Mycokey

Lay summaries

Knowledge transfer to stakeholders

Integrated and innovative key actions for mycotoxin management in the food and feed chain



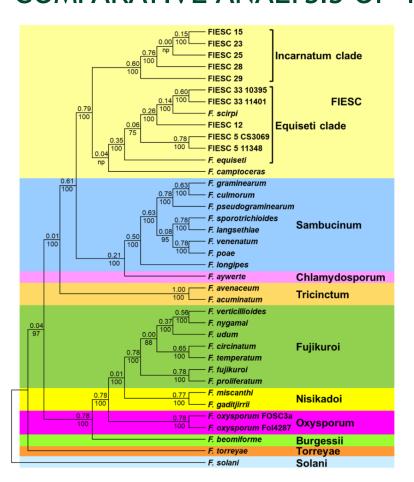








Variation in secondary metabolite Fusarium incarnatum-equiseti species complex production potential in FIESC revealed by COMPARATIVE ANALYSIS OF 13 GENOMES



ISSUE

FIESC consists of over 35 phylogenetically distinct species, which collectively have an almost ubiquitous distribution with respect to geography, climate and ecosystem. However, because the species diversity of FIESC has been recognized only recently, the potential of species to cause mycotoxin contamination of crop plants is unclear, and the evolutionary processes that have contributed to the diversity have not systematically explored yet.

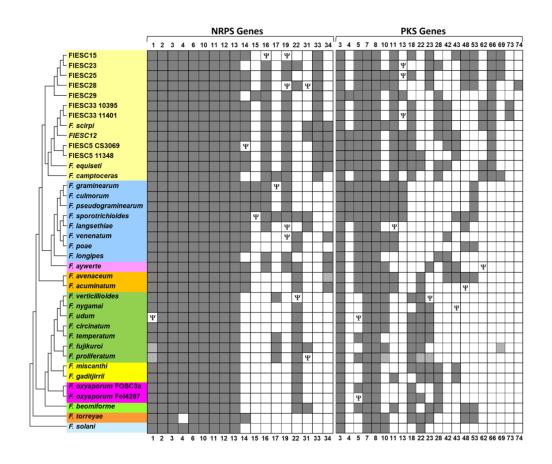


Comparative and evolutionary genomics

Fusarium incarnatum-equiseti species complex

APPROACH

Variation in secondary metabolite (SM) biosynthetic gene content in the FIESC was investigated through a whole genome sequencing approach focusing on the phylogenetic relationships of species, the identification and distribution within the complex of SM biosynthetic gene clusters, and phylogenetic analyses aimed to investigate the frequency with which vertical inheritance, gene loss, gene duplication, and horizontal transfer have contributed to distribution of SM biosynthetic genes within the complex.





Comparative and evolutionary genomics

Fusarium incarnatum-equiseti species complex

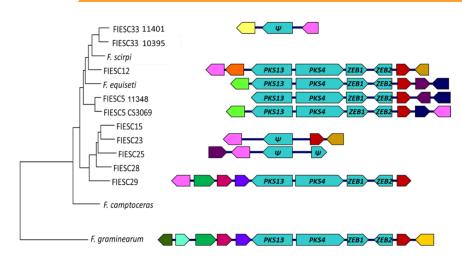
OUTCOMES

Vertical inheritance, gene loss, and HGT have likely contributed to the current distribution of SM biosynthetic genes in FIESC. All three processes have likely affected the distribution of some genes, while recent gene duplication events have not contributed to distribution of NRPS/PKS genes in FIESC.

Understanding which members of FIESC can produce which mycotoxins, may concretely impact growers response to fungal surveys in their fields, and support regulators to develop accurate assessments of the risks that members of FIESC pose to the food and feed supply.

Villani A, Proctor RH, Brown DW, Kim H-S, Logrieco AF, Amatulli MT, Moretti A, Susca A. 2019. BMC Genomics.

DOI: 10.1186/s12864-019-5567-7



			Evidence for HGT				
			Manual Tree				
Gene	Donor	Recipient	Comparison	Bootstrap	NOTUNG	SH-AU	d _S
NRPS4	Tricinctum complex	FIESC (Incarnatum clade)	+	100	+	+	+
NRPS11	Sambucinum complex (or close relative)	FIESC	-	-	+	-	-
NRPS14	Sambucinum complex (or close relative)	FIESC	-	100	+	+	-
NRPS16	F. longipes (or close relative)	FIESC	+	77	+	-	±
NRPS22	Fujikuroi complex (African clade)	FIESC (Incarnatum clade)	+	100	+	+	+
PKS10	Tricinctum complex	F. scirpi (or recent ancestor)	+	100	+	+	+
PKS10	Sambucinum complex	FIESC (Incarnatum clade)	+	100	+	+	-
PKS22	F. torreyae relative	FIESC (Equiseti clade)	-	100	+	+	-
PKS23	Fujikuroi complex	FIESC (Incarnatum clade)	+	100	+	+	+
PKS48	Tricinctum complex (F. avenaceum relative)	FIESC (Incarnatum clade)	+	100	+	+	-
PKS69	Fujikuroi complex	FIESC	+	90	NA	+	±

