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SEXUAL REPRODUCTION IN DERMATOPHYTES

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Abstract

Sexual reproduction is a rich source of genetic variation and commonly observed among fungi. Basically two different modes of sexual reproduction are observed in fungi, namely heterothallism where two compatible mating types are required to undergo mating and homothallism in which the organism is self-fertile. The genomic region governing the process of sexual reproduction and sex determination is called the mating type (*MAT*) locus. In filamentous ascomycetes including dermatophytes, the *MAT* locus harbors two different transcription factor genes in two different mating types. This review focuses on sexual reproduction and the structure of the *MAT* locus in dermatophytes. The reproductive modes and the observed mating types are summarized for different phylogenetic clades of dermatophytes. In addition, the question of whether or not unisexual reproduction, an interesting form of homothallism, may be the sexual reproduction mode especially in anthropophilic dermatophytes is raised.

Keywords

Sexual reproduction; mating; mating type (*MAT*) locus; dermatophytes; unisexual reproduction

Introduction

Sexual reproduction is commonly observed among eukaryotes. Although the mechanisms and how sex is determined differ, the basic features of sexual reproduction are conserved between different organisms such as the processes of meiosis, ploidy change and cell-cell fusion [1]. Why sex is so pervasive in spite of being a costly process is an intriguing question. Finding a suitable partner and undergoing the entire process require time and energy. Also, well-adapted genomic configurations are disrupted. To overcome these costs, there must be potential counterbalancing benefits. These include removal of deleterious mutations from the genome and forming progeny with diverse genotypes, which increases the chance to adapt to changing environments [2].

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In humans and many other animals, sex is determined by the X and Y chromosomes, which are dramatically different in size and structure as heteromorphic sex chromosomes. Similarly in fungi, sex determination is governed by a specialized genomic region called the mating type locus (*MAT*) [3]. Filamentous ascomycetes have only one *MAT* locus in their genome that harbors two divergent loci called idiomorphs in the two mating types. While one of these loci, *MAT1-1*, harbors the gene encoding an alpha box domain transcription factor, *MAT1-1-1*, the other locus, *MAT1-2*, contains a gene that codes for a high mobility group (HMG) domain transcription factor, *MAT1-2-1* [4]. In filamentous ascomycetes, the *MAT* locus is closely linked to a gene encoding a cytoskeletal assembly protein, *SLA2*, on one side, and a DNA lyase gene, *APN2*, on the other side [5]. Although the transcription factor genes are the key components of the *MAT* locus, the size, the gene content, and the structure of the *MAT* locus is specific to each fungus.

Fungi have evolved to undergo two basic modes of sexual reproduction termed heterothallism and homothallism. Heterothallic fungi require two compatible mating types to undergo sexual reproduction, and this pattern is observed in *Aspergillus fumigatus*, *Neurospora crassa* and others [6–8]. In contrast, homothallic fungi are self-fertile and can complete the sexual cycle without the need for a partner of opposite mating-type. There are several types of homothallism. First, in some homothallic fungi, both the *MAT1-1* and *MAT1-2* idiomorphs are present in the genome, in some cases they are fused or closely linked on the same chromosome such as those of *Gibberella zeae* [9] and some *Cochliobolus* species [10]; in other cases they exist in two unlinked locations in the genome, such as those of *Aspergillus nidulans* [11] and *Neosartorya fischeri* [12]. This type of homothallism is called primary homothallism. A second type of homothallism is named pseudohomothallism, in which nuclei of compatible mating types are packed into a single spore, after which it germinates to produce a self-fertile heterokaryotic mycelium [13]. *Neurospora tetrasperma* and *Podospora anserina* are examples of pseudohomothallic fungi [14–15]. Third, some fungi such as *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe* are able to change their mating types via gene conversion between the active *MAT* locus and one of the two linked but silent *MAT* loci, which is named mating-type switching [16–17]. Lastly, an unusual form of homothallism is described as unisexual reproduction, which is different from primary homothallism in that there is only one *MAT* allele in the genome of the organism [2, 18]. In unisexual reproduction or same-sex mating, a single isolate can undergo sexual reproduction in solo culture without the need for a compatible mating partner.

An example of unisexual reproduction is observed in the basidiomycetous pathogenic yeast *Cryptococcus neoformans*. *Cryptococcus* has a well-defined mating system in which two compatible mating types, α and **a**, fuse to form dikaryotic hyphae leading to basidia and infectious basidiospores [19]. Although there is a defined sexual cycle between α and **a** mating types, the α mating type predominates almost exclusively among both environmental and clinical isolates [20]. An answer to the intriguing question of how sexual reproduction potential is maintained within this largely unisexual population was the discovery of unisexual reproduction, which involves both diploidization and meiosis [18, 21–22]. Same-sex mating is commonly observed in α isolates, but some **a** isolates were also shown to

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undergo unisexual reproduction [23]. There is also growing evidence obtained from population genetic studies that shows unisexual reproduction also occurs in nature [24–30]. Unisexual reproduction observed in the fungal kingdom is not unique to *Cryptococcus* species. Another human fungal pathogen, *Candida albicans*, was also shown to undergo unisexual reproduction [31]. It is quite interesting that two of the most common systemic human fungal pathogens (*C. neoformans*, *C. albicans*, and *A. fumigatus*) have evolved to reproduce unisexually in addition to their heterothallic sexual or parasexual cycles. There are also other examples of unisexual reproduction. Some *Neurospora* species such as *N. africana*, *N. galapagosensis*, *N. dodgei*, and *N. lineolata* [32–36], a group of *Stemphylium* isolates [37], and *Huntiella moniliformis* [38] have also been shown to be homothallic species with only one *MAT* idiomorph in their genomes. These species are also examples of unisexual reproduction.

Adapting a reproductive style that sometimes involves two genetically identical genomes must have some potential benefits. These might include avoiding the time and energy consumption typically necessary to find a compatible mating partner. In addition, in unisexual reproduction, there is only limited genetic diversity that might be generated by aneuploidy or chromosomal translocations, which might enhance the fitness of the progeny without disturbing a well-adapted genotype and phenotype [18].

Sexual reproduction and the *MAT* locus in dermatophytes

Dermatophytes are members of the genera *Trichophyton*, *Microsporum* and *Epidermophyton*, with their teleomorphic states defined in the genus *Arthroderma*. When compatible partners encounter each other, typical *Arthroderma*-type fruiting bodies (gymnothecia but sometimes named cleistothecia as well) are observed. Asci and ascospores are embedded within the ascomatal wall comprising interwoven peridial hyphae with spiral appendages.

Sexual reproduction is readily observed among soil-related geophilic dermatophytes. The zoophilic animal pathogens also frequently reproduce sexually. However, human-related anthropophilic dermatophytes were suggested to have lost the ability for sexual reproduction [39]. Because sexual reproduction is common among geophilic organisms, it has been suggested that the formation of fruiting bodies is favored on humid soil containing keratinous materials as debris; therefore, while sexual reproduction is seen in zoophilic dermatophytes associated with ground-dwelling animals, species that evolved to associate with non-ground-dwelling animals and humans appear to reproduce asexually [40]. On the other hand, fungal pathogens once thought to be strictly clonal or asexual because of the lack of population genetic or morphological evidence or lack of a compatible partner have been recently found to have cryptic sexual or parasexual cycles including *A. fumigatus* and *C. albicans* [6, 41].

Stockdale [42] observed that non-mating isolates produce a mating reaction indicative of their mating type when co-cultured with tester strains of *Arthroderma simii*. Both the Stockdale test and also more recent molecular data have shown that most recognized non-mating dermatophyte species comprise just one mating type [43]. Because sexual

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reproduction is observed in almost all phylogenetic branches in dermatophytes, the clonal lineages are thought to have arisen from a sexual ancestor and the other mating type might have been lost or extremely rare or the species might have been derived from one mating type [40]. This process might have been induced by a mutation that confers the ability to adapt to a new ecological niche such as a new host and before or during this process, the species might have lost one of the mating types and become genetically distinct because of the lack of suitable conditions for mating for a long time or due to niche separation [44–45].

Generally clonality is thought to be associated with asexuality, but it might also be the result of recombination between very similar genotypes. Examples include pathogens such as *C. neoformans* and *C. albicans* having highly clonal populations which were shown to be able to undergo unisexual mating [22, 31]. If this might also be the case for “apparently” asexual dermatophytes with a highly clonal population structure is an as yet unanswered question.

The structure of the *MAT* locus, orchestrating sexual reproduction and sex determination, is very similar among dermatophytes. Interestingly in dermatophytes, while the *APN2* and *COX13* genes are linked to the *MAT* locus, they are present in the 5′ side linked to *SLA2* instead of flanking the locus on the 3′ side as in other Pezizomycotina species (Figure 1) [5, 46–48]. The boundaries of the *MAT* locus have only been determined in *Arthroderma benhamiae* and *Microsporum gypseum*, because both mating types are available and the whole locus has been characterized for these species. In *A. benhamiae*, the *MAT* locus includes the 3′ end of the *MAT1-1-4* gene and the 5′ end of a *MAT*-associated gene that we named *HYP1* in addition to the transcription factor gene in between these two. The *MAT* locus of *M. gypseum* is very similar to *A. benhamiae*, but instead of capturing only the 3′ end, the *MAT* locus harbors a larger portion of the *MAT1-1-4* gene. The orthologues of *HYP1* are also seen in the *MAT* loci of *Histoplasma capsulatum*, *Coccidioides immitis* and *A. fumigatus*, but only in the *MAT1-2* isolates. Only the 3′ end of the *MAT1-1-4* gene is included in the *MAT1-2* locus of *H. capsulatum*, whereas the entire *MAT1-1-4* gene has been captured into the *MAT1-1* locus of *C. immitis* together with *APN2*, *COX13* and another gene. While the *H. capsulatum MAT* locus (~5.5 kb) is larger than the *MAT* loci of the dermatophytes (~ 3 kb), *C. immitis* has an even larger *MAT* locus spanning ~ 9 kb.

According to phylogenetic studies, dermatophytes can be classified into different clades, namely the *Arthroderma vanbreuseghemii* clade, the *Arthroderma simii* clade, the *A. benhamiae* clade, the *Trichophyton rubrum* clade, the *M. gypseum* clade and related species, the *Microsporum canis* clade, the *Microsporum cookei* clade and basal clades containing geophilic species [39, 43, 49]. The presence of sexual reproduction and analysis of *MAT* locus genes in dermatophytes are discussed below and summarized in Table 1.

***Arthroderma vanbreuseghemii* clade**

The *A. vanbreuseghemii* clade comprises the anthropophilic species *Trichophyton tonsurans* and *Trichophyton interdigitale* and the zoophilic species *Trichophyton equinum* in addition to the teleomorphic species *A. vanbreuseghemii* [49]. *Arthroderma vanbreuseghemii* is a heterothallic species when strains that were isolated from humans, mice, or chinchillas are co-cultured [50–51]. The *MAT* locus specific genes, the alpha box and the HMG box genes, were identified in *A. vanbreuseghemii* (−) and (+) strains, respectively [52]. Co-culture of *T.*

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interdigitale strains with *A. vanbreuseghemii* tester strains leads to infertile pseudocleistothecia suggesting that *T. interdigitale* is a humanized species derived from the sexual relative *A. vanbreuseghemii* [51]. In addition, Kano et al. [52] observed that among 15 *A. vanbreuseghemii* isolates (initially considered as veterinary isolates of *T. interdigitale*), 5 contain the alpha box gene and 10 harbor the HMG gene; however, all 72 human isolates of *T. interdigitale* have the HMG gene in their MAT locus.

Trichophyton equinum and *T. tonsurans* are clonal species in this clade containing only the *MAT1-2* or the *MAT1-1* idiomorph, respectively [53–54]. The two species have very similar ITS regions that might be indicative of recent divergence [43–44].

Arthroderma simii clade

This clade is composed of an anthropophilic species, *Trichophyton schoenleinii*, and the zoophilic species *A. simii* and *Trichophyton mentagrophytes* [49]. The teleomorph in this group is *A. simii*, and is described as a heterothallic species forming cleistothecia when two opposite mating partners are co-cultured under suitable conditions [55]. While *A. simii* (−) strains contain the alpha box gene, (+) strains have the HMG gene in their *MAT* locus [52].

Arthroderma benhamiae clade

The *A. benhamiae* clade is a group of dermatophytes containing both zoophilic and anthropophilic species. The clade includes *A. benhamiae*, *Trichophyton verrucosum*, *Trichophyton concentricum*, *Trichophyton erinacei*, *Trichophyton bullosum*, and *Trichophyton eriotrephon* and the only anthropophilic species in this clade is *T. concentricum* [49].

Arthroderma benhamiae is a heterothallic species and when strains of two different mating types, (+) and (−), meet under suitable conditions, cleistothecia with asci and ascospores are observed [56–58]. In the study by Kano *et al.* [59], (−) mating type *A. benhamiae* strains were shown to contain the alpha box gene, the *MAT1-1* idiomorph, while (+) mating type strains were found to have the HMG gene, the *MAT1-2* idiomorph. These findings are indicative of a heterothallic nature for this fungus. The genome of *A. benhamiae* has recently been sequenced and the *MAT* locus of the sequenced strain was identified as *MAT1-2* [47]. When the *MAT* locus of an opposite mating type strain was also sequenced, the *A. benhamiae MAT1-2* locus was shown to contain the 3′ end of the *MAT1-1-4* gene, an HMG gene and the 5′ end of a *MAT*-associated gene, *HYP1*, while the *MAT1-1* locus harbors an alpha box gene and the 5′ end of *HYP1* in the *MAT* locus in between the genes *SLA2*, *COX13*, *APN2* in the 5′ and *HYP2* in the 3′ flanking regions (Figure 1) [47].

Symoens *et al.* [58] identified two intraspecific groups among *A. benhamiae* strains based on both phylogenetic analysis and colony morphology. While they observed both mating types in group I, group II contained only one mating type. In addition, while strains from both groups mate with the tester strains of *A. benhamiae*, which form a third group intermediate between group I and group II, no interfertility was observed between group I and group II.

Trichophyton verrucosum is a zoophilic dermatophyte species frequently isolated from cattle. The species is closely related to *A. benhamiae* according to phylogenetic analysis

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using ITS sequences [60]. In the study by Kano *et al.* [60], 22 *T. verrucosum* isolates (4 from Czech Republic and 18 from Japan) were analyzed by PCR and all were found to contain the *MAT1-2* idiomorph, which is defined as the (+) mating type based on an *A. benhamiae* mating test [59]. The genome of *T. verrucosum* has recently been sequenced and its *MAT* locus was found to be very similar to the *MAT1-2* strain of *A. benhamiae* [47]. These findings suggest that *T. verrucosum* is a clonal lineage closely related to *A. benhamiae*.

Trichophyton rubrum clade

This clade is composed of the anthropophilic dermatophytes *T. rubrum* and *Trichophyton violaceum* and has no closely related teleomorphic species [49, 61]. *Trichophyton rubrum* is the most common agent of human dermatophytoses. No teleomorph has been found for this species and research shows that all isolates have the *MAT1-1* mating type [62]. However, Anzawa *et al.* [63] conducted a successful mating experiment between *T. rubrum* and *A. simii*, where they obtained one hybrid progeny among 35 ascospores that were characterized. In addition, mating and meiosis genes were found to be conserved not only in *T. rubrum* but also in other dermatophytes whose genomes have been sequenced [53]. These findings suggest that *T. rubrum* might be capable of sexual reproduction, but because of the loss of a mating partner, the species may reproduce clonally or unisexually in nature.

The *T. rubrum* clade also encompasses a lineage corresponding to the morphospecies *Trichophyton megninii*. It is the only member of the *T. rubrum* complex that is known to be (+) in mating type [61, 64]. However, it has not been described as a separate species by Cafarchia *et al.* [49] because its ITS region is only a few bases different from *T. rubrum*. In the study by Sequeira *et al.* [64], 41 isolates of *T. megninii* were examined and all were found to be of (+) mating type according to the Stockdale test, contrary to *T. rubrum*. Although mating has not been observed between *T. rubrum* and *T. megninii*, the question of whether *T. megninii* might be a missing mating partner of *T. rubrum* requires further research.

Microsporum gypseum clade and related species

The geophilic *M. gypseum* complex has two defined teleomorphic species: *Arthroderma gypseum* and *Arthroderma incurvatum* [65–66]. Both species produce cleistothecia with asci containing eight ascospores after incubation on agar plates with a source of keratin as well as nonkeratinous media based on oatmeal agar [67]. They form the characteristic peridial hyphae with appendages containing straight or spiral hyphae and macroconidia [66]. The two species are not cross compatible, that is, crosses between the two do not lead to cleistothecia [68]. Both species are heterothallic and compatibility in each species is controlled by a single locus with two alleles [68]. The *MAT* locus of *A. gypseum* contains an alpha domain/HMG gene, the *MAT1-1-4* gene and the 5′ end of the *MAT*-related gene, *HYP1* (Figure 1) [46].

Species related to *A. gypseum* and *A. incurvatum* are *Arthroderma fulva* (*Microsporum fulvum*), *Arthroderma obtusum* (*Microsporum nanum*), *Arthroderma persicolor* (*Microsporum persicolor*), and *Arthroderma corniculatum* (*Microsporum corniculatum*) which are also heterothallic with cleistothecia containing asci with eight ascospores. The

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peridium structure and appendages of these species are similar to *A. gypseum* and *A. incurvatum* [66, 69–73].

Microsporum canis clade

This clade consists of three distinct subgroups, the anthropophilic species *Microsporum audouinii* and *Microsporum ferrugineum*, and the zoophilic species *Microsporum canis*, which is associated mainly with cats [43]. The sexually reproducing species in this clade is *Arthroderma otae* and while *M. audouinii* and *M. ferrugineum* strains are sterile, the *M. canis* strains are able to mate with *A. otae* tester strains [74]. While the (+) mating type of *A. otae* is represented by only a limited number of isolates, the (−) mating type is the predominant one [74]. The *MAT* locus of the sequenced strain of *M. canis* was determined to contain an alpha domain gene and the locus structure is very similar to the *MAT1-1* loci of *M. gypseum*, *T. rubrum* and *T. tonsuran*s [46]. In the study by Sharma *et al.* [75], *M. canis* strains were subdivided into three populations (I–III) according to genetic variation and only population III was found to contain evidence of recombination. While this population contains the majority of veterinary isolates, population I contains 74% of strains isolated from humans, which may indicate the emergence of a clonal virulent genotype that has an improved ability to infect the human host.

Microsporum cookei clade

All five species described in this clade have defined teleomorphs. *Arthroderma cajetani* (*Microsporum cookei*), *Arthroderma cookiellum* (*Microsporum cookiella*) and *Arthroderma grubyi* (*Microsporum vanbreuseghemii*) are described as heterothallic fungi leading to cleistothecia typical of *Arthroderma* when compatible mating types meet [76–78]. The perfect state of *Microsporum racemosum* was described as *Arthroderma racemosum* with cleistothecia displaying the characteristic *Arthroderma*-type peridial hyphae and numerous spiral appendages with occasional macroconidia [79]. The first isolation of *M. racemosum* was in fact its perfect stage with numerous cleistothecia, but single ascospore isolates later revealed that the fungus is heterothallic [79]. A newly described species in this clade is *Microsporum mirabile* and its teleomorph *Arthroderma mirabile* [80]. It was shown to be a heterothallic fungus with the characteristic *Arthroderma*-type cleistothecia. Interspecies mating experiments within this clade showed mycelial stimulation between *M. mirabile* and *A. racemosum* and *A. cajetani* strains, pseudocleistothecia with no asci between *M. mirabile* and *A. cookiellum*, and cleistothecial, ascus-like structures with no liberated ascospores between *M. mirabile* and *A. cajetani* strains [80].

Basal clades of dermatophytes

The basal clades of dermatophytes mainly constitute geophilic fungi with a fairly large number of teleomorphic species including *Arthroderma gloriae* (*Trichophyton gloriae*), *Arthroderma gertleri* (*Trichophyton vanbreuseghemii*), *Arthroderma lenticularum* (*Trichophyton terrestre*), *Arthroderma insingulare* (*Trichophyton terrestre*), *Arthroderma uncinatum* (*Trichophyton ajelloi*), *Arthroderma quadrificum* (*Trichophyton terrestre*), *Arthroderma multifidum* (*Chrysosporium multifidum*), *Arthroderma flavescens* (*Trichophyton flavescens*), *Arthroderma melis*, *Trichophyton onychocola*, *Arthroderma ciferrii* (*Trichophyton georgiae*), *Arthroderma cuniculi*, *Arthroderma tuberculatum*

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(*Chrysosporium* sp.), *Arthroderma curreyi* (*Chrysosporium* sp.), *Ctenomyces serratus*, *Arthroderma olidum* (*Trichophyton eboreum*) and *Arthroderma borellii* (*Microsporum amazonicum*) [43, 69, 81–96].

Among these, only *A. ciferrii* (*T. georgiae*) and *A. curreyi* were reported to be homothallic fungi [89–90]. *Arthroderma ciferrii* produces abundant cleistothecia with asci containing 8 ascospores on soil agar with horse hair. Its homothallic nature has been confirmed by single ascospore cultures [89]. *Arthroderma curreyi* was reported to be homothallic, readily producing ascocarps on oatmeal agar [90].

The only molecular study in this clade that has been performed is for *T. onychocola*, a recently described geophilic species related to *A. melis* [96]. The only two isolates of this species were co-incubated on several media with or without blond hair of children as the keratin source at 17°C and 25°C in the dark [97]. Ascomata (gymnothecia) were only observed at 17°C with hair of children. Peridial hyphae were observed to be claw-like and hiding spiral appendages without macroconidia [97]. The mating system was found to be heterothallic. Although PCR amplification of a partial *MAT1-2* sequence was successful, that of the *MAT1-1* sequence from the other strain could not be obtained with the primers used [97].

Conclusions

Dermatophytes are keratinolytic fungi whose phylogeny is greatly influenced by ecology. The geophilic species generally form the basal clades and among these sexual reproduction is commonly observed. While only two species have a homothallic nature, the majority of the geophilic dermatophytes are heterothallic, which might indicate that the ancestral mode of sexual reproduction was heterothallism. While mating is common among geophiles, only some zoophilic species have the ability to undergo sexual reproduction and mating is not observed among anthropophilic species. Also, the majority of the anthropophilic species retain only one mating type. These findings have led to the hypothesis that sexual reproduction occurs on soil for geophilic and ground-dwelling zoophilic dermatophytes, while non-ground-dwelling zoophiles and anthropophiles do not have the necessary conditions for mating, so they may have evolved to reproduce primarily asexually leading to highly clonal population structures. However, examples of other pathogenic fungi that have clonal population structures have been found to undergo sexual reproduction which reveals they have evolved to undergo an interesting mode of homothallism, called unisexual reproduction. Whether this is also the case for dermatophytes is an interesting question and one which has not as yet been answered.

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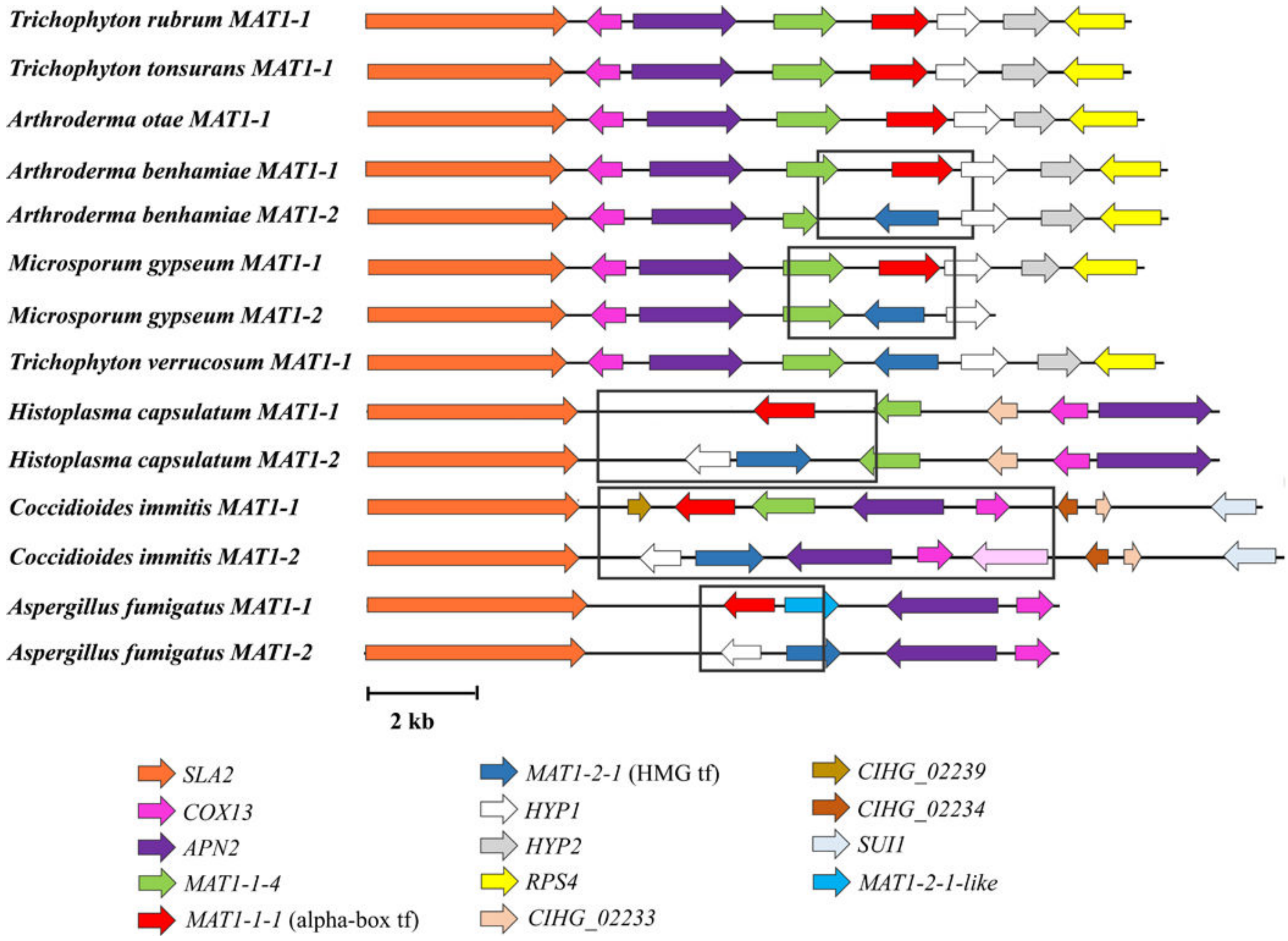

Fig. 1.

The *MAT* locus structure in dermatophytes and closely related pathogenic fungi. Black boxes represent the boundaries of the *MAT* loci. Among the dermatophytes, boundaries can be determined for *Arthroderma benhamiae* and *Microsporum gypseum* because both mating types are available and *MAT* loci sequences from each mating type are known. For *Trichophyton rubrum*, *Trichophyton tonsurans*, *Arthroderma otae* and *Trichophyton verrucosum*, the boundaries are not known; however, the highly similar configuration of the *MAT* loci among dermatophytes is remarkable. The *MAT* locus structures of closely related pathogenic fungi, namely *Histoplasma capsulatum*, *Coccidioides immitis* and *Aspergillus fumigatus*, are also included for comparison.

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Table 1

The host specificity, mating competency and the observed mating types for dermatophytes within different phylogenetic clades (only teleomorphic species were given for the basal clades)

Clade	**Species**	**Host**	**Mating**	**Mating types**	**Reference**
A. vanbreuseghemii clade	*T. tonsurans*	anthropophilic	−	*MAT1-1*	43, 44, 53, 54
	T. equinum	zoophilic	−	*MAT1-2*	43, 44, 53, 54
	T. interdigitale	anthropophilic	−	*MAT1-2*	51, 52
	A. vanbreuseghemii	zoophilic	+, heterothallic	both	50, 51, 52
A. simii clade	*T. schoenleinii*	anthropophilic	−	unknown	43, 49
	A. simii	zoophilic	+, heterothallic	both	52, 55
	T. mentagrophytes	zoophilic	−	unknown	43, 49
A. benhamiae clade	*A. benhamiae*	zoophilic	+, heterothallic	both	47, 56, 57, 58, 59
	T. verrucosum	zoophilic	−	*MAT1-2*	59, 60
	T. concentricum	anthropophilic	−	unknown	43, 49
	T. erinacei	zoophilic	−	unknown	43, 49
	T. bullosum	zoophilic	−	unknown	43, 49
	T. eriotrephon	zoophilic	−	unknown	43, 49
T. rubrum clade	*T. rubrum*	anthropophilic	−	*MAT1-1*	49, 61, 62
	T. violaceum	anthropophilic	−	(−) (*MAT1-1*)	49, 61
	T. megninii	anthropophilic	–	(+) (*MAT1-2*)	61, 64
M. gypseum clade and related species	*A. gypseum*	geophilic	+, heterothallic	both	46, 65, 68
	A. incurvatum	geophilic	+, heterothallic	both	66, 68
	A. fulva (*M. fulvum*)	geophilic	+, heterothallic	both	66
	A. obtusum (*M. nanum*)	geophilic	+, heterothallic	both	69
	A. persicolor (*M. persicolor*)	geophilic	+, heterothallic	both	71
	A. corniculatum (*M. corniculatum*)	geophilic	+, heterothallic	both	72, 73
M. canis clade	*A. otae* (*M. canis*)	zoophilic	+, heterothallic	*MAT1-2* predominant	43, 46, 74
	M. audouinii	anthropophilic	–	unknown	43, 74
	M. ferrugineum	anthropophilic	–	unknown	43, 74
M. cookei clade	*A. cajetani* (*M. cookei*)	geophilic	+, heterothallic	both	76

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Clade	Species	Host	Mating	Mating types	Reference
	A. cookiellum (*M. cookiella*)	geophilic	+, heterothallic	both	77
	A. grubyi (*M. vanbreuseghemii*)	geophilic	+, heterothallic	both	78
	A. racemosum (*M. racemosum*)	geophilic	+, heterothallic	both	79
	A. mirabile (*M. mirabile*)	geophilic	+, heterothallic	both	80
Basal clades	*A. gloriae* (*T. gloriae*)	geophilic	+, heterothallic	both	82
	A. gertleri (*T. vanbreuseghemii*)	geophilic	+, heterothallic	both	81, 83
	A. lenticularum (*T. terrestre*)	geophilic	+, heterothallic	both	81, 84
	A. insingulare (*T. terrestre*)	geophilic	+, heterothallic	both	81, 85
	A. uncinatum (*T. ajelloi*)	geophilic	+, heterothallic	both	69, 81
	A. quadrificum (*T. terrestre*)	geophilic	+, heterothallic	both	69, 81
	A. multifidum (C. multifidum)	geophilic	+, heterothallic	both	86
	A. flavescens (*T. flavescens*)	geophilic	+, heterothallic	both	81, 87
	A. melis	geophilic	+, heterothallic	both	88
	A. ciferrii (*T. georgiae*)	geophilic	+, homothallic	–	81, 89
	A. cuniculi	geophilic	+, heterothallic	both	86
	A. tuberculatum (*Chrysosporium* sp.)	geophilic	+, heterothallic	both	91
	A. curreyi (*Chrysosporium* sp.)	geophilic	+, homothallic	–	90
	Ctenomyces serratus	geophilic	+, heterothallic	both	93, 94
	A. olidum (*T. eboreum*)	geophilic	+, heterothallic	both	92
	A. borellii (*M. amazonicum*)	geophilic	+, heterothallic	both	81, 95
	T. onychocola	geophilic	+, heterothallic	both	96, 97