Functional and Expression Analyses of the Pneumocystis MAT Genes Suggest Obligate Sexuality through Primary Homothallism within Host Lungs

Richard, S.; Almeida, J. M. G. C. F.; Cissé, O. H.; Luraschi, A.; Nielsen, Olaf; Pagni, M.; Hauser, P. M.

Published in:
mbio

DOI:
10.1128/mBio.02201-17

Publication date:
2018

Document version
Publisher's PDF, also known as Version of record

Document license:
CC BY

Citation for published version (APA):
Functional and Expression Analyses of the Pneumocystis MAT Genes Suggest Obligate Sexuality through Primary Homothallism within Host Lungs

S. Richard,a J. M. G. C. F. Almeida,b O. H. Cissé,a* A. Luraschi,a O. Nielsen,c M. Pagni,d P. M. Hausera

aInstitute of Microbiology, Lausanne University Hospital, Lausanne, Switzerland
bUCIBIO-REQUIMTE, Faculdade de Ciências e Tecnologia, Universidade Nova de Lisboa, Caparica, Portugal
cDepartment of Biology, University of Copenhagen, Copenhagen, Denmark
dVital-IT Group, SIB Swiss Institute of Bioinformatics, Lausanne, Switzerland

ABSTRACT Fungi of the genus Pneumocystis are obligate parasites that colonize mammals’ lungs and are host species specific. Pneumocystis jirovecii and Pneumocystis carinii infect, respectively, humans and rats. They can turn into opportunistic pathogens in immunosuppressed hosts, causing severe pneumonia. Their cell cycle is poorly known, mainly because of the absence of an established method of culture in vitro. It is thought to include both asexual and sexual phases. Comparative genomic analysis suggested that their mode of sexual reproduction is primary homothallism involving a single mating type (MAT) locus encompassing plus and minus genes (matMc, matMi, and matPi; Almeida et al., mBio 6:e02250-14, 2015). Thus, each strain would be capable of sexual reproduction alone (self-fertility). However, this is a working hypothesis derived from computational analyses that is, in addition, based on the genome sequences of single isolates. Here, we tested this hypothesis in the wet laboratory. The function of the P. jirovecii and P. carinii matMc genes was ascertained by restoration of sporulation in the corresponding mutant of fission yeast. Using PCR, we found the same single MAT locus in all P. jirovecii isolates and showed that all three MAT genes are often concomitantly expressed during pneumonia. Extensive homology searches did not identify other types of MAT transcription factors in the genomes or cis-acting motifs flanking the MAT locus that could have been involved in MAT switching or silencing. Our observations suggest that Pneumocystis sexuality through primary homothallism is obligate within host lungs to complete the cell cycle, i.e., produce asci necessary for airborne transmission to new hosts.

IMPORTANCE Fungi of the genus Pneumocystis colonize the lungs of mammals. In immunosuppressed human hosts, Pneumocystis jirovecii may cause severe pneumonia that can be fatal. This disease is one of the most frequent life-threatening invasive fungal infections in humans. The analysis of the genome sequences of these uncultivable pathogens suggested that their sexual reproduction involves a single partner (self-fertilization). Here, we report laboratory experiments that support this hypothesis. The function of the three genes responsible for sexual differentiation was ascertained by the restoration of sexual reproduction in the corresponding mutant of another fungus. As predicted by self-fertilization, all P. jirovecii isolates harbored the same three genes that were often concomitantly expressed within human lungs during infection. Our observations suggest that the sexuality of these pathogens relies on the self-fertility of each isolate and is obligate within host lungs to complete the cell cycle and allow dissemination of the fungus to new hosts.

KEYWORDS complementation, fission yeast, RT-PCR, gene expression, heterologous gene expression
The genus *Pneumocystis* includes fungal species that colonize the lungs of mammals. Each of these species is specific for a single mammalian species. *Pneumocystis jirovecii* infects humans, whereas *Pneumocystis carinii* infects rats. In immunosuppressed individuals, *P. jirovecii* can turn into an opportunistic pathogen and cause severe pneumonia (Pneumocystis pneumonia [PCP]) that can be fatal if not treated. This disease is one of the most frequent life-threatening invasive fungal infections in humans (1). Despite numerous endeavors, culture of *Pneumocystis* species *in vitro* has remained elusive. A method of coculturing *P. jirovecii* with lung epithelial cells at the liquid-air interface was recently described (2), but it has not been established in other laboratories yet. Analysis of the *Pneumocystis* genome sequences revealed the loss of several synthesis and assimilation pathways, showing that these fungi are obligate parasites (3–6). Their requirement of thiamine and their lack of inorganic nitrogen and sulfur assimilation are hallmarks of obligate biotrophs (7), i.e., parasites that retrieve energy and compounds from host cells without killing them. Other hallmarks of obligate biotrophs present in *Pneumocystis* species include (i) the absence of massive destruction of host cells, (ii) a lack of virulence factors, (iii) having a sex life cycle within the host, and (iv) being difficult to culture *in vitro* (5, 8–10). *Pneumocystis* species were the first described obligate animal biotrophs (10).

Mainly because of the absence of an *in vitro* culture method, the cell cycle of *Pneumocystis* species is still poorly known. Since they are obligate parasites, their cell cycle takes place entirely within the host’s lungs. It would include asexual multiplication of haploid trophic cells by binary fission, as well as a sexual phase initiated by the fusion of two trophic cells of compatible mating types (11). The sexual cycle would culminate by the production of an ascus containing eight haploid daughter cells. However, quantitative experiments suggested that meiotic division might account for all of the cell multiplication that occurs during infection (12–14). These observations suggested that an asexual cycle may not occur at all or be facultative and, consequently, that sexuality is obligatory in *Pneumocystis* species. Obligate sexuality would also be consistent with the facts that (i) asci are present in the vast majority of, if not all, human infections and are used for diagnosis by staining of their wall and (ii) asci are believed to be the aerially transported particles that ensure transmission of the fungus between hosts (15, 16).

Recently, we used comparative genomics to investigate the mode of sexual reproduction of *Pneumocystis* species (17). We used sex-related genes of the Taphrinomycotina relative *Schizosaccharomyces pombe* as sequence queries to identify homologues in the *P. jirovecii* and *P. carinii* genomes. Approximately 60 of the 103 genes investigated were identified in each species, further suggesting that sexuality is part of the *Pneumocystis* cell cycle. Importantly, in each species, we identified only three candidate homologues (*matMc*, *matPi*, *matMi*) of the four MAT genes present in *S. pombe*. The latter genes encode transcription factors and cofactors and are responsible for sexual differentiation into plus (P) and minus (M) mating types, as well as for induction of meiosis (18). The organization of these genes in each *Pneumocystis* genome as a fusion of the MAT M and P loci suggested the working hypothesis that *Pneumocystis* species are primary homothallic organisms, i.e., each strain would be self-fertile and could produce asci on its own. This contrasts sharply with the closely related yeast *S. pombe*, which uses switching of mating types involving one expressed MAT locus and two silenced loci (secondary homothallism) (19).

The present work was aimed at testing the hypothesis of obligate sexuality through primary homothallism in *Pneumocystis* species. Consistent with this hypothesis, we found the same MAT locus in all of the *P. jirovecii* isolates investigated and frequent concomitant expression of the three MAT genes within human lungs during PCP. Furthermore, the function of one putative *P. jirovecii* and *P. carinii* MAT gene was ascertained by complementation in fission yeast and new *in silico* analyses of the genomes further supported primary homothallism.
RESULTS

The *P. jirovecii* and *P. carinii* matMc genes functionally complement an *S. pombe* matMc null strain. The function of the *Pneumocystis* MAT genes remained putative, and in the absence of an in vitro culture method, the issue was investigated by functional complementation of *S. pombe* because it is closely related to *Pneumocystis* species and offers numerous genetic tools. The *P. jirovecii* and *P. carinii* matMc, matMi, and matPi genes were expressed separately on plasmids in the corresponding *S. pombe* mutants. The *S. pombe* matMc mutant is null because of an opal codon at the beginning of the open reading frame (ORF), whereas the matMi and matPi mutants have nonfunctional alleles because of mutations (see Materials and Methods). The empty plasmid and a recombinant plasmid expressing the corresponding wild-type *S. pombe* MAT gene were used as controls. A tester strain of the opposite mating type was crossed with each recombinant strain. Consistently in all experiments, the negative-control crosses with the tester strain of the same mating type or with the strain harboring the empty plasmid did not complement the mutant, as revealed by iodine staining and microscopic observation (e.g., matMc in Fig. 1). On the other hand, the positive-control crosses with the tester strain or the strain expressing the wild-type *S. pombe* matMc gene on a plasmid did complement. These experiments revealed that the *P. jirovecii* and *P. carinii* matMc genes rescued the function of the *S. pombe* transcription factor matMc null mutant, ascertaining the

![FIG 1](http://mbio.asm.org/) Complementation of the *S. pombe* matMc mutant by expression of the *P. jirovecii* (*Pj*), *P. carinii* (*Pc*), or control *S. pombe* (*Sp*) matMc gene on a plasmid. Tester strain *P* was crossed with various strains by using a plasmid expressing or not expressing a heterologous gene by mixing them in liquid, spotting an aliquot on the mating plate, and incubating it to allow sporulation. Complementation was assessed after 6 days of incubation at 30°C by iodine staining of spore wall starch, as well as by the presence of zygotes containing four spores (asci) upon microscopic observation. Triplicate recombinant strain isolates gave similar results.
function of these genes. This conclusion strongly suggested that the Pneumocystis matPi and matMi genes are also MAT genes because of their significant similarity and synteny to the S. pombe MAT genes (17).

The same single MAT locus is present in all P. jirovecii isolates. The three P. jirovecii MAT genes were clustered in a region spanning about 10 kb on a single contig of the genome sequence. Primary homothallism implies that all isolates harbor the same MAT locus. To investigate the issue, we used long-range PCR with primers located at the ends of the MAT locus, as well as PCRs with internal primers generating three overlapping products covering the whole locus (Fig. 2). Six of the 11 PCP patients analyzed were positive by long-range PCR, and 3 were positive by the three overlapping PCRs (Fig. 3; Table 2). The five patients negative by long-range PCR presented a lighter fungal load than the other patients, as revealed by real-time PCR targeting the mitochondrial 26S rDNA (mt26S). Long-range PCR is notoriously demanding, so that it was not surprising that it required a substantial fungal load to be positive. These observations demonstrated that the same fused MAT locus is present in all P. jirovecii isolates, which is consistent with primary homothallism as a mode of sexual reproduction.

The P. jirovecii MAT genes are often expressed concomitantly during infection within human lungs. The Pneumocystis MAT loci do not present sequence motifs involved in silencing, such as the repeats resembling those of centromeres observed in S. pombe (cenH) or the actual telomere in close proximity as in Saccharomyces cerevisiae (17, 20). Consequently, expression of all three P. jirovecii MAT genes was expected to occur during PCP to ensure mating and maturation of the ascis because the latter are most often, if not always, present. To investigate this issue, we used reverse transcriptase PCR (RT-PCR) analysis of total RNAs extracted from bronchoalveolar lavage (BAL) fluid samples from the 11 patients with PCP that we also investigated for the presence of the MAT locus (as described in the previous section). Proper RT-PCR from the BAL fluid specimens was assessed by (i) a negative PCR result with RNAs not reverse transcribed and (ii), given that the Pneumocystis MAT genes do not include introns, absence of the intron from the PCR product of the unrelated gene for β-tubulin (β-tub;

![FIG 2](image-url) Structure of the single MAT locus of P. jirovecii corresponding to a fusion of loci P and M. The approximate locations of the primers used to confirm the presence of the locus in several isolates are shown. As in S. pombe, the gene encoding the huntingtin-interacting protein (end4) located between the MAT genes might be essential under most conditions, whereas the gene encoding a heat shock protein (hsp104) is probably not. The synteny of these genes, as well those flanking the MAT locus, is fully conserved in P. carinii and P. murina (17).

<table>
<thead>
<tr>
<th>Tester strain P crossed with*</th>
<th>Expt</th>
<th>Cells</th>
<th>% of zygotes with 4 spores</th>
<th>% SD between crosses</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tester strain M</td>
<td>3</td>
<td>1,088</td>
<td>3.7</td>
<td>0.9</td>
</tr>
<tr>
<td>matMc mutant + pREP1</td>
<td>3</td>
<td>1,592</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>matMc mutant + pREP1 + S. pombe matMc</td>
<td>3</td>
<td>971</td>
<td>2.8</td>
<td>0.2</td>
</tr>
<tr>
<td>matMc mutant + pREP1 + P. jirovecii matMc</td>
<td>3</td>
<td>921</td>
<td>1.3</td>
<td>0.4</td>
</tr>
<tr>
<td>matMc mutant + pREP1 + P. carinii matMc</td>
<td>3</td>
<td>1,847</td>
<td>0.9</td>
<td>0.2</td>
</tr>
</tbody>
</table>

TABLE 1 Proportions of zygotes with four spores in matMc complementation assay crosses

Richard et al. January/February 2018 Volume 9 Issue 1 e02201-17 mbio.asm.org

Downloaded from http://mbio.asm.org on July 17, 2018 at DANISH CONSORTIA
Fig. 4). Of 11 patients, 5 were positive for all three MAT genes, 3 were positive only for one MAT gene, and 3 were negative for all MAT genes (Table 2). The latter patients were also negative for β-tub, suggesting that RNA degradation could have occurred during the uncontrolled period between the collection of a sample and its arrival at our laboratory. The three patients positive for only one MAT gene may reflect low expression of MAT genes. This might be due to the collection of BAL fluid at a late stage of infection, i.e., after the peak of MAT gene expression. Consistent with their expression, two or three potential TATA boxes matching that of 7 bp described by Bucher (21) were identified between 6 and 108 bp upstream of the start codons of the ORFs of all the P. jirovecii and P. carinii MAT genes (see Fig. S1 in the supplemental material). These observations suggested that concomitant expression of the three MAT genes occurs in human lungs at some stage of PCP and leads to ascus production. This is consistent with primary homothallism as the mode of reproduction and suggests that sexuality is obligatory during the infection of host lungs.

**Absence of MATα1 and amphipathic alpha-helix MAT transcription factors in Pneumocystis genomes.** *S. pombe* harbors MAT transcription factors with homeobox or high-motility-group (HMG) DNA binding domains. Consequently, our searches using *S. pombe* MAT genes as sequence queries (17) could not identify MAT transcription factors with MATα1 or amphipathic alpha-helix domains that are present in ascomycetous subphyla other than Taphrinomycotina, such as Saccharomycotina and Pezizomycotina (19). Extensive homology searches using tBLASTn involving bait sequences

### TABLE 2  
Amplification of the *P. jirovecii* MAT locus and MAT transcripts from BAL fluid samples from 11 patients with pneumonia

<table>
<thead>
<tr>
<th>Patient</th>
<th>mt26S (no. of copies/ml [10⁶])</th>
<th>MAT locus</th>
<th>RT-PCR</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>matMc</td>
<td>matMi</td>
</tr>
<tr>
<td>1</td>
<td>+ (1,111)</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>2</td>
<td>+ (233)</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>3</td>
<td>+ (89)</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>4</td>
<td>+ (23)</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>5</td>
<td>+ (18)</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>6</td>
<td>+ (3)</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>7</td>
<td>+ (0.7)</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>8</td>
<td>+ (0.25)</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>9</td>
<td>+ (0.15)</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>10</td>
<td>+ (0.03)</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>11</td>
<td>+ (0.01)</td>
<td>–</td>
<td>+</td>
</tr>
</tbody>
</table>

*+, positive PCR result; −, negative PCR result. The RT-PCR used to amplify the three MAT genes included a seminested procedure. The PCR used to amplify the mt26S gene included a real-time procedure (see Materials and Methods).  

Three overlapping PCRs were used (see text).
recruited through InterPro references did not detect any such transcription factors in the \textit{P. jirovecii} and \textit{P. carinii} genomes or in that of \textit{Pneumocystis murina}, the species that infects mice. This observation further suggested that, consistent with primary homothallism, the \textit{MAT} locus we identified is the only one present in \textit{Pneumocystis} genomes.

Absence of \textit{cis}-acting sequences flanking the \textit{MAT} locus in \textit{Pneumocystis} genomes. \textit{S. pombe} harbors \textit{cis}-acting sequences of 57 to 135 bp flanking each of its three \textit{MAT} loci that are involved in switching of the locus expressed by homology recombination, as well as in the silencing of two \textit{MAT} loci (20). \textit{cis}-acting sequences flanking \textit{MAT} loci are also present in other secondary heterothallic fungi (22), as well as in the recently described secondary homothallism based on inversion of the loci (23). We extensively compared the regions flanking the \textit{Pneumocystis} \textit{MAT} genes to each other with the help of local and global alignment tools (24), as well as that of Dotlet for visual appraisal of the distribution of local similarity (25). No such \textit{cis}-acting sequences were identified within the three \textit{Pneumocystis} genomes. This observation further suggested that the mode of reproduction of \textit{Pneumocystis} species is primary homothallism and not secondary homothallism.

**DISCUSSION**

Sexuality is believed to play a crucial role in the life cycle of a number of human microbial pathogens, e.g., \textit{Plasmodium}, \textit{Cryptococcus}, and \textit{Candida} species, for generating genetic diversity and maintaining virulence (26–29). In the present study, we studied this process in the fungal obligate parasites of the genus \textit{Pneumocystis}. We performed functional, structural, expression, and \textit{in silico} genomic analyses that support the hypothesis that primary homothallism is their mode of sexual reproduction. Our observations also suggest that sexuality is obligatory within host lungs during infection to complete the cell cycle, i.e., to produce asci, which are necessary to allow dissemination of the fungus to new hosts by the air route.

**Primary homothallism of \textit{Pneumocystis} species.** Three of our observations are strongly suggestive of primary homothallism in \textit{Pneumocystis} species, (i) the presence of the same \textit{MAT} locus in all \textit{P. jirovecii} isolates investigated, (ii) the lack of other \textit{MAT} transcription factors in the genomes and of any sequences used for switching or silencing, and (iii) the frequent concomitant expression of the three \textit{MAT} genes during PCP. Primary homothallism is thought to be advantageous for human microbial pathogens such as \textit{Candida}, \textit{Cryptococcus}, and \textit{Aspergillus} species (27–29). It would alleviate the need to find a compatible partner, and although it involves a single strain, it would avoid accumulating deleterious mutations, as well as increase genetic diversity and
virulence (30). However, the exact mechanisms involved in Pneumocystis primary homothallism remain to be understood. The absence of the matPc transcription factor suggests that only M cells could be present in Pneumocystis populations. However, the genes coding for the receptors of both M and P factors are present in Pneumocystis genomes (map3, mam2) (17), suggesting that cells of both mating types are produced. The two transcription factors present in the MAT locus (matPi and matMc) are probably sufficient to trigger mating. Thus, the MAT pathways may be wired differently from those of S. pombe since matPi induces meiosis in the latter fungus but not mating (18). A caveat to the hypothesis of primary homothallism is that most, if not all, P. jirovecii infections are polyclonal, i.e., due to several strains (31), including all of those we analyzed in the present study (not shown; determined as described in reference 32). Accordingly, an alternative hypothesis is that each strain produces only, or mostly, M or P cells. This could occur by the expression at a higher level or exclusively one of the two transcription factors mentioned above through transcription regulation or by an unknown mechanism. Such a strategy might further increase genetic diversity by inducing outbreeding and would constitute a previously undescribed mode of secondary homothallism. Analyses at the gene expression level are required to characterize Pneumocystis sexuality further.

**Obligate sexuality of Pneumocystis species during infection.** Obligate sexuality is strongly suggested by our findings that (i) all three MAT genes are often concomitantly expressed during human infections and (ii) the MAT locus does not include any silencing sequence motifs. Obligate sexuality would be compatible with the hypothesis that the asci are the transmission particles (15, 16). The production of asci would allow dissemination to new hosts and thus survival of the fungus, which renders it obligate. The necessity of sexuality might also ensure antigenic variation through the frequent recombination events that occur between the genes encoding surface antigens localized within the subtelomeres (32). Indeed, the bouquet of telomeres formed during meiosis is believed to favor ectopic recombinations at subtelomeres (33, 34). Interestingly, dissemination by asci may also ensure the polyclonality of the infections, i.e., their descent from several cells, which might be of importance. If sexuality is indeed obligate, then it is likely that it also occurs in colonized hosts without overt disease because colonized humans are thought to constitute a source of the infection (35, 36). Obligate sexuality does not imply that asexual reproduction of the trophic forms does not occur. Indeed, multiplication of the trophic forms could be facultative, depending on the conditions encountered. Treatment with echinocandins eliminates asci but not the trophic forms from infected rodents, suggesting that asexual multiplication of the trophic forms may persist under these conditions (15). Antipneumocystis prophylaxis has been shown to reduce the proportion of asci within the population (37). Two other cases harboring few asci were reported (38), but it remained unclear if they were due to prophylaxis or an unknown factor. It is also possible that asexual reproduction is preponderant in early stages of infection, when growth is relatively fast, until the niche is filled with Pneumocystis cells. When nutriments become limited, asexual reproduction might be followed by mating and sporulation.

**Conclusions.** Our observations suggest that the sexuality of Pneumocystis species occurs by primary homothallism (self-fertility of each strain) and that it is obligatory within the host’s lungs during infection. Obligate sexuality may allow completion of the cell cycle, i.e., production of asci that would be the airborne particles that allow transmission of the fungus to new hosts, and thus its survival. Further work is needed to understand the mechanisms of this reproduction, as well as the relative importance of the sexual and asexual phases.

**MATERIALS AND METHODS**

**Strains and growth conditions.** Eg2772 is a haploid S. pombe strain with a null mutation due to an opal codon at the seventh position of the ORF of the gene encoding the matMc HMG transcription factor (h- mat1-Mc-H1:ura4-leu1 ura4-D18 ade6-M210). It is an unpublished derivative of strain Eg575 (20). Eg903 is a haploid S. pombe strain with a nonfunctional mutated allele of the matPi homebox transcription factor (h90 mat2-Pm-B102 ura4-D18 leu1-32) (39). Eg904 is a haploid S. pombe strain with a
In the present study, these strains are named the pantothenate at 81 mM, nicotinic acid at 81 mM, inositol at 4.2 mM, and biotin at 41 mM, respectively (plasmids pSK138 [41], pUS130, and pON656 [42]). Each recombinant plasmid was then introduced into the corresponding S. pombe tester strains, respectively, LFWA01000009.1:221185.221394 (no locus defined), and LFWA01000009.1:211902.211243 (locus T551_02162). Those of the P. carinii matMc, matMi, and matPi gene sequences are, respectively, LFVZ01000001.1:819058.80260 (locus T552_02831), LFVZ01000001.1:81265.81480 (no locus defined), and LFVZ01000001.1:72050.71358 (locus T552_02829). The ORFs of all of these MAT genes harbor no introns and were thus directly amplified by PCR from the genomic DNA extracted from a BAL fluid specimen obtained from an HIV-positive patient with PCP (see PCR amplification section) or from P. carinii genomic DNA (pat 876/4-1997, kindly provided by the late A. E. Wakefield, University of Oxford). Each PCR product was cloned into the vector pREPl (40) downstream of a promoter, ensuring strong constitutive expression of the heterologous gene in S. pombe. Transformation of the heterologous constructs into S. pombe was performed with the two primers used for amplification, as well as the BigDye Terminator DNA sequencing kit and an ABI PRISM 3100 automated sequencer (both from PerkinElmer Biosystems).

The real-time PCR specific for P. jirovecii amplifies a 77 bp fragment of the mitochondrial 26S rDNA (mt265), a gene present in multiple copies per cell. Total DNA was extracted from 200 μl of thalidomide BAL fluid and finally eluted in 100 μl with the MagNA Pure LC robot and DNA isolation kit I (both from Roche). A Pipetting Tecan EVO 150 robot (eight channels) was used to prepare a reaction mixture containing ABI TaqMan universal PCR master mix, forward primer TGGAAAACTTCAAGAATTGGTGTA, reverse primer TTGGCAGAAAACCAGCTATCTCC, and minor groove binding probe 6-carboxyfluorescein–CCGATTGTGTA TTTCCACAT–Black Hole Quencher 1. Each PCR included a 15 μl reaction mixture and 5 μl of extracted DNA. Real-time PCR was performed with TaqMan 7900 (Applied Biosystems). After 2 min at 50°C and 10 min at 95°C, 45 cycles of 15 s at 95°C and 1 min at 60°C were performed. The specificity of the PCR was assessed by the absence of amplification with genomic DNA of microorganisms commonly found in BAL fluids. Its sensitivity was determined by amplification of successive dilutions of a control plasmid, which was dosed with a known value to the target concentration was obtained by using a calibration curve obtained by amplification of successive dilutions of the control plasmid, which was dosed with a NanoDrop ND-1000 spectrophotometer. Absence of inhibition was tested for by using a reaction mixture containing both the test DNA and 1,000 copies of the control plasmid. Each sample was analyzed in duplicate.

RT-PCR amplification. RT-PCRs were performed with cDNAs synthesized from total RNAs that were extracted with the RiboPure yeast kit (Ambion) from 1 ml of BAL fluid from a patient with PCP. The BAL fluids were previously preserved at −80°C in RNA later (Ambion) immediately upon receipt. cDNAs were synthesized from 8 μl of an RNA preparation with the Qiagen REPLi-g WTA Single Cell kit involving random amplification. cDNA was then purified by LiCl-ethanol precipitation (Qiagen supplementary protocol) in the presence of 5 μl of glycogen (stock 20 mg/ml; Thermo Scientific). Random amplification
of cDNA included in the kit proved to be necessary for detection of the low-abundance P. jirovecii cDNAs among the human ones. The PCR procedure was as described above, and the primers and parameters specific to each PCR are shown in Table S1. A seminested procedure was used to amplify the MAT genes in a second round with 2 μl (0.5 μl for the positive control) of the first-round reaction product as the template.

**Bioinformatic analyses.** Potential genes encoding MATα1 or amphiathic alpha-helix transcription factors were searched for in the P. jirovecii, P. carinii, and P. murina genomes (respective accession numbers LFWA01000000, LFVZ00000000, and AFWA00000000) by matching these genomes against large pools of representative bait sequences by using BLASTN (NCBI BLAST suite, 64-bit version). These pools of bait sequences were recruited through the InterPro annotations (IPR006856 (mating type protein MAT alpha 1, HMG-box) and IPR031472 (MAT1-1-2/MatA-2/Smr1 family). To avoid missing candidates because of the use of too stringent conditions, the BLASTN searches were conducted with relaxed parameters (E value > 10^-4 down to the default E value). Each match with a suitable E value (<=1) was investigated by looking for preexisting annotations. If no coding sequence (CDS) annotations were available, the matched region was assessed for putative novel CDSs and their translated sequence were submitted to the InterProScan4 tool to detect the required reference signature matches.

### SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at https://doi.org/10.1128/mBio.02201-17.

**FIG S1,** PDF file, 0.04 MB.

**TABLE S1,** PDF file, 0.03 MB.

### ACKNOWLEDGMENTS

O.H.C. was supported by Swiss National Science Foundation fellowship grant 151780. This work was supported by Swiss National Science Foundation grant 310030_146135 to P.M.H. and M.P. The Swiss National Science Foundation had no role in any steps of this study.

### REFERENCES


