



Supplement

The following supplementary materials are available for this article: Liu, S.-H., C.-C. Huang, C.-K. Liao. 2021. Rediscovery of an ‘extinct’ species *Scleria sumatrensis* Retz. in Taiwan using both morphological and molecular authentications. *Taiwania* 66(3): 398-407. Doi: 10.6165/ta.2021.66.398

#NEXUS

BEGIN TAXA;

TITLE Taxa;
DIMENSIONS NTAX=29 NCHAR=2917;
FORMAT DATATYPE = DNA GAP = - MISSING = ?;
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Bisboeckelera_microcephala

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S_terrestris CGTAGGTGAACCTGCGGAAGGATCATTGTCCG--
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END;
begin trees;
tree ML = [&R]
(Bisboeckelera_microcephala:0.024119,(S_sphacelata:0.053128,(((S_scabra:0.041378,(S_melanomphala:0.044936,(S_foliola:0.047753,(S_naumanniana:0.017156,(((S_terrestris:0.00469,(S_scribiculata:0.003165,(S_kerrii:0.005099,S_oblata:0.007704)[&label=44]:5.17E-4)[&label=27]:3.79E-4)[&label=59]:4.62E-



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tree BI = [&U] (Bisboeckelera_microcephala[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.0253458377,length_median=0.0254710821,length_95%HPD={0.0174454898,0.0344058131}]:0.025471,Calyptrocarya_glomerulata[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.0459432518,length_median=0.0450639159,length_95%HPD={0.0341234181,0.057283297}]:0.045064,((((((((S_baronii[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.0146549326,length_median=0.0144861543,length_95%HPD={0.00912382232,0.0205364127}]:0.014486,((S_latifolia[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.0108369134,length_median=0.0106841483,length_95%HPD={0.00692596006,0.0150683989}]:0.010684,S_splitgerberiana[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.0079639365,length_median=0.00779908473,length_95%HPD={0.00453565846,0.0111239769}]:0.007799)[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.00480561082,length_median=0.00455364842,length_95%HPD={0.00215913325,0.0082138311}]:0.004554,S_microcarpa[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.0210130066,length_median=0.0206636465,length_95%HPD={0.0152013473,0.0273010168}]:0.020664)[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.00580798441,length_median=0.0056301798,length_95%HPD={0.00275180818,0.0094192743}]:0.00563)[&prob=0.969194313,prob_stddev=0.0100536509,prob_range={0.962085308,0.976303318},prob(percent)="97",prob+-sd="97+-1",length_mean=0.00277636978,length_median=0.00257781521,length_95%HPD={3.42592954E-4,0.00552750517}]:0.002578,((S_ciliaris[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.00589856132,length_median=0.00569231746,length_95%HPD={0.00293418372,0.00904196746}]:0.005692,(S_polycarpa[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.0129293652,length_median=0.0123468981,length_95%HPD={0.00635684811,0.0207923014}]:0.012347,(S_purpurascens[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.00396425252,length_median=0.00396341136,length_95%HPD={0.0015632844,0.00662779143}]:0.003963,(((S_sumatrensis_1[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.00170892504,length_median=0.00154192482,length_95%HPD={1.42011682E-4,0.00344115866}]:0.001542,S_sumatrensis_2[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+-0",length_mean=4.2012673E-4,length_median=2.95553893E-4,length_95%HPD={3.06245496E-7,0.00128117556}]:2.96E-4)[&prob=0.54028436,prob_stddev=0.0134048679,prob_range={0.530805687,0.549763033},prob(percent)="54",prob+-sd="54+-1",length_mean=6.95500708E-4,length_median=5.56690283E-4,length_95%HPD={4.9584168E-6,0.00197650203}]:5.57E-4,S_sumatrensis_4[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=7.22790817E-4,length_median=5.99224478E-4,length_95%HPD={1.20477796E-5,0.00177687012}]:5.99E-4)[&prob=0.696682464,prob_stddev=0.0402146037,prob_range={0.668246445,0.725118483},prob(percent)="70",prob+-sd="70+-4",length_mean=8.25247904E-4,length_median=6.86328029E-4,length_95%HPD={2.23472857E-5,0.00199332499}]:6.86E-4,(S_sumatrensis_3[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=8.6324486E-4,length_median=7.47509876E-4,length_95%HPD={3.51641855E-5,0.00213855754}]:7.48E-4,S_sumatrensis_5[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=8.27506692E-4,length_median=6.78427498E-4,length_95%HPD={1.30576469E-5,0.00203498922}]:6.78E-4)[&prob=0.751184834,prob_stddev=0.0167560849,prob_range={0.739336493,0.763033175},prob(percent)="75",prob+-sd="75+-2",length_mean=7.23590129E-4,length_median=5.75322516E-4,length_95%HPD={4.85420339E-6,0.0017366408}]:5.75E-4,S_sumatrensis[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.00146985191,length_median=0.00130186763,length_95%HPD={2.74948386E-4,0.0031069844}]:0.001302)[&prob=1.0,prob_stddev=0.0,prob_range={1.0,1.0},prob(percent)="100",prob+-sd="100+",length_mean=0.0106561473,length_median=0.0103843825,length_95%HPD={0.00722258545,0.0159355764}]:0.010384)[&prob=0.765402844,prob_stddev=0.0167560849,prob_range={0.753554502,0.777251185},prob(percent)="77",prob+-sd="77+-2",length_mean=0.00216863344,length_median=0.00193080268,length_95%HPD={2.12838416E-5,0.004819538}]:0.001931)[&prob=0.997630332,prob_stddev=0.00335121697,prob_range={0.995260664,1.0},prob(percent)="100",prob+-sd="100+-0",length_mean=0.00406959963,length_median=0.00395726862,length_95%HPD={9.67690789E-4,0.00685831802}]:0.003957)[&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```

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END;

```

```

## 1- 683 ITS
## 684-1828 ndhF
## 1829-2917 rps16

```

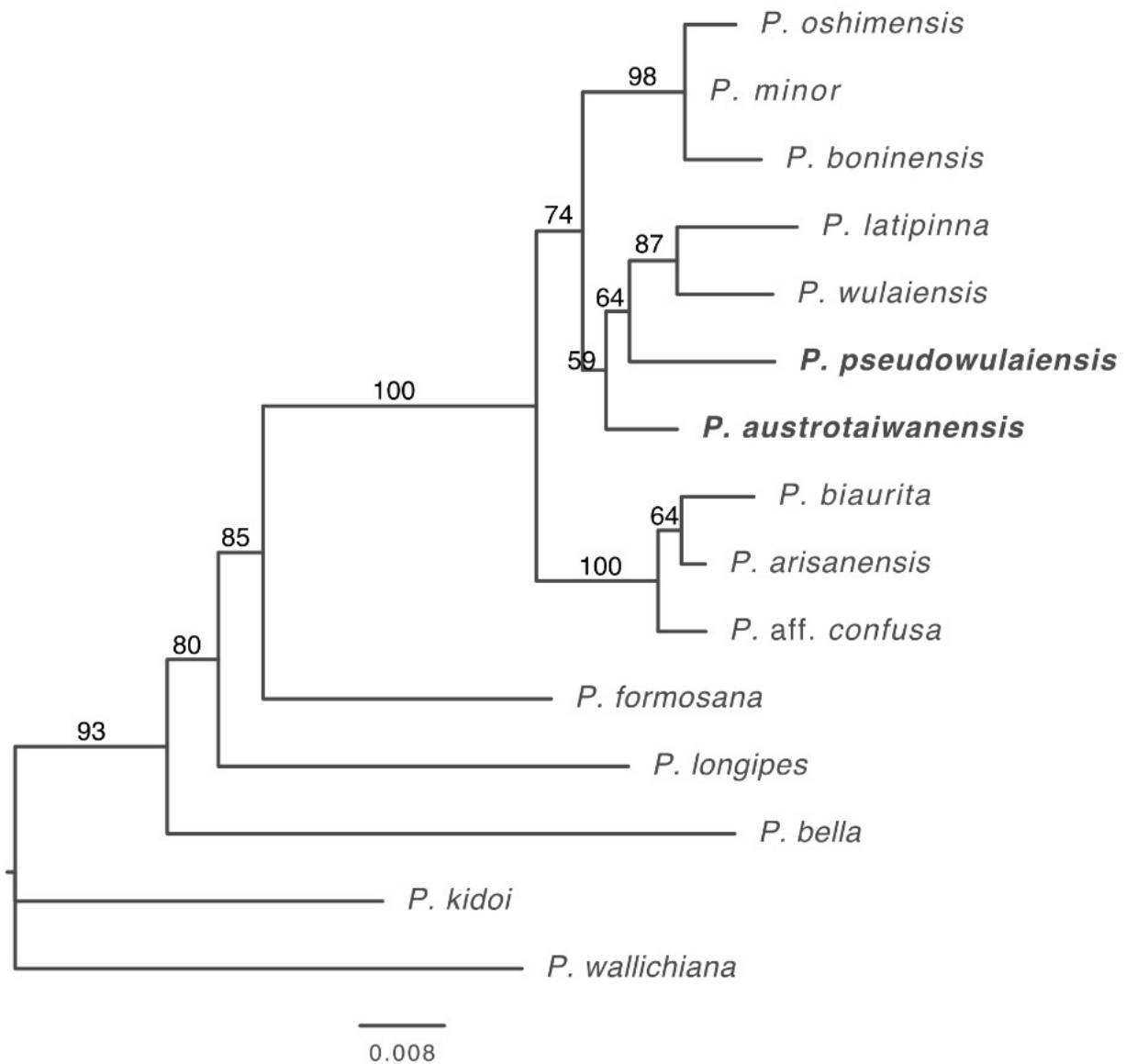


Fig. S2. Nuclear DNA phylogenetic tree of *Pteris austrotaiwanensis* and *P. pseudowulaiensis*, and related taxa in the *P. fauriei* group. Branch support is displayed in ML bootstrap. The dataset was based on *Knox* 3 gene (*KNOTTED*-like homeobox 3 genes), including 493 characters with 41 parsimony-informative sites. Outgroups were *Pteris kidoi* and *P. wallichiana*. The ML tree was inferred by GARLI; conducted by the same settings with the cpDNA tree. The log-likelihood score was -1570.5717. The two new species, *Pteris austrotaiwanensis* and *P. pseudowulaiensis* are phylogenetically separated from their morphologically similar species, *P. latipinna* and *P. wulaiensis*, respectively.