

Agaricus devoniensis Complex Comprises a Group of Heterothallic Isolates Constituting a Basis for Breeding

P. Callac*, C. Spataro; E. Lataillade; P. Blasi; J. Guinberteau

*INRA, MYCSA, BP 81, 33883 Villenave d'Ornon Cedex, France
callac@inra.bordeaux.fr

A recent phylogenetic reconstruction of *Agaricus* section *Duploannulati* revealed that *A. devoniensis* and *A. subfloccosus* are two complexes of species close to *A. bisporus*. The *A. subfloccosus* complex comprises two homothallic entities, while the *A. devoniensis* complex was never studied until now. A sample of 26 isolates, some being unreliably determined, were examined to (i) confirm their identity using a PCR-RFLP marker revealing a characteristic *A. devoniensis* ITS polymorphism, and (ii) for their ability to fruit in standard conditions used for *A. bisporus* cultivation. Twenty one isolates were confirmed as *A. devoniensis*, and only two collections from USA were unable to fruit. The five remaining isolates were excluded from the complex and were unable to fruit; their ITS1+2 regions were sequenced and alignments indicated that four of them were similar to *A. campestris* and that one belonged to a new entity close to *A. bitorquis* and *A. cappellianus*. For the 19 fruitifying isolates of the complex, we attempted intrastock and interstock mating tests with single spore isolates: for three isolates, we did not get spore germination; and for seven isolates, we observed partial to complete intersterility between strains. The nine remaining isolates exhibited a unifactorial system of sexual incompatibility for which eight different mating type alleles were detected. Within this group, the heterothallic and presumably interfertile isolates differed in their origin (Greece, France), their habitat (dune, coniferous trees), and their morphology (mean spore length: 5.6 to 6.6 μm); they constitute a diversified genetic basis usable to select smooth white and attractive cultivars for this tasteful edible and cultivable species.