

## SUPPLEMENTARY TABLES

### LIST OF TABLES

1	List of universal and diagnostic primer . . . . .	1
3	Genbank sequence accessions (cytoplasmic) . . . . .	1
4	Genbank sequence accessions (nuclear) . . . . .	2
2	List of secondary specimens (lemongrass and carnation) . . . . .	5
5	Anatomical diagnostic key . . . . .	6
6	BLOG bamboo tribe classification results . . . . .	7

**Table 1.** List of universal and diagnostic (ARMS) primer used in the current study. The table includes primer names and sequences, melting temperatures (Tm) of each individual primer, the annealing temperatures (An) for each primer pair and references to corresponding publications.

Name	Sequence (5'...3')	Tm (°C)	An (°C)	Design
rbcLa_f <sup>u</sup>	ATGTCACCACAAACAGAGACTAAAGC	62.2	58	Kondo et al. [1996]
rbcLa_rev <sup>u</sup>	GTAAAATCAAGTCCACCRCG	74.7		Fofana et al. [1997]
rbcLb-Sf <sup>u</sup>	AGACCTTTTGAGAAGGTTCTGT	62.2	55	Dong et al. [2014]
rbcLb-Sr <sup>u</sup>	TCGGTCAGAGCAGGCATATGCCA	74.7		
1R_KIM_r <sup>u</sup>	ACCCAGTCCATCTGGAAATCTTGGTTC	72.1	52	Ki-Joong Kim <sup>p</sup>
3F_KIM_f <sup>u</sup>	CGTACAGTACTTTGTGTTACGAG	60.6		
ITS5 <sup>u</sup>	GGAAGTAAAAGTCGTAAACAAGG	58.4	56	White et al. [1990]
ITS4 <sup>u</sup>	TCCTCCGCTTATTGATATGC	61.5		
Bbo-C-407-r <sup>d</sup>	AGGBGGRCCTS <u>GRAAGTTT</u> CGA	58.7		current study
Dian-T-223-r <sup>d</sup>	CGGGCTCGATGTGGTAGTAA	64.9		
Cym-A-254-r <sup>d</sup>	AGCTACATAACAGATATATTGAT <u>CAGG</u>	59.5		

<sup>d</sup> diagnostic primer (ARMS), destabilizing nucleotide underlined

<sup>u</sup> universal primer

<sup>p</sup> unpublished

**Table 3.** GenBank sequence accessions of two plastid DNA regions (rbcL and matK) used in the current study.

Taxon	rbcL	matK
<b>Arundinarieae</b>		
<i>Arundinaria gigantea</i> subsp. <i>tecta</i>	AJ746179	EF125165
<i>Borinda emeryi</i>	EF125079	EF125167
<i>Chimonobambusa marmorea</i>	AJ746176	EF125168
<i>Drepanostachyum falcatum</i>	AJ746265	EF125170
<i>Fargesia dracocephala</i>	AJ746266	KP685610
<i>Fargesia</i> sp. <i>Asmussen</i>	AM110249	AM114722
<i>Indocalamus latifolius</i>	AJ746177	EF125173
<i>Phyllostachys aurea</i>	HE573324	AF164390
<i>Phyllostachys bambusoides</i>	AB088833	AB088805
<i>Phyllostachys nigra</i>	HE573325	EU434241
<i>Pleioblastus maculatus</i>	JN247242	JN247148
<i>Pseudosasa amabilis</i>	AJ746273	KP093752
<i>Pseudosasa japonica</i>	FN870405	HG794001
<i>Thamnochalamus spathiflorus</i>	EF125087	KP685639
<b>Bambuseae</b>		
<i>Bambusa multiplex</i>	M91626	EF125166

**Table 3.** GenBank sequence accessions of two plastid DNA regions (rbcL and matK) used in the current study. (continued)

Taxon	rbcL	matK
<i>Bambusa valida</i>	AJ746171	EU434255
<i>Bambusa vulgaris</i>	HE573326	JX428392
<i>Chusquea culeou</i>	HE575810	HE575860
<i>Greslania multiflora</i>	HE575811	HE575861
<i>Melocanna baccifera</i>	EF125082	EF125174
<i>Olmeca recta</i>	AJ746269	HQ847275
<i>Otatea acuminata</i>	AJ746271	HQ847256
<i>Thyrsostachys siamensis</i>	EF125088	EU434261
<b><i>Olyreae</i></b>		
<i>Cryptochloa strictiflora</i>	JN205319	EU434281
<i>Olyra latifolia</i>	EF125090	AF164386
<i>Pariana radiciflora</i>	AY632369	AF164387
<b><i>Oryzoideae</i></b>		
<i>Oryza sativa Japonica Group</i>	KF731173	KF731059
<i>Porteresia coarctata</i>	HE577876	AF148669
<b><i>Panicoideae</i></b>		
<i>Cymbopogon citratus</i>	EF125117	GQ434093
<i>Cymbopogon goeringii</i>	KC164298	KF163712
<i>Lophatherum gracile</i>	HM167472	JN407183
<b><i>Pooideae</i></b>		
<i>Triticum aestivum</i>	AY328025	AF164405
<i>Triticum dicoccum</i>	LN626623	HQ894423
<i>Triticum monococcum</i>	AY836162	HM540031
<b><i>Caryophyllaceae</i></b>		
<i>Silene baccifera</i>	KM360741	JF956236
<i>Silene conica</i>	EF418564	FJ589520
<i>Silene gallica</i>	HM850354	FJ589528
<i>Silene otites</i>	KC171366	FJ589547
<i>Silene pendula</i>	EF418561	FJ589550
<i>Silene schafta</i>	EF418563	FJ589556
<i>Silene vulgaris</i>	KT178142	EU749399

**Table 4.** GenBank sequence accessions of one nuclear DNA region (ITS) used in the current study.

Taxon	ITS
<b><i>Caryophyllaceae</i></b>	
<i>Dianthus albens</i>	GU440775
<i>Dianthus algetanus</i>	GU440776
<i>Dianthus anatolicus</i>	GU440777
<i>Dianthus andrzejowskianus</i>	JN589032
<i>Dianthus anticarius</i>	GU440778
<i>Dianthus armeria</i>	GU440780
<i>Dianthus barbatus</i>	GU440783
<i>Dianthus benearnensis</i>	GU440784
<i>Dianthus biflorus</i>	GU440785

**Table 4.** GenBank sequence accessions of one nuclear DNA region (ITS) used in the current study.  
(continued)

Taxon	ITS
<i>Dianthus bolusii</i>	GU440786
<i>Dianthus broteri</i>	GU065884
<i>Dianthus broteroii</i>	JN589117
<i>Dianthus caespitosus</i>	GU440789
<i>Dianthus capitatus</i>	GU440792
<i>Dianthus carthusianorum</i>	GU440794
<i>Dianthus caryophyllus</i>	JN589053
<i>Dianthus caucaseus</i>	JN589024
<i>Dianthus charidemi</i>	GU440795
<i>Dianthus chinensis</i>	GU440796
<i>Dianthus corymbosus</i>	GU440801
<i>Dianthus costae</i>	GU440802
<i>Dianthus cretaceus</i>	GU440804
<i>Dianthus crinitus</i>	GU440806
<i>Dianthus cruentus</i>	GU440807
<i>Dianthus cyri</i>	GU440808
<i>Dianthus deltoides</i>	GU440809
<i>Dianthus diffusus</i>	GU440811
<i>Dianthus eretmopetalus</i>	GU440813
<i>Dianthus excelsus</i>	GU440815
<i>Dianthus ferrugineus</i>	GU440803
<i>Dianthus giganteiformis</i>	GU440818
<i>Dianthus giganteus</i>	GU440819
<i>Dianthus glacialis</i>	GU440821
<i>Dianthus gracilis</i>	GU440822
<i>Dianthus gratianopolitanus</i>	JQ307857
<i>Dianthus haematocalyx</i>	GU440824
<i>Dianthus hyssopifolius</i>	GU440826
<i>Dianthus imereticus</i>	JN589026
<i>Dianthus inamoenus</i>	JN589070
<i>Dianthus integer</i>	GU440827
<i>Dianthus knappii</i>	GU440828
<i>Dianthus laingsburgensis</i>	GU440829
<i>Dianthus langeanus</i>	JQ307858
<i>Dianthus libanotis</i>	GU440835
<i>Dianthus lusitanus</i>	GU440838
<i>Dianthus micranthus</i>	GU440839
<i>Dianthus microlepis</i>	GU440840
<i>Dianthus micropetalus</i>	GU440841
<i>Dianthus mooiensis</i>	GU440842
<i>Dianthus multiceps</i> subsp. <i>multiaffinis</i>	GU440843
<i>Dianthus myrtinervius</i>	GU440845
<i>Dianthus namaensis</i>	GU440846
<i>Dianthus orientalis</i>	GU440847
<i>Dianthus pungens</i>	GU440852
<i>Dianthus pygmaeus</i>	GU440853
<i>Dianthus repens</i>	JN589124
<i>Dianthus seguieri</i>	JN589106
<i>Dianthus serotinus</i>	GU440857
<i>Dianthus serratifolius</i>	GU440858
<i>Dianthus serrulatus</i>	GU440859

**Table 4.** GenBank sequence accessions of one nuclear DNA region (ITS) used in the current study.  
(continued)

Taxon	ITS
<i>Dianthus sinaicus</i>	JQ307884
<i>Dianthus sp. cdK73</i>	FJ593175
<i>Dianthus squarrosus</i>	JN589065
<i>Dianthus stenopetalus</i>	GU440861
<i>Dianthus strictus</i>	GU440862
<i>Dianthus strymonis</i>	GU440863
<i>Dianthus superbus</i>	FJ980409
<i>Dianthus sylvestris</i>	GU440870
<i>Dianthus tenuiflorus</i>	GU440871
<i>Dianthus trifasciculatus</i>	GU440874
<i>Dianthus tripunctatus</i>	GU440875
<i>Dianthus viscidus</i>	GU440879
<i>Dianthus webbianus</i>	GU440814
<i>Dianthus zeyheri</i>	GU440881
<i>Dianthus zonatus</i>	GU440882
<i>Ixoca quadrifida</i>	JX274534
<i>Lychnis coronata</i>	JX274529
<i>Melandrium keiskei</i>	DQ908643
<i>Silene dianthoides</i>	KJ918494
<i>Silene jenisseensis</i>	KF267895
<i>Silene multicaulis</i>	KF267891
<i>Silene multiflora</i>	KF274511
<i>Silene occidentalis</i>	DQ908656
<i>Silene sibirica</i>	JX274521
<i>Silene uralensis</i> subsp. <i>apetala</i>	JX274519
<i>Silene vulgaris</i>	KJ918500

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**Table 2.** Specimen accessions (Acc) of lemongrass (*C.*, *Cymbopogon*, *Panicoideae*, L1 - L2) and carnation (*D.*, *Dianthus*, *Caryophyllaceae*, D1 - D10) their taxon names and GenBank sequence accessions of three plastid DNA regions (rbcLa, rbcLb and matK-KIM) and for carnation accessions also for one nuclear DNA region (ITS).

Acc	Taxon	rbcLa	rbcLb	matK-KIM	ITS
<b><i>Panicoideae</i></b>					
L1	<i>C. citratus</i>	KU722908	KU748525	KU722906	
L2	<i>C. citratus</i>	KU722907	KU748524	KU722905	
<b><i>Caryophyllaceae</i></b>					
D1	<i>D. caryophyllus</i>	KU722895	KU722853	KU722867	KU722881
D2	<i>D. chinensis</i>	KU722896	KU722854	KU722868	KU722882
D3	<i>D. deltoides</i>	KU722898	KU722856	KU722870	KU722884
D4	<i>D. deltoides</i>	KU722897	KU722855	KU722869	KU722883
D5	<i>D. gratianopolitanus</i>	KU722899	KU722857	KU722871	KU722885
D6	<i>D. imereticus</i>	KU722900	KU722858	KU722872	KU722886
D7	<i>D. longicalyx</i>	KU722901	KU722859	KU722873	KU722887
D8	<i>D. superbus</i>	KU722902	KU722860	KU722874	KU722888
D9	<i>D. superbus</i>	KU722903	KU722861	KU722875	KU722889
D10	<i>D. turkestanicus</i>	KU722904	KU722862	KU722876	KU722890

**Table 5.** Anatomical diagnostic key used to microscopically differentiate between Bamboo, lemongrass and Carnation leaf fragments present in Bamboo tea products. General features (GF) of adaxial and abaxial epidermis cells and cell walls (CW) are described in addition to characteristics of bulliforme cells (BC), stomata (ST), trichomes (TR) and wax structures (WS). Further features are derived from trichomes of the leaf margin (TM) and structures of the mesophyll (MP).

	Bamboo	Lemongrass	Carnation
Epidermis-abd			
GF	long cells, sinuous curved CW and short cells alternately	polygonal cells, mostly straight CW	
BC	10-30 x 10-20 um CW polygonal, thick, straight to slightly sinuous curved	70 x 30 um CW polygonal, thick, straight none	
ST	none or dumbbell-shaped guard cells	dumbbell-shaped guard cells	diacytic / anisocytic , numerous
TR	none or unicellular, short, thick-walled, acute	unicellular, short, thick walled, acuminate 1-2 celled, short, minute, thin-walled, papil- late	none or a few, unicellular, short, thick walled
WS		inconspicuous	
Epidermis-ab			
GF	long cells, sinuous curved CW and short cells alternately	polygonal cells, mostly straight CW	
BC	none	none	none
ST	dumbbell-shaped guard cells difficult to see because of wax papilla	dumbbell-shaped guard cells conspicuous	diacytic / anisocytic
TR	unicellular, long / short, thick-walled, acute 1-2 celled, short, minute, thin- walled, papillate	unicellular, short, thick-walled, acuminate none or unicellular, thick-walled	none or unicellular, thick-walled
WS	papilla		inconspicuous
TM	mostly unicellular, short, thick-walled, acuminate	1-3 celled, short acuminate mostly unicellu- lar, short, acuminate	
MP	main veins running parallel vein pattern tessellate, visible at 40x mag- nification <sup>a</sup>	only main veins visible at 40 x magnifica- tion glandular cells	many relatively large crystal druses along main veins and in intercostal regions

<sup>a</sup> except *Bambusa*

**Table 6.** BLOG bamboo tribe (Aru = *Arundinarieae*, Bam = *Bambuseae*, Oly = *Olyreae*) classification results. BLOG results using bamboo tribes for classification with single marker datasets (*rbcLa*, *rbcLb*, *matKK*) and combined marker datasets (*rbcL*: *rbcLa* + *rbcLb*, *rbcL+matK*: *rbcL* + *matKK*). The diagnostic (LOGic) formulas cover (C) a certain proportion of the sequences, ideally 100 %. Proportion of false positive (FP) and negative (FN) classifications as well as the ratio false to true positive (TP) classifications are shown. The score refers to the Laplace score

Classes	C (%)	FN (%)	FP (%)	Score	FP/TP	Formulas
<b>rbcLa</b>						
Aru	96.0	4.0	0.0	0.93	0.00	pos45=T
Bam	100.0	0.0	3.6	0.80	0.09	pos234=C AND pos538=T
Oly	100.0	0.0	0.0	0.67	0.00	pos526=T
<b>rbcLb</b>						
Aru	100.0	0.0	0.0	0.93	0.00	pos343!=G AND pos497!=G
Bam	100.0	0.0	0.0	0.86	0.00	pos204=C AND pos771=C
Oly	100.0	0.0	0.0	0.67	0.00	pos546=A
<b>rbcL</b>						
Aru	100.0	0.0	0.0	0.93	0.00	pos252=G AND pos1103!=C
Bam	100.0	0.0	0.0	0.86	0.00	pos526=C AND pos1103=C
Oly	100.0	0.0	0.0	0.67	0.00	pos878=A
<b>matKK</b>						
Aru	100.0	0.0	0.0	0.93	0.00	pos632=G
Bam	100.0	0.0	0.0	0.86	0.00	pos667=G AND pos688=A
Oly	100.0	0.0	0.0	0.67	0.00	pos536=A
<b>rbcL + matK</b>						
Aru	100.0	0.0	0.0	0.93	0.00	pos1788=G
Bam	100.0	0.0	0.0	0.86	0.00	pos1485=C AND pos1844=A
Oly	100.0	0.0	0.0	0.67	0.00	pos1692=A