

PR1.8

Variation in sequence and location of the fumonisin mycotoxin biosynthetic gene cluster in *Fusarium*

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Several *Fusarium* species in the *Gibberella fujikuroi* species complex (GFSC) and rare strains of *F. oxysporum* can produce fumonisins, a family of mycotoxins associated with multiple health disorders in humans and animals. In *Fusarium*, the ability to produce fumonisins is governed by a 17-gene fumonisin biosynthetic gene (*FUM*) cluster. Here, we examined the cluster in *F. oxysporum* strain O-1890 and nine other species (e.g. *F. proliferatum* and *F. verticillioides*) selected to represent a wide range of the genetic diversity within the GFSC. Flanking-gene analysis revealed that the *FUM* cluster can be located in one of four genetic environments. Comparison of the genetic environments with a housekeeping gene-based species phylogeny revealed that *FUM* cluster location is correlated with the phylogenetic relationships of species; the cluster is in the same genetic environment in more closely related species and different environments in more distantly related species. Additional analyses revealed that sequence polymorphism in the *FUM* cluster is not correlated with phylogenetic relationships among some species. However, cluster polymorphism is associated with production of different classes of fumonisins in some species. As a result, closely related species can have markedly different *FUM* gene sequences and can produce different classes of fumonisins. The data indicate that the *FUM* cluster has moved within the *Fusarium* genome during evolution of the GFSC and further that sequence polymorphism was sometimes maintained during the movement such that clusters with markedly different sequences are now located in the same genetic environment.

PR1.9

Relationships among *Lasiodiplodia theobromae* isolates associated with tropical fruit plants inferred from the analysis of ITS and EF1- α gene

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Lasiodiplodia theobromae is a phytopathogenic fungus causing gummosis, a threatening disease for cashew plants in Brazil. A collection of isolates of *L. theobromae* obtained from cashew plants and also from others tropical fruit plants was studied on the basis of sequence data from the ITS regions and EF1- α gene. Sequence data and ITS-RFLP patterns indicate a substantial genetic variability among isolates from cashew plants showing symptoms of the disease and also from others tropical fruit plants, such as lemon, *Spondia* sp., passion fruit and graviola plants. However, no difference was found among *L. theobromae* isolates from symptomatic cashew plants and from symptomless cashew plants colonized by the fungus, indicating that possibly the same specie that endophytically colonize the cashew plants with no apparent symptoms is also responsible for the disease. Further studies based on detection of Single Nucleotide Polymorphisms are being carried out and have potential utility for detection of *L. theobromae* strains in cashew plant seedlings.