DEVELOPMENT OF A GENETIC LINKAGE MAP OF *Mycosphaerella fijiensis*, THE CAUSAL AGENT OF BLACK LEAF STREAK DISEASE IN BANANAS (*Musa* spp.) USING SSR AND DArT MARKERS

Ferreira, C.F.[1,2], Van der Lee, T.A.J.[1] Zapater, M.F.[3], Carlier, J[3].Goodwin, S.B.[4], Souza Jr., M.T.[1,5], Kema, G.H.J.[1]

[(1)]*Plant Research International B.V., Wageningen University and Research Centre, P.O. Box 16, 6700 AA, Wageningen, The Netherlands*; [(2)]*Embrapa Cassava and Tropical Fruits, Rua Embrapa S/N, C.P. 007, 4438-000 Cruz das Almas-BA, Brazil 4430-000*; [(3)]*Biologie et Génétique des Interactions Plantes-Parasites, CIRAD-INRA-AGRO.M, TA 41/K, 34398 Montpellier, France*; [(4)]*USDA-ARS, Crop Production and Pest Control Research Unit, Department of Botany and Plant Pathology, 915 West State Street, Purdue University, West Lafayette, IN 47907-2054, USA*; [(5)]*Embrapa-LABEX Europe - Wageningen University and Research Centre, P.O. Box 16, 6700 AA, Wageningen, The Netherlands*

E-mail theo.vanderlee@wur.nl or gert.kema@wur.nl

Mycosphaerella fijiensis is the causal agent of black leaf streak or Black Sigatoka disease in bananas. This pathogen threatens global banana production, as the main export cultivars, Cavendish type, are highly susceptible. As a consequence, commercial banana plantations must be protected chemically with fungicides. The frequency of fungicide applications varies per region but is usually higher than 40 applications per year representing >40% of the total production costs. Ascospores are the major drivers of black leaf streak epidemics and *M. fijiensis* is currently still colonizing new banana-growing areas, which has a huge economic impact on banana producers. The frequent fungicide applications exert a strong selection pressure on *M. fijiensis* populations resulting in abrupt resistance development to strobilurins and a gradual increase of resistance to azole fungicides. To provide the community with necessary genetic tools we developed a genetic linkage map of *M. fijiensis*.. One-hundred and thirty-six F_1 individuals from the CIRAD086 (Cameroon, *Mat*1-1) x CIRAD 139A (Colombia, *Mat*1-2) cross were evaluated. Eighty-seven SSR (Simple-Sequence Repeat) markers, 3 VNTR (Variable Number of Tandem Repeat) markers, the mating type (*Mat*) locus and 235 DArT (Diversity Arrays Technology) markers were positioned in 19 linkage groups covering 1417 cM of the genome. The arrays containing individual fragments of the genomic representation of *M. fijiensis* generated DArT markers with a 90% genotype call rate and 98.8% reliability score. In total, 87% of the markers could be positioned reliably with high LOD scores (LOD <10). Due to its excellent genome coverage and high quality we decided to sequence the DArT markers to align this genetic map with the genome sequence of CIRAD086, which will considerably assist the genome assembly of this important fungus.