

Supplementary Table S1. Specimen source information; herbarium abbreviations follow Thiers (continuously updated).

Species ¹	Family	Voucher number [Collector number (herbarium)]	GenBank accession
Pandanales			
<i>Carludovica palmata</i> Ruiz & Pav.	Cyclanthaceae	M.W. Chase 14836, K	KP462882.1
<i>Cyclanthus bipartitus</i> Poit. ex A. Rich	Cyclanthaceae	M.W. Chase 1237, K	KT205192 - KT205273
<i>Freycinetia banksii</i> A. Cunn	Pandanaceae	S.W. Graham 02-03-14, UBC	KT205110 - KT205191
<i>Sararanga sinuosa</i> Hemsl.	Pandanaceae	Gallaher 461, BISH, HAW	KT204539 - KT204619
<i>Croomia japonica</i> Miq.	Stemonaceae	Rothwell & Stockey 43, ALTA	KT204620 - KT204701
<i>Stemona tuberosa</i> Lour.	Stemonaceae	Rothwell & Stockey 46, ALTA	KT204702 - KT204783
<i>Stichoneuron caudatum</i> Ridl.	Stemonaceae	Rothwell & Stockey 45, ALTA	KT204946 - KT205027
<i>Pentastemona sumatrana</i> Steenis	Stemonaceae	B.G. Leiden 910375, K	KT205028 - KT205109
<i>Sciaphila densiflora</i> Schltr.	Triuridaceae	Pillon Y. <i>et al.</i> 88, NOU, P	KR902497.1
<i>Xerophyta retinervis</i> Baker	Velloziaceae	B.G. Reeves 14, NBG	KT204784 - KT204865
Dioscoreales			
<i>Lophiola aurea</i> Ker Gawl.	Nartheciaceae	Whitten 95028, K	KT204866 - KT204945

¹ Additional sequences: *Acorus calamus* L. (NC_007407), *Alstroemeria aurea* Graham (KC968976), *Amborella trichopoda* Baill. (NC_005086), *Buxus microphylla* Siebold & Zucc. (NC_009599), *Calycanthus floridus* var. *glaucus* (Willd.) Torr. & A.Gray (NC_004993), *Dioscorea elephantipes* (NC_009601), *Drimys granadensis* L.f. (NC_008456), *Elaeis oleifera* (Kunth) Cortés (EU016883–EU016962), *Fritillaria taipaiensis* P.Y. Li (NC_023247), *Hordeum vulgare* L. (NC_008590), *Illicium oligandrum* Merr. & Chun (NC_009600), *Japonolirion osense* Nakai (JQ068951- JQ069028), *Lemna minor* L. (NC_010109), *Lilium longiflorum* Thunb. (KC968977), *Liriodendron tulipifera* L. (NC_008326), *Musa acuminata* Colla (EU016983–EU017063), *Nandina domestica* Thunb. (NC_008336), *Nuphar advena* (Aiton) W.T.Aiton (NC_008788), *Oncidium* Sw. Gower Ramsey (NC_014056), *Orontium aquaticum* L. (NC_010109), *Oryza sativa* L. (NC_001320), *Phalaenopsis aphrodite* Rchb.f. subsp. *formosana* (NC_007499.1), *Phoenix dactylifera* L. (NC_013991), *Piper cenocladum* C.DC. (NC_008457), *Plantanus occidentalis* L. (NC_008335), *Saccharum officinarum* L. (NC_006084), *Smilax china* L. (HM536959), *Sorghum bicolor* (L.) Moench (NC_008602), *Spirodela polyrhiza* (L.) Schleid. (NC_015891), *Triticum aestivum* L. (NC_002762), *Typha latifolia* L. (NC_013823), *Veratrum patulum* Loes. (NC_022715), *Vitis vinifera* L. (NC_007957), *Wolffia australiana* (Benth.) Hartog & Plas (NC_015899), *Wolffiella lingulata* (Hegelm.) Hegelm. (NC_015894), *Yucca schidigera* Ortgies (DQ069337–DQ069702, EU016681– EU016700), *Zea mays* L. (NC_001666). For additional taxa, see Givnish *et al.* (2010) (Arecales, Asparagales, Commelinales, Dasygogonales, Poales), Barrett *et al.* (2013) (Arecales, Commelinales, Dasygogonales, Zingiberales), and Mennes *et al.* (2015) (Liliales and Pandanales)

Supplementary Table S2. Data partitioning schemes inferred using PartitionFinder or PartitionFinderProtein with the BIC criterion. (a) “Codon” partitioning scheme for the nucleotide matrix; (b) “GxC” (gene x codon) partitioning scheme; (c) Amino-acid partitioning scheme; and (d) GxC (gene x codon) partitioning scheme for matrix with re-alignments for *accD*, *rpl20* and *rps18* (see text for details). Plastid genes are indicated before the underscore; the ‘pos’ term after an underscore indicates the codon position (not applicable for *rrn* genes).

Partition no.	Best Model	Partition subsets
a)		
1	GTR + G	codon_pos1
2	GTR + G	codon_pos2
3	GTR + G	codon_pos3
4	GTR + G	rrn16, rrn23, rrn4.5, rrn5
b)		
1	GTR + G	accD_pos1, accD_pos2, clpP_pos3, lhbA_pos3, matK_pos2, ndhF_pos1, ndhF_pos2, petG_pos3, psbE_pos3, psbH_pos2, psbJ_pos2, psbJ_pos3, psbL_pos2, rpl16_pos1, rpl22_pos1, rpl22_pos2, rpl32_pos1, rps14_pos3, rps16_pos2, rps4_pos3, ycf3_pos2, ycf3_pos3
2	GTR + G	accD_pos3, atpB_pos3, atpE_pos3, atpF_pos3, atpI_pos3, matK_pos1, ndhC_pos3, ndhJ_pos3, ndhK_pos3, petN_pos3, psaI_pos2, psbA_pos3, psbD_pos3, psbH_pos3, psbK_pos3, rpl14_pos3, rpl20_pos3, rpl32_pos2, rpl33_pos3, rpoA_pos3, rpoB_pos3, rpoC1_pos3, rps2_pos3, rps8_pos3
3	GTR + G	5rps12_pos3, atpA_pos1, atpA_pos2, atpF_pos1, clpP_pos1, ndhA_pos1, psaC_pos2, psaI_pos3, psbH_pos1, psbM_pos2, rbcL_pos1, rbcL_pos2, rpl20_pos2, rpoC2_pos1, rps15_pos1, rps16_pos1, rps18_pos3, rps3_pos1, rps8_pos1, ycf4_pos1
4	GTR + G	atpA_pos3, matK_pos3, ndhE_pos3, petD_pos3, psaC_pos3, rpl16_pos3, rpl36_pos3, rps3_pos3
5	GTR + G	3rps12_pos3, 5rps12_pos2, atpB_pos1, atpI_pos1, clpP_pos2, infA_pos2, lhbA_pos2, ndhB_pos3, ndhI_pos1, ndhJ_pos1, ndhJ_pos2, petB_pos1, petB_pos2, petD_pos2, psaB_pos1, psbA_pos1, psbA_pos2, psbB_pos2, psbC_pos2, psbD_pos2, psbK_pos2, psbL_pos1, psbM_pos1, psbN_pos1, psbT_pos2, rpl23_pos3, rpl36_pos2, rpoB_pos1, rpoB_pos2, rpoC1_pos2, rps11_pos1, rps14_pos2, rps15_pos2, rps2_pos2, rps3_pos2, rps4_pos2, rps7_pos3, ycf2_pos1, ycf2_pos2, ycf2_pos3, ycf3_pos1
6	GTR + G	atpB_pos2, atpF_pos2, ccsA_pos1, ccsA_pos2, lhbA_pos1, ndhA_pos2, ndhD_pos1, ndhD_pos2, ndhG_pos1, ndhK_pos1, petD_pos1, petL_pos1, petL_pos3, psaB_pos2, psaI_pos1, psbB_pos1, psbD_pos1, psbE_pos2, psbF_pos2, psbF_pos3,

7	GTR + G	psbJ_pos1, psbN_pos3, rpl16_pos2, rpl20_pos1, rpl36_pos1, rpoC2_pos2, rps8_pos2 5rps12_pos1, atpE_pos1, atpE_pos2, atpI_pos2, cemA_pos1, cemA_pos2, infA_pos1, ndhC_pos1, ndhE_pos1, ndhG_pos2, ndhH_pos1, ndhH_pos2, ndhI_pos2, ndhK_pos2, petA_pos1, petA_pos2, petL_pos2, psaA_pos1, psaA_pos2, psaC_pos1, psaJ_pos1, psaJ_pos2, psbC_pos1, psbL_pos3, psbN_pos2, rpl14_pos1, rpl2_pos3, rpl33_pos1, rpl33_pos2, rpoA_pos1, rpoA_pos2, rpoC1_pos1, rps11_pos2, rps14_pos1, rps18_pos1, rps18_pos2, rps19_pos1, rps19_pos2, rps2_pos1, rps4_pos1, ycf4_pos2
8	GTR + G	3rps12_pos1, 3rps12_pos2, atpH_pos1, atpH_pos2, ndhB_pos1, ndhB_pos2, ndhC_pos2, ndhE_pos2, petG_pos1, petG_pos2, petN_pos1, petN_pos2, psbE_pos1, psbF_pos1, psbI_pos1, psbI_pos2, psbT_pos1, rpl14_pos2, rpl23_pos1, rpl23_pos2, rpl2_pos1, rpl2_pos2, rps7_pos1, rps7_pos2, rrn16, rrn23, rrn4_5, rrn5
9	GTR + G	atpH_pos3, cemA_pos3, infA_pos3, ndhG_pos3, ndhI_pos3, petA_pos3, petB_pos3, psaA_pos3, psaB_pos3, psbB_pos3, psbC_pos3, psbI_pos3, psbM_pos3, psbT_pos3, rbcL_pos3, rpoC2_pos3, rps15_pos3, rps19_pos3, ycf4_pos3
10	GTR + G	ccsA_pos3, ndhD_pos3, ndhH_pos3, psbK_pos1, rpl22_pos3, rps16_pos3
11	GTR + G	ndhA_pos3, psaJ_pos3, rpl32_pos3, rps11_pos3
12	GTR + I + G	ndhF_pos3

c)		
1	JTT + G + F	accD
2	CPREV + I + G	atpA, psbC
3	JTT + G	atpB
4	JTT + G	atpE, clpP, ndhI
5	JTT + G	atpF
6	CPREV+G	atpH
7	JTT+G	5rps12, atpI
8	JTT+G+F	ccsA
9	JTT+G+F	cemA, ndhA
10	JTT+G	infA
11	CPREV+G	lhbA
12	JTT+G+F	matK
13	JTT+G+F	ndhB
14	CPREV + G	ndhC
15	CPREV + G	ndhD
16	MTMAM+G	ndhE
17	JTT + G + F	ndhF
18	JTT + G	ndhG
19	JTT + I + G	ndhH
20	JTT + G	ndhJ
21	JTT + G	ndhK
22	JTT + G	petA, rpoC1
23	JTT + G	petB
24	JTT + G	petD, psbH
25	CPREV + G	petG
26	MTMAM+G	petL
27	MTMAM+G	petN

28	CPREV + I + G	psaA
29	CPREV + I + G	psaB
30	JTT + I + G	psaC
31	CPREV + G	psaI
32	CPREV + G	psaJ
33	CPREV + I + G	psbA
34	JTT + I + G	psbB
35	CPREV + I + G	psbD
36	JTT + G	psbE
37	JTT + G	psbF, rps11
38	CPREV + G	psbI
39	MTMAM+G	psbJ
40	CPREV + G	psbK
41	MTMAM+G	psbL
42	CPREV + G	psbM
43	MTMAM+G	psbN
44	JTT + G	psbT
45	LG + G	rbcL
46	JTT + G	rpl2
47	JTT + G	rpl14
48	CPREV + G	rpl16
49	JTT + G	rpl20
50	JTT + G	rpl22
51	JTT + G	rpl23
52	JTT + G	rpl32
53	JTT + G	rpl33
54	CPREV + G	rpl36
55	JTT + G	rpoA
56	JTT + G	rpoB
57	JTT + G + F	rpoC2
58	JTT + G	rps2
59	JTT + G	rps3
60	JTT + G	rps4
61	JTT + G	rps7
62	CPREV + G	rps8
63	CPREV + G	3rps12
64	JTT + G	rps14
65	JTT + G	rps15
66	JTT + G	rps16
67	JTT + G + F	rps18
68	JTT + G	rps19
69	JTT + G + F	ycf2
70	JTT + G	ycf3
71	CPREV + G	ycf4
d)		
1	GTR + G	5rps12_pos3, accD_pos1, accD_pos2, clpP_pos3, ndhA_pos1, psaI_pos3, psbE_pos3, psbH_pos2, psbJ_pos1, psbJ_pos2, psbJ_pos3, rbcL_pos1, rbcL_pos2, rpl16_pos1, rpl22_pos1, rpl22_pos2, rpl33_pos1, rpl33_pos2, rpoC2_pos1, rps14_pos3, rps4_pos3, ycf3_pos2
2	GTR + G	accD_pos3, atpB_pos3, atpE_pos3, atpF_pos3, atpI_pos3, matK_pos1, ndhC_pos3, ndhJ_pos3, ndhK_pos3, petN_pos3, psaI_pos2, psbA_pos3, psbD_pos3, psbH_pos3, psbK_pos3, rpl14_pos3, rpl32_pos2, rpl33_pos3, rpoA_pos3, rpoB_pos3, rpoC1_pos3, rps2_pos3, rps8_pos3

3	GTR + G	atpA_pos1, atpB_pos2, atpF_pos1, ccsA_pos1, ndhG_pos1, ndhH_pos1, psaC_pos2, psaI_pos1, psbB_pos1, psbH_pos1, psbM_pos2, rpl16_pos2, rpl20_pos1, rpoA_pos1, rps11_pos1, rps15_pos1, rps3_pos1, rps8_pos1, ycf4_pos1
4	GTR + G	5rps12_pos1, atpA_pos2, atpE_pos1, atpE_pos2, atpF_pos2, atpI_pos2, ccsA_pos2, cemA_pos1, cemA_pos2, clpP_pos1, clpP_pos2, infA_pos1, infA_pos2, lhbA_pos1, ndhA_pos2, ndhC_pos1, ndhD_pos1, ndhD_pos2, ndhE_pos1, ndhG_pos2, ndhH_pos2, ndhI_pos2, ndhK_pos1, ndhK_pos2, petA_pos1, petA_pos2, petD_pos1, petL_pos1, petL_pos2, petL_pos3, psaA_pos1, psaB_pos2, psaC_pos1, psaJ_pos1, psbA_pos2, psbC_pos1, psbD_pos1, psbE_pos2, psbF_pos2, psbF_pos3, psbL_pos3, psbN_pos3, rpl20_pos2, rpl2_pos3, rpl36_pos1, rpoA_pos2, rpoC1_pos1, rpoC2_pos2, rps11_pos2, rps14_pos1, rps18_pos1, rps18_pos2, rps19_pos1, rps19_pos2, rps2_pos1, rps2_pos2, rps3_pos2, rps4_pos1, rps4_pos2, rps8_pos2, ycf4_pos2
5	GTR + G	atpA_pos3, matK_pos3, ndhE_pos3, petD_pos3, psaC_pos3, rpl16_pos3, rpl36_pos3, rps3_pos3
6	GTR + G	3rps12_pos3, 5rps12_pos2, atpB_pos1, atpI_pos1, lhbA_pos2, ndhB_pos3, ndhE_pos2, ndhI_pos1, ndhJ_pos1, ndhJ_pos2, petB_pos1, petB_pos2, petD_pos2, petG_pos1, psaB_pos1, psaJ_pos2, psbA_pos1, psbC_pos2, psbD_pos2, psbK_pos2, psbL_pos1, psbM_pos1, psbN_pos1, psbT_pos1, psbT_pos2, rpl14_pos1, rpl23_pos3, rpl2_pos1, rpl36_pos2, rpoB_pos1, rpoB_pos2, rpoC1_pos2, rps14_pos2, rps15_pos2, rps7_pos1, rps7_pos3, ycf2_pos1, ycf2_pos2, ycf2_pos3, ycf3_pos1
7	GTR + G	3rps12_pos1, 3rps12_pos2, atpH_pos1, atpH_pos2, ndhB_pos1, ndhB_pos2, ndhC_pos2, petG_pos2, petN_pos1, petN_pos2, psaA_pos2, psbB_pos2, psbE_pos1, psbF_pos1, psbI_pos1, psbI_pos2, psbN_pos2, rpl14_pos2, rpl23_pos1, rpl23_pos2, rpl2_pos2, rps16_pos1, rps7_pos2, rrn16, rrn23, rrn4_5, rrn5
8	GTR + G	atpH_pos3, cemA_pos3, infA_pos3, ndhG_pos3, ndhI_pos3, petA_pos3, petB_pos3, psaA_pos3, psaB_pos3, psbB_pos3, psbC_pos3, psbI_pos3, psbM_pos3, psbT_pos3, rbcL_pos3, rpoC2_pos3, rps15_pos3, rps19_pos3, ycf4_pos3
9	GTR + G	ccsA_pos3, ndhA_pos3, ndhD_pos3, ndhH_pos3, psaJ_pos3, psbK_pos1, rpl22_pos3, rpl32_pos3, rps11_pos3, rps16_pos3
10	GTR + G	lhbA_pos3, matK_pos2, ndhF_pos1, ndhF_pos2, petG_pos3, psbL_pos2, rpl20_pos3, rpl32_pos1, rps16_pos2, rps18_pos3, ycf3_pos3
11	GTR + I + G	ndhF_pos3

Supplementary Table S3. Log likelihoods of branch models for the 18 genes retained in the *Sciaphila* plastome (note that the trans-spliced exons of *rps12* are treated operationally as two genes below; see text for further details).

Gene	Model	lnL ^a	LRT ^b	<i>P/P</i> -corrected ^c
3'- <i>rps12</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.149$	-610.263		
	M1: $\omega_{\text{MHT}} = 0.202, \omega_{\text{green}} = 0.115$	-609.869	0.789	--/--
5'- <i>rps12</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.150$	-506.460		
	M1: $\omega_{\text{MHT}} = 0.312, \omega_{\text{green}} = 0.115$	-506.460	2.672	--/--
<i>accD</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.309$	-8167.290		
	M1: $\omega_{\text{MHT}} = 0.255, \omega_{\text{green}} = 0.316$	-8166.681	1.218	--/--
<i>clpP</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.174$	-2868.960		
	M1: $\omega_{\text{MHT}} = 0.288, \omega_{\text{green}} = 0.154$	-2866.248	5.423	* / *
<i>matK</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.367$	-12771.087		
	M1: $\omega_{\text{MHT}} = 0.491, \omega_{\text{green}} = 0.358$	-12769.319	3.536	--/--
<i>rpl2</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.252$	-2303.569		
	M1: $\omega_{\text{MHT}} = 0.280, \omega_{\text{green}} = 0.235$	-2303.389	0.360	--/--
<i>rpl14</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.111$	-1630.594		
	M1: $\omega_{\text{MHT}} = 0.240, \omega_{\text{green}} = 0.096$	-1627.974	5.240	* / *
<i>rpl16</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.169$	-2310.496		
	M1: $\omega_{\text{MHT}} = 0.093, \omega_{\text{green}} = 0.185$	-2308.459	4.075	* / --
<i>rpl20</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.353$	-1930.838		
	M1: $\omega_{\text{MHT}} = 0.313, \omega_{\text{green}} = 0.360$	-1930.759	0.158	--/--
<i>rpl36</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.103$	-522.304		
	M1: $\omega_{\text{MHT}} = 0.100, \omega_{\text{green}} = 0.103$	-522.303	0.001	--/--
<i>rps2</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.183$	-3730.279		
	M1: $\omega_{\text{MHT}} = 0.258, \omega_{\text{green}} = 0.171$	-3728.948	2.663	--/--
<i>rps3</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.178$	-3847.162		
	M1: $\omega_{\text{MHT}} = 0.224, \omega_{\text{green}} = 0.173$	-3846.696	0.931	--/--
<i>rps4</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.174$	-3056.894		
	M1: $\omega_{\text{MHT}} = 0.211, \omega_{\text{green}} = 0.168$	-3056.556	0.677	--/--
<i>rps7</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.330$	-1147.401		
	M1: $\omega_{\text{MHT}} = 0.611, \omega_{\text{green}} = 0.203$	-1144.219	6.364	* / *
<i>rps8</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.259$	-2262.744		
	M1: $\omega_{\text{MHT}} = 0.403, \omega_{\text{green}} = 0.244$	-2261.666	2.156	--/--
<i>rps11</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.097$	-2310.140		
	M1: $\omega_{\text{MHT}} = 0.129, \omega_{\text{green}} = 0.093$	-2309.673	0.933	--/--
<i>rps14</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.218$	-1449.355		
	M1: $\omega_{\text{MHT}} = 0.138, \omega_{\text{green}} = 0.233$	-1448.617	1.400	--/--
<i>rps18</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.214$	-1416.231		
	M1: $\omega_{\text{MHT}} = 0.192, \omega_{\text{green}} = 0.217$	-1416.198	0.065	--/--
<i>rps19</i>	M0: $\omega_{\text{MHT}} = \omega_{\text{green}} = 0.160$	-1249.963		
	M1: $\omega_{\text{MHT}} = 0.111, \omega_{\text{green}} = 0.171$	-1249.468	0.320	--/--

Abbreviations for ω ratios: ω_{MHT} = *Sciaphila* and ω_{green} = green outgroups.

^a Log likelihood of the data for the model.

^b Log likelihood ratio test statistic $-2(\ln L \text{ M0} - \ln L \text{ M1})$ to evaluate differences in model fit.

^c *P*-values for uncorrected/Bonferroni corrected χ^2 tests, where * = $P < 0.05$ and dashes (--) indicates not significant.

Supplementary Table S4. Likelihoods of branch-site models for the 18 genes retained in the *Sciaphila* plastome. “Staggered” refers to analyses performed on a realigned matrix for *accD*, *rpl20* and *rps18* (note that the trans-spliced exons of *rps12* are treated operationally as two genes below; see text for further details).

Gene	LRT ^a	<i>P/P</i> corrected ^b	LRT (staggered)	<i>P/P</i> -corrected (staggered)
3'- <i>rps12</i>	0	--/--		
5'- <i>rps12</i>	1.259	--/--		
<i>accD</i>	18.740	*** / ***	2.679	--/--
<i>clpP</i>	0	--/--		
<i>matK</i>	2.095	--/--		
<i>rpl2</i>	0	--/--		
<i>rpl14</i>	0.004	--/--		
<i>rpl16</i>	0	--/--		
<i>rpl20</i>	10.480	** / **	0	--/--
<i>rpl36</i>	0	--/--		
<i>rps2</i>	0	--/--		
<i>rps3</i>	0	--/--		
<i>rps4</i>	0.207	--/--		
<i>rps7</i>	0.124	--/--		
<i>rps8</i>	0	--/--		
<i>rps11</i>	0	--/--		
<i>rps14</i>	0	--/--		
<i>rps18</i>	3.887	* / --	0	--/--
<i>rps19</i>	0	--/--		

^a Log likelihood ratio test statistic $-2(\ln L_{H0} - \ln L_{H1})$ to evaluate differences in model fit.

^b *P*-values for uncorrected/Bonferroni corrected χ^2 tests, where * = $P < 0.05$, ** = $P < 0.01$, *** = $P < 0.001$ and dashes (--) indicates not significant.