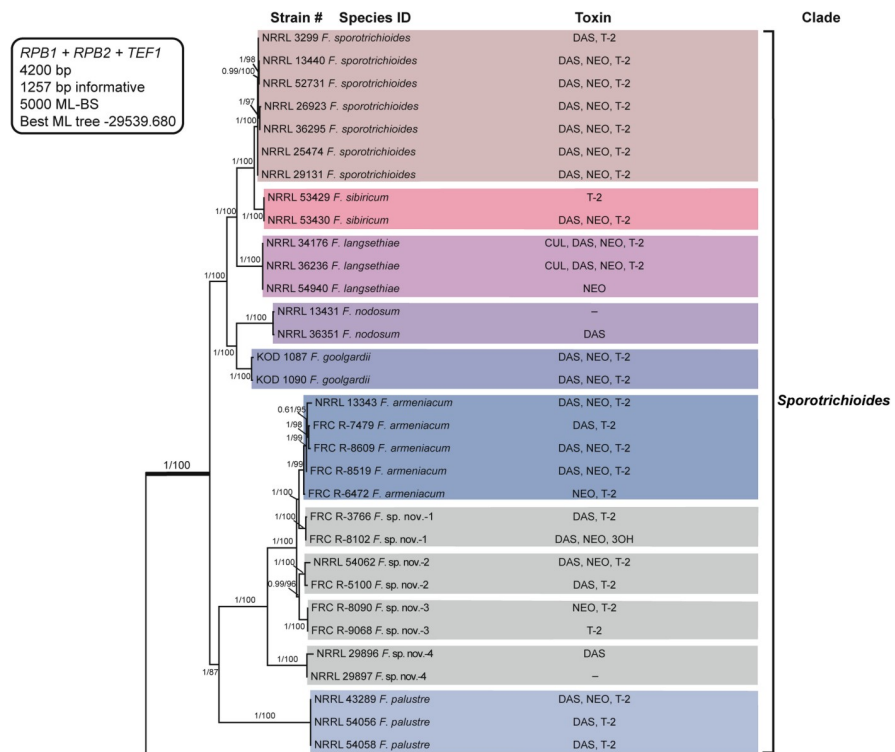
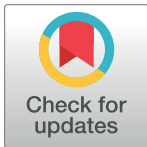


CORRECTION

# Correction: Phylogenetic diversity, trichothecene potential, and pathogenicity within *Fusarium sambucinum* species complex

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Fig 1 in the original article [1] is incorrect. Fig 1 should have been individual figures, rather than one consolidated figure. The authors have provided correct versions of Fig 1 as new figures below. Figs 4–7 correspond with the originally published Fig 1. Please view Figs 4–7 here.



**Fig 4. *Fusarium sambucinum* species complex. Bayesian and maximum likelihood phylogeny of the Sporotrichioides Clade inferred from partial RPB1 + RPB2 + TEF1 data set.** Support values above internodes are Bayesian posterior probabilities (BPP)/maximum likelihood bootstrap (ML-BS) values. BPP were calculated using MrBayes 3.2.7a [71]. ML-BS values were determined using IQ-TREE 1.6.12 [66]. The Sporotrichioides Clade (defined by thickened internode) was strongly supported as monophyletic (BPP = 1; ML-BS = 100%). Putatively novel species resolved within the Sporotrichioides Clade are designated *F. sp. nov.-1* to *-4*. Toxins mapped on the phylogeny were determined via gas chromatography-mass spectrometry. CUL, culmorin; DAS, diacetoxyscirpenol; NEO, neosolaniol; T-2, T-2 toxin; 3OH, isotrichodermol; -, none detected.

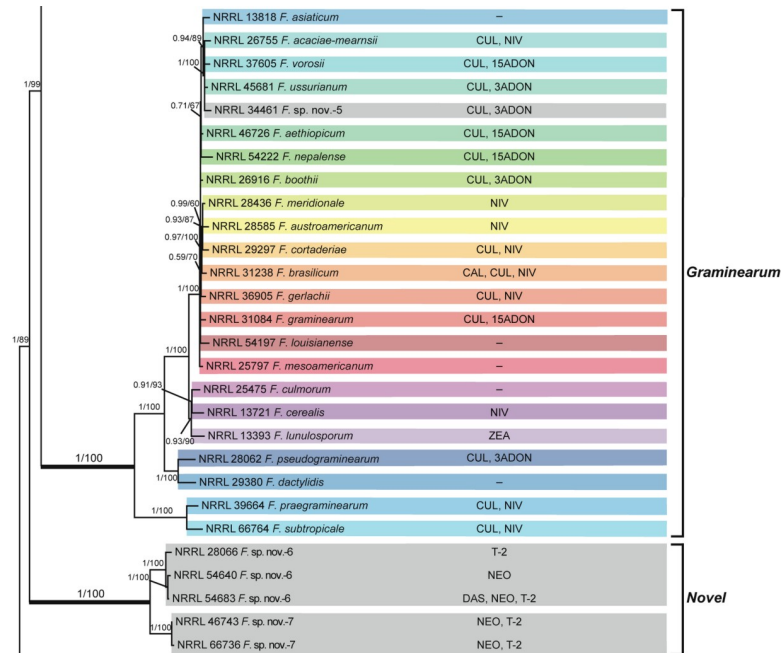
<https://doi.org/10.1371/journal.pone.0250812.g001>

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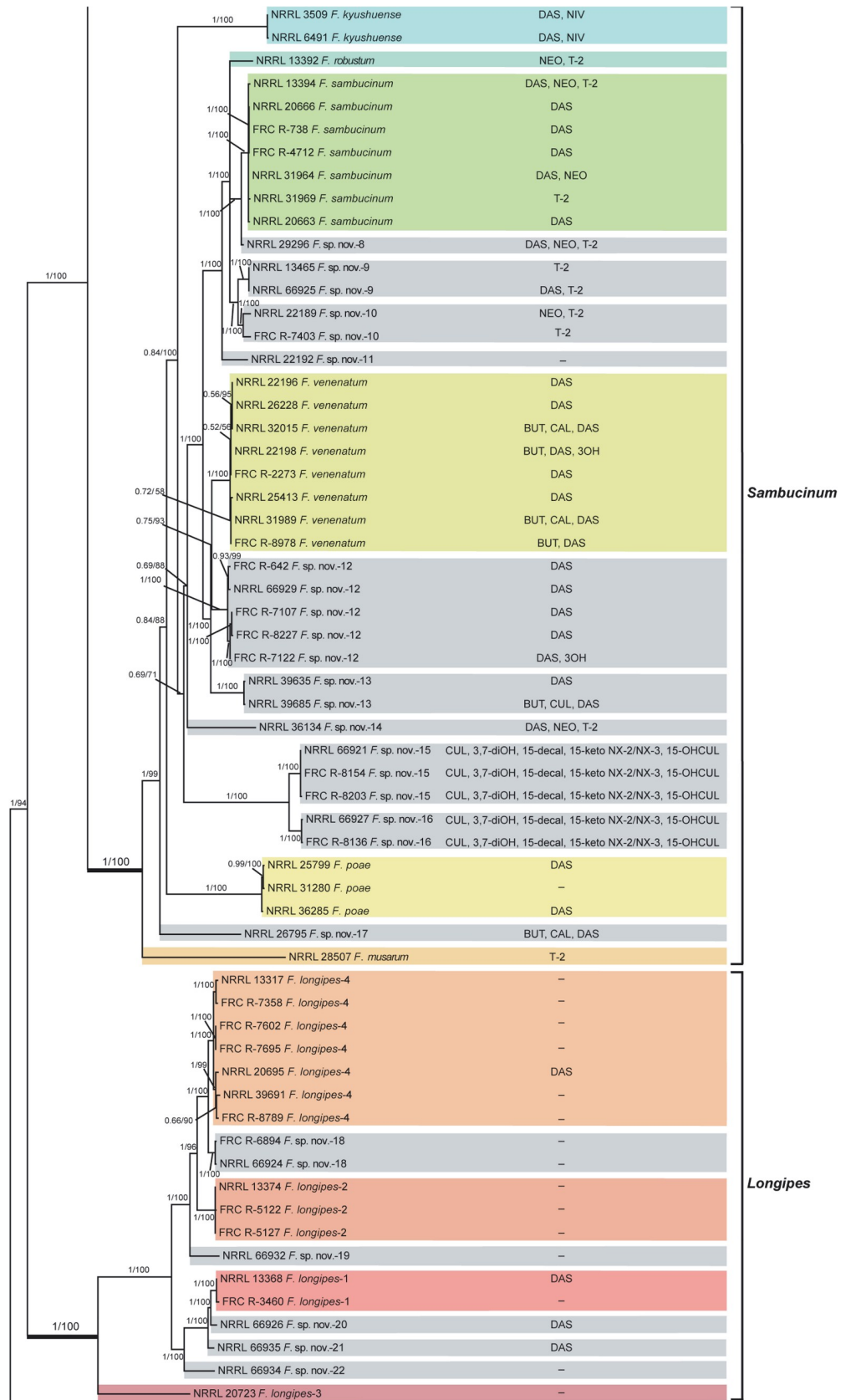
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**Fig 5. *Fusarium sambucinum* species complex. Bayesian and maximum likelihood phylogeny of the Graminearum and Novel Clades inferred from partial *RPB1* + *RPB2* + *TEF1* data set.** Support values above internodes are Bayesian posterior probabilities (BPP)/maximum likelihood bootstrap (ML-BS) values. BPP were calculated using MrBayes 3.2.7a [71]. ML-BS values were determined using IQ-TREE 1.6.12 [66]. The Graminearum and Novel Clades (defined by thickened internodes) were strongly supported as monophyletic (BPP = 1; ML-BS = 100%). Putatively novel species resolved within the Graminearum and Novel Clades are designated *F. sp. nov.-5* to *-7*. Toxins mapped on the phylogeny were determined via gas chromatography-mass spectrometry. CAL, calonectrin; CUL, culmorin; DAS, diacetoxyscirpenol; NEO, neosolanol; NIV, nivalenol; T-2, T-2 toxin; ZEA, zearalenone; 3ADON, 3-acetyldeoxynivalenol; 15ADON, 15-acetyldeoxynivalenol; -, none detected.

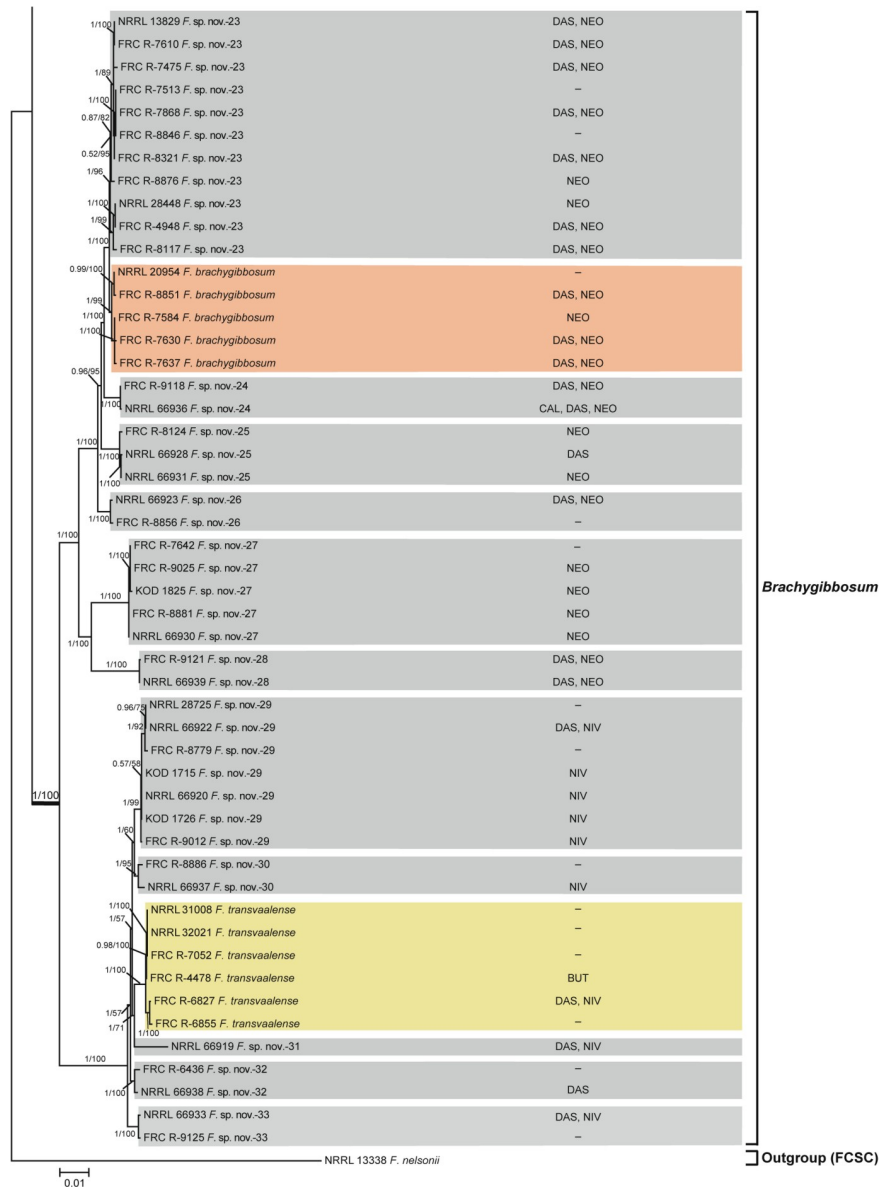
<https://doi.org/10.1371/journal.pone.0250812.g002>



**Fig 6. *Fusarium sambucinum* species complex. Bayesian and maximum likelihood phylogeny of the *Sambucinum* and *Longipes* Clades inferred from partial *RPB1* + *RPB2* + *TEF1* data set.** Support values above internodes are Bayesian posterior probabilities (BPP)/maximum likelihood bootstrap (ML-BS) values. BPP were calculated using MrBayes 3.2.7a [71]. ML-BS values were determined using IQ-TREE 1.6.12 [66]. The *Sambucinum* and *Longipes*

Clades (defined by thickened internodes) were strongly supported as monophyletic (BPP = 1; ML-BS = 100%). Putatively novel species resolved within the *Sambucinum* and *Longipes* clades are designated *F. sp. nov.*-8 to -22. Four phylogenetically distinct species within the *Longipes* Clade previously reported in other studies are identified by unique Arabic numbers (1 to 4). Toxins mapped on the phylogeny were determined via gas chromatography-mass spectrometry. BUT, butenolide; CAL, calonectrin; CUL, culmorin; DAS, diacetoxyscirpenol; NEO, neosolaniol; NIV, nivalenol; T-2, T-2 toxin; 3OH, isotrichodermol; 3,7-diOH, 7-hydroxy isotrichodermol; 15-decal, 15-decalonectrin; 15-keto NX-2 and 15-keto NX-3, novel type A trichothecenes; 15-OHCUL, 15-hydroxy culmorin; -, none detected.

<https://doi.org/10.1371/journal.pone.0250812.g003>



**Fig 7. *Fusarium sambucinum* species complex.** Bayesian and maximum likelihood phylogeny of the *Brachy gibbosum* Clade inferred from partial *RPB1* + *RPB2* + *TEF1* data set. Support values above internodes are Bayesian posterior probabilities (BPP)/maximum likelihood bootstrap (ML-BS) values. BPP were calculated using MrBayes 3.2.7a [71]. ML-BS values were determined using IQ-TREE 1.6.12 [66]. The ingroup *Fusarium sambucinum* species complex was rooted on sequences of NRRL 13338 *F. nelsonii* from its sister group, the *F. chlamydosporum* species complex. The *Brachy gibbosum* Clade (defined by thickened internode) was strongly supported as monophyletic (BPP = 1; ML-BS = 100%). Putatively novel species resolved within the *Brachy gibbosum* Clade are designated *F. sp. nov.*-23 to -33. Toxins mapped on the phylogeny were determined via gas chromatography-mass spectrometry. BUT, butenolide; CAL, calonectrin; DAS, diacetoxyscirpenol; NEO, neosolaniol; NIV, nivalenol; -, none detected.

<https://doi.org/10.1371/journal.pone.0250812.g004>

## Reference

1. Laraba I, McCormick SP, Vaughan MM, Geiser DM, O'Donnell K (2021) Phylogenetic diversity, trichothecene potential, and pathogenicity within *Fusarium sambucinum* species complex. PLoS ONE 16(1): e0245037. <https://doi.org/10.1371/journal.pone.0245037> PMID: 33434214