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Acquisition of an animal gene by microsporidian intracellular parasites

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Abstract

Parasites have adapted to their specialised way of life by a number of means, including the acquisition of genes by horizontal gene transfer. These newly acquired genes seem to come from a variety of sources, but seldom from the host, even in the most intimate associations between obligate intracellular parasite and host [1]. Microsporidian intracellular parasites have acquired a handful of genes, mostly from bacteria, that help them take energy from their hosts or protect them from the environment [2,3]. To date, however, no animal genes have been documented in any microsporidian genome. Here, we have surveyed the genome of the microsporidian *Encephalitozoon romaleae*, which parasitises arthropods for evidence of animal genes. We found one protein-encoding gene that is absent from publicly available sequence data from other microsporidia. The gene encodes a component of the purine salvage pathway, and has been independently acquired by other parasites through horizontal gene transfer from other donors. In this case, however, the gene shows a very strong phylogenetic signal for arthropod origin.

We created a 20-fold coverage survey of the *E. romaleae* genome, resulting in 165 contigs, with an average length of 13,350 bp. Search for genes of potential animal origin revealed the presence of only one candidate, a purine nucleotide phosphorylase (PNP). Interestingly, this gene is absent from any other publicly available microsporidian sequence data, including complete genomes from other members of the genus *Encephalitozoon* [4]. *Encephalitozoon* genomes share a high level of co-linearity, and the *E. romaleae* PNP gene is flanked by genes with high sequence similarity and gene order conservation from regions of chromosome 1 of *E. cuniculi* and *E. intestinalis*, respectively (Supplemental information). This protein is involved in a pathway that is notoriously reduced in other members of the lineage, but otherwise essential for salvaging purines in other eukaryotes [4], and its inclusion in the genome of *E. romaleae* was confirmed by PCR and conventional DNA sequencing.

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Supplemental Information

Supplemental Information includes a supplemental figure and experimental procedures and can be found with this article online at doi: 10.1016/j.cub.2011.06.017.

The origin of the PNP gene was assessed using a variety of models and methods for phylogenetic reconstruction. The phylogeny consistently showed the microsporidia to cluster not just with animals, but specifically with arthropods with high support (Figure 1). The exclusion of the more divergent arthropod sequences (i.e., crustaceans and *Pediculus*) had no effect on either tree topology or support (Supplemental information). *E. romaleae* is unusual in that it is the first described species or *Encephalitozoon* isolated from an insect [5]; all other members of the genus are only known to infect vertebrates. The arthropod origin of its PNP might suggest a recent, insect host origin, so we also searched an ongoing genome project from a putative sister species, the human parasite *E. hellem*, for the presence of PNP. Interestingly, the arthropod PNP is also found in the same genomic context in *E. hellem* (Figure 1), and we confirmed that these two species are indeed sister-species using a multigene phylogeny (Supplemental information).

Overall, these data indicate that the PNP gene was acquired from an insect in the ancestor of *E. romalea* and *E. hellem*, which raises the question: was this insect the host? The exceedingly narrow distribution of this gene in the sister species *E. hellem* and *E. romaleae* is most consistent with a recent gain of the gene. But *E. hellem*, like all other described members of this genus, is a parasite of vertebrates. It is possible that our current understanding of host-range in *Encephalitozoon* species is limited by sampling bias, or ancestral types had broader host-ranges. Indeed, infection of both insects and vertebrate hosts by microsporidia has been documented in *Anncalia algerae* [6], *Trachipleistophora hominis* [7] and *Trachipleistophora extenrec* [8]. This is particularly plausible given that *E. romaleae* is an insect parasite, so some host switching must have occurred in the ancestor of *E. romaleae* and *E. hellem*. The alternative explanation — that an ancestral intracellular parasite that specifically infected vertebrates somehow acquired an insect gene — is difficult to imagine since exposure of the parasite to insect genes would presumably be very limited.

The function of the PNP gene in parasite biology is also of interest because many parasites depend on salvage pathways for their nucleotides. In the apicomplexan *Cryptosporidium*, the pyrimidine salvage enzyme thymidine kinase was acquired from a bacterium [9], as was the PNP itself in the diplomonad *Giardia* [10]. These three lineages acquired similar functions in parallel by acquiring new genes through HGT, but only in microsporidia was it apparently derived from the host. The genome-level data from microsporidia now available also raise the interesting question of why some species of *Encephalitozoon* get by without PNP while these two species have retained it, despite their otherwise highly reduced gene repertoire. Neither the long-term fate of such genes acquired by HGT, nor the short-term implications of their integration into cellular pathways are well understood, but the relatively tractable genomes of *Encephalitozoon* make this an appealing genus in which to address such questions.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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References

1. Anderson MT, Seifert HS. Opportunity and means: horizontal gene transfer from the human host to a bacterial pathogen. mBio. 2011; 2
2. Chan KW, Slotboom DJ, Cox S, Embley TM, Fabre O, van der Giezen M, Harding M, Horner DS, Kunji ER, Leon-Avila G, et al. A novel ADP/ATP transporter in the mitosome of the microaerophilic human parasite *Entamoeba histolytica*. Curr Biol. 2005; 15:737–742. [PubMed: 15854906]
3. Fast NM, Law JS, Williams BA, Keeling PJ. Bacterial catalase in the microsporidian *Nosema locustae*: implications for microsporidian metabolism and genome evolution. Eukaryot Cell. 2003; 2:1069–1075. [PubMed: 14555490]
4. Corradi N, Pombert JF, Farinelli L, Didier ES, Keeling PJ. The complete sequence of the smallest known nuclear genome from the microsporidian *Encephalitozoon intestinalis*. Nat Comm. 2010; 1 10 1038/ncomms1082.
5. Lange CE, Johny S, Baker MD, Whitman DW, Solter LF. A new *Encephalitozoon* species (Microsporidia) isolated from the lubber grasshopper, *Romalea microptera* (Beauvois) (Orthoptera: Romaleidae). J Parasitol. 2009; 95:976–986. [PubMed: 20050002]
6. Coyle CM, Weiss LM, Rhodes LV, Cali A, Takvorian PM, Brown DF, Visvesvara GS, Xiao L, Naktin J, Young E, et al. Fatal myositis due to the microsporidian *Brachiola algerae*, a mosquito pathogen. New Eng J Med. 2004; 351:42–47. [PubMed: 15229306]
7. Weidner E, Canning EU, Rutledge CR, Meek CL. Mosquito (Diptera: Culicidae) host compatibility and vector competency for the human myositic parasite *Trachipleistophora hominis* (Phylum Microspora). J Med Entomol. 1999; 36:522–525. [PubMed: 10467783]
8. Vavra J, Kamler M, Modry D, Koudela B. Opportunistic nature of the mammalian microsporidia: experimental transmission of *Trachipleistophora extenrec* (Fungi: Microsporidia) between mammalian and insect hosts. Parasitol Res. 2010; 108:1565–1573. [PubMed: 21188601]
9. Striepen B, Pruijssers AJ, Huang J, Li C, Gubbels MJ, Umejiego NN, Hedstrom L, Kissinger JC. Gene transfer in the evolution of parasite nucleotide biosynthesis. Proc Natl Acad Sci USA. 2004; 101:3154–3159. [PubMed: 14973196]
10. Morrison HG, McArthur AG, Gillin FD, Aley SB, Adam RD, Olsen GJ, Best AA, Cande WZ, Chen F, Cipriano MJ, et al. Genomic minimalism in the early diverging intestinal parasite *Giardia lamblia*. Science. 2007; 317:1921–1926. [PubMed: 17901334]

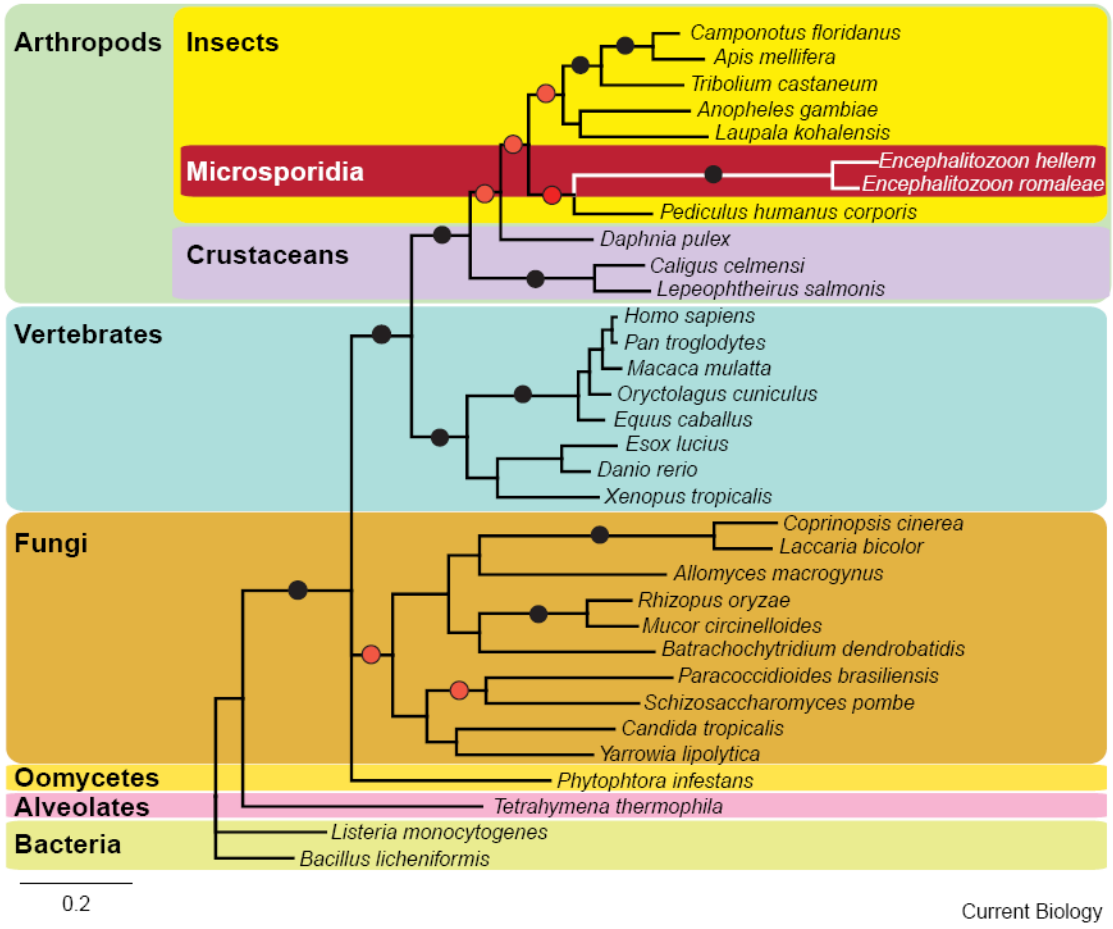

Figure 1. Phylogeny of the PNP genes

Phylogenetic relationships between the PNP genes based on 240 amino acid positions from a broad diversity of eukaryotes and prokaryotes. Major lineages are indicated by coloured boxes, while black circles indicate branches with bootstrap support of over 95% from Maximum likelihood analyses (WAG model of evolution) and over 0.95 posterior probabilities obtained using Mr Bayes (WAG model of evolution) and Phylobayes (CAT and LG models of evolution). Red circles indicate branches with posterior probabilities of 1 using Mr Bayes, but with bootstrap support and posterior probabilities sometimes below 95% and 0.95 for, either, maximum likelihood analyses, or for Bayesian analyses performed under the CAT and LG models of evolution implemented in Phylobayes. Phylogenetic relationships between the PNP genes of several eukaryotic and prokaryotic lineages based on 240 amino acid positions after removal of sequences corresponding to *Pediculus humanus* and Crustaceans (i.e. the longest branches) are shown in Figure S1.