

Tracking of diversity and evolution in the brown rot fungi *Monilinia fructicola*, *Monilinia fructigena*, and *Monilinia laxa*

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Monilinia fructigena



Monilinia fructicola



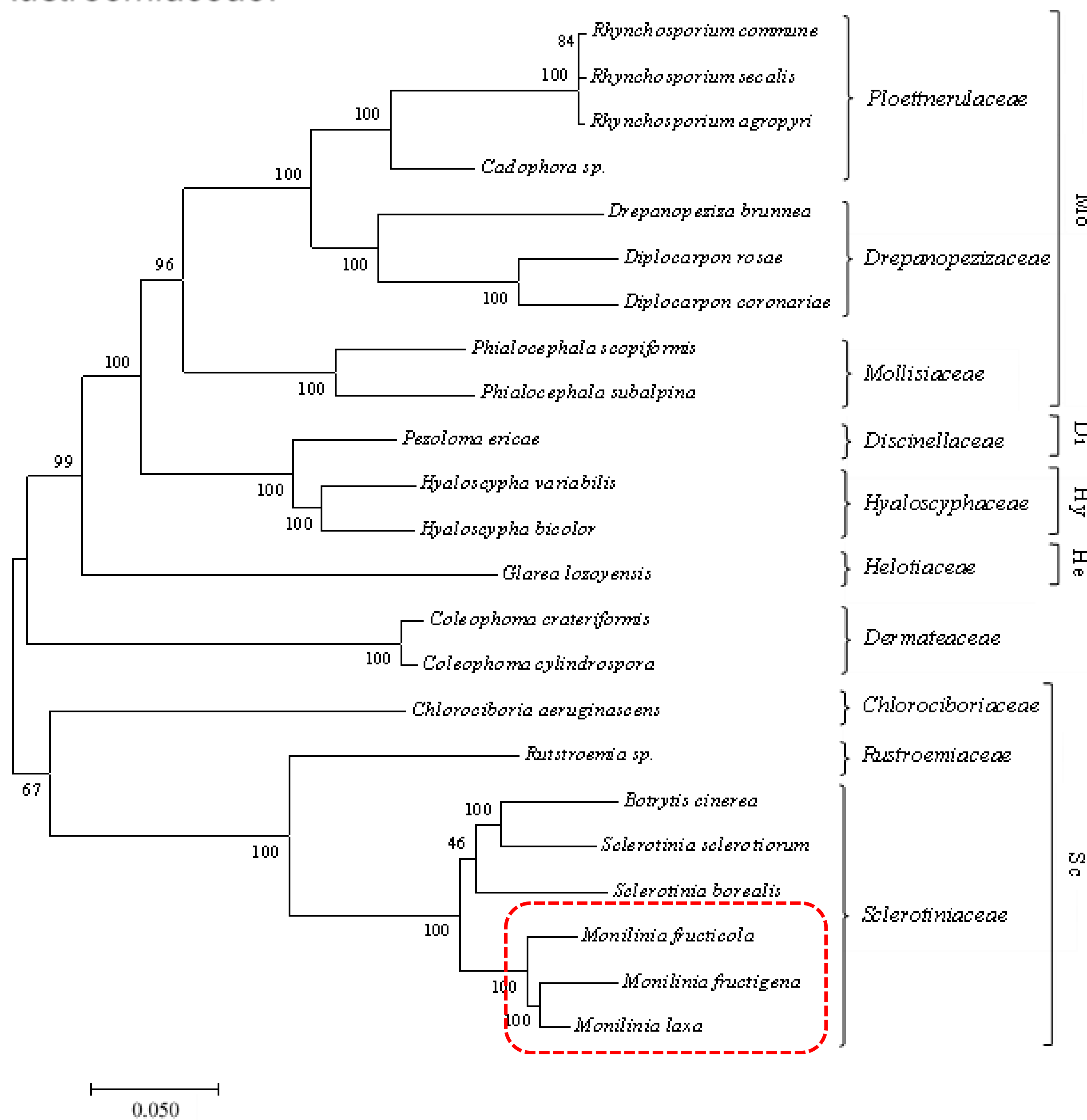
Monilinia laxa

The most important fungi causing brown rot and blossom blight on fruit trees are *Monilinia laxa*, *Monilinia fructigena* and *Monilinia fructicola*. They are Ascomycetes included in the *Sclerotiniaceae* family, causing worldwide severe losses on stone and pome fruits production in pre and postharvest.

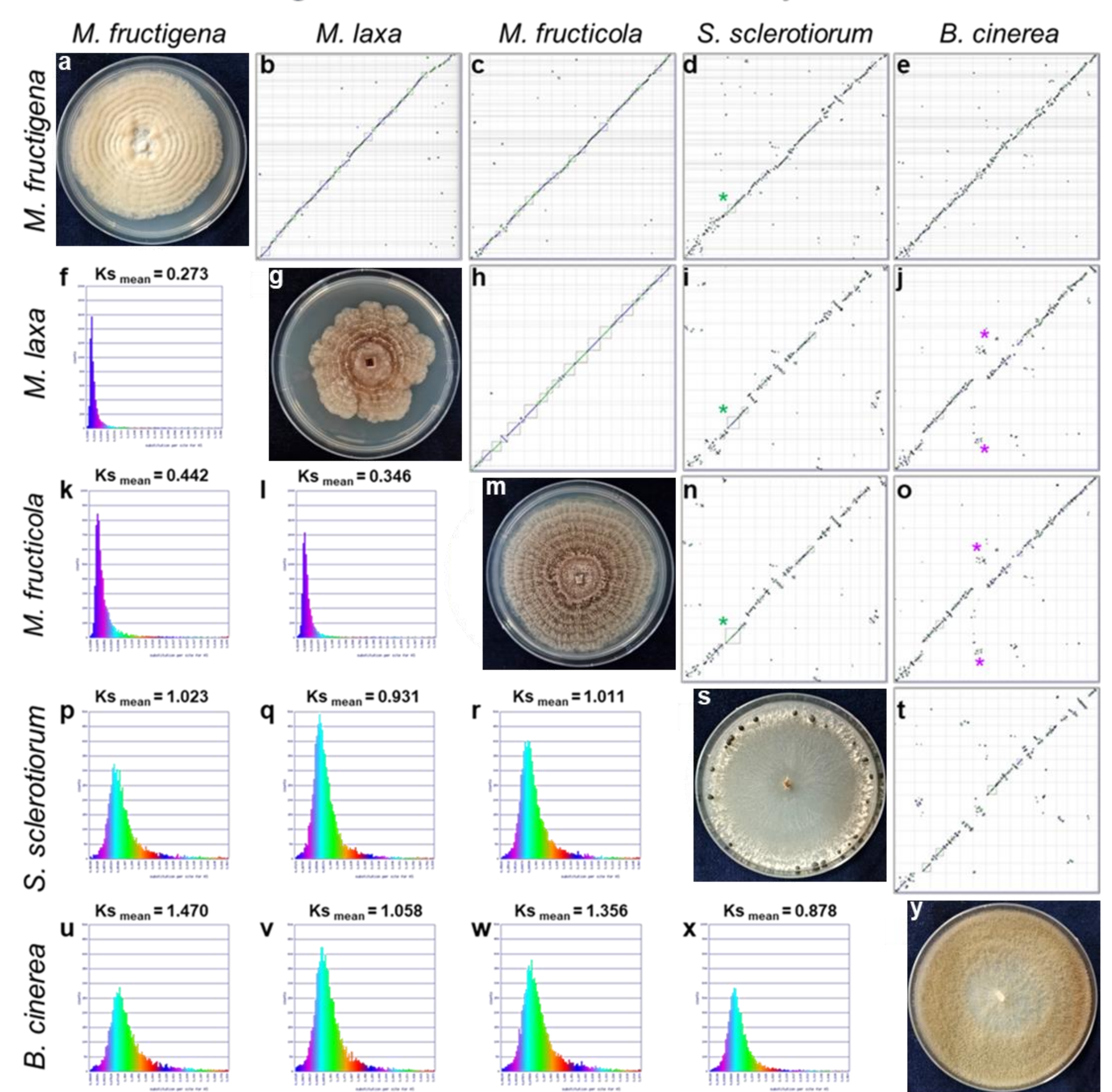
We generated annotated high-quality draft genomes that can represent useful sources for investigations into the evolutionary history of the *Monilinia* genus within the *Sclerotiniaceae* family.

Isolate	Mfrg269	Isolate	Mlax316	Isolate	Mfrc123
<i>M. fructigena</i> (Landi et al., 2018)	Host <i>Prunus domestica</i>	Host <i>Prunus avium</i>	Host <i>Prunus avium</i>	Host <i>Prunus avium</i>	Host <i>Prunus avium</i>
Total length (Mb) 43,125,165	Total length (Mb) 42,814,844	Total length (Mb) 44,047,900	Total length (Mb) 44,047,900	Total length (Mb) 44,047,900	
N° scaffolds 131	N° scaffolds 49	N° scaffolds 20	N° scaffolds 20	N° scaffolds 20	
N° genes 10,502	N° genes 11,163	N° genes 12,118	N° genes 12,118	N° genes 12,118	
CDS 10,811	CDS 12,427	CDS 13,784	CDS 13,784	CDS 13,784	
Scaffolds N50 (pb) 767,732	Scaffolds N50 (pb) 2,449,422	Scaffolds N50 (pb) 2,592,823	Scaffolds N50 (pb) 2,592,823	Scaffolds N50 (pb) 2,592,823	
Scaffolds L50 20	Scaffolds L50 8	Scaffolds L50 7	Scaffolds L50 7	Scaffolds L50 7	
CG% 42.10	CG% 41.26	CG% 40.79	CG% 40.79	CG% 40.79	

Phylogenomic analyses suggest *M. fructicola* genetically distant from *M. laxa* and *M. fructigena*, although the three species likely share a common ancestor. *Botrytis cinerea* and *Sclerotinia sclerotiorum* were the closest related taxa to the *Monilinia* genus in the *Junctoriae* section, and all were in a monophyletic lineage strictly related to *Rustroemiaceae*.



The syntenic studies confirm the close relationship among the three *Monilinia* genomes. The coding sequence divergence (measured by Ks values) confirmed that *M. laxa* and *M. fructigena* are closely related each other, while *M. fructicola* is somewhat divergent. *Monilinia* genomes were closer to those of *S. sclerotiorum* than *B. cinerea*, and *M. laxa* was the closest to the other tested fungi of the *Sclerotiniaceae* family.



List of species within the order *Helotiales* submitted to phylogenetic analysis.

Species (Code/strain)	Family*	Genbank accession number	Number of annotated proteins
<i>Monilinia fructicola</i> (Mfrc123)	<i>Sclerotiniaceae</i>	GCA_008692225.1	13,749
<i>Monilinia fructigena</i> (Mfrg269)	<i>Sclerotiniaceae</i>	GCA_003260565.1	10,800
<i>Monilinia laxa</i> (Mlax316)	<i>Sclerotiniaceae</i>	GCA_009299455.1	12,424
<i>Botrytis cinerea</i> (B05.10)	<i>Sclerotiniaceae</i>	GCF_000143535.2	13,703
<i>Cadophora</i> sp. (DSE1049)	<i>Ploetmerulaceae</i>	GCA_003073865.1	22,762
<i>Chlorociboria aeruginascens</i> (IHIA39)	<i>Chlorociboriaceae</i>	GCA_002276475.2	8,648
<i>Coleophoma cylindrospora</i> (BP6252)	<i>Dermateaceae</i>	GCA_003369665.1	14,177
<i>Coleophoma crateriformis</i> (BP5796)	<i>Dermateaceae</i>	GCA_003369635.1	13,257
<i>Diplocarpon rosae</i> (DortE4)	<i>Drepanopezizaceae</i>	GCA_002317995.1	13,761
<i>Glaea lozoyensis</i> (ATCC 20868)	<i>Helotiaceae</i>	GCA_000409485.1	13,083
<i>Hyaloscypha variabilis</i> (F)	<i>Hyaloscyphaceae</i>	GCA_002865655.1	20,386
<i>Marssonina brunnea</i> (=Drepanopeziza brunnea) (MB_m1)	<i>Drepanopezizaceae</i>	GCA_000298775.1	10,027
<i>Marssonina coronariae</i> (=Diplocarpon coronariae) (NL1)	<i>Drepanopezizaceae</i>	GCA_002204255.1	9,355
<i>Meliniomyces bicolor</i> (=Hyaloscypha bicolor) (E)	<i>Hyaloscyphaceae</i>	GCA_002865645.1	18,604
<i>Pezoloma ericae</i> (UAMH 7357)	<i>Discinellaceae</i>	GCA_002865625.1	16,783
<i>Phialocephala scopiformis</i> (CBS 120377)	<i>Mollisiaceae</i>	GCA_001500285.1	18,567
<i>Phialocephala subalpina</i> (UAMH 11012)	<i>Mollisiaceae</i>	GCA_000143535.1	20,173
<i>Rhynchosporium agropyri</i> (O4CH-RAC-A.6.1)	<i>Ploetmerulaceae</i>	GCA_000074905.1	13,673
<i>Rhynchosporium commune</i> (UK7)	<i>Ploetmerulaceae</i>	GCA_000074885.1	12,211
<i>Rhynchosporium secalis</i> (O2CH4-6a.1)	<i>Ploetmerulaceae</i>	GCA_000074895.1	13,145
<i>Rustroemia</i> sp. (NJR-2017a BBW)	<i>Rustroemiaceae</i>	GCA_002946425.1	10,975
<i>Sclerotinia sclerotiorum</i> (1980 UF-70)	<i>Sclerotiniaceae</i>	GCA_001857865.1	11,130
<i>Sclerotinia borealis</i> (F-4128)	<i>Sclerotiniaceae</i>	GCA_000503235.1	10,166

*According to the CABI database (<http://www.speciesfungorum.org/Names/fundic.asp>)



Syntenic dot plot (b, c, d, e, h, i, j, n, o, t) and synonymous (Ks) analysis (f, k, l, p, q, r, u, v, w, x) of *M. fructigena*, *M. laxa*, *M. fructicola*, *S. sclerotiorum*, and *B. cinerea* genomes. Seven-day-old cultures on PDA are shown on the diagonal (a, g, m, s, y). In dot-plot graphs, horizontal or vertical grey lines delineate scaffolds ordered and oriented according to synteny, using 'Syntenic Path Assembly' (SPA) option (SynMap - COGE GENOME). Each dot represents an orthologous gene pair. Syntenic gene pairs are plotted with colour based on the same forward order (green) or inverted matching (blue). Gray squares underline syntenic blocks. In Ks graphs, younger syntelogs (lower number of synonymous changes) are purple blue coloured (on the left), while older syntelogs (higher number of synonymous changes) are cyan-yellow-green coloured (on the right). Fuchsia * = disjointed alignments was indicated; green * = largest syntenic block among outgroup genomes and *Monilinia* spp.

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