Amoebic gill disease: a growing threat



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The risk of disease outbreaks is predicted to increase due to climate change. For farmed fish an example is amoebic gill disease (AGD). While initially reported only in farmed salmonids in Washington State, USA, and Tasmania, Australia, it has now become an issue for Atlantic salmon farming worldwide and affects a range of other farmed marine fish species. Local high temperature anomalies and a lack of rainfall have been associated with the outbreaks of AGD. This worldwide presence is at least partly due to the cosmopolitan nature of the parasite and its low host-specificity. The disease can be treated using freshwater or hydrogen peroxide baths, but the treatments increase the cost of salmon production. Management of AGD contributes 20% to production costs of Atlantic salmon in Tasmania.

AGD, caused through infection of fish gills by the facultative parasite *Neoparamoeba perurans*, was first documented in sea-caged salmonids in 1985[1]. Since its initial observation AGD has become a primary health concern globally for the marine salmonid industry, resulting in mortalities as great as 80% when left untreated[2]. Clinical signs of AGD include respiratory distress, lethargy and inappetence, which are associated with grossly visible gill lesions[3]. Histologically, gill lesions are characterised by epithelial hyperplasia, interlamellar vesicles with associated amoebae and lamellar fusion[4] (Figure 1).

Because *N. perurans* was only recently identified[5] and shown to cause AGD[6], minimal information is available on its biology and ecology. Amoebae of the genus *Neoparamoeba* (Amoebozoa, Dactylopodida) are ubiquitous in the marine environment[7], and *N. perurans* specifically have been detected throughout the water column on and near Atlantic salmon (*Salmo salar* L.) farms[8,9]. All species from the genus *Neoparamoeba* harbour at least one intracellular endosymbiont known as a *Perkinsela amoebae*-like organism (PLO)[10]. The details of the symbiotic relationship between the PLOs and *Neoparamoeba* are unknown; however, the strict phylogenetic congruence of PLOs and their *Neoparamoeba* hosts suggests that PLOs are vertically transmitted from parent to daughter cells during mitotic division[10]. Species of *Neoparamoeba* all

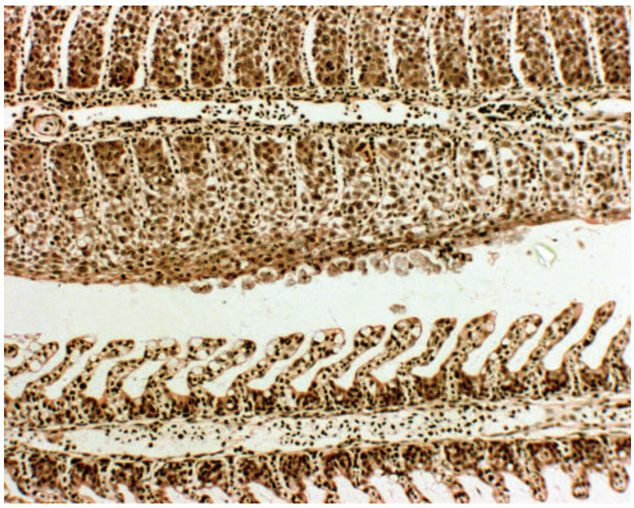

Figure 1. Histological section showing two filaments from gills of infected Atlantic salmon, the top filament is affected and the bottom one is normal. Epithelial hyperplasia and lamellar fusion associated with presence of numerous amoebae can be seen in the top filament.

share the same general ultrastructural characteristics and cannot be differentiated morphologically[11].

Despite numerous studies investigating potential reservoirs of *N. perurans*, no significant reservoir outside farmed salmon has been identified[9]. Extensive surveys of the water column[8,12] and wild fish[13–15] have detected only minimal evidence of *N. perurans*. Studies of metazoan ectoparasites, for example copepods or isopods, on farmed salmon have detected low frequencies of *N. perurans*[16,17], but no evidence of a reservoir population. Additional studies using genus specific identification methods detected *Neoparamoeba* spp. in sediment samples[18] and net biofouling[19], but as yet no species specific testing has been conducted to detect *N. perurans* in these potential reservoirs.

Along with seemingly no reservoir, *N. perurans* is also an opportunistic parasite with no apparent host specificity. The pathogen has been detected not only in the commercially important Atlantic salmon[20], but also in a variety of farmed and non-farmed finfish species around the world[9] (Figure 2). Presently AGD is a major issue for aquaculture in Tasmania, Ireland, Scotland, Norway and the United States with varying levels of impact from 10% to 82% mortality in some cases[9]. Additional outbreaks have been reported in Chile, France, Spain, South Africa, and most recently Canada and the Faroe Islands[9,21].

Beyond salmon, *N. perurans* has been found on the gills of an additional 14 finfish species including ayu in Japan[22], sea bass in the Mediterranean[23], and olive flounder in Korea[24]. There is no traceable pattern from one of these outbreaks to another making it unlikely that it is a specific sub-population that causes the disease or that amoebae are transferred from one outbreak site to another. What is known of its lifecycle suggests an asexual clonal evolutionary pattern. It has been postulated by statistical analysis that the sheer number of individuals in any given microbial species is so large that dispersal would rarely be restricted by contrived geographical barriers[25], especially in marine environments[7].

The cosmopolitan nature of *N. perurans* and lack of host specificity make discerning trends and risk factors for AGD challenging. A recent meta-analysis which considered all reports of AGD to date suggests locally high temperature anomalies, rather than absolute temperature, are related to disease outbreak[9]. Salinity also plays an important role in AGD. *N. perurans* is a marine amoeba with minimal tolerance for low salinity. Freshwater bathing for 2–4 hours is the most commonly utilised commercial treatment for AGD[26], and though many reports do not include information on rainfall, the few which have report lower than average rainfall preceding outbreaks[3,27–29]. Given the predicted increase in ocean temperatures and altered rainfall patterns associated with climate change, there is concern that AGD associated costs will continue to increase for the salmonid industry moving forward[30].

Although research into AGD has come a long way in the past 30 years there are still many knowledge gaps in key areas from basic biology

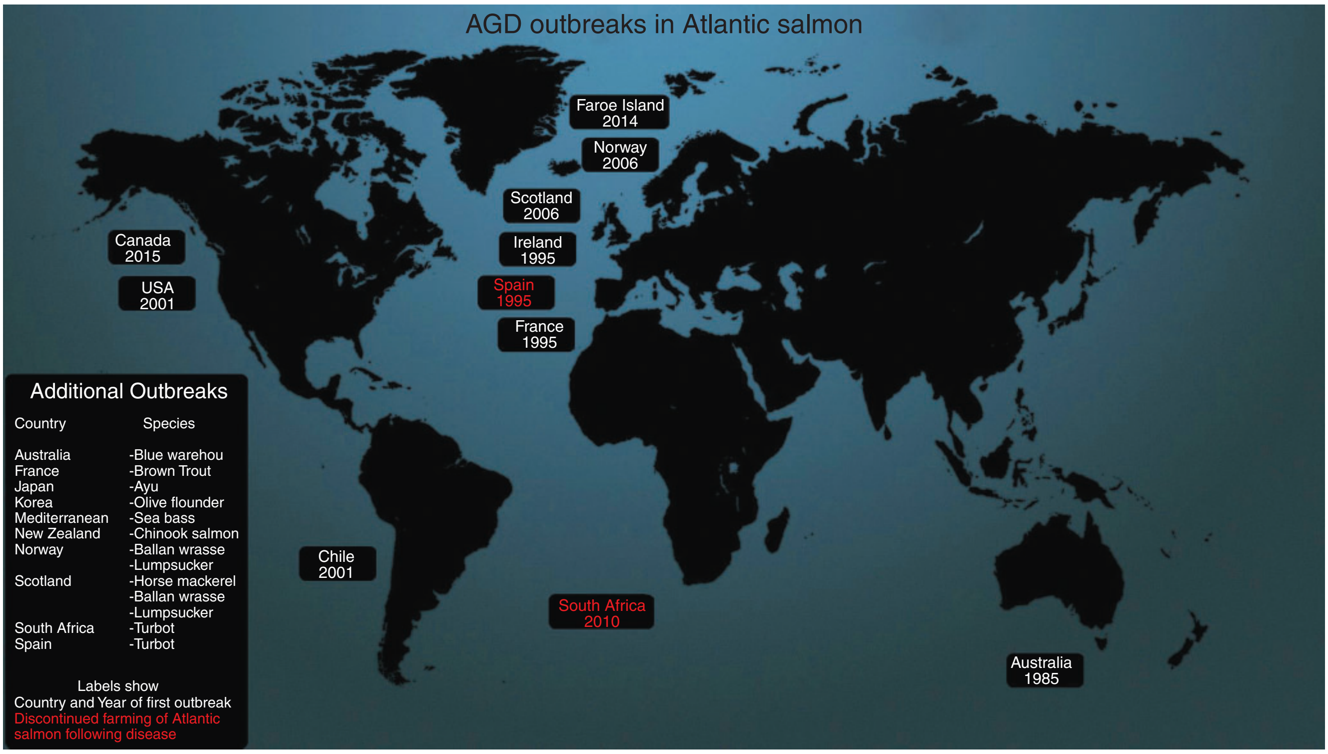

Figure 2. Map showing reported confirmed (PCR and/or ISH) cases of amoebic gill disease (AGD) in farmed Atlantic salmon.

to industry research. For instance, little is known about the parasite *N. perurans*. The mechanisms behind the successful transfer of the PLO from mother to daughter cell, and benefits of the symbiosis, are not yet known. In addition there is little information on how the amoebae cause disease and whether there is potential for vaccines or drug targets. On a more practical side, extensive and thorough testing of sediment, biofouling and other potential reservoirs would also be beneficial for predicting outbreaks and controlling this globally increasing threat.

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Biographies

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