Table S1.   **Nonhybrid *Epichloë* species used in this study**

Endophyte species	Isolate ID	ATCC or CBS number	Host species	Reference or source
E. amarillans	E52	ATCC 200743	*Sphenopholis obtusata*	(1-4)
E. amarillans	E57	ATCC 200744	*Agrostis hyemalis*	(1-5)
E. amarillans	E4668			(6)
E. baconii	As6	ATCC 90167	*Agrostis capillaris*	(7)
E. baconii	E424	ATCC 200746	*Agrostis tenuis*	(8)
	E357 =			
E. baconii	E1031	ATCC 200745	*Calamagrostis villosa*	(2-4, 6, 8)
E. brachyelytri	E1040	ATCC 200752	*Brachyelytrum erectum*	(2-4)
E. brachyelytri	E1045	ATCC 200753	*Brachyelytrum erectum*	(3)

Species	Strain	ATCC	Host	Source/Reference
E. brachyelytri	E1124	ATCC 201560	*Brachyelytrum erectum*	(3)
E. brachyelytri	E4804		*Brachyelytrum erectum*	(5)
E. bromicola	E501	ATCC 200749	*Bromus erectus*	(2, 4, 8)
E. bromicola	E502	ATCC 200750	*Bromus erectus*	(5, 8)
E. bromicola	E799	ATCC 201559	*Bromus benekenii*	(8)
E. elymi	E56	ATCC 201551	*Elymus canadensis*	(1-5, 9)
E. elymi	E184	ATCC 200850	*Elymus virginicus*	(2-4, 9)
E. elymi	EC1		*Elymus canadensis*	S. Marek, Oklahoma State University
E. elymi	EC4		*Elymus canadensis*	S. Marek, Oklahoma State University
E. elymi	WWG2		*Pascopyrum smithii*	C.A. Young, The Samuel Roberts Noble

				Foundation, Oklahoma
E. festucae	E189	ATCC 90661	*Festuca rubra*	(1, 4, 8, 9)
E. festucae	E434	ATCC MYA-434	*Festuca gigantea*	(2, 8)
E. festucae	E1035.33	ATCC MYA-446	NA	(10)
E. festucae	E2368		NA	(5, 10)
E. festucae	Fg1		*Festuca glauca*	(9)
E. festucae	Fl1	ATCC MYA-3407	*Festuca longifolia*	(9, 11)
E. festucae	Frc5		*Festuca rubra* subsp. *commutata*	(9)
E. festucae	Frc7		*Festuca rubra* subsp. *commutata*	(9)
E. festucae	Fr1		*Festuca rubra*	(9, 11)

E. festucae	Frr1		*Festuca rubra* subsp. *rubra*	(9)
E. glyceriae	E2772	ATCC 200755	*Glyceria striata*	(2-4)
E. mollis	E3601 = AL9924		*Holcus mollis*	(6)
E. sylvatica	E354	ATCC 200748	*Brachypodium sylvaticum*	(2-4, 8)
E. sylvatica	E503	ATCC 200751	*Brachypodium sylvaticum*	(2-4, 8)
E. typhina	E8	ATCC 200736	*Lolium perenne*	(3-5, 8, 9)
E. typhina	E505	ATCC 200739	*Brachypodium pinnatum*	(2-4, 8)
E. typhina	ORE04		*Dactylis glomerata*	C.A. Young, The Samuel Roberts Noble Foundation, Oklahoma

				C.A. Young, The Samuel Roberts Noble
E. typhina	ORE06		*Dactylis glomerata*	Foundation, Oklahoma
E. typhina subsp. *clarkii*	Holcus 3	ATCC 90168	*Holcus lanatus*	(7)
E. typhina subsp. *poae*	E1022	ATCC 201668	*Poa nemoralis*	(4, 8)
E. typhina subsp. *poae*	E5819		*Poa nemoralis*	(5)

Table S2.   *Epichloë* **species from endophyte-infected plant material used in this study**

Species	Isolate ID	Plant ID	Host Species	Reference or source
E. typhina	OR10	Collected from field plant in Oregon	*Dactylis glomerata*	C.A. Young, The Samuel Roberts Noble Foundation, Oklahoma
E. typhina subsp. *poae* BlaTG-1	NFe671	BRLA-671	*Bromus laevipes*	(12)
E. amarillans	NFe-708	ELCA-708	*Elymus canadensis*	C.A. Young, The Samuel Roberts Noble Foundation, Oklahoma
E. elymi	NFE728	ELVI-728	*Elymus virginicus*	C.A. Young, The Samuel Roberts Noble Foundation, Oklahoma
E. elymi	NFE741	ELVI-741	*Elymus virginicus*	C.A. Young, The Samuel

				Roberts Noble Foundation, Oklahoma
				C.A. Young, The Samuel Roberts Noble Foundation, Oklahoma
E. festucae var. *lolii*	NFe243	LOPE-243	*Lolium perenne*	
E. cabralii BlaTG-2	NFe661	BRLA-661	*Bromus laevipes*	(12)
E. cabralii BlaTG-2	NFe688	BRLA-688	*Bromus laevipes*	(12)
E. sp. BlaTG-3 (G1)	NFe79	BRLA-79	*Bromus laevipes*	(12)
E. sp. BlaTG-3 (G2)	NFe82	BRLA-82	*Bromus laevipes*	(12)
E. sp. BlaTG-3 (G3)	NFe83	BRLA-83	*Bromus laevipes*	(12)
E. canadensis	NFe699	ELCA-699	*Elymus canadensis*	C.A. Young, The Samuel Roberts Noble Foundation, Oklahoma
E. amarillans	NFe715	ELCA-715	*Elymus canadensis*	C.A. Young, The Samuel Roberts Noble

				Foundation, Oklahoma
	NFe1001 =			
E. canadensis	NFe727	ELCA-727	*Elymus canadensis*	(13)
E. canadensis	NFe716	ELCA-716	*Elymus canadensis*	(13)
	e19 = ATCC			
E. coenophiala	90664	LOAR-00437	*Lolium arundinaceum*	(4, 14)
E. coenophiala	AR584	LOAR-00405	*Lolium arundinaceum*	(15, 16)
		LOAR-00245		
		(BarOptima		C.A. Young, The Samuel
		PLUS E34,		Roberts Noble
E. coenophiala	E34	Barenbrug	*Lolium arundinaceum*	Foundation, Oklahoma
E. coenophiala	NFe45078	LOAR-00190	*Lolium arundinaceum*	(17)
E. sp. FaTG-2 G2	NFe45079	LOAR-00193	*Lolium arundinaceum*	(17)
E. sp. FaTG-2 G3	NFe45115	LOAR-00210	*Lolium arundinaceum*	(17)
E. sp. FaTG-3	NFe1100	LOAR-00488	*Lolium arundinaceum*	(6, 16)

E. sp. FaTG-4	e4305	4305	*Lolium sp.*	(6, 16)
	e167 = CBS			
E. uncinata	102646	FEPR-00400	*Lolium pratense*	(6, 18-20)
E. siegelii	e915	955	*Lolium pratense*	(20, 21)
E. sp.	e4678	4678	*Poa alsodes*	C.L. Schardl, University of Kentucky
E. sp.	e4742	4742	*Poa autumnalis*	C.L. Schardl, University of Kentucky
E. sp.	e4755	4755	*Poa autumnalis*	C.L. Schardl, University of Kentucky
E. sp. PauTG-1	e55		*Poa autumnalis*	(4)
E. sp.	e4427	4427	*Sphenopholis sp.*	C.L. Schardl, University of Kentucky
E. sp.	e4768	4768	*Festuca versuta*	C.L. Schardl, University of Kentucky

E. sp.	e4672	4672	*Agrostis hyemalis*	C.L. Schardl, University of Kentucky
E. sp.	e4676	4676	*Agrostis hyemalis*	C.L. Schardl, University of Kentucky

Table S3.   PCR primers used in this study

Target[1]	Primers used	Product size (bp)[2]
mfsA	mfsA_F: ACGATGGATTGGTCTTCTC	1362
	mfsA_R: GCAGACGAGCAACGCAACG	
qcrA	qcrA_F: TTCCGAGATTGTCGAGG	639
	qcrA_R: TCACTCTCCTGCTGCTG	
perA A1-domain	perA-5'_F3: ATGACGAGCTCGGAGCGAGTTG	1691
	perA-A1_R: AGACTTCCATCTGCACAGTATC	
perA T1-domain	perA1_4: TCGGAAAGGTCGGCTGTAC	1073
	perA1_R: TTGCTTCATCCCAGTCAGC	
perA C-domain	perA2_F: ATCCAAGACGCATATCCC	878
	perA-C_R: ATCATCTCGGCGGCTTCC	
perA A2-domain	perA2_1: ACAGCTTTGCCACTCCAAG	2363
	perA2_R: ATCCACGCCTATGTAGCTC	
perA M-domain	perA3_F: GCTTGCTGCGTTTGTCAC	1298
	perA-M_R: TGGGAAATCGGAACAAGG	
perA T2-domain	perA-T2_F: TCTTCAGGCATCGCAGGAAC	600
	perA-T2_R: TCGGCCACCTCCAGCCTGATG	
perA R*-domain	perA3_3: AGGAAGGCATCAGGCTGG	1376
	perA3_R: CTAGCCTCCAGATCTTGTG	
perA R*-domain deletion	perA-T2_F: TCTTCAGGCATCGCAGGAAC	742
	perA-17bp_R: GTACGGATAACCTCAAC	(E2368)

perA-1	perA1_F: ATGGACGCGGAGCCTTTTG	2905
	perA1_R: TTGCTTCATCCCAGTCAGC	
	Additional sequencing primers:	
	perA1_1: TTTGCAGTCCGGCGAAGC	
	perA1_2: ACGCCTAGAGTTCTGCAT	
	perA1_3: ATACTCACGCACACCAAC	
	perA1_4: TCGGAAAGGTCGGCTGTAC	
perA-2	perA2_F: ATCCAAGACGCATATCCC	2973
	perA2_R: ATCCACGCCTATGTAGCTC	
	Additional sequencing primers:	
	perA2_1: ACAGCTTTGCCACTCCAAG	
	perA2_2: AGATTTGGCAGTGGAACG	
	perA2_3: GTCTCCATCAGCAACATC	
perA-3	perA3_F: GCTTGCTGCGTTTGTCAC	3058
	perA3_R: CTAGCCTCCAGATCTTGTG	
	Additional sequencing primers:	
	perA3_1: TATCTCTTCAACATCATCCAG	
	perA3_2: ATCGCAGGAACACTCATCG	
	perA3_3: AGGAAGGCATCAGGCTGG	
	perA3_4: ATTCGCCAGGATGTAGAG	
perA-3ΔR*	perA3_F: GCTTGCTGCGTTTGTCAC	1864
	perA-17bp_R: GTACGGATAACCTCAAC	(E2368)
	Additional sequencing primers:	
	perA3_1: TATCTCTTCAACATCATCCAG	

	perA3_2: ATCGCAGGAACACTCATCG	
	perA3_3: AGGAAGGCATCAGGCTGG	
perA-qcrA intergenic region	perA-mid2_F2: CATCAGGCTGGAGGTGGCCGA	1451
	Ef104_R: CTAAGCTTTGGTCCAAGCTGCG	(E2368)

[1] Abbreviations: A = adenylation, T = thiolation, C = condensation, M = methylation and R* = reductase*.

[2] Product fragment sizes are for amplification of *E. festucae* Fl1 genomic DNA unless *E. festucae* E2368 is indicated in brackets.

Table S4.   Details of sequenced *perA* alleles

Species	Isolate	Allele progenitor[a]	*perA* type	Notes[b]	Accession #[c]
Nonhybrid species					
E. amarillans	E57	*E. amarillans*	*perA*		**JN640285**
E. amarillans	E4668	*E. amarillans*	*perA*		
E. baconii	As6	*E. baconii*	*perA*-ΔR		KP347847
	E357/E1031	*E. baconii*	*perA*		KP347874
	E424	*E. baconii*	*perA*-ΔR		KP347851
E. brachyelytri	E4804	*E. brachyelytri*	*perA*		**JN613323**
E. bromicola	AL0434	*E. bromicola*	*perA*		KP347845
	AL0426_2	*E. bromicola*	*perA*-ΔR	START	KP347846, KP719965
	E501	*E. bromicola*	*perA*		KP347854
	E502	*E. bromicola*	*perA*		**JX441995**
	E799	*E. bromicola*	*perA*-ΔR	STOP@7051	KP347855
E. elymi	E56	*E. elymi*	*perA*		**JX402755**
E. festucae	E189	*E. festucae*	*perA*-ΔR		KP347868
	E2368	*E. festucae*	*perA*-ΔR		**JN640287**
	Fg1	*E. festucae*	*perA*	-236@3652	KP347869
	Fl1	*E. festucae*	*perA*		**AB205145**
E. mollis	E3601	*E. mollis*	*perA*	+1@1412,	KP347873

				+2@3470, +4@6153, +7@6162	
E. sylvatica	E354	*E. sylvatica*	*perA*-ΔR	+1@992, -259@1891, +2@4200	KP347850, KP719966
	E503	*E. sylvatica*	*perA*-ΔR	+1@992, -259@1891, +2@4200	KP347852
E. typhina	E8	*E. typhina*	*perA*		**JX402754**
	E505	*E. typhina*	*perA*-ΔR	STOP@2116	KP347853, KP719967
	E1022	*E. typhina*	*perA*-ΔR		KP347856
	ORE04	*E. typhina*	*perA*-ΔR	STOP@7045	KP347848, KP719969
	ORE06	*E. typhina*	*perA*-ΔR	STOP@7045	KP347849
	OR10	*E. typhina*	*perA*-ΔR	incomplete	KP347870
E. typhina subsp. *clarkii*	Holcus 3	*E. typhina* subsp. *clarkii*	*perA*-ΔR	STOP@6628	KP347859, KP719968
E. typhina subsp. *poae*	BlaTG-1	*E. typhina* subsp. *poae*	*perA*	incomplete	KP347875
	E5819	*E. typhina* subsp. *poae*	*perA*-ΔR		**JN640289**, KP719970
Hybrid species					
E. cabralii	BlaTG-2	*E. amarillans*	*perA*	incomplete	KP347876

	BRLA-00661				
		E. typhina	*perA*	incomplete	KP347877
E. siegelii	e915	*E. festucae*	*perA*-ΔR		KP347857, KP719971-KP719973
		E. bromicola	*perA*-ΔR	STOP@2839	KP347858
E. uncinata	e167	*E. bromicola*	*perA*	-1@5044	KP347860
		E. typhina	*perA*	+1@7972	KP347861
E. sp. FaTG-2 G2	NFe45079	LAE	*perA*	+1@1031, -621@1251, -328@3970	KP347862
		E. festucae	*perA*		KP347863
E. sp. FaTG-2 G3	NFe45115	LAE	*perA*	+1@1031, -621@1251, -328@3970	KP347864
		E. festcuae	*perA*	STOP@525	KP347865
E. sp. FaTG-3	NFe1100	LAE	*perA*	+1@1031, -621@1251, -328@3970	KP347866
		E. typhina	*perA*		KP347867
E. sp.	e4768	*E. festucae*	*perA*-ΔR	incomplete	KP347871
		E. typhina	*perA*	incomplete	KP347872

aLAE = *Lolium*-associated endophyte

[b]The sign indicates if bases have been deleted (-) or inserted (+), the following number shows the number of bp affected and the number after the "@" symbol shows the coordinates at which, or immediately before which, the insertion or deletion begins, respectively. Small deletions or insertions that do not cause a frameshift mutation are not detailed here. The sizes of large deletions are given relative to the *perA* sequence from *E. festucae* Fl1. STOP indicates a nonsense mutation, with the number following "@" detailing the coordinate of the causative SNP. START indicates the ATG start codon has been disrupted, though a nearby ATG codon may fill this role.

[c]Accession numbers shown in bold are from previous publications (5, 22).

1. **Schardl CL, Leuchtmann A, Tsai HF, Collett MA, Watt DM, Scott DB.** 1994. Origin of a fungal symbiont of perennial ryegrass by interspecific hybridization of a mutualist with the ryegrass choke pathogen, *Epichloë typhina*. Genetics **136:**1307-1317.

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5. **Schardl CL, Young CA, Hesse U, Amyotte SG, Andreeva K, Calie PJ, Fleetwood DJ, Haws DC, Moore N, Oeser B, Panaccione DG, Schweri KK, Voisey CR, Farman ML, Jaromczyk JW, Roe BA, O'Sullivan DM, Scott B, Tudzynski P, An Z, Arnaoudova EG, Bullock CT, Charlton ND, Chen L, Cox M, Dinkins RD, Florea S, Glenn AE, Gordon A, Gueldener U, Harris DR, Hollin W, Jaromczyk J, Johnson RD, Khan AK, Leistner E, Leuchtmann A, Li C, Liu J, Liu J, Liu M, Mace W, Machado C, Nagabhyru P, Pan J, Schmid J, Sugawara K, Steiner U, Takach JE, Tanaka E, Webb JS, Wilson EV, Wiseman JL, Yoshida R, Zeng Z.** 2013. Plant-symbiotic fungi as chemical engineers: Multi-genome analysis of the Clavicipitaceae reveals dynamics of alkaloid loci. PLoS Genet. **9**.

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from aphids in a grass-endophyte mutualism. Mol. Plant-Microbe Interact. **13:**1027-1033.

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