



**Supplementary Figure S1.** Phylogenetic analysis of 28 Aeridinae species based on 68 protein coding genes. Numbers near the nodes are bootstrap percentages and Bayesian posterior probabilities (BSML left, BSMP middle, and PP right). - indicates that a node is inconsistent between the topology of the MP/ML trees and the Bayesian tree. \* indicates that the node is 100 bootstrap percentage or 1.00 posterior probability.

**Supplementary Table S1** Source and voucher information for this study. *P. labukensis* and *P. denevel* were introduced and cultivated in Shanghai Chen Shan Botanical Garden, Shanghai province, China. *P. laycockii* 'semi-alba' was introduced and cultivated in the China National Botanical Garden, Beijing province, China. And other voucher specimens were deposited in the herbariums of National Center for Biotechnology Information (NCBI).

Species	Source	Voucher	GenBank accession numbers
<i>Paraphalaenopsis denevel</i>	This study		OR159903
<i>Paraphalaenopsis labukensis</i>	This study		OR159902
<i>Paraphalaenopsis laycockii</i> 'semi-alba'	This study		OR159904
<i>Holcoglossum wangii</i>	Li et al., 2019	13881	NC041520
<i>Holcoglossum amesianum</i>	Li et al., 2019	9419	NC041511
<i>Holcoglossum tsii</i>	Chen et al., 2020	LDKAe67	NC048459
<i>Holcoglossum flavescens</i>	Li et al., 2019	8943	NC041512
<i>Vanda falcata</i>	Kim et al., 2017	PDBK 2014-0010	KT726907
<i>Vanda richardsiana</i>	Kim et al., 2017	PDBK 2014-0945	KT726908
<i>Vanda xichangensis</i>	Liu et al., 2019	Z.J. Liu 2747	NC047197
<i>Vanda brunnea</i>	Li et al., 2019	13059	NC041522
<i>Schoenorchis tixieri</i>	Liu et al., 2020	Liu4123	MN124407
<i>Schoenorchis seidenfadenii</i>	Liu et al., 2020	Liu5230	MN124434
<i>Smitinandia micrantha</i>	Liu et al., 2020	Liu21119	MN124406
<i>Robiquetia spathulata</i>	Liu et al., 2020	Liu5248	MN124410
<i>Diploprora championii</i>	Liu et al., 2020	Liu4480	MN124409
<i>Vandopsis gisantea</i>	Liu et al., 2020	Liu7990	MN124403
<i>Vandopsis lissochiloides</i>	Liu et al., 2020	Lior070	MN124443
<i>Gastrochilus obliquus</i>	Liu et al., 2020	Liu4191	MN124429
<i>Gastrochilus bellinus</i>	Liu et al., 2020	Lior011	MN124427
<i>Cymbilabia undulata</i>	Liu et al., 2020	Lior078	MN124402
<i>Phalaenopsis stobartiana</i>	Zhou et al., 2021	-	NC059917
<i>Phalaenopsis wilsonii</i>	Wang et al., 2021	-	NC057488
<i>Phalaenopsis zhejiangensis</i>	Jiang et al., 2021	-	MZ326749
<i>Phalaenopsis mannii</i>	Zhou et al., 2020	HDL-YN2019-12A	NC050940
<b>Outgroup</b>			
<i>Tridactyle tridactylites</i>	D'hajjère et al., 2022	-	MW760855
<i>Polystachya bennettiana</i>	Jiang et al., 2022	-	NC066148
<i>Polystachya concreta</i>	Jiang et al., 2022	-	NC066150

**Supplementary Table S2.** The details information of long repeats.

seq len	species	<i>P. labukensis</i>	<i>P. denevel</i>	<i>P. laycockii</i> 'semi-alba'
≥40	Complement	0	0	0
	Forward	5	5	7
	Palindrome	9	7	9
	Reverse	2	5	1
30-39	Complement	1	2	2
	Forward	3	6	7
	Palindrome	9	7	8
	Reverse	5	11	6
20-29	Complement	0	0	0
	Forward	6	3	6
	Palindrome	4	2	3
	Reverse	5	1	0

**Supplementary Table S3.** The details information Small simple repeats.

species	mono	di	tri	tetra	penta	hexa	total
<i>P. laycockii</i> 'semi-alba'	39	13	9	7	4	0	72
<i>P. denevel</i>	49	13	10	2	3	1	78
<i>P. labukensis</i>	47	9	4	6	3	2	71

species	LSC	SSC	IR	total
<i>P. laycockii</i> 'semi-alba'	51	15	6	72
<i>P. denevel</i>	60	14	4	78
<i>P. labukensis</i>	53	16	2	71

**Supplementary Table S4.** The nucleotide diversity of three *Paraphalaenopsis* Chloroplast genomes.

Sliding window test of nucleotide diversity ( $\pi$ ) in the *Paraphalaenopsis* chloroplast genomes.  
Win-dow length: 600 bp; step size: 200 bp.