BAYOUD OF DATE PALM (PHOENIX DACTYLIFERA L.): POPULATION STRUCTURE AND GENETIC CHARACTERIZATION OF FUSARIUM OXYSPORUM F. SP. ALBEDINIS

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Bayoud, the Fusarium wilt of date palm tree (*Phoenix dactylifera* L.), has caused the death of millions of trees. The disease occurred since 1870 in Morocco and since the beginning of the XXth century in the western and central parts of the Algerian Sahara. It has never been reported in any other area of date palm cultivation throughout the world (Louvet and Toutain, 1981).

Detection and identification of *Fusarium oxysporum* f. sp. albedinis remain difficult, mainly because inoculation tests are still required to assess the pathogenicity of the *F*. oxysporum isolates. In addition, the pathogen can be easily disseminated by exchange of some contaminated material, and, at present, strict phytosanitary rules are applied at borders of date palm growing countries that remain free of Bayoud.

Studies on the genetic characterization of the pathogen have been undertaken in order to assess the genetic diversity and the population structure of F. o. albedinis and to develop diagnostic tools for its detection. Vegetative compatibility and genomic analyses have allowed characterization of a single clonal lineage within the Algerian and Moroccan F. o. albedinis (Tantaoui et al., 1996; Fernandez et al., 1997). All isolates tested belonged to a single vegetative compatibility group (VCG 0170) and displayed identical mitochondrial DNA (mtDNA) restriction fragment length polymorphism (RFLP) patterns and random amplified polymorphic DNA (RAPD) profiles, whatever the host genotype or their geographical origin (Tantaoui et al., 1996; Fernandez et al., 1997). Genomic analyses have also shown that the fungus carries repetitive DNA sequences homologous to the DNA transposable element Fot1, cloned in F. oxysporum f. sp. melonis (Daboussi et al., 1992) and widely distributed in F. oxysporum. Depending on the F. o. albedinis strain, 15-26 EcoRI-fragments hybridizing with the Fot1 sequence were found and several were conserved among the isolates. Use of the Fot1 element as a dispersed repetitive DNA probe has allowed to characterize more than 64 closely related repetitive patterns (genotypes) among 120 F. o. albedinis isolates (Tantaoui et al., 1996; Ouinten, 1996).

These results support the hypothesis that the Algerian and Moroccan isolates of F. o. albedinis were probably founded by a single virulent clone that originated from the Moroccan oases where the date palm wilt (Bayoud disease) was first detected (Tantaoui et al., 1996; Fernandez et al., 1997). However, some geographic substructuring was apparent in Algeria,

suggesting that local diversification of the pathogen might have occurred. Based on similarity of RAPD patterns and Fot1-genotypes occurring in different oases, and on historical records of the Bayoud disease in Algeria, spread of the pathogen in the different Algerian regions could be partially recounted (Fernandez et al., 1997; Ouinten, 1996).

In addition, all molecular patterns differred radically between F. o. albedinis isolates and other non-pathogenic F. oxysporum isolated from palm-grove soil (Tantaoui, 1994). We have taken advantage of the high genetic relatedness among isolates pathogenic to date palm to develop a sensitive PCR assay (Fernandez et al., sub). Several DNA clones containing a copy of the transposable element Fot1 were isolated from a genomic library of the date palm pathogen. Partial sequencing of the clones was undertaken to obtain the flanking sequences of the Fot1 copies in the genome of the fungus and we designed PCR primers to amplify the DNA regions overlapping each Fot1 insertion site.

When tested on a large sample of Fusarium isolates including 286 F. o. albedinis, 17 other formae speciales, non-pathogenic Fusarium oxysporum isolated from palm-grove soils and 8 Fusarium species, the primer pair TL3/FOA28 allowed specific amplification of a 400-bp fragment from the F. o. albedinis DNA. In addition, sequence analysis showed that one of the Fot1 copies was truncated, lacking 182-bp at its 3' terminus. The primer pair BIO3/FOA1, amplifying 204-bp overlapping the Fot1 truncated-copy and its 3' region of insertion in the albedinis genome, enabled identification of 95% of the isolates. Less than 100 pg of purified albedinis DNA could be efficiently detected. The primer pairs BIO3/FOA1 and FOA28/TL3 used in PCR assays thus provide a useful diagnostic tool for F. o. albedinis.

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