

Reviews, Critiques and New Technologies

Diversity and evolution of *Fusarium* species in the *Gibberella fujikuroi* complexKvas, M.^{1*}, Marasas, W.F.O.¹, Wingfield, B.D.², Wingfield, M.J.¹ and Steenkamp, E.T.^{1,*}¹Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), Faculty of Natural and Agricultural Sciences, University of Pretoria, South Africa²Department of Genetics, DST/NRF Centre of Excellence in Tree Health Biotechnology (CTHB), Forestry and Agricultural Biotechnology Institute (FABI), Faculty of Natural and Agricultural Sciences, University of Pretoria, South AfricaKvas, M., Marasas, W.F.O., Wingfield, B.D., Wingfield, M.J. and Steenkamp, E.T. (2009). Diversity and evolution of *Fusarium* species in the *Gibberella fujikuroi* complex. *Fungal Diversity* 34: 1-21.

From agricultural, medical and veterinary points of view, the genus *Fusarium* represents a very important group of fungi. *Fusarium* species can colonize all vegetative and reproductive organs of plants, where they are capable of causing devastating diseases (Fig. 1). Some species can also affect humans and animals. *Fusarium* species also produce a wide range of toxic secondary metabolites or mycotoxins that contaminate food/feed worldwide. Among the known *Fusarium* species, one of the best-studied groups is the *Gibberella fujikuroi* complex (GFC).



Fig. 1. Disease symptoms caused by *Fusarium* species. (a) maize cob rot caused by *F. verticillioides*; (b) pitch canker caused by *F. circinatum*; (c) mango malformation caused by *F. mangiferae*; (d) sorghum stalk rot caused by *F. thapsinum*.

GFC is a group of *Fusarium* species with similar and overlapping morphological traits descended from a common ancestor. Many of the *Fusarium* species within the GFC are well known plant pathogens and cause diseases such as cob rot of maize, pitch canker of pines, mango malformation, vascular wilt of coffee, bakane disease of rice, pokkah boeng disease of sugar cane, etc. (Fig. 1). Due to the limited number of available diagnostic characters (Fig. 2) needed to differentiate species, DNA sequence information and phylogenetic analyses are increasingly used. In fact, the application of DNA-based data has revolutionized the taxonomy and diagnostics of the GFC, which currently include at least 50 distinct phylogenetic lineages. Of these, 34 species have been formally described based on morphological characters, while 10 have been described based on sexual fertility (Fig. 3). At least 20 of these species produce mycotoxins such as fumonisins, moniliformin, beauvericin, fusaproliferins, fusaric acid and enniatins.

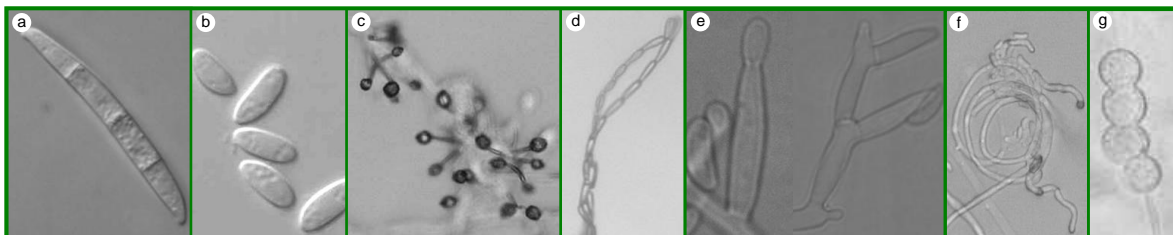


Fig. 2. Morphological characters observed within GFC. (a) macroconidia; (b) microconidia; (c) microconidia produced in false heads; (d) microconidia produced in chains; (e) conidiogenous cells; (f) sterile coils; (g) chlamydozoospores.

From an evolutionary point of view, the GFC species are grouped into three major clades (Fig. 3). Although these clades have not been formally named, their current designations (i.e. African, Asian and American) are controversial and thought to reflect the geographic origins of the plant hosts from which the *Fusarium* species were isolated. This biogeographic hypothesis appears to be true for most of the *Fusarium* species in the GFC. However, there are a number of notable exceptions (e.g. the association of the “African” fungus *F. verticillioides* with the “American” host *Zea mays*) and recent human activity is frequently invoked to explain the apparent distribution of fungi in this complex. Furthermore, in terms of morphology, the traits typically applied in GFC taxonomy appear not be phylogenetically informative. This also appears to be true for mycotoxin production, although very little information regarding the evolution of the genes and pathways involved in mycotoxin production is available for the GFC.

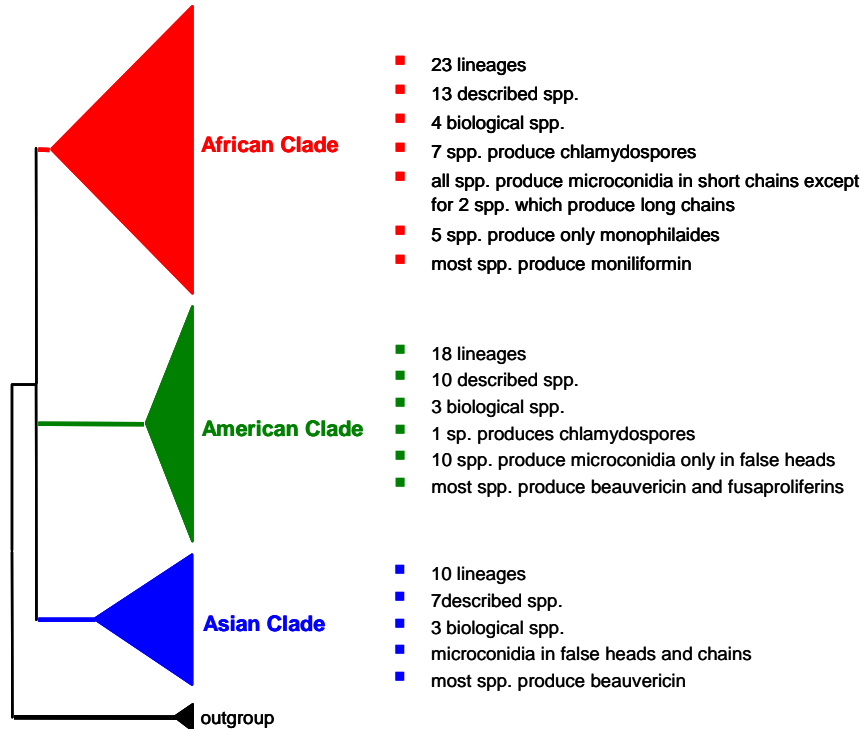


Fig. 3. Phylogenetic clades the *Gibberella fujikuroi* complex. Morphological, biological and phylogenetic diversity of complex is presented. The morphological traits and mycotoxicological properties of *Fusarium* species in with respect to their phylogeny are summarised.

To fully explain the existence and biological significance of the clades of the GFC, it will be necessary to study *Fusarium* species in their natural or indigenous habitats. The sampling in such areas will certainly reveal numerous new species which will improve the phylogenetic resolution of the GFC. Such studies will allow rejection, modification or the eventual acceptance of the biogeographic hypothesis and will further help in clarifying the role of the host in the evolution of *Fusarium* species. As the utility of genomes becomes easily available, comparative and phylogenomic approaches will aid us in better understanding the evolution of *Fusarium* species within the GFC.