MATERIALS AND METHODS

Amplified fragment length polymorphism (AFLP) analysis

We used an AFLP Microbial Fingerprinting kit (Life Technologies, Carlsbad, CA, USA) for AFLP analysis, according to manufacturer's instructions. T4 DNA ligase, EcoRI, and MseI (New England Biolabs, Beverly, MA, USA) were used in the simultaneous restriction–ligation reaction. Preselective and selective polymerase chain reactions (PCRs) were performed in an iCycler thermal cycler (Bio-Rad Laboratories Hercules, CA, USA). A fluorescent dye-labelled EcoRI primer with two-base selection (FAM-EcoRI +AC, NED-EcoRI +AT, or JOE-EcoRI +AG) and an unlabelled MseI primer with two-base selection (MseI +CA) were used in the selective PCR. The FAM-EcoRI +AC, NED-EcoRI +AT, or JOE-EcoRI +AG reaction mixture was mixed in a 1:3:1 (v:v:v) ratio after the selective PCR. Hi-Di formamide (9.95 μL; Life Technologies) and standard size GeneScan 500 (ROX; 0.05 μL; Life Technologies) were added to 1.5 μL of each mixed sample. The samples were analysed with the modified conditions of injection, voltage 2.0, and time 44 using a 3100 Genetic Analyser with a 36-cm 16-capillary array, a Performance Optimized Polymer 6 (POP6) separation matrix, and GeneScan collection software (Life Technologies). The obtained

data were processed using GeneMapper software (Life Technologies) to produce the binary matrix for phylogenetic analysis.

Phylogenetic analysis

The binary data for a total of 66 AFLP markers of EACMCAB (FAM-EcoRI +AC), EATMCAY (NED-EcoRI +AT), and EAGMCAG (JOE-EcoRI +AG) from 95 taxa were compiled into a single data matrix. Neighbour-joining (NJ) analysis (Saitou and Nei 1987) of the binary data was performed using PAUP* (version 4.0β10) (Swofford 2002). Ties were broken randomly when encountered.

The sequence datasets combined the data for *TEF1α* and *RPB2* from 35 taxa including an outgroup (*Fusarium hostae* NRRL29889). The sequences obtained in the present study were aligned with MAFFT (version 7) using the E-INS-i option online (Katoh et al 2002, Katoh et al 2005, Katoh et al 2009). The sequences were truncated at the 5′ - and 3′ -ends, and manually aligned when necessary using ChromasPro. Phylogenetic trees were obtained using maximum parsimony (MP), maximum likelihood (ML), and Bayesian phylogenetic analyses. The best-fit evolutionary model was determined for each dataset by comparing different evolutionary models via the corrected Akaike information criterion (AICc) (Akaike 1974, Sugiura 1978) for MP and ML analyses, and the Bayesian information criterion (BIC) (Schwarz 1978) for the Bayesian analysis.

Kakusan4 (Tanabe 2007) and PAUP* were used for likelihood calculations. As a result of the calculations, the TEF1α regions were fitted to a J2 model with a gamma-shaped distributed rate. RPB2 regions were fitted to a TN93ef model with a gamma-shaped distributed rate. The combined dataset of the TEF1α and the RPB2 regions was fitted to a J2ef model with a gamma-shaped distributed rate. MP analysis with the selected evolutionary model was carried out using PAUP*. MP analysis was performed for 1,000 replications with different random starting points using the step-wise addition option to increase the likelihood of finding the most parsimonious tree. Alignment gaps were treated as new state data, and all characters were unordered and had equal weight. The branch-swapping algorithm was tree bisection and reconstruction (TBR). Branches of zero length were collapsed and all multiple, equally parsimonious trees were saved. The best tree topology of the MP trees was established using the Kishino–Hasegawa likelihood test (Kishino and Hasegawa 1989) on PAUP*. We calculated the tree length (TL), consistency index (CI), retention index (RI), homoplasy index (HI), and rescaled consistency index (RC). The ML analysis was performed by the likelihood ratchet method (Vos 2003). For the ML tree search, 1,000 sets of 25% site-upweighted data were created using the pgresampleseq command in Phylogears 1.0.2009.07.17 (Tanabe 2007), and ML trees with upweighted data were estimated using Treefinder (June 2008

release) (Jobb et al 2005) by applying the best-fit model. The strength of the internal branches from the resulting tree was tested by bootstrap (BS) analysis (Felsenstein 1985) using 10,000 replications in NJ, MP, and ML analysis. Bayesian phylogenetic analyses with the selected evolutionary model were carried out using MrBayes (version 3.2.5) (Ronquist and Huelsenbeck 2003). It was launched with random starting trees for 5 × 106 generations, and the Markov chains were sampled every 500 generations. To ensure that the Markov chain did not become trapped in local optima, we used the Metropolis-coupled Markov chain Monte Carlo (MCMCMC) algorithm, performing the estimation with four incrementally heated Markov chains. In each of these analyses, the first 461,000 generations were discarded as burn-in. The remaining trees were summarized in a 50% majority-rule consensus tree, yielding the probabilities of each clade being monophyletic.

Single nucleotide polymorphism analysis

Polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP) experiments for TEF_C447A, FUM1_G423A, FUM78_C41T, FUM8_G2834A, FUM18_G51T, and RPB2_C3250T were performed using the following primers/restriction enzymes: HS434/HS435/NspI, HS482/HS483/NruI,

HS576/HS577/NruI, HS576/HS577/HincII, HS506/HS519/MseI, and HS833/HS834/BmrI, respectively, under the same conditions used for HIS PCR-RFLP (Suga et al 2014) except that the annealing temperature for HS576/HS577 was 58°C, 2% Metaphor agarose gel (Cambrex Bio Science) was used for HS434/HS435/NspI and HS482/HS483/NruI, and 2.5% agarose gel was used for HS833/HS834/BmrI. The derived cleaved amplified polymorphic sequence (dCAPS) primers (HS435, HS482, and HS834) for PCR-RFLP were designed using dCAPS Finder 2.0 (Table S1) (Neff et al 2002). The PCR-sequencing for CPR_C1152A and P4504_C842T were performed as PCR and sequencing in MATERIALS AND METHODS in the original paper.

A multiplex PCR was performed to prepare template DNA for allele-specific primer extension (ASPE) reactions. The PCR components for *TEF1α* and *FUM* amplification comprised 0.025 units of rTaq polymerase (TaKaRa Bio Inc.) in a 10 μL reaction mixture containing 1 × reaction buffer, 200 μM dNTPs, 1 μM of each HS438 and HS439 primer (Table S1) (Suga et al 2014), 0.5 μM of each HS576 and HS577 primer (Table S1), and 5 ng of genomic DNA. The PCR components for CPR and P450-4 amplification comprised 1 μM of each P138-5, HS556, HSP450-4-GD1, and P450-4-GD2 primer (Table S1) (Malonek et al 2005). The PCR was performed in an iCycler thermal cycler (Bio-Rad Laboratories) using the following cycling parameters: 94°C for

2 min, 35 cycles of 94°C for 1 min, 58°C for 1 min, and 72°C for 1 min. Each 2.5-μL PCR mixture comprising *TEF1α*/*FUM* and *CPR*/*P450-4*, 0.2 μL of ExoSAP-IT (GE Healthcare Life Sciences, Uppsala, Sweden), and 1.8 μL of water was kept at 37°C for 30 min, then at 80°C for 15 min. The ASPE reactions were performed according to the manufacturer’s instructions using Platinum Genotype Tsp DNA Polymerase (Invitrogen Life Technologies, Carlsbad, CA) and HS641, HS642, HS704, HS705, HS700, HS7001, HS557, HS558, HS559, and HS560 primers (Table S1) constituting a volume of 20 μL and with a 1-min extension step at 50°C. The biotin-labelled products were sorted by hybridization with polystyrene microspheres coated with the following anti-tag sequences: LUA-12, -65, -87, -97, -67, -76, -16, -28, -2, and -14. The hybridizations were performed in 45-μL volumes using 1 × Tm hybridization buffer (0.2 M NaCl, 0.1 M Tris, 0.08% Triton X-100) at pH 8.0 with 20 μL of the extension product. The samples were incubated for 90 s at 96°C, followed by 30 min at 37°C, and were then transferred to a 96-well filtration plate (MultiScreen HTS; Millipore Corp., Billerica, MA, USA). The liquid was removed using a vacuum manifold, and 100 μL of 1 × Tm hybridization buffer was added; this procedure was repeated twice, and the liquid was removed again by vacuum manifold. The microspheres were resuspended in 100 μL of 1 × Tm hybridization buffer containing 2 μg/mL streptavidin-R-

phycoerythrin (Invitrogen Life Technologies). The median fluorescence intensity (MFI) of 100 microspheres was measured with a Luminex 100 flow cytometer (Luminex Corporation, Austin, TX, USA) after incubation for 15 min at 37°C. SNP was determined from more than 100 MFI values after subtracting the background MFI value obtained using water instead of the extension product. SNP was determined based on ratios of more than twice the MFI value between the paired microspheres corresponding to SNPs: LUA-12/-65, -87/-97, -67/-76, -16/-28, and -2/-14. The SNPs of the *F. fujikuroi* strains used by Niehaus et al. (2017) were obtained from the BioProject at the NCBI, as described above.

Fumonisin analysis

A mycelial plug was transferred in sterile rice medium. Sterile rice medium was prepared as follows; 5 g of rice grain was soaked with 4 ml water in an Erlenmeyer flask for 3 hr and then autoclaved. After fungal growth for 10 days at 25℃, fumonisins were extracted with 25 mL methanol/water (3:1, v/v) by reciprocal shaking for 30 min. The extract filtered through paper was purified by a strong anion exchange column (Sep-Pak Accell Plus QMA Short Cartridge (360 mg), Waters, Milford, MA, USA). A Visiprep™ SPE Vacuum manifold (Supelco Inc., Bellefonte, PA, USA) was used for

the purification. Five mL of the extract was loaded onto the column that is previously washed by 5 mL of methanol and then 10 mL of methanol/water (3:1, v/v). Then 5 mL methanol/water (3:1, v/v) and 5 mL methanol were successively loaded on the column for washing. The fumonisins were eluted with final 5 mL of a solution methanol/acetic acid (99:1, v/v). The eluent 1.4 mL was transferred into a glass tube and the solvent was evaporated under a nitrogen gas stream at 50 °C. The residue was dissolved in 0.2 mL of acetonitrile/water (1:1, v/v) and subjected to ultra-performance liquid chromatography–tandem mass spectrometry (UPLC-MS/MS) analysis. It was performed using an ACQUITY UPLC^{TM} system coupled to a Xevo QTof mass spectrometer (Waters, Milford, MA, USA). An ACQUITY UPLC consisting of a binary pump, an auto-sampler, and a column heater was used. Chromatographic separation was performed at 40 °C on a AQUITY UPLC BEH C18 column, 100 x 2.1 mm i.d., 1.7 μm particle size (Waters). Eluents were composed of formic acid/water (1:999, v/v) (eluent A), and methanol/acetonitrile (1:1, v/v) (eluent B), respectively. Sample injection was conducted at a volume of 2 μL. Elution was conducted at the flow rate of 0.3 mL/min with a linear gradient. After starting with the initial portion of B at 60 %, it was hold for 0.5 min and then increased linearly to 100 % B within 4.5 min. Thereafter, the portion of B was decreased linearly to 60 % within 0.1 min, and hold for 1.9 min. It was kept at

60 % prior to the next sample injection. Ionization was conducted with an electro-spray ionization (ESI) probe in positive polarity. The operating parameters were optimized under the following conditions: capillary voltage, 1.0 kV (positive mode)); sample cone voltage, 50 V; extraction cone voltage 4 kV; ion source temperature, 120 °C; desolvation temperature, 400 °C; cone gas flow 50 L/h; desolvation gas flow, 1000 L/h (both gases were nitrogen); and argon gas was used for collision. Conditions of collision energies and multiple reaction monitoring (MRM) transitions were set for each FBs: 30 eV and precursor ion 722/ product ion 705 (*m/z*); FB_1, 30 eV and 706/689 (*m/z*); FB_2 and FB_3. Data acquisition was performed for 7 min after injection. Under the above conditions, fumonisins were detected at the retention time of 1.0 min (FB_1), 1.5 min (FB_3), and 1.9 min (FB_2), respectively. The fumonisins FB_1 (Enzo Life Sciences, Lausen, Switzerland), FB_2 (Enzo Life Sciences) and FB_3 (Iris Biotech, Marktredwitz, Germany) were used as standard. Working solutions containing FB_1, FB_2 and FB_3 at concentrations between 0.05-5.0 mg/L (FB_1/ FB_2: 0.1, 0.2, 0.5, 1.0, 2.0, 5.0 mg/L, FB_3: 0.05, 0.1, 0.2, 0.4, 0.6, 1.0 mg/L, respectively in 6 bottles) were prepared in acetonitrile/water (1:1, v/v), and used for calibration curve. The concentration (X) (FB_1, FB_2 and FB_3) and corresponding peak area ratio (Y) were plotted for the 6 bottles of the working solution. The limits of quantification (LOQs) for the fumonisin analysis was

the lowest concentration (FB_1/ FB_2: 0.1 mg/L, FB_3: 0.05 mg/L) on the calibration curves for FB_1, FB_2, and FB_3. The concentration of the analyte was calculated from the corresponding Y value with the linear regression line. In cases in which the concentration of the sample exceeded the range given by the calibration curve, the sample was diluted 10 times and re-analyzed.

Gibberellin analysis

A mycelial plug was transferred in 20 mL of 10% ICI medium (Geissman et al 1966) and grown for 7 days on a reciprocal shaker (123 rpm) at 25°C with 0.02% of the trace elements reported by Correl et al. (1987) instead of 0.2% of the original trace elements. After removing the mycelium using filter paper, the gibberellins in the culture filtrate were analysed by thin-layer chromatography (TLC) or by UPLC-MS/MS. The gibberellins GA_3 (Wako Pure Chemicals Ind., Ltd., Osaka, Japan), GA_1, GA_4, and GA_7 (Olchemim Ltd., Olomouc, Czech Republic) were dissolved in 10% ethanol and used as standard solutions, and GA_3 and $GA_{4/7}$ were analysed by TLC according to the method described by Linnemannstons et al. (1999). The culture filtrate (10 µL) was applied to a 60F254 TLC silica gel plate (Merck KG, Darmstadt, Germany) and separated using a mobile chloroform/ethyl acetate/acetic acid phase (90:60:5). After air drying, HCl was sprayed to the TLC plate and left for 30 min. The GAs were visualized in UV light (356

nm) after heating at 120°C for 10 min. GA_3, GA_4, and the GA_7 mixture (5 μL, 100 mg/L each) were used as standards.

The concentrations of the gibberellins (GA_1, GA_3, GA_4, and GA_7) were quantified by UPLC-MS/MS analysis with the same equipment as fumonisin analysis. The experimental cultures were repeated in triplicate, and the resulting broths were subjected to UPLC-MS/MS analysis. Chromatographic separation was performed at 40°C on a AQUITY UPLC BEH C18 column (Waters). The eluents comprised water containing 5 mM ammonium acetate (eluent A) and methanol containing 5 mM ammonium acetate (eluent B). Both solvents (water and methanol) were LC/MS or high-performance liquid chromatography (HPLC) grade. The injection samples were 5 μL in volume, and the elution was conducted at a flow rate of 0.3 mL/min with a linear gradient of methanol. Starting with 10% eluent B, the proportion of B was increased linearly to 65% within 11.5 min, further increased to 95% within 1.5 min, and held for 1.5 min at 95%. Thereafter, the proportion of B was decreased to 10% within 0.1 min, and kept at 10% prior to the next sample injection. Ionization was conducted with an electro-spray ionization (ESI) probe with negative polarity. The optimum operating parameters were: capillary voltage, 0.5 kV (negative mode); sample cone voltage, 40 V; extraction cone voltage, 4 kV; ion source temperature, 120°C; desolvation temperature, 400°C; cone gas

flow, 50 L/h; desolvation gas flow, 1000 L/h (both gases were nitrogen); and argon gas was used for collision. The collision energies and multiple reaction monitoring (MRM) transitions were set for each GA: GA_1, 25 eV and precursor ion 347/product ion 229 (m/z); GA_3, 30 eV and 345/227 (m/z); GA_4, 15 eV and 331/257 (m/z); and GA_7, 30 eV and 329/211 (m/z). The data were acquired for 17 min after injection. Under the conditions described above, the gibberellins were detected at the retention times of 4.6 min (GA_1/GA_3), 9.0 min (GA_7), and 9.3 min (GA_4). Working solutions containing GA_1, GA_3, GA_4, and GA_7 at concentrations of 0.5–5.0 mg/L (GA_3/GA_7: 0.5, 1.0, 2.0, 5.0 mg/L; GA_1/GA_4: 0.5, 1.0, 1.5, 2.0 mg/L, in four bottles) were prepared in ethanol/water (1/9, v/v), and used to create a calibration curve. The concentration (X) (GA_1, GA_3, GA_4, and GA_7) and corresponding peak area ratio (Y) were plotted for the four bottles of the working solution. The limit of quantification (LOQ) for the gibberellin analysis was the lowest concentration (0.5 mg/L) on the calibration curves for GA_1, GA_3, GA_4, and GA_7. The concentration of the analyte was calculated from the corresponding Y value from the linear regression line. In cases in which the concentration of the sample exceeded the range given by the calibration curve, the sample was diluted 4 and 10 times and re-analyzed..

Table S1 Polymerase chain reaction (PCR) primer list

Primer sequence (5'- -3')				Objective	Reference
Forward		Reverse			
P138-5	AACCCCTACATTGCCCCTATC	P138-6	TCGGCAACCAAAGAACAAGAGTG	PCR and sequence of *CPR*	Malonek et al 2005
HS438	GTGTCAAACTAAACATTCGACAATAGGAAG	HS439[a]	ATGATATGTTAGTATGAATAAGTAGAAT	PCR and sequence of *TEF* and PCR for ASPE of TEF_T618G	Suga et al 2014
EF-11	GTGGGGCATTTACCCCGCC			Sequence of *TEF*	O'Donnell et al 1998
EF-21	GAGTGGCGGGGTAAATGCC			Sequence of *TEF*	O'Donnell et al 1998
HS398	TTGGAAGTGGCCTACGAGTGT	HS399	GAAGATGGCATTGATTGCCT	PCR and sequence of *FUM1*	
HS482[a]	TATGCAATCTTCGGGCCAAACCGATTCGCG	HS483	ATGGCAAAGTCATGCCCACCGGAGACGC	PCR-RFLP (*Nru* I) of FUM1_G423A	
HS576	TTCCATCAGATAGCTGATAA	HS577	GACAGCAGGGGTCTTGGAAA	PCR for Luminex ASPE of FUM78_C41T and FUM8_G2834A	
P138-5	see above	HS556	GGTTCATCTCAGCCTTGATA	PCR for Luminex ASPE of CPR_C1152A	
P450-4-GD1	TTTCTCGGTCCAGAGCACTGCCGC	P450-4-GD2	CGTGGTCTTCCTTTCCCATCTGGC	PCR and sequence of *P450-4* , PCR for Luminex ASPE of P4504_C842T	Malonek et al 2005
HS641	TACACTTTCTTTCTTTCTTTCTTTGTATGAATAAGTAGAATTAC			Luminex ASPE of TEF_T618G, signal detection with LUA-12 (FlexMAPxtag)	
HS642	CTTTTCATCAATAATCTTACCTTTGTATGAATAAGTAGAATTAA			Luminex ASPE of TEF_T618G, LUA-65	
HS704	AAACTAACATCAATACTTACATCATATAACTATATCTTARCATCG			Luminex ASPE of FUM78_C41T, LUA-87	
HS705	AATCTCATAATCTACATACACTATTATAACTATATCTTARCATCA			Luminex ASPE of FUM78_C41T, LUA-97	
HS700	TCATTTACTCAACAATTACAAATCACAATCAGGATGTCCCTCGC			Luminex ASPE of FUM8_G2834A, LUA-67	
HS701	AATCTAACAAACTCATCTAAATACACAATCAGGATGTCCCTCGT			Luminex ASPE of FUM8_G2834A, LUA-76	
HS557	AATCAATCTTCATTCAAATCATCATCATCGTTGGGAGCAAATGCG			Luminex ASPE of CPR_C1152A, LUA-16	
HS558	CTACAAACAAACAAACATTATCAATCATCGTTGGGAGCAAATGCT			Luminex ASPE of CPR_C1152A, LUA-28	
HS559	CTTTATCAATACATACTACAATCATCCGCGTTGTCCCCCATATC			Luminex ASPE of P4504_C842T, LUA-2	
HS560	CTACTATACATCTTACTATACTTTTCCGCGTTGTCCCCCATATT			Luminex ASPE of P4504_C842T, LUA-14	
7cf	ATGGGYAARCAAGCYATGGG	11ar	GCRTGGATCTTRTCRTCSACC	PCR and sequence of *RPB2*	O'Donnell et al 2010
HS833	GTACGAACCACCAAGATTCCTCAA	HS834[a]	TGCTAAGAAGACACTCAATCAACTG	PCR-RFLP(*Bmr* I) of RPB2_C3250T	
HS576	see above	HS577	see above	PCR and sequence of *FUM8* including *FUM8*/*FUM7* intergenic region, PCR-RFLP (*Hinc* II) of FUM8_G2834A or (*Nru* I) for FUM78_C41T	
HS434	GAGAAGGTTAGTCACTTTCCCTTCGATC	HS435[a]	CCGAGCTCAGCGGCTTCCTATTGTCGCAT	PCR-RFLP (*Nsp* I) of TEF_C447A	
HS506	ATGCGGCCGCGGRCCGAAAGAAGCATCCGA	HS519	AGCCAAAGAAACTTGGCAGT	PCR and sequence of *FUM18* including *FUM18*/*FUM19* intergenic region, PCR-RFLP (*Mse* I) of FUM18_G51T	

[a]Primers were designed with dCAPS (derived cleaved amplified polymorphic sequence) Finder 2.0 (Neff et al 2002)

Table S2 GenBank accession numbers of translation elongation factor 1α (*TEF1α*) and RNA polymerase II second largest-subunit (*RPB2*) used in the present study

Species	Strain	GenBank accession No. for gene		Reference
		TEF [a]	*RPB2* [b]	
F. verticillioides (MP-A)	NRRL22172	AF160262	EF470122	
F. sacchari (MP-B)	NRRL13999	AF160278	JX171580	
F. proliferatum (MP-D)	NRRL22944	AF160280	HM068352	
	MAFF236459	AB725609	LC133068 (obtained in this study)	
F. subglutinans (MP-E)	NRRL22016	AF160289	JX171599	
F. thapsinum (MP-F)	NRRL22045	AF160270	JX171600	
F. nygamai (MP-G)	NRRL13448	AF160273	EF470114	
F. circinatum (MP-H)	NRRL25331	AF160295	JX171623	
F. concentricum	NRRL25181	AF160282	LC133069 (obtained in this study)	
F. fractiflexum	NRRL28852	AF160288	LC133070 (obtained in this study)	
F. globosum	NRRL26131	AF160285	KF466406	
F. mangiferae	NRRL25226	AF160281	JX171622	
F. hostae	NRRL29889	AY329034	JX171640	used as outgroup of phylogenetic analysis of *F.fujikuroi* species complex based on *TEF* and *RPB2* sequence

[a] *TEF* is *translation elongation factor 1α*.

[b] *RPB2* is *RNA polymerase II second largest-subunit.*

Table S3 Results of amplified fragment length polymorphism (AFLP) marker assays

AFLP Marker — EACMCAB

Fumonisin production	Strain	AFLP haplotype	52	58	90	92	100	105	107	109	127	145	152	159	167	180	184	208	213	218	256
Non-producer	MAFF235949	1	0	1	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0801001	2	0	1	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0801002	3	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	0	1	1	1
	Gfc0801003	4	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	MYG92-10	5	0	0	0	1	0	0	1	1	1	1	1	0	1	0	0	1	1	1	1
	SMN86-2	6	0	0	0	1	0	0	0	1	1	1	1	0	1	0	0	1	1	1	1
	MIE92-4	7	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc9424702	8	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc9424703	9	0	0	0	1	0	1	0	1	0	1	1	0	1	0	0	1	1	1	1
	Gfc9424707	10	0	0	0	1	0	1	0	1	0	1	1	0	1	0	0	1	1	1	1
	Gfc0625001	11	0	1	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0625002	12	1	0	1	1	0	1	0	1	1	1	1	0	0	0	0	1	1	1	1
	Gfc0625004	12	1	0	1	1	0	1	0	1	1	1	1	0	0	0	0	1	1	1	1
	Gfc0625005	12	1	0	1	1	0	1	0	1	1	1	1	0	0	0	0	1	1	1	1
	Gfc0625006	12	1	0	1	1	0	1	0	1	1	1	1	0	0	0	0	1	1	1	1
	Gfc0625007	12	1	0	1	1	0	1	0	1	1	1	1	0	0	0	0	1	1	1	1
	Gfc0625008	13	0	1	0	1	0	1	0	1	1	1	0	0	1	0	0	1	1	1	1
	Gfc0625010	14	1	0	1	1	0	1	1	1	1	0	0	0	1	0	1	1	1	1	1
	Gfc0925005	15	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	0
	Gfc0925010	16	0	0	0	1	0	0	1	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0925011	17	0	0	0	1	0	0	0	1	0	1	1	0	1	0	0	1	1	1	0
	Gfc0925012	18	0	0	0	1	0	0	0	1	0	1	1	0	1	0	0	1	1	0	0
	APF06083	19	0	1	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc8707123	20	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc8707182	20	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc8707117	21	0	0	1	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	0
	Gfc8707249	22	0	0	0	1	0	0	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc8707642	23	0	0	0	1	0	0	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0825001	24	1	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0825002	24	1	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0825003	24	1	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0825004	24	1	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0825005	24	1	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0825006	24	1	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0901002	25	0	0	0	1	0	0	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0901005	25	0	0	0	1	0	0	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc0901009	26	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	0	1
	Gfc1004001	27	0	0	0	0	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc1004002	28	0	0	1	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	Gfc1034001	29	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	GL24	19	0	1	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	GL25	30	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	GL27	31	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
	GL28	32	0	0	0	1	0	1	0	1	1	1	1	0	1	0	0	1	1	1	1
Producer	MAFF235463	33	0	0	1	0	0	1	1	1	0	1	0	0	1	1	0	1	0	0	0
	Gfc1004003	34	1	0	1	1	1	1	1	1	1	1	0	0	1	0	1	1	1	1	1
	Gfc1006001	35	1	1	1	1	0	1	1	1	1	1	0	0	0	0	1	1	1	1	1
	Gfc1006002	36	1	1	1	1	1	1	0	1	1	0	0	0	1	0	1	1	1	1	0
	Gfc1006007	37	1	1	1	1	1	1	0	0	0	1	0	0	1	0	0	1	1	1	1
	Gfc1019001	38	0	1	1	0	0	1	0	1	0	0	0	0	1	0	0	1	1	1	1
	Gfc1019003	39	1	1	1	1	0	1	0	1	1	0	0	0	1	0	0	1	1	1	0
	Gfc1019004	40	1	1	1	0	0	1	1	1	0	1	0	0	0	0	0	1	1	1	1
	Gfc1016022	41	0	0	1	1	1	1	0	1	1	0	0	0	1	0	0	1	1	1	1
	Gfc1016024	42	0	0	1	1	1	1	0	1	0	0	0	0	1	0	0	1	1	1	1
	Gfc1016025	43	0	0	1	1	1	1	0	1	0	1	0	0	1	0	0	1	1	1	1
	Gfc1016026	43	0	0	1	1	1	1	0	1	0	1	0	0	1	0	0	1	1	1	1
	Gfc0821004	44	1	1	1	1	0	1	0	0	1	1	0	0	1	0	0	1	1	1	1
	Gfc0921001	45	1	0	1	1	1	1	0	1	0	1	0	0	0	0	1	1	1	1	1
	Gfc0921002	46	1	0	1	1	0	1	0	1	0	0	0	0	1	0	1	1	1	0	0
	Gfc0921009	47	1	0	1	1	0	1	0	1	0	0	0	0	1	0	0	1	1	1	1
	Gfc0921014	48	0	0	1	1	0	1	0	1	0	0	0	0	0	1	1	1	1	1	0
	Gfc0921034	49	0	1	1	1	0	1	0	1	0	0	0	0	1	0	0	1	1	1	1
	Gfc0921039	50	1	0	1	1	0	1	0	1	0	1	0	0	0	0	0	1	1	1	0
	Gfc0921040	51	0	1	1	1	0	1	0	1	0	0	0	0	1	0	0	1	1	1	0
	Gfc0921041	52	0	0	1	1	0	1	0	1	1	0	0	0	1	0	0	1	1	1	1
	Gfc1025029	53	1	1	1	1	0	1	0	1	1	1	0	0	1	0	0	1	1	1	1
	Gfc1025037	53	1	1	1	1	0	1	0	1	1	1	0	0	1	0	0	1	1	1	1
	Gfc1025091	54	0	0	1	0	0	1	0	1	1	0	0	0	1	0	0	1	1	1	1
	Gfc1034002	55	0	0	1	1	0	1	0	1	1	1	0	1	1	0	0	0	1	1	1
	Gfc1041003	56	1	1	1	1	0	1	0	1	0	1	0	0	1	0	0	1	1	1	1
	Gfc1041010	57	1	1	1	1	0	1	0	1	0	1	0	0	1	0	0	1	1	1	1
	Gfc1041011	56	1	1	1	1	0	1	0	1	0	1	0	0	1	0	0	1	1	1	1
	Gfc1043032	58	1	0	1	1	0	1	0	1	0	1	0	0	0	0	0	1	1	1	1
	Gfc1043035	59	1	0	1	1	0	1	0	1	0	1	0	0	0	0	1	1	1	1	1
	Gfc1043037	60	1	0	1	1	0	1	0	1	1	0	0	0	0	0	0	1	1	1	1
	Gfc1043045	60	1	0	1	1	0	1	0	1	1	0	0	0	0	0	0	1	1	1	1
	Gfc1043046	58	1	0	1	1	0	1	0	1	0	1	0	0	0	0	0	1	1	1	1
	Gfc1043047	58	1	0	1	1	0	1	0	1	0	1	0	0	0	0	0	1	1	1	1
	Mo78	61	1	0	1	0	0	1	0	1	0	1	0	0	1	0	1	1	1	1	1
	Mo80	62	1	1	1	1	1	1	0	1	0	1	0	0	1	0	0	1	1	0	0
	Mo141	63	0	0	1	1	0	1	0	1	1	1	0	0	1	0	0	1	1	1	1
	Mo136	64	1	0	1	0	0	1	1	1	1	1	0	0	0	1	0	1	1	1	1
	Mo309	65	1	0	1	1	0	1	0	1	1	0	0	0	1	0	1	1	1	1	1
	IBR89-1	66	0	0	1	0	0	1	0	1	0	1	0	0	1	0	0	1	1	1	1
	Gfc0825007	67	0	0	1	1	0	1	0	1	0	1	1	0	0	0	1	1	0	0	0
	Gfc0825009	68	1	1	1	1	0	1	0	1	0	1	0	0	1	0	0	1	1	1	1
	Gfc0825011	69	0	0	1	1	0	1	0	1	1	0	0	0	1	0	0	1	1	1	1
	Gfc0009063	70	1	0	0	1	1	1	0	1	0	1	0	0	1	0	1	0	1	0	0
	Gfc0009105	71	0	0	1	1	0	1	0	1	1	0	0	0	1	0	0	1	1	0	1
	Gfc0009110	72	0	0	1	1	0	1	0	1	1	0	0	0	1	0	0	0	0	1	1
	Gfc0009117	73	1	0	1	1	0	1	1	1	0	0	0	0	0	0	1	1	0	0	0
	41-79	74	0	1	1	1	0	1	0	1	1	0	0	0	1	0	0	1	1	1	1
	41-84	75	0	0	1	1	0	1	0	1	1	1	0	1	1	0	0	1	1	1	0
	41-116	76	1	0	1	1	0	1	0	1	0	1	0	0	1	0	0	1	1	1	1
	41-108	77	1	1	1	1	0	1	1	1	0	1	0	0	1	0	0	1	1	1	1

AFLP Marker — EATMCAY

Strain	58	61	63	65	66	96	104	107	120	126	150	174	190	209	212	261	264	283	315	319	328	352
MAFF235949	0	1	1	1	1	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	1	1
Gfc0801001	0	1	1	1	1	0	1	0	1	1	0	0	1	1	1	1	0	0	0	0	1	1
Gfc0801002	0	0	1	1	1	0	1	0	1	1	0	0	1	1	1	1	0	0	0	0	1	1
Gfc0801003	0	1	1	1	1	0	1	0	1	1	0	0	1	1	1	1	0	0	0	0	1	1
MYG92-10	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
SMN86-2	0	1	0	1	1	0	1	0	1	1	0	0	0	1	1	0	0	0	0	0	1	1
MIE92-4	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc9424702	0	1	1	1	1	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc9424703	0	1	1	1	1	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc9424707	0	1	0	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0625001	0	1	1	1	1	0	1	0	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc0625002	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0625004	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0625005	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0625006	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0625007	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0625008	0	1	1	1	1	0	1	0	0	1	0	0	0	1	1	0	0	0	0	0	1	1
Gfc0625010	0	1	1	1	1	0	1	0	1	1	0	0	0	0	1	0	0	0	0	0	1	1
Gfc0925005	0	1	0	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0925010	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0925011	0	1	1	1	1	0	1	0	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc0925012	0	1	1	1	1	0	1	0	0	1	0	0	1	0	1	0	0	0	0	0	1	1
APF06083	0	1	1	1	1	0	1	0	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc8707123	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc8707182	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc8707117	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc8707249	0	1	1	1	1	0	1	0	1	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc8707642	0	1	1	1	1	0	1	0	1	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0825001	0	1	1	1	1	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0825002	0	1	1	1	1	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0825003	0	1	1	1	1	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0825004	0	1	1	1	1	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0825005	0	1	1	1	1	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0825006	0	1	1	1	1	0	0	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0901002	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0901005	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc0901009	0	1	1	1	1	0	1	0	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc1004001	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc1004002	0	1	1	1	1	0	1	0	1	1	0	0	1	1	1	0	0	0	0	0	1	1
Gfc1034001	0	1	1	1	1	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	1	1
GL24	0	1	1	1	1	0	1	0	0	1	0	0	1	0	1	0	0	0	0	0	1	1
GL25	0	0	1	0	1	1	1	0	0	1	0	0	1	0	1	0	0	0	0	0	1	1
GL27	0	0	1	0	1	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0	1	1
GL28	0	1	1	0	1	0	1	0	0	1	0	0	1	1	1	0	0	0	0	0	1	1
MAFF235463	0	1	1	0	1	0	1	1	0	1	1	0	1	0	1	0	0	0	0	0	1	1
Gfc1004003	0	1	1	1	1	0	1	1	0	1	0	1	0	0	1	0	0	0	0	0	1	0
Gfc1006001	0	1	0	1	1	0	0	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
Gfc1006002	0	0	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	1	1
Gfc1006007	0	1	0	1	1	1	0	1	0	1	1	0	1	0	1	0	0	0	0	0	1	1
Gfc1019001	0	1	1	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
Gfc1019003	0	1	1	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
Gfc1019004	0	0	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	1	1
Gfc1016022	0	0	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	1	1	0
Gfc1016024	0	0	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	1	1	0
Gfc1016025	0	0	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	1	1	0
Gfc1016026	0	0	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	1	1	0
Gfc0821004	1	0	1	1	1	0	1	1	0	1	0	0	1	0	1	0	0	0	0	0	1	0
Gfc0921001	1	1	1	1	1	0	0	1	0	1	1	0	0	0	1	0	0	0	1	0	1	1
Gfc0921002	1	0	1	1	1	0	1	1	0	1	0	0	1	0	1	0	1	0	1	0	1	1
Gfc0921009	1	0	1	1	1	0	1	1	0	1	0	0	1	0	1	0	1	0	1	0	1	1
Gfc0921014	1	1	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	1	1	1
Gfc0921034	0	0	1	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
Gfc0921039	0	1	1	1	1	0	1	1	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc0921040	0	0	1	1	1	0	1	1	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc0921041	0	1	0	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
Gfc1025029	0	1	1	1	1	0	0	1	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc1025037	0	1	1	1	1	0	0	1	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc1025091	0	1	1	1	1	0	0	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
Gfc1034002	1	1	1	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
Gfc1041003	0	1	1	1	1	0	1	1	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc1041010	0	1	1	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
Gfc1041011	0	1	1	1	1	0	1	1	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc1043032	1	1	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	1	1
Gfc1043035	0	1	1	1	1	1	1	1	0	1	0	1	1	0	1	0	1	0	0	0	1	1
Gfc1043037	1	1	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	1	1
Gfc1043045	1	1	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	1	1
Gfc1043046	1	1	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	1	1
Gfc1043047	1	1	1	1	1	0	1	1	0	1	1	0	0	0	1	0	0	0	0	0	1	1
Mo78	1	1	1	1	1	0	1	1	0	0	0	0	0	0	1	0	0	0	0	0	1	1
Mo80	1	0	1	1	1	0	0	1	0	1	1	0	1	0	1	0	0	0	0	0	1	0
Mo141	0	1	1	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
Mo136	0	1	0	1	1	0	1	1	0	1	1	1	1	0	1	0	0	0	0	0	1	1
Mo309	0	1	1	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
IBR89-1	0	1	0	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
Gfc0825007	1	1	1	1	1	0	1	1	0	1	0	1	1	0	1	0	1	0	0	0	1	1
Gfc0825009	1	1	1	1	1	0	1	1	0	1	0	0	1	0	1	0	0	0	0	0	1	0
Gfc0825011	0	0	1	1	1	0	1	1	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc0009063	0	0	1	1	1	1	1	1	0	1	0	0	1	0	1	0	0	0	1	0	1	1
Gfc0009105	0	1	1	1	1	1	1	1	0	1	0	0	1	0	1	0	0	0	0	0	1	1
Gfc0009110	0	1	0	1	1	0	1	1	0	1	0	0	1	0	1	0	1	0	1	0	1	1
Gfc0009117	0	1	1	1	1	0	1	1	0	1	0	0	1	0	1	0	0	0	0	0	1	1
41-79	0	1	1	1	1	0	0	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
41-84	0	0	1	0	1	0	0	1	0	1	0	0	0	0	1	0	0	0	0	0	1	0
41-116	0	1	0	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1
41-108	0	1	0	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	1	1

AFLP Marker — EAGMCAG

Strain	92	98	101	117	121	170	194	198	213	236	239	243	250	279	281	297	308	333	358	379	381	407	410	415	418
MAFF235949	1	1	0	0	1	1	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0801001	1	1	0	0	1	1	1	1	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0801002	1	1	0	1	1	0	1	1	0	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0801003	1	1	0	0	1	1	0	1	1	0	1	1	0	0	1	0	0	1	1	1	0	0	1	0	0
MYG92-10	1	1	0	0	1	1	1	0	1	1	0	1	1	0	1	0	0	1	1	1	1	0	1	0	0
SMN86-2	1	1	0	0	1	0	1	1	1	0	0	1	1	0	1	0	0	1	1	1	1	0	1	0	0
MIE92-4	1	1	0	0	1	0	1	0	1	0	1	1	1	0	1	0	0	1	1	1	1	0	0	0	0
Gfc9424702	1	1	0	1	1	1	1	0	1	1	1	1	1	0	1	0	0	1	1	1	1	0	1	0	0
Gfc9424703	1	1	0	1	1	1	1	0	1	1	1	1	1	0	1	0	0	1	1	1	1	0	1	0	0
Gfc9424707	1	1	0	1	1	0	1	0	1	0	1	1	1	0	1	0	0	0	1	1	1	0	0	0	0
Gfc0625001	1	1	0	0	1	0	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0625002	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	0	1	1	1	0	0	1	0	0
Gfc0625004	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	0	1	1	1	0	0	1	0	0
Gfc0625005	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	0	1	1	1	0	0	1	0	0
Gfc0625006	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	0	1	1	1	0	0	1	0	0
Gfc0625007	0	1	0	1	1	0	1	0	1	0	1	0	1	0	1	0	0	1	1	1	0	0	1	0	0
Gfc0625008	1	1	0	0	1	1	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0625010	1	1	0	0	1	1	1	1	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0925005	1	1	0	0	1	0	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0925010	1	1	0	0	1	1	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0925011	1	1	0	0	1	0	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0925012	1	1	0	0	1	1	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
APF06083	1	1	0	0	1	1	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc8707123	1	1	0	0	1	1	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc8707182	1	1	0	0	1	1	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc8707117	1	1	0	0	1	1	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc8707249	1	1	0	0	1	0	1	1	1	1	0	1	0	0	1	0	0	1	1	1	1	0	1	1	0
Gfc8707642	1	1	0	1	1	0	1	0	1	0	0	1	1	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0825001	1	1	0	0	1	1	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0825002	1	1	0	0	1	1	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0825003	1	1	0	0	1	1	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0825004	1	1	0	0	1	1	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0825005	1	1	0	0	1	1	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0825006	1	1	0	0	1	1	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0901002	1	1	0	0	1	1	1	0	1	0	1	1	1	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0901005	1	1	0	0	1	1	1	0	1	0	1	1	1	0	1	0	0	1	1	1	1	0	1	0	0
Gfc0901009	1	1	0	0	1	0	1	0	1	1	0	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc1004001	1	1	0	1	1	1	1	0	1	0	0	1	0	0	1	0	0	1	1	1	1	0	1	0	0
Gfc1004002	1	1	0	0	1	0	1	1	1	1	1	1	1	0	1	0	0	1	1	1	1	0	1	0	0
Gfc1034001	1	1	0	0	1	1	1	0	1	0	1	1	1	0	1	0	0	1	1	1	1	0	1	0	0
GL24	1	1	0	0	1	1	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	1	0	0
GL25	1	1	0	0	1	1	1	0	1	0	1	1	0	0	1	0	0	1	1	1	0	0	1	0	0
GL27	1	1	0	0	1	1	1	0	1	0	1	1	1	0	1	0	0	1	1	1	0	0	0	0	0
GL28	1	1	0	0	1	1	1	0	1	0	1	1	1	0	1	0	0	1	1	1	1	0	1	0	0
MAFF235463	1	1	0	1	1	0	1	0	1	1	1	1	0	1	0	0	0	1	0	1	1	0	0	1	0
Gfc1004003	1	1	0	1	1	0	1	0	1	0	0	1	1	0	1	0	0	1	1	1	1	1	0	0	0
Gfc1006001	1	1	0	1	1	0	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Gfc1006002	1	1	1	1	1	0	1	0	1	0	1	1	0	1	1	0	0	1	1	1	1	1	0	1	0
Gfc1006007	1	1	1	1	1	0	1	0	1	0	1	1	0	1	0	0	0	1	1	1	1	1	0	1	0
Gfc1019001	1	1	0	1	1	0	1	0	1	0	1	1	0	1	0	0	0	1	1	1	1	1	0	1	0
Gfc1019003	1	1	0	1	1	0	1	0	1	0	1	1	0	1	0	0	0	1	1	1	0	1	0	1	0
Gfc1019004	1	1	1	0	1	0	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Gfc1016022	1	1	0	1	1	0	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Gfc1016024	1	1	0	1	1	0	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Gfc1016025	1	1	0	1	1	0	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Gfc1016026	1	1	0	1	1	0	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Gfc0821004	1	1	0	0	1	0	1	0	1	0	1	1	0	1	0	0	0	1	1	1	1	1	0	1	0
Gfc0921001	1	1	1	1	1	0	1	0	1	0	1	1	0	1	1	0	0	1	1	1	1	1	0	0	0
Gfc0921002	1	1	1	1	1	0	1	0	1	0	1	1	0	1	1	0	0	1	1	1	1	1	0	1	0
Gfc0921009	1	1	0	1	1	0	1	0	1	1	1	1	0	1	1	0	0	1	1	1	1	1	0	1	0
Gfc0921014	1	1	0	1	1	1	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Gfc0921034	1	1	0	1	1	0	1	0	1	0	1	1	1	1	1	0	0	1	1	1	1	1	0	1	0
Gfc0921039	1	1	0	1	1	0	1	0	1	0	1	1	1	1	1	0	0	1	1	1	1	1	0	1	0
Gfc0921040	1	1	0	1	1	0	0	0	1	0	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Gfc0921041	1	1	1	1	1	0	1	0	1	0	1	1	0	0	0	0	0	1	1	1	1	1	0	1	0
Gfc1025029	1	1	1	1	1	0	1	0	1	0	1	1	1	1	0	0	0	1	1	1	1	1	0	1	0
Gfc1025037	1	1	1	1	1	0	1	0	1	0	1	1	1	1	0	0	0	1	1	1	1	1	0	1	0
Gfc1025091	1	1	1	1	1	0	1	1	1	0	1	1	0	1	0	0	0	1	1	1	1	1	0	1	0
Gfc1034002	1	1	1	1	1	0	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Gfc1041003	1	1	0	1	1	0	1	0	1	1	1	1	0	1	0	1	0	1	1	1	1	1	0	1	0
Gfc1041010	1	1	0	1	1	0	1	0	1	1	1	1	0	1	0	1	0	1	1	1	1	1	0	1	0
Gfc1041011	1	1	0	1	1	0	1	0	1	1	1	1	0	1	0	1	0	1	1	1	1	1	0	1	0
Gfc1043032	1	1	1	1	1	0	1	0	1	0	1	1	0	1	0	0	0	1	1	1	1	1	0	1	0
Gfc1043035	1	1	1	0	1	0	1	0	1	0	1	1	0	1	0	1	0	1	1	1	1	1	0	0	0
Gfc1043037	1	1	1	1	1	0	1	0	1	0	1	1	0	1	0	0	0	1	1	1	1	1	0	1	0
Gfc1043045	1	1	1	1	1	0	1	0	1	0	1	1	0	1	0	0	0	1	1	1	1	1	0	1	0
Gfc1043046	1	1	1	1	1	0	1	0	1	0	1	1	0	1	0	0	0	1	1	1	1	1	0	1	0
Gfc1043047	1	1	1	1	1	0	1	0	1	0	1	1	0	1	0	0	0	1	1	1	1	1	0	1	0
Mo78	1	1	1	1	1	0	0	0	1	0	0	1	0	1	1	0	0	1	1	1	1	1	0	1	0
Mo80	1	1	0	1	1	0	0	0	1	0	1	1	0	0	1	0	0	1	1	1	1	1	0	0	0
Mo141	1	1	1	0	1	0	0	0	1	1	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Mo136	1	1	1	1	1	0	0	0	1	0	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Mo309	1	1	0	1	1	0	1	0	1	1	0	1	0	0	0	0	0	1	1	1	0	1	0	1	0
IBR89-1	1	0	1	1	1	0	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Gfc0825007	1	1	1	1	1	0	1	0	1	0	1	1	0	1	1	0	0	1	1	1	1	1	0	1	0
Gfc0825009	1	1	1	0	1	0	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	1	0	0	0
Gfc0825011	1	1	1	0	1	0	1	0	1	0	1	1	1	0	1	1	0	1	1	1	1	1	0	1	0
Gfc0009063	1	1	1	0	1	0	1	0	1	1	1	1	0	0	1	0	0	1	1	1	1	1	0	0	0
Gfc0009105	1	0	1	1	1	0	1	0	1	0	1	1	1	0	1	0	0	1	1	1	1	1	0	0	0
Gfc0009110	1	1	0	1	1	0	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	1	0	1	0
Gfc0009117	1	1	0	1	1	0	1	0	1	0	1	1	0	1	1	0	0	1	1	1	1	1	0	1	0
41-79	1	1	1	1	1	0	1	0	1	0	1	1	0	1	0	0	0	1	1	1	1	1	0	0	0
41-84	1	1	1	1	1	0	1	0	1	0	1	1	0	0	1	0	0	1	1	1	1	0	0	1	0
41-116	1	0	1	1	1	0	1	0	1	0	0	1	0	0	1	0	0	1	1	1	1	0	0	0	0
41-108	1	0	1	1	1	0	1	0	1	0	1	1	1	0	1	0	0	1	1	1	1	0	0	0	0

REFERENCES

Akaike H. 1974. A new look at the statistical model identification. IEEE Trans Autom Control **19:**716–723.

Correll JC, Klittich CJR, Leslie JF. 1987. Nitrate nonutilizing mutant of *Fusarium oxysporum* and their use in vegetative compatibility tests. Phytopathology **77:**1640-1646.

Felsenstein J. 1985. Confidence limits on phylogenies: an approach using the bootstrap. Evolution **39:**783–791.

Geissman TA, Verbiscar AJ, Phinney BO, Cragg G. 1966. Studies on the biosynthesis of gibberellins from (−)-kaurenoic acid in cultures of *Gibberella fujikuroi*. Phytochemistry **5:**933-947.

Jobb G, von Haeseler A, Strimmer K. 2004 TREEFINDER: a powerful graphical analysis environment for molecular phylogenetics. BMC Evol Biol **4:**18.

Katoh K, Asimenos G, Toh H. 2009. Multiple alignment of DNA sequences with MAFFT, p 39–64. *In* Posada D (ed), Bioinformatics for DNA sequence analysis. Methods in Molecular Biology **537**. Springer, Humana Press.

Katoh K, Kuma K, Toh H, Miyata T. 2005. MAFFT version 5: improvement in accuracy of multiple sequence alignment. Nucleic Acids Res **33:**511–518.

Katoh K, Misawa K, Kuma K, Miyata T. 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res **30:**3059–3066.

Kishino H, Hasegawa M. 1989 Evaluation of the maximum likelihood estimate of the evolutionary tree topologies from DNA sequence data, and the branching order in Hominoidea. J Mol Evol **29:**170–179.

Linnemannstöns P, Voß T, Hedden P, Gaskin P, Tudzynski B. 1999. Deletions in the gibberellin biosynthesis gene cluster of *Gibberella fujikuroi* by restriction enzyme-

mediated integration and conventional transformation-mediated mutagenesis. Appl Environ Microbiol **65:**2558–2564.

Malonek S, Bömke C, Bornberg-Bauer E, Rojas MC, Hedden P, Hopkins P, Tudzynski B. 2005. Distribution of gibberellin biosynthetic genes and gibberellin production in the *Gibberella fujikuroi* species complex. Phytochemistry **66:**1296-1311.

Neff MM, Turk E, Kalishman M. 2002. Web-based primer design for single nucleotide polymorphism analysis. Trends Genet **18:**613-615.

Niehaus E-M, Kim H-K, Munsterkotter M, Janevska S, Arndt B, Kalinina SA, Houterman PM, Ahn I-P, Alberti I, Tonti S, Kim D-W, Sieber CMK, Humpf H-U, Yun S-H, Guldener U, Tudzynski B. 2017. Comparative genomics of geographically distant Fusarium fujikuroi isolates revealed two distinct pathotypes correlating with secondary metabolite profiles. PLoS Pathog **13:**e1006670.

O'Donnell K, Cigelnik E, Nirenberg HI. 1998. Molecular systematics and phylogeography of the *Gibberella fujikuroi* species complex. Mycologia **90:**465-493.

O'Donnell K, Sutton DA, Rinaldi MG, Sarver BAJ, Balajee SA, Schroers H-J, Summerbell RC, Robert VARG, Crous PW, Zhang N, Aoki T, Jung K, Park J, Lee Y-H, Kang S, Park B, Geiser DM. 2010. Internet-accessible DNA sequence database for identifying fusaria from human and animal infections. J Clin Microbiol **48:**3708-3718.

Ronquist F, Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics **19:**1572–1574.

Saitou N, Nei M. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol **4:**406–425.

Schwarz G. 1978. Estimating the dimension of a model. Ann Stat **6:**461–464.

Suga H, Kitajima M, Nagumo R, Tsukiboshi T, Uegaki R, Nakajima T, Kushiro M, Nakagawa H, Shimizu M, Kageyama K, Hyakumachi M. 2014. A single nucleotide polymorphism in the translation elongation factor 1alpha gene correlates

with the ability to produce fumonisin in Japanese *Fusarium fujikuroi*. Fungal Biol **118:**402-412.

Sugiura N. 1978. Further analysis of the data by Akaike's information criterion and the finite corrections. Comm Stat Theory Methods **7:**13–26.

Swofford DL. 2002 PAUP*: phylogenetic analysis using parsimony and other methods, 4.0β10. Sinauer, Sunderland

Tanabe AS. 2007. Kakusan: a computer program to automate the selection of a nucleotide substitution model and the configuration of a mixed model on multilocus data. Mol Ecol Notes **7:**962–964.

Vos RA. 2003 Accelerated likelihood surface exploration: the likelihood ratchet. Syst Biol **52:**368–373.