The use of repellents to reduce biting by nuisance mosquitoes is well known. As Hoffman and Miller comment, ‘We suggest a combination of directed wind and volatile repellent might be developed as a mosquito deterrent strategy for the backyard setting’ [3]. Indeed, the combination of DEET and permethrin in a coconut base (Mosbar) as a malaria control measure looks promising (M. Rowlands et al., unpublished). Volatile oils from plants can serve as effective repellents [4,5] and these oils can be burnt in lamps [6]. The use of volatile oils are being studied by J. Lines and M. Rowlands (London School of Tropical Medicine and Hygiene, UK) as part of the malaria programme funded by the Bill and Melinda Gates Foundation (http://www.gatesfoundation.org/). Given that the Egyptians had used both towers [7,8] and impregnated nets to avoid mosquitoes, and that they knew a thing or two about herbs, the rediscovery of Kiki and an examination of its possible repellent effects might seem apposite.

Are hydrothermal vents oases for parasitic protists?

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Two recent 18S ribosomal RNA-based surveys of protist diversity near hydrothermal vents in the Pacific and Atlantic oceans allowed the identification of a variety of sequences related to several parasitic protist lineages. These include the Apicomplexa, Perkinsozoa, Syndiniales and Kinetoplastida. This diversity of parasitic protists could be hosted by the dense animal populations that thrive around these hydrothermal vents which contrasts with the scarcely populated cold deep-sea waters. These protist parasites might explain some of the mysterious sudden mortality episodes affecting the hydrothermal vent fauna.

In 1977, a wealth of endemic exotic animals was discovered thriving around deep-sea hydrothermal vents in the Galapagos area. Most of them are invertebrates that establish flourishing colonies close to the vent chimneys expelling hot and reduced hydrothermal fluids. In addition to many other animal species, vent areas in the Atlantic ocean are dominated by shrimps (Rimicaris spp.), whereas those in the Pacific host conspicuous tube-building worms such as polychaete species of the genera Alvinella and Paralvinella, and the giant vestimentiferan Riftia pachyptila. Dense populations of bivalves (Calyptogena spp. and Bathy modiolus spp.) can be found in diffuse low temperature habitats at hydrothermal vents and cold seeps in both oceans [1]. Sudden massive mortality episodes affecting some of these animal species, in particular bivalves, have been attributed to fluctuations in hydrothermal fluid flux, although the precise cause remains unknown [2]. Sterility and mortality might also be due to bacterial infections [3]. This is not a surprising hypothesis in that together with animals, hydrothermal vents are occupied by a vast diversity of prokaryotic species (some of which are chemolithoautotrophic), but the lifestyle of most of these prokaryotic species is unknown [4]. Moreover, microscope examinations of gill and gonad tissues from seep mussel populations in some areas of the Gulf of Mexico have revealed a high prevalence of parasites, including intracellular bacteria morphologically related to Rickettsia and Chlamydia, in addition to Bucephalus-like trematodes. Bucephalus infections were so extensive that 40% of these mussel populations showed a severely compromised reproductive potential because most individuals of these populations had very degraded gonadal tissues [3].

Deep-sea discoveries

Since the first explorations of deep-sea hydrothermal vents, the animal and prokaryotic communities have been extensively studied using classical and molecular approaches [1,4]. However, until recently, little attention was paid to the diversity of protists in these areas. In 2000, Atkins et al. furnished conclusive evidence of protist presence with the isolation of nine species from vents in the Eastern Pacific ocean [5]. Direct PCR amplification of 18S ribosomal RNA (rRNA) genes from environmental samples provides an alternative powerful tool to examine protist diversity [6]. Thus, two recent molecular surveys have uncovered a rich protist diversity in Pacific [7] and Atlantic [8] deep-sea vents. An interesting result shared by

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both molecular analyses is the identification of several 18S rRNA sequences that most probably belong to parasitic protist lineages. Figure 1 presents bayesian phylogenetic trees, showing the evolutionary relationships of these sequences.

Most of these putative parasitic protists affiliate to the alveolates (comprising well-known groups such as the Perkinsozoa, Apicomplexa, dinoflagellates and ciliates; Figure 1a). Perkinsus spp. parasitize a variety of bivalves [9]. The Atlantic clone AT2–6 [8] is a close relative of the

Figure 1. Bayesian phylogenetic trees showing the relationships of Pacific and Atlantic deep-sea vent environmental sequences with (a) alveolate and (b) kinetoplastid parasitic protists. Trees were constructed using MrBayes [Huelsenbeck, J.P. and Ronquist, F. (2003) MrBayes: A Program for the Bayesian Inference of Phylogeny, Uppsala University], by applying a gamma distribution with a proportion of sites invariant to model rate variation across sites. A million generations were used, with trees begin sampling every 100 generations (the first 1000 trees were discarded). Environmental sequences are indicated in green, those labeled 'C' are from Pacific [7], and those labeled 'AT' and 'IN'' are from Atlantic[8] hydrothermal areas. Parasites related to these hydrothermal environmental sequences are indicated in bold; names in parentheses correspond to hosts of the respective parasites. Numbers at nodes are posterior probabilities (only those >0.5 are shown). The very long branches of several gregarine species have been shortened to half of their actual length and appear as broken in the tree. Scale bar = 0.1 substitutions per site.

http://parasites.trends.com
oyster parasite Perkinsus marinus (18S rRNA sequence identity of 99%) and emerges within a compact group of sequences from parasitic Perkinsus spp. This clone was retrieved from a colonization substrate, adjacent to a colony of Bathymodiolus azoricus, so it is probable that these hydrothermal mussels are also parasitized by Perkinsus as their coastal relatives. Two additional sequences (AT4–98 and IN242) branch at the base of the Perkinsus group [8]. The Pacific sequence C1_E016 is related to Parvilucifera infectans, a species distantly related to the genus Perkinsus that parasitizes other protists [10]. The entire group of the Perkinsozoa is probably parasitic, including the environmental deep-sea vent sequences. Still within the alveolates, some Pacific (C3_E014, C2_E016, and C1_E017) and Atlantic (AT4–16) clones branch among the gregarines within the Apicomplexa. Gregarines, as are all of the known species of Apicomplexa, are parasites, most of them of the digestive tract or body cavities of invertebrates [11]. They are generally homoxenous (adapted to parasitize a single host species), hence the discovery of several distantly related gregarine species in these environments suggests that they are parasites of different deep-sea vent invertebrate species. The Pacific clone C1_E047, distantly related to Cryptosporidium parvum, also belongs to Apicomplexa. One Atlantic (AT4–21) and several Pacific (CS_E040, CS_E001, C1_E010, CS_E006, and A2_E046) clones are relatives of Hematodinium and Amoebophrya spp. These are endoparasites of invertebrates and protists ascribed to the parasitic dinoflagellate order Syndiniales [12]. Amoebophrya-related sequences are abundantly retrieved from marine plankton samples at all depths and different oceanic regions, indicating that this putative parasitic group is ubiquitous in the ocean [6,13,14]. In addition to this wide variety of parasitic alveolates, a deep-sea vent clone (AT4–56) related to the fish ectoparasitic kinetoplastid Ichthyobodo necator (Figure 1b) was also detected. Although it is generally difficult to extrapolate the way of life of organisms from their 18S rRNA sequences, these results show that a significant proportion of sequences retrieved from both Pacific and Atlantic deep-sea vent areas are related to parasitic protist lineages that might target a broad spectrum of hosts.

Perspective

In sharp contrast to the cold abyssal oceanic regions, hosting scattered animal populations, deep-sea vent areas are colonized by exceptionally dense populations, which can facilitate parasite transmission and then favour elevated parasite prevalence values [3,15]. In this sense, deep-sea vents can be regarded as oases for parasites. However, deep-sea vents configure extremely fragmented landscapes (vent areas can be many kilometres distant from each other). Hence, endemic vent animals are characterized by developing a metapopulation distribution, with a rapid turnover rate and colonization–recolonization events [16,17]. The discovery of a variety of parasitic protists in deep-sea vents adds a new factor that has to be considered to understand deep-sea vent ecology and population dynamics. The identification and characterization of these parasites beyond their 18S rRNA sequences will be of great interest to investigate the peculiarities (mode of transmission, eventual co-speciation, prevalence) of parasitism in metapopulation communities.

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