

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*

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 of 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 moved to the same genetic environment.