

Table 1 Suppl. The sources of *Phaelanopsis* species used in this study. ^a -The endemic species of moth orchids have been commonly used as parental strains in breeding program (personal communication, Dr. Wen-Huei Chen).

Species ^a	Orchid nursery	Address	Purpose
<i>^aP. equestris</i>	Chane Ya Orchids	41-9 Shulin, Qigu Dist., Tainan 724, Taiwan	Endemic species of moth orchids used for screening mtDNA markers
<i>^aP. aphrodite</i>	Mainshow Orchid Nursery	2, Aly. 2 Ln. 314, Wanciao Village, Jhuci , Chiayi County 604, Taiwan	
<i>^aP. schilleriana</i>	Mainshow Orchid Nursery	2, Aly. 2 Ln. 314, Wanciao Village, Jhuci , Chiayi County 604, Taiwan	
<i>^aP. stuartiana</i>	Mainshow Orchid Nursery	2, Aly. 2 Ln. 314, Wanciao Village, Jhuci , Chiayi County 604, Taiwan	
<i>^aP. sanderiana</i>	Mainshow Orchid Nursery	2, Aly. 2 Ln. 314, Wanciao Village, Jhuci , Chiayi County 604, Taiwan	
<i>^aP. lueddemanniana</i>	Mainshow Orchid Nursery	2, Aly. 2 Ln. 314, Wanciao Village, Jhuci , Chiayi County 604, Taiwan	
<i>^aP. amboinensis</i>	Mainshow Orchid Nursery	2, Aly. 2 Ln. 314, Wanciao Village, Jhuci , Chiayi County 604, Taiwan	
<i>^aP. pulcherrima</i>	Unknown source	Unknown	Hybrid moth orchids used for studying mtDNA inheritance mode
<i>^aP. fasciata</i>	Chane Ya Orchids	29 Ln. 425, Sec. 2, Yung-Ho Rd., Yung-Ho, New Taipei City 234, Taiwan	
<i>^aP. venosa</i>	Chane Ya Orchids	2 Aly. 2, Ln. 314, Wanciao Village, Jhuci, Chiayi County 604, Taiwan	
<i>^aP. gigantea</i>	Chane Ya Orchids	41-9 Shulin, Qigu Dist., Tainan 724, Taiwan	
<i>^aP. mannii</i>	Mainshow Orchid Nursery	2, Aly. 2 Ln. 314, Wanciao Village, Jhuci , Chiayi County 604, Taiwan	
<i>P. javanica</i>	Chane Ya Orchids	41-9 Shulin, Qigu Dist., Tainan 724, Taiwan	
<i>P. parishii</i>	Chane Ya Orchids	41-9 Shulin, Qigu Dist., Tainan 724, Taiwan	
<i>^aP. amabilis</i>	Mainshow Orchid Nursery	2, Aly. 2, Ln. 314, Wanciao Village, Jhuci, Chiayi County 604, Taiwan	
<i>^aP. bellina</i>	Native Orchid	7, Shancha Ln., Caotun, Nantou County 542, Taiwan	
<i>^aP. fuscata</i>	Mainshow Orchid Nursery	2, Aly. 2, Ln. 314, Wanciao Village, Jhuci, Chiayi County 604, Taiwan	
<i>^aP. pulchra</i>	Tung-Hai Orchids	16-6, Niguan, Dapi, Yunlin County 631, Taiwan	
<i>^aP. violacea</i>	Native Orchids	7, Shancha Ln., Caotun, Nantou County 542, Taiwan	
<i>Dtps. Han Ben's Girl</i>	Taoyuan District Agricultural Research and Extension Station	139, Sec. 2, Dongfu Rd., Xinwu, Taoyuan County 327, Taiwan	
<i>P. Timothy Christopher</i>	Taoyuan District Agricultural Research and Extension Station	139, Sec. 2, Dongfu Rd., Xinwu, Taoyuan County 327, Taiwan	
<i>P. Yungho Gelb Canary</i>	Taoyuan District Agricultural Research and Extension Station	139, Sec. 2, Dongfu Rd., Xinwu, Taoyuan County 327, Taiwan	
<i>Dtps. Sogo Golden</i>	Taoyuan District Agricultural Research and Extension Station	139, Sec. 2, Dongfu Rd., Xinwu, Taoyuan County 327, Taiwan	

Table 2 Suppl. Primers used in this study.

Location	Markers/introns	Primer name	Sequence (5'→3')	Purpose
Intergenic spacers	MT1	M1-I-F	AAAGGGTAAAGGCAAGGATCTGA	for PCR amplification of markers
		M1-I-R	TCGCCACTTGAGCCGTATGC	
	MT2	M2-I-F	ACAGAACCTGAATAGGCTCCATAC	
		M2-I-R	GAGAGGTAGGACACAAGGAACATT	
	MT3	M3-I-F	TCCAACCCAAGCGGTAGCGAGTG	
		M3-I-R	CACAAAATCTCTGCAAAAACCTCCGC	
	MT4	M4-I-F	CCTACTCCTATGACTCCTCCTTATC	
		M4-I-R	AATATCTAGAGGAATGAGACTTGAG	
	MT5	M6-I-F	TCATTGATTTGAGTCCACTTTAC	
		M6-I-R	AACTTCTTGACCCGTTTACCC	
	MT6	M7-I-F	CAGGTCCCAGATTTGGAGAGGC	
		M7-I-R	CTGGCATATCTGGAAAAAGCGTAAT	
	MT7	M8-I-F	AGATATTTTCTTGGGTTGAACAAG	
		M8-I-R	GCTAGTTAAGGGTGGACGTAGTGA	
	MT8	M11-I-F	CGGGATCACTCACTAATACTAAAAAC	
		M11-I-F	TTTCGTGCTTTGGTGAGTCG	
	MT9	M12-I-F	GACAAGACTACCCCCAATTATCCA	
		M12-I-R	CGAGTCCTTTACAAAGTCTTTCCAA	
	MT10	M12a-I-F	TCATTCAATTGCTCCGTCATAAAG	
		M12a-I-F	GAGAGATCTATTAGTGATTGGGCCA	
	MT11	M16-I-F	AAGAAGACTCAGCACCTCCCGC	
		M16-I-R	AAGAGAAGACGGCCGCTATTGAATT	
	MT12	M19-I-F	CCTTTCTGTCTCAAACCTTGGAG	
		M19-I-R	GCTTTTTTGCTCTGATCTTCTGG	
	MT13	M20-I-F	AGTCGCAACGGCTTACTTCACAC	
		M20-I-R	TAACATGGCTCCAATTTTCGCTC	
	MT2S	M2a-I-F	CACCTGAGACACATCCTTCCCCCT	for PCR amplification across marker regions and sequencing
		M2a-I-R	TTTCTGCCCTCATTCCTGACATTT G	
	MT3S	M3a-I-F	TCAGGTGAGTGTGTGCATGGC	
		M3a-I-R	CACAAAATCTCTGCAAAAACCTCCGC	
	MT9S	MT9S-F	GAATTTGCGTGAATGGGCTCTAGC	
		MT9S-R	ACTGCAACAACCTCGTACACCGGAT	
	MT12S	MT12S-F	ATGGGGAGAGAACAAGAATCAGAAT	
		MT12S-R	GCATCAAAAGTGACCTGAAAGTAAA	
Introns	<i>ccmFc</i>	ccmFc-F	TCGAAGGTTTTGGGCCTGTAG	for PCR amplification of introns and sequencing
		ccmFc-R	CAGGTCGGCACGAAGTGATTC	
	<i>rpl2</i>	rpl2-F	AAGCCGAAGGCGGATCAAG	
		rpl2-R	ACCATCTGACCCGCTTCCAA	
	<i>nad2-1</i>	c24-nad2-F	GTTAGTCAGTAATGTGGGTTGGC	
		c24-nad2-R	AAGCCGAGATCATTAAGAGCATA	
	<i>nad2-3</i>	c9-nad2-F	TAGCTTACCGAATCAGTTGCGA	
		c9-nad2-R	TAGTAGTAACGACTTGTACGATCC	
	<i>nad5-1</i>	c2-nad5-F	CATGGATCTCATCGGAAATGTTTG	
		c2-nad5-R	AAATGGAATAAAGATGGACCAAGCT	
	<i>nad5-4</i>	c19-nad5-F	TTTACCACATCATGGGGGTTTACA	
		c19-nad5-R	CCGAATCCGAGTTTGCTGC	
	<i>nad7-3</i>	c10-nad7-F	GGCAACCGTATCTGGAA	
		c10-nad7-R	CGAACACTTTGTGCGATC	
	<i>rps10</i>	rps10-F	CATAAAAACGGAAACGCATGAATT	
		rps10-R	GGAGTTTGCCCTTATCCGAAC	

Table 3 Suppl. The number of simple sequence repeats in the mitochondrial DNA of *P. aphrodite*. Includes unclear! only > 5 iterations of mononucleotides; > 2 iterations of di-, tri-, tetra-, and penta-nucleotides; and ≥ 2 iterations of hexa-, hepta-, octa-, nona-, and deca-nucleotides.

Repeat motif	No. of iterations											Total [%]
	2	3	4	5	6	7	8	9	10	11	12	
Mononucleotide	—	—	—	—	828	336	124	78	37	15	6	1424 (32.8)
Dinucleotide	—	1,303	175	23	5	0	0	0	0	0	0	1506 (34.7)
Trinucleotide	—	328	17	0	0	0	0	0	0	0	0	345 (7.9)
Tetranucleotide	—	58	0	0	0	0	0	0	0	0	0	58 (1.3)
Pentanucleotide	—	3	0	0	0	0	0	0	0	0	0	5 (0.1)
Hexanucleotide	726	0	0	0	0	0	0	0	0	0	0	726 (16.7)
Heptanucleotide	193	0	0	0	0	0	0	0	0	0	0	193 (4.4)
Octanucleotide	48	0	0	0	0	0	0	0	0	0	0	48 (1.1)
Nonanucleotide	29	0	0	0	0	0	0	0	0	0	0	29 (0.7)
Decanucleotide	8	0	0	0	0	0	0	0	0	0	0	8 (0.2)
Total	1004	1692	192	23	833	336	124	78	37	15	6	4340 (100)

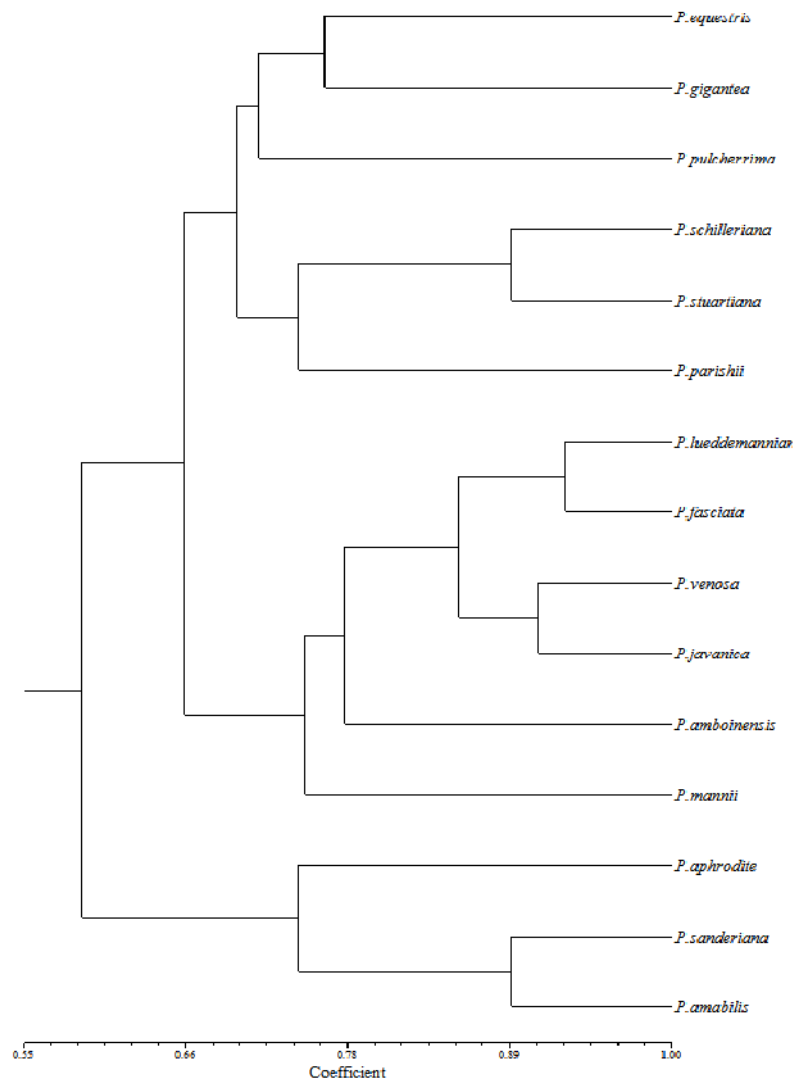


Fig. 1 Suppl. Dendrograms generated using unweighed pair-group method with arithmetic mean (UPGMA) clustering analysis showing relationships among 15 endemic moth orchids. The 13 mtDNA simple sequence repeat markers (Table 1) were amplified from 15 moth orchids indicated, separated by 8 % (m/v) polyacrylamide gel electrophoresis, and then stained with ethidium bromide.

rps10 intron

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1. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
2. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
3. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
4. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
5. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
6. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AGAAACGTC-GGTTGA...
7. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
8. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
9. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--GAAACGTC-GGTTGA...
10. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
11. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
12. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
13. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--GAAACGTC-GGTTGA...
14. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
15. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...
16. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGAG--AG--AAACGTCGCGTTGA...
17. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGGGAG--AAACGTCGCGT-GA...
18. ...CTGTGCTT-----AG.....TTGGCT.....GAGGGGGGGGGG--GAAACGTC-GGTTGA...
19. ...CTGTGCTTGTGCTTAG.....TTG-CT.....GAGGGGGGGGG--AG--AACGTC-GGTTGA...

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rpl2 intron

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1. ...AAGGCC.....GATCTTCTATTACCAAGT.....CAGGGGCC---TTAGGTC-AA--C
2. ...AAGG-CC.....GATCT---ATTACCA-GT.....CAGGGGC---TTAGGTC-AA--C
3. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AAA-C
4. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AAA-C
5. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGG----TTATTAGGTC-AA--C
6. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AA--C
7. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AA--C
8. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AAA-C
9. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AAA-C
10. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AA--C
11. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AA--C
12. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AAA-C
13. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AA--C
14. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AAA-C
15. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AA--C
16. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AA--C
17. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AA--C
18. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AA--C
19. ...AAGG-CC.....GATCT---ATTACCAAGT.....CAGGGGC---TTAGGTC-AA--C

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ccmFe intron

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1. ...TATTTTTTCA.....CCTTTTTTAC.....TAGGGTCGGTTTTTGG.....CCTT-TCA...
2. ...TATTTTTTCA.....CCTTTTTTAC.....TAGGGTCGGTTTTTGG.....CCTT-TCA...
3. ...TATTTTTT-CA.....CCTTTTTTAC.....TAGGGTCGGTTTTTGG.....CCTT-TCA...
4. ...TATTTTTT-CA.....CCTTTTTTAC.....TAGGGTCGGTTTTTGG.....CCTT-TCA...
5. ...TATTTTTTCA.....CCTTTTTTAC.....TAGGGTCGGTTTTTGG.....CCTT-TCA...
6. ...TATTTTTTCA.....CCTTTTTTAC.....TAGG-TCGGTTTTTGG.....CCTTATCA...
7. ...TATTTTTTCA.....CCTTTTTTAC.....TAGG-TCGGTTTTTGG.....CCTTATCA...
8. ...TATTTTTTCA.....CCTTTTTTAC.....TAGGGTCGGTTTTTGG.....CCTT-TCA...
9. ...TATTTTTTCA.....CCTTTTTTAC.....TAGG-TCGGTTTTTGG.....CCTTATCA...
10. ...TATTTTTTCA.....CCTTTTTTAC.....TAGG-TCGGTTTTTGG.....CCTTATCA...
11. ...TATTTTTTCA.....CCTTTTTTAC.....TAGGGTCGGTTTTTGG.....CCTTATCA...
12. ...TATTTTTTCA.....CCTTTTTTAC.....TAGGGTCGGTTTTTGG.....CCTTATCA...
13. ...TATTTTTTCA.....CCTTTTTTAC.....TAGG-TCGGTTTTTGG.....CCTTATCA...
14. ...TATTTTTTCA.....CCTTTTTTAC.....TAGGGTCGGTTTTTGG.....CCTT-TCA...
15. ...TATTTTTTCA.....CCTTTTTTAC.....TAGGGTCGGTTTTTGG.....CCTT-TCA...
16. ...TATTTTTTCA.....CCTTTTTTAC.....TAGG-TCGGTTTTTGG.....CCTTATCA...
17. ...TATTTTTTCA.....CCTTTTTTAC.....TAGG-TCGGTTTTTGG.....CCTTATCA...
18. ...TATTTTTTCA.....CCTTTTTTAC.....TAGG-TCGGTTTTTGG.....CCTTATCA...
19. ...TATTTTTTCA.....CCTTTTTTAC.....TAGG-TCGGTTTTTGG.....CCTTATCA...

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nad5-1 intron

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1. ...TCAAAAAAAAAAGC.....ACAAAAAA-CT.....GCAAA--TG.....ATGGGAA.....AAGGGG-AG...
2. ...TCAAAAAAAAAAGC.....ACAAAAAA-CT.....GCAAA--TG.....ATGGGAA.....AAGGGG-AG...
3. ...TCAAAAAAAAAAGC.....ACAAAAAA-CT.....GCAAA--TG.....ATGGGAA.....AAGGGG-AG...
4. ...TCAAAAAAAAAAGC.....ACAAAAAA-CT.....GCAAA--TG.....ATGGGAA.....AAGGGG-AG...
5. ...TCAAAAAAAAAAGC.....ACAAAAAA-CT.....GCAAA--TG.....ATGGGAA.....AAGGGG-AG...
6. ...TCAAAAAA---GC.....ACAAAAAA-CT.....GCAGA--TG.....ATGGGAA.....AAGGGG-AG...
7. ...TCAAAAAA---GC.....ACAAAAAACT.....GCAGA--TG.....ATGGGAA.....AAGGGG-AG...
8. ...TCAAAAAA---GC.....ACAAAAAA-CT.....GCAGAGATG.....ATGGGAA.....AAGGGG-AG...
9. ...TCAAAAAA---GC.....ACAAAAAA-CT.....GCAGA--TG.....ATGGGAA.....AAGGGG-AG...
10. ...TCAAAAAA---GC.....ACAAAAAACT.....GCAGA--TG.....ATGGGAA.....AAGGGG-AG...
11. ...TCAAAAAA---GC.....ACAAAAAA-CT.....GCAGA--TG.....ATGGGAA.....AAGGGG-AG...
12. ...TCAAAAAA---GC.....ACAAAAAA-CT.....GCAGA--TG.....ATGGGAA.....AAGGGG-AG...
13. ...TCAAAAAAAAAAGC.....ACAAAAAA-CT.....GCAAA--TG.....ATGGGAA.....AAGGGGAG...
14. ...TCAAAAAAAAAAGC.....ACAAAAAA-CT.....GCAAA--TG.....ATGG-AA.....AAGGGG-AG...
15. ...TCAAAAAAAAAAGC.....ACAAAAAA-CT.....GCAAA--TG.....ATGGGAA.....AAGGGG-AG...
16. ...TCAAAAAA---GC.....ACAAAAAACT.....GCAGA--TG.....ATGGGAA.....AAGGGG-AG...
17. ...TCAAAAAA---GC.....ACAAAAAA-CT.....GCAGA--TG.....ATGGGAA.....AAGGGG-AG...
18. ...TCAAAAAA---GC.....ACAAAAAA-CT.....GCAGA--TG.....ATGGGAA.....AAGGGG-AG...
19. ...TCAAAAAA---GC.....ACAAAAAACT.....GCAGA--TG.....ATGGGAA.....AAGGGG-AG...

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nad7-2 intron

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1. ...CTGGCGGGGCC-----AT.....CCTCTTT-----CT.....AC-----AA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
2. ...CTGGCGGGGCCCGCGGCCAT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
3. ...CTGGCGGGGCC-----AT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
4. ...CTGGCGGGGCC-----AT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
5. ...CTGGCGGGCCGCGGCCAT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
6. ...CTGGCGGGGCC-----AT.....CCTCTTTCTTTCT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
7. ...CTGGCGGGCCGCGGCCAT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
8. ...CTGGCGGGGCC-----AT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
9. ...CTGGCGGGGCC-----AT.....CCTCTTTCTTTCT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
10. ...CTGGCGGGGCC-----AT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
11. ...CTGGCGGGGCC-----AT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
12. ...CTGGCGGGCCGCGGCCAT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
13. ...CTGGCGGGGCC-----AT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
14. ...CTGGCGGGGCC-----AT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
15. ...CTGGCGGGGCC-----AT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
16. ...CTGGCGGGGCC-----AT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
17. ...CTGGCGGGCCGCGGCCAT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
18. ...CTGGCGGGGCC-----AT.....CCTCTTTCTTTCT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...
19. ...CTGGCGGGGCC-----AT.....CCTCTTT-----CT.....ACCCCAAAGGGAA.....TGAAGG.....AGTTTTTTTTT--GGGGGGGAA...

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Fig. 2 Suppl. Variable sequence tandem repeats in mitochondrial introns of moth orchids. The polymorphic sequence tandem repeats (red, blue, or green) in five introns of moth orchids are shown. Dots indicate not shown sequences. Dashes indicate nucleotide deletions. Squares indicate exons. The species of moth orchids were 1. *Phalaenopsis equestris*, 2. *P. aphrodite*, 3. *P. schilleriana*, 4. *P. stuartiana*, 5. *P. sanderiana*, 6. *P. lueddemanniana*, 7. *P. amboinensis*, 8. *P. pulcherrima*, 9. *P. fasciata*, 10. *P. venosa*, 11. *P. gigantea*, 12. *P. mannii*, 13. *P. javanica*, 14. *P. parishii*, 15. *P. amabilis*, 16. *P. bellina*, 17. *P. fuscata*, 18. *P. pulchra*, and 19. *P. violacea*.



Fig. 3 Suppl.. The genealogy of hybrid moth orchids registered at the Royal Horticultural Society. The genealogy of four hybrid moth orchids, *Dtps. Sogo Golden*, *P. Yungho Gelb Canary*, *Dtps. Han-Ben's Girl*, and *P. Timothy Christopher*, were retrieved from the Royal Horticultural Society database. The male parent is on the top and the female parent on the bottom. Only the female parents were traced.

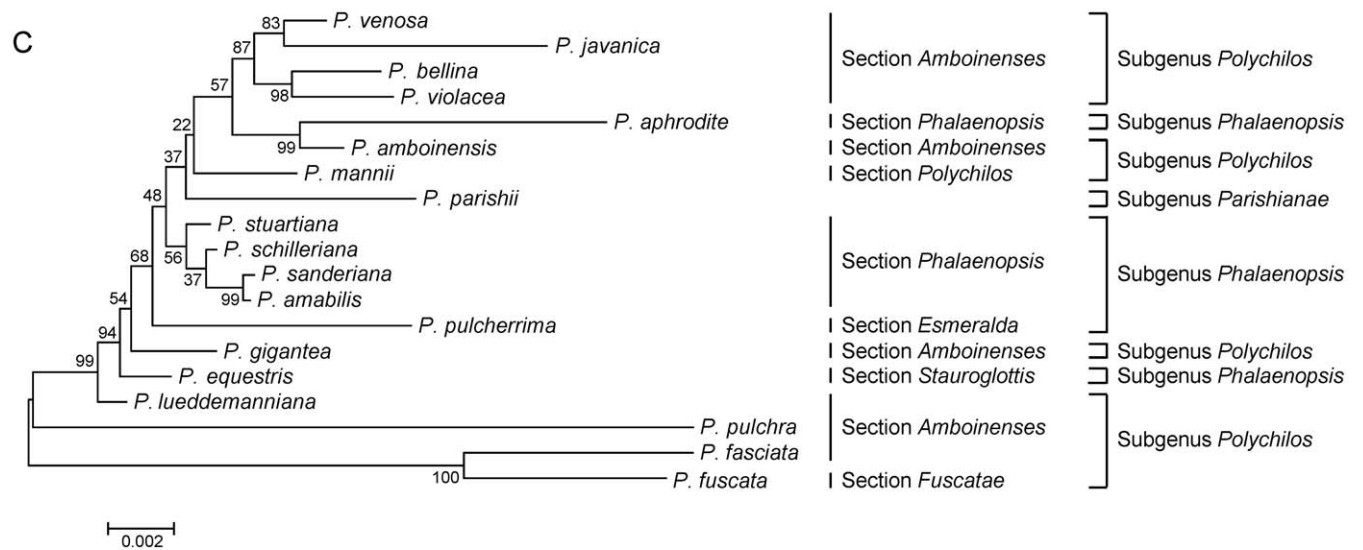
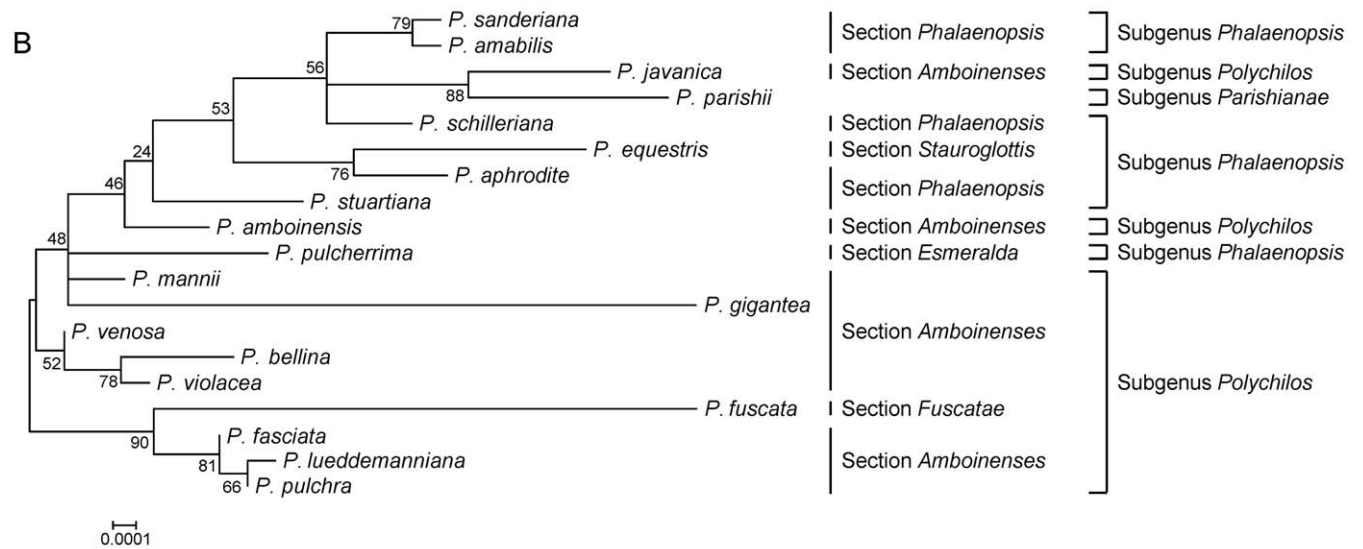
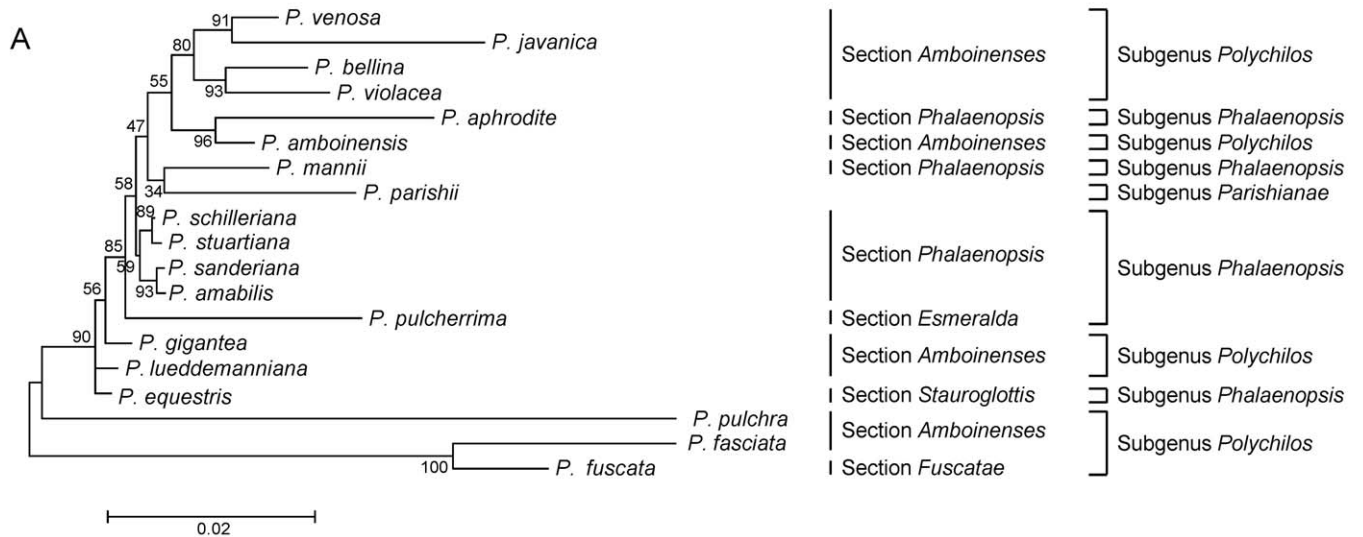


Fig. 4 Suppl. Phylogenetic relationships among 19 moth orchids based on mtDNA. Sequences from four intergenic spacer regions across marker regions (MT2, MT3, MT9, and MT12) and eight introns (Table 2) were multiple aligned with use of Muscle in MEGA5.2, respectively, and then concatenated. Phylogenetic analysis involved the maximum likelihood method with all sites retained at 1,000 bootstrap replications. Bootstrap support values are shown beside branches. The ruler is the substitution rate. A phylogenetic tree based on four intergenic spacer regions (A); eight introns (B), and the concatenation of intergenic spacer regions and introns (C). The right panel is the taxonomic classification of species in the *Phalaenopsis* genus according to Tsai *et al.* 2010.