

Session 1: Pathogen variability

1.2 Analysis of *Ustilago scitaminea* genetic diversity using microsatellite markers provides evidence of selfing and dispersal of a unique lineage over America and Africa

Raboin L.-M.¹, Selvi A.², Miranda Oliveira K.³, Paulet F.⁴, Calatayud C.⁴, Zapater M.-F.⁵, Brottier P.⁶, Garsmeur O.⁴, Carlier J.⁵ and D'Hont A.⁴

¹. CIRAD (Centre de coopération internationale en recherche agronomique pour le développement) - UMR PVBMT, Pôle de Protection des Plantes, Ligne Paradis, 97410 Saint-Pierre, Réunion, France ; ². Sugarcane Breeding Institute, Coimbatore, India; ³. Universidade Estadual de Campinas, Brazil; ⁴. CIRAD - UMR 1096, PIA, TA40/03, Avenue Agropolis, 34398 Montpellier cedex 5, France ; ⁵. CIRAD - UMR BGPI, TA 41 / K, Campus International de Baillarguet, 34398 Montpellier Cedex 5, France ; ⁶. Genoscope, Centre National de Séquençage, 2 rue Gaston Crémieux, 91057 Evry, France.

Ustilago scitaminea Sydow, which causes sugarcane smut disease, has been spreading throughout Africa and America since the 1950s. The objectives of the present study were (1) to confirm and further describe the global population structure of *U. scitaminea* on the basis of a larger number of isolates and (2) to infer its reproduction system. Microsatellite markers, that present the advantage of being highly polymorphic, PCR-based, reproducible and codominant, were therefore developed for *U. scitaminea* and used to analyse a sample of single-teliospore isolates from various sugarcane-producing countries around the world. We surveyed 142 single-spore isolates of *Ustilago scitaminea* for genetic diversity. The fungal samples were teliospores from 77 single whips (sori) collected on various cultivars and at different locations in 15 sugarcane-growing countries throughout the world. The overall genetic structure of this fungus was investigated using 17 polymorphic microsatellite loci. All isolates but one were homozygous for all loci, indicating that selfing could be the highly preferential predominant reproductive mode of *U. scitaminea*. In America and Africa, genetic diversity was found to be extremely low and all isolates belonged to a single inbred lineage. This inbred lineage was also found in some parts of the Asian continent where most *U. scitaminea* genetic diversity was detected. These observations support the hypothesis that the fungus originated in Asia. The strong founder effect observed in the global genetic structure of *U. scitaminea* suggests that the fungus migrated from Asia to other continents on rare occasions.