

Co-evolution of the parasitic fungi *Pneumocystis* and their Muridae rodent hosts in Southeast Asia

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Pneumocystis species are opportunistic and airborne-transmitted fungi that infect the lungs of numerous mammalian species. These highly diversified fungi are characterized by strong host specificity, probably associated with co-speciation. In this study, we investigate the *Pneumocystis* genetic diversity and infection rate in Muridae rodents of Southeast Asia in relation to environmental habitats. A total of 445 wild rodents belonging to 18 Southeast Asian Muridae species were tested for the presence of *Pneumocystis* in their lungs through PCR amplification of two *Pneumocystis* mitochondrial genes (mtLSU rRNA and mtSSU rRNA).

Pneumocystis DNA was detected in 215 (48.3%) out of these 445 rodents. Eight highly divergent *Pneumocystis* lineages were retrieved in our phylogenetic tree. Three of these lineages correspond to the described species *Pneumocystis murina* (infecting *Mus* species), *P. carinii* (infecting *Rattus* species) and *P. wakefieldiae* (also infecting *Rattus* species). Three individuals belonging to *Rattus norvegicus* were found co-infected by both *P. carinii* and *P. wakefieldiae*. The five remaining lineages may correspond to several new undescribed *Pneumocystis* species and infect the lungs of *Cannomys* (lineage 1), *Bandicota* (lineage 2), *Berylmys* (lineage 3), *Rattus* (lineage 4) and *Maxomys*, *Niviventer* and *Leopoldamys* (lineage 5) Muridae genera. The congruence between phylogenies of *Pneumocystis* and their rodent hosts has been tested using co-phylogenetic analyses and the number of inferred co-speciation events is significantly greater than expected by chance. Rodent species, age and sex have no influence on the *Pneumocystis* infection rate among Muridae rodents but individuals trapped close to human settlements in patchy habitat were more likely infected by *Pneumocystis* parasites.