

Title: Transcriptome of *Pneumocystis carinii* and the Concept of a Compatible Parasite

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To better understand the basic biological and pathological processes of the fungal pathogen, *Pneumocystis carinii*, 4500 ESTS derived from sequencing of the poly(A) tail ends of *P. carinii* during fulminate infection were annotated and functionally characterized as unassembled reads; clustered and reduced to a unigene set with 1055 members. BLAST analysis of the unassembled reads revealed 56% had identity to existing polypeptides at $p < 10^{-6}$, with most (70%) having identity to fungal or existing *P. carinii* sequences. Gene Ontology analysis using BLAST2GO revealed *P. carinii* dedicated most of its transcripts to cellular and physiological processes (80%); to binding and catalytic activities in the molecular function categories (70%); and to cell and organellar compartments (80%). KEGG Pathway mapping showed the putative *P. carinii* genes represented most standard metabolic pathways and cellular processes, with carbohydrate metabolism garnering the most transcripts. Several gene homologs specific for a sexual mode of reproduction and sterol biosynthesis were identified. Genes encoding the major surface glycoprotein family, heat shock, and proteases were the most abundantly expressed of known *P. carinii* genes. The apparent presence of many metabolic pathways in *P. carinii*, sexual reproduction within the host, and other known characteristics suggest members of the genus *Pneumocystis* are adapted parasites and their relationship with the host may be a compatible one.

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