



Thank to organizer committee

Re-classification of Fusarium species by taxonomy and phylogeny molecular using micro-sequences of DNA of orthologous genes.



Re-classification of *Fusarium* species by taxonomy and phylogeny molecular using micro-sequences of DNA of orthologous genes.

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Vs

GCTTCGGACTTCCGCAACGGTCGCTACCTGACCTGCT--CGGCCATTGTGAGTGA
GCTTCGGACTTCCGCAACGGTCGCTACCTGACCTGCT--CGGCCATTGTGAGTGA
GCTTCGGACTTCCGCAACGGTCGCTACCTGACCTGCT--CGGCCATTGTGAGTGA
GCTTCGGACTTCCGCAACGGTCGCTACCTGACCTGCT--CGGCCATTGTGAGTGA
GCTTCGGACTTCCGCAACGGTCGTTACCTGACCTGCT--CGGCCATTGTGAGTGA
GCCCTCCGACTTCCGCAACGGTCGTTACCTGACCTGCT--CTGCCATCTT-----
GCGTTCCAGAGCTGCCCCAGCAGATACTTGACCCCCAT--GGACCRAGATGGTGA
ATTTCAAAGATCCGCGAGGA--ATTCCCCGACCGAATGATGGCCACCTTCTCG
ATTTCAAAGATCCGCGAGGA--ATTCCCCGACCGAATGATGGCCACCTTCTCG
GCTAACCAAATCGGTGCTTCTGGCAGACCCATCTC-TGGCGAGCATGGCCTCGA
GCTAACCAAATCGGTGCTTCTGGCAGACCCATCTC-TGGCGAGCATGGTCTCGA
GCTAACCAAATCGGTGCTTCTGGCAGACCCATCTC-TGGCGAGCATGGCCTCGA



My plant has
Fusarium

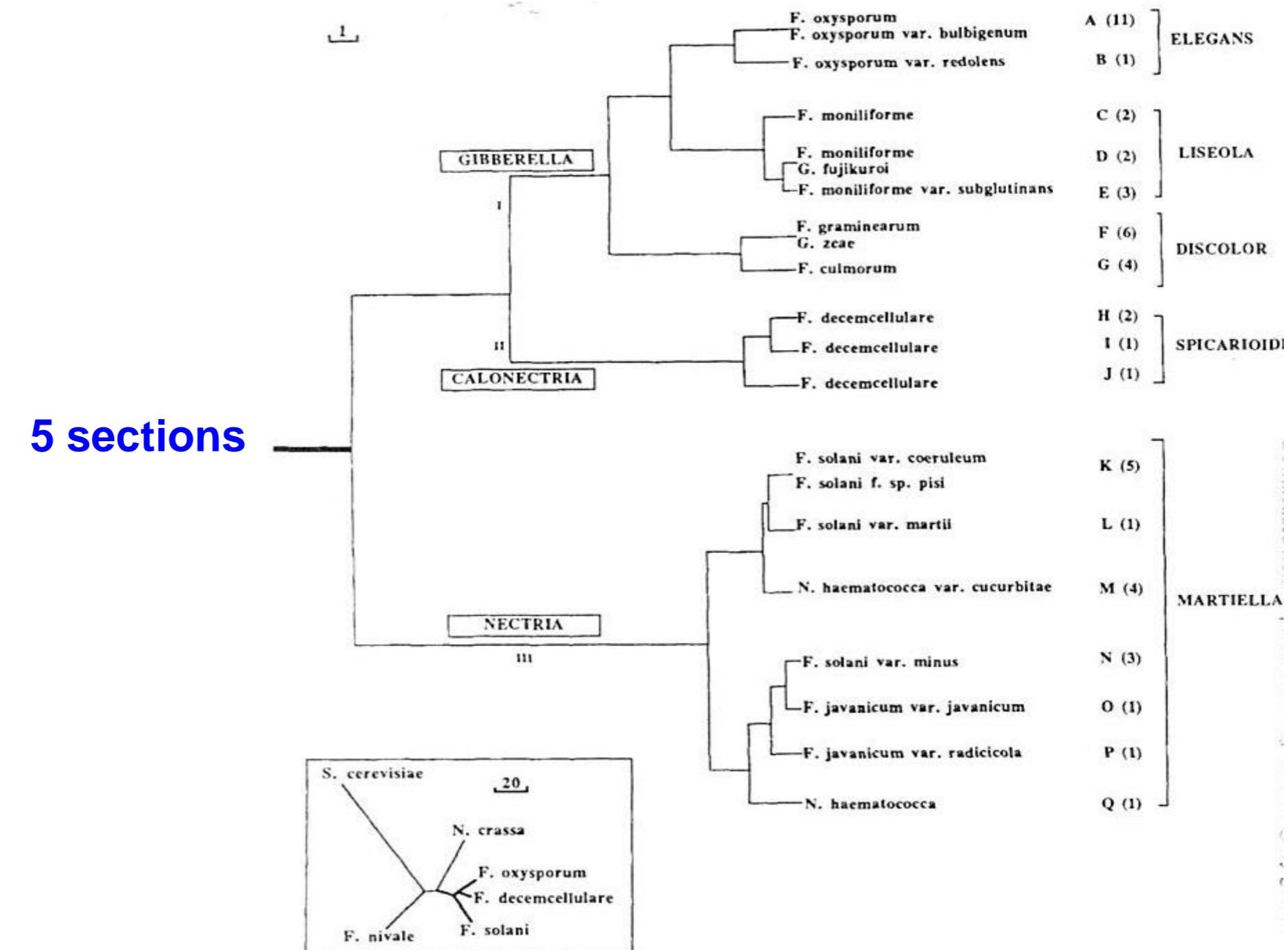
Which ones?



The plant pathologist and mycologist are confronted continually with the problem of identifying the widely distributed members of the genus *Fusarium*, so frequently associated with the disorders of plants.

Some of History

- 1809: Link create the genus *Fusarium*
- 1910: Appel and Wollenweber grouped all the perfect fungi in the family Tubulariaceae, macroconidia with the croissant shape
- 1935: 16 sections and 65 species (Wollenweber and Reinking)
- 1940: only 10 species (Snyder and Hansen)
- 1971: C. Booth recognize 44 species
- 1982 Gerlach and Niremberg recognize 73 species and 23 varieties
- 1983: Nelson & et.al. only 30 species
- 2006: Leslie and Summerell recognize 70 species
- 2011: Watanabe more than 1000 species
- 2017: 1200 species

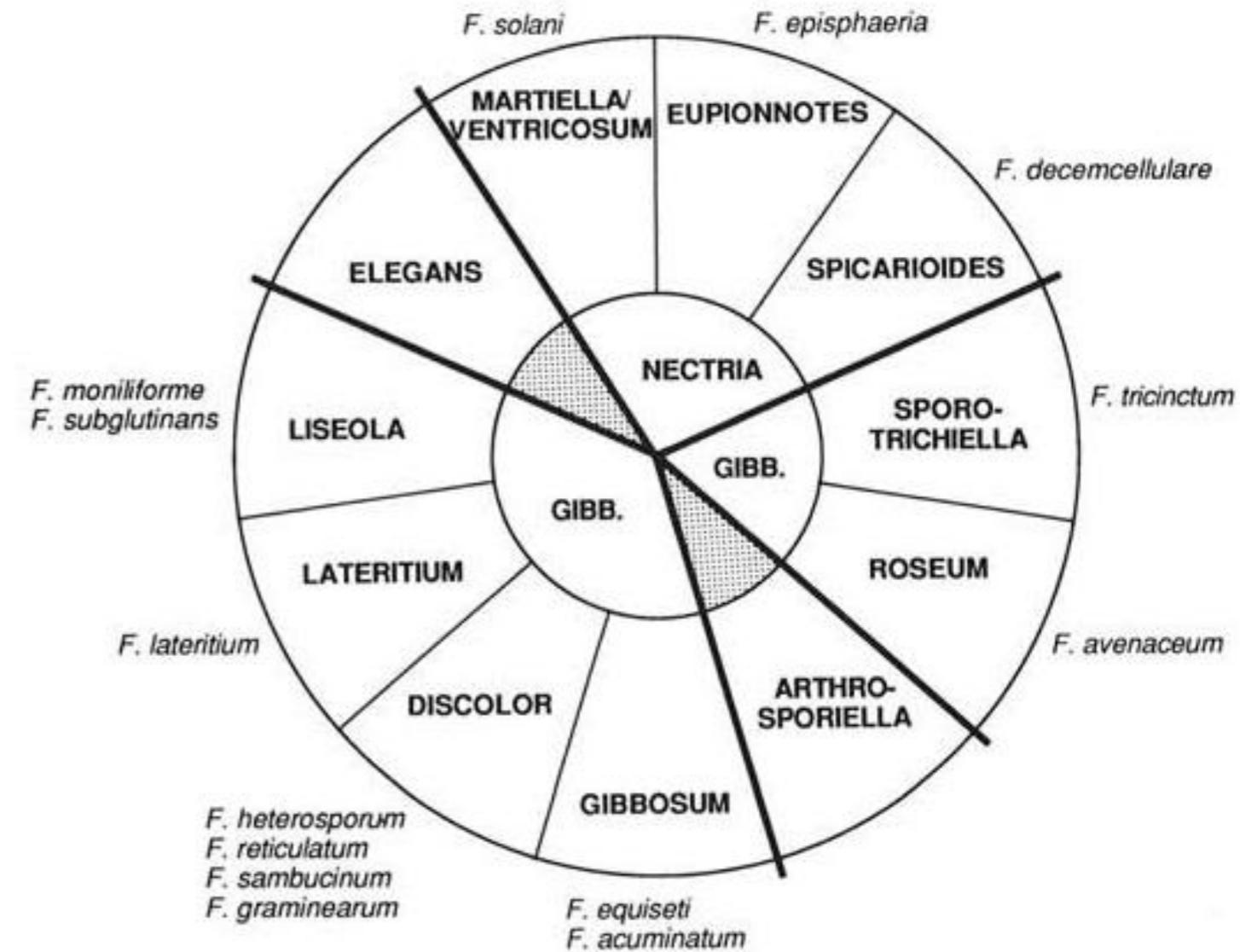




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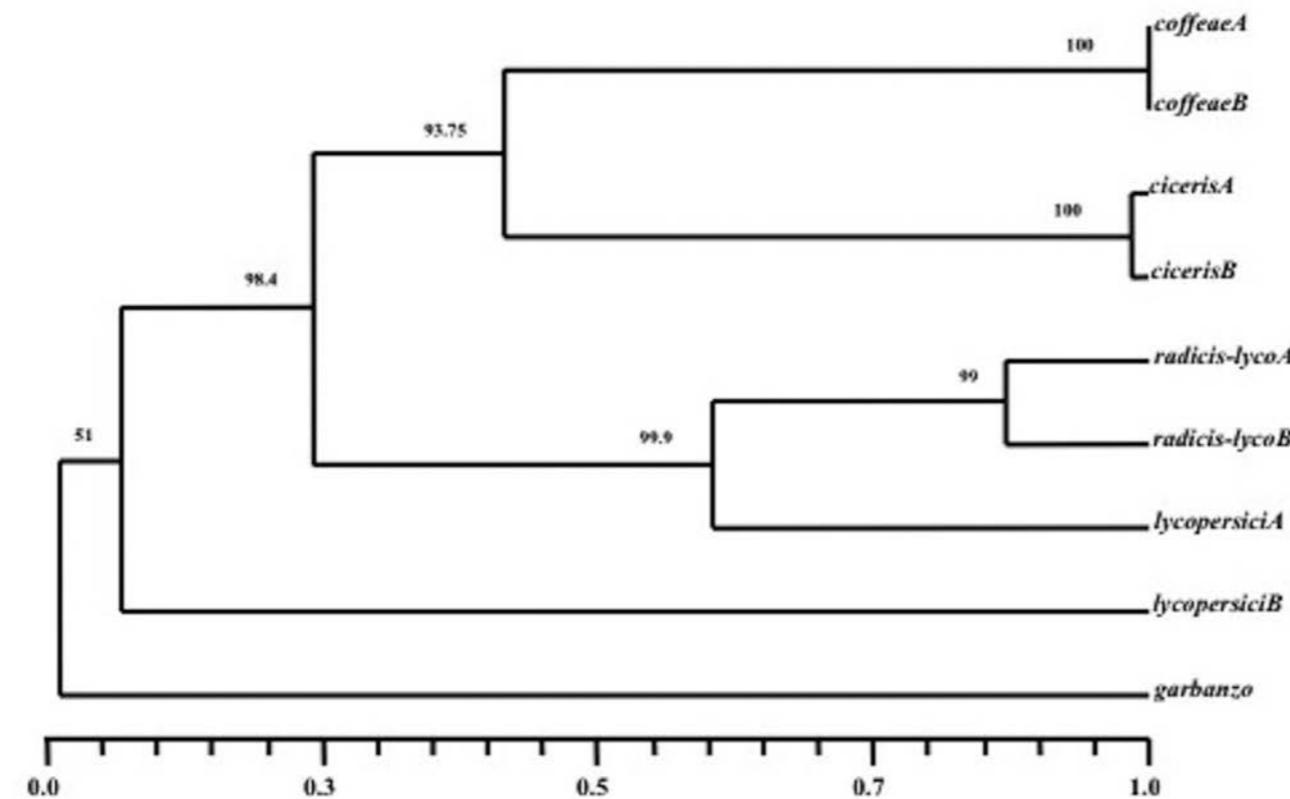
13 sections

- *Arachnites*
- *Arthrosporiella*
- *Discolour*
- *Elegans*
- *Eupionnotes*
- *Gibbosum*
- *Lateritium*
- *Liseola*
- *Martiella*
- *Ventricosum*
- *Roseum*
- *Spicarioides*
- *Sporotrichiella*





- *Fusarium acaciae*^[1]
 - *Fusarium acaciae-mearnsii*^[1]
 - *Fusarium acicola*^[1]
 - *Fusarium acremoniopsis*^[1]
 - *Fusarium acridiorum*^[1]
 - *Fusarium acutatum*^[1]
 - *Fusarium aderholdii*^[1]
 - *Fusarium adesmiae*^[1]
 - *Fusarium aduncisporum*^[1]
 - *Fusarium aecidi-tussilaginis*^[1]
 - *Fusarium aeruginosum*^[1]
 - *Fusarium aethiopicum*^[1]
 - *Fusarium affine*^[1]
 - *Fusarium agaricorum*^[1]
 - *Fusarium ailanthinum*^[1]
 - *Fusarium alabamense*^[1]
 - *Fusarium albedinis*^[1]
 - *Fusarium albertii*^[1]
 - *Fusarium albidoviolaceum*^[1]
 - *Fusarium albiziae*^[1]
 - *Fusarium albocarneum*^[1]
 - *Fusarium album*^[1]
 - *Fusarium aleurinum*^[1]
 - *Fusarium aleyrodis*^[1]
 - *Fusarium alkanophilum*^[1]
 - *Fusarium allescheri*^[1]
 - *Fusarium allescherianum*^[1]
 - *Fusarium allii-sativi*^[1]
 - *Fusarium alluviale*^[1]
 - *Fusarium aloës*^[1]
 - *Fusarium ambrosium*^[1]
 - *Fusarium amenti*^[1]
 - *Fusarium amentorum*^[1]
 - *Fusarium amethysteum*^[1]
 - *Fusarium ampelodesmii*^[1]
 - *Fusarium andinum*^[1]
 - *Fusarium andiyazi*^[1]
 - *Fusarium andropogonis*^[1]
 - *Fusarium anguoides*^[1]
 - *Fusarium angustum*^[1]
 - *Fusarium anisophilum*^[1]
 - *Fusarium annulatum*^[1]
 - *Fusarium annum*^[1]
 - *Fusarium anomalum*^[1]
 - *Fusarium anthophilum*^[1]
 - *Fusarium apii*^[1]
 - *Fusarium apio-genum*^[1]
 - *Fusarium*^[1]
 - *Fusarium armeniacum*^[1]
 - *Fusarium arthrosporioides*^[1]
 - *Fusarium arundinis*^[1]
 - *Fusarium arvense*^[1]
 - *Fusarium asclepiadeum*^[1]
 - *Fusarium asclerotium*^[1]
 - *Fusarium asiaticum*^[1]
 - *Fusarium asparagi*^[1]
 - *Fusarium asperifoliorum*^[1]
 - *Fusarium aspidioti*^[1]
 - *Fusarium atrovirens*^[1]
 - *Fusarium audinum*^[1]
 - *Fusarium aurantiacum*^[1]
 - *Fusarium aurantiacum*^[1]
 - *Fusarium candidulum*^[1]
 - *Fusarium candidum*^[1]
 - *Fusarium cactacearum*^[1]
 - *Fusarium cacti-maxoni*^[1]
 - *Fusarium asparagi*^[1]
 - *Fusarium calcaratum*^[1]
 - *Fusarium calidariorum*^[1]
 - *Fusarium callosporum*^[1]
 - *Fusarium camerunense*^[1]
 - *Fusarium audinum*^[1]
 - *Fusarium campyloceras*^[1]
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 - *Fusarium carniformis*^[1]
 - *Fusarium carpineum*^[1]
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 - *Fusarium castagneti*^[1]
 - *Fusarium castaneicola*^[1]
 - *Fusarium capitatum*^[1]
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 - *Fusarium carneolum*^[1]
 - *Fusarium catenulatum*^[1]
 - *Fusarium caucasicum*^[1]
 - *Fusarium caudatum*^[1]
 - *Fusarium cavispermum*^[1]
 - *Fusarium celosiae*^[1]
 - *Fusarium celtidis*^[1]
 - *Fusarium cepae*^[1]
 - *Fusarium cerasi*^[1]
 - *Fusarium cydoniae*^[1]
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 - *Fusarium apio-genum*^[1]
 - *Fusarium brasiliense*^[1]
 - *Fusarium biseptatum*^[1]
 - *Fusarium brassicae*^[1]
 - *Fusarium brevicatenulatum*^[1]
 - *Fusarium briosianum*^[1]
 - *Fusarium bubl*^[1]
 - *Fusarium bufonicolae*^[1]
 - *Fusarium bugnoutii*^[1]
 - *Fusarium buharicum*^[1]
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 - *Fusarium eucaalypticola*^[1]
 - *Fusarium eucommiae*^[1]
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 - *Fusarium expansum*^[1]
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 - *Fusarium falciforme*^[1]
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 - *Fusarium ferruginosum*^[1]
 - *Fusarium fiji-kuroi*^[1]
 - *Fusarium filiferum*^[1]
 - *Fusarium filisporum*^[1]
 - *Fusarium fissum*^[1]
 - *Fusarium flavidum*^[1]
 - *Fusarium flavum*^[1]
 - *Fusarium flocciferum*^[1]
 - *Fusarium foeni*^[1]
 - *Fusarium foetens*^[1]
 - *Fusarium foliicola*^[1]
 - *Fusarium fractiflexum*^[1]
 - *Fusarium fractum*^[1]
 - *Fusarium fragrans*^[1]
 - *Fusarium dianthi*^[1]
 - *Fusarium didymum*^[1]
 - *Fusarium diffusum*^[1]
 - *Fusarium dimerum*^[1]
 - *Fusarium dimorphum*^[1]
 - *Fusarium diplasporum*^[1]
 - *Fusarium discoideum*^[1]
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 - *Fusarium diversisporum*^[1]
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 - *Fusarium enterolobii*^[1]
 - *Fusarium entomophilum*^[1]
 - *Fusarium epicoccum*^[1]
 - *Fusarium gallinae*^[1]
 - *Fusarium gaudichaudii*^[1]
 - *Fusarium globosum*^[1]
 - *Fusarium globulosum*^[1]
 - *Fusarium gloeosporioides*^[1]
 - *Fusarium gloeosporioides*^[1]
 - *Fusarium glumarum*^[1]
 - *Fusarium gracile*^[1]
 - *Fusarium graminearum*^[1]
 - *Fusarium graminum*^[1]
 - *Fusarium granulare*^[1]
 - *Fusarium granulosum*^[1]
 - *Fusarium guttiforme*^[1]
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 - *Fusarium gyneri*^[1]
 - *Fusarium hakeae*^[1]
 - *Fusarium heidelbergense*^[1]
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 - *Fusarium heterosporum*^[1]
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 - *Fusarium hordearium*^[1]
 - *Fusarium hordei*^[1]
 - *Fusarium hostae*^[1]
 - *Fusarium hydnicae*^[1]
 - *Fusarium hymenula*^[1]
 - *Fusarium hyperoxysporum*^[1]
 - *Fusarium hypocreoides*^[1]
 - *Fusarium idahoanum*^[1]
 - *Fusarium illosporioides*^[1]
 - *Fusarium illudens*^[1]
 - *Fusarium inaequale*^[1]
 - *Fusarium incarcerans*^[1]
 - *Fusarium incarnatum*^[1]
 - *Fusarium inflexum*^[1]
 - *Fusarium inexpectatum*^[1]
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 - *Fusarium iridis*^[1]
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 - *Fusarium limosum*^[1]
 - *Fusarium linearis*^[1]
 - *Fusarium linii*^[1]
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 - *Fusarium longipes*^[1]
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 - *Fusarium longissimum*^[1]
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 - *Fusarium lunulosporum*^[1]
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 - *Fusarium oidioides*^[1]
 - *Fusarium opuli*^[1]
 - *Fusarium opuntiarum*^[1]
 - *Fusarium orchidis*^[1]
 - *Fusarium orobanches*^[1]
 - *Fusarium orthoceras*^[1]
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 - *Fusarium orthoconium*^[1]
 - *Fusarium orthosporum*^[1]
 - *Fusarium oryzae*^[1]
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 - *Fusarium otomycosis*^[1]
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 - *Fusarium oxysporum*^[1]
 - *Fusarium oxysporum*^[1]
 - *Fusarium palczewskii*^[1]
 - *Fusarium pallens*^[1]
 - *Fusarium pallidoroseum*^[1]
 - *Fusarium pallidulum*^[1]
 - *Fusarium pallidum*^[1]
 - *Fusarium pampini*^[1]
 - *Fusarium pandani*^[1]
 - *Fusarium pannosum*^[1]
 - *Fusarium parasiticum*^[1]
 - *Fusarium parasiton*^[1]
 - *Fusarium paspalum*^[1]
 - *Fusarium paspalicola*^[1]
 - *Fusarium mikaniae*^[1]



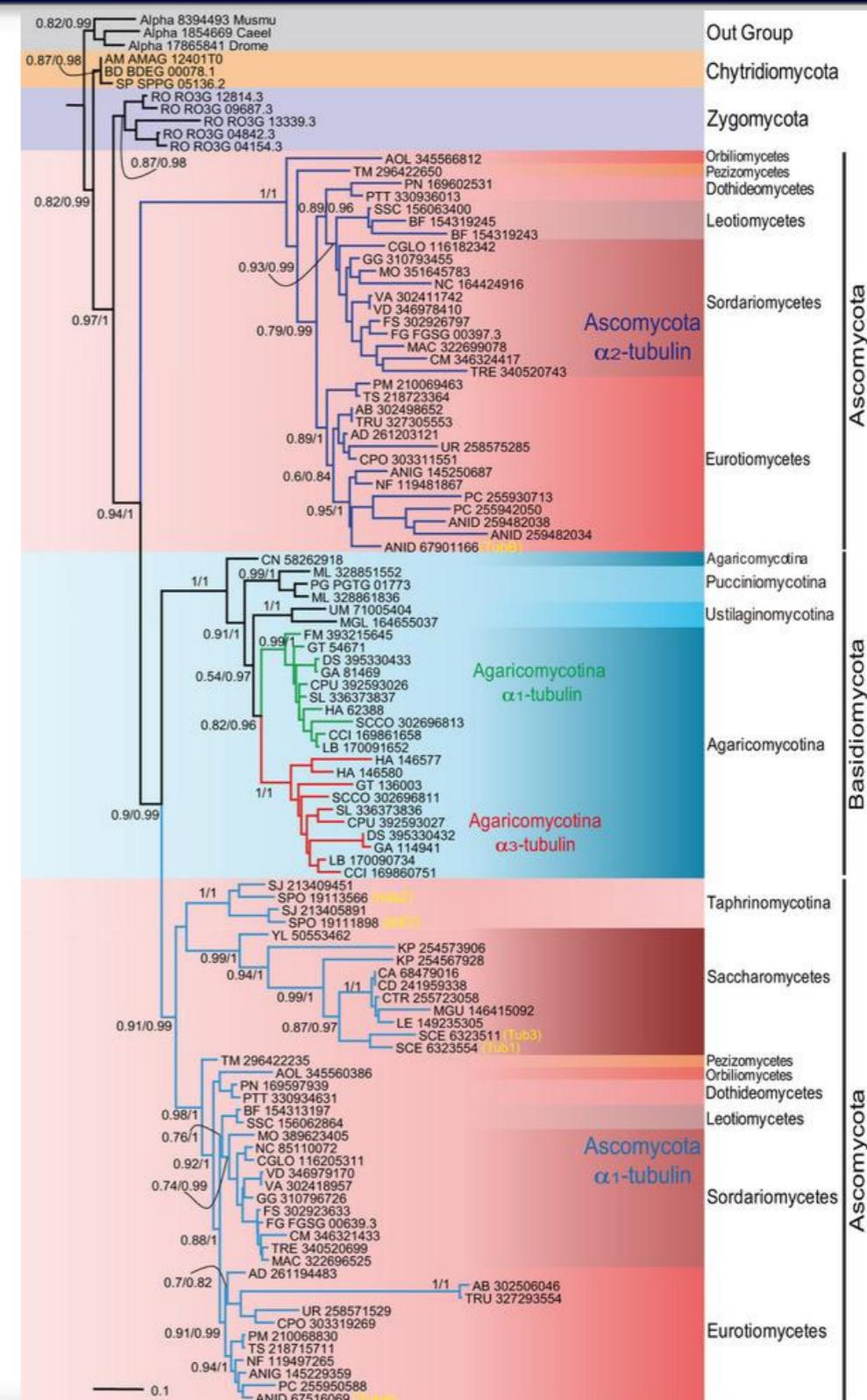
- Genus
- Subgenera
- Species
- f.sp.
- Races
- Isolates



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Molecular evolution and functional divergence of tubulin superfamily in the fungal tree of life, 2012.

•Zhongtao Zhao, Huiquan Liu, Yongping Luo, Shanyue Zhou, Lin An, Chenfang Wang, Qiaojun Jin, Mingguo Zhou & Jin-Rong Xu





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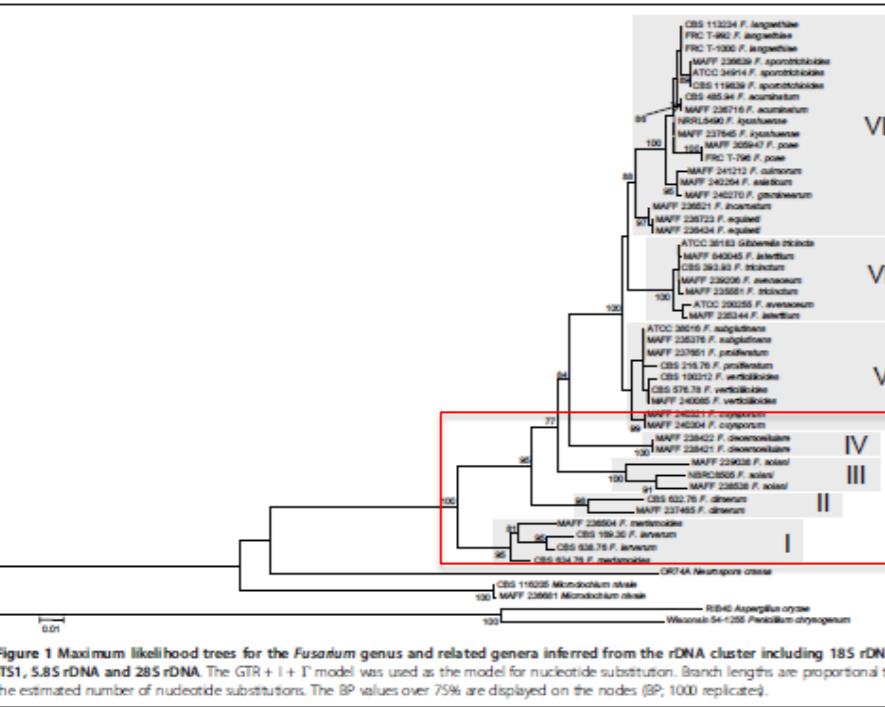


Figure 1 Maximum likelihood trees for the *Fusarium* genus and related genera inferred from the rDNA cluster including 18S rDNA, ITS1, 5.8S rDNA and 28S rDNA. The GTR + I + T model was used as the model for nucleotide substitution. Branch lengths are proportional to the estimated number of nucleotide substitutions. The BP values over 75% are displayed on the nodes (BP; 1000 replicates).

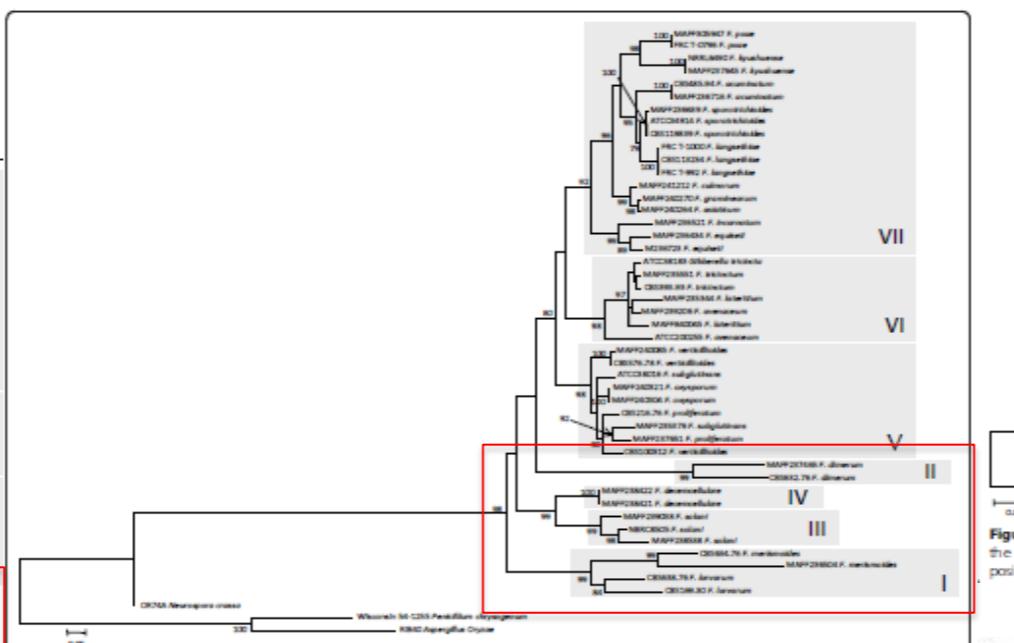


Figure 3 Maximum likelihood trees for the *Fusarium* genus and related genera inferred from EF-1 α . The GTR + I + T model was used as the model for nucleotide substitution. Branch lengths are proportional to the estimated number of nucleotide substitutions. Each codon position was analysed separately. The BP values over 75% are displayed on the nodes (BP; 1000 replicates).

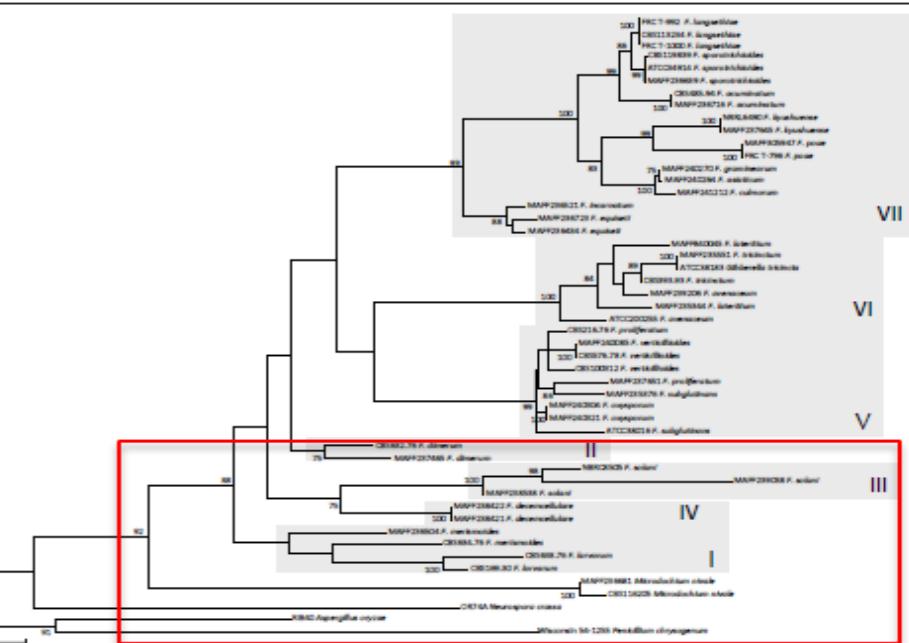


Figure 2 Maximum likelihood trees for the *Fusarium* genus and related genera inferred from β -tub. The GTR + I + T model was used as the model for nucleotide substitution. Branch lengths are proportional to the estimated number of nucleotide substitutions. Each codon position was analysed separately. The BP values over 75% are displayed on the nodes (BP; 1000 replicates).

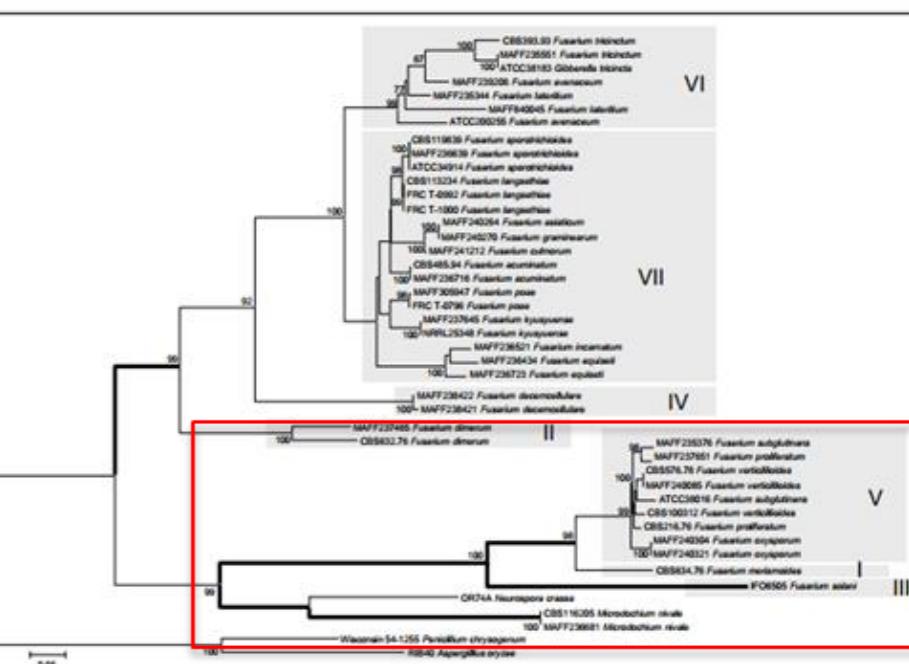


Figure 4 Maximum likelihood trees for the *Fusarium* genus and related genera inferred from lys2. The GTR + I + T model was used as the model for nucleotide substitution. Branch lengths are proportional to the estimated number of nucleotide substitutions. Each codon position was analysed separately. The BP values over 75% are displayed on the nodes (BP; 1000 replicates). The branches with bold lines indicate the lineages in which positive selection has occurred with the p-value under the null hypothesis that the ω (synonymous substitutions per synonymous site/non-synonymous substitutions per non-synonymous site) of the positively selected sites is equal to 1.0. ($p < 0.001$).

Molecular phylogeny of the higher and lower taxonomy of the *Fusarium* genus and differences in the evolutionary histories of multiple genes

Maiko Watanabe¹*, Takahiro Yonezawa², Ken-ichi Lee³, Susumu Kumagai³, Yoshiko Sugita-Konishi¹, Keiichi Goto⁴ and Yukiko Hara-Kudo¹ BMC Evolutionary Biology 2011, 11:322.

F. oxysporum



F. verticillioides



Filgueira, J.J., Quinche, C.G., y Soto, J.C.: 2007. ¿Es el Fusarium verticillioides responsable del decaimiento de la variedad Nelson en la Sabana de Bogota?. Asocolflores. No 69. p51-54.

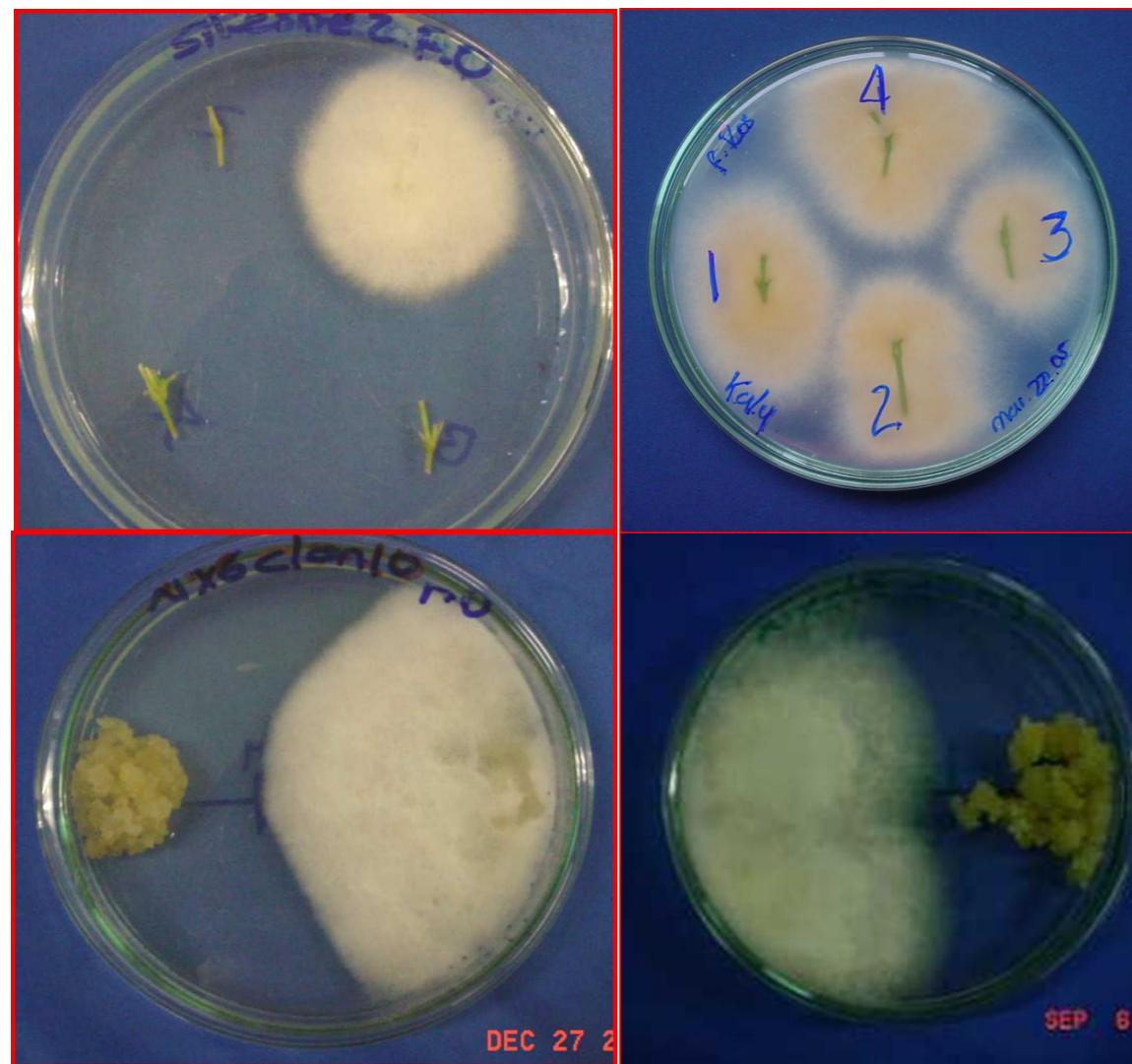


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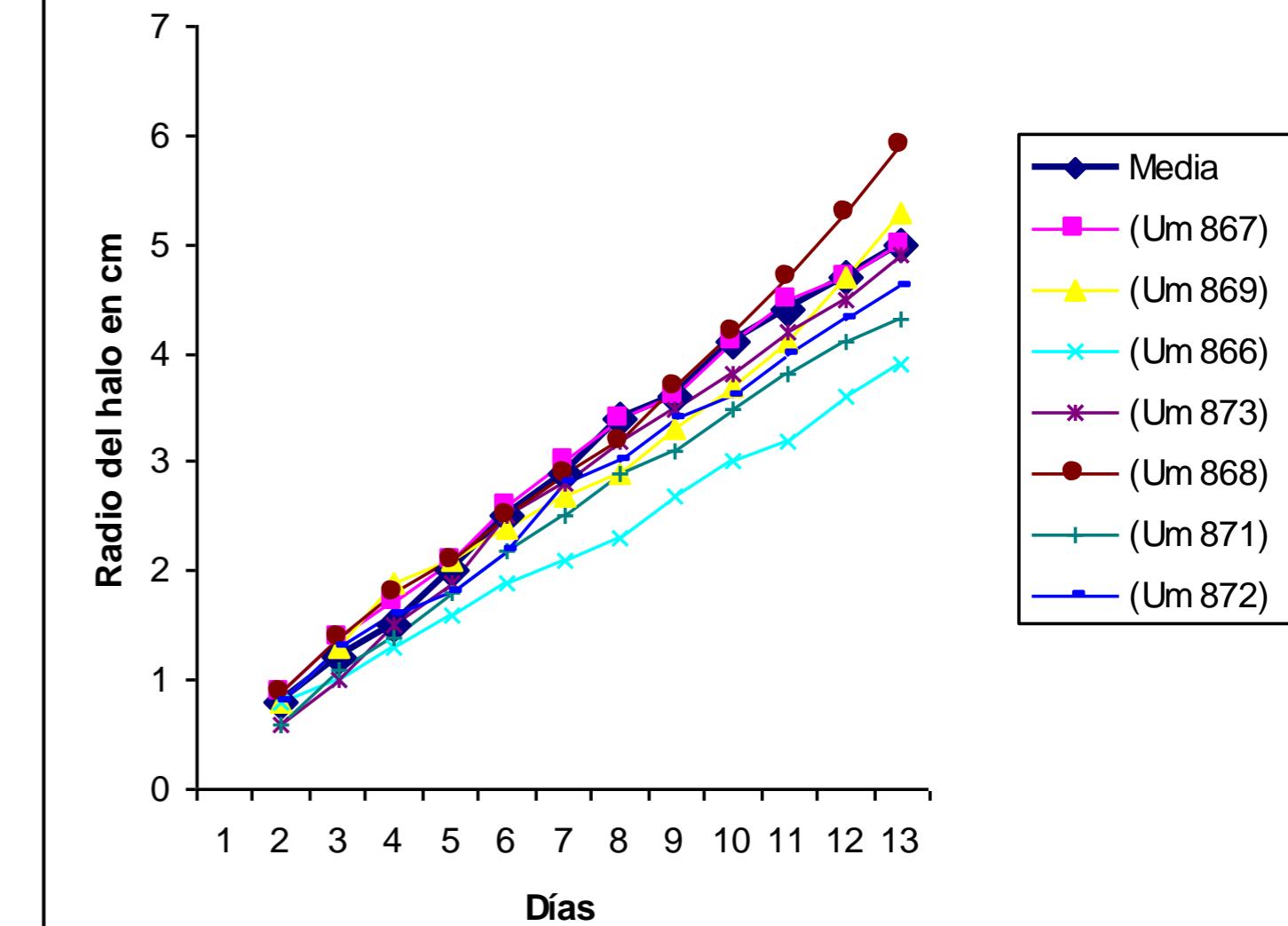
F. verticillioides - CARNATION INTERACTION IN COLOMBIA

Quinche C.Y., Soto J.C., Pabón F. and Filgueira J.J.*

Department of Science, Biotechnology Laboratory, Military University "Nueva Granada",
Bogotá - Colombia * jfilgdu@umng.edu.co



Resultado ensayo dual callos de los clones de la linea híbrida 8 frente a *Fusarium verticillioides*



ESTUDIO DE *Fusarium foetens* ASOCIADO A LA PUDRICIÓN BASAL EN CLAVEL (*Dianthus caryophyllus L.*) VARIEDAD NELSON

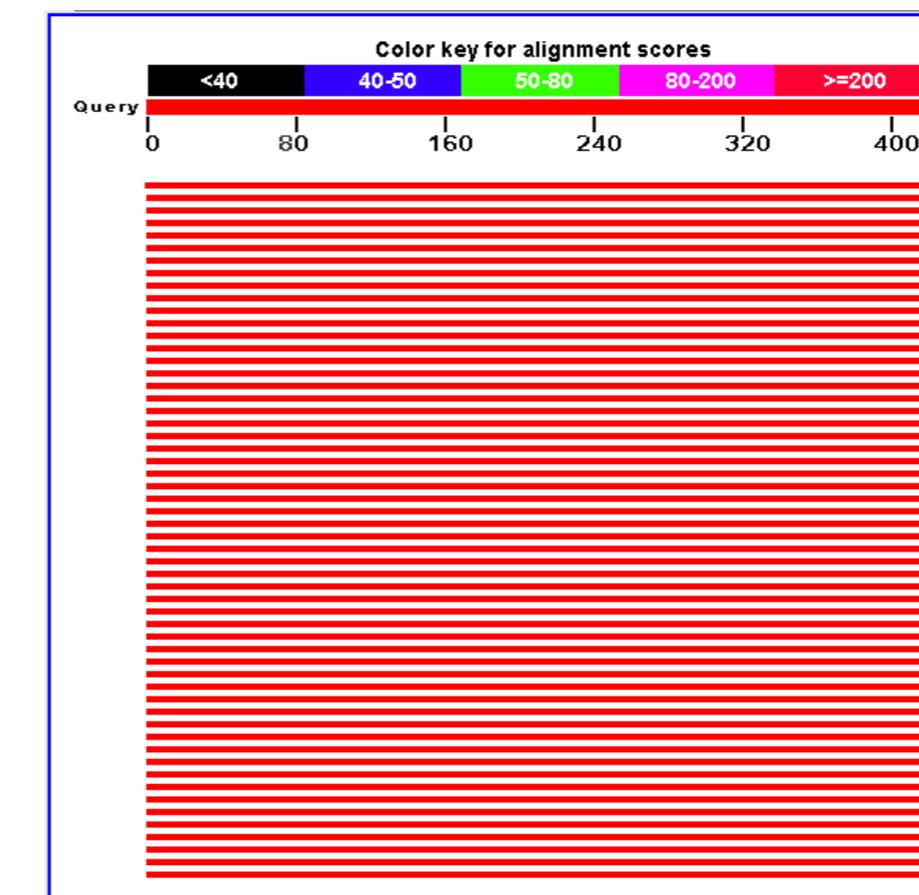
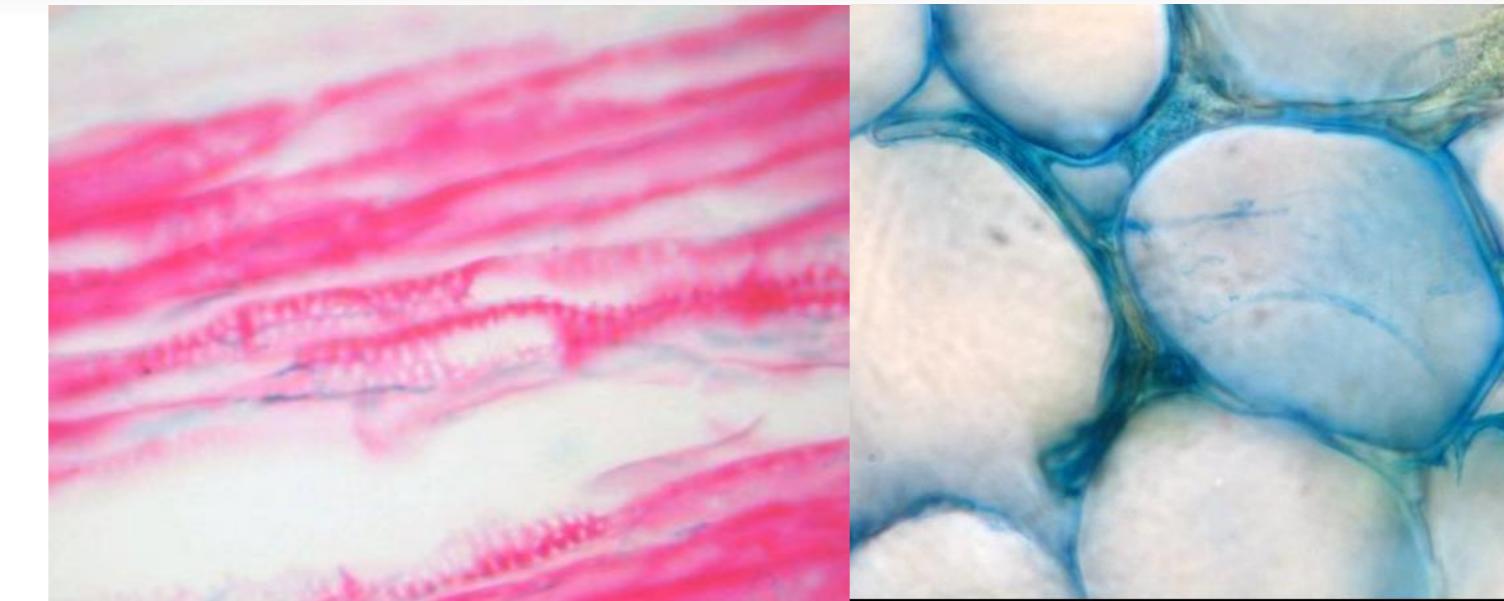
BURAGLIA OSORIO, Guillermo Andrés- FILGUEIRA DUARTE, Juan Jose

Grupo de Fitopatología Molecular, Universidad Militar Nueva Granada – Colombia

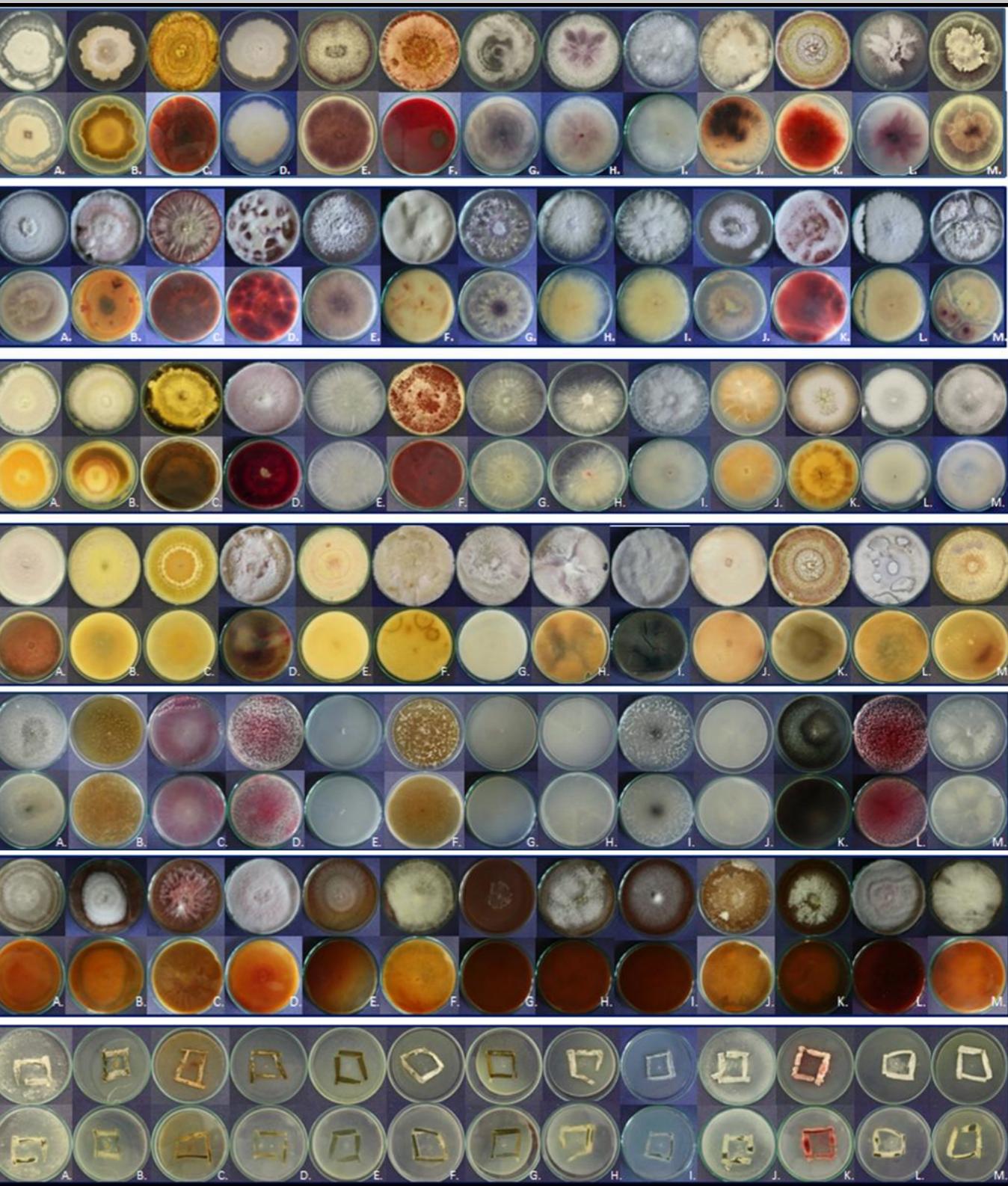
muin24@g...



du.co



13 Fusarium Species 7 different culture media



Uso de microsecuencias de genes útiles para hacer filogenia molecular para resolver problemas de clasificación taxonómica en el género *Fusarium*. Cindy Melissa Rincón. Universidad Nacional de Colombia. Maestría en Microbiología, Bogotá Colombia.



MACROCONIDIA

MICROCONIDIA

ID. No.

Forma

Apical

Pie

Forma

Fialide

Clamidosporas

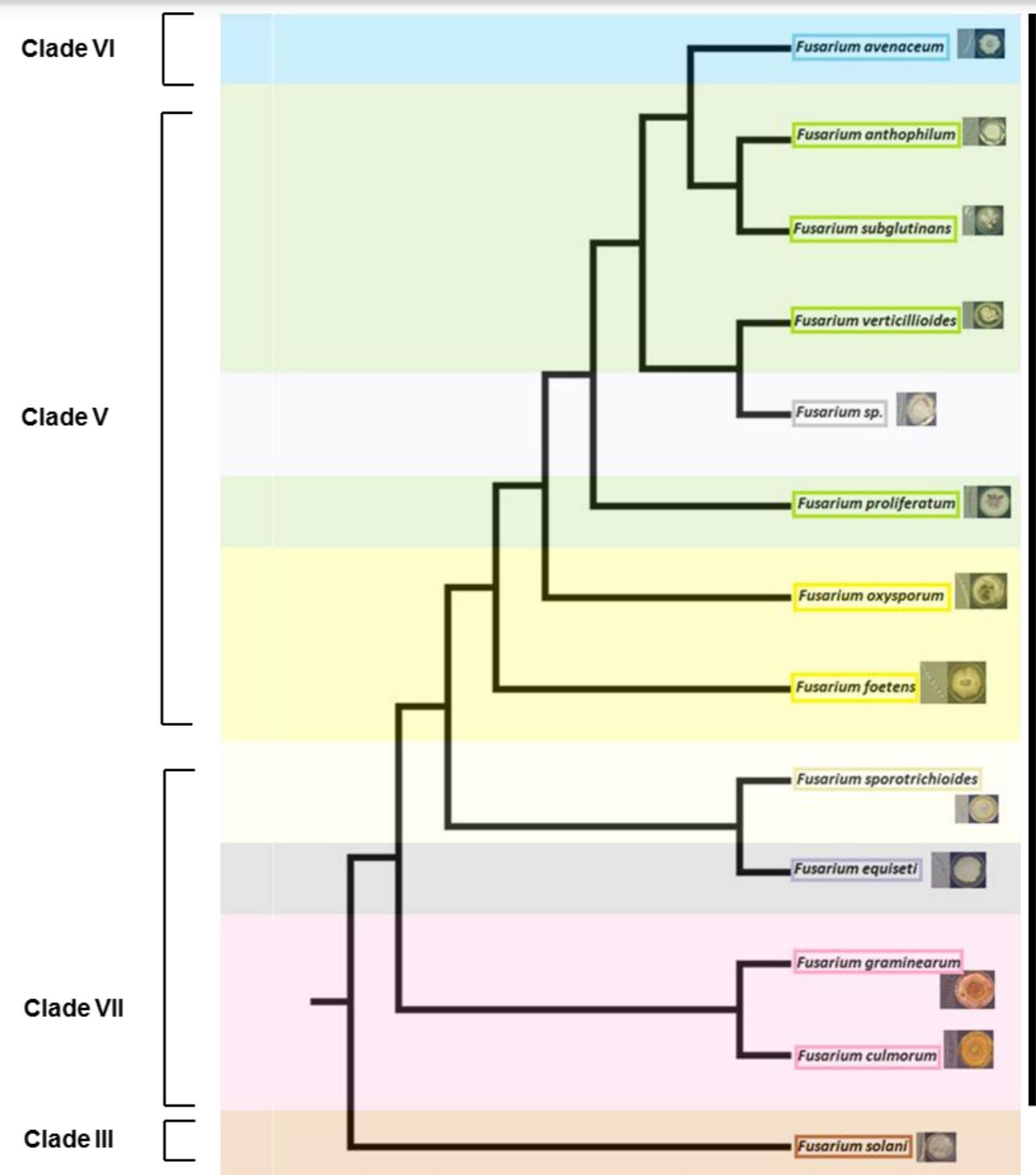
<i>Fusarium anthophilum</i>	delgadas, poca curvatura, pared delgada	Curvada	Definido	piriforme, globosa, ovoide	si	no
<i>Fusarium avenaceum</i>	largas y delgadas	Larga	con una muesca	fusoide	si	no
<i>Fusarium culmorum</i>	Robusta	redondeada y roma	no definido	ausente	no	si
<i>Fusarium equiseti</i>	largas y delgadas	ahusada y elongada	Elongado	elipsoidal	si	si
<i>Fusarium foetens</i>	Falcada	Curvada	Redondeado	ovoide, elipsoidal	si	si
<i>Fusarium graminearum</i>	delgadas, pared gruesa, longitud media	Hoz	Definido	ausente	no	si
<i>Fusarium oxysporum</i>	recta o levemente curvada, relativamente delgada	ahusada y curvada	Definido	ovoide, elipsoidal, arriñonada	si	si
<i>Fusarium proliferatum</i>	delgadas, relativamente rectas, pared delgada	Curvada	poco definido	claviforme	si	no
<i>Fusarium solani</i>	relativamente anchas, rectas, gruesas y robustas	redondeada y roma	Redondeado	ovoide, elipsoidal, fusiforme	si	si
<i>Fusarium sp.</i>	largas y delgadas	Curvada	Definido	ovaladas	no	no
<i>Fusarium sporotrichioides</i>	Luna	curvada y ahusada	con una muesca	piriforme, elipsoidal, ovoide	si	si
<i>Fusarium subglutinans</i>	relativamente delgadas, pared delgada	Curvada	poco definido	ovoide	si	no
<i>Fusarium verticillioides</i>	largas y delgadas	Curvada	Definido	ovaladas	no	no

Especie	Área (μm)	Perímetro (μm)	Longitud eje mayor (μm)	Longitud eje menor (μm)
<i>Fusarium anthophilum</i>	59	524	216,5	34,5
<i>Fusarium avenaceum</i>	156	982	329	60
<i>Fusarium culmorum</i>	204	953	377	69
<i>Fusarium equiseti</i>	96	860	277	44
<i>Fusarium foetens</i>	163	1216	411	51
<i>Fusarium graminearum</i>	184,7	970	364,7	64,7
<i>Fusarium oxysporum</i>	123	779,5	290,5	53,75
<i>Fusarium proliferatum</i>	81,3	646	272	38
<i>Fusarium solani</i>	109	687,5	272,5	51
<i>Fusarium sp.</i>	104,5	807	324	41,5
<i>Fusarium sporotrichioides</i>	-	-	-	-
<i>Fusarium subglutinans</i>	53	462,5	217	31
<i>Fusarium verticillioides</i>	101	911	363,5	36

**Character matrix built
with Mesquite software
V.2.5.**

Taxon \ Character	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Microcondia-absent	1	0	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Microcondia-absent	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Micro_chains-absent	1	0	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Micro_chains-absent	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Micro_heads-absent	1	0	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Micro_heads-absent	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Monophilia-absent	1	0	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Monophilia-absent	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Polyphilia-absent	1	0	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Polyphilia-absent	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Macrocondia-absent	1	0	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Macrocondia-absent	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Basal_cat-foot-shaped	1	0	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Basal_cat-foot-shaped	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
1-2_spatulae	1	0	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
1-2_spatulae	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
3-7_spatulae	1	0	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
3-7_spatulae	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Many_dospores-absent	1	0	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0
Many_dospores-absent	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	1	0

Dendrogram of the characters matrix using Mezquite



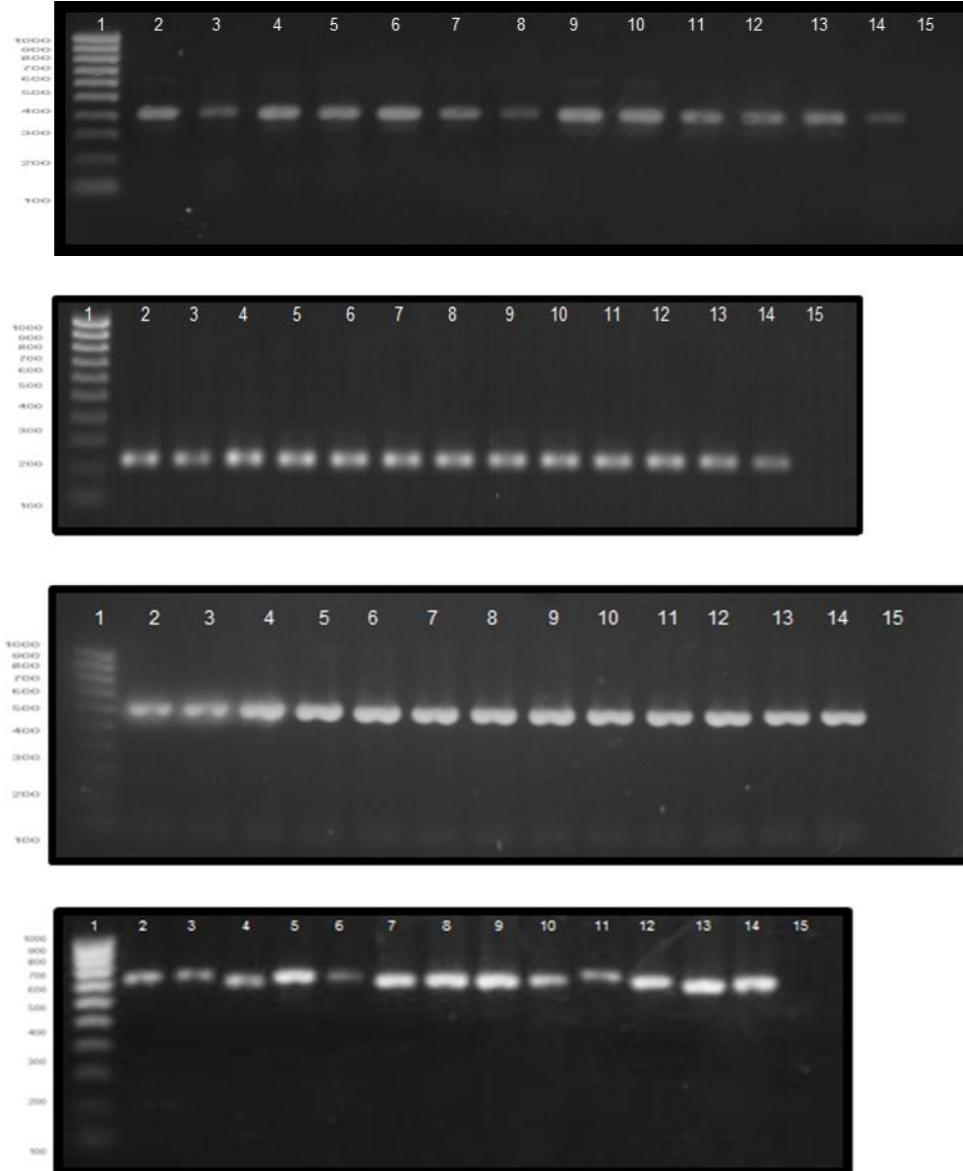
*

Gibberella clade

*

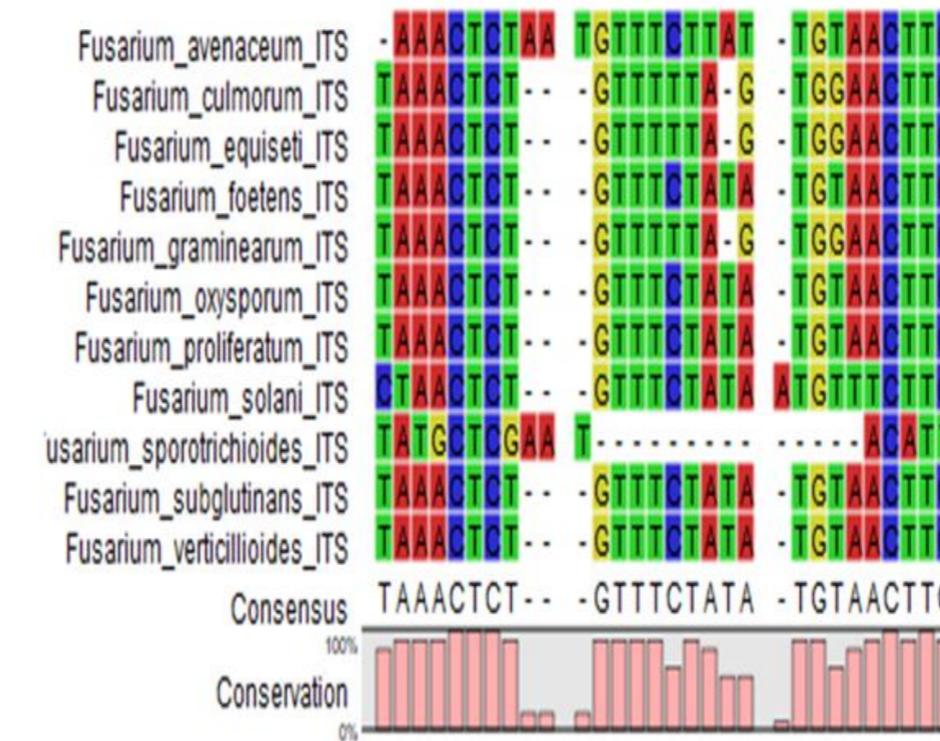
- What is *Fusarium*?
- Are *Nectria*, *Gibberella*, and *Fusarium* monophyletic?
- Are the sections natural?
- Can a phylogenetic species concept (PSC) be applied, and to what extend is it congruent with morphological and biological species concepts?
- Can sister group relationships of all taxa be resolved?
- How can the DNA database best be used to design molecular tools for the detection, and rapid and accurate identification of all species of *Fusarium*?

F. verticillioides – Aislamiento Sopo

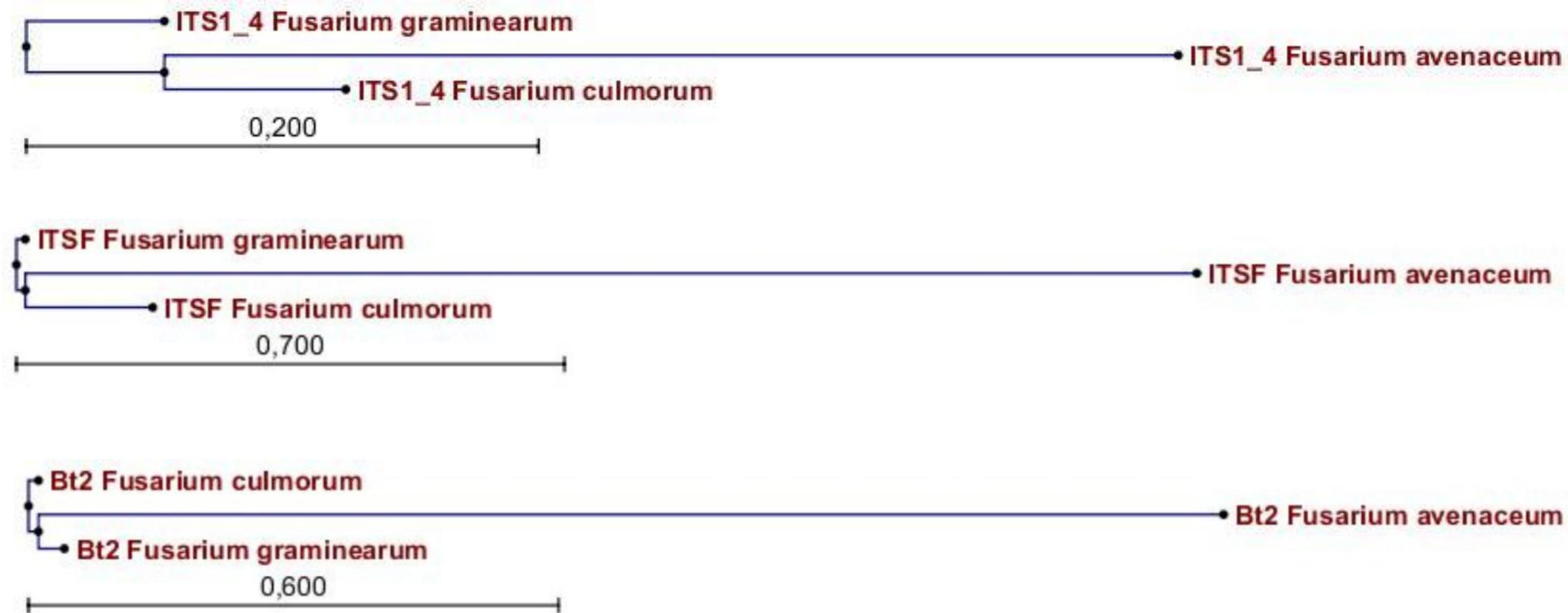


Sequences producing significant alignments:

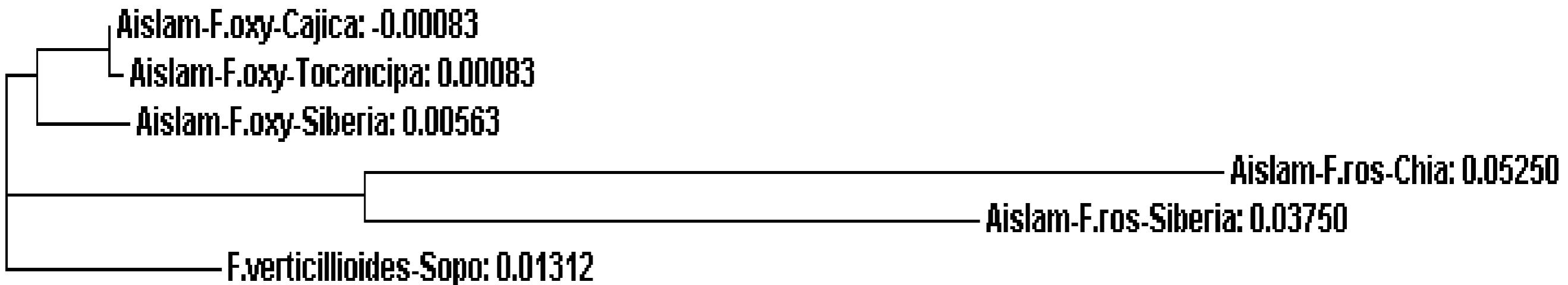
	Score (Bits)	E Value
gi 90855308 emb AM162679.1 	Uncultured Fusarium sp. 18S rRNA ...	696 0.0
gi 55793450 gb AY662326.1 	Gibberella moniliformis strain KSU...	696 0.0
gi 21666881 gb AF455450.1 	Gibberella sacchari isolate wb395 ...	696 0.0
gi 20531669 gb AF502862.1 	Leaf litter ascomycete strain its3...	696 0.0
gi 3320362 gb U61688.1 FSU61688	Fusarium sp. NRRL25195	696 0.0
gi 45479262 gb AY533376.1 	Gibberella moniliformis small subu...	696 0.0
gi 83272594 gb DQ297569.1 	Fusarium subglutinans isolate ZMS-...	696 0.0
gi 83272593 gb DQ297568.1 	Fusarium subglutinans isolate ZMS-...	696 0.0
gi 83272592 gb DQ297567.1 	Fusarium subglutinans isolate ZMS-...	696 0.0
gi 83272588 gb DQ297563.1 	Fusarium pseudonygamai isolate ZMS...	696 0.0



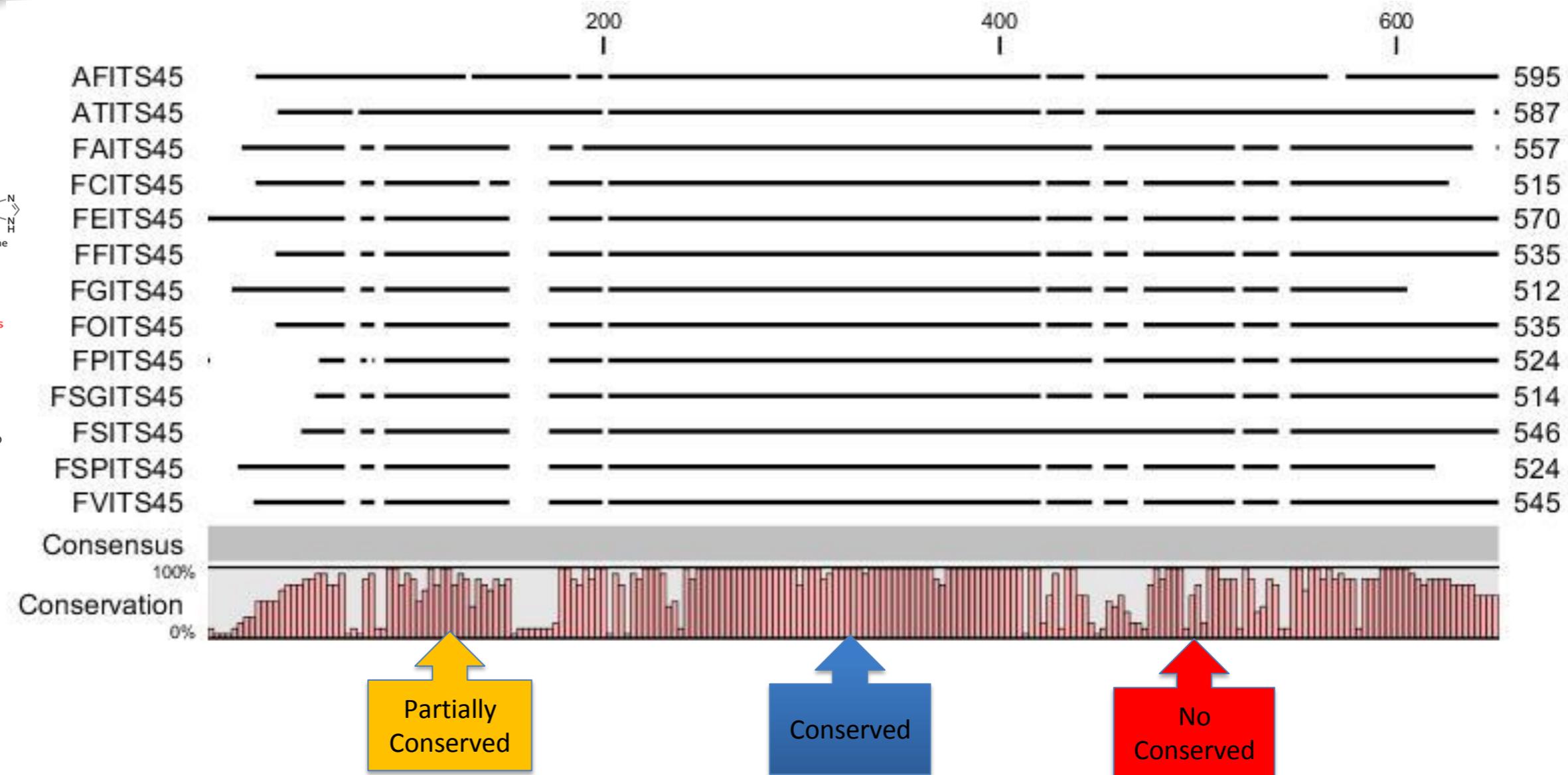
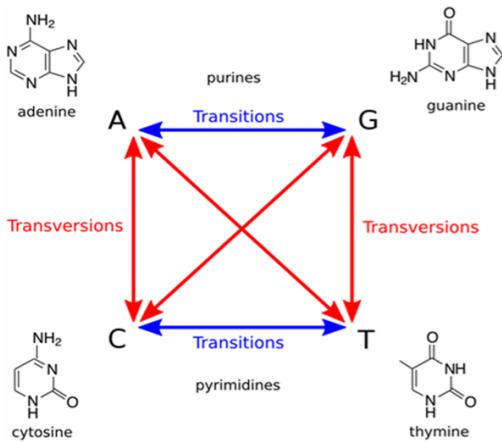
Genetic differences between regions of the same locus



Genetic variations between different FOX isolates in different farms



DNA Micro-Sequences Obtaining



Calculate the Sequence variation (Sv)

$$Sv = \frac{GAPs (0.5) + Tv (0.375) + Ti (0.125)}{(GAPs + Tv + Ti)}$$

Tv = Transversions Ti = Transitions

MicSeq

Select file

Select example.fa Calculate

Result

Microsequence	Initial position	Final position	Transitions	Transversions	Indels	Ci index
1	31	100	45	8	0	0.01760204...
2	154	166	10	10	0	0.05494505...
3	217	229	10	2	0	0.02197802...
4	235	289	37	7	0	0.01883116...
5	337	349	8	3	0	0.02335164...
6	355	383	14	8	0	0.02339901...

Export

Ci values Micro-sequences



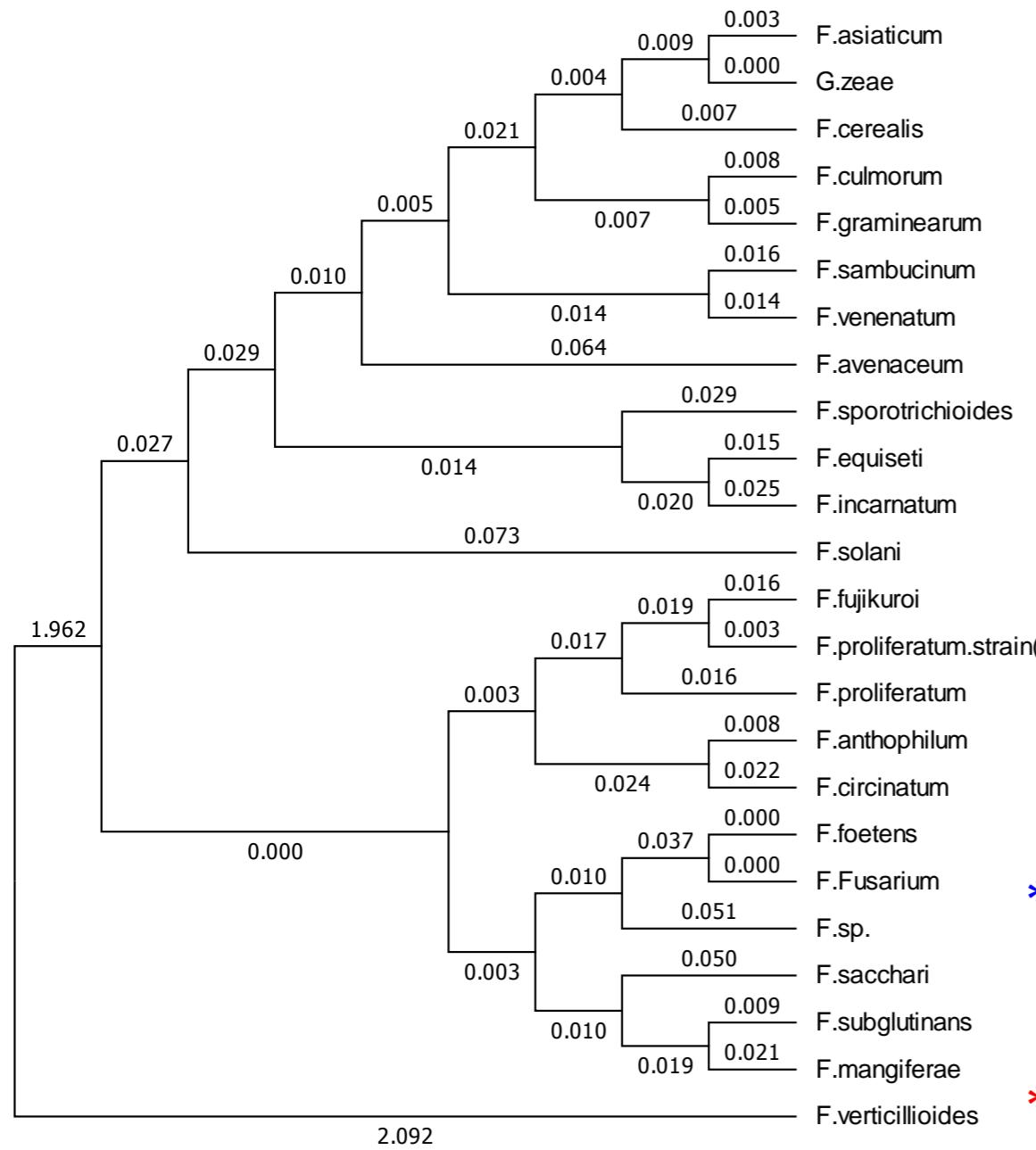
24 Fusarium species

16 Genes evaluados

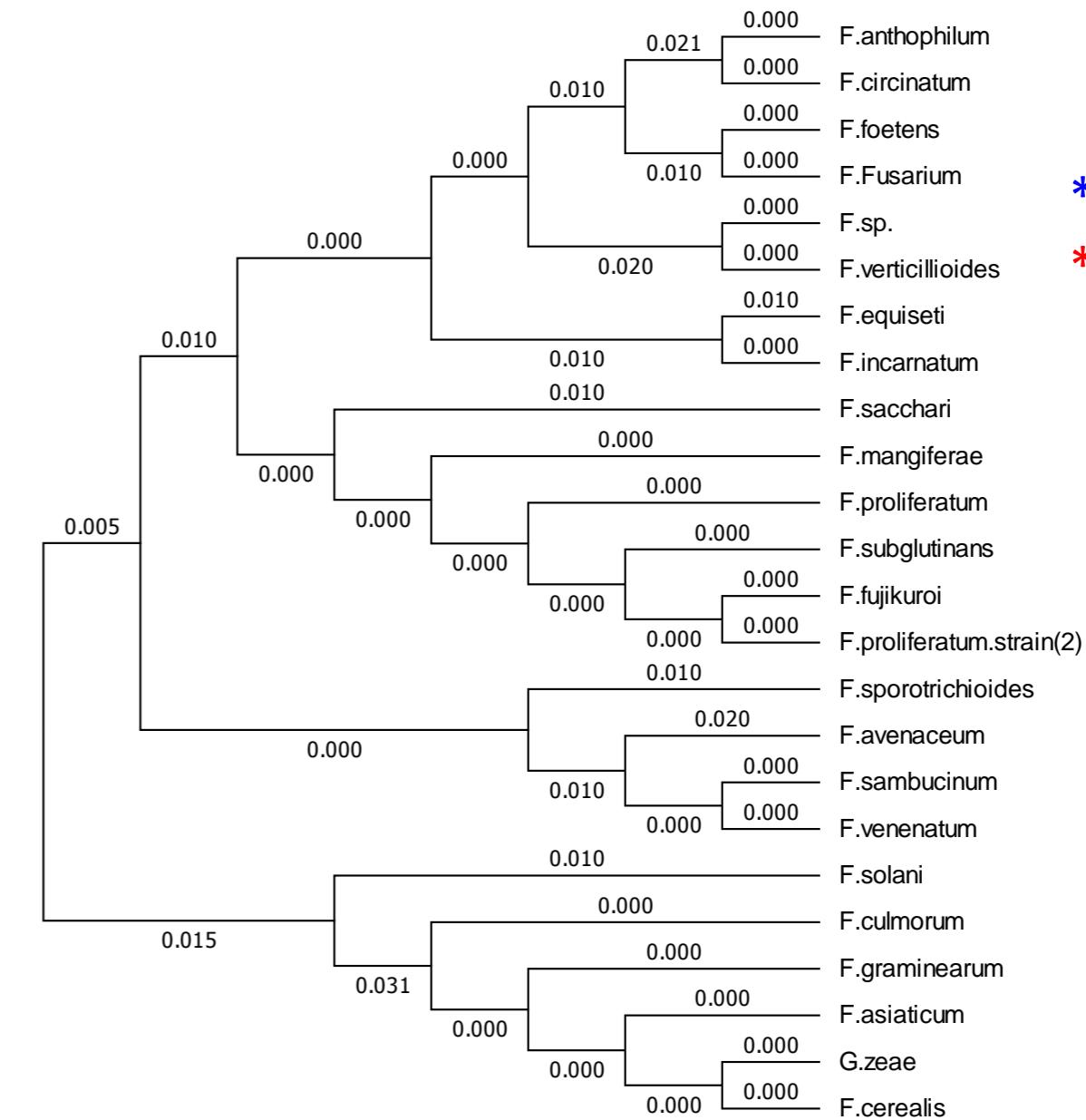


Molecular Phylogenetic analysis by Maximum Likelihood method

H3 amplicon

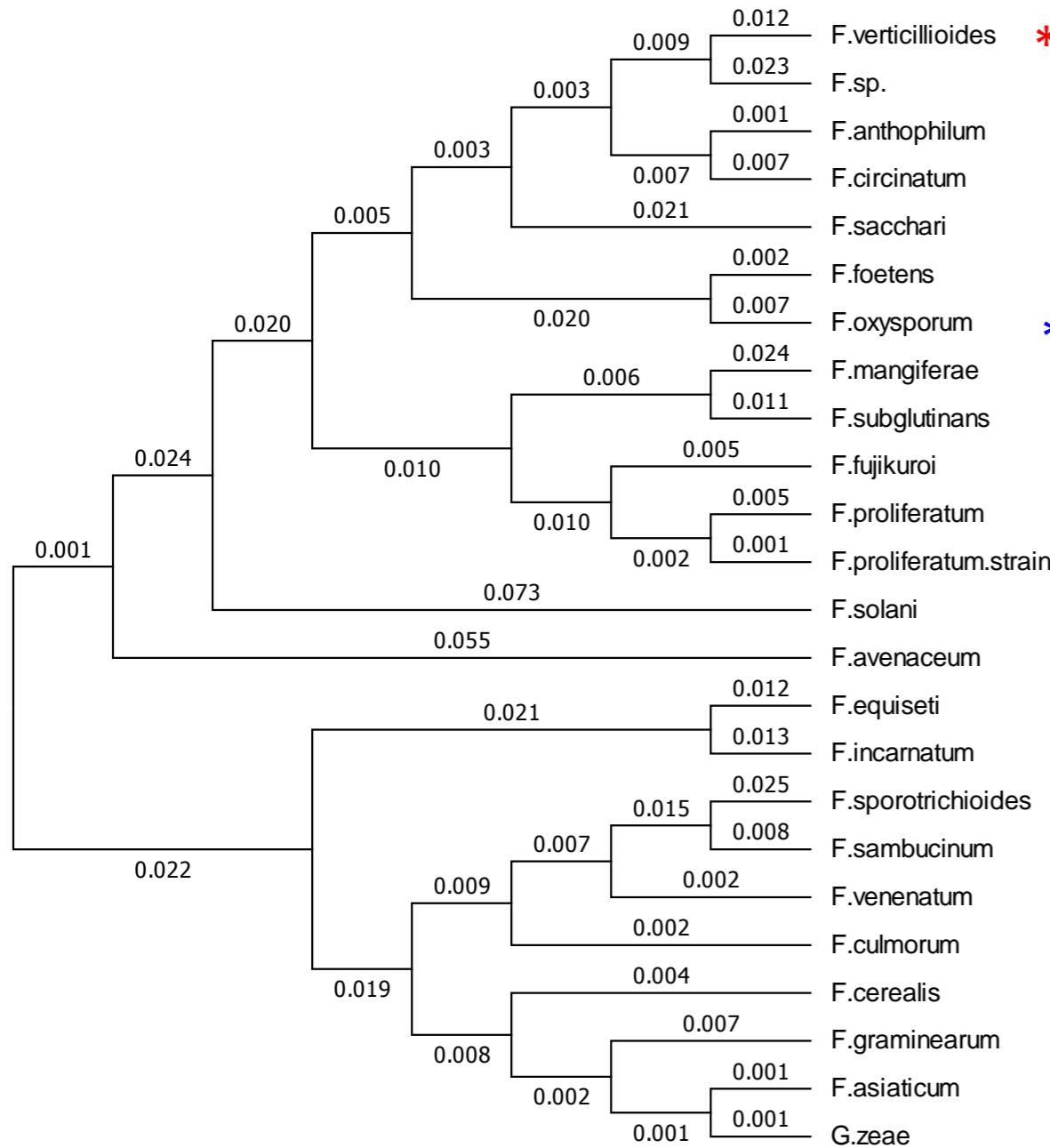


H3 MicroSec

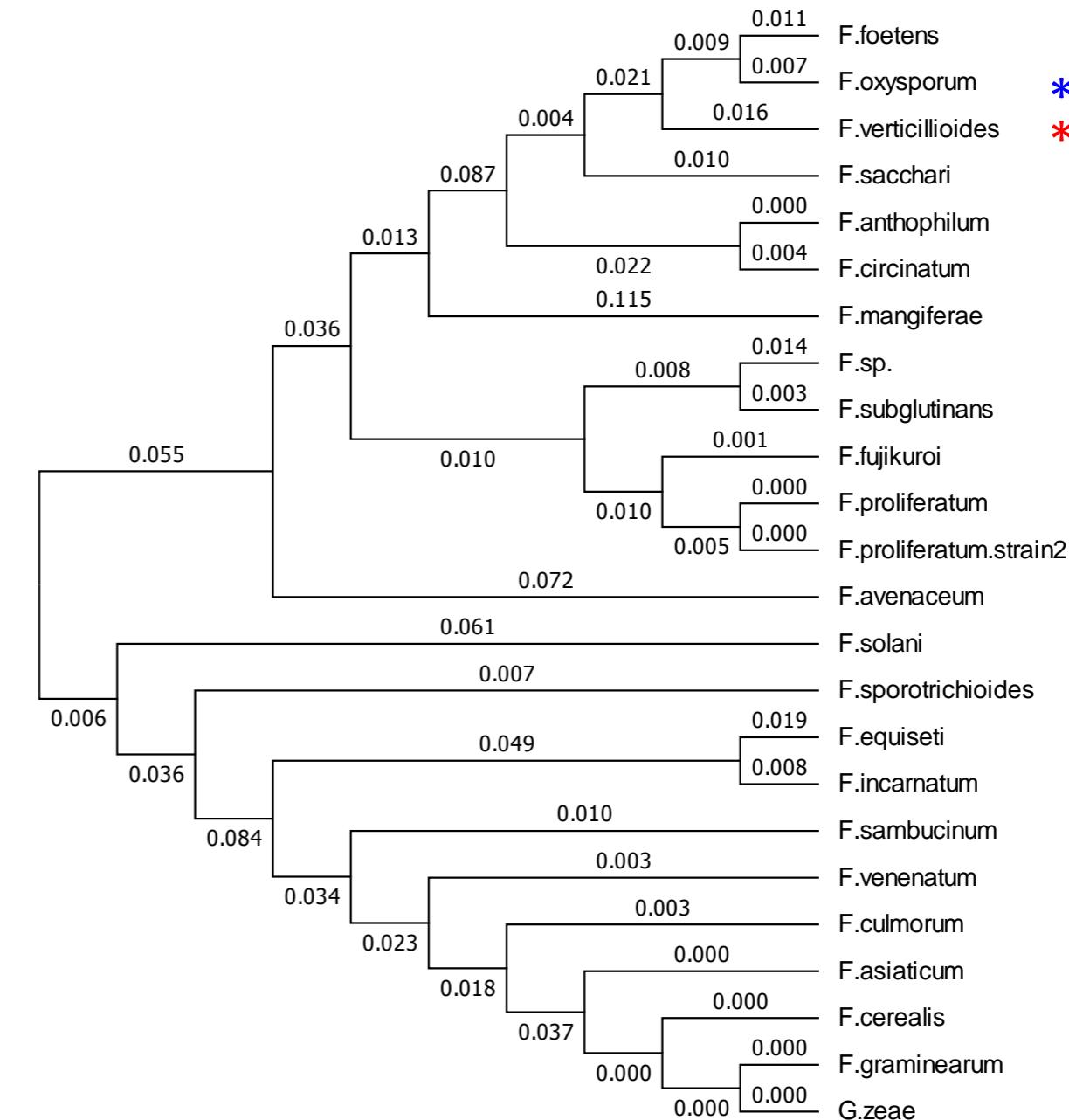


Molecular Phylogenetic analysis by Maximum Likelihood method

EF-1 H3 mtSSU ITS 2-4 amplicon



EF-1 H3 mtSSU ITS 2-4 MicroSeq



*

Bt1a/Bt1b

Bt2a/Bt2b

Ahy-FuF/AHyFuR

EF-1H/EF-2T

H3-1a/H3-1b

H4-1a/H4-1b

ITS FuR/ITS FuF

ITS-1/ITS-2

ITS-1/ITS-4

ITS-4/ITS-5



Bt2a/Bt2b

Bt1a/Bt1b

Ahy-FuF/AHyFuR

EF-1H/EF-2T

H3-1a/H3-1b

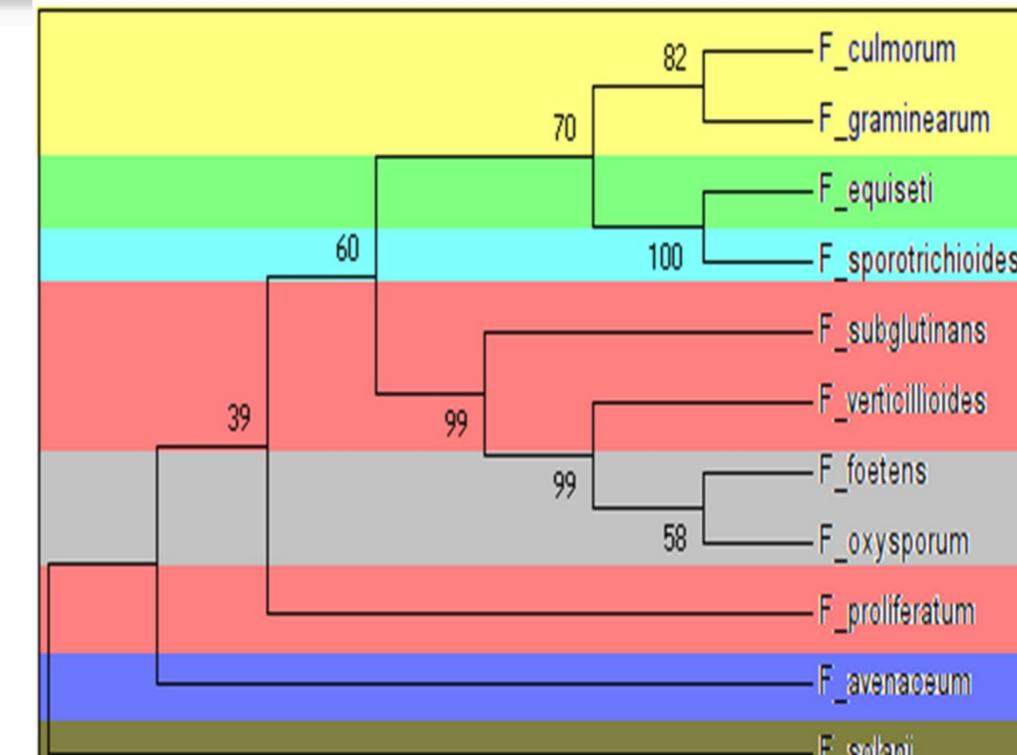
H4-1a/H4-1b

ITS FuR/ITS FuF

ITS-1/ITS-2

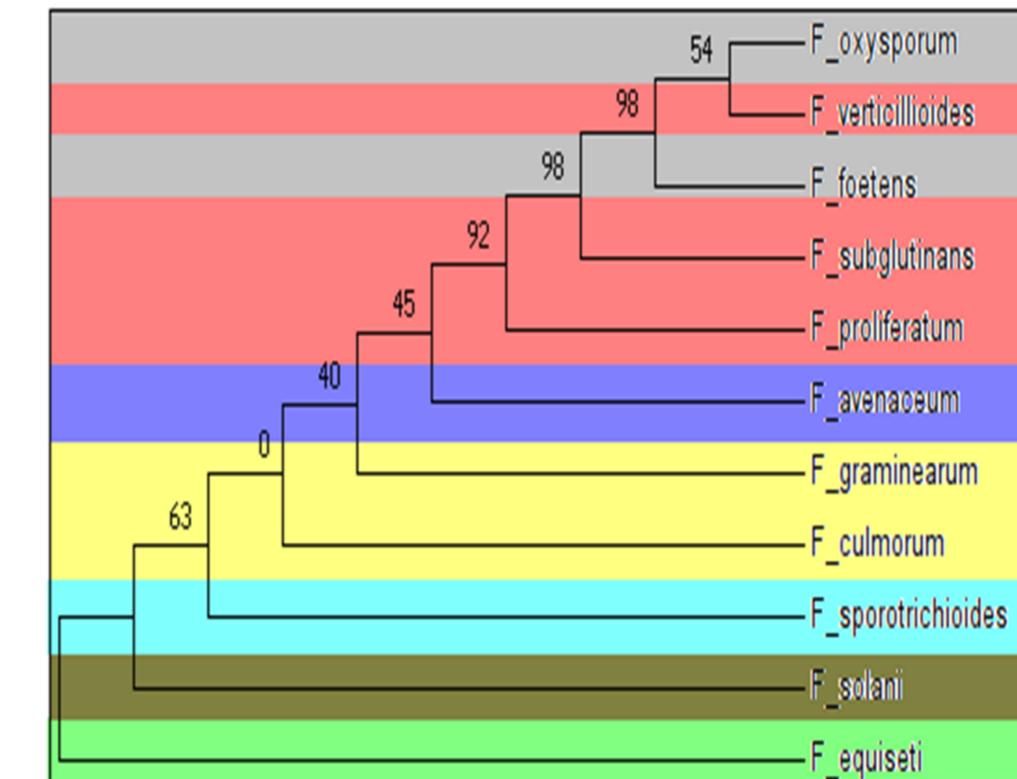
ITS-1/ITS-4

ITS-4/ITS-5



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*



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*

Advances in Computational Biology
Advances in Intelligent Systems and Computing Volume 232, 2014, pp 97-102

“Head to Tail” Tool Analysis through
ClustalW Alignment Algorithms and
Construction of Distance Method
Neighbor-Joining Trees Based on Genus
Fusarium Genomic Distances

Neighbour-joining Distance Matrices

	Species					
Genes	Amplicones	EF-1	H3	ITS	mtSSU	Promedio
	Ver/Foe	0,026	3,838	0,000	0,006	0,967
	Ver/Oxy	0,032	3,838	0,004	0,006	0,970
	Foe/Oxy	0,032	0,000	0,004	0,000	0,009
	Pro/Strain	0,005	0,035	0,000	0,006	0,012
	Pro/Fuji	0,018	0,049	0,000	0,008	0,019
	Strain/Fuji	0,018	0,019	0,000	0,002	0,010
	Sacha/Mang	0,026	0,069	0,312	0,002	0,102

Monogen

	Species					
Genes	MicroSeq	EF-1	H3	ITS	mtSSU	Promedio
	Ver/Foe	0,018	0,040	0,000	0,021	0,020
	Ver/Oxy	0,018	0,040	0,011	0,021	0,023
	Foe/Oxy	0,018	0,000	0,011	0,000	0,007
	Pro/Strain	0,000	0,000	0,000	0,021	0,005
	Pro/Fuji	0,009	0,000	0,000	0,029	0,009
	Strain/Fuji	0,009	0,000	0,000	0,007	0,004
	Sacha/Mang	0,037	0,010	1,144	0,014	0,301

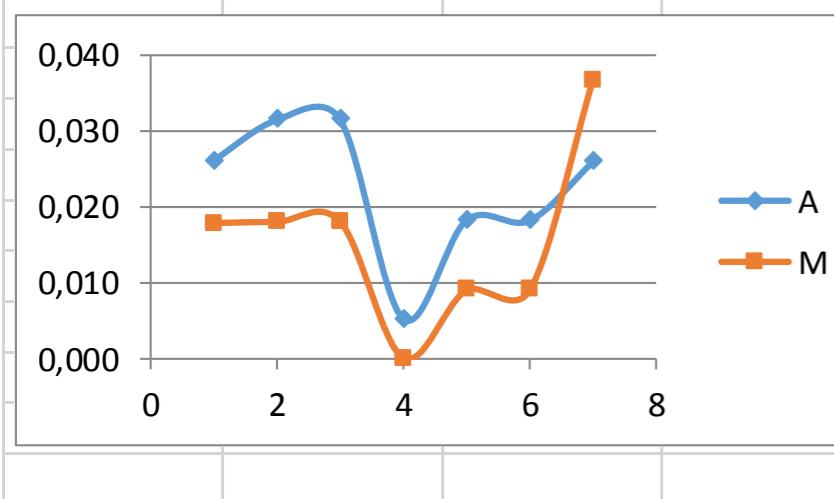
Poligen

	Species				
Genes	Amplicones	EF-1+H3	EF+H3+mtSSU	EF+H3+mtSSU+ITS	Promedios
	Ver/Foe	0,018	0,045	0,036	0,033
	Ver/Oxy	0,073	0,047	0,040	0,053
	Foe/Oxy	0,014	0,009	0,009	0,011
	Pro/Strain	0,010	0,009	0,006	0,009
	Pro/Fuji	0,022	0,019	0,012	0,017
	Strain/Fuji	0,016	0,012	0,009	0,013
	Sacha/Mang	0,050	0,032	0,051	0,044

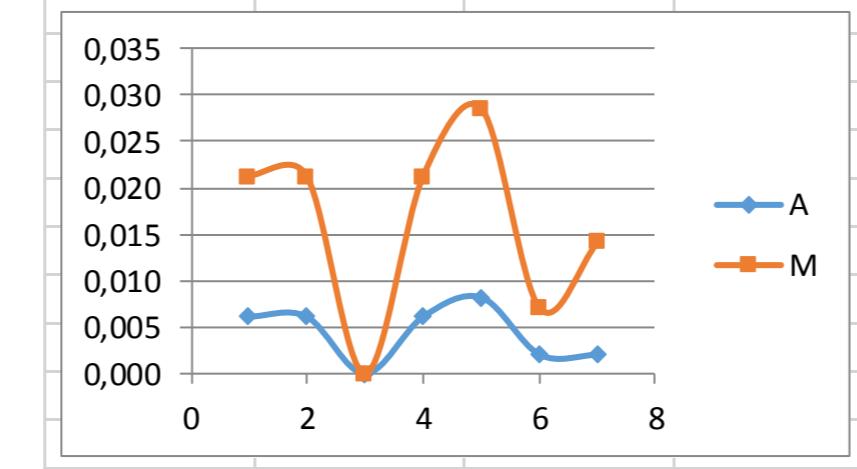
	Species				
Genes	MicroSeq	EF-1+H3	EF+H3+mtSSU	EF+H3+mtSSU+ITS	Promedios
	Ver/Foe	0,018	0,043	0,032	0,031
	Ver/Oxy	0,014	0,043	0,032	0,030
	Foe/Oxy	0,043	0,014	0,018	0,025
	Pro/Strain	0,000	0,000	0,000	0,000
	Pro/Fuji	0,007	0,007	0,004	0,006
	Strain/Fuji	0,007	0,007	0,004	0,005
	Sacha/Mang	0,043	0,029	0,208	0,093

Differences in gene variability and microsequence

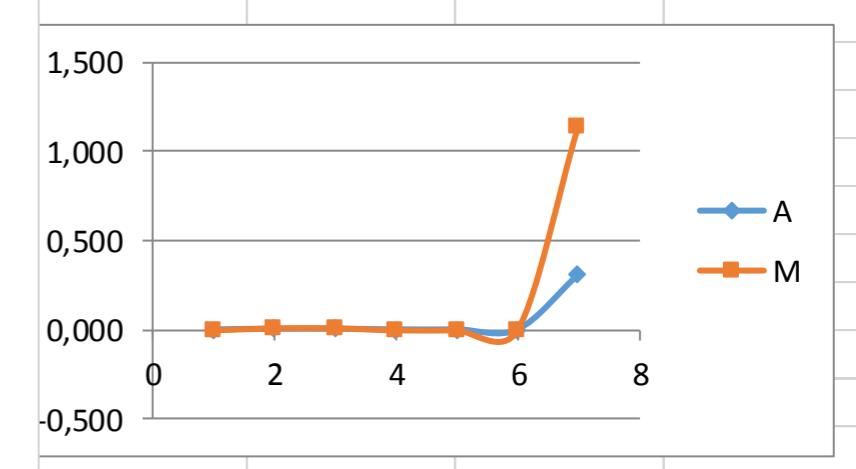
EF-1	A	M
VF	0,026	0,018
VO	0,032	0,018
FO	0,032	0,018
PS	0,005	0,000
PF	0,018	0,009
SF	0,018	0,009
SM	0,026	0,037



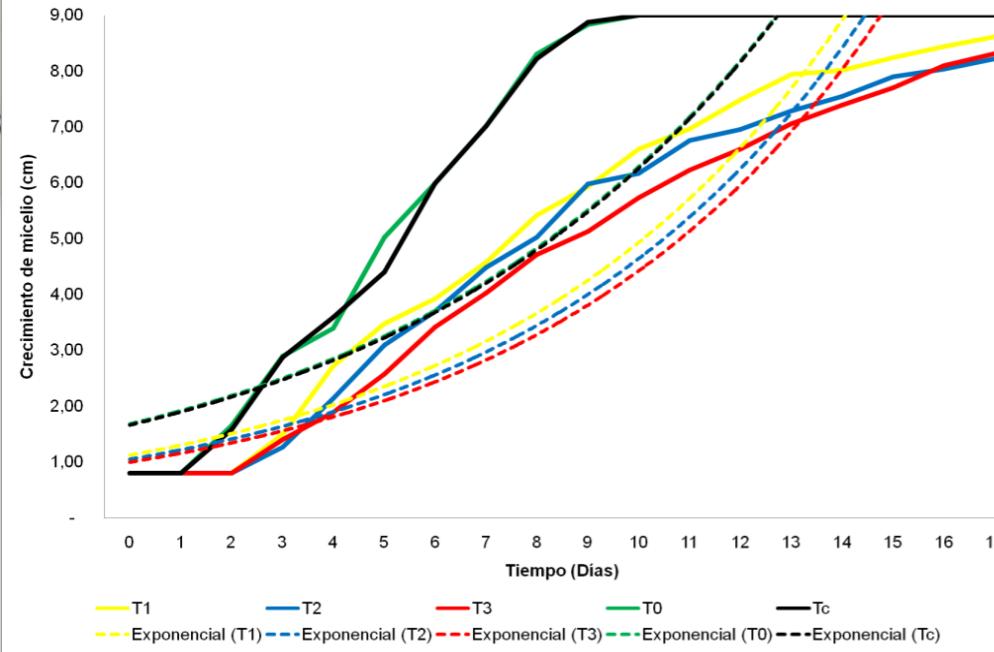
mtSSU	A	M
VF	0,006	0,021
VO	0,006	0,021
FO	0,000	0,000
PS	0,006	0,021
PF	0,008	0,029
SF	0,002	0,007
SM	0,002	0,014



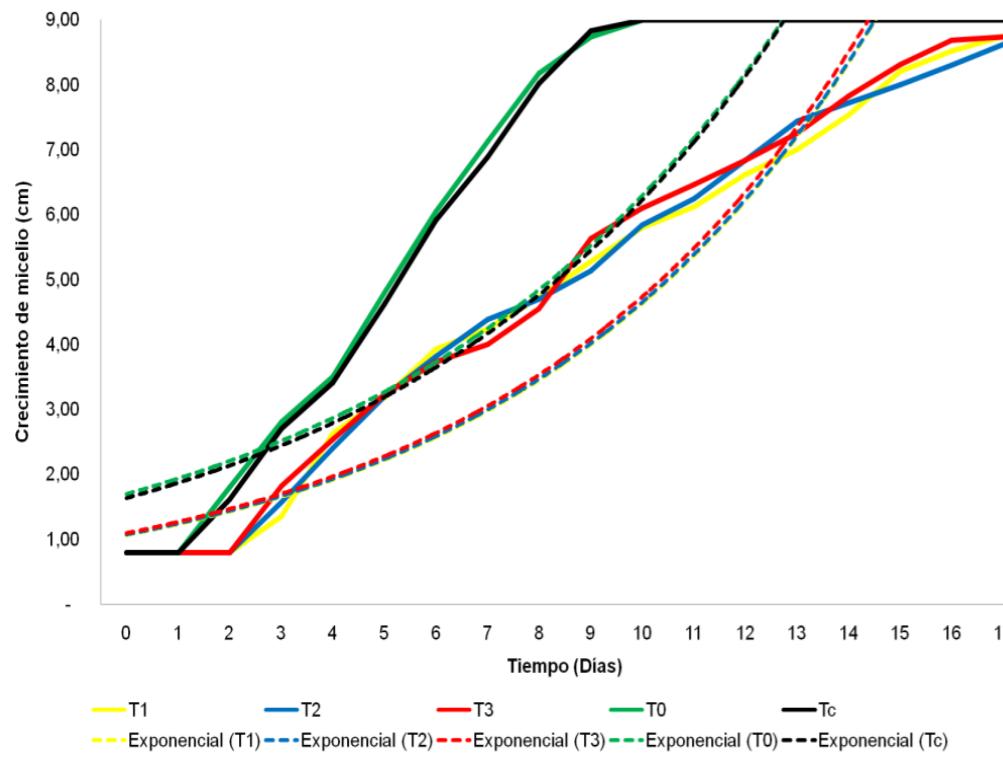
ITS	A	M
VF	0,000	0,000
VO	0,004	0,011
FO	0,004	0,011
PS	0,000	0,000
PF	0,000	0,000
SF	0,000	0,000
SM	0,312	1,144



Efecto en el crecimiento de micelio de *F. oxysporum* generado por el fungicida Prochloraz



Efecto en el crecimiento de micelio de *F. oxysporum* generado por el fungicida Difenoconazole



EVALUACIÓN DEL EFECTO DE FUNGICIDAS EN SEIS ESPECIES DE *Fusarium* PATÓGENOS DEL CLÁVEL (*Dianthus caryophyllus*)

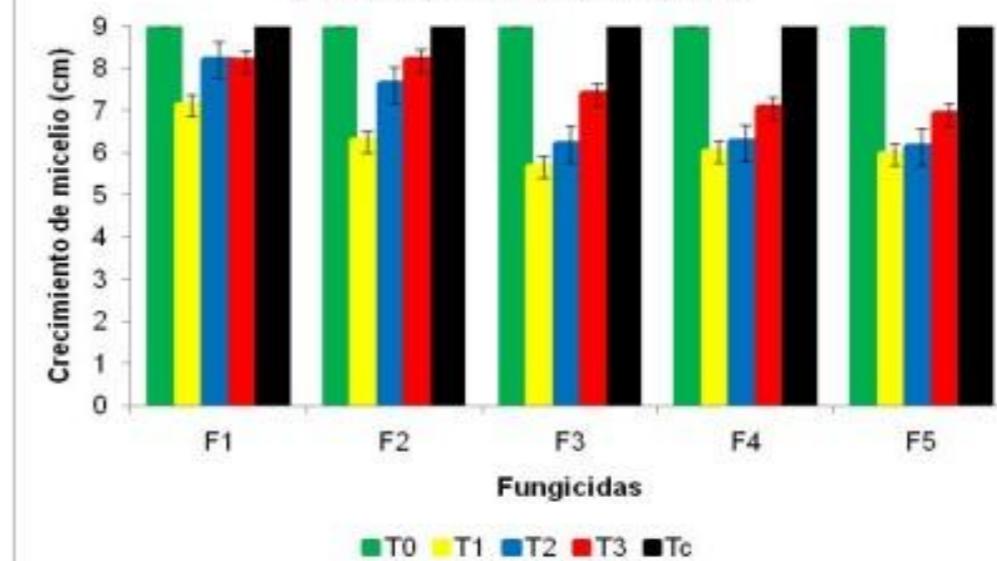
TRIANA BARROTE, Diana Lorena ; ARBELAEZ TORRES, Germán; FERNANDEZ DIAZ, Gina Paola;

FILGUEIRA DUARTE, Juan José

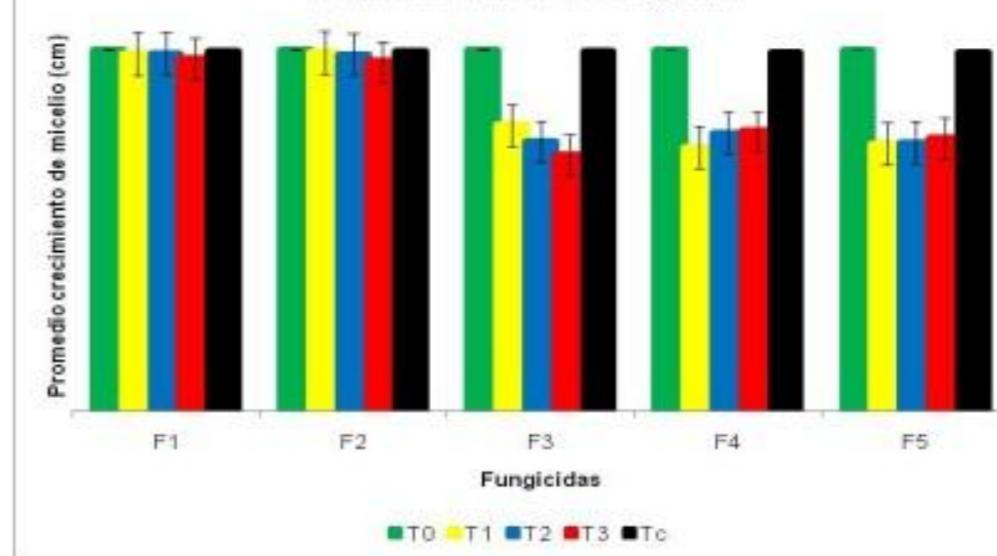
Programa Biología Aplicada, Universidad Militar Nueva Granada – Colombia

juan.filgueira@unimilitar.edu.co

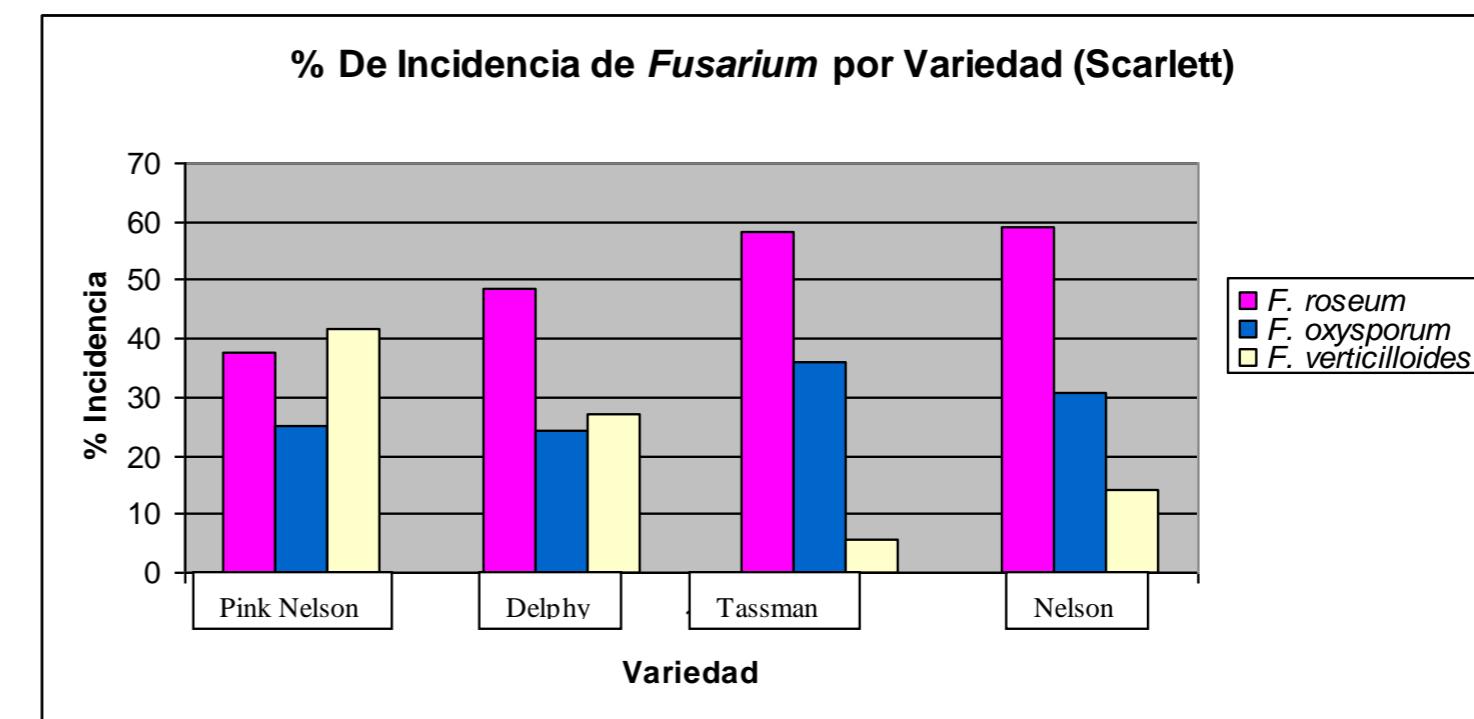
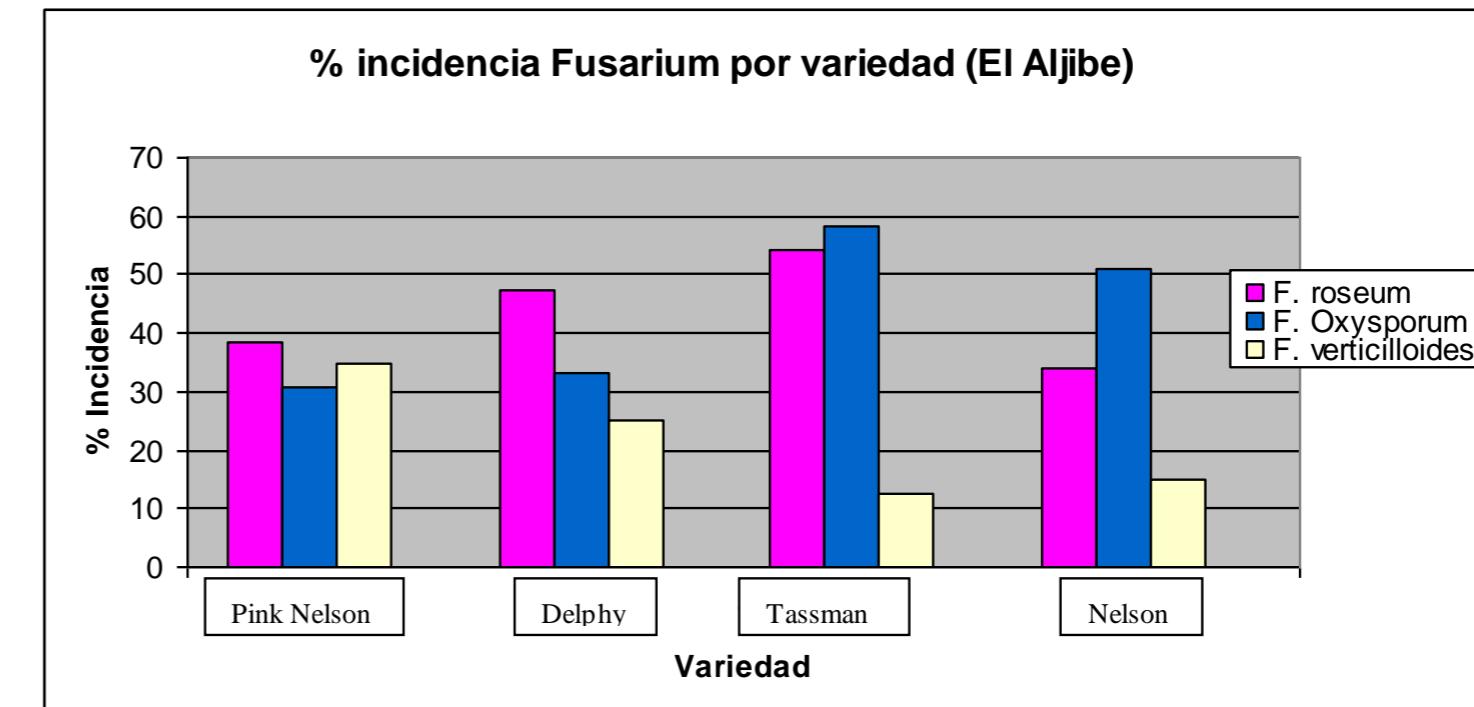
Efecto en el crecimiento de micelio de *F. avenaceum* generado por diferentes fungicidas



Promedio final del efecto causado por diferentes fungicidas en el crecimiento de micelio de *F. oxysporum*

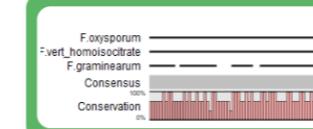


Variation of the incidence of different Fusarium species in different varieties of carnation and different farms.

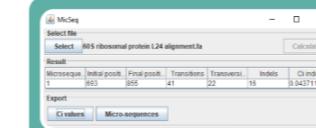




Búsqueda de genes ortólogos



Alineamientos de los genes ortólogos



Análisis Cuantitativo de las microsecuencias



Análisis de taxonomía molecular



Análisis de filogenia molecular

Especie	Total genes	Orthologous genes
<i>Fusarium oxysporum</i> f.sp <i>Lycopersici</i>	27.348	402
<i>Fusarium graminearum</i>	14.144	
<i>Fusarium verticillioides</i>	20.575	

Microsequences in orthologos genes

Nombre	Total Microsecuencias	Promedio de Transiciones	Promedio de Transversiones	Promedio de Indels	Promedio de índice Mi	Promedio de Longitud Microsecuencias (pb)
30S ribosomal protein S12	2	20,5	14,5	5	0,033	100,5
50S ribosomal protein L14	1	20	19	86	0,124	141
Atp-dependent RNA helicase DBP4	6	15,2	9,8	0	0,025	72,8
Chorismate synthase	4	13,5	11,3	3	0,032	73,8
COP9 signalosome complex subuni	3	11	7,7	0	0,025	56
Diphosphomevalonate decarboxyla	1	15	6	0	0,020	69
Diphthamide biosynthesis protei	6	17,7	15	0	0,031	84,5
DNA primase small subunit	2	29,5	13	3	0,021	139,5
Ferrochelatase	2	16	4	0	0,015	73,5
Formyltetrahydrofolate deformyl	1	13	3	0	0,014	66
Histone acetyltransferase type	5	27,2	17,4	0	0,027	114
Homoisocitrate dehydrogenase	2	158,5	144,5	5	0,035	723,5
Ornithine decarboxylase	3	17,7	14	22,7	0,074	88,7
Palmitoyltransferase PFA3	4	14,3	8	1,5	0,028	65,75
Quinate dehydrogenase	4	12,5	13	0	0,030	70,25
Rhomboid protein 2	4	33,8	21,3	19	0,052	141,5
RNA exonuclease 4	4	18,5	10,3	1,5	0,029	82,25
Swr1-complex protein 5	5	20	14,8	8,4	0,045	90,8
Transcription elongation factor	6	14	4,8	2	0,022	66,5
Transcription factor IWS1	3	35,3	30,3	10	0,048	141,3
Transcription initiation factor	1	13	8,0	6	0,042	60

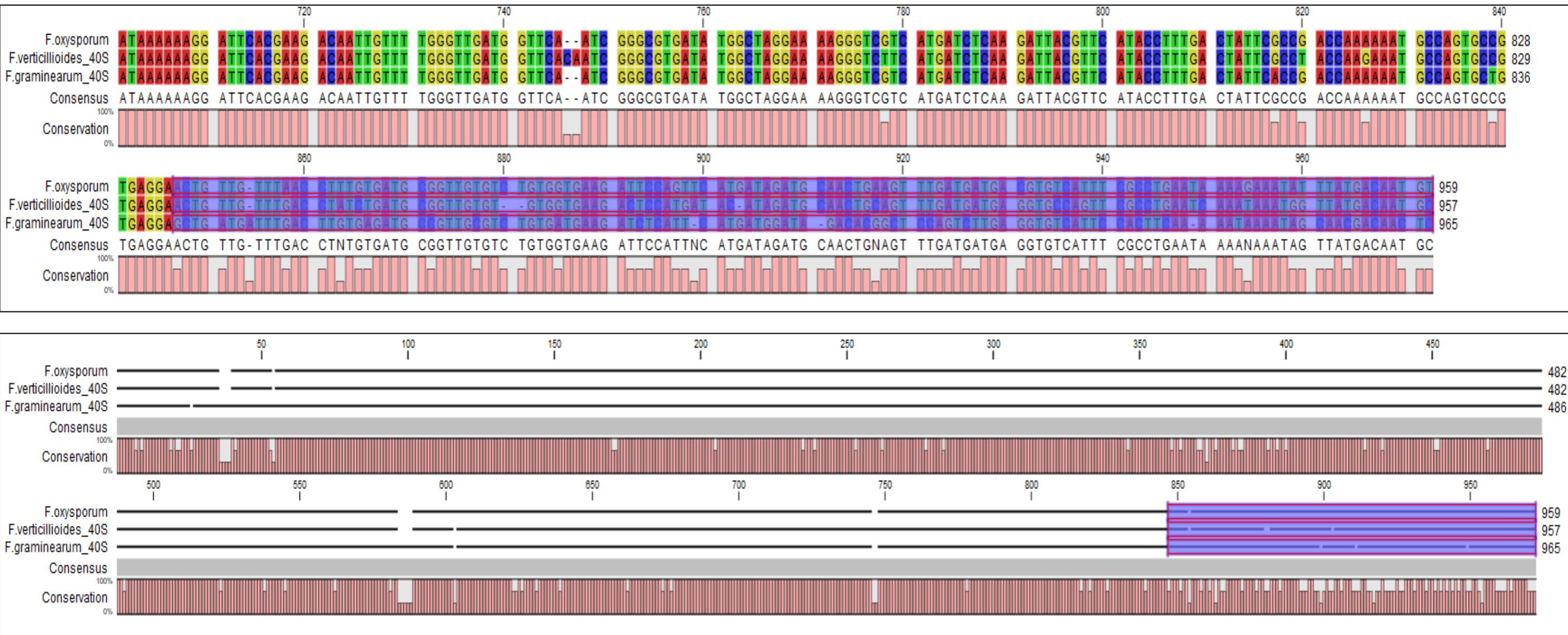
Matrices of distance N-J Microsequences of orthologous genes

	Ferrochelatase	Quinate dehydrogenase	Transcription elongation factor	Diphthamide biosynthesis protein	COP9 signalosome complex subunit 5	Atp-dependent RNA helicase	Histone acetyltransferase type B
F.oxy/F.gram	0,255	0,339	0,449	0,500	0,422	0,457	0,532
F.ver/F.gram	0,300	0,364	0,457	0,565	0,530	0,530	0,604
F.ver/F.oxy	0,064	0,245	0,087	0,155	0,200	0,200	0,155

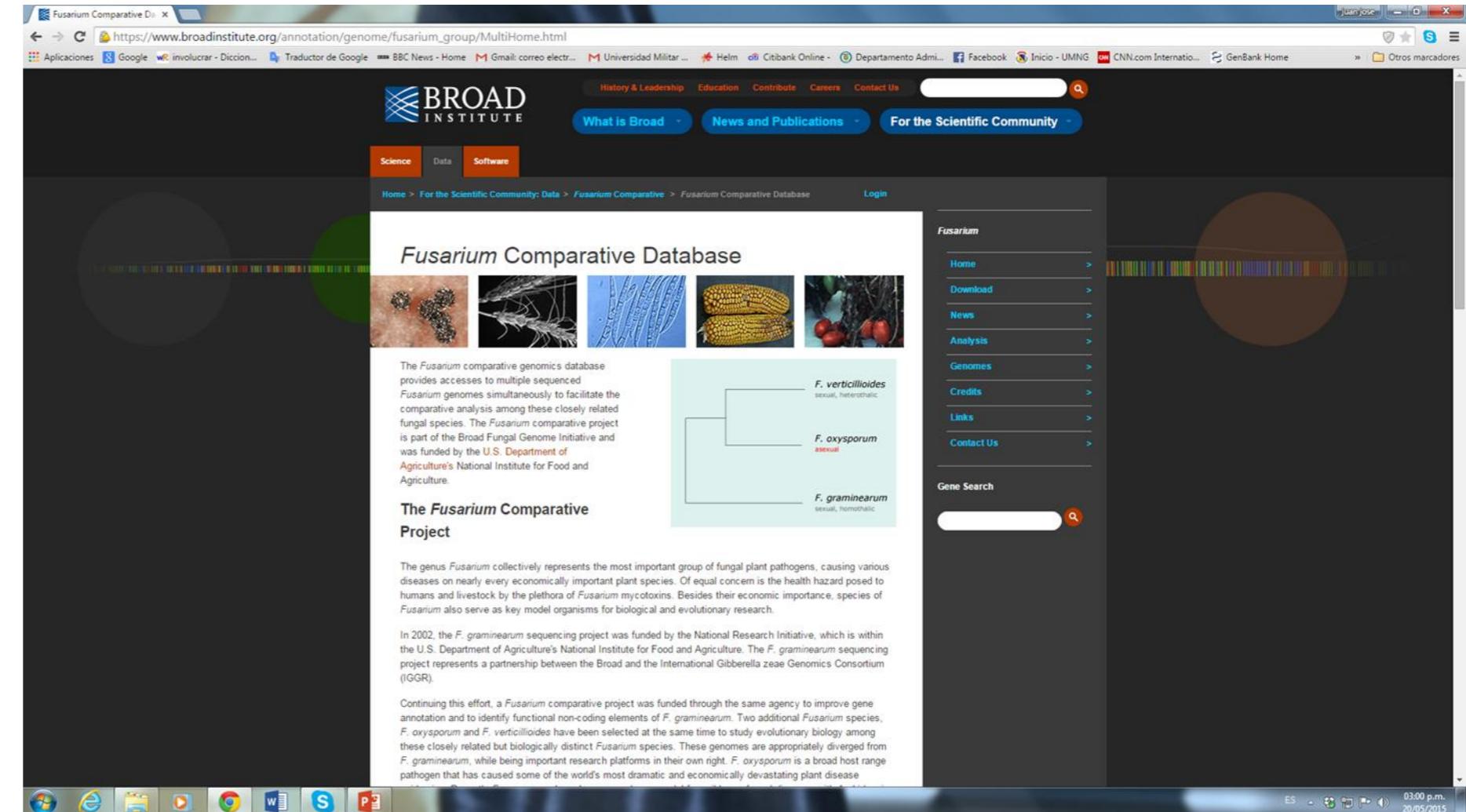
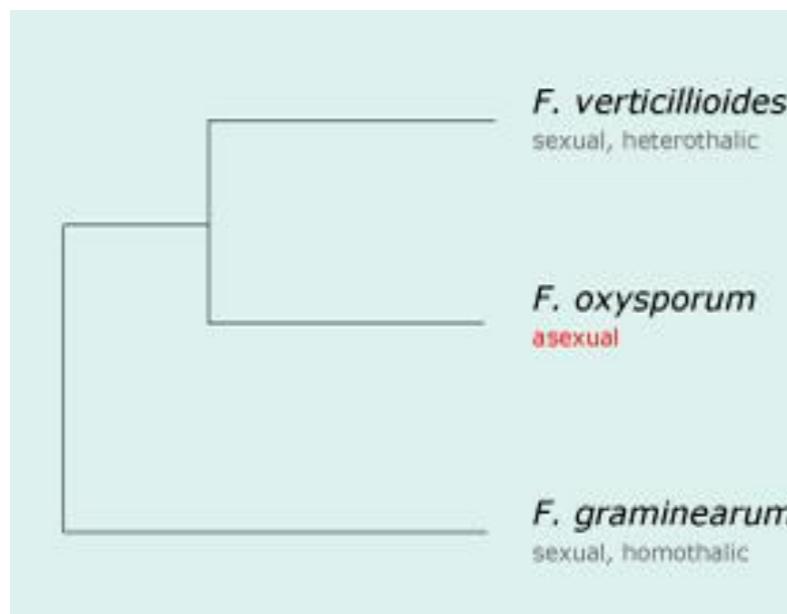
Orthologous genes, grouped in the same way to the species
 They present similar distances despite being different genes



Conservation map obtained for the Ribosomal 40S protein gene for 3 species of the genus *Fusarium*.



Fusarium Comparative Database



The Fusarium comparative genomics database provides access to multiple sequenced Fusarium genomes simultaneously to facilitate the comparative analysis among these closely related fungal species. The Fusarium comparative project is part of the Broad Fungal Genome Initiative and was funded by the U.S. Department of Agriculture's National Institute for Food and Agriculture.

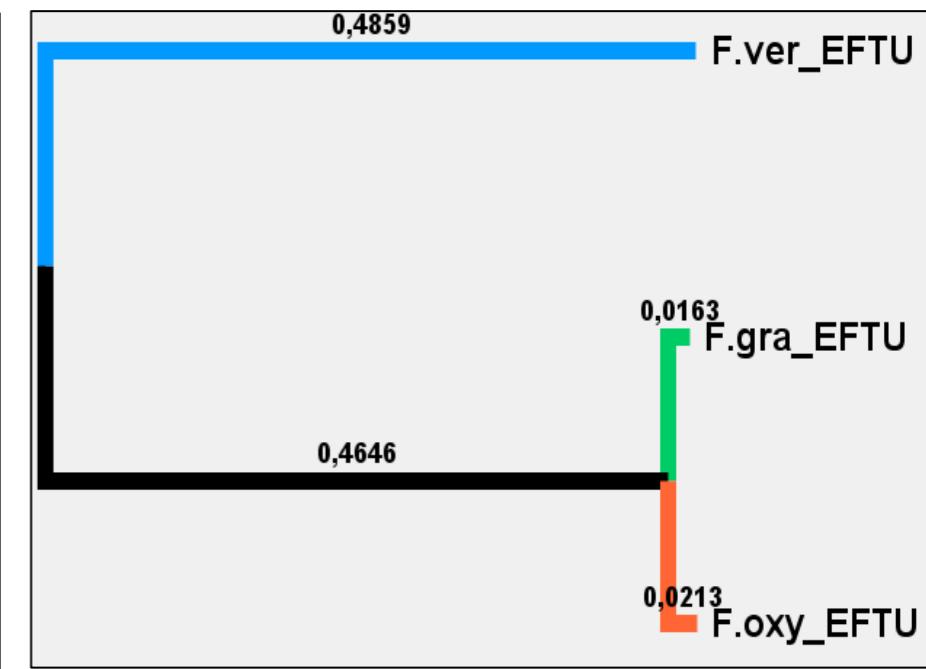
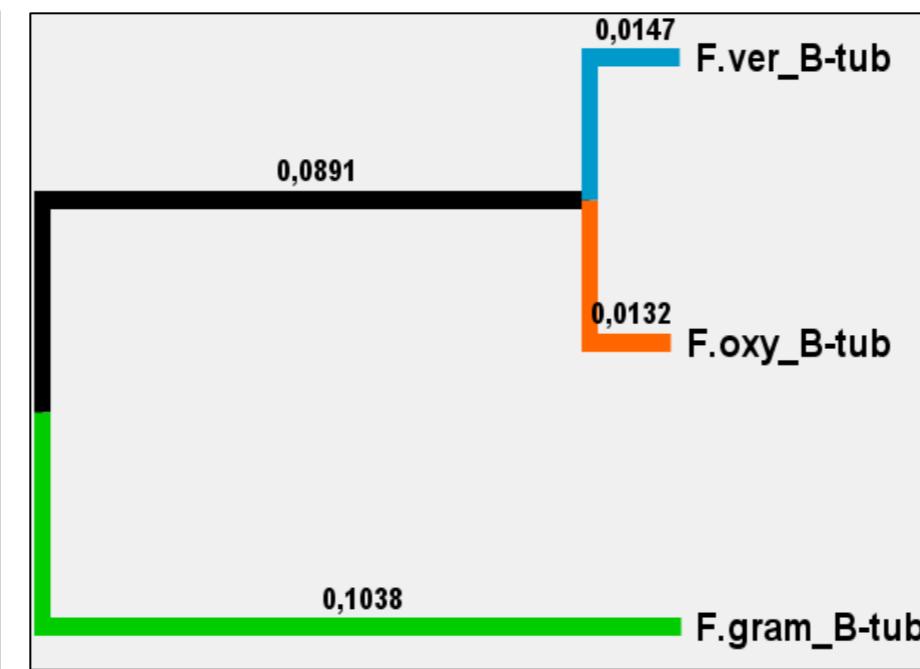
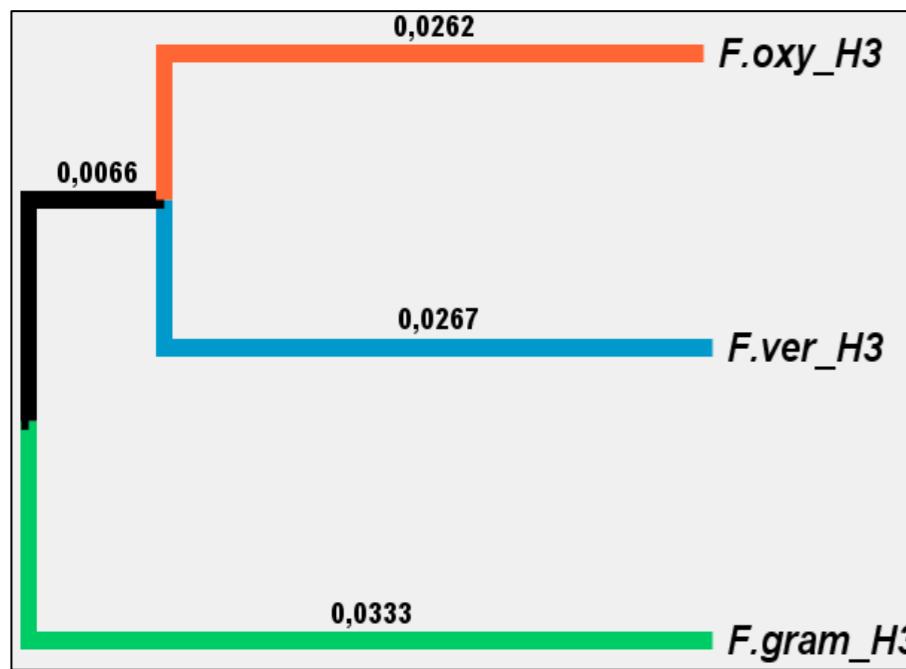
The Fusarium Comparative Project

The genus *Fusarium* collectively represents the most important group of fungal plant pathogens, causing various diseases on nearly every economically important plant species. Of equal concern is the health hazard posed to humans and livestock by the plethora of *Fusarium* mycotoxins. Besides their economic importance, species of *Fusarium* also serve as key model organisms for biological and evolutionary research.

In 2002, the *F. graminearum* sequencing project was funded by the National Research Initiative, which is within the U.S. Department of Agriculture's National Institute for Food and Agriculture. The *F. graminearum* sequencing project represents a partnership between the Broad and the International *Gibberella zeae* Genomics Consortium (IGGR).

Continuing this effort, a *Fusarium* comparative project was funded through the same agency to improve gene annotation and to identify functional non-coding elements of *F. graminearum*. Two additional *Fusarium* species, *F. oxysporum* and *F. verticillioides* have been selected at the same time to study evolutionary biology among these closely related but biologically distinct *Fusarium* species. These genomes are appropriately diverged from *F. graminearum*, while being important research platforms in their own right. *F. oxysporum* is a broad host range pathogen that has caused some of the world's most dramatic and economically devastating plant disease

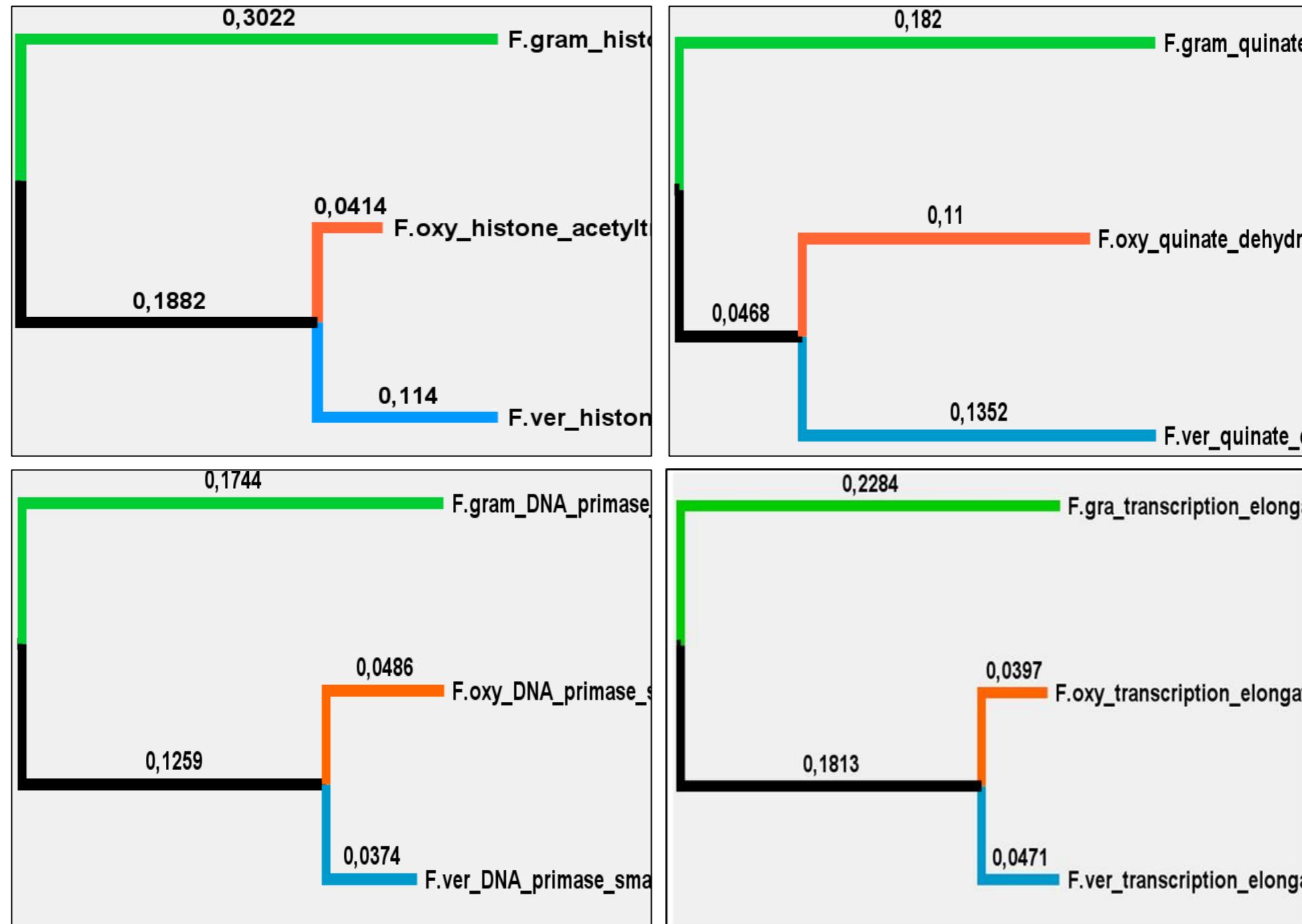
Dendograms with complete genes





UNIVERSIDAD MILITAR
NUEVA GRANADA

Phylogeny using orthologous genes



Thanks

