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Fusarium: Molecular Taxonomy and Phylogeny Using Microsequences of DNA of Orthologous

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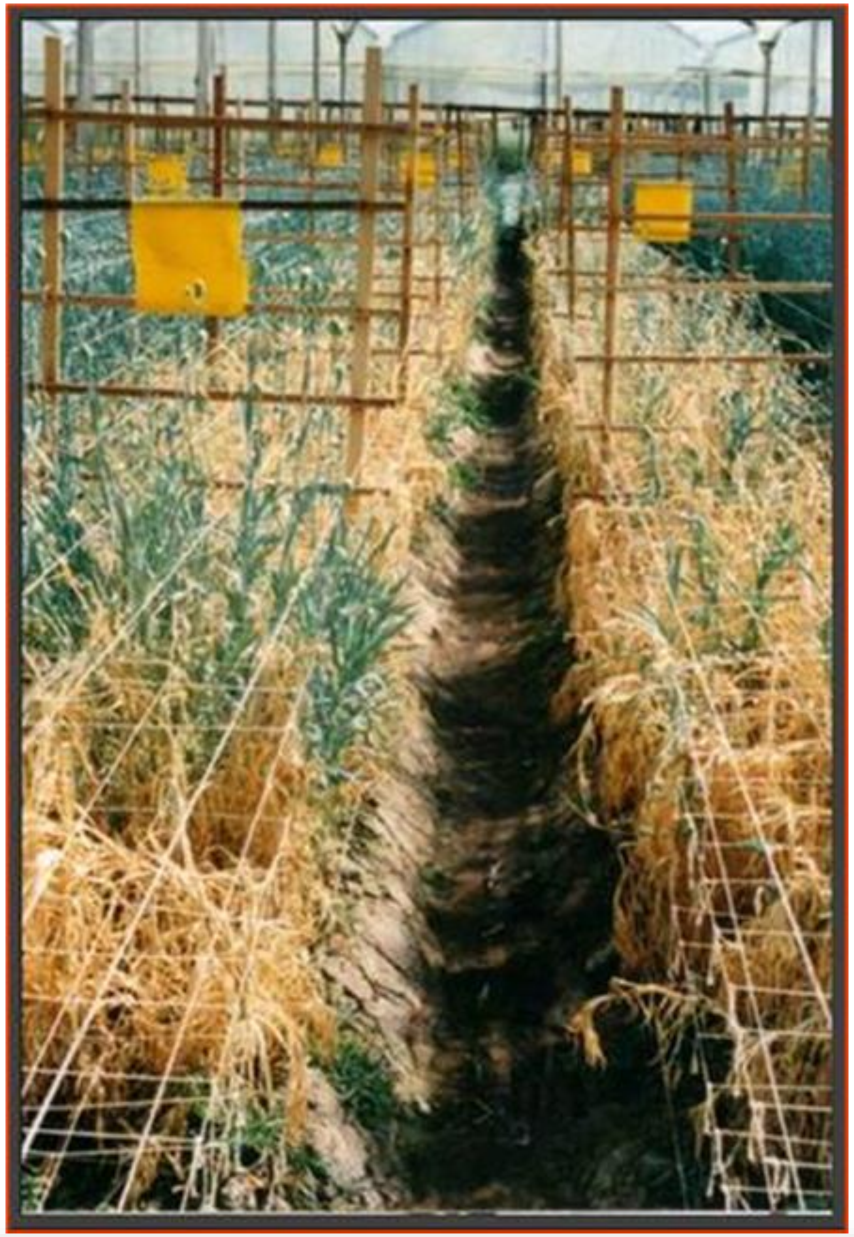
Disease Vs Simptoms



https://www.outlookindia.com/magazine/story/no-more-bananas-on-your-breakfast-table/300937

My plant has Fusarium

Which ones?

https://pnwhandbooks.org/plantdisease/pesticide-articles/fungicides-disease-management-home-landscape

Fungicides Market

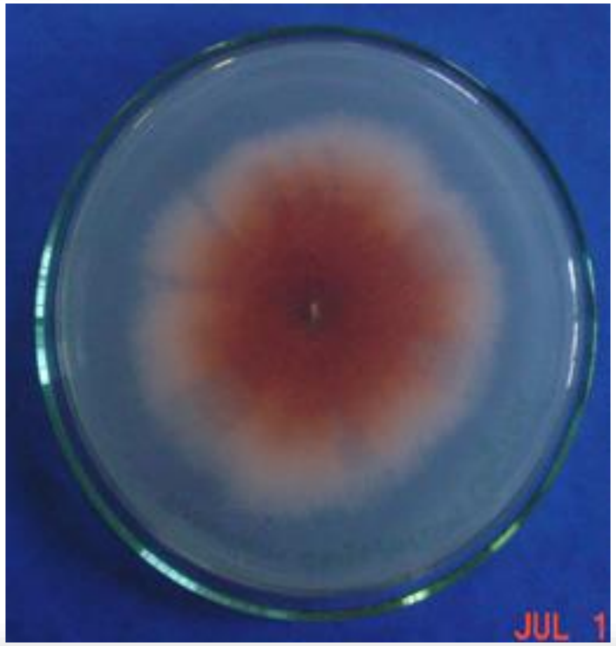
https://www.slideshare.net/KanchanGaikwad8/fungicides-market-expected-to-grow-faster-with-key-winning-strategies

F. oxysporum

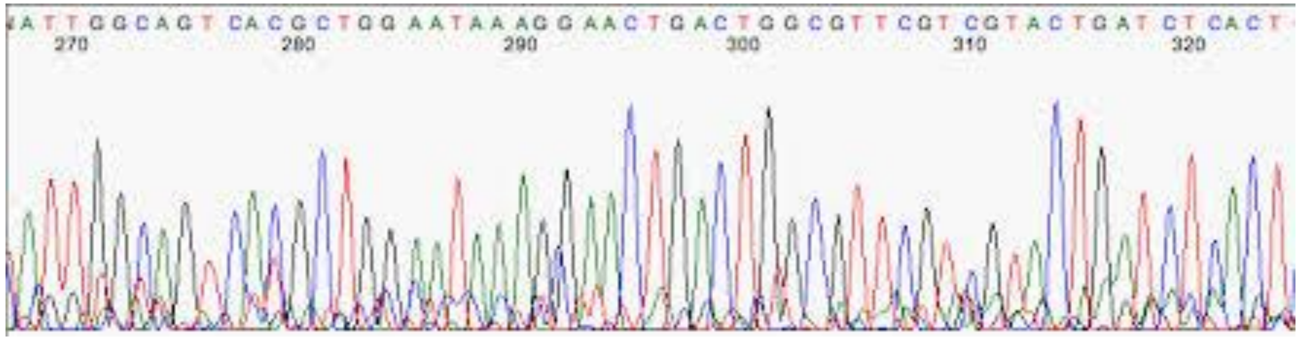
F. verticillioides

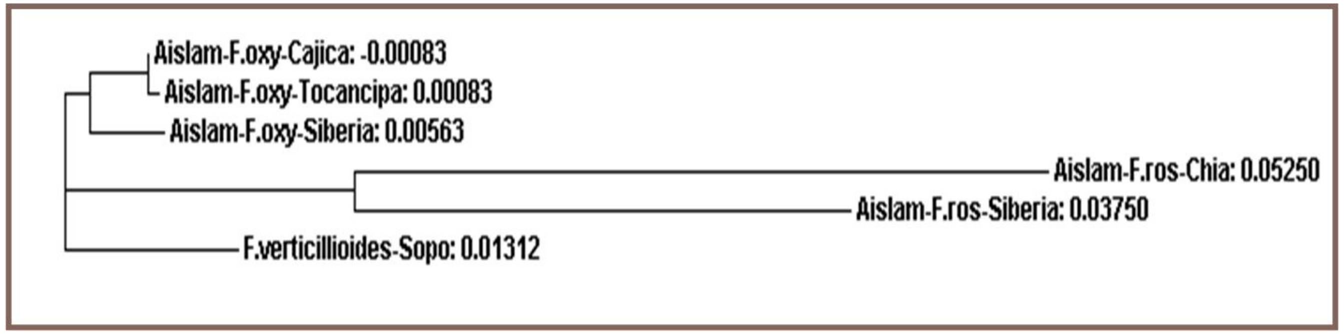
Filgueira, J.J., Quinche, C.G., y Soto, J.C.: 2007. ¿Es el Fusarium verticillioides responsable del decaimiento de la variedad Nelson en la Sabana de Bogota?. Asocolflores. No 69. p51-54.

Taxonomy and phylogeny / Morphology traits vs. Molecular traits



Vs.





What's the difference between taxonomy, binomial nomenclature, and phylogeny?

Explanation:

Taxonomy is the study of the classification of organisms. Taxonomists study the characteristics of organisms in order to classify them into the appropriate taxonomic groups, such as kingdom, phylum, class, etc.

Phylogeny, or phylogenetics, is the study of the evolutionary development of organisms and relationships between them. Phylogeny is a useful tool for taxonomists.

https://socratic.org/questions/whats-the-difference-between-taxonomy-binomial-nomenclature-and-phylogeny

Some of History

- 1909: Link create the genus *Fusarium*
- 1910: Appel and Wollenweber grouped all the perfect fungi in the family Tuberculariacea, 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
- 2000: Leslie and Summerell recognize 70 species
- 2011: Watanabe more than 1000 species
- 2019: 300 species

- *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 aecidii-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 ampelodesmi*[1]
- *Fusarium andinum*[1]
- *Fusarium andiyazi*[1]
- *Fusarium andropogonis*[1]
- *Fusarium anguioides*[1]
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- *Fusarium annulatum*[1]
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- *Fusarium anomalum*[1]
- *Fusarium anthophilum*[1]
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- *Fusarium apiogenum*[1]
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- *Fusarium arachnoideum* [1]
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- *Fusarium arcuosporum*[1]
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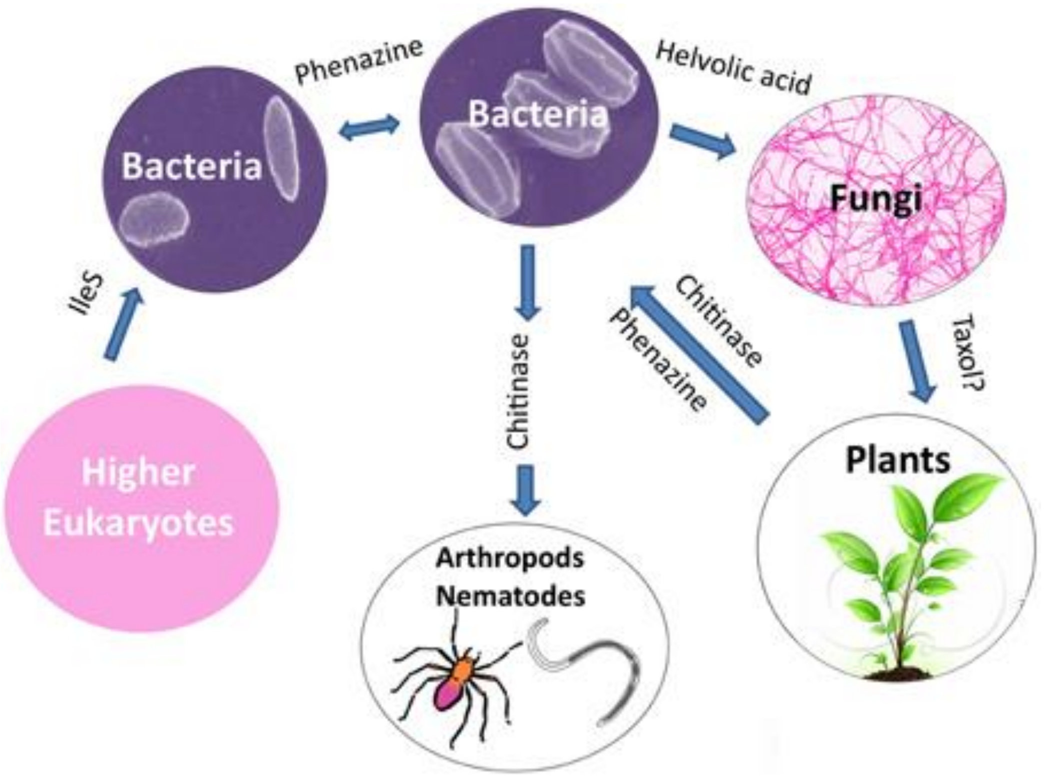
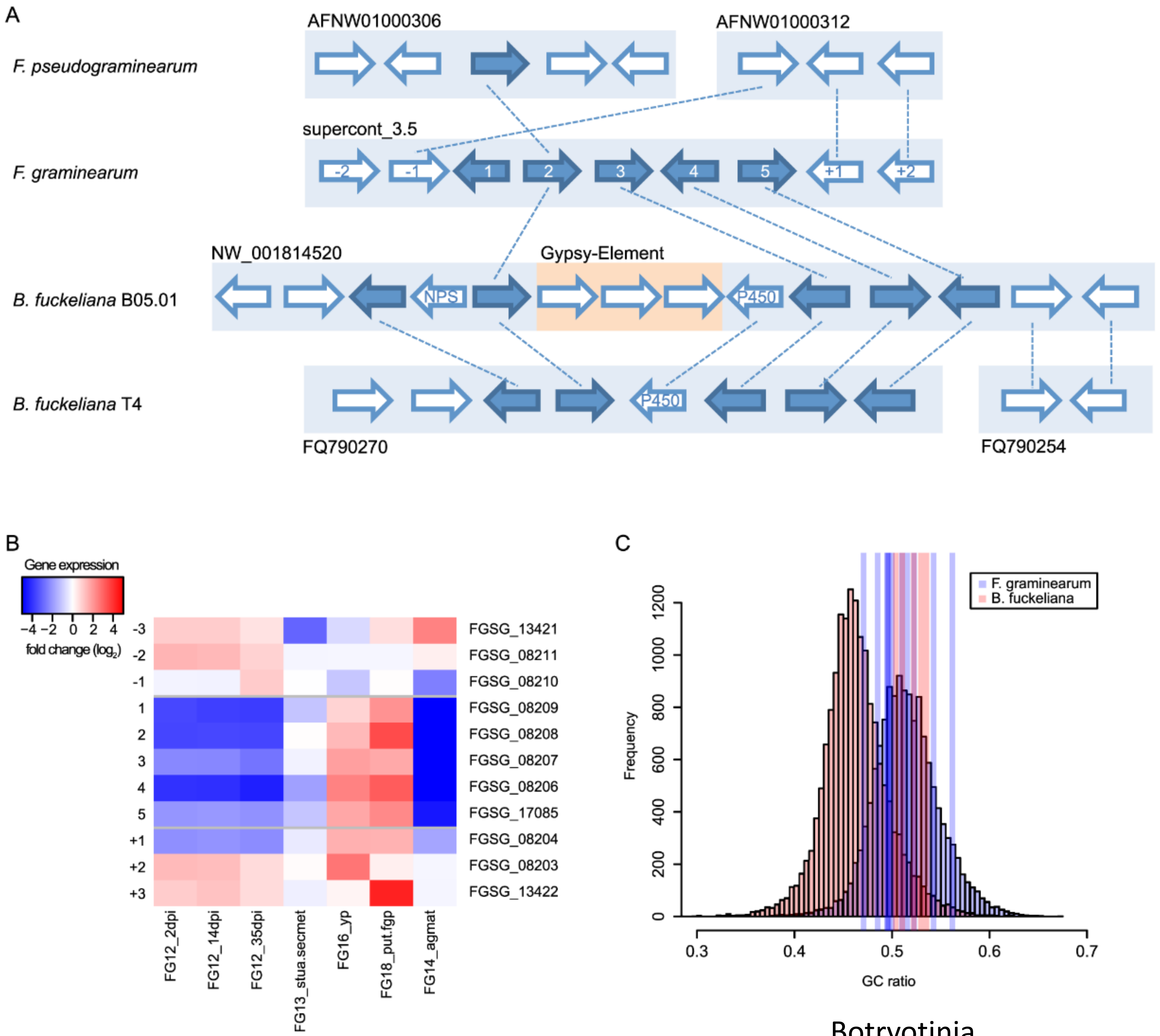
- *Fusarium pampini*[1]
- *Fusarium pandani*[1]
- *Fusarium pannosum*[1]
- *Fusarium parasiticum*[1]
- *Fusarium parasiton*[1]
- *Fusarium paspali*[1]
- *Fusarium paspalicola*[1]

Horizontal gene transfer





Botryotinia

Mousa, Walaa. Raizada, Manish. 2015/04/10. 231. Biodiversity of genes encoding anti-microbial traits within plant associated microbes. DOI:10.3389/fpls.2015.00231. Frontiers in plant science

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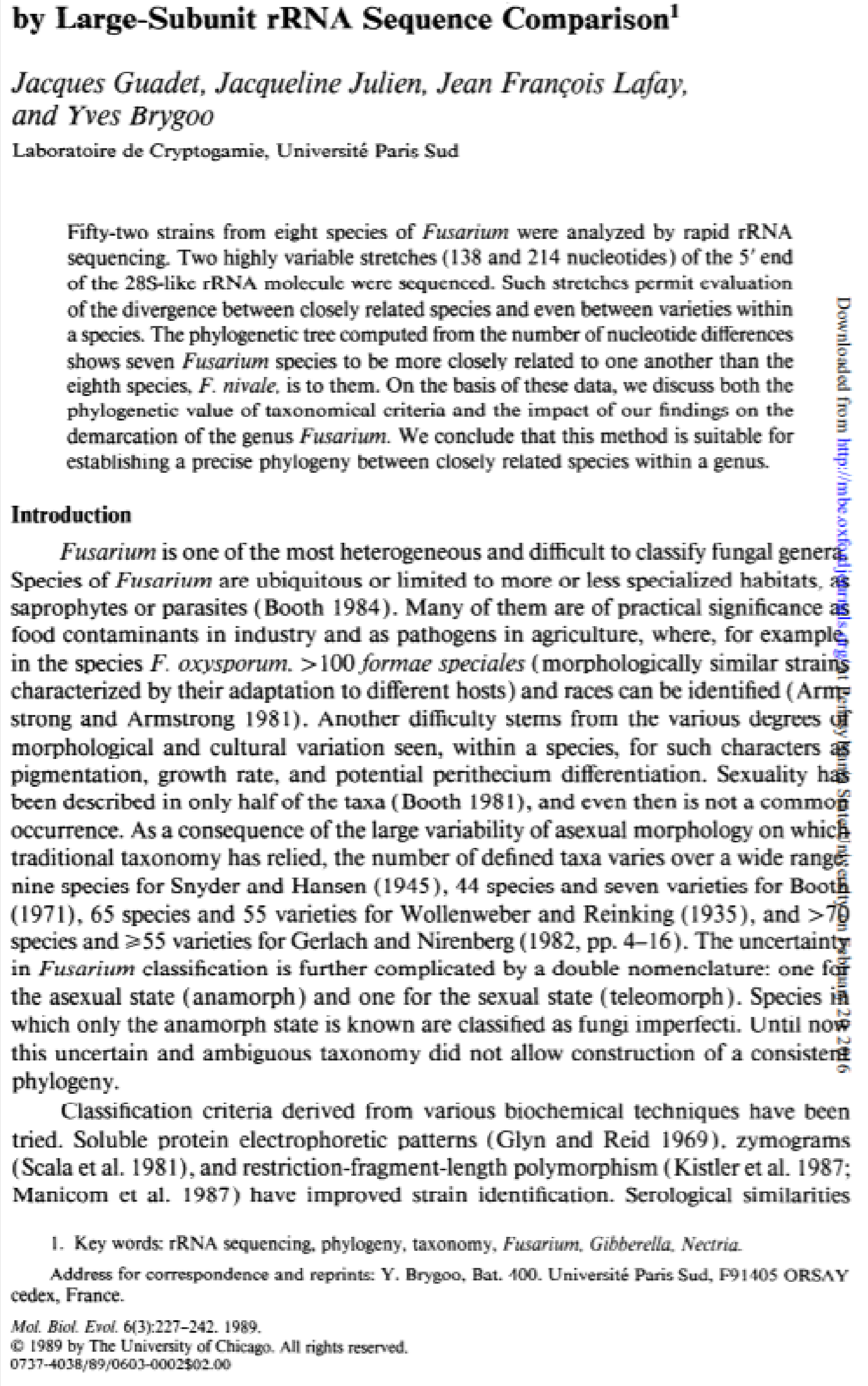

Phylogeny of Some *Fusarium* Species, as Determined by Large-Subunit rRNA Sequence Comparison[1]

Jacques Guadet, Jacqueline Julien, Jean François Lafay, and Yves Brygoo
Laboratoire de Cryptogamie, Université Paris Sud

Fifty-two strains from eight species of *Fusarium* were analyzed by rapid rRNA sequencing. Two highly variable stretches (138 and 214 nucleotides) of the 5′ end of the 28S-like rRNA molecule were sequenced. Such stretches permit evaluation of the divergence between closely related species and even between varieties within a species. The phylogenetic tree computed from the number of nucleotide differences shows seven *Fusarium* species to be more closely related to one another than the eighth species, *F. nivale*, is to them. On the basis of these data, we discuss both the phylogenetic value of taxonomical criteria and the impact of our findings on the demarcation of the genus *Fusarium*. We conclude that this method is suitable for establishing a precise phylogeny between closely related species within a genus.

Introduction

Fusarium is one of the most heterogeneous and difficult to classify fungal genera. Species of *Fusarium* are ubiquitous or limited to more or less specialized habitats, as saprophytes or parasites (Booth 1984). Many of them are of practical significance as food contaminants in industry and as pathogens in agriculture, where, for example, in the species *F. oxysporum*, >100 *formae speciales* (morphologically similar strains characterized by their adaptation to different hosts) and races can be identified (Armstrong and Armstrong 1981). Another difficulty stems from the various degrees of morphological and cultural variation seen, within a species, for such characters as pigmentation, growth rate, and potential perithecium differentiation. Sexuality has been described in only half of the taxa (Booth 1981), and even then is not a common occurrence. As a consequence of the large variability of asexual morphology on which traditional taxonomy has relied, the number of defined taxa varies over a wide range: nine species for Snyder and Hansen (1945), 44 species and seven varieties for Booth (1971), 65 species and 55 varieties for Wollenweber and Reinking (1935), and >70 species and ⩾55 varieties for Gerlach and Nirenberg (1982, pp. 4–16). The uncertainty in *Fusarium* classification is further complicated by a double nomenclature: one for the asexual state (anamorph) and one for the sexual state (teleomorph). Species in which only the anamorph state is known are classified as fungi imperfecti. Until now this uncertain and ambiguous taxonomy did not allow construction of a consistent phylogeny.

Classification criteria derived from various biochemical techniques have been tried. Soluble protein electrophoretic patterns (Glyn and Reid 1969), zymograms (Scala et al. 1981), and restriction-fragment-length polymorphism (Kistler et al. 1987; Manicom et al. 1987) have improved strain identification. Serological similarities

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[1] Key words: rRNA sequencing, phylogeny, taxonomy, *Fusarium*, *Gibberella*, *Nectria*.

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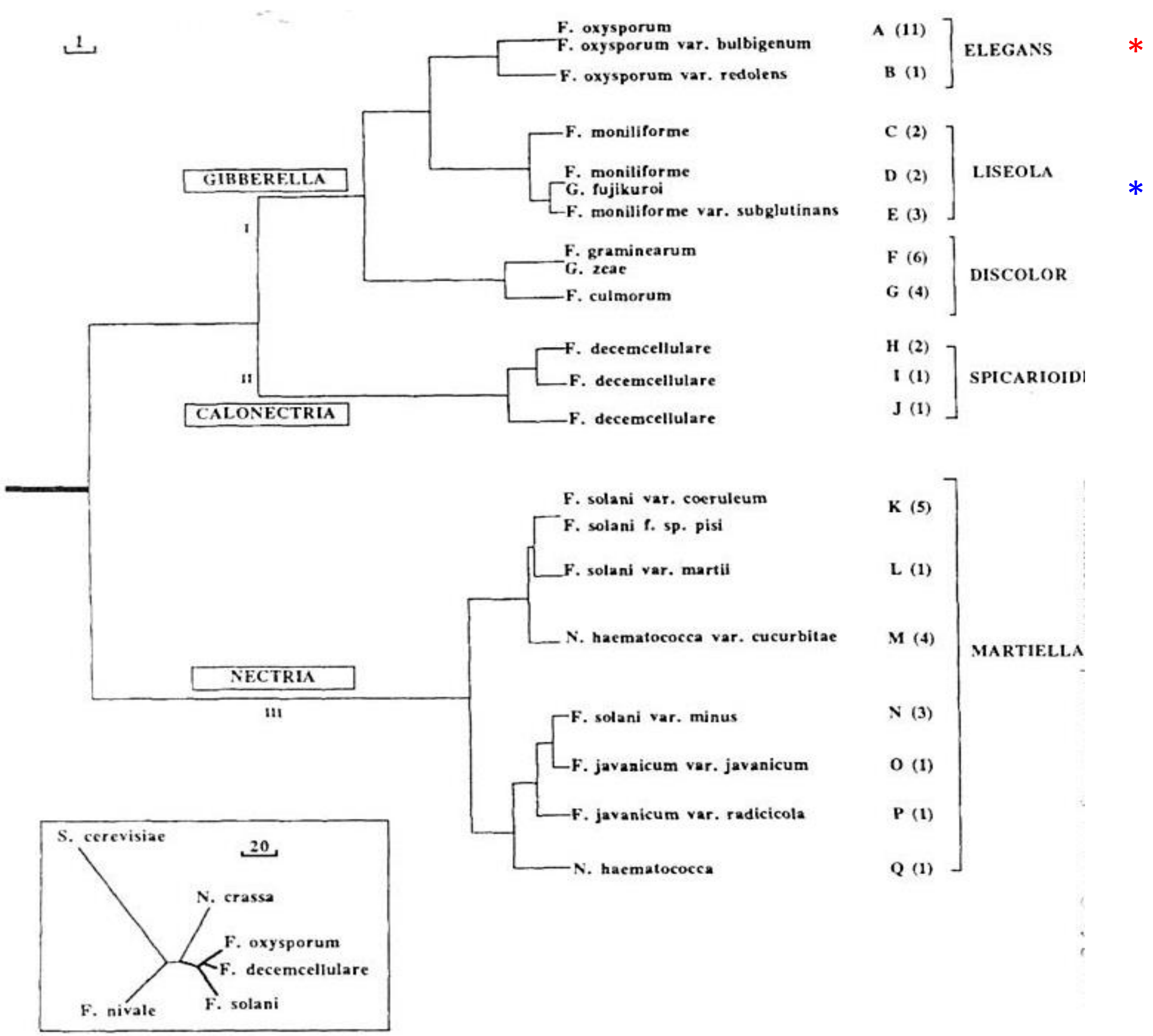
Mol. Biol. Evol. 6(3):227–242. 1989.

0737-4038/89/0603-0002$02.00



ANNUAL REVIEWS

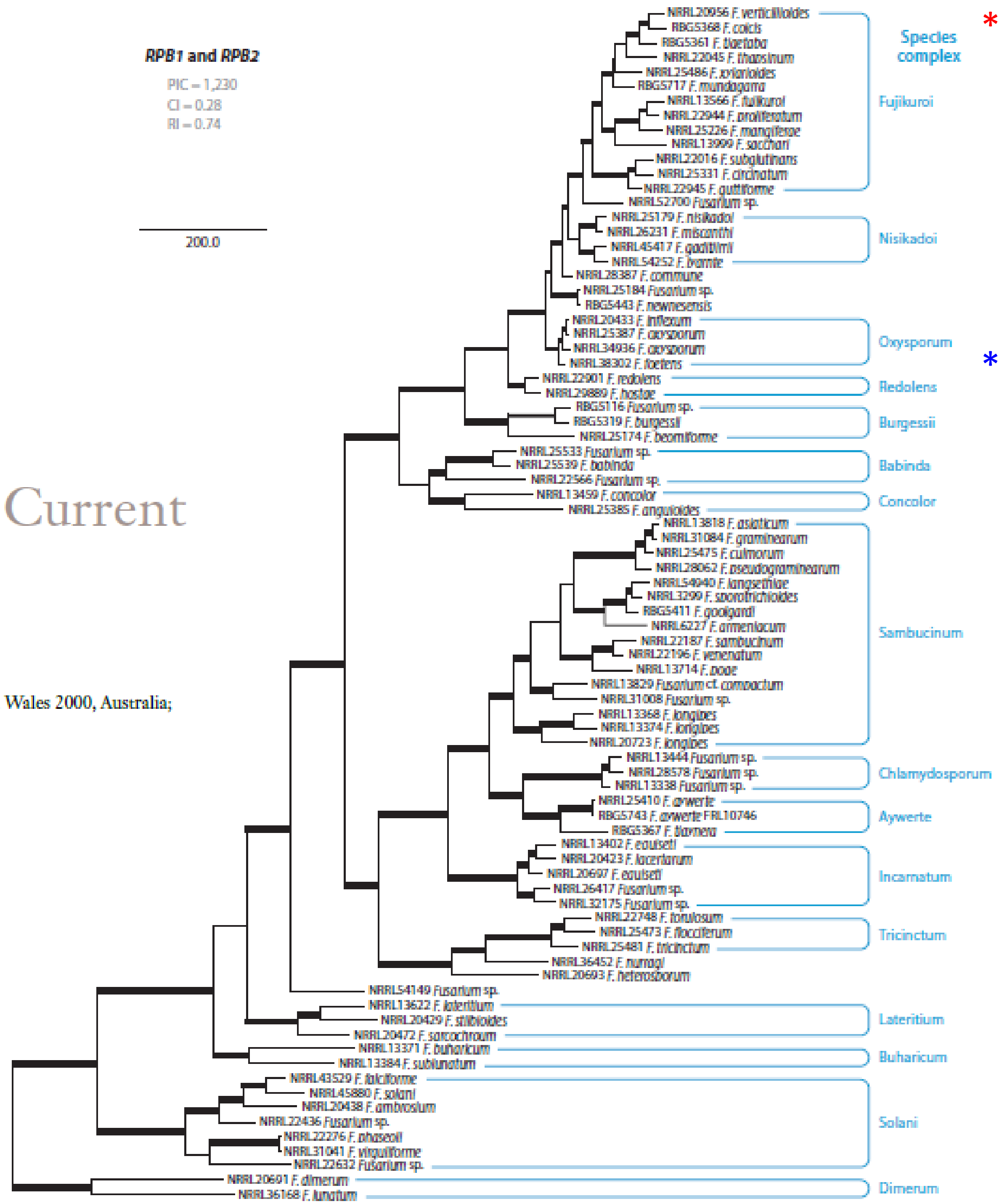
Annual Review of Phytopathology

Resolving *Fusarium*: Current Status of the Genus

Brett A. Summerell

Royal Botanic Garden and Domain Trust, Sydney, New South Wales 2000, Australia;
email: brett.summerell@rbgsyd.nsw.gov.au

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



(Caption appears on following page)

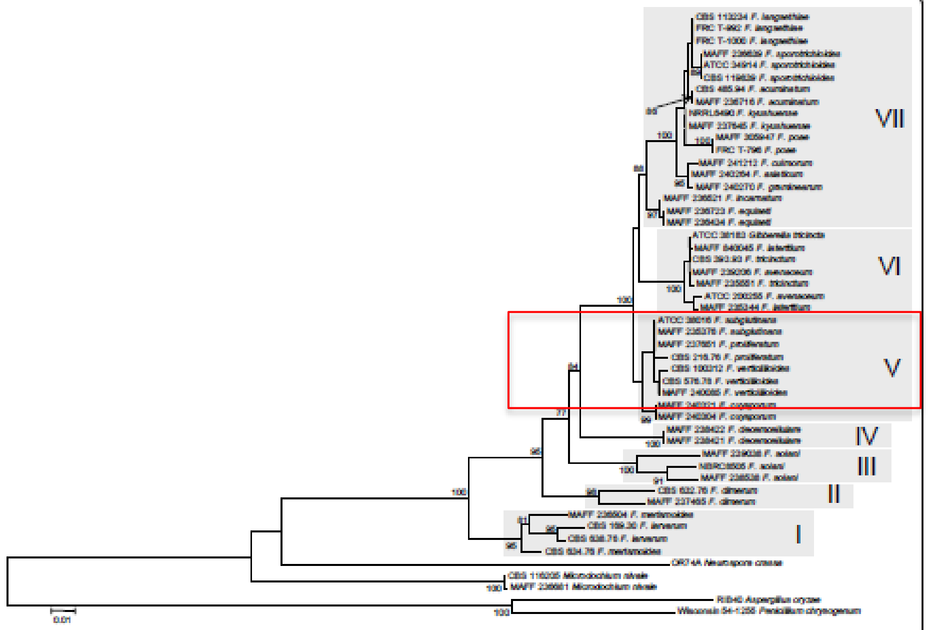


Figure 1 Maximum likelihood trees for the *Fusarium* genus and related genera inferred from the rDNA cluster including 18S rDNA, ITS1, 5.8S rDNA and 28S rDNA. The GTR + I + Γ model was used as the model for nucleotide substitution. Branch lengths are proportional to the estimated number of nucleotide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

18S, 5.8S, 28S and ITS

β-tub

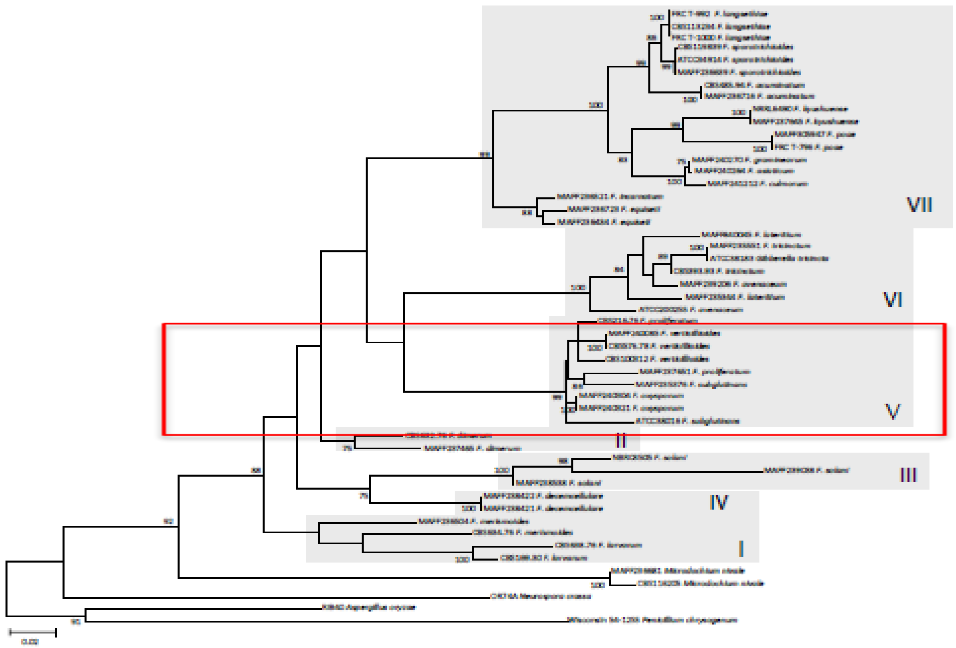


Figure 2 Maximum likelihood trees for the *Fusarium* genus and related genera inferred from *β-tub*. The GTR + I + Γ model was used as the model for nucleotide substitution. Branch lengths are proportional to the estimated number of nucleotide substitutions. Each codon position was analysed separately.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

Figure 3 Maximum likelihood trees for the *Fusarium* genus and related genera inferred from *EF-1α*. The GTR + I + Γ 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).

EF-1α

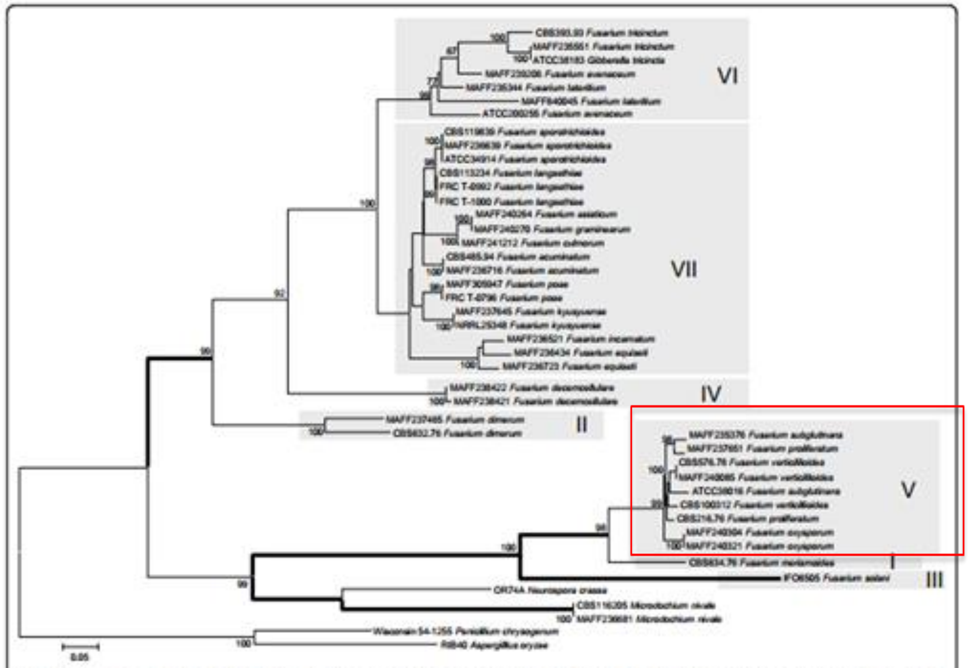


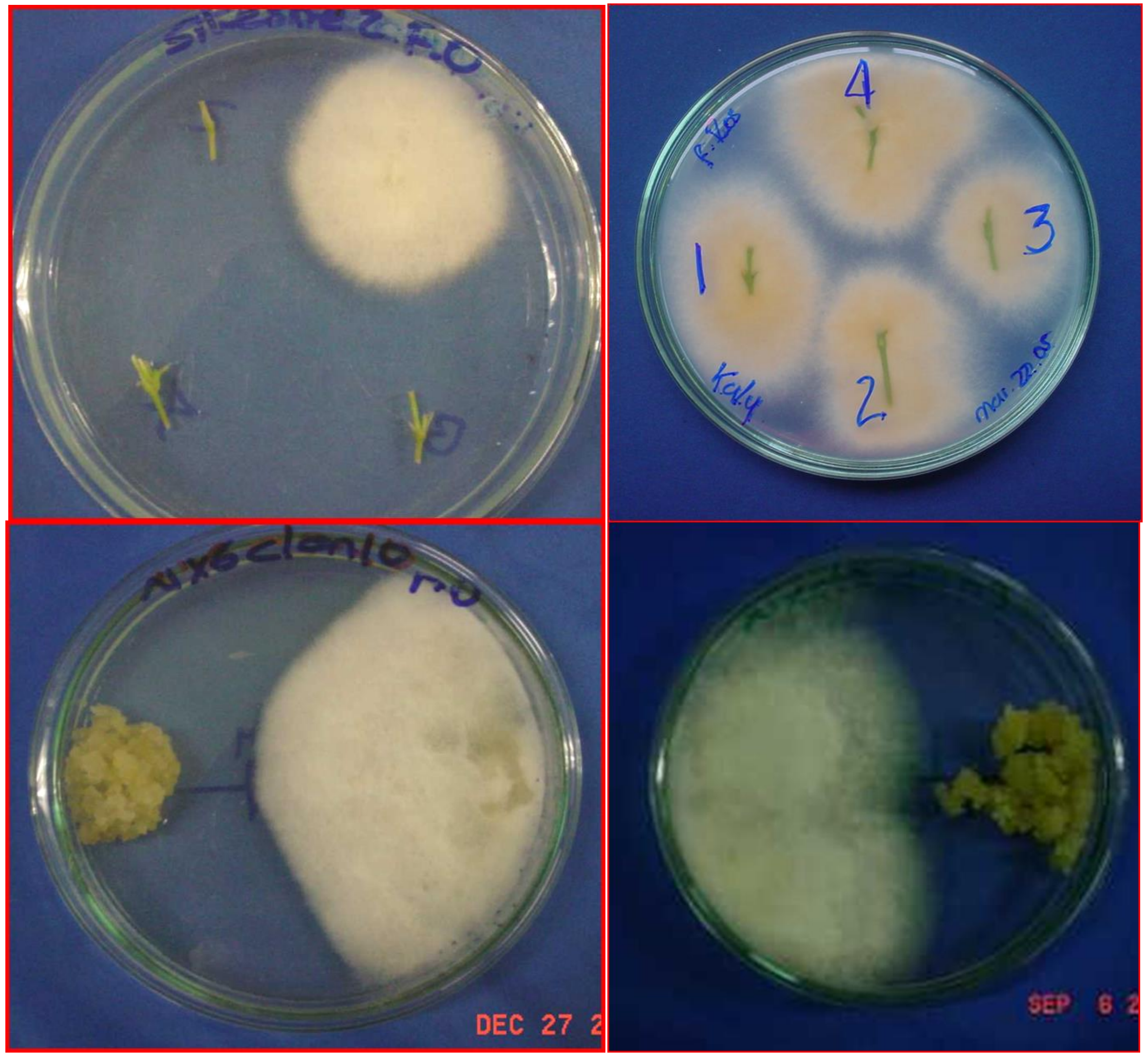
Figure 4 Maximum likelihood trees for the *Fusarium* genus and related genera inferred from *lys2*. The GTR + I + Γ model was used as the model for nucleotide substitution. Branch lengths are proportional to the estimated number of nucleotide substitutions. Each codon position was analysed separately. 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. ($p < 0.001$).

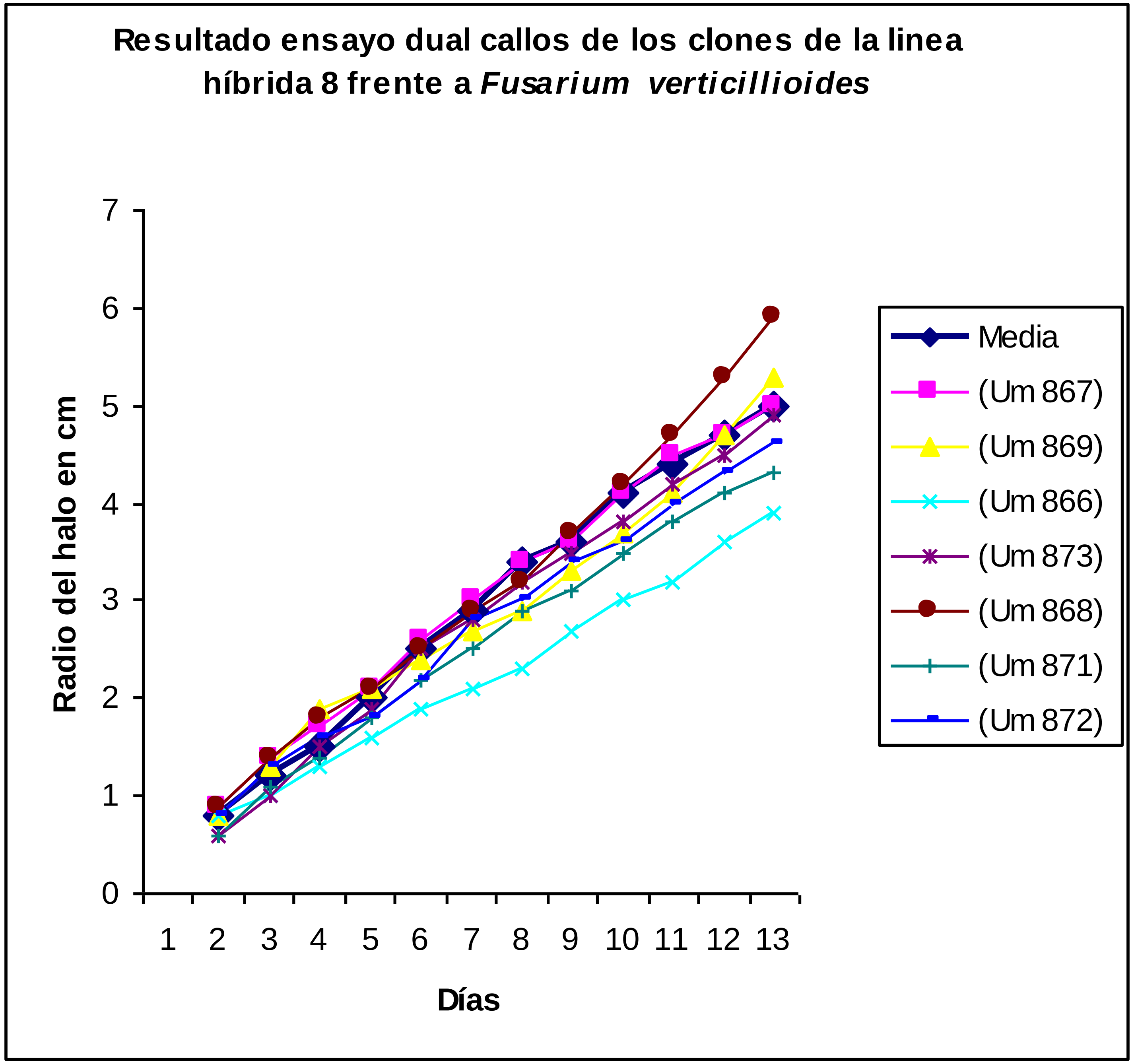
L-2-aminoadipate reductase

Molecular phylogeny of the higher and lower taxonomy of the Fusarium genus and differences in the volutionary 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. 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



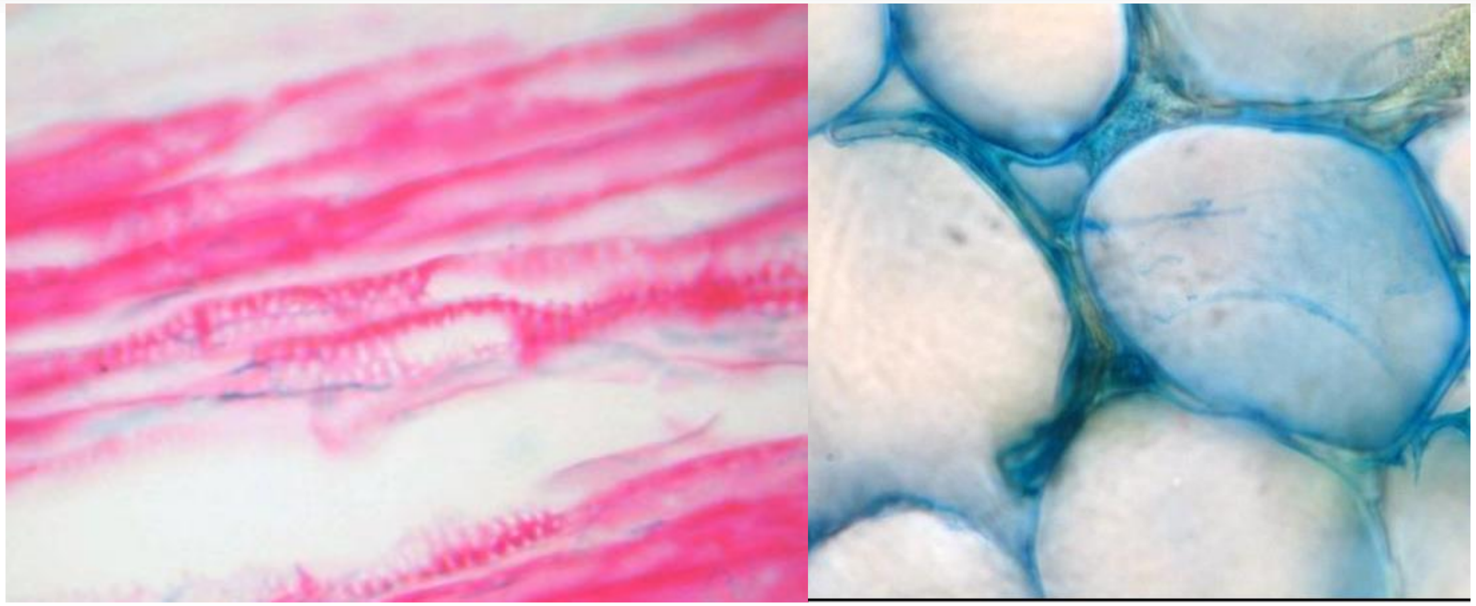


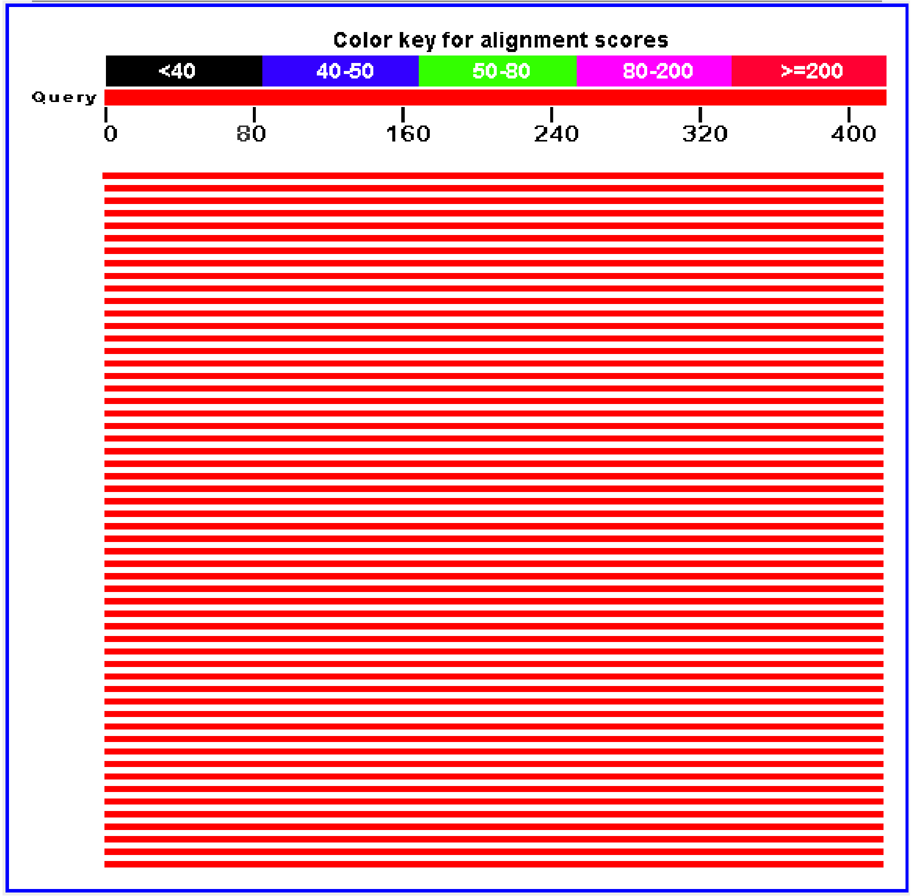
Resultado ensayo dual callos de los clones de la linea híbrida 8 frente a *Fusarium verticillioides*

UNIVERSIDAD MILITAR
NUEVA GRANADA

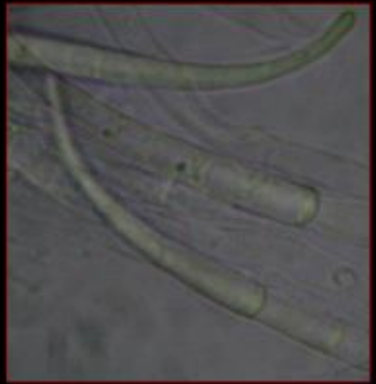
ESTUDIO DE *Fusarium foetens* ASOCIADO A LA PUDRICIÓN BASAL EN CLAVEL *(Dianthus caryophyllus* L.) VARIEDAD NELSON

BURAGLIA OSORIO, Guillermo Andrés- FILGUEIRA DUARTE, Juan Jose
Grupo de Fitopatología Molecular, Universidad Militar Nueva Granada – Colombia
muin24@gmail.com - juan.filgueira@unimilitar.edu.co

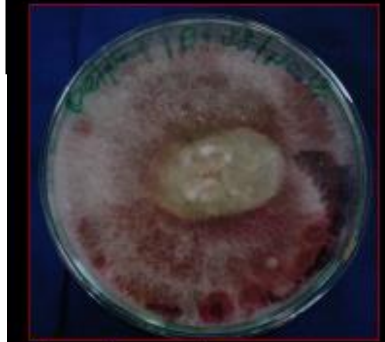




Fusarium avenaseum

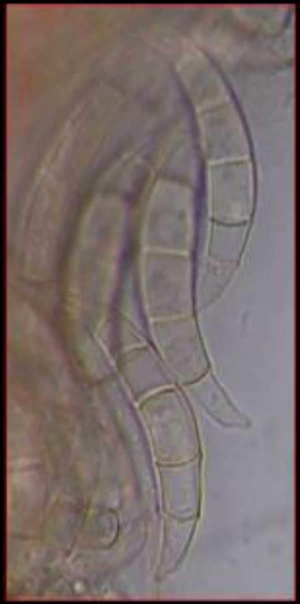


Macroconidias

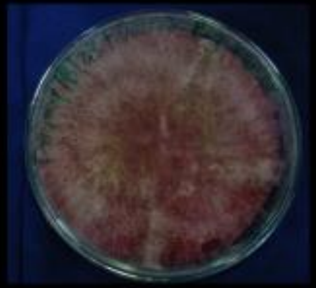


Fusarium culmorum

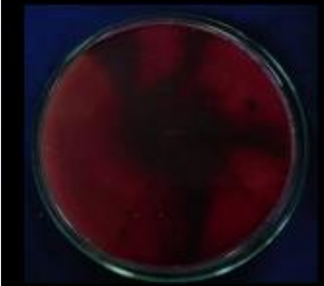
Clamidosporas



Macroconidias

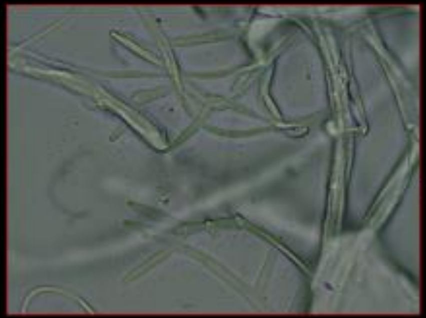


Fusarium graminearum



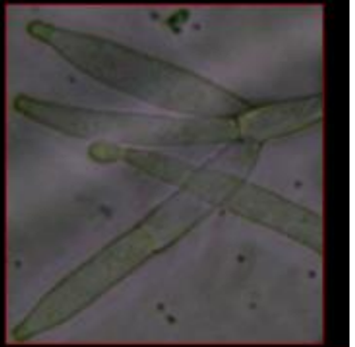
Macroconidias

Micelio de *Fusarium verticillioides*

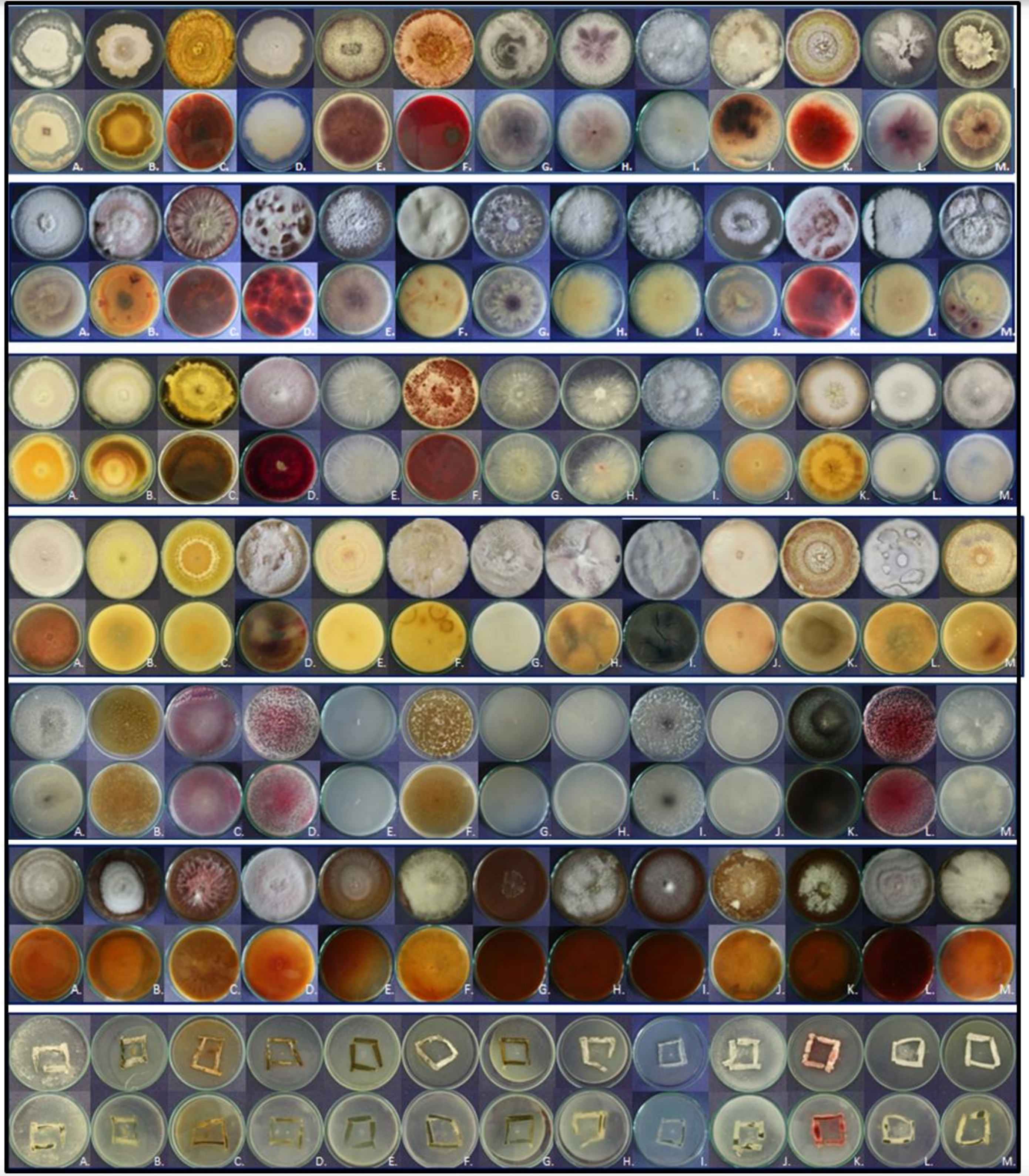


Fialides

Microconidios



Elizabeth
Monroy



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. 2014.

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

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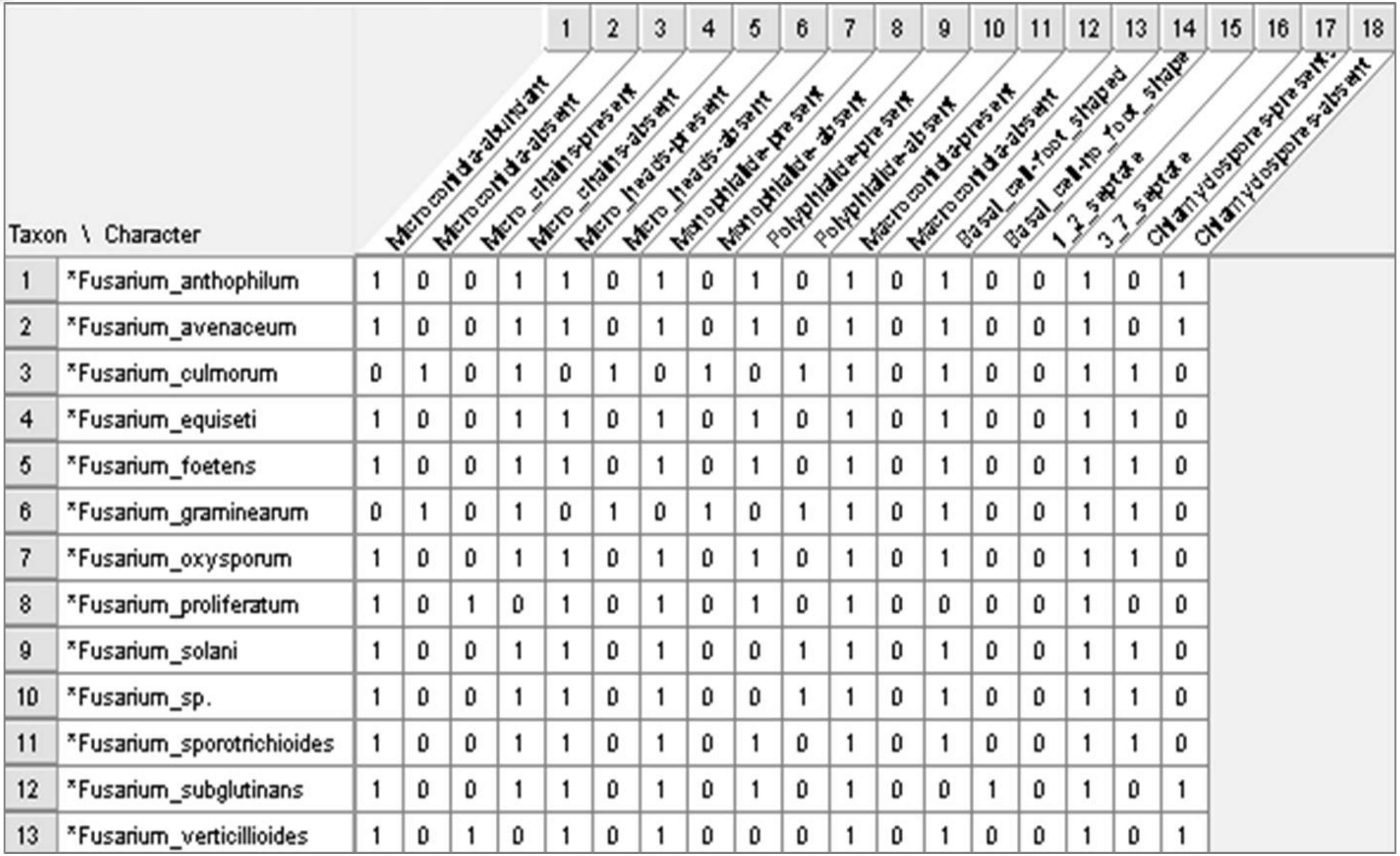
Especie	Área (µm)	Perímetro (µm)	Longitud eje mayor (µm)	Longitud eje menor (µm)
Fusarium anthophilum	59	524	216,5	34,5
Fusarium avenaceum	156	982	329	60
Fusarium culmorum	204	953	377	69
Fusarium equiseti	96	860	277	44
Fusarium foetens	163	1216	411	51
Fusarium graminearum	184,7	970	364,7	64,7
Fusarium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

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.

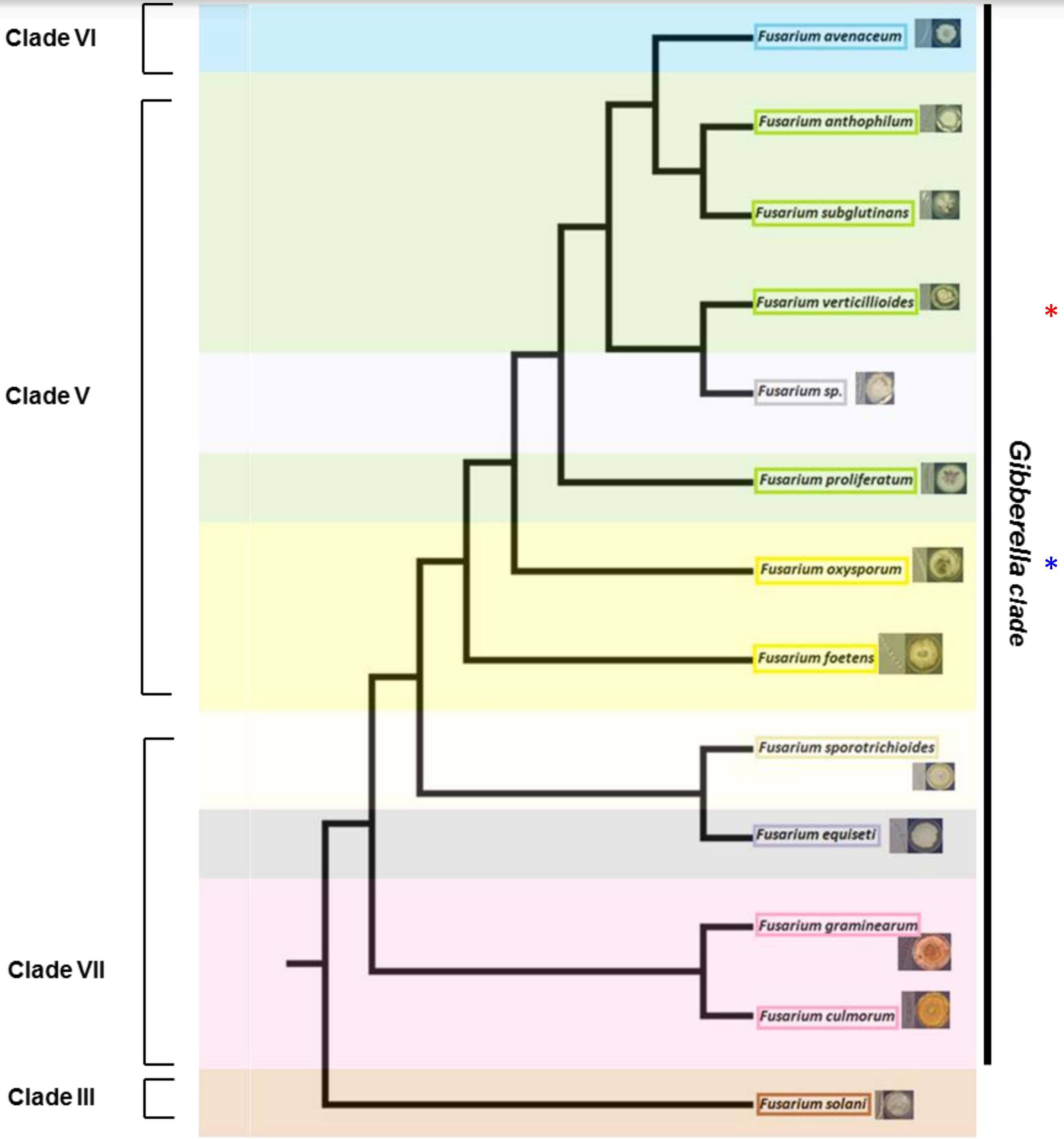
Character matrix built with Mesquite software V.2.5.



	Taxon \ Character	1 Microconidia-abundant	2 Microconidia-absent	3 Micro_chains-present	4 Micro_chains-absent	5 Micro_heads-present	6 Micro_heads-absent	7 Monophialide-present	8 Monophialide-absent	9 Polyphialide-present	10 Polyphialide-absent	11 Macroconidia-present	12 Macroconidia-absent	13 Basal_cell-foot_shaped	14 Basal_cell-no_foot_shape	15 1_3_septate	16 3_7_septate	17 Chlamydospores-present	18 Chlamydospores-absent
1	*Fusarium_anthophilum	1	0	0	1	1	0	1	0	1	0	1	0	1	0	0	1	0	1
2	*Fusarium_avenaceum	1	0	0	1	1	0	1	0	1	0	1	0	1	0	0	1	0	1
3	*Fusarium_culmorum	0	1	0	1	0	1	0	1	0	1	1	0	1	0	0	1	1	0
4	*Fusarium_equiseti	1	0	0	1	1	0	1	0	1	0	1	0	1	0	0	1	1	0
5	*Fusarium_foetens	1	0	0	1	1	0	1	0	1	0	1	0	1	0	0	1	1	0
6	*Fusarium_graminearum	0	1	0	1	0	1	0	1	0	1	1	0	1	0	0	1	1	0
7	*Fusarium_oxysporum	1	0	0	1	1	0	1	0	1	0	1	0	1	0	0	1	1	0
8	*Fusarium_proliferatum	1	0	1	0	1	0	1	0	1	0	1	0	0	0	0	1	0	0
9	*Fusarium_solani	1	0	0	1	1	0	1	0	0	1	1	0	1	0	0	1	1	0
10	*Fusarium_sp.	1	0	0	1	1	0	1	0	0	1	1	0	1	0	0	1	1	0
11	*Fusarium_sporotrichioides	1	0	0	1	1	0	1	0	1	0	1	0	1	0	0	1	1	0
12	*Fusarium_subglutinans	1	0	0	1	1	0	1	0	1	0	1	0	0	1	0	1	0	1
13	*Fusarium_verticillioides	1	0	1	0	1	0	1	0	0	0	1	0	1	0	0	1	0	1

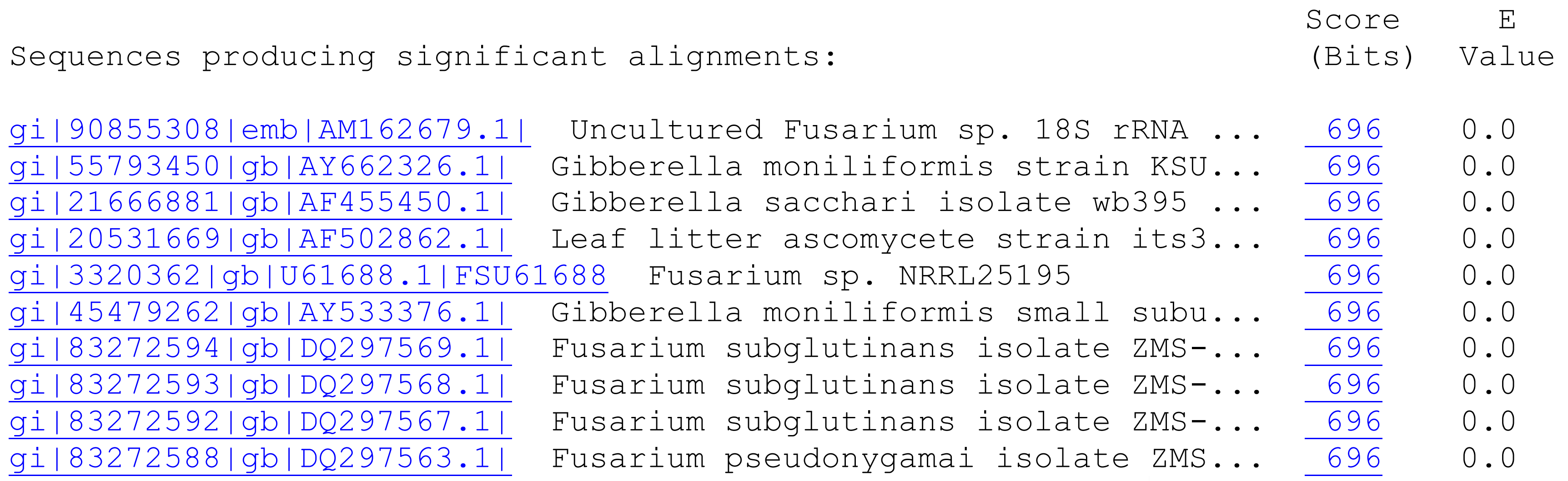
Uso de microsecuencias de genes útiles para hacer filogenia molecular para resolver problemas de clasificación taxonómica en el género *Fusarium*. **Cindy Melissa Rincón**. Universidad Nacional de Colombia. Maestría en Microbiología, Bogotá Colombia.

Dendrogram of the characters matrix using Mezquite



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.

F. verticilliodes – Aislamiento Sopo



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                                                                Score     E
Sequences producing significant alignments:                     (Bits)  Value

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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
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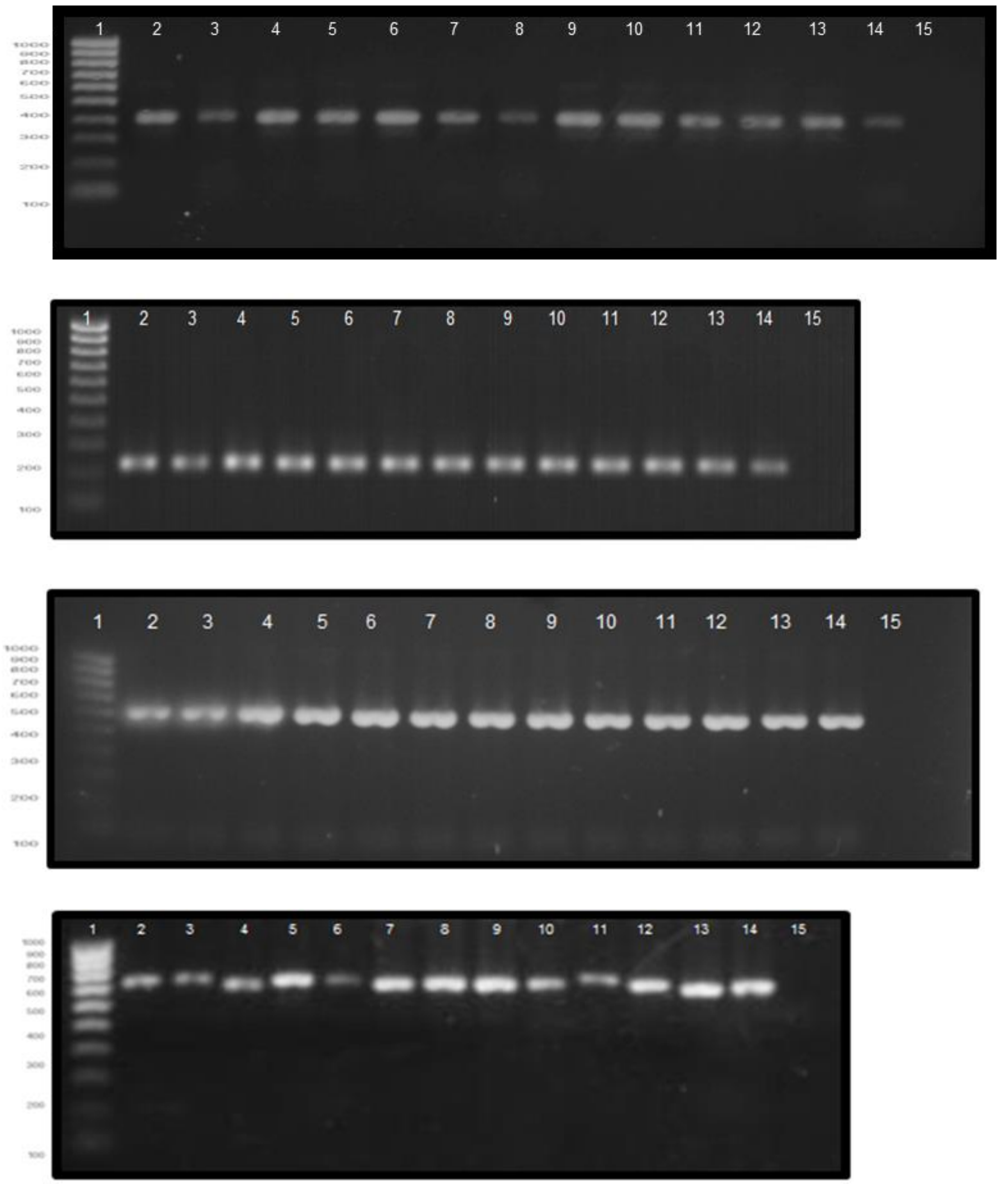

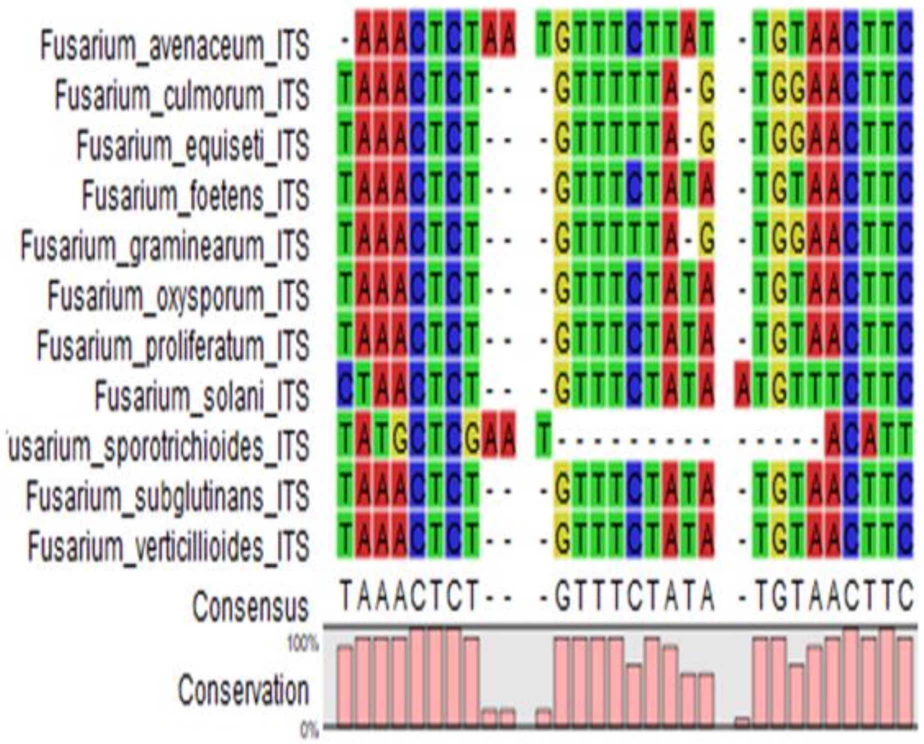

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Fusarium_avenaceum_ITS          -AAACTCTAA  TGTTTCTTAT  -TGTAACTTC
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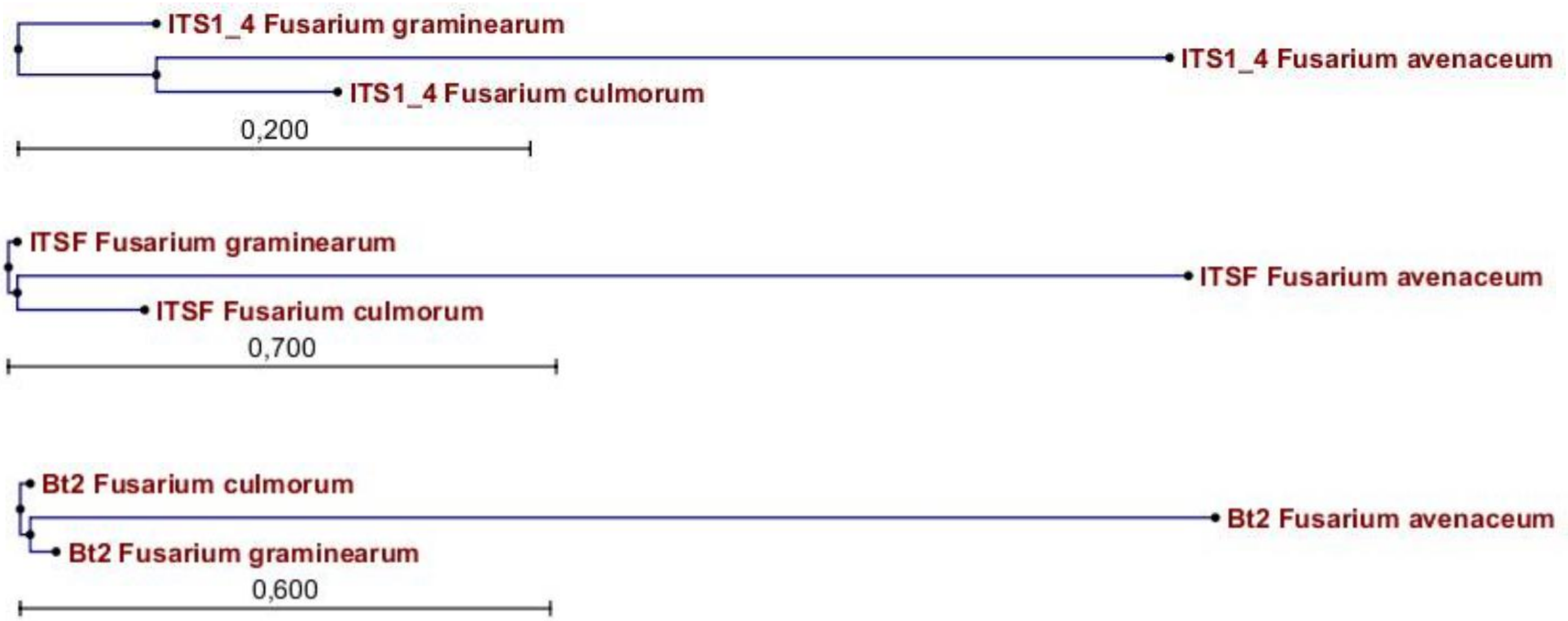
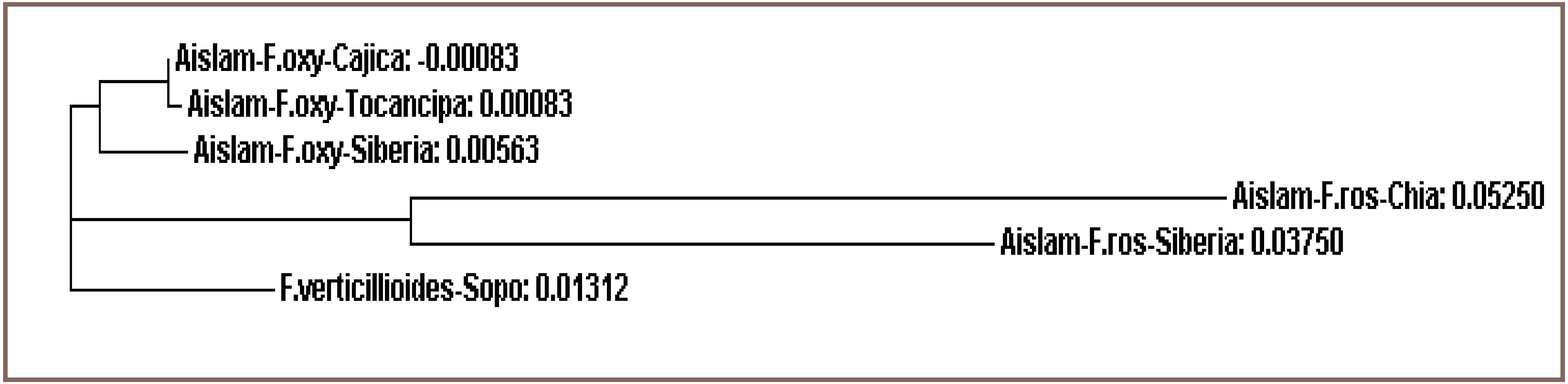
Fusarium_equiseti_ITS           TAAACTCT--  -GTTTTTA-G  -TGGAACTTC
Fusarium_foetens_ITS            TAAACTCT--  -GTTTCTATA  -TGTAACTTC
Fusarium_graminearum_ITS        TAAACTCT--  -GTTTTTA-G  -TGGAACTTC
Fusarium_oxysporum_ITS          TAAACTCT--  -GTTTCTATA  -TGTAACTTC
Fusarium_proliferatum_ITS       TAAACTCT--  -GTTTCTATA  -TGTAACTTC
Fusarium_solani_ITS             CTAACTCT--  -GTTTCTATA  ATGTTTCTTC
usarium_sporotrichioides_ITS    TATGCTCGAA  T---------  -----ACATT
Fusarium_subglutinans_ITS       TAAACTCT--  -GTTTCTATA  -TGTAACTTC
Fusarium_verticillioides_ITS    TAAACTCT--  -GTTTCTATA  -TGTAACTTC

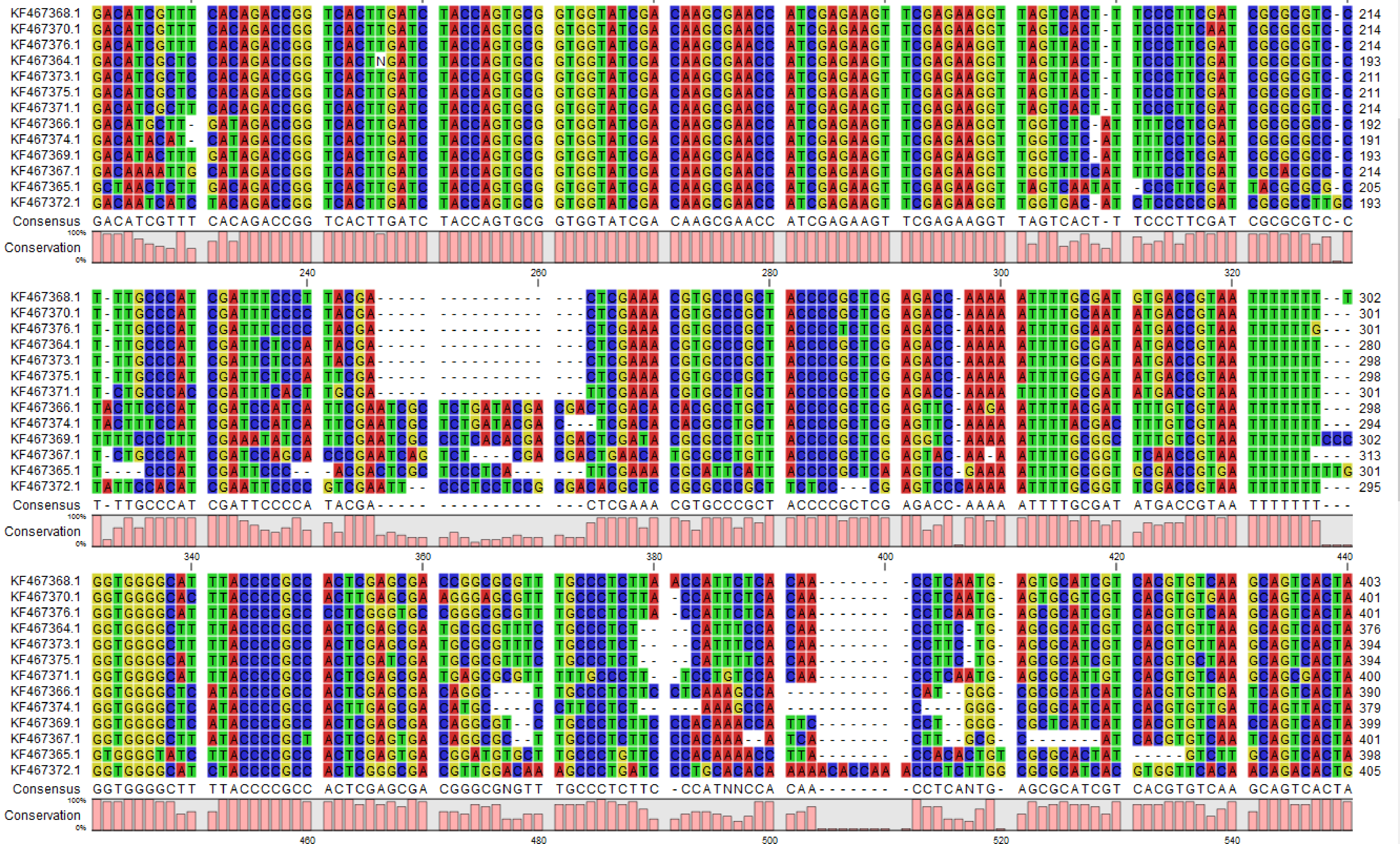
Consensus                       TAAACTCT--  -GTTTCTATA  -TGTAACTTC
```

Genetic differences between regions of the same locus



Genetic variations between different FOX isolates in different farms





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KF467370.1  GACATCGTTT CACAGACCGG TCACTTGATC TACCAGTGCG GTGGTATCGA CAAGCGAACC ATCGAGAAGT TCGAGAAGGT TAGTCACT-T TCCCTTCAAT CGCGCGTC-C 214
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KF467367.1  GACAAAATTG CATAGACCGG TCACTTGATC TACCAGTGCG GTGGTATCGA CAAGCGAACC ATCGAGAAGT TCGAGAAGGT TGGTTTCCAT TTTCCTCGAT CGCACGCC-C 214
KF467365.1  GCTAACTCTT GACAGACCGG TCACTTGATC TACCAGTGCG GTGGTATCGA CAAGCGAACC ATCGAGAAGT TCGAGAAGGT TAGTCAATAT -CCCTTCGAT TACGCGCG-C 205
KF467372.1  GACAATCATC TACAGACCGG TCACTTGATC TACCAGTGCG GTGGTATCGA CAAGCGAACC ATCGAGAAGT TCGAGAAGGT TGGTGAC-AT CTCCCCCGAT CGCGCCTTGC 193
Consensus   GACATCGTTT CACAGACCGG TCACTTGATC TACCAGTGCG GTGGTATCGA CAAGCGAACC ATCGAGAAGT TCGAGAAGGT TAGTCACT-T TCCCTTCGAT CGCGCGTC-C
Conservation
                               240                   260                   280                   300                   320

KF467368.1  T-TTGCCCAT CGATTTCCCT TACGA----- ---------- ---CTCGAAA CGTGCCCGCT ACCCCGCTCG AGACC-AAAA ATTTTGCGAT GTGACCGTAA TTTTTTT--T 302
KF467370.1  T-TTGCCCAT CGATTTCCCC TACGA----- ---------- ---CTCGAAA CGTGCCCGCT ACCCCGCTCG AGACC-AAAA ATTTTGCAAT ATGACCGTAA TTTTTTT--- 301
KF467376.1  T-TTGCCCAT CGATTTCCCC TACGA----- ---------- ---CTCGAAA CGTGCCCGCT ACCCCTCTCG AGACC-AAAA ATTTTGCAAT ATGACCGTAA TTTTTTG--- 301
KF467364.1  T-TTGCCCAT CGATTCTCCA TACGA----- ---------- ---CTCGAAA CGTGCCCGCT ACCCCGCTCG AGACC-AAAA ATTTTGCGAT ATGACCGTAA TTTTTTT--- 280
KF467373.1  T-TTGCCCAT CGATTCTCCA TACGA----- ---------- ---CTCGAAA CGTGCCCGCT ACCCCGCTCG AGACC-AAAA ATTTTGCGAT ATGACCGTAA TTTTTTT--- 298
KF467375.1  T-TTGCCCAT CGATTCTCCA TTCGA----- ---------- ---CTCGAAA CGTGCCCGCT ACCCCGCTCG AGACC-AAAA ATTTTGCGAT ATGACCGTAA TTTTTTT--- 298
KF467371.1  T-CTGCCCAC CGATTTCACT TGCGA----- ---------- ---TTCGAAA CGTGCCTGCT ACCCCGCTCG AGACC-AAAA TTTTTGCGAT ATGACCGTAA TTTTTTT--- 301
KF467366.1  TACTTCCCAT CGATCCATCA TTCGAATCGC TCTGATACGA CGACTCGACA CACGCCTGCT ACCCCGCTCG AGTTC-AAGA ATTTTACGAT TTTGTCGTAA TTTTTTT--- 298
KF467374.1  TACTTTCCAT CGATCCATCA TTCGAATCGC TCTGATACGA C---TCGACA CACGCCTGCT ACCCCGCTCG AGTTC-AAAA ATTTTACGAC TTTGTCGTAA TTTTTTT--- 294
KF467369.1  TTTTCCCTTT CGAAATATCA TTCGAATCGC CCTCACACGA CGACTCGATA CGCGCCTGTT ACCCCGCTCG AGGTC-AAAA ATTTTGCGGC TTTGTCGTAA TTTTTTTCCC 302
KF467367.1  T-CTGCCCAT CGATCCAGCA CCCGAATCAG TCT----CGA CGACTGAACA TGCGCCTGTT ACCCCGCTCG AGTAC-AA-A ATTTTGCGGT TCAACCGTAA TTTTTT---- 313
KF467365.1  T----CCCAT CGATTCCC-- -ACGACTCGC TCCCTCA--- ---TTCGAAA CGCATTCATT ACCCCGCTCA AGTCC-GAAA ATTTTGCGGT GCGACCGTGA TTTTTTTTTG 301
KF467372.1  TATTCCACAT CGAATTCCCC GTCGAATT-- CCCTCCTCCG CGACACGCTC CGCGCCCGCT TCTCC---CG AGTCCCAAAA ATTTTGCGGT TCGACCGTAA TTTTTTT--- 295
Consensus   T-TTGCCCAT CGATTCCCCA TACGA----- ---------- ---CTCGAAA CGTGCCCGCT ACCCCGCTCG AGACC-AAAA ATTTTGCGAT ATGACCGTAA TTTTTTT---
Conservation
                               340                   360                   380                   400                   420                   440

KF467368.1  GGTGGGGCAT TTACCCCGCC ACTCGAGCGA CCGGCGCGTT TGCCCTCTTA ACCATTCTCA CAA------- -CCTCAATG- AGTGCATCGT CACGTGTCAA GCAGTCACTA 403
KF467370.1  GGTGGGGCAC TTACCCCGCC ACTTGAGCGA AGGGAGCGTT TGCCCTCTTA -CCATTCTCA CAA------- -CCTCAATG- AGTGCGTCGT CACGTGTGAA GCAGTCACTA 401
KF467376.1  GGTGGGGCAT TTACCCCGCC CCTCGGGTGC CGGGCGCGTT TGCCCTCTTA -CCATTCTCA CAA------- -CCTCAATG- AGCGCATCGT CACGTGTCAA GCAGTCACTA 401
KF467364.1  GGTGGGGCTT TTACCCCGCC ACTCGAGCGA TGCGCGTTTC TGCCCTCT-- --CATTTCCA CAA------- -CCTTC-TG- AGCGCATCGT CACGTGTTAA GCAGTCACTA 376
KF467373.1  GGTGGGGCTT TTACCCCGCC ACTCGAGCGA TGCGCGTTTC TGCCCTCT-- --CATTTCCA CAA------- -CCTTC-TG- AGCGCATCGT CACGTGTTAA GCAGTCACTA 394
KF467375.1  GGTGGGGCAT TTACCCCGCC ACTCGATCGA TGCGCGTTTC TGCCCTCT-- --CATTTTCA CAA------- -CCTTC-TG- AGCGCATCGT CACGTGCTAA GCAGTCACTA 394
KF467371.1  GGTGGGGCAT TTACCCCGCC ACTCGAGCGA TGAGCGCGTT TTTGCCCTT- -TCCTGTCCA CAA------- -CCTCAATG- AGCGCATTGT CACGTGTCAA GCAGCGACTA 400
KF467366.1  GGTGGGGCTC ATACCCCGCC ACTCGAGCGA CAGGC----T TGCCCTCTTC CTCAAAGCCA ---------- -CAT--GGG- CGCGCATCAT CACGTGTTGA TCAGTCACTA 390
KF467374.1  GGTGGGGCTC ATACCCCGCC ACTTGAGCGA CATGC----C CTTCCTCT-- ---AAAGCCA ---------- -C----GGG- CGCGCATCAT CACGTGTTGA TCAGTTACTA 379
KF467369.1  GGTGGGGCTC ATACCCCGCC ACTCGAGCGA CAGGCGT--C TGCCCTCTTC CCACAAACCA TTC------- -CCT--GGG- CGCTCATCAT CACGTGTCAA CCAGTCACTA 399
KF467367.1  GGTGGGGCTT ATACCCCGCT ACTCGAGTGA CAGGCGC--T TGCCCTCTTC CCACAAA--A TCA------- -CTT--GCG- C-------AT CACGTGTCAA TCAGTCACTA 401
KF467365.1  GTGGGGTATC TTACCCCGCC ACTCGAGTGA CGGATGTGCT TGCCCTGTTC CCACAAAACC TTA------- -CCACACTGT CGCGCACTAT -----GTCTT GCAGTCACTA 398
KF467372.1  GGTGGGGCAT CTACCCCGCC ACTCGGGCGA CGTTGGACAA AGCCCTGATC CCTGCACACA AAAACACCAA ACCCTCTTGG CGCGCATCAC GTGGTTCACA ACAGACACTG 405
Consensus   GGTGGGGCTT TTACCCCGCC ACTCGAGCGA CGGGCGNGTT TGCCCTCTTC -CCATNNCCA CAA------- -CCTCANTG- AGCGCATCGT CACGTGTCAA GCAGTCACTA
Conservation
                               460                   480                   500                   520                   540
```
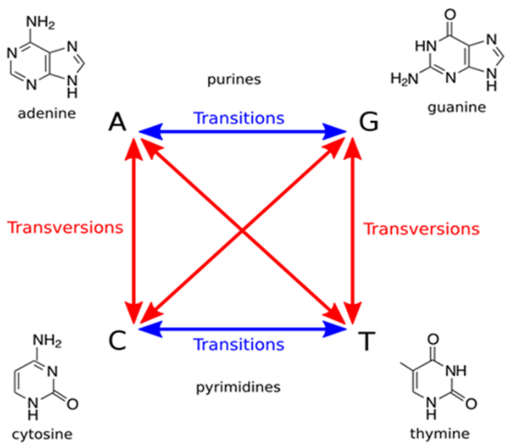
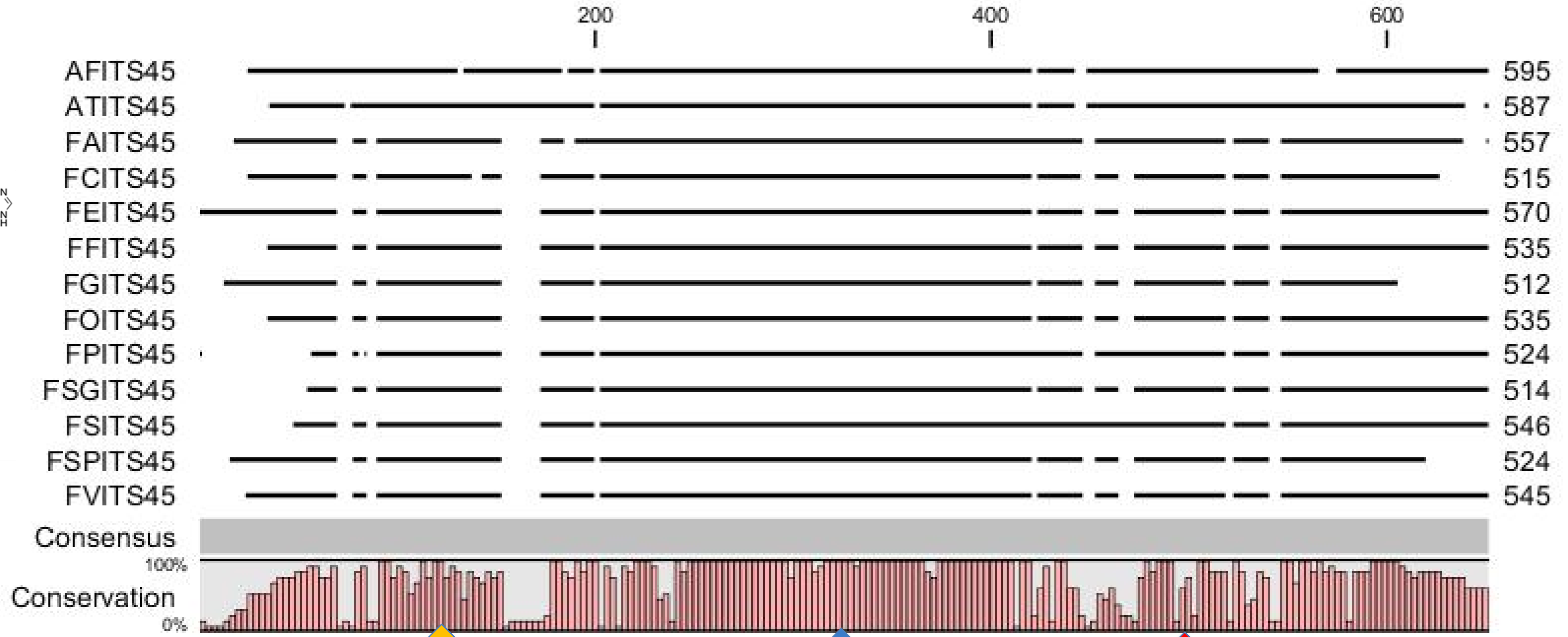

DNA Micro-Sequences Obtaining





Partially Conserved

Conserved

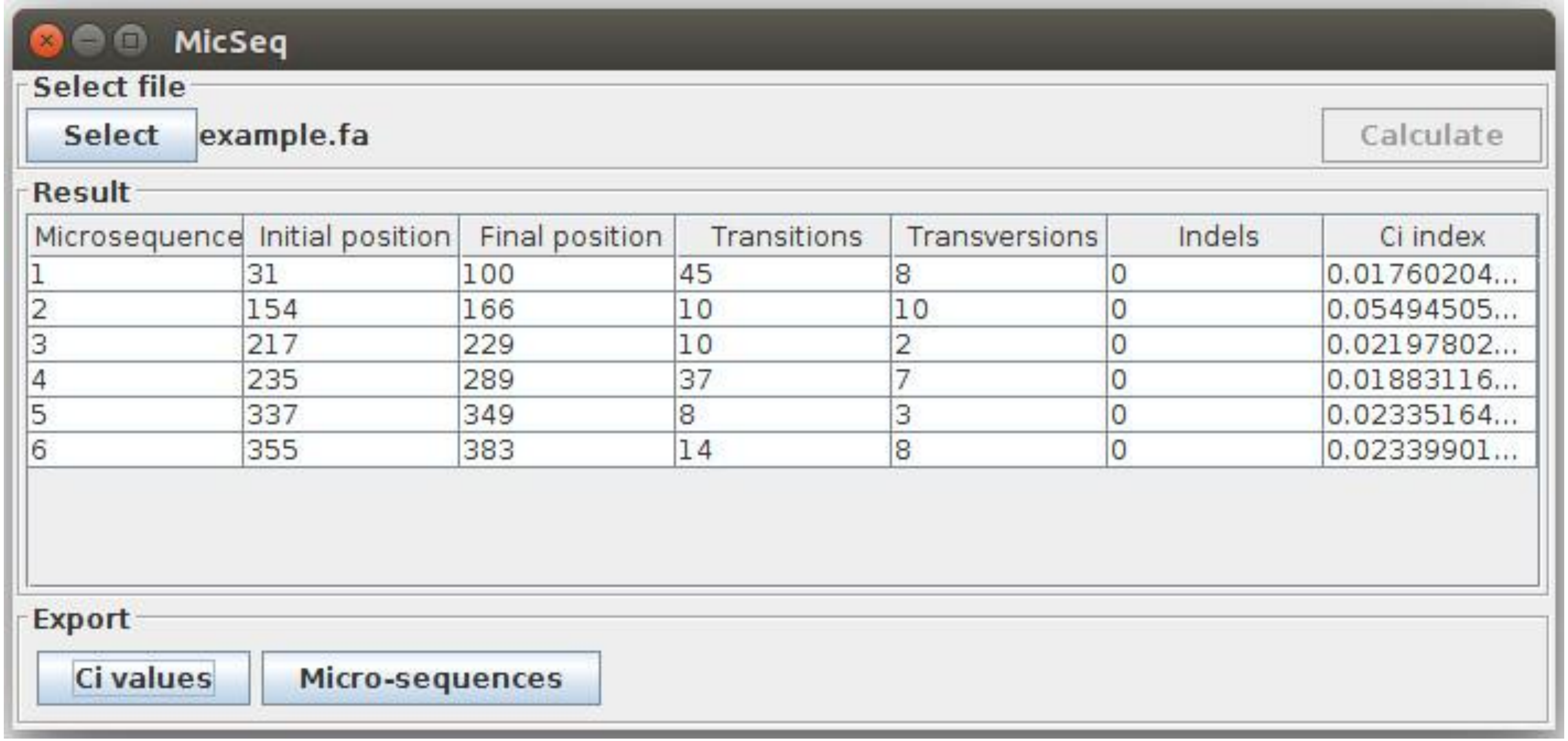
No Conserved

Calculate the Sequence variation (Sv)

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

Tv = Transversions Ti = Transitions

Phylogenetic analysis of a group of species of the genus *Fusarium* using DNA microsequences
J. J. FILGUEIRA-DUARTE (1), M. Rincon (1)
(1) Universidad Militar Nueva Granada, Bogotá, Colombia
Phytopathology 102:S4.39

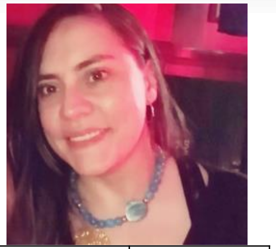


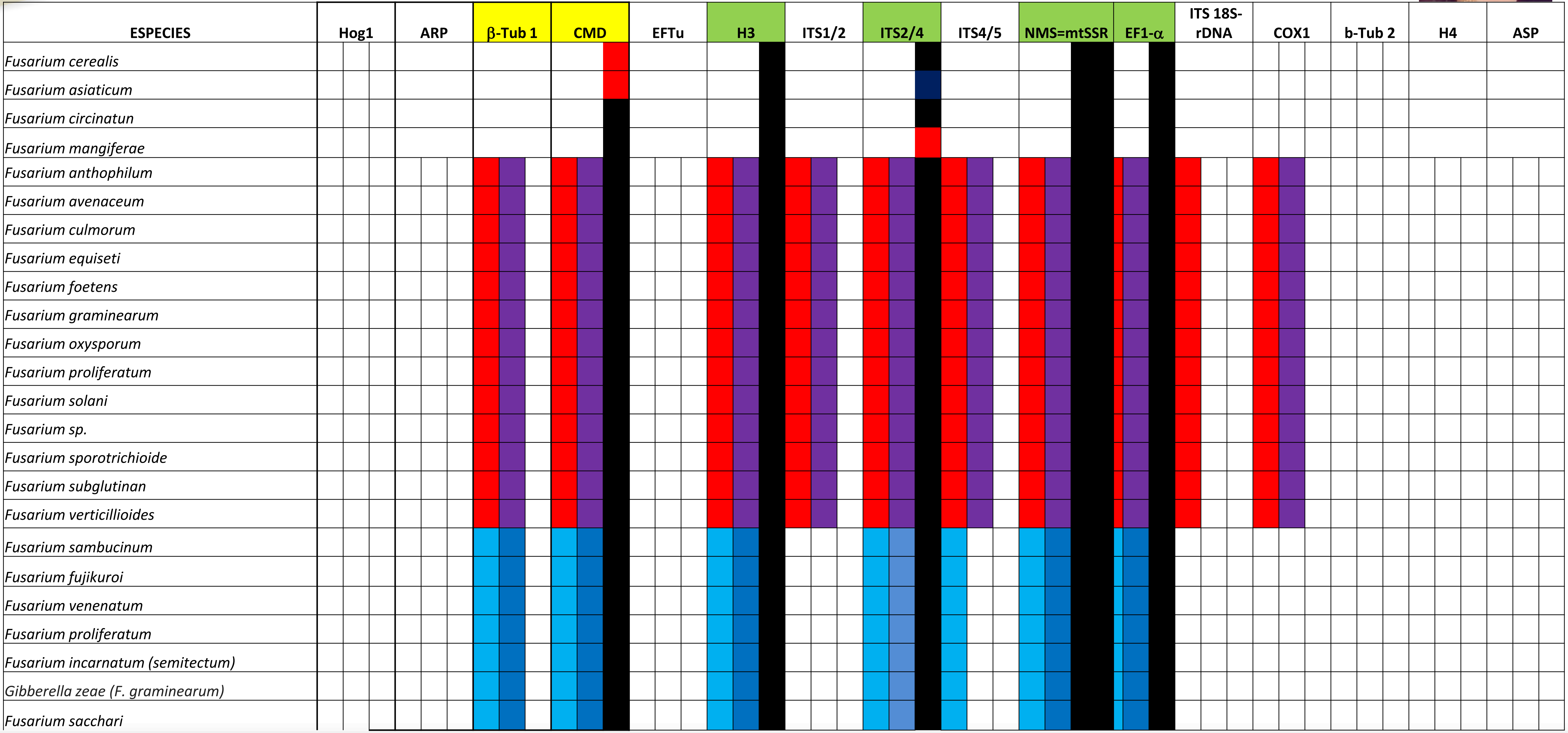
example.fa

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...

24 Fusarium species
16 Genes evaluados

María Fernanda Cadena



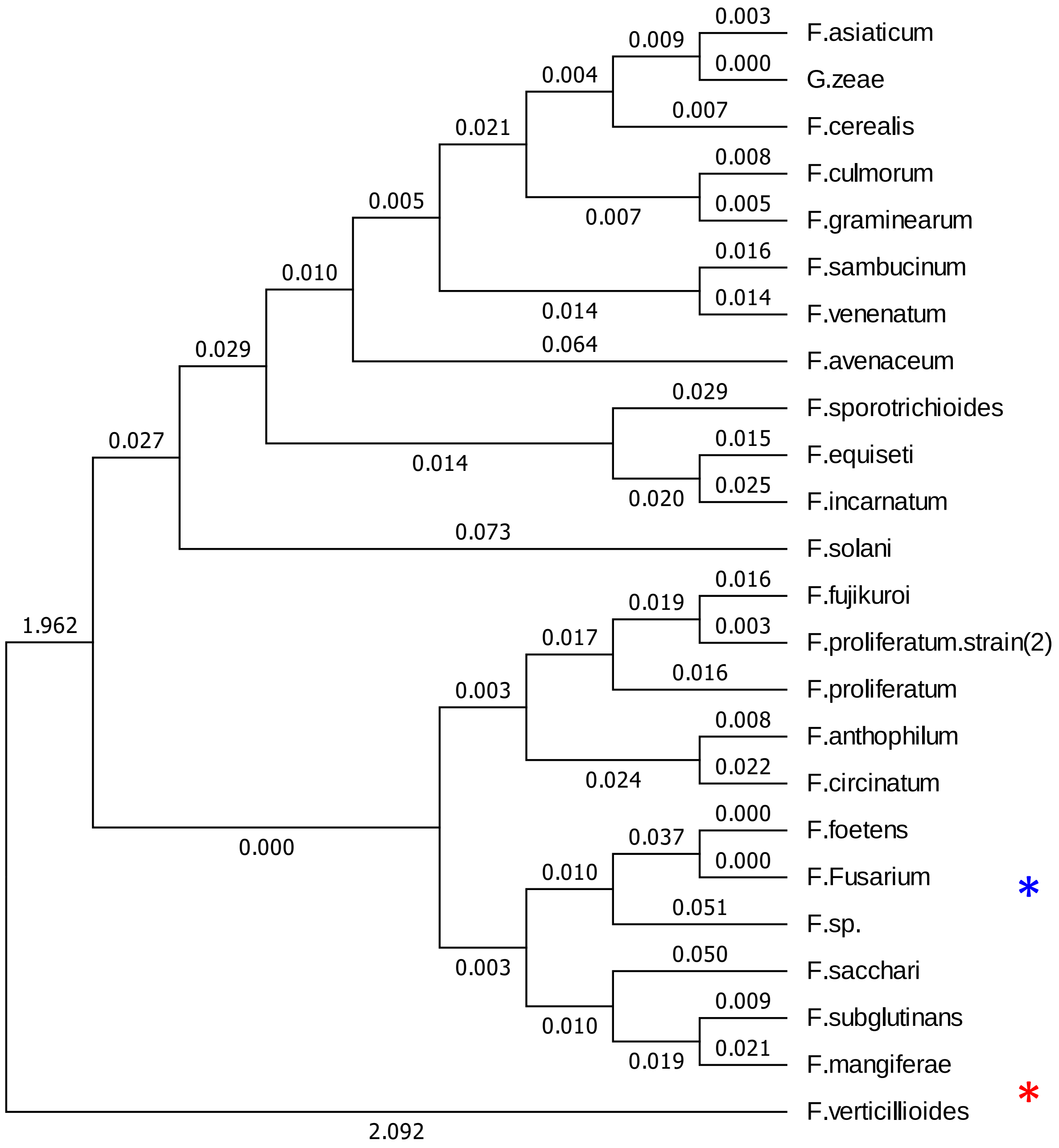


ESPECIES	Hog1	ARP	β-Tub 1	CMD	EFTu	H3	ITS1/2	ITS2/4	ITS4/5	NMS=mtSSR	EF1-α	ITS 18S-rDNA	COX1	b-Tub 2	H4	ASP
Fusarium cerealis				🟥		⬛		⬛		⬛	⬛					
Fusarium asiaticum				🟥		⬛		🟦		⬛	⬛					
Fusarium circinatun				⬛		⬛		⬛		⬛	⬛					
Fusarium mangiferae				⬛		⬛		🟥		⬛	⬛					
Fusarium anthophilum			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium avenaceum			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium culmorum			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium equiseti			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium foetens			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium graminearum			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium oxysporum			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium proliferatum			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium solani			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium sp.			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium sporotrichioide			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium subglutinan			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium verticillioides			🟥🟪	🟥🟪⬛		🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪	🟥🟪⬛	🟥🟪⬛	🟥	🟥🟪			
Fusarium sambucinum			🟦🟦	🟦🟦⬛		🟦🟦⬛		🟦🟦⬛	🟦	🟦🟦⬛	🟦🟦⬛					
Fusarium fujikuroi			🟦🟦	🟦🟦⬛		🟦🟦⬛		🟦🟦⬛	🟦	🟦🟦⬛	🟦🟦⬛					
Fusarium venenatum			🟦🟦	🟦🟦⬛		🟦🟦⬛		🟦🟦⬛	🟦	🟦🟦⬛	🟦🟦⬛					
Fusarium proliferatum			🟦🟦	🟦🟦⬛		🟦🟦⬛		🟦🟦⬛	🟦	🟦🟦⬛	🟦🟦⬛					
Fusarium incarnatum (semitectum)			🟦🟦	🟦🟦⬛		🟦🟦⬛		🟦🟦⬛	🟦	🟦🟦⬛	🟦🟦⬛					
Gibberella zeae (F. graminearum)			🟦🟦	🟦🟦⬛		🟦🟦⬛		🟦🟦⬛	🟦	🟦🟦⬛	🟦🟦⬛					
Fusarium sacchari			🟦🟦	🟦🟦⬛		🟦🟦⬛		🟦🟦⬛	🟦	🟦🟦⬛	🟦🟦⬛					

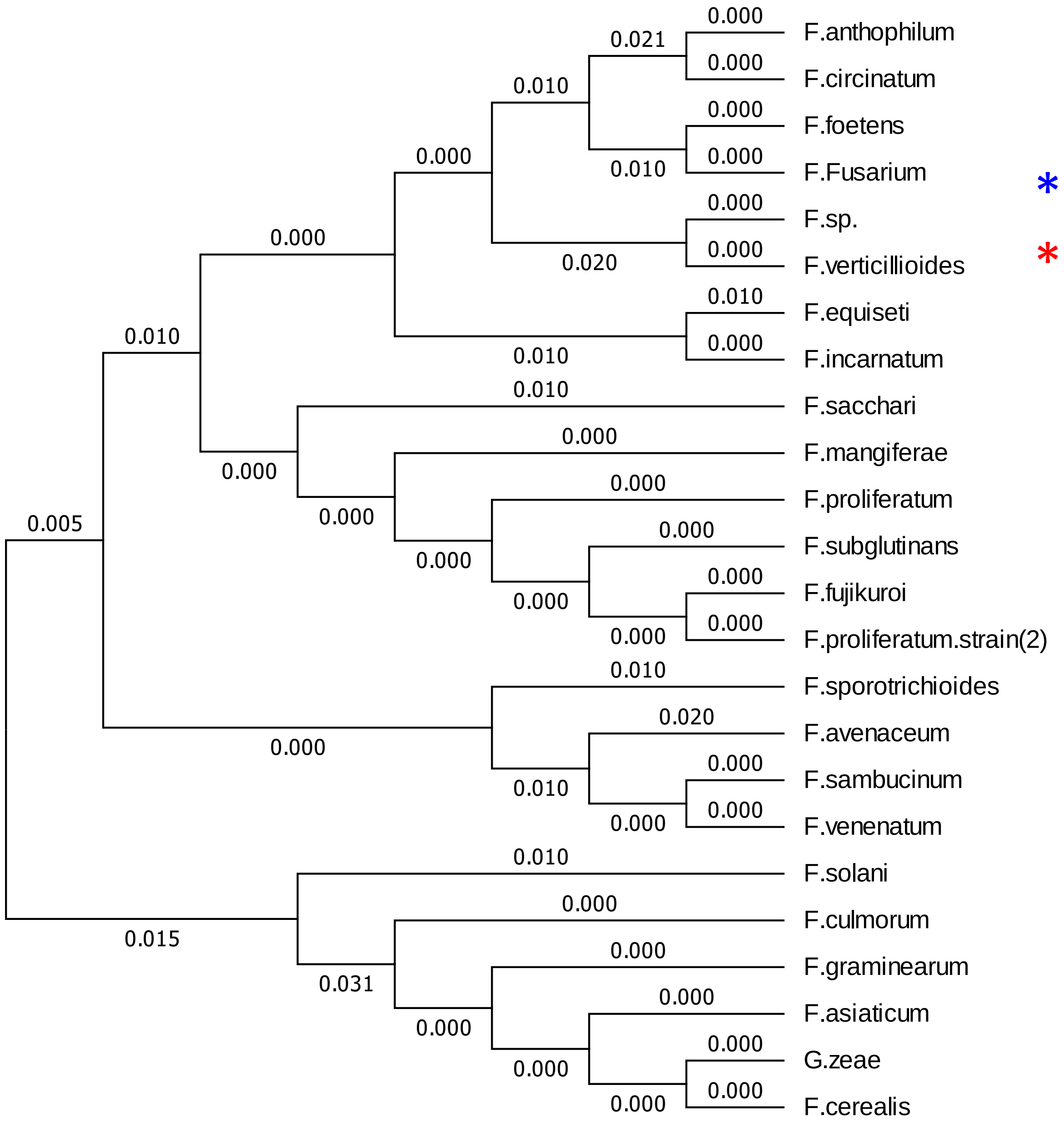
UNIVERSIDAD MILITAR NUEVA GRANADA

Molecular Phylogenetic analysis by Maximum Likelihood method

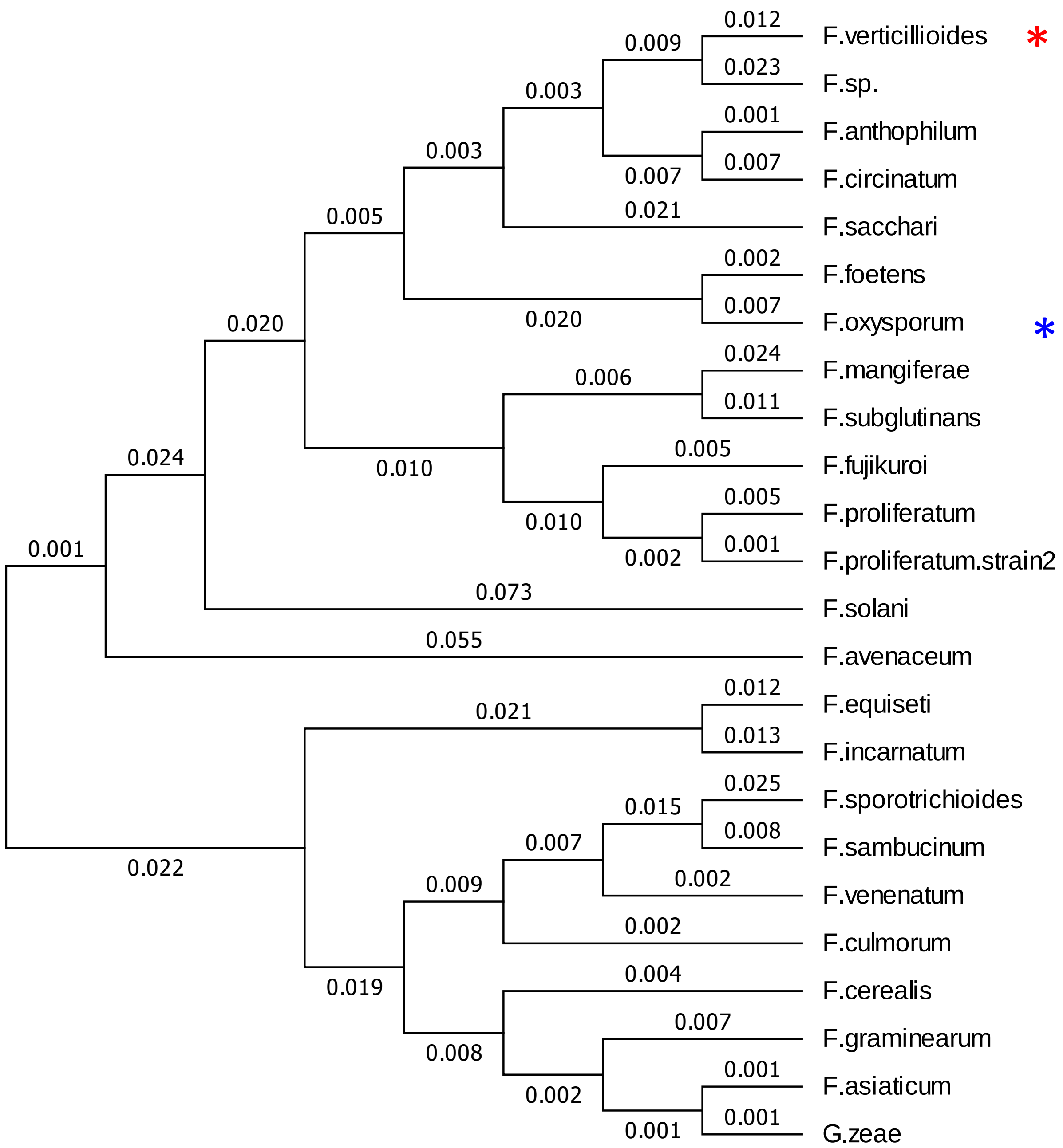
H3 amplicon



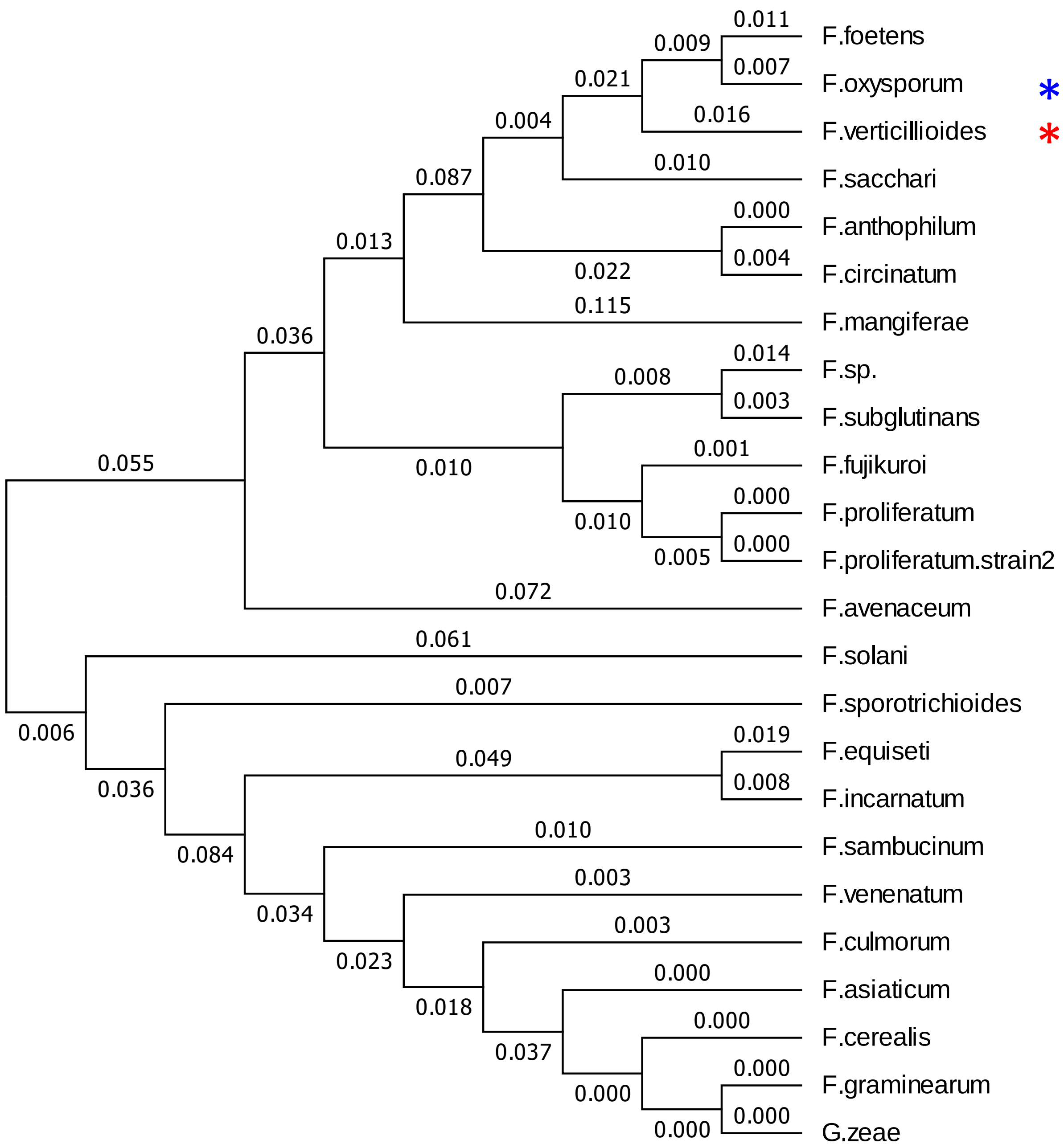
H3 MicroSeq



Molecular Phylogenetic analysis by Maximum Likelihood method



EF-1 H3 mtSSU ITS 2-4 amplicon

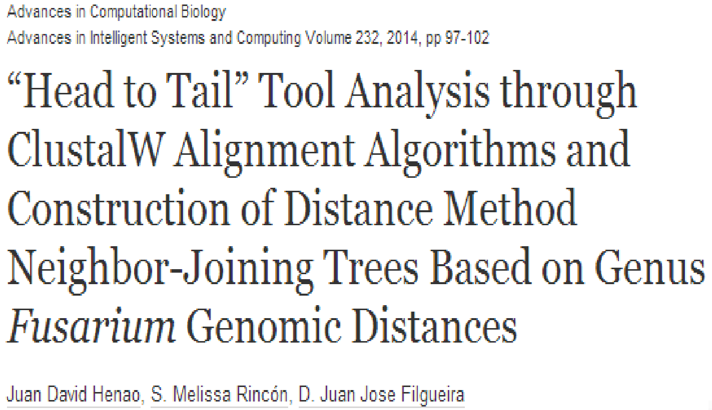


EF-1 H3 mtSSU ITS 2-4 MicroSeq

10 Genes

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

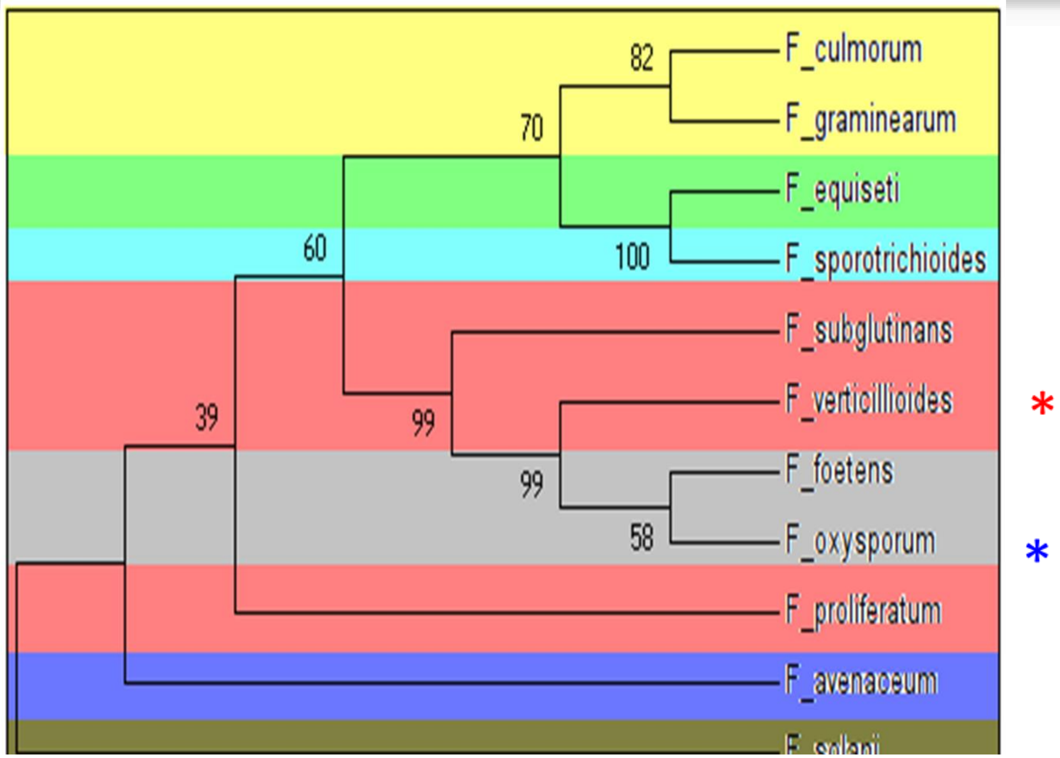
Bt2a/Bt2b
Bt1a/Bt1b
Ahy-FuF/AHyFuR
EF-1H/EF-2T
H3-1a/H3-1b
H4-1a/H4-1b
ITS FuR/ITS FuF
ITS-1/ITS-2
ITS-1/ITS-4
ITS-4/ITS-5

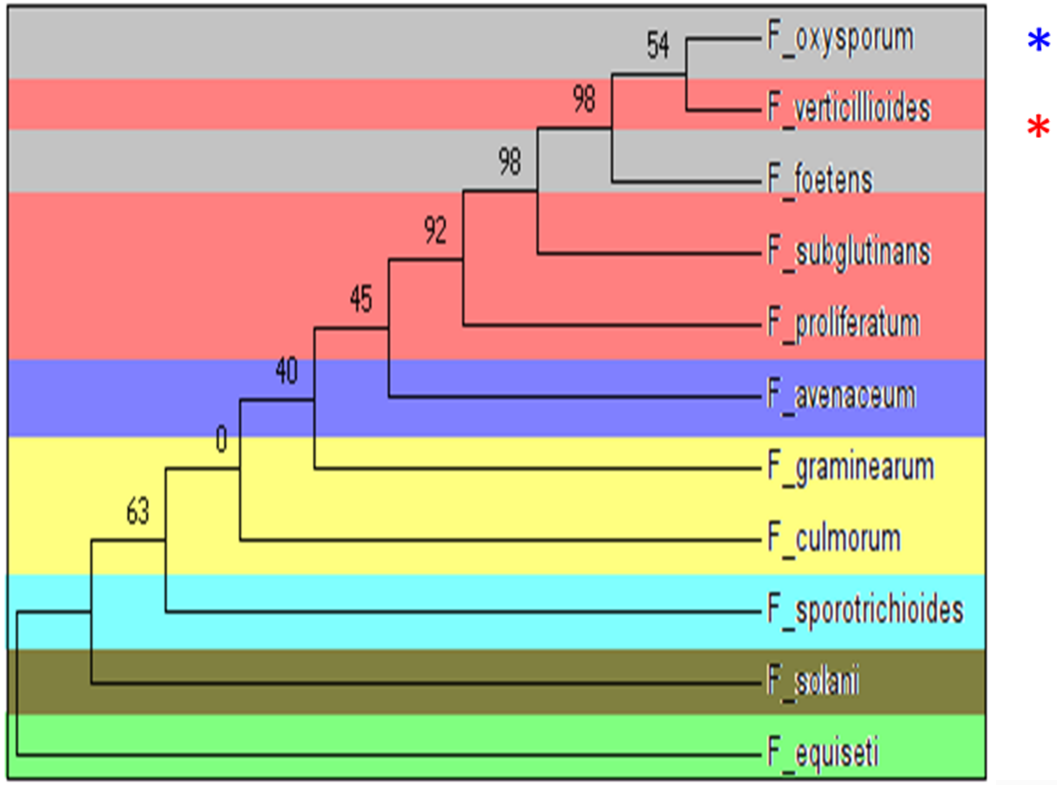


Advances in Computational Biology
Advances in Intelligent Systems and Computing Volume 232, 2014, pp 97-102

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

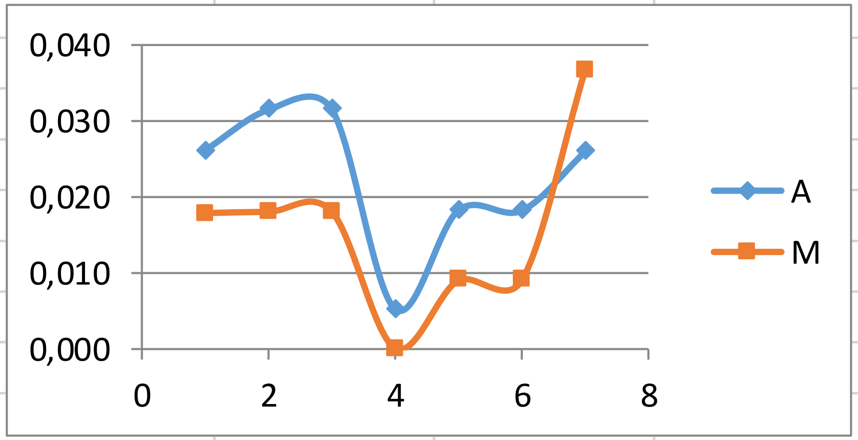
Juan David Henao, S. Melissa Rincón, D. Juan Jose Filgueira



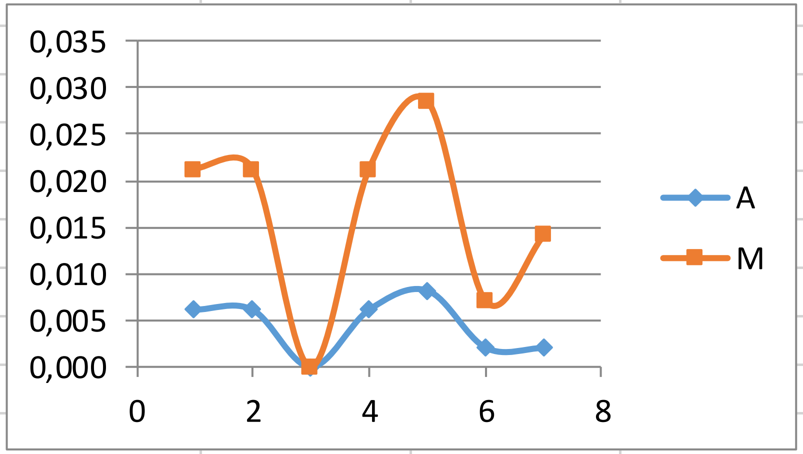


Differences in gene variability and microsequence

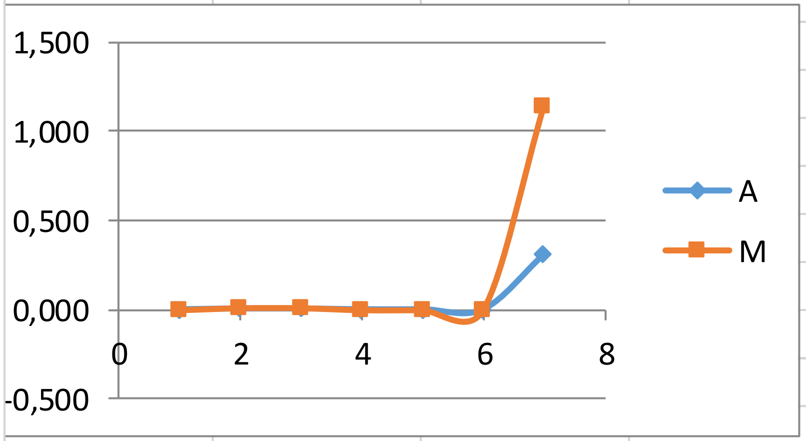
EF-1	A	M
VF	0,026	0,018
VO	0,032	0,018
FO	0,032	0,018
PS	0,005	0,000
PF	0,018	0,009
SF	0,018	0,009
SM	0,026	0,037



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



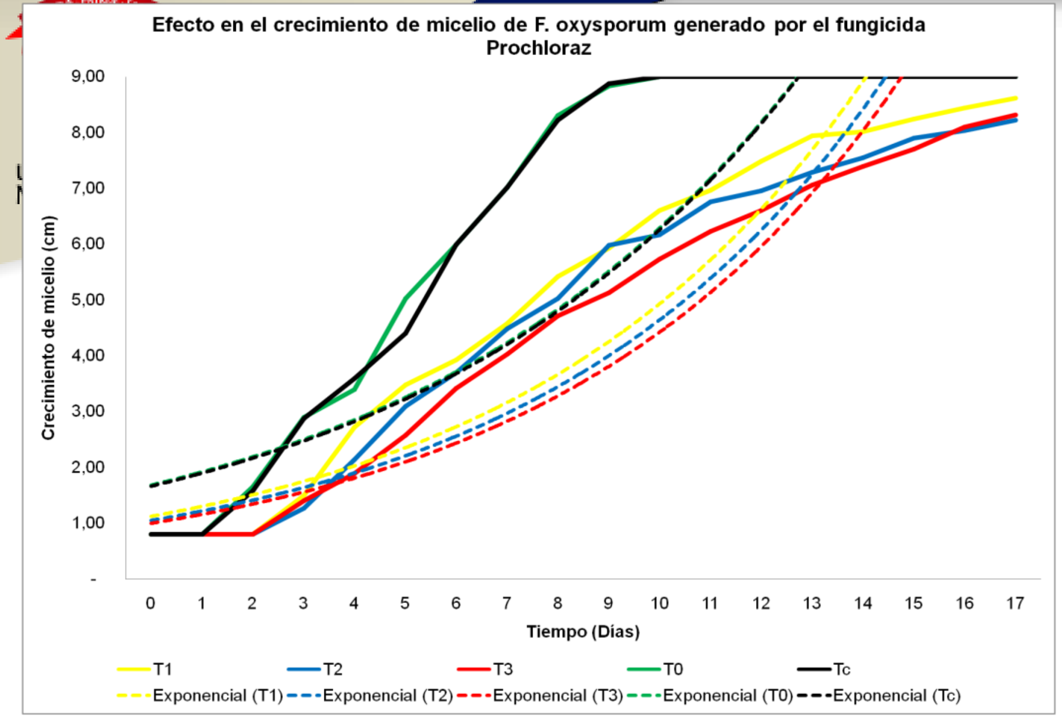
ITS	A	M
VF	0,000	0,000
VO	0,004	0,011
FO	0,004	0,011
PS	0,000	0,000
PF	0,000	0,000
SF	0,000	0,000
SM	0,312	1,144

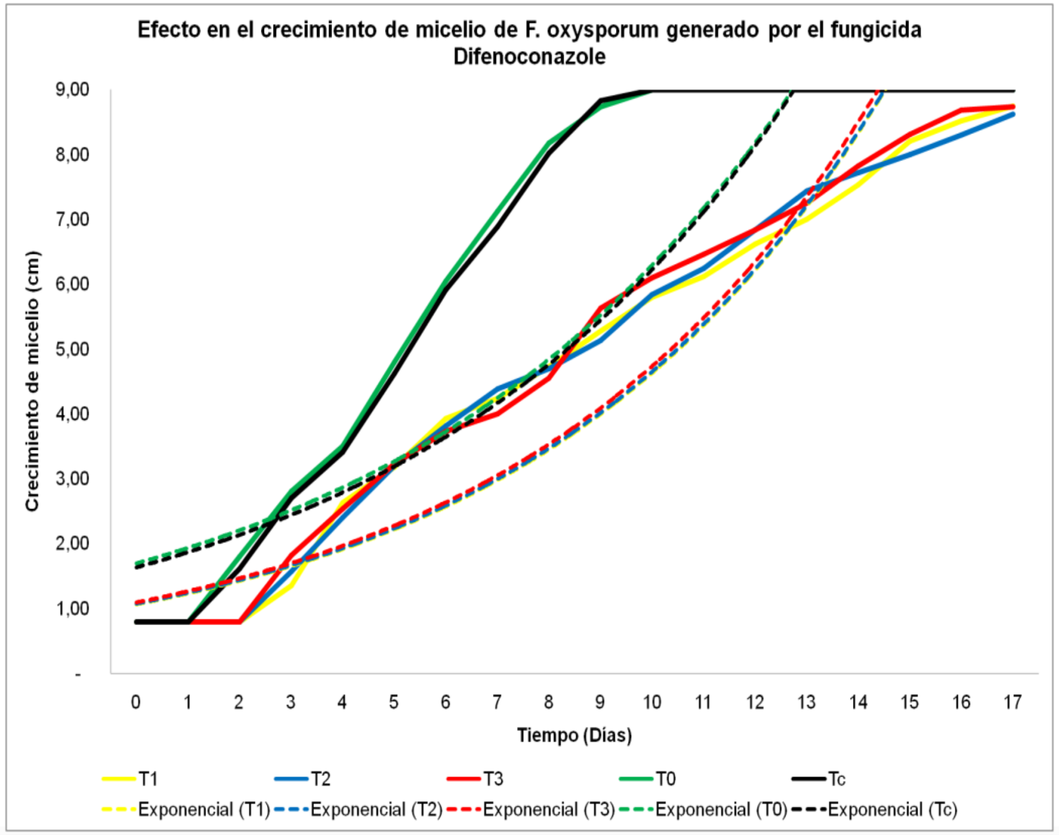


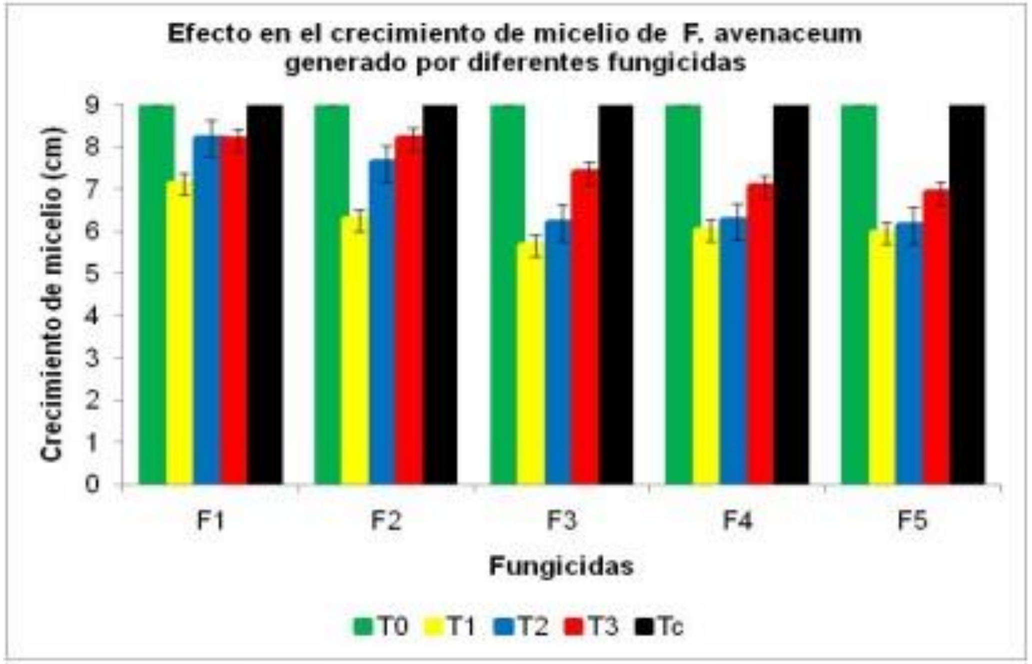
A: amplicon M: microsequence

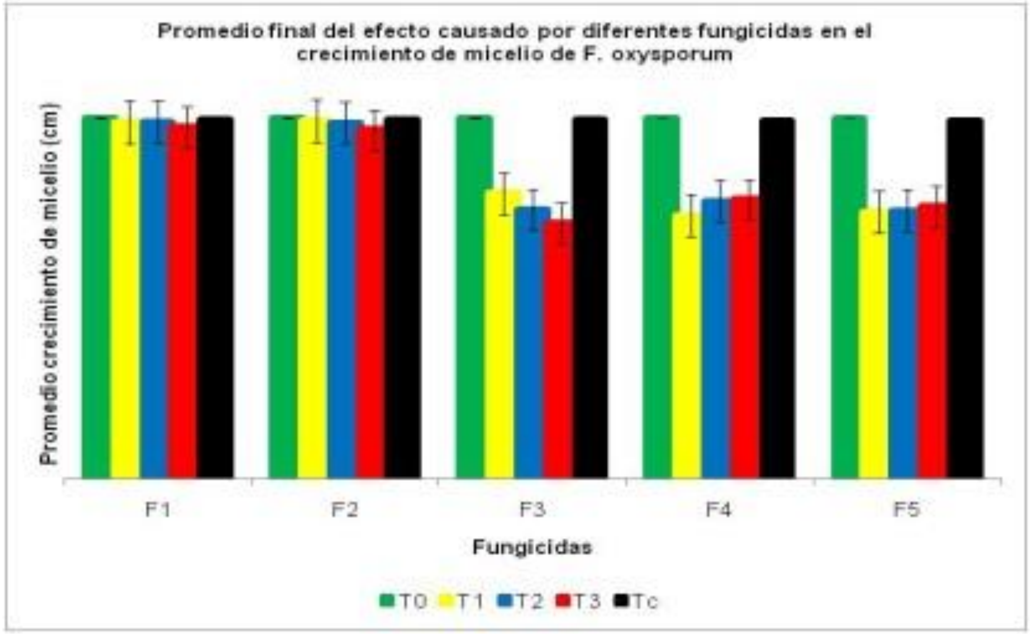
EVALUACIÓN DEL EFECTO DE FUNGICIDAS EN SEIS ESPECIES DE Fusarium PATÓGENOS DEL CLAVEL (*Dianthus caryophyllus*)

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

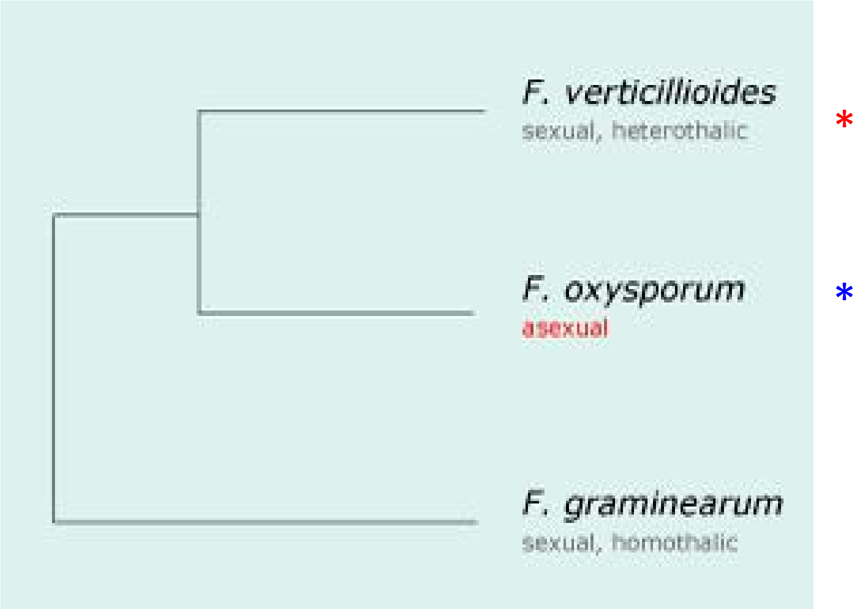


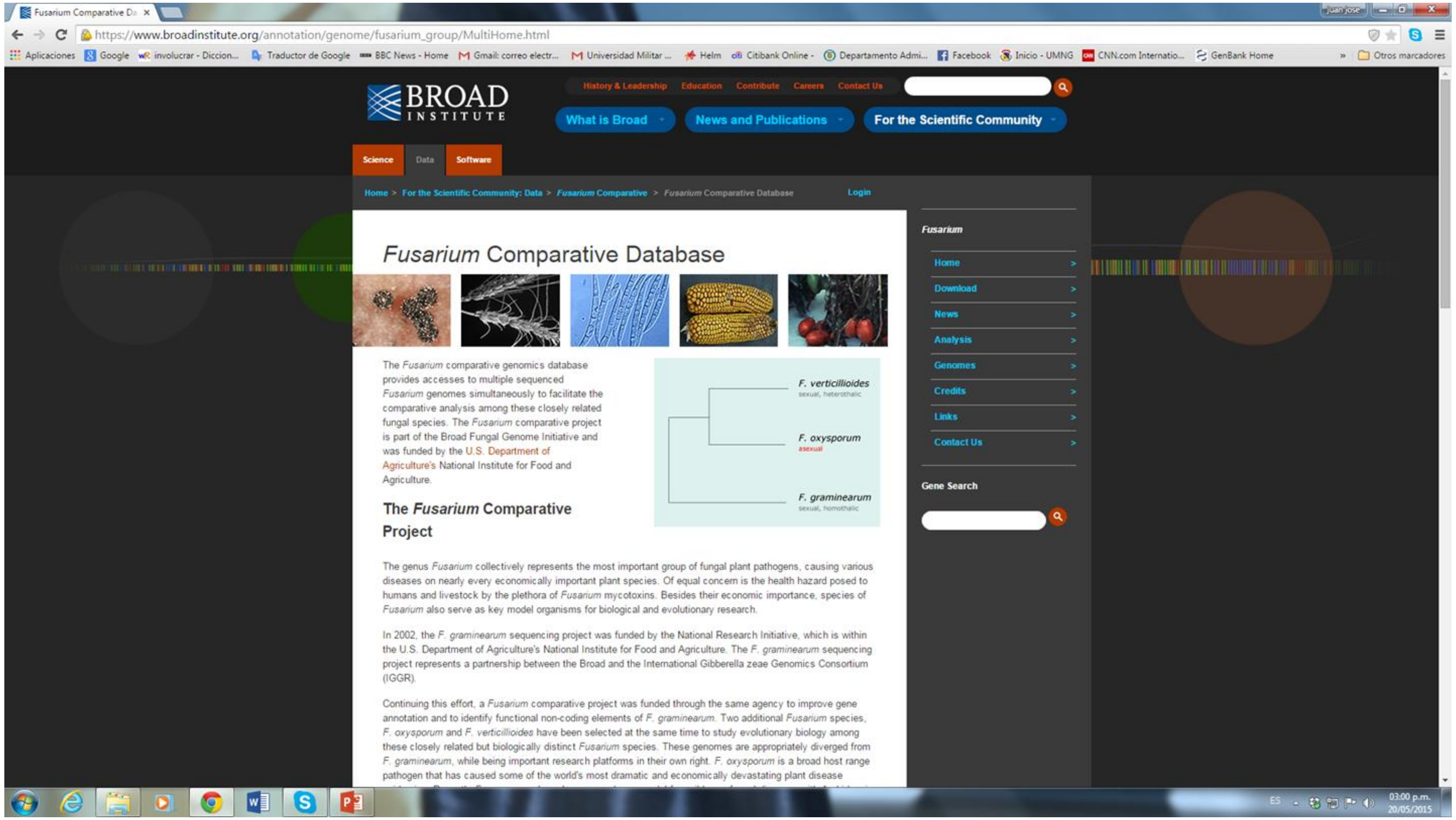






Fusarium Comparative Database





Fusarium Comparative Database

The *Fusarium* comparative genomics database provides accesses 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

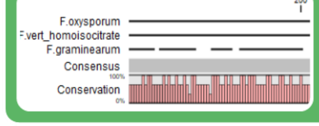
The genus *Fusarium* collectively represents the most important group of fungal plant pathogens, causing various diseases on nearly every economically important plant species. Of equal concern is the health hazard posed to humans and livestock by the plethora of *Fusarium* mycotoxins. Besides their economic 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).

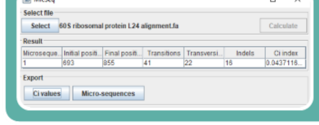
Continuing this effort, a *Fusarium* comparative project was funded through the same agency to improve gene annotation and to identify functional non-coding elements of *F. graminearum*. Two additional *Fusarium* species, *F. oxysporum* and *F. verticillioides* have been selected at the same time to 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

NCBI National Center for Biotechnology Information

Búsqueda de genes ortólogos



Alineamientos de los genes ortólogos



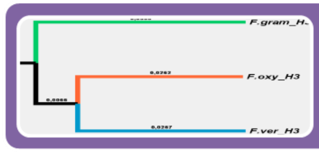
60S ribosomal protein L24 alignment.fa

Microseque...	Initial positi...	Final positi...	Transitions	Transversi...	Indels	Ci index
1	693	855	41	22	16	0.0437118...

Análisis Cuantitativo de las microsecuencias

Nucleotide BLAST
nucleotide ▶ nucleotide

Análisis de taxonomía molecular



Análisis de filogenia molecular

Búsqueda de microsecuencias de ADN útiles para hacer taxonomía y filogenia molecular en genes del género fusarium en bases de datos biológicas.

Ángela Maria Niño Nova., Juan, D. Henao., Daniela Londoño., Adrian R. Gómez P., Juan J. Filgueira D.,

Especie	Total genes	Orthologous genes
Fusarium oxysporum f.sp *Lycopersisi*	27.348	402
Fusarium graminearum	14.144	
Fusarium verticilloides	20.575	

Microsequences in orthologos genes

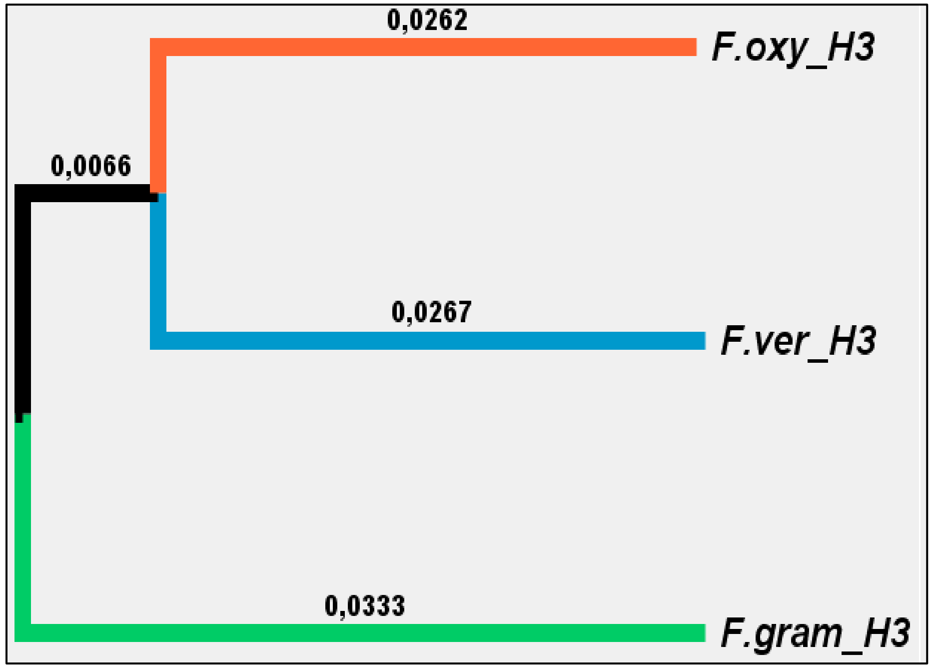
Nombre	Total Microsecuencias	Promedio de Transiciones	Promedio de Transversiones	Promedio de Indels	Promedio de índice Mi	Promedio de Longitud Microsecuencias (pb)
30S ribosomal protein S12	2	20,5	14,5	5	0,033	100,5
50S ribosomal protein L14	1	20	19	86	0,124	141
Atp-dependent RNA helicase DBP4	6	15,2	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

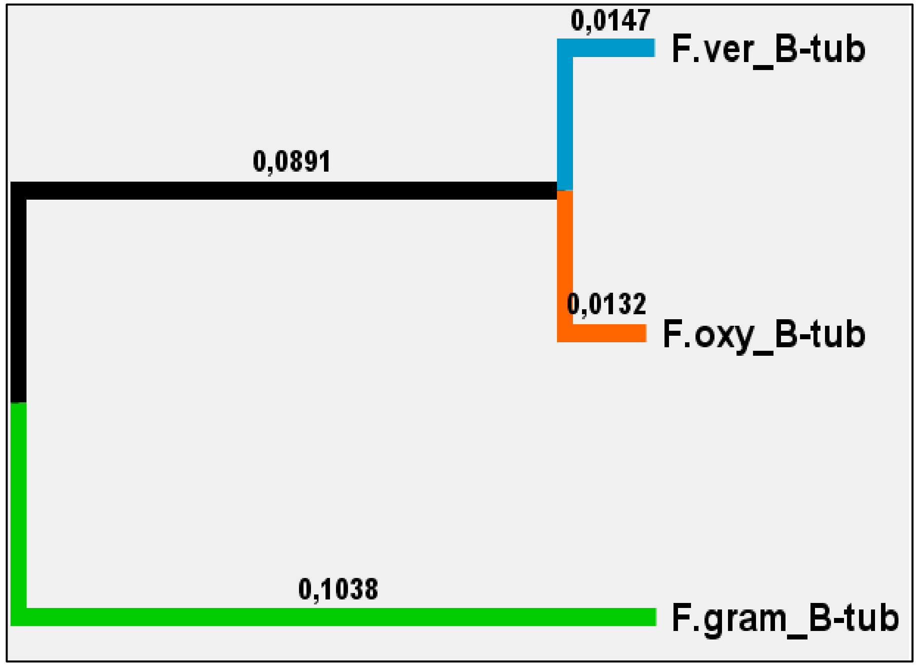
Matrices of distance N-J Microsequences of orthologous genes

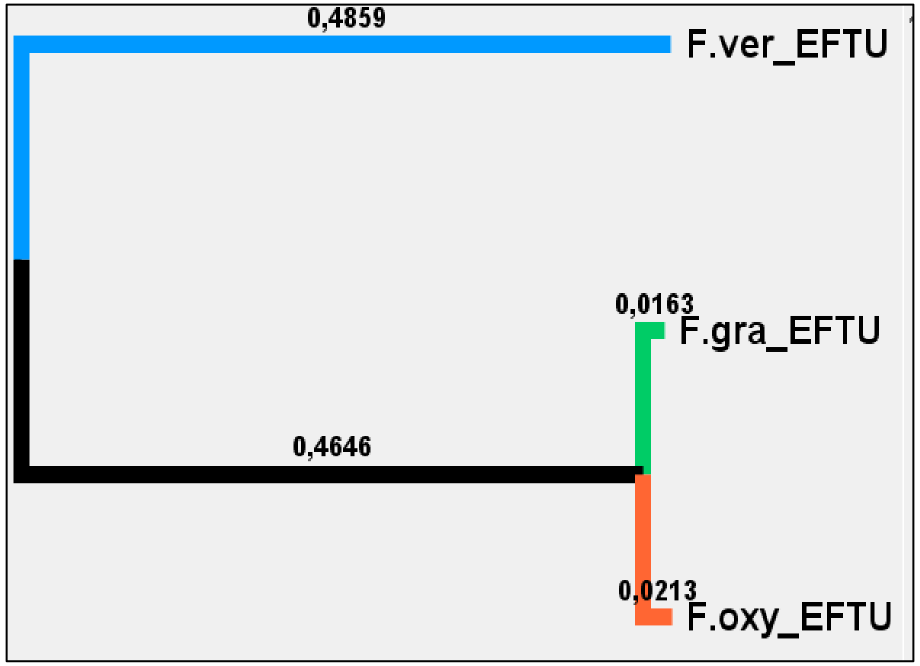
	Ferrochelatase	**Quinate dehydrogenase**	**Transcription elongation factor**	**Diphthamide biosynthesis protein**	**COP9 signalosome complex subunit 5**	**Atp-dependent RNA helicase**	**Histone acetyltransferase type B**
F.oxy/F.gram	0,255	0,339	0,449	0,500	0,422	0,457	0,532
F.ver/F.gram	0,300	0,364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

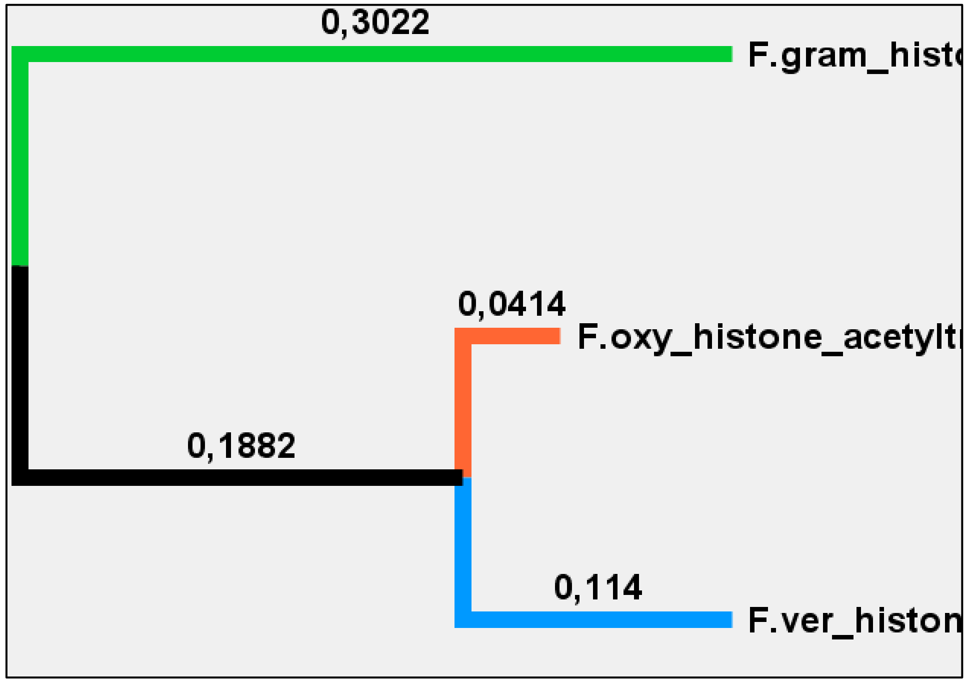
Dendrograms with complete genes

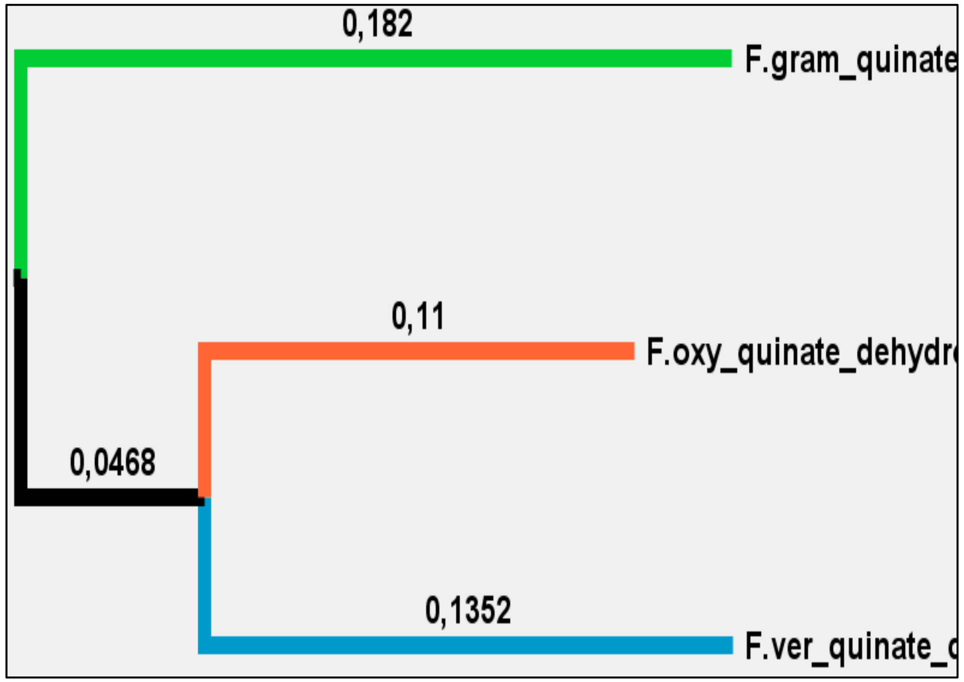


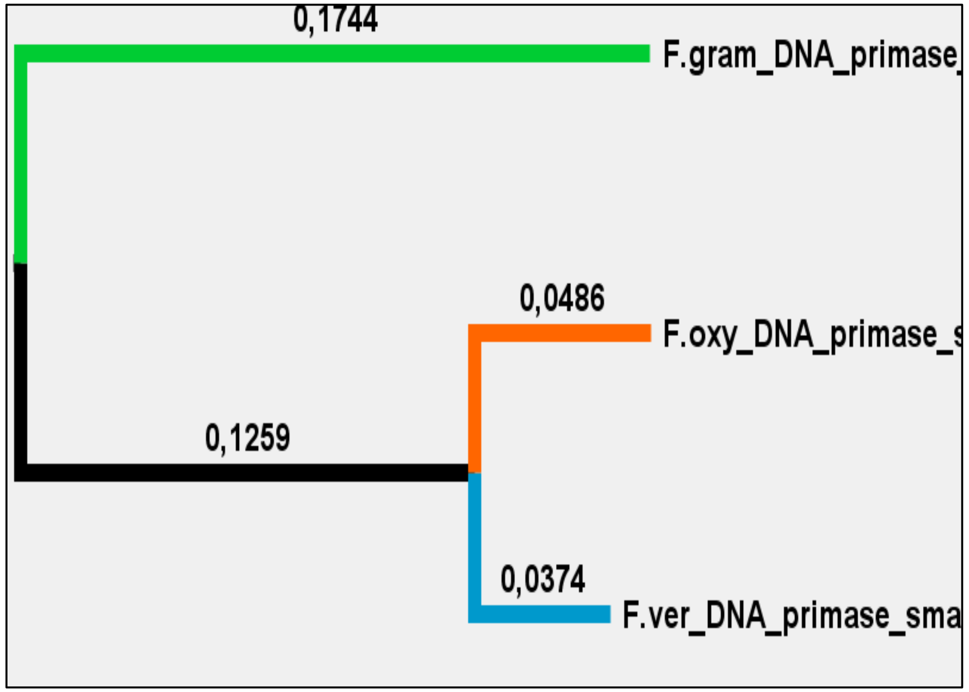


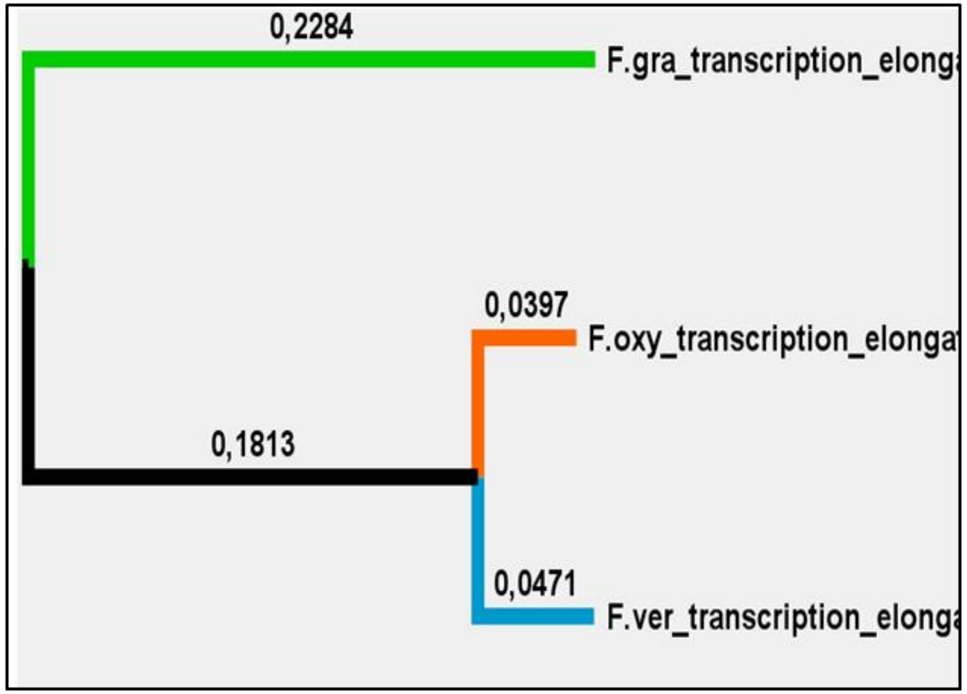


Phylogeny using microsequences of orthologous genes









Tasas de cambio

1. Frecuencias de cada uno de los nucleótidos y gaps en las microsecuencias.

$$gA = \frac{\sum(A/\mathbb{N})}{0t} \quad gT = \frac{\sum(T/\mathbb{N})}{0t} \quad gG = \frac{\sum(G/\mathbb{N})}{0t} \quad gC = \frac{\sum(C/\mathbb{N})}{0t}$$

$$gGaps = \frac{\sum(Gaps/\mathbb{N})}{0t}$$

N: longitud de las secuencias, 0t: número de especies analizadas

2. Frecuencia de las purinas, pirimidinas y gaps.

$$gR = gA + gG$$

$$gY = gT + gC$$

$$gZ = gGap$$

Siendo gR: frecuencia de purinas, gY: frecuencia de pirimidinas y gZ: frecuencia de gaps.

3. Frecuencias de cambios:
   a. Frecuencia de transiciones purina-purina.

$$P1ij = \frac{\sum A - G + \sum G - A}{N}$$

   a. Frecuencias de transiciones pirimidina-pirimidina.

$$P2ij = \frac{\sum C - T + \sum T - C}{N}$$

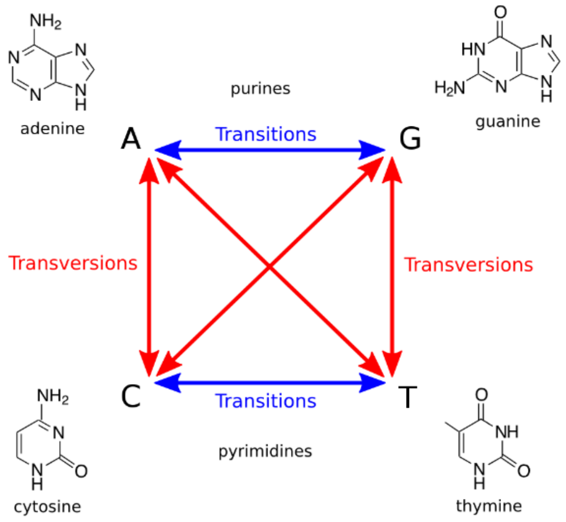
   a. Frecuencia de transversiones purina- pirimidina y pirimidina- purina.

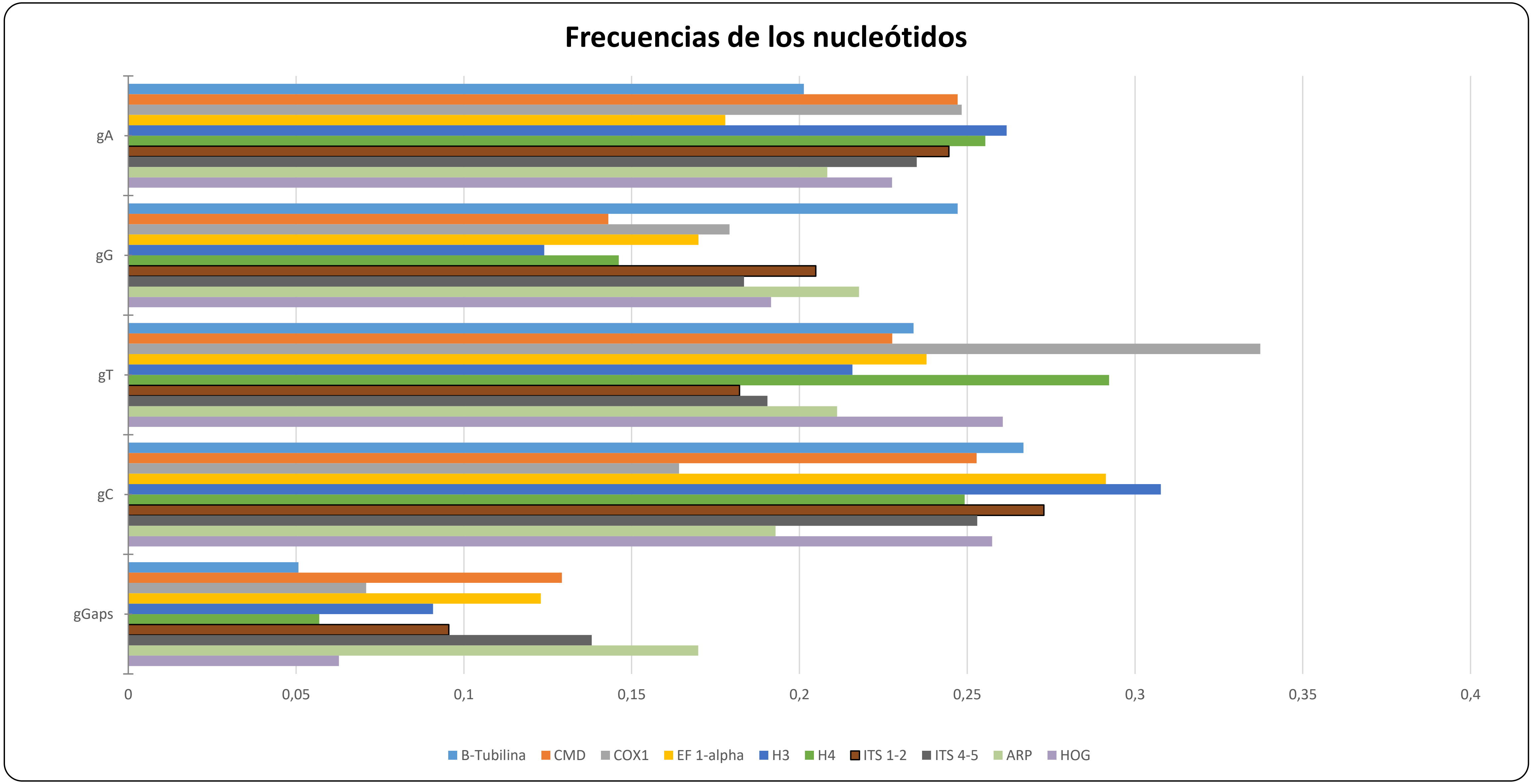
$$Qij = \frac{\sum A - T + \sum T - A + \sum G - C + \sum C - G + \sum A + C + \sum C - A + \sum G - T + \sum T - G}{N}$$

   a. Frecuencia de gap gaps-nucleótido y nucleótido-gap.

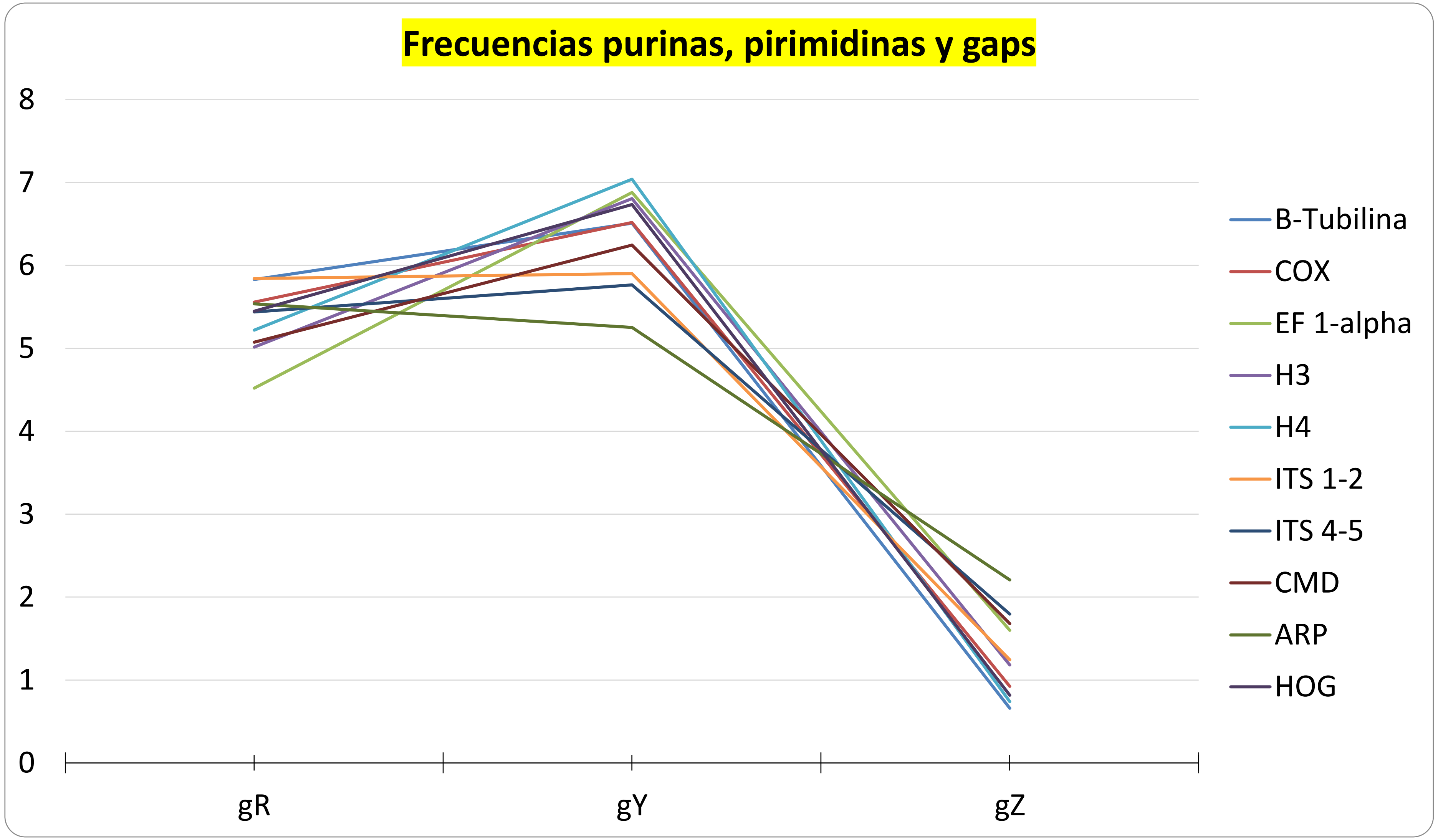
$$Gap, ij = \frac{\sum Gap - Ni + \sum Ni - Gap}{N}$$

Siendo Ni: nucleótido eliminado o adicionado.

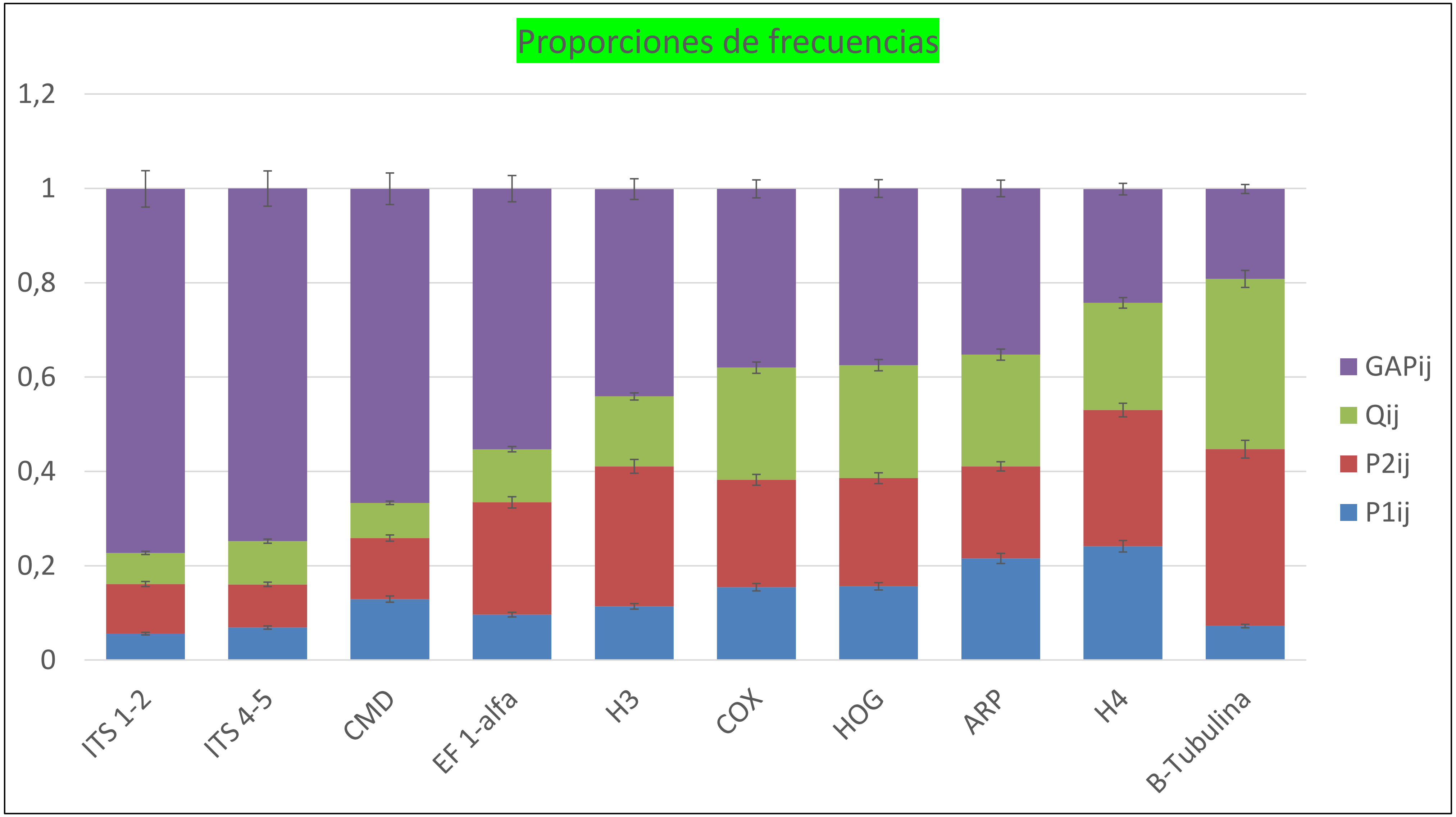



Frecuencias de los nucleótidos
gA
gG
gT
gC
gGaps
0
0,05
0,1
0,15
0,2
0,25
0,3
0,35
0,4
B-Tubilina
CMD
COX1
EF 1-alpha
H3
H4
ITS 1-2
ITS 4-5
ARP
HOG

Frecuencias de las purinas (gR), pirimidinas (gY) y gaps (gZ) para micro sequencias de cada gen ortólogo.



Proporciones de las frecuencias de cambio para transiciones purina-purina (P1ij), transiciones pirimidina-pirimidina (P2ij), transversiones (Qij) y gaps (GAPij)



Proporciones de cambio

Proporciones de cambio (transiciones, transversiones y gaps) en los diferentes genes ortólogos, esto se realizó en tres pasos:

1. Se calcularon las frecuencias de todos los genes usados en las microsecuencias de los diferentes genes.

a. Frecuencias de transiciones purina-purina para todas microsecuencias.

$$RP1 = \frac{\sum_{n=0}^{n} P1}{nt}$$

a. Frecuencias de transiciones pirimidina-pirimidina para todas las microsecuencias.

$$RP2 = \frac{\sum_{n=0}^{n} P2}{nt}$$

a. Frecuencia de transversiones purina- pirimidina y pirimidina- purina para todas las microsecuencias.

$$RQ = \frac{\sum_{n=0}^{n} Q}{nt}$$

a. Frecuencia de gap gaps-nucleótido y nucleótido-gap para todos las microsecuencias.

$$RGap = \frac{\sum_{n=0}^{n} Gap}{nt}$$

Siendo nt: número de genes totales usados para el análisis.

2. Luego se sumaron las frecuencias anteriormente calculadas para todos los tipos de cambios.

$$Rt = RP1 + RP2 + RQ + RGap$$

1. Por último, se calcularon las proporciones de las sumas de las frecuencias para cada caso.

$$Rt1 = \frac{RP1}{Rt} \quad Rt2 = \frac{RP2}{Rt} \quad Rt3 = \frac{RQ}{Rt} \quad Rt3 = \frac{RQ}{Rt}$$

Tasas de cambio

4. Tasas de transiciones, transversiones vs gaps.
   a. Tasa de purina vs transversiones.

$$K1 = \frac{\mathrm{P1ij/gA * gG}}{\mathrm{Qij/(gR * gY * gZ)}}$$

   a. Tasa de pirimidina vs transversiones.

$$K2 = \frac{\mathrm{P2ij/gT * gC}}{\mathrm{Qij/(gR * gY * gZ)}}$$

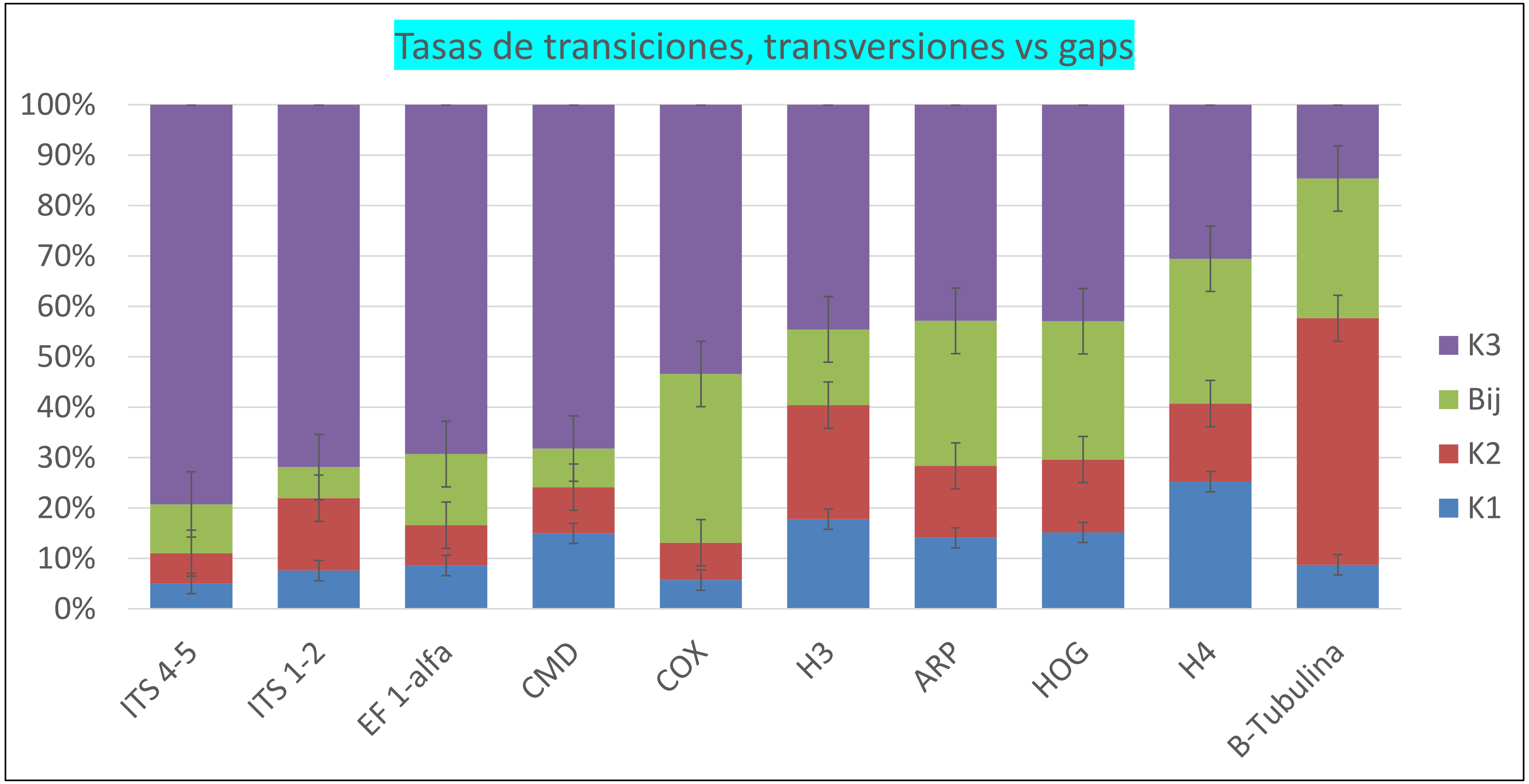
   a. Tasa de transversiones.

$$Bij = \frac{\mathrm{Qij}}{\mathrm{4(gR * gY * gZ)}}$$

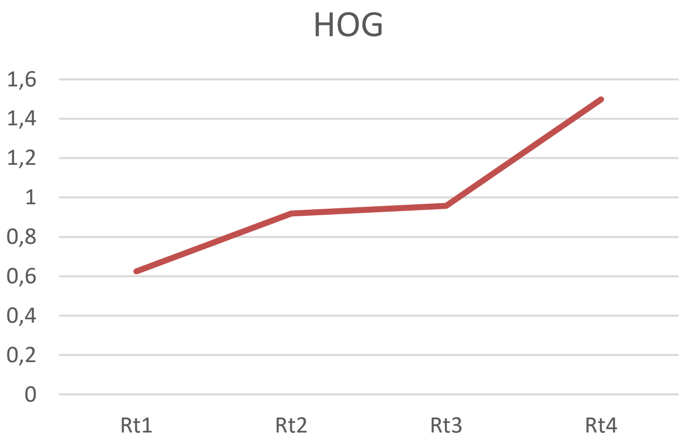
   a. Tasa de gaps.

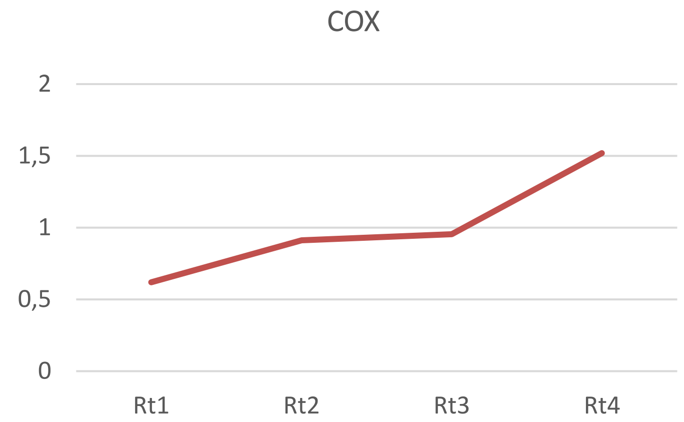
$$K3 = \frac{\mathrm{Gap, ij}}{\mathrm{4(gR * gY * gZ)}}$$

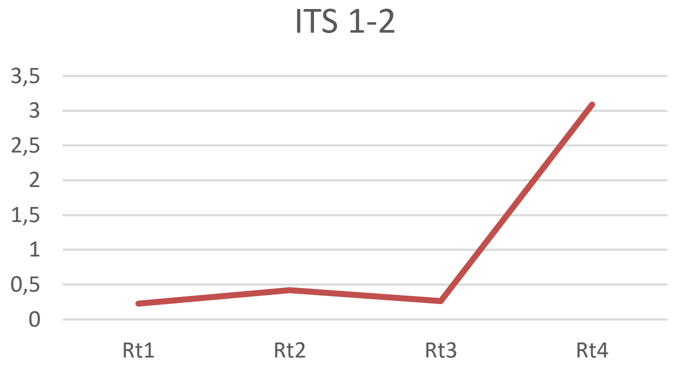
Tasas de las transiciones purina-purina (K1), transiciones pirimidina-pirimidina (K2), transversiones (Bij) y gaps (K3)

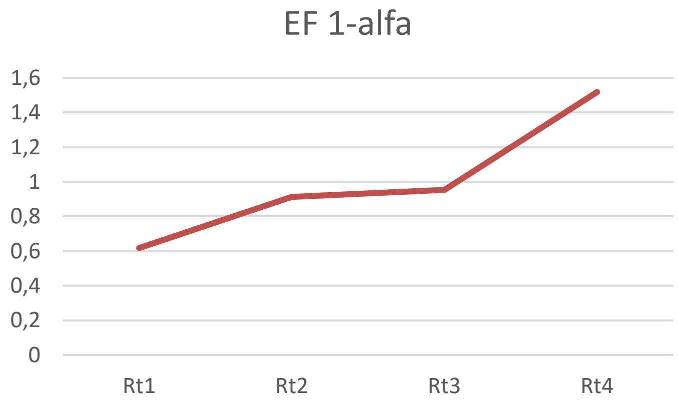


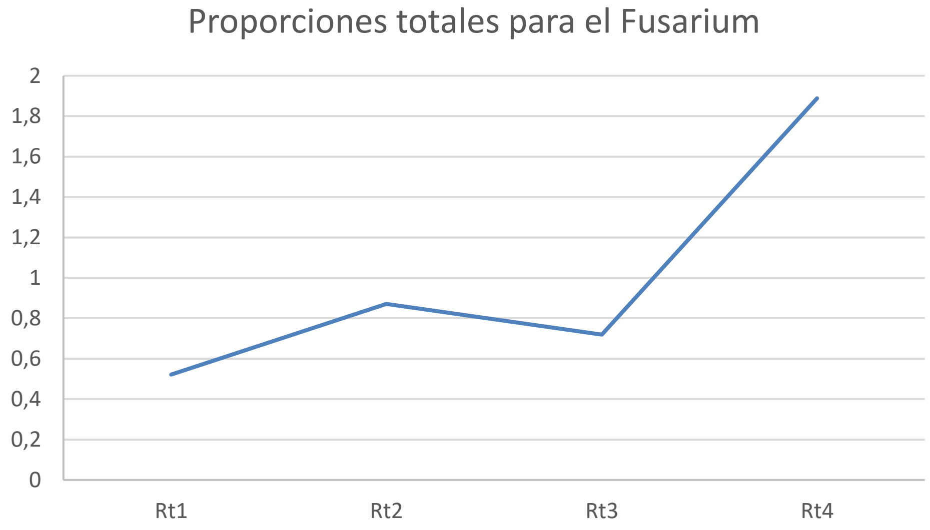
Tasas de cambio genes para análisis Taxonómico y filogénico


HOG

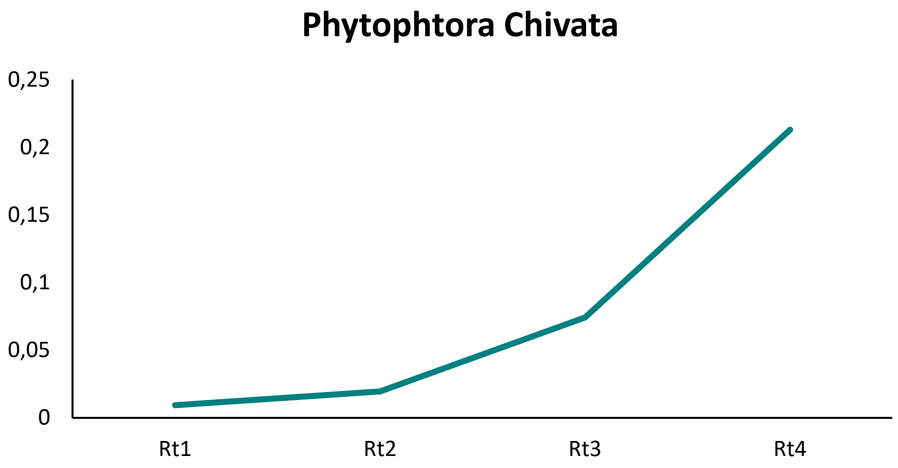

COX


ITS 1-2

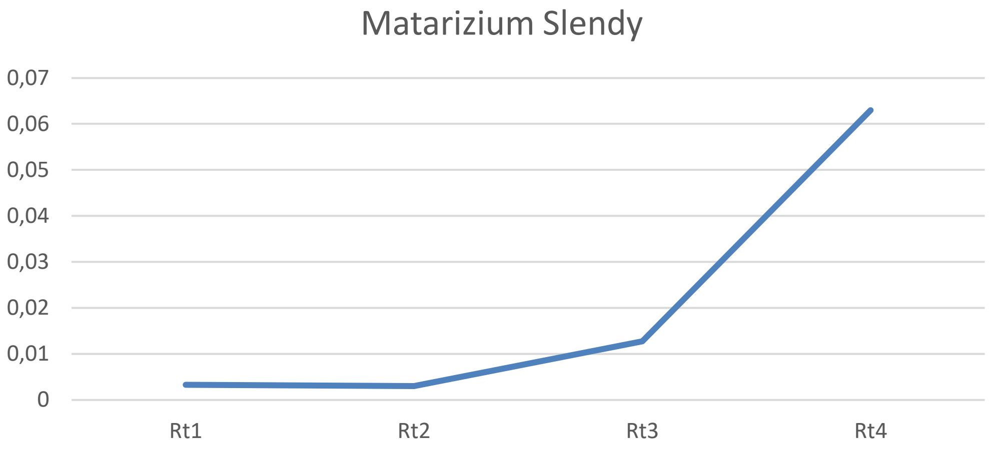

EF 1-alfa


Proporciones totales para el Fusarium

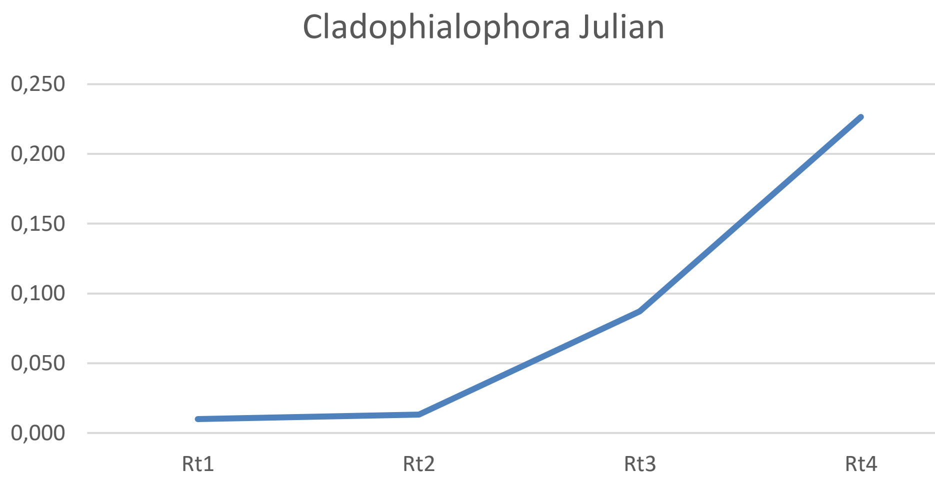
Tasas de cambio otros géneros con genes para Taxonómico y filogénico



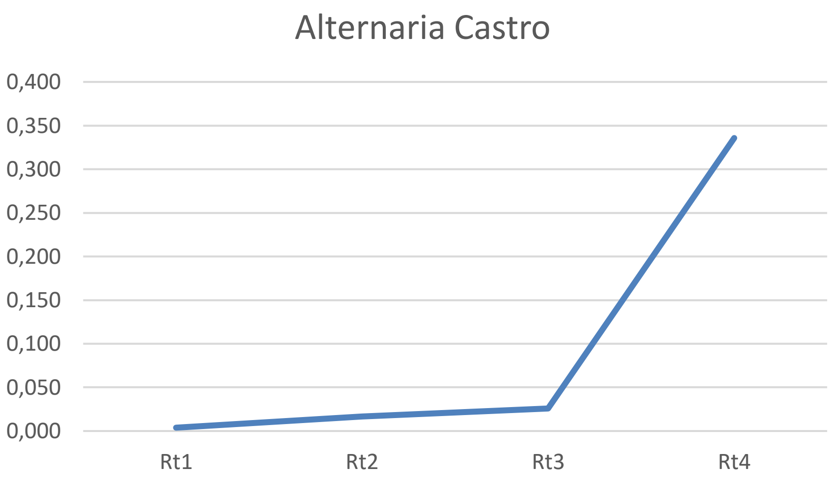
Phytophtora Chivata



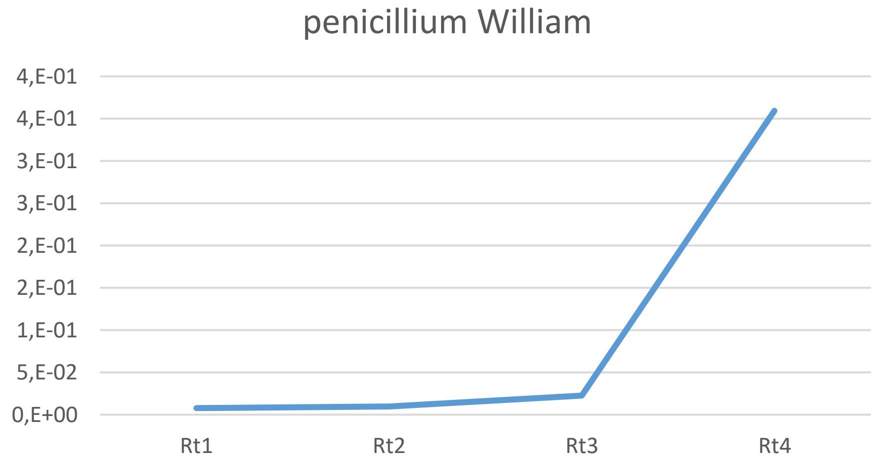
Matarizium Slendy



Cladophialophora Julian

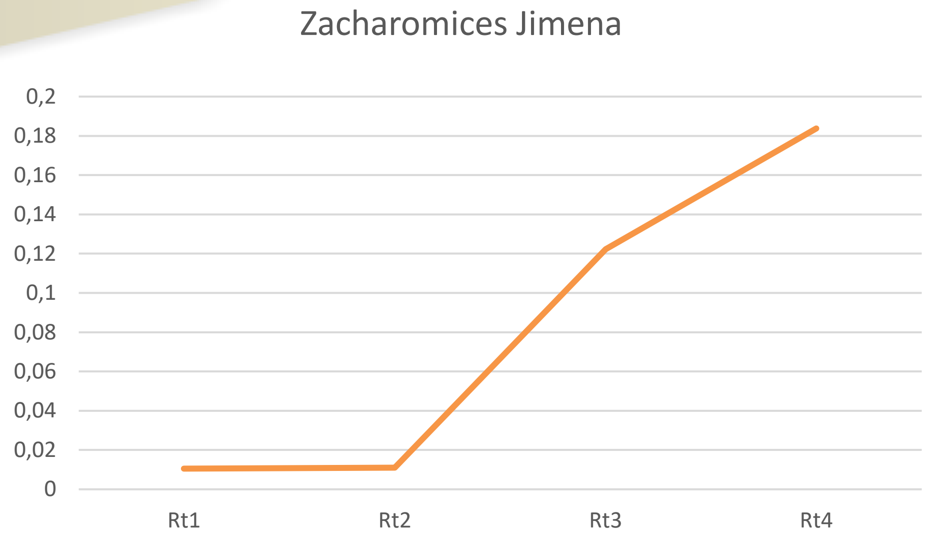


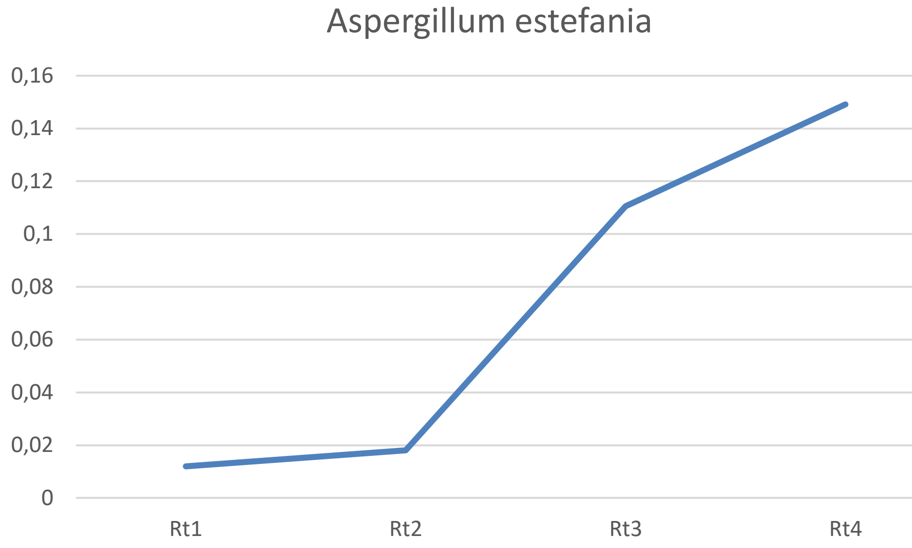
Alternaria Castro

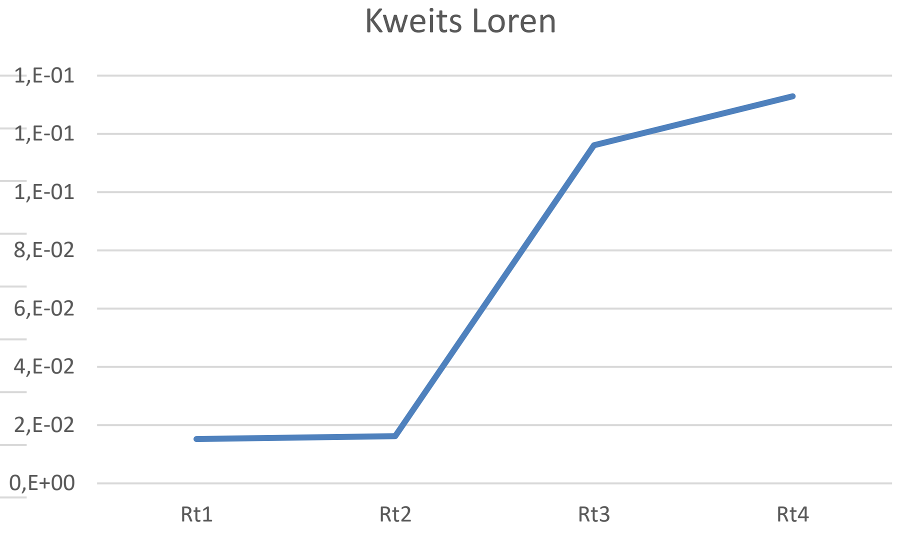


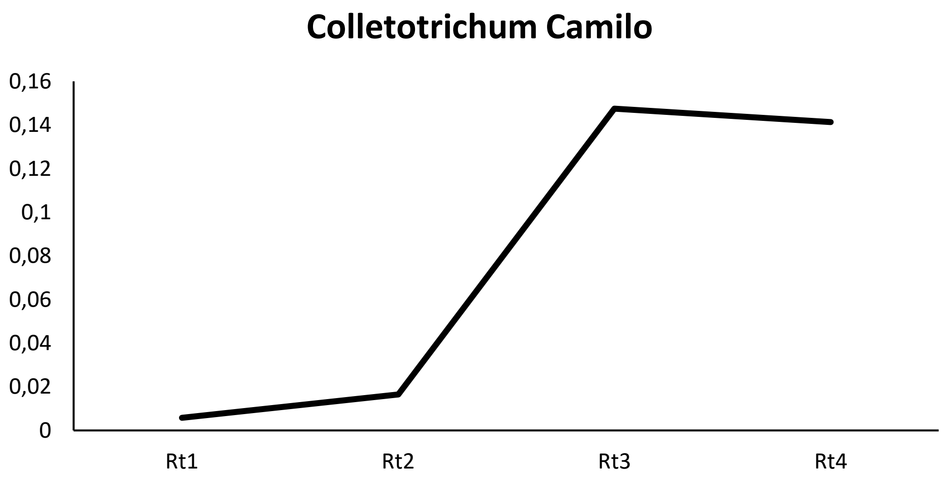
penicillium William

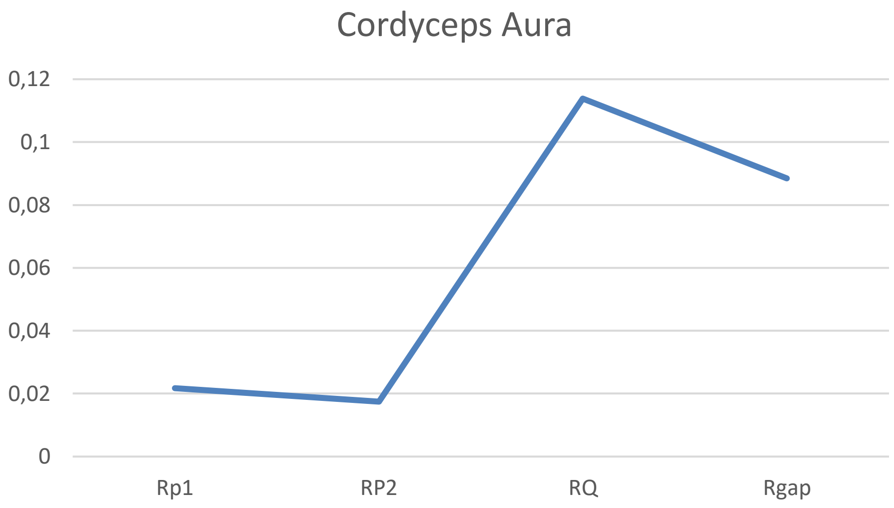
Tasas de cambio otros géneros con genes para Taxonómico y filogénico


Zacharomices Jimena

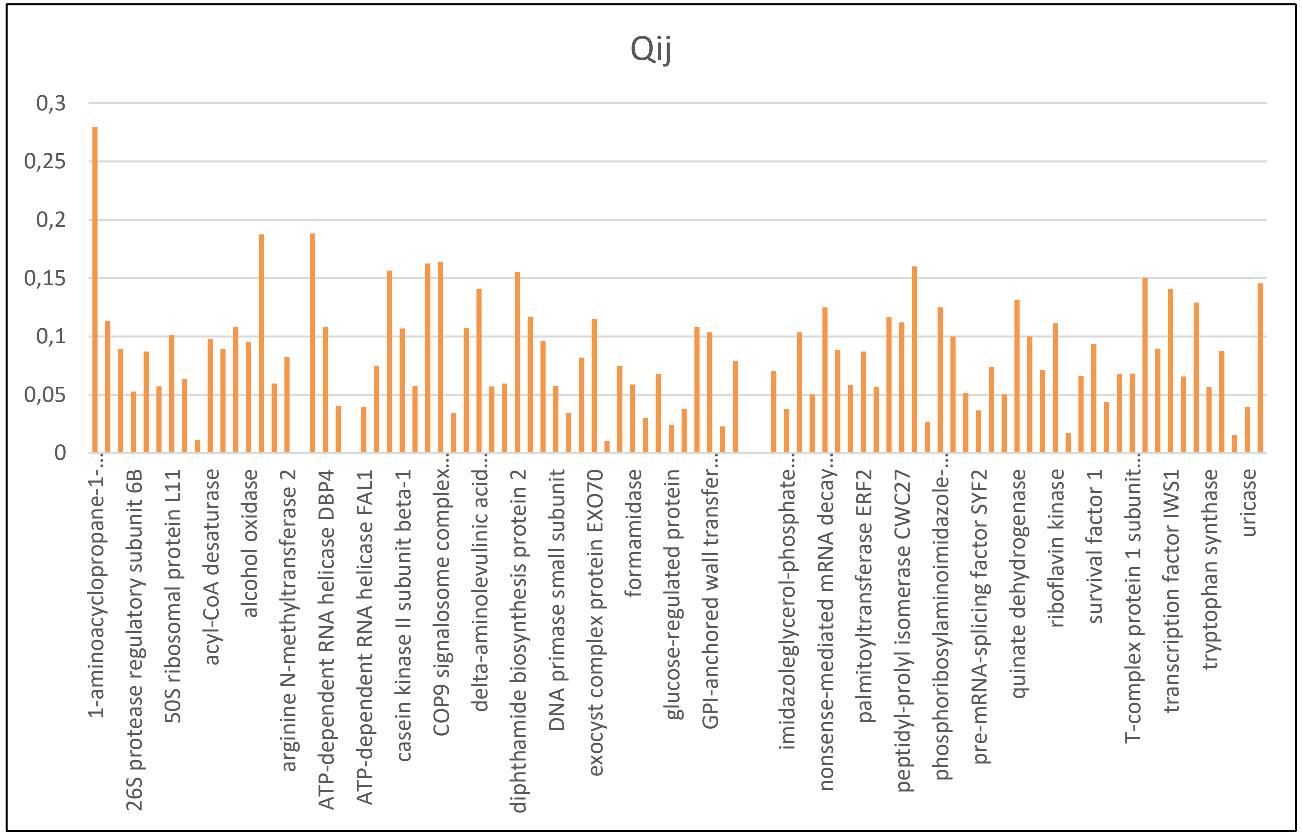

Aspergillum estefania

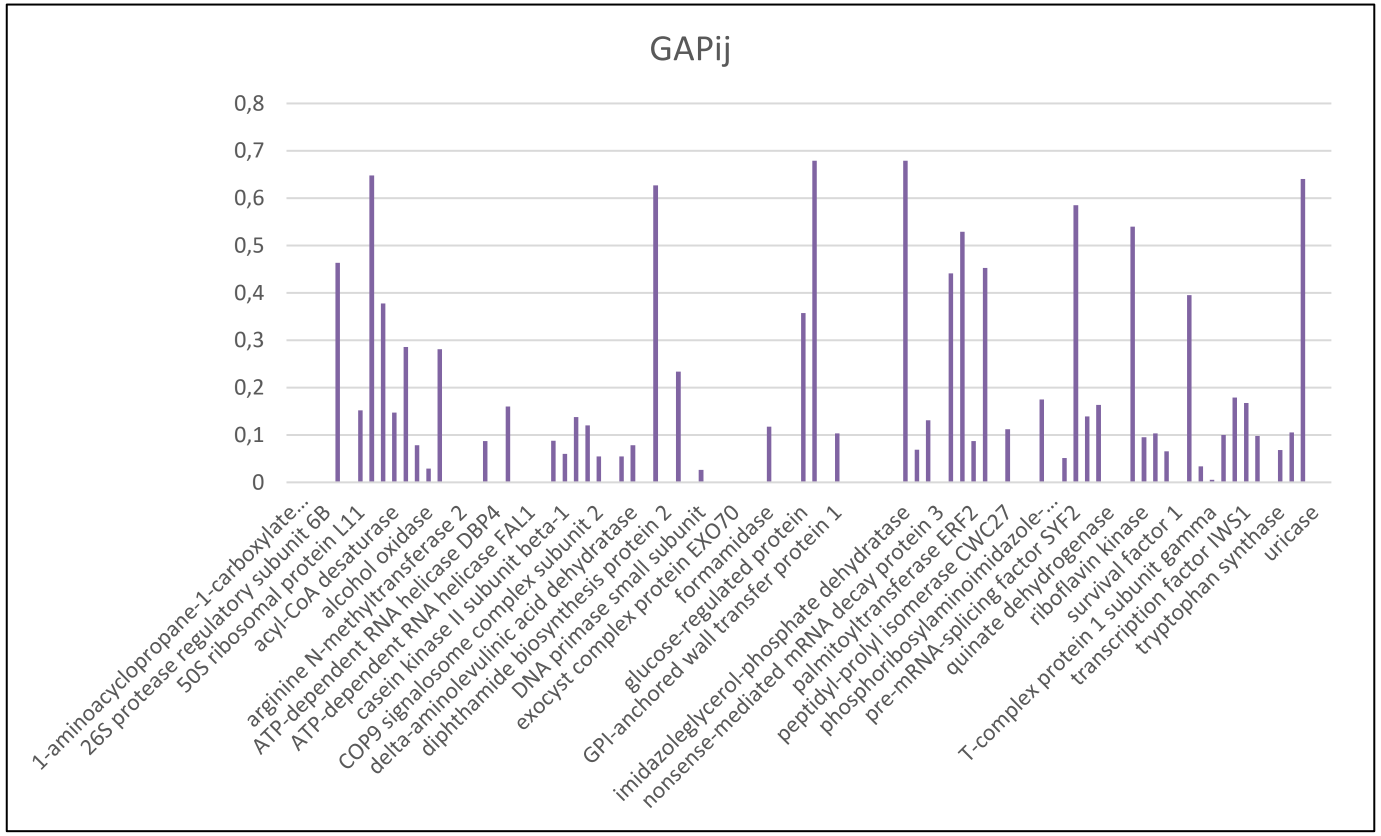

Kweits Loren


Colletotrichum Camilo


Cordyceps Aura

Tasas de cambio Fusarium con ortólogos no para Taxonómico y filogénico

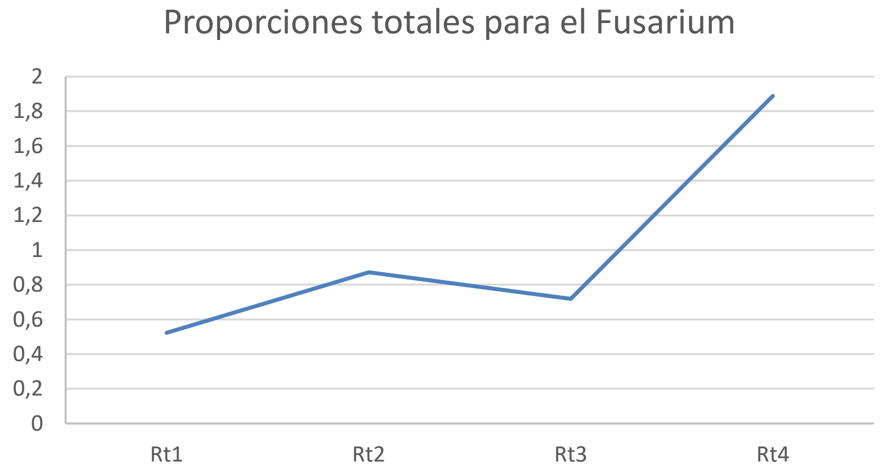




Transversiones

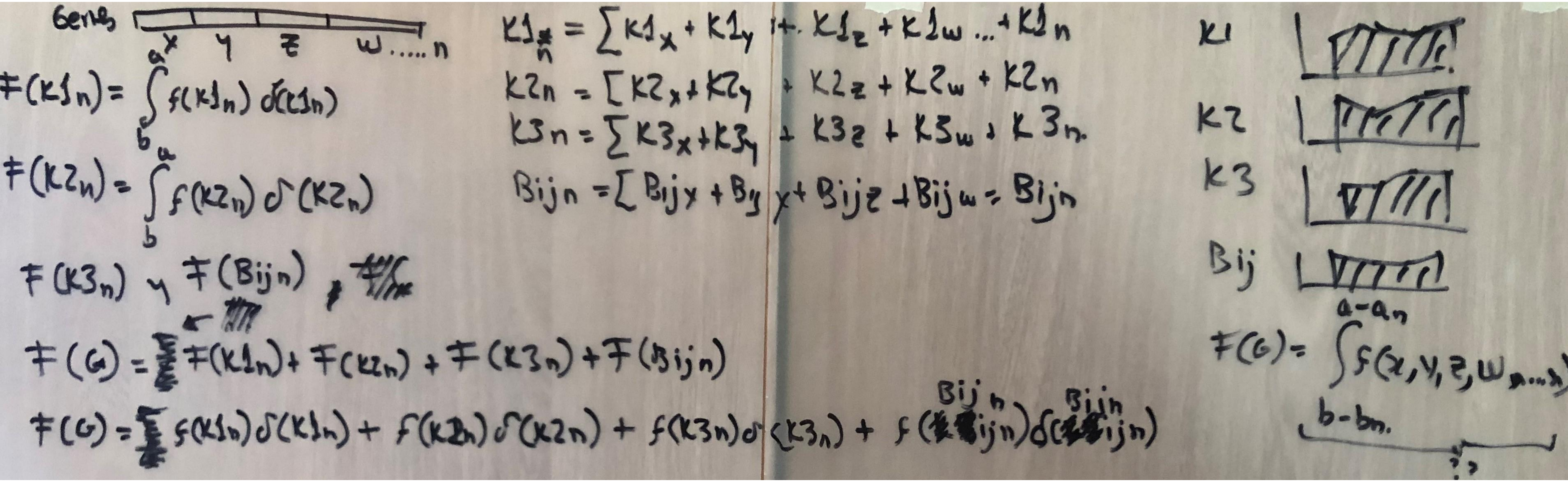
Gaps

Tasas de cambio genes para análisis T&P



Tasas de cambio Fusarium con ortólogos no para T&P

Rt1: purina-purina
Rt2: pirimidina-pirimidina
Rt3: transversiones
Rt4: gaps



Genes

x y z w ..... n

$F(K1_n) = \int_b^a f(K1_n)\,\delta(K1_n)$

$F(K2_n) = \int_b^a f(K2_n)\,\delta(K2_n)$

$F(K3_n)$ y $F(Bij_n)$

$F(G) = F(K1_n) + F(K2_n) + F(K3_n) + F(Bij_n)$

$F(G) = f(K1_n)\,\delta(K1_n) + f(K2_n)\,\delta(K2_n) + f(K3_n)\,\delta(K3_n) + f(\overset{Bij_n}{ij_n})\,\delta(\overset{Bijn}{ij_n})$

$K1_{\underset{n}{\cancel{x}}} = \sum K1_x + K1_y + K1_z + K1_w \dots + K1_n$

$K2_n = \sum K2_x + K2_y + K2_z + K2_w + K2_n$

$K3_n = \sum K3_x + K3_y + K3_z + K3_w + K3_n$

$Bij_n = \sum Bij_x + Bij_x + Bij_z + Bij_w = Bij_n$

K1

K2

K3

Bij

$F(G) = \int_{b-b_n}^{a-a_n} f(x, y, z, w_{n \dots n})$

??

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Thanks