Mating Type Protein Mat1-2 from Asexual *Aspergillus fumigatus* Drives Sexual Reproduction in Fertile *Aspergillus nidulans*†

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The lack of an experimentally amenable sexual genetic system in *Aspergillus fumigatus* is a major limitation in the study of the organism’s pathogenesis. A recent comparative genome analysis revealed evidence for potential sexuality in *A. fumigatus*. Homologs of mating type genes as well as other genes of the “sexual machinery” have been identified in anamorphic *A. fumigatus*. The mat1-2 gene encodes a homolog of MatA, an HMG box mating transcriptional factor (*MatHMG*), that regulates sexual development in fertile *Aspergillus nidulans*. In this study, the functionalities of *A. fumigatus* mat1-2 and the Mat1-2 protein were determined by interspecies gene exchange between sterile *A. fumigatus* and fertile *A. nidulans*. Ectopically integrated *A. fumigatus mat1-2* (driven by its own promoter) was not functional in a sterile *A. nidulans ΔmatA* strain, and no sexual development was observed. In contrast, the *A. fumigatus mat1-2* open reading frame driven by the *A. nidulans matA* promoter and integrated by homologous gene replacement at the *matA* locus was functional and conferred full fertility. This is the first report showing that cross species mating type gene exchange between closely related *Ascomycetes* did not function in sexual development. This is also the first report demonstrating that a *MatHMG* protein from an asexual species is fully functional, with viable ascospore differentiation, in a fertile homothallic species. The expression of mat1-2 was assessed in *A. fumigatus* and *A. nidulans*. Our data suggest that mat1-2 may not be properly regulated to allow sexuality in *A. fumigatus*. This study provides new insights about *A. fumigatus* asexuality and also suggests the possibility for the development of an experimentally amenable sexual cycle.

Mating type genes (mat loci) have been characterized in a number of homothallic, heterothallic, and asexual filamentous *Ascomycetes*. In fertile fungi, the mat locus functions as a master regulatory locus controlling sexual reproduction (8–10, 21). *Aspergillus* (*Emericella*) *nidulans* is a homothallic, self-fertile ascomycete. It has both sexual and asexual reproductive strategies and provides a robust genetic system for the study of euukaryotic development and cell biology (6, 35). Sexual reproduction in *A. nidulans* is a complex multistep process that involves coordinated differentiation of three tissue types: Hülle cells, ascogenous hyphae, and cleistothecium wall. Hülle cells function as nurse cells for fruiting body development in *A. nidulans*, which forms mature cleistothecia that are hard and highly pigmented (6). However, Hülle cells are not required for sexual reproduction per se and, Hülle cell production varies among *A. nidulans* strains. Other fertile *Aspergillus* species lack Hülle cells and produce cleistothecia that are soft and lightly pigmented (6). Sexual conjugation is believed to occur within the foci of Hülle cells, where mating and fertilization between cells that are equivalents of male and female gametangia take place. Upon fertilization, parental nuclei divide synchronously and ascogenous hyphae proliferate within the female organ. Pairs of nuclei are ultimately segregated into dikaryotic cells where karyogamy, meiosis, and two additional mitoses lead to the formation of asci filled with eight binucleate ascospores.

Vegetative hyphae of female origin grow in a circular fashion surrounding the fertile ascogenous tissue and eventually form the hard cleistothecial wall (3, 4, 6, 48). As in other fertile *Ascomycetes*, the mating type regulatory genes *matA* (HMG box) and *matB* (alpha box) are required for mating and completion of sexual development, with *matA* being required to initiate fruiting body development (*matA*, accession number AF328028 and locus identification number [ID] AN4734; *matB*, accession number AY399600 and locus ID AN2755) (B. L. Miller and K. Y. Miller, unpublished data).

*Aspergillus fumigatus* is an opportunistic human pathogen and major cause of life-threatening invasive aspergillosis in immunodeficient individuals, with an overall mortality rate of about 50%. The species has been classified among the “imperfect fungi” (17). No sexual cycle has been observed to date. The lack of a sexual cycle significantly limits the application of genetic analyses to the study of mechanisms involved in pathogenesis. However, a high degree of genetic diversity among clinical and environmental isolates suggests existing latent, recently lost, or rare sexual activity within populations of *A. fumigatus*. (11, 13, 15, 32, 36, 37). Comparative genome analysis provides further evidence for sexual ability in *A. fumigatus*. The homologs of mating type genes (*mat1-1* and *mat1-2*), as well as all key components of the core meiotic program, pheromone signaling, and genes involved in fruiting body development have been identified in *A. fumigatus* (12, 45). Two supplementary *A. fumigatus* mating types with heterothallic structures at the mat locus are equally distributed in nature (13). The expression of putative mating type genes and other sex-related genes have been detected at low abundance during mycelial growth (29). However, neither pheromone nor pher-
omone receptor genes are expressed in a mating type-specific pattern. It is possible that the lack of *A. fumigatus* sexuality could be a result of a mutation in one of the key genes of the “sexual machinery” that blocks sexual development. A study of the mating type genes in sterile *A. fumigatus* is essential for understanding the basis for asexual and may provide important insights for potential reconstruction or induction of a viable sexual cycle. The availability of an experimentally amenable sexual state in *A. nidulans* will have a major impact upon the study of the pathogenesis and biology of this species.

The *A. fumigatus* *mat1*-2 gene encodes a homolog of the *A. nidulans* MatA, an HMG box mating type transcriptional factor (MatHMG) that is a key regulator of sexual development in fertile *A. nidulans* (B. L. Miller and K. Y. Miller, unpublished data). This mating type-specific, high-mobility-group, DNA-binding domain is highly conserved among the Ascomycetes. The main goal of this study was to use the *A. nidulans* genetic system to address the hypothesis that the *A. fumigatus* *mat1*-2 gene and encoded Mat1-2 protein carry functional mating type information and can regulate sexual development in *A. nidulans*. Our data demonstrate that the *A. fumigatus* *mat1*-2 gene is not properly expressed or developmentally regulated and, consequently, cannot support the sexual cycle in an *A. nidulans* *ΔmatA* mutant. By contrast, *A. fumigatus* Mat1-2 protein expressed under control of the *A. nidulans* matA promoter is functional and can drive sexual reproduction in *A. nidulans*. Although *mat1*-2 may not be properly expressed in *A. fumigatus*, our results provide evidence for the potential ability of *A. fumigatus* to undergo sexual reproduction and the possibility of constructing compatible mating partners by manipulation of *mat loci.

### MATERIALS AND METHODS

Strains, growth conditions, and genetic manipulations of *A. nidulans*. *A. nidulans* strains used in this study are listed in Table 1. Appropriately supplemented media were prepared as described previously by Pontecorvo et al. (35), Kafer (19), and Vallim et al. (43). Standard *A. nidulans* culture conditions and genetic techniques were used as described previously by Pontecorvo et al. (35). DNA and RNA isolation, standard molecular manipulations, and Southern blot analysis were performed as described previously by Miller et al. (26, 27, 43). DNA-mediated transformation of *A. nidulans* was performed according to the protocols of Miller et al. (27) and Yelton et al. (50).

### Table 1. Aspergillus strains used in this study

| Strain | Genotype | Source |
|--------|----------|--------|
| FGSCA26 | biA1 | Fungal Genetics Stock Center |
| FGSCA237 | pabaA2 yA2; trpC801 | Fungal Genetics Stock Center |
| UI401 | pyrG89 yA2 biA1; argB2 | B. L. Miller and K. Y. Miller |
| UI404 | pyrG89 yA2 biA1; argB2 | B. L. Miller and K. Y. Miller |
| UI414 | pyrG89pWP1-pyrG biA1 pabaA1; ΔmatA:argB | This study |
| UI412 | biA1 pabaA1; matA:Af1mat1-2 ORF | This study |
| UI421 | yA2 biA1 pabaA1; ΔmatA:Af1mat1-2 ORF | This study |
| UI422 | yA2 biA1 pabaA1; matA:Af1mat1-2 ORF | This study |
| UI423 | biA1 pabaA1; matA:Af1mat1-2 ORF | This study |
| UI435 | pyrG1 | G. S. May (MD Anderson) |

### Table 2. Primers used in this study

| Primer | Sequence |
|--------|----------|
| AnMatAR1 | TGC CGT ATG CTA CCT GAG |
| AnMatAF11 | TGG GAG TGT ATC AGC TTC ATG |
| AnpyrG1 | GAA TTC GAT ACC TGT GGA AAG |
| AnpyrG2 | TGA TCA GTG CTT GTC TAC CAG |
| AnmatAF33 | CGG ACA GCA TCA CGG AGC TCC |
| AnmatAR29 | GGT GTG CGC AGA ACA CGG AGA |
| AnbenA2 | GAT GTT CGA CCC CAA GAA CA |
| AnbenAR2 | CTT GAA GAG CTC CTG GAT GG |
| AfmatA(AGT) | ATG GCT GCA ATC GCA ATC GCC |
| AfmatA(TAG) | CTA GAA GCA ATC AGA GAT AAA ATC |
| Afmat1-2F4 | ATG TGA CCG ACA TSG TCG GCC AGG |
| Afmat1AF6 | GCA AGC CTG ACA GAG CAC |
| Afmat1-2R5 | TGT CTT GAC TTC ACC GTG |
| AfmatAR4 | CTT TCT ACC TAC GTC GGG ACC CTG |
| AfbenAF1 | GGC CTC AAA ATG TCC CTG ACC |
| AfbenAR1 | CTC GGC GTA CTC CTG CT |

**Database analyses of the *A. fumigatus* genome.** The matA locus encoding the HMG box domain mating type protein has been analyzed in *A. nidulans* (B. L. Miller and K. Y. Miller, unpublished data). To identify the homolog of the *A. nidulans* matA gene in *A. fumigatus* genome, the translated open reading frame (ORF) of the *A. nidulans* matA gene (location ID AN47343; accession number NY23288) was used in a BLASTP search of the TIGR *A. fumigatus* database (www.tigr.org) and in comparative analysis of three aspergilli genomes (12). *A. nidulans* genome sequences are available from the Broad Institute (www.broad.mit.edu/annotation/genome/aspergillus_nidulans/home.html). The locus ID for *A. fumigatus* mat1-2 is Afu3gb06710.

**Plasmid construction.** Plasmid pWP1 was constructed using the pCR8-TOPO vector, TOPO TA cloning kit for entry into the Gateway technology and AccuPrime Pfu polymerase (Invitrogen) (41). Genomic DNA from the *A. fumigatus* strain AF293.139 was extracted according to standard protocol (50). The *A. fumigatus* mat1-2 gene (Afu3gb06710), including the ORF, the 1.2-kb upstream flank, and the 1.7-kb downstream flank, was amplified from the genomic DNA with primers AfmatAF6 and AfmatAR4 (Table 2). The resulting plasmid was subsequently subjected to a recombination reaction with pAN7, a destination plasmid containing the Gateway RIC reading frame cassette and the *A. nidulans* pyrG selectable marker cloned into pDK101 (20). The final vector created upon recombination contained both the *A. fumigatus* mat1-2 gene and the *A. nidulans* pyrG marker. The mat1-2 gene was sequenced to confirm the correct sequence and to determine its orientation in pWP1.

The destination vector pAnmA An/Af ORF swap containing the *A. fumigatus* mat1-2 ORF under the *A. nidulans* matA promoter and terminator was created by using the pCR4-TOPO and pCR8-TOPO vectors, the TOPO TA cloning kit for entry into the Gateway technology (Invitrogen), and Phusion high-fidelity PCR master mix (New England Biolabs). Genomic sequences containing the *A. nidulans* matA ORF flanked by 1-kb upstream and 1.8-kb downstream regulatory regions were amplified from FGSCA26 (wild-type [WT]) genomic DNA with primers AnmatAF11 and AnmatAR1 (Table 2). The PCR product was cloned into the pCR4-TOPO vector (41). Subsequently, 990 bp of the 1,054-bp coding region was removed by CiaI and Apal digestion. Blunt ends were generated with Klenow fragment, and the vector was ligated with the Gateway RIA reading frame cassette. The *A. fumigatus* mat1-2 coding region beginning with ATG and ending with TAG was amplified from the genomic DNA of AF293.139 strain with primers AfmatA (ATG) and AfmatA (TAG) and cloned into pCR8 vector. Both pCR8 and pCR4 constructs were subjected to recombination reaction, resulting in the formation of a destination vector that contained the *A. fumigatus* mat1-2 ORF incorporated at the CiaI/Apal site and flanked by *A. nidulans* 1-kb promoter and 1.8-kb terminator sequences. The region of transgene between priming sites of AnmatAF11 and AnmatAR1 was sequenced to confirm in-frame cloning and correct sequence. Both plasmids, pWP1 and pAnmA An/Af ORF swap, were propagated using TOP10 Escherichia coli strain (Invitrogen). Standard methods for the manipulation of E. coli cells and DNA were performed as described previously (38).
with NotI and SpeI restriction enzymes to promote gene replacement at the ORF construct. A linear fragment with the transgene was generated by digestion in sexual development. The UI404 strain was transformed with the pmatA An/Af A. nidulans pyrG locus were isolated based on argB FGSCA237 to obtain homokaryotic single-spore isolates of primary transformants and Southern blot analysis was performed to discriminate single-copy gene replacement from multiple tandem or ectopic integrations. The presence of a single copy of the A. fumigatus mat1-2 ORF at the A. nidulans matA locus was confirmed by two different digests using Sall and ApLI restriction enzymes (Fig. 3). Three progeny were isolated and designated UI421, UI422, and UI423.

Induction of sexual development and fruiting body analysis. A total of 10^4 conidia per plate were spread onto 1.2% agar plates containing rich medium (YGMTV [yeast extract, glucose, MgSO_4, trace elements, and vitamins]). Cultures were grown at 37°C, and plates were sealed 24 h after inoculation to promote sexual development. Cleistothecial tissue and Hülle cells were subjected to microscopy observations from 4 to 24 days (43). The efficiency of fruiting body formation was calculated based on the percentage of proteolysinithia that developed into mature cleistothecia. Proteolysinithia in *Aspergillus nidulans* are defined as female coiled hyphal elements found within clusters of Hülle cells. Successful mating and fertilization lead to cleistothecium development. Three plates of each strain with developmental cultures were examined under a dissecting scope, and the average number of proteolysinithia and number of cleistothecia/cm^2 were determined. Ten individual cleistothecia of the WT and each of the ORF swap strains were collected for size measurements. The diameter of each fruiting body was measured using a standardized microscope ruler. The production and viability of ascospores were assessed by counting 20 individual cleistothecia on 3% agar plates and crushing them in 1.5-mL Eppendorf tubes containing 0.1% Tween 80. Aliquots of ascospores were loaded onto a hemacytometer chamber, and the total number of ascospores per cleistothecium was obtained. The ascospore viability was determined as the percentage of ascospores that germinated on solid minimal medium out of the total number of spores that were plated.

Light microscopy. Photomicrographs of developmental cultures on petri dishes were taken by using a Nikon Coolpix 5400 camera and a Zeiss SV8 stereomicroscope. Fruiting bodies were suspended in 15 μL of sterile water on a glass slide and crushed under a coverslip. Fruiting body tissue was examined by differential interference contrast optics using a Zeiss Axioskop. Photographs were taken with either a Nikon Coolpix 5400 or a Photometrics CoolSnap ES camera and MetaVue software (Universal Imaging Corp.).

Comparative quantitative PCR (QTPCR) analysis. Developmental tissues of FGSCA26 (WT), UI422, UI412, UI414, and AI293.139 were collected 6 days postinduction. Strains FGSCA26 and UI412 were analyzed for the expression of mat4 at resident and ectopic loci. Strains UI422 and UI414 were analyzed for A. fumigatus mat1-2 expression in A. nidulans, at either resident or ectopic locus. Additionally, the natural expression of mat1-2 in AI293.139 was assessed. Total RNA was extracted, treated with Turbo DNase (Ambion), and reverse transcribed from oligo(dT) primers by using SuperScript First-Strand synthesis system for reverse transcription-PCR (RT-PCR) (Invitrogen). Transcript levels were quantitated using either the threshold cycle (ΔΔCT) method or a relative standard curve. SYBR green sequence detection was performed using the StepOne real-time PCR system (Applied Biosystems). To monitor the expression of mat4 in the reference sample FGSCA26 (mat4 at its resident locus) and in UI412 (mat4 at ectopic loci), the primers AnmatAR29 and AnmatAF33 and AnmatAR29 were used (Table 2). To detect A. fumigatus mat1-2 expression in A. nidulans and A. fumigatus, the primers AmtAf2-4F and AmtAf2-25R were used. β-tubulin (bent4) was used as the endogenous control to normalize expression of the mat gene in both A. nidulans and A. fumigatus. AmtenAF2 and AmtenAR2 primers were used to amplify bent4 in all A. nidulans strains. AmtenF1 and AmtenAR1 primers were used to amplify the A. fumigatus bent6 homolog. Validation experiments of target and control genes for the comparative ΔΔCT method were performed according to the instructions of Applied Biosystems (1). SYBR green exhibits some sequence-specific DNA binding with higher preference for AT-rich sequences (52). To avoid fluorescence differences resulting from different DNA sequences between mat4 and mat1-2, we analyzed both genes separately. For a valid ΔΔCT method calculation, the efficiency of the target amplification and the efficiency of reference amplification must be approximately equal. The direct comparison of A. fumigatus mat1-2 expressions in A. fumigatus and A. nidulans was possible and valid since amplification efficiencies of endogenous control genes, A. nidulans bent4 and A. fumigatus bent4, were nearly equal. Relative quantitation, by the ΔΔCT method, is expressed as a difference in target gene expression with respect to an endogenous control in different samples. Each cDNA sample was assayed in triplicate, and RINs were obtained from three separate biological samples.

**RESULTS**

The *A. fumigatus* mat1-2 gene cannot complement an *A. nidulans* ΔmatA mutant. The *A. nidulans* genetic system was
employed to investigate the potential functionality of *A. fumigatus* mat1-2 in sexual development. All *A. nidulans* ΔmatA strains are sterile and form only undifferentiated protocleistothecia within the foci of Hülle cells. Fruiting bodies (cleistothecia), ascogenous hyphae, and ascospores are not observed (K. Y. Miller and B. L. Miller, unpublished data) (Fig. 2C and D). (This ΔmatA phenotype differs from that described previously by Paoletti et al. [30], where fruiting bodies are formed at reduced numbers and these lack ascospores.) Therefore, matA is not needed for Hülle cell formation and acts downstream of key initiators of sexual development. *A. fumigatus* mat1-2 encodes a structural homolog of the *A. nidulans* MatA HMG box mating type protein. *A. nidulans* MatA and *A. fumigatus* Mat1-2 display 53% identity and 70% similarity at the amino acid level. The HMG box of *A. fumigatus* Mat1-2 is the region of highest homology to *A. nidulans* MatA with 74% identity. Outside the HMG box, the N termini of the two proteins share 69% identity, while there is only limited identity (33%) in the C termini. At the DNA level, the HMG box has 75% sequence similarity, but there is no significant sequence similarity outside this domain. *A. fumigatus* mat1-2 has previously been identified and annotated (11, 12, 32). A comparison of mat loci in fertile *A. nidulans* and sterile *A. fumigatus* revealed extensive synteny (12). The function of the putative protein encoded by *A. fumigatus* mat1-2 is unknown. The sexual reproduction of *A. fumigatus* has been proposed but never observed in nature or the laboratory. To determine whether *A. fumigatus* mat1-2 can function in *A. nidulans* as a mating type regulator, we performed a complementation assay by using an *A. nidulans* ΔmatA strain.

We first tested whether *A. fumigatus* mat1-2 can confer mating function and drive sexual reproduction in *A. nidulans*. The sterile ΔmatA UI404 strain was transformed with the pWP1 plasmid containing the *A. fumigatus* mat1-2 gene (ORF plus the 1-kb promoter region and the 1.8-kb transcription termination region) and a selectable marker, *A. nidulans* pyrG. Due to a lack of extensive DNA sequence homology between *A. nidulans* matA and *A. fumigatus* mat1-2 outside the HMG box domain, recovered transformants were screened for single-copy ectopic integration of *A. fumigatus* mat1-2 at *A. nidulans* pyrG (Fig. 1). Two transformants, T1 and T5, were analyzed in detail. These transformants were induced to undergo sexual development. Six days after induction, the control strain FGSCA26 had differentiated mature fruiting bodies: cleistothecia filled with ascospores. Neither T1 nor T5 had differentiated fruiting bodies by day 6, but formed only foci of Hülle cells. No sexual

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**FIG. 2.** Phenotype of the *A. nidulans* transformant UI412 with resident ΔmatA and ectopic *A. fumigatus* mat1-2 at 6 days postinduction of the sexual cycle. (A) Dark purple-pigmented WT cleistothecia (black arrows) and mature green conidiophores. (B) Contents of broken WT cleistothecium at 6 days postinduction. A, mature ascospores; AH, ascogenous hyphae; IAc, immature transparent ascus; MAc, mature red-pigmented ascus with ascospores. (C) Clusters of white Hülle cells (white arrow) in UI414 at 6 days postinduction. (D) UI414 protocleistothecium within a cluster of Hülle cells under higher magnification. H, individual Hülle cells; VH, vegetative hyphae; Pc, protocleistothecium. Magnification, 700 μm (A and C) and 20 μm (B and D).
development was observed beyond this developmental block, which is characteristic of the UI404 matA deletion strain (Fig. 2).

Therefore, the A. fumigatus mat1-2 gene did not complement the A. nidulans matA deletion. By contrast, ectopically integrated A. nidulans matA (the ORF plus the 1-kb promoter region and 1.8-kb transcription termination region) complemented UI404 and fully restored fruiting body development.

Construction of an ORF swap strain by replacement of the endogenous A. nidulans matA ORF with the A. fumigatus mat1-2 ORF. We performed an ORF swap experiment to determine whether the Mat1-2 protein was functional in sexual development. A transcriptional fusion gene was created in which the expression of the A. fumigatus mat1-2 ORF is driven by the A. nidulans matA promoter, and potential posttranscriptional regulation is under control of A. nidulans matA 5' and 3' untranscribed regions. This construct, with the A. fumigatus mat1-2 ORF flanked by 5' and 3' sequences of A. nidulans matA, was used to replace the endogenous A. nidulans ∆matA allele by homologous recombination at the matA locus (Fig. 3A). Transformants created upon gene replacement at the matA deletion were argB2 auxotrophs. Transformant T4 was crossed to FGSCA237 to restore argB prototrophy and ensure that the ORF swap transformant was homokaryotic. Three argB/+/H11001 progeny, P1, P4, and P5, were isolated, and the presence of a single copy of the A. fumigatus mat1-2 ORF at the resident A. nidulans matA locus was confirmed by Southern blot analysis (Fig. 3B). Digestion with SalI was designed specifically to distinguish A. nidulans matA from the FGSCA237 parent and the A. fumigatus mat1-2 ORF swap parent in the selected progeny. A. fumigatus mat1-2 has a unique SalI (SalI*) restriction site in the coding region, whereas A. nidulans matA lacks this site. The 1.88-kb SalI fragment corresponds to WT A. nidulans matA, while the presence of the A. fumigatus mat1-2 ORF was distinguished by a 0.96-kb fragment (Fig. 3A and B). ApaL1 digestion was designed to confirm the presence of a single copy of the A. fumigatus mat1-2 ORF at the resident A. nidulans matA locus. The A. fumigatus mat1-2 ORF has a unique ApaLI (ApaLI*) restriction site. The 10.06-kb ApaLI fragment represents ∆matA control of the UI404 recipient strain. Single 2.33-kb ApaLI fragments in P1, P4, and P5 indicate a single
copy of the *A. fumigatus* mat1-2 ORF (Fig. 3B). Two or more tandem integrations would be indicated by an additional fragment of 3.5 kb.

The *A. fumigatus* Mat1-2 protein supports differentiation of atypical hypertrophic cleistothecia in *A. nidulans*. ORF swap strains UI421 (P1), UI422 (P4), UI423 (P5), and WT FGSCA26 were induced to undergo sexual development, and developmental tissue was examined 10 days postinduction. All ORF swap strains developed extremely large fruiting bodies that were ~300 times bigger per volume than those of the WT. The abundance of ORF swap cleistothecia was significantly lower than the value for the WT. In the WT, 100% of the protocleistothecia developed into mature cleistothecia by 10 days postinduction. By contrast, ORF swap strains had abundant undeveloped protocleistothecia within clusters of Hülle cells. Only 1.2% of all protocleistothecia underwent successful mating and fertilization which resulted in fruiting body formation (Table 3; Fig. 4).

Developmental time points (6, 8, 12, and 24 days postinduction) were selected based upon different stages of *Aspergillus nidulans* sexual development. Four separate sexual cycle inductions were analyzed. Samples of fruiting body tissue from each time point were examined microscopically. By 5 days postinduction, the WT and all ORF swap strains differentiated foci of Hülle cells that represent the earliest identifiable stage of sexual development. Within the foci of Hülle cells, mating and fertilization occur to trigger fruiting body development. After 6 days, the WT strain differentiated small pink cleistothecia, within which all ascogenous hyphae had differentiated into distinct asci with transparent or red-pigmented ascospores (Fig. 5A) In contrast, UI421, UI422, and UI423 at 6 days had differentiated significantly larger transparent cleistothecia containing a mass of proliferating ascogenous hyphae but no distinct asci (Fig. 5D). Sexual development of all ORF swap strains was apparently delayed at this time. After 8 days postinduction, the WT strain had abundant, almost fully mature, purple cleistothecia that were filled with ascospores. However, not all ascospores were released from asci at that time (Fig. 5B). Cleistothecia formed by the ORF swap strains were less abundant but much bigger than those formed by the WT as described previously. Large cleistothecia were dark purple pigmented and filled with asci at various developmental stages, with little or no differentiated ascospores at that time (Fig. 5E). Small amounts of debris, apparently coming from lysis of undeveloped asci and ascospores, were present in all ORF swap strains. After 12 days of sexual development, cleistothecia of the WT had reached full maturity. All ascospores were released from the asci and were ready for discharge (Fig. 5C). Similarly, development in UI421 and UI423 was completed. Ascospores were released from asci, but a large number of asci failed to develop, leading to the accumulation of debris (Fig. 5G). UI422 was not yet fully mature at 12 days and had large amounts of ascogenous hyphae and asci at different stages of development, and small numbers of mature released ascospores were present (Fig. 5F). UI422 continued to develop up to 24 days postinduction, at which time fruiting bodies were full of released ascospores and small amounts of ascospores enclosed in asci (Fig. 5H). All ORF swap strains represent different progeny from a cross between the original transformant and FGSC237 as described in Materials and Methods. The influence of genetic backgrounds of the parental stains may explain an observed variation in sexual morphogenesis among ORF swap progeny.

*A. fumigatus* Mat1-2 protein confers full fertility in *A. nidulans*. The total number and viability of ascospores were examined to confirm fertility of the ORF swap strains. Twenty mature cleistothecia from the WT and each ORF swap strain were collected at the same developmental stage, when they released ascospores. The average number of ascospores per cleistothecium in the WT was 0.59 × 10^5. The number of ascospores in UI421 was similar to that in the WT (average, 0.85 × 10^5). By contrast UI422 and UI423 differentiated significantly larger amounts of ascospores: 3.1 × 10^5 and 2.2 × 10^5, respectively, which represents a four- to fivefold increase over the value for the WT (Fig. 6A). Ascospore viability in the WT was an average of 37%, and similar viabilities were observed for UI421 and UI423, whereas UI422 ascospore viability was about twofold lower (Fig. 6B).

| Strain    | Average size C (μm) | Average no./cm² | % Fertilized P |
|-----------|---------------------|-----------------|----------------|
|           | P                   | C               |                |
| FGSCA26   | 145                 | 0               | 866            | 100            |
| UI421     | 650                 | 213.5           | 2.6            | 1.2            |

*P*, protocleistothecia; *C*, cleistothecia.
A. fumigatus Mat1-2 protein supports outcrossing in A. nidulans. WT A. nidulans strains (matA) are readily able to outcross. Crossed cleistothecia differentiate ascospore progeny with meiotic recombination frequencies consistent with established recombination units found in the A. nidulans genetic linkage map. To examine whether A. fumigatus Mat1-2 can also function in an outcross, we crossed the yellow conidial strain FGSCA237 and the green conidial strain UI421. Large cleistothecia were picked from a region of well-balanced and stable vegetative heterokaryon. Crossed cleistothecia were initially selected based upon conidial color of the progeny. Progeny from each cleistothecium were then analyzed for recombination frequency between markers on dropout medium. Recombination frequencies between the linked markers yA (Chr 1R) and bIA (Chr 1R) and the unlinked markers yA and trpC (Chr VIII) were analyzed for 100 progeny. For the linked markers, progeny were ~93% parental-to-7% recombinant, which is consistent with the established genetic linkage of seven recombination units. The segregation of unlinked markers was ~50% parental-to-50% recombinant as predicted. Therefore, the A. fumigatus Mat1-2 protein supports self-fertility, cross-fertility, and meiotic recombination.

A. fumigatus mat1-2 gene expression in A. nidulans is significantly higher than the natural transcript levels in A. fumigatus. Functionalities of the A. fumigatus mat1-2 gene and A. fumigatus mat1-2 ORF were correlated with the level of transcript expressed under conditions favorable for sexual development. The expression of the A. nidulans matA gene in A. nidulans and the A. fumigatus mat1-2 gene in both A. nidulans and A. fumigatus were analyzed using comparative QTPCR. Developmental tissues of four A. nidulans strains, FGSCA26 (WT), UI412, UI414, and UI422, and A. fumigatus strain Af293.139 were collected 6 days postinduction.
The FGSCA26 and UI422 are comparable because the promoter at the ectopic locus. Relative expression levels in mat1 with reference to expression in transcript levels in UI422 (H11011 A. fumigatus mat1 transcript level expressed from the promoter is not sufficient to support fruiting body for- sion at its resident locus (Fig. 7A). This level of expression was in strain UI422 is fully capable of driving sexual reproduction as robust as that of the A. nidulans sponds to upstream matA of the ORF swap strain UI422 (Fig. 7B). While expression in refer- ence strain UI421 was 60% of A. nidulans matA expression in UI414, we 1.8 kb downstream) was the ectopic copy of A. fumigatus mat1 (ORF plus 1.2 kb upstream and 1.7 kb from each strain. Statistical significance was determined by the one-way analysis of variance (P < 0.05).

In this study, we investigated the function of the mat1-2 mating type gene and its encoded protein to elucidate possible reasons for asexuality in the opportunistic human pathogen Aspergillus fumigatus. Mating ability and sexual development in filamentous Ascomycetes are controlled by two alternate forms of the mat locus, one encoding an HMG box protein and the other encoding an alpha box protein (8–10). The discovery of mat1-1 (alpha box) and mat1-2 (HMG box) A. fumigatus iso-lates that express putative mating type genes suggests a potential for sexual compatibility and fertility or already existing, but cryptic, sexual activity (29, 45). However, the physical presence and expression of mat loci, as reported for many assexual spe- cies, is not sufficient to confer sexuality. The mat genes may carry mutations rendering them nonfunctional or redirecting their regulatory functions to another biological process not related to the sexual cycle. Alternatively, other genes of the “sexual machinery” may have been lost. To clarify the basis for A. fumigatus asexuality, it is important that the functionality of proteins encoded by mating type genes is determined (1a, 11). Therefore, the main goal of this study was to determine func- tionality of the A. fumigatus mat1-2 gene and the Mat1-2 pro- tein by using the well-characterized genetic system of fertile homothallic A. nidulans. We used two approaches to separately analyze gene function and protein function.

We first determined the functionality of A. fumigatus mat1-2 by interspecies gene exchange between sterile heterothallic-like A. fumigatus and fertile homothallic A. nidulans. Interspe- cies mating type gene exchanges and heterologous expression have previously been used to understand the role and function of the mat locus in homothallic, heterothallic, and sterile As- comycetes. Mating type gene exchanges between members of the Sordariaceae (homothallic Sordaria macrospora and het- erothallic Podospora anserina and Neurospora crassa) revealed cross-species functionality. Mating type genes were inter- changeable between these species with respect to mating and fruiting body development but were not interchangeable with regard to postfertilization functions, such as meiosis and ascospore formation (2, 34). Similar results were obtained when mating type genes from asexu-al Alternaria alternata were ec- topically integrated and expressed in fertile heterothallic Cochliobolus heterostrophus (1a). Turgeon et al. reported that the mating type gene MAT-2 from assexual Bipolaris sacchari was able to support full fertility with normal ascospore differenti- ation in a ΔMAT C. heterostrophus strain (40, 42). Therefore, in

postinduction and RNA prepared as described in Materials and Methods. Genomic position appears to play an important role in proper developmental expression of mating type genes (2, 34, 46, 47). Therefore, to analyze ectopic mat1-2 expression in UI414, we included two reference control strains, FGSCA26, expressing A. nidulans matA at its resident locus (Chr III), and UI412, expressing A. nidulans matA at the ectopic site (Chr I). The expression of the ectopic copy of A. nidulans matA (ORF plus 1 kb upstream and 1.8 kb downstream) was ~60% of A. nidulans matA expression at its resident locus (Fig. 7A). This level of expression was sufficient to confer fruiting body development in A. nidulans. To correlate expression and functionality of A. fumigatus mat1-2, we analyzed two A. nidulans strains expressing the mat1-2 transcript: UI422 (mat1-2 ORF driven by the A. nidulans matA promoter at the A. nidulans matA resident locus) and UI414 (A. fumigatus mat1-2 gene with ORF driven by the native A. fumigatus pro- moter at the ectopic locus). Relative expression levels in FGSCA26 and UI422 are comparable because the matA4 promoter at its resident locus drives transcription in both strains. The A. fumigatus mat1-2 gene (ORF plus 1.2 kb upstream and 1.7 kb downstream) expressed by its own promoter was ~36% of the transcript level expressed from the A. nidulans matA promoter in the ORF swap strain UI422 (Fig. 7B). While expression in refer- ence strain UI422 is fully capable of driving sexual reproduction in A. nidulans, the level of expression driven by the native A. fumigatus promoter is not sufficient to support fruiting body for- mation in A. nidulans. Therefore, the A. fumigatus promoter re- sponds to upstream A. nidulans regulators, but this response is not as robust as that of the A. nidulans promoter. Native mat1-2 transcript levels in A. fumigatus strain AF293.139 were evaluated with reference to expression in A. nidulans. Significantly, mat1-2 expression from its resident locus in A. fumigatus was only about 1.1% relative to that in UI422 (Fig. 7B). These data suggest that there may exist a critical threshold level of mating type gene expression that is required to initiate fruiting body formation. Similar threshold specificities have been observed for other A. nidulans developmental transcription factors (28). If the above suggestion is the case, the level of mat1-2 expression in A. nidulans (UI414) and A. fumigatus (AF293.129) would be below this threshold. It is also significant that a comparison of UI414 and AF293.139 suggests that the A. fumigatus mat1-2 promoter is not responding to an important upstream regulator(s) in A. fumigatus or that these critical regulators are missing/nonfunctional in A. fumigatus.

**DISCUSSION**

In this study, we investigated the function of the mat1-2 mating type gene and its encoded protein to elucidate possible reasons for asexuality in the opportunistic human pathogen Aspergillus fumigatus. Mating ability and sexual development in filamentous Ascomycetes are controlled by two alternate forms of the mat locus, one encoding an HMG box protein and the other encoding an alpha box protein (8–10). The discovery of mat1-1 (alpha box) and mat1-2 (HMG box) A. fumigatus iso-lates that express putative mating type genes suggests a potential for sexual compatibility and fertility or already existing, but cryptic, sexual activity (29, 45). However, the physical presence and expression of mat loci, as reported for many assexual spe- cies, is not sufficient to confer sexuality. The mat genes may carry mutations rendering them nonfunctional or redirecting their regulatory functions to another biological process not related to the sexual cycle. Alternatively, other genes of the “sexual machinery” may have been lost. To clarify the basis for A. fumigatus asexuality, it is important that the functionality of proteins encoded by mating type genes is determined (1a, 11). Therefore, the main goal of this study was to determine func- tionality of the A. fumigatus mat1-2 gene and the Mat1-2 pro- tein by using the well-characterized genetic system of fertile homothallic A. nidulans. We used two approaches to separately analyze gene function and protein function.

**FIG. 6.** Ascospore production and viability in WT and ORF swap strains (UI421, UI422, and UI423). Illustrated are the means and standard errors (error bars) of the means for 20 separate cleistothecia per strain. Statistical significance was determined by the one-way analysis of variance (P < 0.05).
all reported cases, mating type function is conserved among both closely and distantly related species, even though gene structure was highly divergent. Turgeon et al. concluded that the reason for *B. sacchari* asexuality was not due to a defective *mat* gene but to another function required for sexual reproduction (40, 42). By contrast, our data demonstrate that *A. fumigatus* *mat1*-2 introduced ectopically into an *A. nidulans*/*H9004 matA strain was not properly expressed and, consequently, did not function to support either cleistothecia or ascospore development. To our knowledge, this is the first report showing that mating type gene exchange between closely related asexual and fertile *Ascomycetes* did not function in any aspect of sexual development. In line with observations of Turgeon et al., our data suggest that *A. fumigatus* asexuality might be caused by defective regulation of *mat1*-2 expression. The lack of proper *A. fumigatus* *mat1*-2 expression in *A. nidulans* might be due to an *A. fumigatus* *mat1*-2 promoter that does not respond appropriately to upstream regulators so that the level of expression is less than the threshold required to drive sexual reproduction. Other possible reasons for reduced expression could be position effect or subtle differences in mechanisms that regulate the expression of mating type genes in homothallic fertile *A. nidulans* and heterothallic sterile *A. fumigatus*. Our data further provide evidence that *mat1*-2, as it exists in the genome of the sequenced clinical isolate Afu293, is expressed at such a low level that it may not be sufficient to drive sexual reproduction. The expression of *mat1*-2 at its resident locus in *A. fumigatus* represents only 1.1% of the level of *mat1*-2 expression required to confer fertile fruiting body differentiation in *A. nidulans*. This level of expression in *A. fumigatus* is also significantly less than *mat1*-2 expression driven by its native promoter in *A. nidulans*. Therefore, the absence of a critical upstream regulator may also explain a deficiency in *mat1*-2 expression and asexuality in *A. fumigatus*. Many other *A. fu-
migatus isolates may be similar to the sequenced strain AF293 used in this study, and this phenomenon may be widespread throughout the worldwide A. fumigatus population. Paolletti et al. also observed very low expression levels of mating type genes in A. fumigatus environmental and clinical strains by using a reverse transcription-PCR/gel analysis approach (29). Detectable expression of both mating type genes required 35 cycles, a cycle threshold similar to what we observed for strain AF293.139 in our QTPCR analysis. In two independent studies, 50 and 70 A. fumigatus strains of clinical and environmental origin, respectively, were subjected to pair-wise matings in all possible combinations and on various mycological media promoting fungal mating. No signs of mating or sexual development were observed for any combination of strains (G. S. May and J. Kwon-Chung, personal communication). These studies support the argument that although there are two extant A. fumigatus mating type idiomorphs, the mat genes are not responding to key upstream regulators or key transcriptional factors for initiating sexual reproduction are missing. It remains possible that undetected strains that do express mat1-2 at functional levels may still exist in the current world population. Because A. fumigatus sexual reproduction has not been observed in nature or in the laboratory, these strains may be quite rare.

Because the mat1-2 gene was nonfunctional in A. nidulans, we were prompted to determine whether the Mat1-2 protein was functional by using the ORF swap approach. We created a gene replacement strain in which the A. nidulans matA ORF was effectively replaced with the A. fumigatus mat1-2 ORF. The expression of the A. fumigatus mat1-2 ORF was therefore driven by the A. nidulans matA promoter at the resident matA locus on Chr III. All ORF swap transformants were fertile, although sexual development was delayed and cleistothecium morphogenesis and ascosporogenesis were altered. Previous studies have shown that heterologous expression of functional mating type proteins conferred the differentiation of fruiting bodies that were indistinguishable from the WT in size and shape but had no, or only few, asci and ascospores (1a, 2, 34, 40, 42). By contrast, we observed the very unique formation of atypical hypertrophic fruiting bodies when the sexual cycle was driven by A. fumigatus Mat1-2 when it was expressed under control of the A. nidulans matA promoter. These atypical cleistothecia were filled with proliferating ascogenous hyphae and asci at various stages of maturation. The ascogenous tissue did not completely fill the entire volume of the cleistothecium. Hence, the cleistothecium was very soft and fragile. The A. fumigatus Mat1-2 protein has the highly conserved mating type HMG box DNA binding domain. Therefore, it probably binds to the same set of target genes as A. nidulans MatA does and supports full fertility. However, limited homology at the N and C termini of the two proteins could influence interactions with other transcription factors and affect the transcript abundance of target genes. These differences would, in turn, alter sexual cycle progression and fruiting body development. For example, ascospore differentiation and meiosis in Saccharomyces cerevisiae diploids are induced in the presence of the mating type a1/alpha2 heterodimer which represses the expression of RME1 (repressor of meiosis) (5). The formation of a MatAHMG/MatB alpha box (MatBalpha) mating type heterodimer has not yet been demonstrated for A. nidulans. However, Jacobsen et al. have shown that the alpha box and HMG box mating type proteins of homothallic Sordaria macrospora are able to form heterodimers (18). Our results suggest that the A. fumigatus Mat1-2 HMG box protein may not interact with the A. nidulans MatB alpha box mating factor to form a functional heterodimer. Alternatively, the protein-protein interaction may not be sufficiently stable. In addition to self-fertility, A. fumigatus Mat1-2 supports cross fertility and meiotic recombination when mated with a WT (matA) strain. It was previously shown that the Saccharomyces pombe mating type genes are required for both mating and meiosis and also influence meiotic recombination (25, 44). It has also been shown that HMG box proteins bind to, and potentially stabilize, the four-way (Holliday) DNA junction, an intermediate in homologous genetic recombination (49). In Ascomycetes, the expression of genes encoding proteins required for meiotic homologous recombination could be regulated by MatHMG transcription factors, including A. fumigatus Mat1-2, when expressed in A. nidulans.

Fruiting body development in Ascomycetes is a complex process of cellular differentiation that is under polygenic control and requires specific intrinsic signals and environmental conditions (31). Sexual morphogenesis in A. nidulans has been described previously; however, the molecular mechanisms controlling coordinated development of ascogenous hyphae and cleistothecium wall remain largely unknown (6). It has previously been demonstrated that the HMG box mating type transcription factor is necessary for fruiting body development in homothallic as well as in heterothallic fungi. MatHMG is required for the expression of different sets of target genes directly involved in male and female fertility, fruiting body morphogenesis, fruiting body abundance, and ascospore formation (7, 8, 21, 33). Sexual cycle genes include not only those encoding pheromones, pheromone receptors, and components of signal transduction pathways but also enzymes involved in cell wall biogenesis and metabolism (31). The delay in sexual development of the ORF swap strains may be due to unfavorable metabolic conditions created by reduced activities of critical enzymes when regulated by A. fumigatus Mat1-2. One of the essential enzymes being expressed at the onset of sexual development is endo-1,3-beta-glucanase. This enzyme is required to degrade glucan as a carbon source for fruiting body formation. Reduced endo-1,3-beta-glucanase expression could result in lowered carbon source availability and cause a delay in development. The delay in cleistothecia and ascospore development in the ORF swap strains might also be due to altered regulation of genes encoding components of signal transduction cascades that control expression of enzymes involved in cell wall biogenesis. These would also be important determinants of cleistothecium size and efficiency of development. Two well-characterized signaling pathways, the cyclic AMP-dependent protein kinases protein kinase A and mitogen-activated protein kinase, are known to regulate fruiting body formation in response to external stimuli. In particular, mating type proteins are known to regulate genes of the pheromone-mediated mitogen-activated protein kinase signaling pathway. N. crassa strains with a Galpha subunit mutation (Delta gna-I) form fewer protoperithecia with no ascospores (22). Fewer cleistothecia and ascospores were reported for A. nidulans gprA and gprB mutants that encode putative G protein-coupled pheromone receptors (39). Therefore, reduced efficiency of cleistothecia formation in ORF swap strains could be explained by
the altered expression of genes encoding important components of pheromone signaling, including G proteins, pheromones, and pheromone receptors, when regulated by the A. fumigatus Mat1-2 transcription factor.

In conclusion, our results confirm that the A. fumigatus Mat1-2 protein is not only a structural but also a functional homolog of the A. nidulans MatA HMG box mating type transcription factor and alone is able to regulate sexual development in A. nidulans. Additionally, A. fumigatus Mat1-2, like A. nidulans MatA, supports self-fertility, cross-fertility, and normal meiotic recombination frequency when expressed in the A. nidulans genetic background under control of the A. nidulans matA promoter. By contrast, the A. fumigatus mat1-2 gene in A. nidulans is not expressed at levels sufficient to confer biological function for sexual reproduction. Therefore, we infer that improper developmental regulation of mat1-2 could be a reason for asexuality in A. fumigatus. This may result from differences in mat1-2 promoter function or from key initiators of sexual development acting upstream of mat1-2 that are missing or not functional. Several lines of evidence demonstrate both functional conservation of the mat loci and distinctive plasticity in reproductive life style. Within the Ascomycetes, it has been possible with some success to change the reproductive mode by using intraspecies manipulation of mating type loci in Gibberella zeae and interspecies mating type gene exchanges among Cochliobolus sp. (23, 51). Intergenus mating type gene exchanges between asexual Bipolaris sacchari and heterothallic Cochliobolus heterostrophus, between homothallic Sordaria macrospora and heterothallic Podospora anserina, and between heterothallic Neurospora crassa and heterothallic Podospora anserina are also functional (2, 34, 40). Furthermore, in separate studies, Magee and Magee (24) and Hull et al. (16) were able to alter the mating-type like (MTL) locus in the asexual pathogen Candida albicans to create compatible mating partners able to mate in vitro. Hull et al. also showed evidence of mating in vivo within a mammalian host during infection (16). Overall, these data suggest that in most species, conservation of mating type function allows intraspecies, interspecies, and intergenus gene exchanges and supports alternate reproductive life styles. Further studies using a combination of genetic manipulations of mat loci and interspecies gene exchanges between sterile A. fumigatus and fertile Aspergillus, such as A. nidulans, Emericella heterothallica, and Neurospora fischeri, would be a next step in clarifying the expression of A. fumigatus mating type genes and their potential roles in A. fumigatus asexuality. These investigations should help elucidate whether A. fumigatus is truly asexual or has a cryptic sexual activity; moreover, they may reveal ways to manipulate mat loci to reconstruct compatible mating partners able to undergo a successful sexual cycle.

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