

# Berkeleyomyces rouxiae—A Pathogen Causing the Black Root Rot of Tobacco

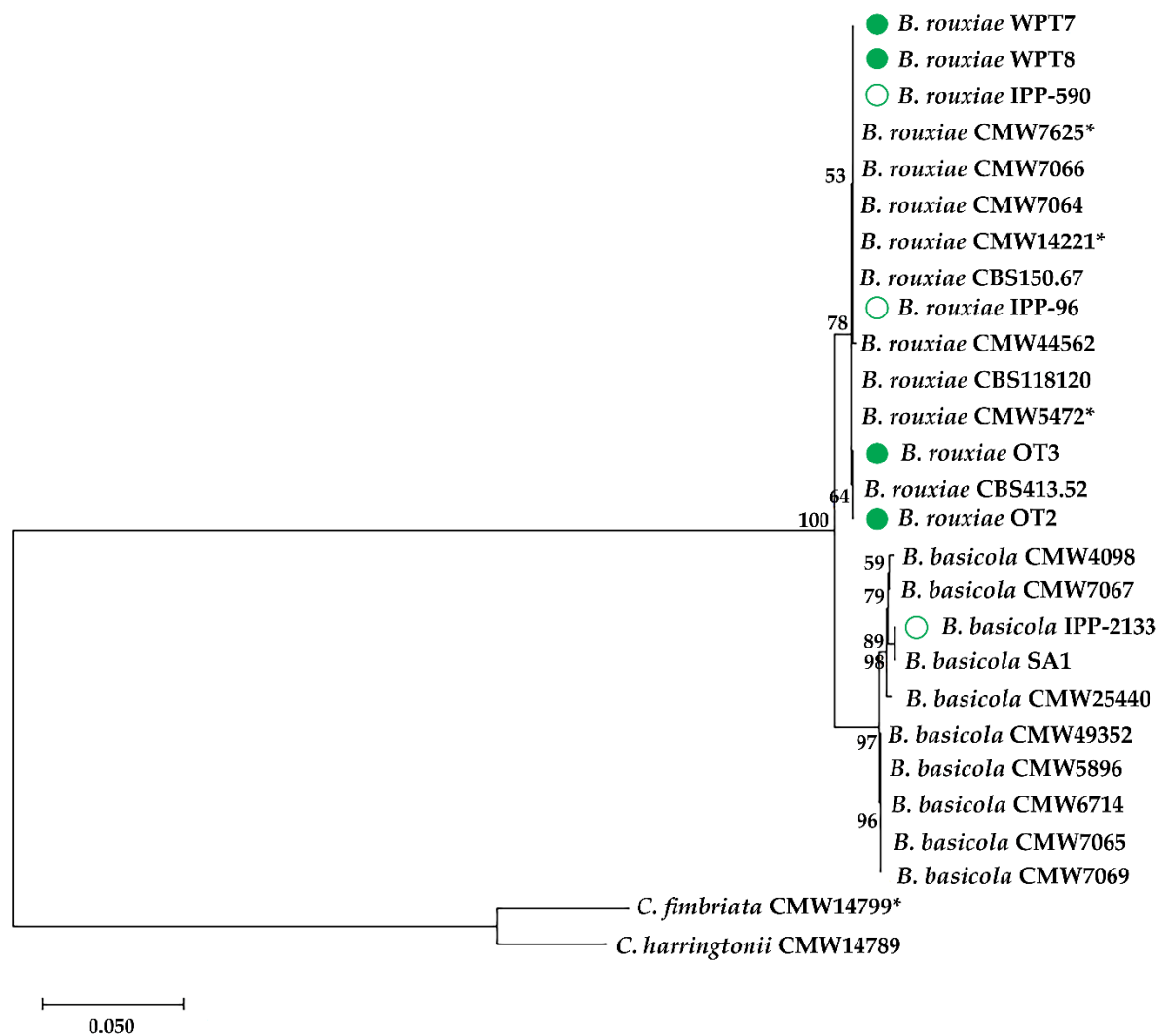
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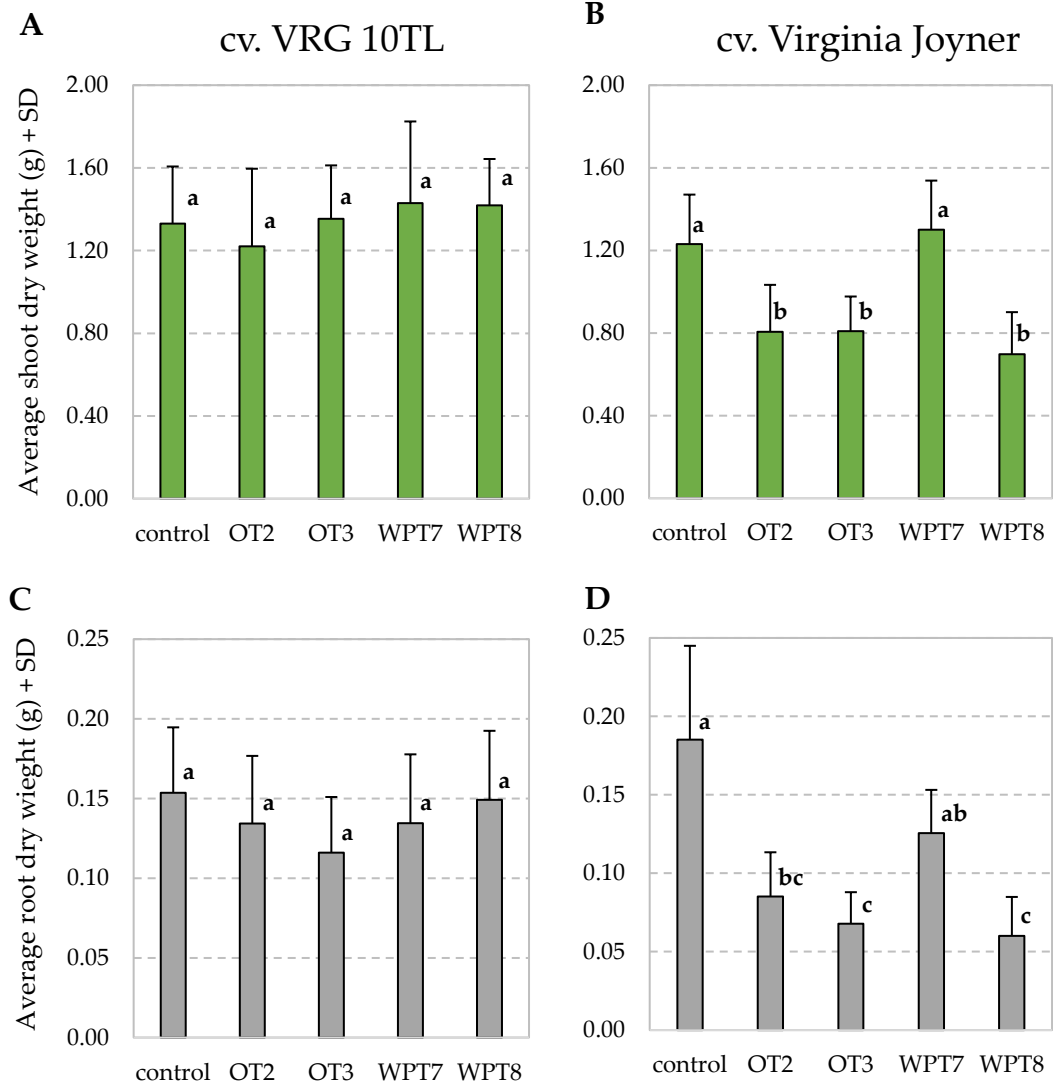
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**Table S1** Accession numbers of the sequences and isolates used in phylogenetic analyses. Data obtained in this study is indicated in green.

Species name	Isolate name/culture collection no.	CBS culture collection no.	ITS	MCM7	ACT
<i>Berkeleyomyces basicola</i>	CMW4098		MF952421	MF967078	MF967131
<i>Berkeleyomyces basicola</i>	CMW5896		MF952422	MF967100	MF967141
<i>Berkeleyomyces basicola</i>	CMW6714		MF952423	MF967079	MF967142
<i>Berkeleyomyces basicola</i>	CMW7065	CBS341.33	MF952424	MF967082	MF967144
<i>Berkeleyomyces basicola</i>	CMW7067	CBS487.48	MF952425	MF967084	MF967146
<i>Berkeleyomyces basicola</i>	CMW7069		MF952420	MF967085	MF967147
<i>Berkeleyomyces basicola</i>	CMW49352	CBS142796	MF952429	MF967102	MF967148
<i>Berkeleyomyces basicola</i>	CMW25440	CBS142829	MF952428	MF967088	MF967129
<i>Berkeleyomyces basicola</i>	SA1		MF952430	MF967108	MF967115
<i>Berkeleyomyces basicola</i>	IPP-2133		PQ511483	PQ553447	PQ553440
<i>Berkeleyomyces rouxiae</i>		CBS118120	MF952413	MF967098	MF967117
<i>Berkeleyomyces rouxiae</i>	CMW5472	CBS117825	MF952406	MF967080	MF967140
<i>Berkeleyomyces rouxiae</i>	CMW7064	CBS194.26	MF952407	MF967081	MF967143
<i>Berkeleyomyces rouxiae</i>	CMW7066	CBS342.33	MF952408	MF967083	MF967145
<i>Berkeleyomyces rouxiae</i>		CBS413.52	MF952417	MF967106	MF967120
<i>Berkeleyomyces rouxiae</i>		CBS150.67	MF952416	MF967107	MF967118
<i>Berkeleyomyces rouxiae</i>	CMW7625	CBS117828	MF952412	MF967112	MF967151
<i>Berkeleyomyces rouxiae</i>	CMW14221	CBS142830	MF952404	MF967113	MF967125
<i>Berkeleyomyces rouxiae</i>	CMW44562		MF952395	MF967089	MF967132
<i>Berkeleyomyces rouxiae</i>	LXBR1		ON679637	ON711036	-
<i>Berkeleyomyces rouxiae</i>	LT1		LC341294	LC421984	-
<i>Berkeleyomyces rouxiae</i>	BRR1		OK526425	OK526429	-
<i>Berkeleyomyces rouxiae</i>	OT2		PQ511477	PQ553441	PQ553434
<i>Berkeleyomyces rouxiae</i>	OT3		PQ511478	PQ553442	PQ553435
<i>Berkeleyomyces rouxiae</i>	WPT7		PQ511479	PQ553443	PQ553436
<i>Berkeleyomyces rouxiae</i>	WPT8		PQ511480	PQ553444	PQ553437
<i>Berkeleyomyces rouxiae</i>	IPP-590		PQ511481	PQ553445	PQ553438
<i>Berkeleyomyces rouxiae</i>	IPP-96		PQ511482	PQ553446	PQ553439
<i>Ceratocystis harringtonii</i> (syn. <i>Ceratocystis populicola</i> )	CMW14789	CBS119.78	EF070418	KM495435	MF967155
<i>Ceratocystis fimbriata</i>	CMW14799	CBS114723	KC493160	KJ601542	MF967156
<i>Ceratocystis eucalypticola</i>	CMW11536		FJ236723	KM495428	-
<i>Ceratocystis diversiconidia</i>	CMW22445	CBS123013	FJ151440	KM495423	-
<i>Chalaropsis ovoidea</i>	CMW22733		FJ411343	KM495487	-
<i>Chalaropsis thielavioides</i>	CMW22736		FJ411342	KM495489	-
<i>Thielaviopsis cerberus</i>	CMW36668		JX518348	KM495415	-
<i>Thielaviopsis musarum</i>	CMW1546		JX518325	KM495445	-
<i>Thielaviopsis paradoxa</i>	CMW36689		JX518342	KM495451	-
<i>Thielaviopsis radicola</i>	CMW1032		KF612023	KM495459	-
<i>Endoconidiophora douglasii</i>	CMW26367		NR_120295	KM495424	-
<i>Graphium laricis</i>	CMW5601		AY148183	KM495476	-



**Figure S1** Maximum likelihood tree constructed from concatenated nucleotide sequences of three regions (ITS, *MCM7*, *ACT*) showing relative relationship of 27 accessions belonging to *Berkeleyomyces* and *Ceratocysis* genera. Numbers next to the nodes are bootstrap values of 1000 replicates (only values greater than 50% are shown). Isolates sequenced in this study are indicated in green: tobacco isolates (closed circles), isolates obtained from the Bank of Pathogens IPP-NRI (open circles). Asterisks indicate ex-type strains.



**Figure S2** Average dry weight of the shoots and roots of two tobacco cultivars (VRG 10TL and Virginia Joyner) subjected to testing pathogenicity of the four isolates of *B. rouxiae* (OT2, OT3, WPT7, WPT8). The plotted values are averages + standard deviation. Lowercase letters indicate results of post-hoc tests performed after ANOVA (in case of cv. VRG 10TL; Fig. A and C) or rank ANOVA (Kruskal-Willis test in case of data for cv. Virginia Joyner; Fig. B and D). The same letter assigned for two experimental groups in the same graph indicates a lack of statistically significant differences among them.