

Genetic Diversity in the Coffee Wilt Pathogen (*Gibberella Xylarioides*) Populations: Differentiation by Host Specialization and RAPD Analysis

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SUMMARY

Gibberella xylarioides (*Fusarium xylarioides*) causes vascular wilt disease, tracheomycosis, in almost all coffee species in Africa. Coffee wilt disease is endemic with certain outbreaks on Arabica coffee (*Coffea arabica* L.) in Ethiopia and re-emerged as a major threat to Robusta coffee (*C. canephora*) in Congo (Zaire), Uganda and Tanzania. The population structure of the pathogen was studied in recent and historic strain collections employing pathogenicity and RAPD-PCR analysis. In the pathogenicity test that consisted of 11 isolates and 9 cultivars from Arabica and Robusta coffee, the Arabica isolates were pathogenic only to seedlings of *C. arabica* with significantly varying degrees of aggressiveness across cultivars, but incompatible with seedlings of *C. canephora*. In contrast, the Robusta strain was specifically compatible with seedlings of *C. canephora* without showing any infection symptom in all *C. arabica* cultivars. This result is the first cross-inoculation evidence proving host specialization of *G. xylarioides* populations to the two economically important coffee species. There existed also highly significant differences among cultivars, isolates and cultivars-isolates interactions. In the RAPD-PCR analysis of 22 *G. xylarioides* strains of the recent and historic collections from Arabica, Robusta and Excelsa coffee, the Ethiopian Arabica isolates clustered into a single homogeneous population although distinctly polymorphic to the recent and old strains from *C. canephora* and *C. excelsa*. The recent Robusta isolate from Uganda showed close genetic relatedness to the historic strain collected from *C. excelsa* in Central African Republic (CAR) suggesting that the current tracheomycosis outbreaks might have been caused by the fungus inculum originated from *C. excelsa* in CAR spread to Uganda via Congo. The historic Arabica isolate (1971) was slightly different from the recent (2001) collections in Ethiopia illustrating little genetic change in the population structure over the last 3 decades. This in turn implies that the sexual (teleomorphic) state of the fungus has little contribution to the population genetics rather serving for survival and dissemination mechanisms. The findings of both host-pathogen interactions and RAPD-PCR markers corroborated existence of host specialization into at least two pathogenic forms within *G. xylarioides* populations. Thus two *formae speciales*, namely; *G. xylarioides* f.sp. *abyssiniae* (anamorph: *F. xylarioides* f.sp. *abyssiniae*) for the fungus strains attacking only *C. arabica*; and *G. xylarioides* f.sp. *canephorae* (anamorph: *F. xylarioides* f.sp. *canephorae*) pathogenic to *C. canephora* and *C. excelsa* are proposed. This subdivision enables to design effective coffee wilt management strategies, develop resistant cultivars/lines and formulate further breeding programs towards each population group in Africa.