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Positions of carnivorous plant families in the current overall angiosperm phylogeny (Stevens, 2007; relationships within the Lamiales from Müller et al. 2006). © The Author [2008]. Published by Oxford University Press [on behalf of the Society for Experimental Biology].

**Fig. 2.1**
Overview of the cpDNA indicating the positions and organization of the regions studied. Boxes show introns (black), spacers (grey), and flanking genes or exons (ex) (white). LSC (large single copy region); IR_A: inverted repeat A; IR_B, inverted repeat B; SSC (small single copy region). ©2012 Institute of Botany, Chinese Academy of Sciences.

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**Fig. 3.4**
Bayesian phylogenies of Nepenthaceae, Droseraceae, Sarraceniaceae and Roridulaceae based on concatenated plastid markers.
Phylogenetic analysis are based on plastid (ITS and matK) sequence data with posterior probabilities >0.85. Bayesian phylogeny reconstruction obtained by posterior probabilities (BPP) for the nodes in the ML tree. GTR evolutionary model was implemented in MrBayes 3.2 with four chains during 100,000 generations and trees were sampled every 100 generations.

**Fig. 3.5**
Rel TimeTree chronogram for the combined dataset of matK and ITS showing divergence time estimation of Nepenthaceae. Divergence times for all branching points in the user-supplied calibrated topology were calculated using the Maximum Likelihood method based on the Tamura-Nei model. A discrete Gamma distribution was used to model evolutionary rate differences among sites [5 categories (+G, parameter = 2.0910)]. The rate variation model allowed for some sites to be evolutionarily invariable ([+I], 0.0000% sites). Numbers at nodes are median ages in million of years (MYA) with two internal calibration points Evolutionary analyses were conducted in MEGA7.
Fig. 3.6
Comparisons of intra and inter-specific variations among ITS, coxI, matK, rbcL, rps4 and atpB genes of the carnivorous plant families Nepenthaceae, Droseraceae, Sarraceniaceae, Lentibulariaceae and Roridulaceae. The grey and black bars represent the intra- and inter-specific variations, respectively. The thin, black lines indicate the smallest inter-specific variation. Names next to the dark bars indicate the closest species to that listed on the left.

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Fig. 3.8
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Alternative ancestral ranges of nodes (with frequency of occurrence) are shown in pie chart form. Bootstrap support values/Bayesian credibility values (PP) (50 % and higher) are indicated near the pie chart in the Bayesian tree. Colour key to possible ancestral ranges at different nodes represent other ancestral ranges. Biogeographical regions: A, Asia; B, Africa; C, Australasia; D, Europe; E, North America; F, South America; AB, Asia-Africa; ABC, Asia- Africa- Australasia; ABCD, Asia- Africa- Australasia-Europe.

Fig. 4.1 (a-c)
Drosera peltata
(a) Plant in natural habitat; (b) close up view of leaf (c) trapped insect and (d) whole plant.

Fig. 4.2 (a-d)
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Maximum Likelihood (ITS + rbcL) tree of family Droseraceae. *N. khasiana* and *S. flava* were taken as outgroups. Substitutions per site between taxon groups according to the model of best fit (GTR + Γ + I) determined with Modeltest in MEGA 7. Consensus ITS2 core secondary structures drawn in LOCARNA for representative *Drosera* species based on geographical distribution.

Fig. 4.4
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Colour codes represent phylogenetic nodes with percent probability scores. Bayesian phylogeny reconstruction obtained by posterior probabilities (BPP) for the nodes in the ML tree. GTR evolutionary model was implemented in MrBayes 3.2 with four chains during 50,000 generations and trees were sampled every 100 generations.

Fig. 4.5
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Fig. 4.6
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Fig. 4.7
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(a) Plant in natural habitat; (b) close up view of leaf (c) Bladders; bar-1mm and (d) whole plant.

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(a) Plant in natural habitat; (b) close up view of leaf (c) Bladders; bar-1mm and (d) whole plant.

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Fig. 5.4
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Fig. 5.5
Ancestral area reconstruction along with distribution world map of species belonging to Lentibulariaceae family using RASP (S-DIVA and BBM).
Alternative ancestral ranges of nodes (with frequency of occurrence) are shown in pie chart form. Bootstrap support values/Bayesian credibility values (PP) (50 % and higher) are considered in the overall Bayesian tree. Colour key to possible ancestral ranges at different nodes represent other ancestral ranges. *A. vesiculosa* and *D. capillaris* are taken as outgroups.