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STRUCTURE AND FUNCTION OF MATING-TYPE GENES IN *FUSARIUM* SPECIES

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Members of the genus *Fusarium* are worldwide-distributed filamentous fungi. Many of them are responsible for various plant diseases and may cause animal and human toxicoses. The reproductive structure of these fungi is crucial from a plant pathological point of view as the sexual recombination helps to maintain the genetic diversity of the population yielding new pathotypes and mycotoxin profiles. Moreover, the ascospores survive during winter and serve as a primary inoculum source in the next vegetation period.

Most *Fusarium* species reproduce themselves solely asexually by vegetative spores (conidia). However, certain species are able to complete the sexual part of their life cycle resulting in the production of ascospores. These species can be homothallic (self-compatible, the sexual reproduction is carried out within the same thallus) or heterothallic (self-incompatible, an interaction between two genetically distinct strains is needed for initiating sexual reproduction). The heterothallic sexual behaviour is governed by a single locus named mating-type (*MAT*) locus. The sexual process starts when the interacting strains have the opposite mating-type loci [1]. In *Fusarium verticillioides* (teleomorph *Gibberella fujikuroi*) the *MAT1* locus contains three genes (*MAT1-1, MAT1-2* and *MAT1-3*), whereas the *MAT2* locus contains only one (*MAT2-1*). This organisation of the mating-type loci is very similar to that found in the heterothallic type-species *Neurospora crassa* as well as in *Podospora anserina* which is a pseudohomothallic fungus. The genome of the homothallic *Fusarium graminearum* (teleomorph *Gibberella zeae*) contains all these four *MAT* genes, mentioned above, which are tightly linked together. The asexual fungus, *Fusarium oxysporum* also contains *MAT* genes whose sequences and arrangements are similar to that of the *MAT* genes present in *Fusarium verticillioides* [2]. The putative function of the *MAT1-1* and *MAT2-1* genes is the control of the mating process; *MAT1-2* and the *MAT1-3* are presumably involved in the ascosporogenesis [3].

Our scientific goal was to establish whether mating-type sequences exist in asexual, toxigenic *Fusarium* species. In order to answer this question two pairs of degenerate oligonucleotide primers were designed – based on known fungal mating type sequences – and used for PCR amplification of the mating-type specific DNA fragments in 62 strains of *F. camptoceras* (2), *F. cerealis* (5), *F. culmorum* (16), *F. poae* (8), *F. pulverosum* (3), *F. semitectum* (6) and *F. sporotrichioides* (10). *Fusarium avenaceum* (*Gibberella avenacea*, 12 isolates) was also included in this experiment as the sexual behaviour of this fungus is not clear. In general, *G. avenacea* is regarded as a heterothallic fungus, but weak homothallism has also been observed. Using this technique, each of the two conserved mating-type sequences, i.e. the ALPHA box derived from the *MAT1-1* gene and the HMG box derived from *MAT2-1* gene could be detected. All of the strains were found to contain one or the other of the two mating-type genes, but never both of them indicating the putative heterothallic nature of these fungi. RT-PCR experiments clearly demonstrated that the mating type-genes are transcribed in asexual *Fusarium* species. The results suggest that asexual *Fusarium* species (or at least some of them) have the potential to complete the sexual part of their life cycle. Under field conditions, such a recombination may result in the emergence of new pathotypes and/or progenies with an altered mycotoxin producing capability.

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