A molecular diagnostic for tropical race 4 of the banana

M.A. Dita[1,2], C. Waalwijk[2], I.W. Buddenhagen[3], M.T. Souza Jr[2,4] and G.H.J. Kema[2]

[1]Embrapa Cassava & Tropical Fruits, Cruz das Almas, 44380-000, Bahia, Brazil; [2]Plant Research International B.V., PO Box 16, 6700 AA Wageningen, the Netherlands; [3]1012 Plum Lane, Davis, California, USA; [4]Embrapa LABEX Europe, PO Box 16, 6700 AA, Wageningen, the Netherlands; e-mail: cees.waalwijk@wur.nl

This study analysed genomic variation of the translation elongation factor 1α(TEF-1) and the intergenic spacer region (IGS) of the nuclear ribosomal operon of *Fusarium oxysporum* f. sp. *cubense* (Foc) isolates, from different banana production areas, representing strains within the known races, comprising 20 vegetative compatibility groups (VCG). Based on two single nucleotide polymorphisms present in the IGS region, a PCR-based diagnostic tool was developed to specifically detect isolates from VCG 01213, also called tropical race 4 (TR4), which is currently a major concern in global banana production. Validation involved TR4 isolates, as well as Foc isolates from 19 other VCGs, other fungal plant pathogens and DNA samples from infected tissues of the Cavendish banana cultivar Grand Naine (AAA). Subsequently, a multiplex PCR was developed for fungal or plant samples that also discriminated Musa acuminata and M. balbisiana genotypes. It was concluded that this diagnostic procedure is currently the best option for the rapid and reliable detection and monitoring of TR4 to support eradication and quarantine strategies.