by impairing the adhesion properties of hemocytes (Choquet et al., 2003). The physiological state and immunity of hosts is also an important factor determining the capacity for parasites to evade defense factors and establish within hosts (Lacoste et al., 2002). *N. crassostreae* appears to enter oyster hosts directly through the digestive tract (Bower et al., 2005). Infection seems to occur primarily during periods of host physiological stress, presumably associated with periods of high metabolism and reproductive maturation when water temperatures rise (Paillard et al., 2004; Bower et al., 2005). Initial signs of brown ring disease also appear to coincide with the reproductive period of *R. philippinarum*, which corresponds to a drop in the clam condition index (Martinez-Manzanares et al., 1998; Paillard, 2004).

Bacterial parasites have also demonstrated the capacity to evade digestion by behaving, at least initially, as external parasites, colonizing the pseudo-internal extrapallial spaces and peripheral compartments (Paillard and Maes, 1994; Allam et al., 1996; Paillard et al., 2004; Boettcher et al., 2000; Boardman et al., 2008). Roseovarians crassostreae, for example, colonizes the inner shell surfaces of *C. virginica*, stimulating the deposition of conchiolin around the outer edge of the mantle margin (Boettcher et al., 2000; Ford and Borrero, 2001). The nature of conchiolin deposition in oysters colonized by *R. crassostreae* is similar to that observed in *R. philippinarum* colonized by *V. tapetis*, which uses a number of adherence factors, including pili, to adhere to the periostracal lamina of its clam host (Paillard et al., 1994; Paillard and Maes, 1994; Allam et al., 1996, 2000). Adherence to the periostracal lamina is a required step in the transmission cycle of *V. tapetis* (Martinez-Manzanares et al., 1998; Lopez-Cortes et al., 1999b), and the attachment of bacteria onto the shell secretion is structurally similar to biofilms formed by other vibrios, including *V. cholerae*, *V. fisheri*, and *V. parahaemolyticus* (Costerton and Stewart, 1999; Yildiz and Visick, 2009; Rodrigues et al., 2014). The biofilm forming capacity of vibrios is directly linked with the pathogenicity of these bacteria (Costerton and Stewart, 1999; Nyholm et al., 2000; Yildiz and Visick, 2009). Once formed along the growing edge of the clam shell, the *V. tapetis* biofilm can advance into internal tissues when environmental conditions permit. Extensive bacterial proliferation ruptures the external epithelium of the mantle and disseminates this parasite throughout the extrapallial fluid and into and through the connective tissue of the mantle (Paillard et al., 1994; Lopez-Cortes et al., 1999b; Allam et al., 2000, 2002; Paillard, 2004).

Some protozoan parasites, such as *B. exitiosa*, appear to enter hosts directly through the digestive tract, escaping digestion in the case of *B. exitiosa* by burrowing under the gut basement membrane (Hine, 1991).

Most protozoans though seem to evade direct feeding and digestion by initiating infections outside the digestive tract, most often in the pallial organs. Initial infections with QPX typically occur in the mantle, gill, and incurrent siphon (Smolowitz et al., 1998; Dahl et al., 2010). This also appears to be the case for infections with *Haplosporidium nelsoni* and *H. costale* in *C. virginica* and *B. ostreae* in *O. edulis*, as these parasites initially infect the gill epithelium before invading nearby connective tissues (Andrews, 1982; Montes et al., 1994; Sunila et al., 2000; Burreson and Ford, 2004). Oysters with Denman Island disease, caused by infection with *Mikrocytos mackini*, have been observed to first develop lesions in the mantle and labial palps (Farley et al., 1988; Carnegie et al., 2003). The initial infective stages of *M. refringens* and *M. syneyi* also enter through the labial palps (Audemard et al., 2002; Kleeman et al., 2002), and all members of the genus *Perkinsus* appear to infect their bivalve hosts through the pallial organs (Azevedo et al., 1990; Rodriguez and Navas, 1995; Villalba et al., 2004; Allam et al., 2013; Soudant et al., 2013). In some instances, such as with QPX and *P. marinus*, the initial source of infectious stages appears to be from the accumulated particles captured by the gills but not ingested that await rejection as pseudofeces along the outer edge of the mantle (Lyons et al., 2005; Allam et al., 2013). Further studies indicate that the mucus covering oyster pallial organs, which provides an efficient protective barrier for these feeding organs, plays a significant role in the pathogenesis of *P. marinus*, enhancing parasite proliferation and infectivity (Pales Espinosa et al., 2013). Although the mechanisms remain unresolved, it appears that contact between *P. marinus* and pallial mucus causes significant changes to the parasite's metabolic processes, increasing the expression of virulence factors to facilitate infections on the pallial organs (Pales Espinosa et al., 2013). In addition, *P. marinus* has demonstrated greater infectivity when cells are incorporated within marine aggregates (Allam et al., 2013). These results implicate a role for marine aggregates, in addition to host factors such as pallial mucus, as abiotic vectors or mediators of parasite transmission through suspension feeding processes.

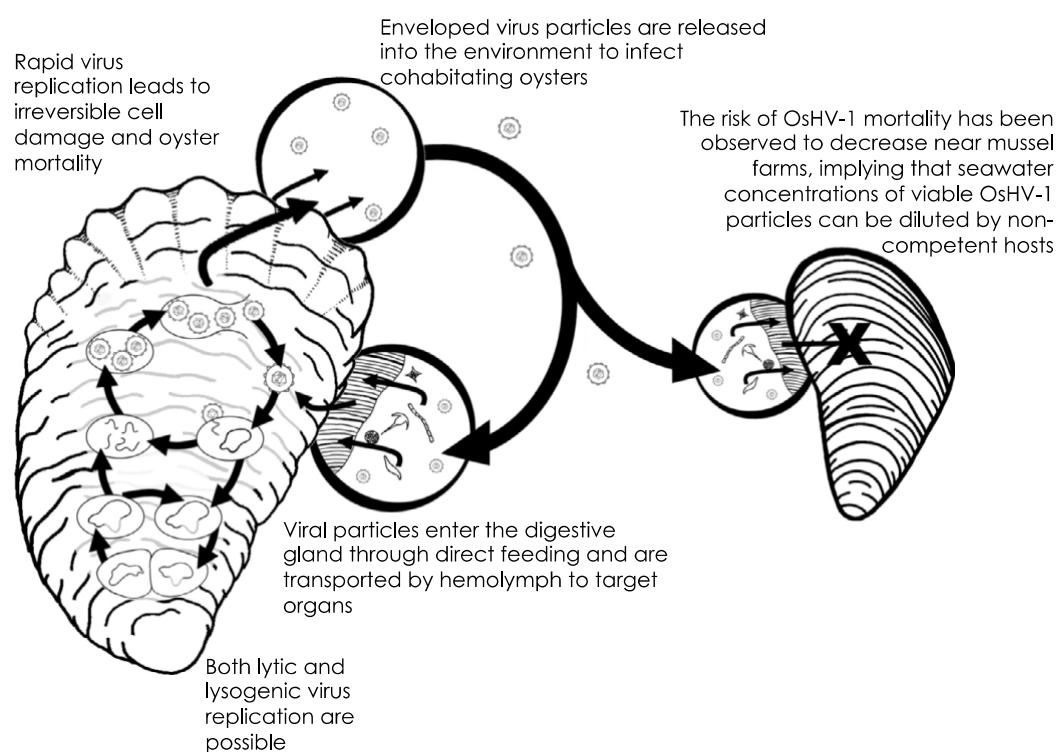
Once established within pallial organs, many protozoan parasites have demonstrated the ability to evade phagocytic and humoral factors (La Peyre et al., 1995, 2010a,b; Volety and Chu, 1995; Kang et al., 2006; Tasumi and Vasta, 2007) and directly infect hemocytes to disseminate throughout host tissues via the open hemolymphatic system (Villalba et al., 2004; Soudant et al., 2013). Interactions between *P. marinus* and its oyster hosts have become a model for the identification of mechanisms of immunoinhibition and dissemination through host tissues. Previous work has shown that this protozoan uses a suite of intricate mechanisms to sequester cellular functions of its host's immune system to assure propagation (La Peyre et al., 1995; Garreis et al., 1996; Sunila and LaBanca, 2003; Villalba et al., 2004; Hughes et al., 2010; Soudant et al., 2013). *P. marinus* can inhibit phagocytic processes (Anderson, 1999; Schott and Vasta, 2003), allowing this parasite to hijack circulating hemocytes for dissemination throughout host tissues by

diapedesis. This parasite can also suppress hemocyte apoptosis (Sunila and LaBanca, 2003; Hughes et al., 2010). Apoptotic death of hemocytes infected with *P. marinus* would likely restrict the spread of this parasite to initial infection foci. Suppressing apoptosis can further help *P. marinus* survive and disseminate throughout host tissues, specifically within host hemocytes. Targeting hemocytes for parasite replication and spread through host tissues is not unique to *Perkinsus* spp. Most microcell haplosporidians, including *B. ostreae*, *B. exitiosa*, and *B. roughleyi* infect and proliferate in hemocytes (Farley et al., 1988; Montes et al., 1994; Culloty et al., 1999; Cochennec-Laureau et al., 2003; Carnegie and CochennecLaureau, 2004). *M. mackini* also occurs in hemocytes but is more conspicuously associated with vesicular connective tissues of the pallial organs and does not appear to proliferate in hemocytes (Farley et al., 1988; Carnegie and Cochennec-Laureau, 2004). These observations demonstrate that hemocytes, while serving a primary role in non-specific immune defense, are often targets of parasitic infection. Infection of hemocytes is directed by host phagocytosis, but even this may not always be the case. Cochennec (2001) demonstrated that live *B. ostreae* are internalized by hemocytes at a greater rate than heat-killed parasites, suggesting that the parasites themselves initiate the infection of these microbial defense agents. This paradoxical role of phagocytes in the pathogenesis of infectious diseases, known as the Trojan horse effect, has been of widespread interest to investigators studying a diversity of host-parasite systems, including *Bacillus anthracis* in livestock and humans, *Streptococcus iniae* in fish, *T. gondii* in mammals, and *Vibrio cholerae* in humans (Roy and Wainberg, 1988; Guidi-Rontani, 2002; Zlotkin et al., 2003; Nguyen and Pieters, 2005; Lambert and Barragan, 2010). The inherent migratory functions of circulating phagocytes appear to make them also a very suitable target for parasites to mediate their dispersion throughout host tissues.

## 5. Parasite life cycles

The diverse mechanisms bivalve parasites use to infect and disperse throughout host tissues directly reflect the diversity of life and replication styles of bivalve parasites. Viruses, most often transmitted directly between bivalve hosts, can have several different replication cycles once established within host tissues. The two most dominant are the lytic, or virulent cycle, and the lysogenic, or latent cycle. Virulent viruses infect a cell or tissue, replicate, and are released throughout host tissues or into the environment by lysis of the host cell. Alternatively, latent viruses infect the host and the viral DNA stays within the host cell, often in the host genome. Here, the viral genome replicates along with the host genome until some factors, such as DNA damage, induce the lytic cycle. It has been suggested that lytic viruses dominate in productive ecosystems, where the abundance and density of target hosts is high which would facilitate host contacts ([Wilcox and Fuhrman, 1994](#); [Suttle, 2005](#); [Breitbart, 2012](#)). Herpesviruses, such as OsHV-1 can

have both virulent and latent cycles (Honess and Roizman, 1974). In herpesviruses the virulent cycle has demonstrated to be induced by a range of host factors, including life stage and environmental stress, and involves a significant increase in viral replication, often leading to an increase in pathogenic effects on hosts (Wolf and Darlington, 1971; Eisenberg et al., 2012). Like human herpesviruses (Schmader, 2001), OsHV-1 appears to be able to persist as latent infections in asymptomatic *C. gigas* (Arzul et al., 2002; Dégremont et al., 2013; Whittington et al., 2015b). Apparent infections have been observed to persist in asymptomatic oysters, particularly during the cooler winter months (Petton et al., 2015) or when OsHV-1 infected oysters are held within aquaria maintained at cooler temperatures (<13 C; Pernet et al., 2015). OsHV-1 transmission and oyster mortalities occur seasonally, when seawater temperatures exceed 16 C (Pernet et al., 2012; Dégremont et al., 2013; Petton et al., 2013; Renault et al., 2014), and the highest rates of OsHV-1 transmission occur at seawater temperatures ranging from 16 to 24 C (Pernet et al., 2012; Petton et al., 2013). This temperature range corresponds to the temperature range that supports the highest clearance rates in *C. gigas* (Bougrier et al., 1995), lending support to direct filtration of OsHV-1 particles in the environment as the portal of entry for viral infection (Fig. 2).



**Fig. 2.** Life cycle of Ostreid herpesvirus 1 (OsHV-1) in *Crassostrea gigas*

The concentration of OsHV-1 particles in the environment can be substantial during herpesvirus epizootics, reaching  $6\text{--}7 \cdot 10^9$  virions per liter of seawater (Vigneron et al., 2004). Such seawater concentrations likely reflect the high prevalence of infection and high rate of mortality during epizootics, and would lead to high concentrations of directly infectious OsHV-1 particles in the environment and a high rate of transmission to new susceptible hosts. Advection of seawater, and its consequences on the dilution of seawater concentrations of OsHV-1, appears to strongly influence the risk and severity of herpesvirus outbreaks. In experimental laboratory tanks holding oysters exposed to OsHV-1 in the field, Petton et al. (2015) manipulated the rate of water renewal demonstrating the risk of OsHV-1 mortality to decrease with increasing rates of water renewal. The observed importance of water renewal agrees with observations of oyster farming practices by Pernet et al. (2012), finding that oysters cemented onto ropes, where water circulation around individual oysters is enhanced, suffered a lower rate of OsHV-1 mortality compared to oysters held in Australian baskets, where the circulation and flushing of water around individual oysters is comparably low. In addition, Pernet et al. (2014) observed that the OsHV-1 mortality risk decreased when oysters were deployed in the vicinity of mussel (*Mytilus galloprovincialis*) farms, suggesting that mussels, which are incompetent hosts for OsHV-1, can further dilute the water column abundance of viral particles through suspension feeding.

Complete life cycles have yet to be fully explored for many bacterial parasites of bivalves, but many of these parasites appear to be members of ambient marine microbial communities. It is well known that environmental factors, such as changes in water temperature and salinity, exert significant controls on the abundance and diversity of *Vibrio* species in the environment (Paillard, 2004; Labreuche et al., 2006; Beaz-Hidalgo et al., 2010), many of which have been described as agents of disease in wild and cultured bivalve molluscs. Infections with *N. crassostreae* have been associated with summer mortalities in wild populations of *C. gigas*, *O. edulis*, and *M. galloprovincialis*, particularly during periods of host physiological stress or in association with other pathogenic *Vibrio* spp. (Friedman et al., 1998; Engelsma et al., 2008; Carella et al., 2013). This parasite reproduces in host tissues by mycelial fragmentation and can be shed from hosts into the water column (Friedman and Hedrick, 1991). Since most terrestrial *Nocardia* are soil saprophytes, it is suggested that *N. crassostreae* infection in wild oyster populations occurs through a parasite reservoir that is regularly present in benthic sediments (Friedman and Hedrick, 1991). However, this parasite has not been demonstrated to transmit directly through sediments from enzootic areas, nor has transmission been observed through cohabitation with infected oysters (Friedman and Hedrick, 1991). Experimental infection has been achieved by inoculation with a relatively high parasite dose (Friedman and Hedrick, 1991), suggesting that, in conjunction with observations of mortality during periods of host physiological stress, *N.*

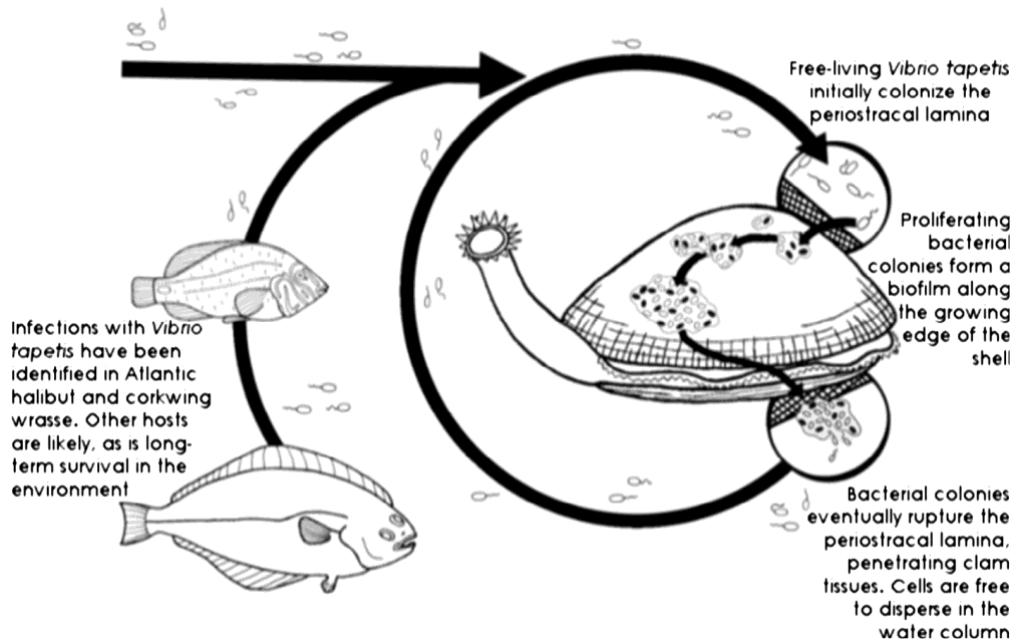
*R. crassostreae* is an opportunistic and facultative parasite that is regularly present in benthic marine sediments (Bower et al., 2005; Engelsma et al., 2008).

Although bacterial parasites appear to behave as members of ambient microbial communities little is known about the source and fate of these parasites outside bivalve hosts. *R. crassostreae* is a member of the marine Roseobacter clade, a diverse group of a-Proteobacteria comprising up to 25% of marine microbial communities in coastal oceans (Wagner-Dobler and Biebl, 2006). Among the cultured members of the Roseobacter clade, only *R. crassostreae* is known to be pathogenic (Boardman et al., 2008). After colonizing the inner shell surface of *C. virginica*, this bacterium divides by budding where new cells either become available to further colonize available shell surfaces or can be transmitted directly to new hosts (Ford and Borrero, 2001). Conchiolin deposition can serve to wall off colonizing bacteria, however, in advanced cases of disease conchiolin deposits eventually cover the entire soft body mass, forming a raised ring around the entire outer edge of the mantle margin (Ford and Borrero, 2001). The inhibition of filter feeding observed in laboratory-challenged oysters suggests that inadequate nutrition is a consequence of advanced infection (Boettcher et al., 2000; Boardman et al., 2008), and smaller and physiologically stressed oysters, with comparatively limited metabolic resources, have a higher incidence of mortality from disease (Davis and Barber, 1999; Ford and Borrero, 2001).

*R. crassostreae* can spread rapidly through shellfish hatcheries and grow-out operations (Lewis et al., 1996), likely from aided host contacts due to dense culture conditions. Population genetic studies confirm that most epizootics result from site-specific acquisition of *R. crassostreae* (Maloy et al., 2007a,b). This result, combined with repeated summer epizootics, suggests that *R. crassostreae* is present but not abundant in the environment. Once established within a bivalve culture facility or grow-out site *R. crassostreae* can be transmitted rapidly when environmental conditions are favorable.

Conchiolin deposition in oysters infected with *R. crassostreae* is similar to that observed in manila clams infected with *V. tapetis*. After colonizing the periostracal lamina, *V. tapetis* begin reproducing alongsurfaces of the external epithelium, particularly during periods of physiological stress when host defenses may be compromised (Allam et al., 1996; Lopez-Cortes et al., 1999a; Paillard, 2004). Parasit replication occurs through binary fission, and in favorable conditions, the bacterial biofilm associated withthis conchiolin deposit can eventually rupture the external epithelium of the mantle, allowing *V. tapetis* to penetrate into and proliferate rapidly in soft tissues (Allam et al., 1996, 2002; Lopez-Cortes et al., 1999a; Paillard, 2004). Results from transmission experiments suggest that direct contact between infected and healthy clams enhances the transmission of *V. tapetis* and the development of brown ring disease (Martinez-Manzanares et al., 1998). *V. tapetis* can also be transmitted through exposure to the feces of infected clams (Maes, 1992). The severe tissue disruption that results from bacterial proliferation (Allam et

al., 2002) also suggests that infective cells are released into the water column from decaying moribund hosts, and available to directly infect new susceptible hosts (Fig. 3).



**Fig. 3.** Life cycle of *Vibrio tapetis* in *Ruditapes philippinarum*.

Like other vibrios, *V. tapetis* is likely to be well adapted for survival in seawater (Yildiz and Visick, 2009; Beaz-Hidalgo et al., 2010; Balboa et al., 2012). Related *V. tapetis* strains have also been detected in moribund Corkwing wrasse (Jensen et al., 2003) and Atlantic halibut (Reid et al., 2003) exhibiting signs of vibriosis. Although these observations of *V. tapetis* infection in finfish were outside the geographic range limits of reported detections of brown ring disease, the association of this parasite with other hosts suggests that *V. tapetis* is a widespread, though not necessarily numerically dominant member of marine microbial communities. Since transmission is likely to occur through direct contact with both water-borne *V. tapetis* and infected clams, the density of hosts, particularly under intensive culture conditions, likely plays an important role in the control of brown ring disease (Paillard and Maes, 1994; Paillard, 2004). Bacterial parasites are not alone in their ability to reproduce outside their internal host environment. QPX can survive and grow on many available nutrient sources in the environment, including various species of macroalgae (Buggé and Allam, 2007; Gast et al., 2008). This is not surprising for a labyrinthulomycete parasite, as these saprotrophic protists commonly occur on or in living marine vascular plants and

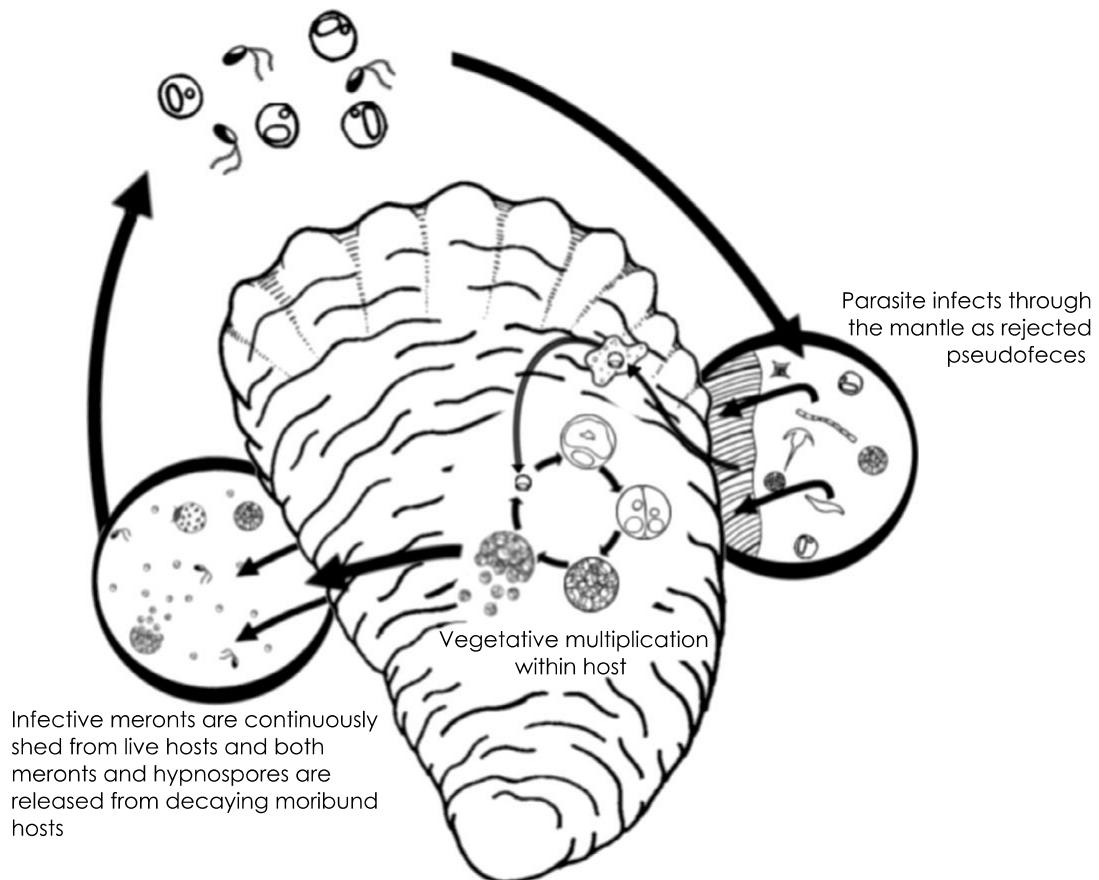
macroalgae, or in association with decomposing plant material and detritus (Tsui et al., 2009). Ectoplasmic nets, used by labyrinthulomycetes to solubilize nutrients in decomposing plant material, have not been identified in foci of QPX-like infections within quahog hosts (Smolowitz et al., 1998) or in association with QPX cells held in culture media (Kleinschuster et al., 1998). Instead, within hosts, QPX thalli and sporangia appear to produce a homogenous mucofilamentous material (Smolowitz et al., 1998), which is unusual for labyrinthulomycetes (Kleinschuster et al., 1998). QPX thalli, endospores, and zoospores have demonstrated the ability to produce the ectoplasmic net however (Kleinschuster et al., 1998). This occurs when QPX cells are suspended in seawater and adhere to substrate, such as culture flasks (Kleinschuster et al., 1998). Vegetative reproduction occurs within hosts and in culture media, where growth and maturation of thalli results in the formation of sporangia containing many vegetative endospores. Endospores are released when sporangia are ruptured, and the endospores form into thalli, repeating the life cycle (Kleinschuster et al., 1998). In seawater, motile zoospores can also form from endospores and thalli; however, zoospores have not been identified in infected clam tissue (Smolowitz et al., 1998). Vegetative reproduction can commence when zoospores are placed in culture media though (Kleinschuster et al., 1998). These observations suggest that zoospores occur in seawater and can infect hosts but do not commonly occur in the internal host environment. These observations of the QPX life cycle in infected hosts and culture media suggest that QPX can alternate between vegetative reproduction within clam hosts and survival and growth on substrates outside clam hosts, which is supported by the detection of QPX in association with a wide range of environmental samples, including seawater, marine aggregates (Lyons et al., 2005), marsh grasses, macroalgae, gastropods, ascidians, amphibians, barnacles, polychaetes, annelids, and bivalves other than quahogs (Gast et al., 2008). Detection of QPX in association with environmental samples increases in regions where QPX disease in quahogs is prevalent, suggesting that alternating between saprotrophy and parasitism may increase the distribution and spread of this labyrinthulomycete. In the absence of quahog hosts, or when environmental conditions do not favor infections within these hosts, QPX is likely to remain a common though inconspicuous component of the coastal marine microbial community.

The capacity for QPX to alternate between parasitism and survival and growth on substrates outside hosts appears to be unique among protozoan parasites infecting bivalves. The majority of these parasites require suitable hosts to complete their life cycles. All protozoans of the genus *Perkinsus* are obligate parasites, but many have proven to be very successful, able to infect a diversity of bivalve hosts and maintain high prevalence and persistence in host populations (Bushek and Allen, 2006; Goggin et al., 1989; Casas et al., 2002; Ragone Calvo et al., 2003; Villalba et al., 2004, 2005; Bushek et al., 2012; Soudant et al.,

2013). Their success is linked to qualities such as their capacity to survive outside hosts for prolonged periods (Chu et al., 2002; Chu and Lund, 2006), a battery of intricate mechanisms to degrade and sequester host immune systems (La Peyre et al., 1995; Garreis et al., 1996; Sunila and LaBanca, 2003; Hughes et al., 2010), and their ability to form chronic infections (Ford et al., 1999) while continuously dispersing from host tissues into the environment (Bushek et al., 2002). All *Perkinsus* species share a common life cycle. Infective trophozoites, or meronts, occur within host tissues as well as outside hosts in the water column, and undergo vegetative proliferation within hosts. After several internal cell divisions, four to 64 daughter cells become aggregated within the wall of schizont stages. Daughter cells are liberated through a tear in the schizont wall, and each daughter cell enlarges into an immature trophozoite, itself eventually dividing to repeat the vegetative reproduction cycle (Perkins, 1988, 1996; Sunila et al., 2001). When host tissues infected by *Perkinsus* spp. are incubated in fluid thioglycollate medium (FTM), trophozoites enlarge and develop a thick cell wall, becoming a prezoosporangium (also referred to as a hypnospore). Zoosporulation begins when prezoosporangia are transferred to seawater or culture media (Perkins, 1988), where numerous zoospores form by multiple fission within the prezoosporangia cell wall (Sunila et al., 2001) and emerge through a single discharge tube (Azevedo et al., 1990; Casas et al., 2002). Prezoosporangia have also been observed in decaying tissues of moribund hosts, and begin zoosporulation when placed in seawater (Perkins, 1996; Casas et al., 2002). Zoosporulation following transfer to seawater or culture media has been observed in all *Perkinsus* spp. except for *P. qugwadi*. In the case of *P. qugwadi*, the development of *P. qugwadi* zoospores has been observed to occur only within the interstitial spaces of scallops infected by this parasite (Blackbourn et al., 1998; Bower et al., 1998). All life stages of *Perkinsus* spp. have been shown experimentally to cause infection in bivalves, and all species can be transmitted directly, without intermediate or secondary hosts. Viable *Perkinsus* spp. trophozoites are released into the water column from live infected bivalves through diapedesis and in feces (Scanlon et al., 1997; Bushek et al., 2002; Casas et al., 2002). Infected hosts appear to provide a continuous source of infectious stages to new hosts, which are exposed to these parasites through feeding processes (Fig. 4). Maximum rates of transmission of *P. marinus* in oysters appear to occur during periods of maximum mortality caused by this parasite, most often in the late summer and early autumn when infection intensities peak (Ragone Calvo et al., 2003). This observation suggests that prezoosporangia, forming in moribund hosts and releasing numerous zoospores into the water column, contribute substantially to *P. marinus* transmission. White et al. (1987) also demonstrated that *P. marinus* could be transmitted through hemolymph meals taken by the ectoparasitic gastropod *Boonea impressa* that had previously been fed *P. marinus*-infected oysters. This vector is not essential for transmission though, since *P. marinus* transmission regularly occurs outside the geographic range of *B. impressa*.

Both the prevalence of infection with *Perkinsus* spp. and the transmission of these parasites are strongly tied to environmental conditions. Long-term field studies monitoring infection with *P. marinus* in its eastern oyster host along estuary salinity gradients, capturing annual variability in temperature and salinity, have identified these two factors as the key drivers of the incidence and expression of disease (Burreson and Ragone Calvo, 1996; Ragone Calvo et al., 2003; Soniat, 1996; Bushek et al., 2012). In temperate regions that experience broad annual temperature fluctuations, such as the mid-Atlantic and New England coasts of the United States, this temperature-dependence leads to a strong annual cycle of *P. marinus* proliferation (Ford et al., 1999). The cycle begins with an initial increase in the intensities of overwintering infections, when water temperatures increase above approximately 20 C (Soniat, 1996; Ford et al., 1999; Bushek et al., 2012). Parasite proliferation and host mortality increase through the summer and early fall, as does the release of viable parasites through the feces of live hosts and decaying tissues of moribund hosts (Ford et al., 1999; Bushek et al., 2002, 2012).

Infective meronts and zoospores can survive in seawater for weeks or more



**Fig. 4.** Life cycle of *Perkinsus marinus* in *Crassostrea virginica*.

Parasite proliferation within hosts and oyster mortality are followed by increases in the water column abundance of free *P. marinus* (Ragone Calvo et al., 2003; Audemard et al., 2006) and transmission to new hosts (Burreson and Ragone Calvo, 1996; Ragone Calvo et al., 2003; Bushek et al., 2012). Remission of infections in oyster populations occurs through the winter and early spring as water temperatures decrease (Ford et al., 1999). An early onset of spring, a delayed onset of winter, or both, allow for longer periods of parasite proliferation, which lead to a greater impact and extent of disease (Burreson and Ragone Calvo, 1996; Ford and Smolowitz, 2007). This temperature-dependence very likely defines the geographic extent of disease impacts as well. The apparent northward range expansion of *P. marinus* in the early 1990s was associated with above average winter and spring temperatures (Ford, 1996; Ford and Chintala, 2006), allowing this parasite to establish in areas it had not previously been reported or known to cause mortalities (Ford and Smolowitz, 2007).

Infections and the transmission of *P. olseni* follow a similar annual cycle. Casas (2002) showed that the prevalence and intensity of *P. olseni* infection in *R. decussatus* in Galicia, Spain increased in the spring when water temperatures exceeded 15 C, and peaked in the late summer when water temperatures reached annual maxima of 19–21 C. As with infection with *P. marinus* in oysters, remission of *P. olseni* infections occurred in the population through the winter and spring (Casas, 2002; Casas et al., 2002). Although not a bivalve host, higher temperatures also predispose greenlip abalone (*Haliotis laevigata*) to *P. olseni* infection and infection-associated mortalities (Goggin and Lester, 1995). Long-term field studies monitoring the prevalence and intensity of infections with *Perkinsus* species other than *P. marinus* and *P. olseni* have been scarce, but limited sampling has revealed that annual proliferation cycles are not always the case. In British Columbia, Canada, *P. qugwadi* proliferates and remains pathogenic to the cultured Japanese scallop *Patinopecten yessoensis* throughout the winter months, where water temperatures fall to as low as 8 C (Blackbourn et al., 1998). Epizootiological studies suggest that Japanese scallops, introduced into British Columbia in 1983, merely serve as an alternative or even aberrant host for *P. qugwadi*, and this parasite is likely enzootic in an unknown native host and co-adapted to the cool waters of this region (Bower et al., 1998). It is worth noting that the classification of *P. qugwadi* is uncertain, as this species is the only member of the genus that does not respond to incubation in Ray's fluid thioglycollate media (Dungan and Bushek, this volume).

Like *Perkinsus* spp., microcell haplosporidian parasites such as *B. ostreae*, *B. exitiosa*, *B. roughleyi*, and *M. mackini* are presumptively transmitted directly between bivalve hosts (Elston et al., 1986; Grizel et al., 1988; Montes et al., 1994; Culloty et al., 1999). These parasites differ from most haplosporidians by their apparent lack of a spore stage, instead infecting bivalve hemocytes and gill epithelial cells as small (2–3 lm), uninucleate, electron-dense or electron-clear forms, giving the microcell haplosporidians their namesake (Elston et al., 1986; Hine, 1991; Carnegie and Cochenne-Laureau, 2004; Engelsma et al., 2014). These cell forms reproduce by binary fission, and dense forms appear to be more numerous in heavily infected hosts (Carnegie and Cochenne-Laureau, 2004). Dense forms are presumed to be the primary infective stage (Hine, 1991) and frequent observations of free dense forms in gill epithelia suggest that parasites are released into the environment through these organs (Montes et al., 1994), but parasites are also likely to be released into the water column in moribund and recently deceased hosts through tissue lysis. Some microcell parasites do express multinucleate plasmodial forms (Hine, 1991; Montes et al., 1994; Carnegie and Cochenne-Laureau, 2004; Carnegie et al., 2006), but the contribution of these forms to parasite transmission is questionable. Only *B. exitiosa* regularly express multinucleate forms, and *B. ostreae* and *B. roughleyi* plasmodia have very rarely been observed and only in moribund hosts (Hine, 1991; Cochenne-Laureau et al., 2003; Carnegie and Cochenne-Laureau, 2004).

The transmission and impact of *B. exitiosa* display a strong seasonal association with the gametogenic and reproductive cycles of its host *Ostrea chilensis* in New Zealand (Hine, 1991; Hine et al., 2001). Initial infections occur when dense cell forms are ingested during feeding. Within-host parasite proliferation occurs after hosts spawn in December, continuing through the summer and autumn months. Here, dense cell forms proliferate and are shed from hosts, with host mortality and parasite transmission to new hosts following. By winter, many cells appear to grow to larger forms intermediate between dense and plasmodial forms, and plasmodial forms begin to dominate within hosts through the winter and early spring (Hine, 1991; Carnegie and Cochenne-Laureau, 2004). Plasmodial forms have been observed to develop toward sporogony, but host defenses, and possibly viral infections, are able to overwhelm and eradicate *B. exitiosa* plasmodia before this can occur (Hine, 1991). Dense forms present within hosts during this time appear to remain inactive though undetected by host defenses, or at least are able to evade host immune factors (Hine, 1991). Overwintering dense forms then incubate within host tissue until hosts spawn the following summer, when the proliferation and transmission cycle repeats (Hine, 1991; Hine et al., 2001). The infection cycles of other directly transmitted microcell haplosporidians do not appear to follow host gametogenic or reproductive cycles, but do show some seasonality. Although infections and mortality have been observed to occur year-round, the prevalence and intensity of *B. ostreae* infections in *O. edulis* are generally greatest in the warmer months (Grizel et al., 1988; Montes et al., 1994; Culloty and Mulcahy, 1996; Carnegie and

Cochennec-Laureau, 2004). On the other hand, signs of *B. roughleyi* infection and mortality in *Saccostrea commercialis* in southeastern Australia occur through cooler winter months (Adlard and Lester, 1995). *M. mackini* has typically been detected by histology only in the late winter and spring, but more sensitive PCR experiments have shown it to be associated with *C. gigas* throughout the year (Carnegie et al., 2003).

Whereas most haplosporidians are often only indirectly transmitted among their known hosts, direct transmission of uninucleate stages has been confirmed for *B. ostreae* in *O. edulis* and is well supported for *B. exitiosa*, *B. roughleyi*, and *M. mackini* in their known hosts (Grizel et al., 1988; Hine, 1991; Hervio et al., 1995; Culloty et al., 1999; Carnegie and Cochennec-Laureau, 2004; Lallias et al., 2008; Engelsma et al., 2014). The microcell parasites are noteworthy for their inconsistent expression of plasmodial forms and apparent lack of a spore stage. Carnegie et al. (2006) did observe sporulation in a novel *Bonamia* sp. infecting *Ostreola equestris* in North Carolina, USA, later characterized as *B. perspora*, but only in a small fraction of confirmed infections and an even smaller fraction of the *O. equestris* examined in the laboratory. The function of plasmodial forms, likely a vestige from an ancestral haplosporidian, seems to have been averted in microcell parasites in their known hosts with the evolution of directly transmitted dense forms (Hine, 1991; Carnegie and Cochennec-Laureau, 2004; Carnegie et al., 2006). However, the occurrence and utility of plasmodial forms and sporulation should not be overlooked. The longest documented and best-studied relationships between microcell parasites and their hosts are in host species of economic importance, many of which have a long history of being introduced and transported for aquaculture and resource restoration or enhancement. In addition to introducing any associated parasites, the expansion and diversification of susceptible host populations, such as by introducing native or nonnative bivalves for aquaculture, has both modified parasite life cycles and amplified the effects of parasites on host populations (Burreson et al., 2000; Hershberger et al., 2010; Blakeslee et al., 2012). It is possible, likely even, that a more conventional haplosporidian life cycle, including plasmodial forms and sporulation, can be identified if and when microcell parasites are observed in other, presumably natural, hosts.

Haplosporidian parasites introduced into naïve bivalve populations have also appeared to stray from the conventional life cycles characterizing these taxa. *H. nelsoni* has caused extensive mortalities in its *C. virginica* host along the mid-Atlantic coast of the United States (Haskin, 1966; Ford and Haskin, 1982) since its likely introduction from Asia, where the parasite appears to be enzootic in *C. gigas* (Kern, 1976; Burreson et al., 2000; Burreson and Ford, 2004; Carnegie and Burreson, 2011). This parasite has two life stages within oyster hosts: (1) multinucleate plasmodia, from which the disease caused by infection with *H. nelsoni*, Multinucleate Sphere Unknown (MSX), gets its name, and (2) spores. An infective stage has not been recognized, and efforts to transmit *H. nelsoni* under controlled laboratory conditions have not been successful. The most ambitious effort to date was by Canzonier (1974), implanting infected tissues into

uninfected recipients. Canzonier (1968) also reported failure to transmit *H. nelsoni* through cohabitation of infected and uninfected but susceptible oysters. Farley (1967) suggested that the infective stage is a uninucleate sporoplasm escaping from the spore. However, this pathogen is rarely observed to complete sporulation within adult *C. virginica* (Haskin, 1966; Andrews, 1982), inhibiting experimental efforts to transmit *H. nelsoni*. Limited sporulation has also led some investigators to conclude that *H. nelsoni* must have an intermediate host to complete sporulation and release infective stages into the environment (Farley, 1967; Andrews, 1982; Ford and Haskin, 1982; Sunila et al., 2000). Later efforts have observed sporulation in the digestive tubule epithelium of young oysters less than 30 mm in shell height (Barber et al., 1991), typically occurring over a brief two to three week period in late June and early July, which coincides with periods of maximum incidence observed in the field (Andrews, 1982; Ford and Haskin, 1982). Nevertheless, the complete life cycle of *H. nelsoni* continues to elude investigators and a suspected intermediate host has yet to be identified (Haskin and Andrews, 1988).

In contrast to *H. nelsoni*, *H. costale*, which causes Seaside Disease in oysters along the mid-Atlantic and northeastern coasts of the United States, appears to be a well-adapted native species exhibiting a conventional haplosporidian life cycle in its natural host, *C. virginica* (Wood and Andrews, 1962; Andrews, 1982). Although the timing unquestionably varies year-to-year (Stokes and Burreson, 2001), this parasite has a short infection period in the late spring and early summer, followed by an incubation period of up to nine months before clinical signs of diseases can be observed (Andrews, 1982). *Haplosporidium costale* sporulates regularly and completely, promptly killing its host following sporulation (Andrews, 1982). This leads to the characteristic pattern of acute mortality first observed by Wood and Andrews (1962, pp. 162–163) where “oysters began to die abruptly in mid-May and stopped dying early in July.” Like *H. nelsoni*, efforts to transmit *H. costale* under controlled laboratory conditions have not been successful, leading to speculation that an unknown intermediate host or hosts are required to complete the transmission cycle.

The detection and identification of intermediate hosts is challenging, limited by the tremendous diversity of potential host species to be screened, the broad spatial and temporal scales required for sufficient screening, and the limitations of tools available for detection (Haskin and Andrews, 1988; Audemard et al., 2001, 2002; Carrasco et al., 2007, 2008). As with the haplosporidian parasites *H. nelsoni* and *H. costale*, the paramyxean parasites of the genus *Marteilia* infect and sporulate in bivalve hosts, but cannot be transmitted directly between hosts, leading investigators to speculate that intermediate hosts are required to complete the transmission cycle (Grizel, 1979; Berthe et al., 1998). When working in semi-enclosed oyster ponds, locally known as ‘claires’ in Marennes-Oléron Bay, France, Berthe et al. (1998) observed new *M. refringens* infections in planted *O. edulis* even though no other *O. edulis* were present in the claire. Owing to their limited size and its consequences on environmental variables such as acute temperature variability

and seawater residence time, claire pond systems harbor fewer species than adjacent coastal bays and estuaries (Audemard et al., 2001), making them ideal experimental systems for detecting potential intermediate hosts. Audemard et al. (2002) systematically screened the entire fauna of the pond, finding that the copepod *Paracartia gralli* can serve as a host of *M. refringens*. Later surveys have confirmed that *Marteilia* parasites can be associated with zooplankton species in larger and more natural bays and estuaries (Carrasco et al., 2007). Within *O. edulis*, *M. refringens* develops from early stages in the epithelia of the upper digestive tract (Berthe et al., 1998). Sporulation takes place within the epithelium of the digestive gland tubules, releasing sporangia into the lumen of the digestive tract (Berthe et al., 1998). Sporulation is often associated with the destruction of the digestive gland epithelia and shedding of sporangia into the water column, becoming available to be ingested by *P. gralli* (Audemard et al., 2002; Carrasco et al., 2008; Boyer et al., 2013). Within *P. gralli*, *M. refringens* cells migrate to gonadal tissue through adjacent connective tissues, where this parasite then forms pseudoplasmodia containing large numbers of small (2–5 lm), presumptively infectious cells (Carrasco et al., 2008).

The involvement of *P. grani* in the life cycle of *M. refringens* is consistent with the phenology of this copepod and the epizootiology of disease caused by *M. refringens*, known as Aber disease. Aber disease is seasonal, beginning in late spring, peaking through the summer and early fall, and decreasing in the winter (Grizel, 1979). *Paracartia grani* is most commonly observed in coastal waters in the spring and summer, where it can become a dominant member of the zooplankton community (Audemard et al., 2002). Transmission experiments have demonstrated that *P. gralli* could be infected from infected *O. edulis*, indicating that these two species are contiguous in the life cycle of the parasite (Audemard et al., 2002; Carrasco et al., 2008). It remains open whether and how *M. refringens* can be transmitted from *P. grani* to *O. edulis* though, as attempts at copepod-to-oyster transmissions have failed (Audemard et al., 2002; Carrasco et al., 2008). These results suggest there may be a second intermediate host, or they may simply reflect a failure for transmission experiments to attain the required inoculum of *M. refringens* in *P. gralli* to lead to successful infection in *O. edulis*. This latter hypothesis is supported by the observations of Boyer et al. (2013), following the dynamics of *M. refringens* in *P. grani* and two bivalve hosts, *M. galloprovincialis* and *R. decussatus*, in Thau lagoon, southern France. Although *M. galloprovincialis* serve as competent hosts, *M. refringens* was observed only as necrotic cells in the digestive epithelia of *R. decussatus*, suggesting this bivalve is a dead end for *M. refringens*. The prevalence of mature *M. refringens* sporangia in *M. galloprovincialis* was observed to increase in the spring, declined through the summer, but increased again in the fall (Boyer et al., 2013). The parasite was also detected in eggs and the copepodid stages of *P. grani* throughout the summer and fall, lending support to the hypothesis of the transmission of *M. refringens*.

from bivalves to copepods and back to bivalves. In addition, it appears this parasite has two cycles per year in Thau lagoon (Boyer et al., 2013).

It is common for parasites with complex life cycles and multiple host species to demonstrate multiple overlapping life cycle phases (Holt et al., 2003; Dobson, 2004). Andrews (1982) described irregular patterns of *H. nelsoni* infection in *C. virginica* inhabiting estuaries along the mid-Atlantic coast of the United States. In Virginia, the timing of infections with *H. nelsoni* can be divided into early-summer and late-summer acquisitions that result in quite different mortality patterns (Andrews, 1982). The early summer infection period for *H. nelsoni* occurs from mid-May through the early summer, with the earliest infections becoming clinical by the mid-summer and first mortalities occurring by the late summer. Late-summer infections with *H. nelsoni* exhibit patterns similar to those described for *H. costale*, where initial infections occur in the late summer but remain subclinical or localized throughout the winter and early spring. These infections eventually become severe by the following spring and lead to mortality by the early summer (Andrews, 1982). In the case of *M. refringens* infection in *M. galloprovincialis*, the increase in prevalence in the early spring observed in Thau lagoon may reflect proliferating overwintered infections that can be shed by bivalve hosts, becoming available to infect intermediate copepod hosts. Parasite development in intermediate hosts lags this event, and infective parasite stages in intermediate hosts then become available to infect new bivalve hosts by the late summer and early fall. Interestingly, Boyer et al. (2013) also demonstrated high retention efficiency of copepod stages contributing to *M. refringens* transmission in *M. galloprovincialis*, suggesting that exposure to infective parasite stages occurs through direct feeding of copepod stages.

## 6. Concluding remarks: an ecological perspective

Parasitic diseases cause substantial community- and ecosystem-wide impacts in marine and estuarine bivalves. The long history of diseases impacting bivalve species of ecological and economic importance has produced a rich body of knowledge describing interactions between bivalves and their parasites. Collectively assembled, we can draw a number of conclusions about parasite transmission in bivalve hosts from this diverse body of work.

1. Parasite transmission rarely occurs through direct contact between bivalve hosts, although *V. tapetis* may be transmitted between clams in very close contact. In most cases, the transmission of bivalve parasites occurs by exposure to water-borne parasite stages through suspension feeding processes.
2. Infections with viral parasites are very likely to be common in wild and cultured bivalves, and may be responsible for many of the cryptic mortality events observed in shellfish hatcheries.

3. Many bacterial parasites, including *N. crassostreae* and *Vibrio* spp., and protozoan parasites such as QPX, can be common, though inconspicuous constituents of ambient marine microbial communities. These facultative parasites appear to adapt to parasitic lifestyles when conditions permit.
4. Some stages of protozoan parasites can survive for days, weeks, or even months in the water column, and can disperse quite far as passive particles, broadly distributing themselves throughout bivalve populations.
5. Many consumed parasites have adapted behaviors to evade direct digestion, instead targeting “safer” portals of entry such as pallial organs and pseudo-internal extrapallial spaces and peripheral compartments.
6. Parasites often target hemocytes for direct infection or dissemination through host tissues.
7. The outcome of interactions between bivalve hosts and their parasites is regulated by intrinsic host factors such as innate immunity and physiology, parasite factors such as virulence, and the interaction of these two factors with environmental variables such as temperature and salinity.
8. Many bivalve parasites, including OsHV-1, *V. tubiashii*, *P. olseni*, *B. ostreae*, *M. mackini*, and *M. refringens*, have adapted to infect multiple hosts. The susceptibility and tolerance of hosts to parasitic infection can vary dramatically by species.

The implications of the final conclusion remain open, and should drive future ecological studies of parasites infecting bivalve hosts. A community of bivalves offers parasites options for host competence. This point is exemplified by the observations of Boyer et al. (2013) in Thau lagoon. There, *M. refringens* infects *M. galloprovincialis*, but occurs only in digestive epithelia of *R. decussatus* as necrotic cells. This parasite has been observed to infect a diversity of bivalve hosts, including *O. edulis*, *O. angasi*, *O. puelchana*, *M. galloprovincialis*, and *M. edulis* (Figueras and Montes, 1988; Le Roux et al., 2001) (Table 1). A diversity of host species, each plausibly offering parasites a range of competency, represents the resources supporting a continuum of outcomes for parasites, from immediate parasite mortality to successful reproduction and spread through host populations. This diversity is not limited to competent hosts. Once released into the environment, free-living parasite stages encounter a multitude of factors that impact their survival and infection success. While associations with abiotic factors such as water temperature and salinity have received much attention here and elsewhere, little is known about the role of ambient fauna. This reductionist approach is often intentional, as much of what we know about the transmission of bivalve parasites is based on experimental systems or models in which hosts and parasites are considered in an ecological vacuum. In reality, hosts exist within diverse ecological communities, and ecological interactions undoubtedly influence the transmission and impact of parasites (Dobson, 2004; Hall

et al., 2007). Pernet et al. (2014), for example, found the risk of OsHV-1 mortality to decrease in *C. gigas* when oysters were held in the vicinity of mussel farms. The observation by Pernet et al. (2014) suggests that nonfocal suspension feeders can dilute the abundance of suspended particles in the water column, minimizing the impact of suspended parasites on their focal hosts. The importance of host diversity has become apparent in a number of case studies of bivalve hosts impacted by trematode parasites. Studying infections with the larval trematode *Curtuteria australis* in the intertidal cockle *Austrovenus stutchburyi*, Mouritsen and Poulin (2003) found that cockles that provided habitat for epifaunal anemones (*Anthopleura aureoradiata*) were significantly less likely to be infected with the larval trematode *C. australis*, compared to control groups free of epibionts. In a similar series of experiments, Thieltges et al. (2008) found cockle hosts (*Cerastoderma edule*) held with co-occurring macrofaunal invertebrates acquired a lower load of cercariae of the trematode *Himasthla elongata* compared to cockles held alone. These studies revealed that the effects of parasites were modified when focal hosts were considered within broader ecological communities. In these examples, the effects of parasites were diluted when focal bivalve hosts were considered within a community of abundant alternative hosts with reduced competence. This general phenomenon of a “dilution effect” has received much attention in disease ecology, with relevant examples including Lyme disease (Schmidt and Ostfeld, 2001; LoGiudice et al., 2003), West Nile virus (Swaddle and Calos, 2008; Allan et al., 2008), and Schistosomiasis (Johnson et al., 2009). In these examples, weakly competent or incompetent hosts play a crucial role in determining the impact of parasites on focal hosts. When these alternative hosts have net negative impacts on focal hosts, via ecological processes such as competition and predation of suspended parasite stages in the water column, the dilution effect is compounded (Schmidt and Ostfeld, 2001; Wood and Lafferty, 2013).

The relationship between the host diversity and parasite effect is scale-dependent and complex (Randolph and Dobson, 2012; Wood and Lafferty, 2013). In the case of bivalve hosts, three separate ecological processes can lead to the attenuation of parasite effects in focal hosts: (1) the consumption of free-living parasite stages by predators in the water column, (2) suspension feeding by non-host species (parasite decoys), and (3) the infection of alternative hosts. Interference competition arising from all three processes, and even between focal hosts, may also result in lower exposure to suspended particles, further lowering the exposure of focal hosts to parasite stages in the water column and diluting the effect of parasites. Connections between the structure of ecological communities and the emergence, spread, and persistence of bivalve diseases are very rarely made, but these connections underscore the importance of understanding the context of and feedbacks to ongoing changes in bivalve populations and their broader ecological communities when considering the impacts of disease.

We encourage future research questions to address these connections directly. How do bivalve diseases respond to changes in host population density? Does the presence of multiple host species influence the impact of bivalve parasites on focal hosts? In turn, how does the abundance and diversity of suspension feeding invertebrates dilute concentrations of parasites in the water column, and what are the effects of parasite dilution on the impact of disease? These questions highlight a critical role for ecological context and host community ecology in the transmission of diseases in populations of bivalve molluscs, which in turn has important consequences for the sustainability of wild and cultured bivalve populations and the function of nearshore ecosystems.

## Acknowledgments

The authors would like to thank E. McGurk, R. MacFarlan, B. Allam, D. Proestou, J. Looney, and W. Schroer for constructive discussions on the content and arrangement of this manuscript. We also thank J.E. Ward for clarity on suspension feeding processes in marine bivalves and we thank one anonymous referee for constructive comments on an earlier version of this manuscript. TBH was supported by a grant from the National Science Foundation program in Ecology and Evolution of Infectious Diseases (OCE-1216220). LH was funded by a National Science Foundation Research Experience for Undergraduates supplement to OCE-1216220. DAN was funded by MINECON – NC120086, Chile.

## Appendix A. Supplementary material

Supplementary data associated with this article can be found, in the online version, at  
<http://dx.doi.org/10.1016/j.jip.2015.07.006>.

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