

Title Molecular characterization of the black *Aspergillus* isolates responsible for ochratoxin A contamination in grapes and wine in relation to taxonomy of *Aspergillus* section *Nigri*

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Abstract

This work examines ochratoxigenic mycobiota in grapes by ap-PCR analysis sequence analysis of the ITS and IGS regions and ability to produce OTA. A comparison was also made with many reference strains of *Aspergillus* section *Nigri*. Based on ap-PCR profiles, derived from two microsatellite primers, three main groups were obtained by UPGMA cluster analysis corresponding to *A. carbonarius*, *A. niger* and *A. tubingensis*. The cophenetic correlation values corresponding to ap-PCR UPGMA analysis revealed a higher genetic variability in *A. niger* and *A. tubingensis* than in *A. carbonarius*. In addition, no genotypical differences could be established between OTA producers and nonproducers in all species analysed. Phylogenetic relationships inferred from ITS and IGS sequences are, mostly, congruent with earlier works. *A. niger* and *A. tubingensis* strains were closely related, but not identical, and they clustered into two distinct groups within the *A. niger* aggregate. Sequence analysis also showed genetic divergences between strains of *A. foetidus* and the rest of the *Aspergillus* section *Nigri*. Additionally, the phylogenetic analysis was consistent in separating a new group of ochratoxigenic strains, frequently isolated from grapes, named *A. tubingensis*-like. All strains of *A. carbonarius* analysed by sequence analysis had identical ITS and IGS sequences confirming the lack of significant genetic variability within this important ochratoxigenic species.