Note: These are the original figures of Wanntorp et al., Taxon 63:89-102, 2014. The networks had to be dropped on editorial advise.

## **Figure legends**

- **Fig. 1.** Distribution of *Hoya*. Circles mark the abundance of *Hoya* in each area (larger circle corresponds to a higher number of species in one area). Different colours correspond to clades I–VI in the text (Results): black = Clade I; yellow = Clade II; olive = Clade III; green = Clade IV; blue = Clade V; red = Clade VI. Further colours: purple = taxa with affinity to clades V and VI; white = taxa of ambiguous or unresolved systematic affinity; light green = Philippine sister taxa of Clade IV. Shown are also the climate diagrams for selected stations [32] within the distribution range of *Hoya*. The Köppen climate classification for each station is indicated following Kottek *et al.*[31].
- Fig. 2. Best-known ML trees based on matrices 1 and 2, including all analysed accessions. Overall, the plastid (left) and nuclear (right) trees found similar groups and clades as annotated with varying support. Colouring of terminals and clades refers to major clades and groups defined by the analyses of the combined data (matrix 3, Figs 3–4): dark grey = Clade I; yellow = Clade II; light and dark olive = Clade III; green = Clade IV; dark green = Clade J; turquoise = Clade M; blue and dark blue = Clade V; red = Clade VI; dark red = Clade P; pink = other members of Group 2. Numbers at branches indicate BS support based on 800 (matrix 1), respectively, 1000 BS (matrix 2) replicates. Individual taxa abbreviated by the first three letters of their names, rogue taxa in bold font. For some taxa (\*) only limited data is available so far, these have been excluded from further analyses.
- Fig. 3. Hoya phylogeny, Clade I–IV. Best-known ML tree based on the combined plastid (*trnT-trnL* and *trnH-psbA* intergenic spacers) and nuclear data set (ITS region, and 5'-41

ETS; matrix 3). Numbers at branches denote bootstrap support under ML (BS<sub>ML</sub>). Symbols left of species names show the distribution of each species: Open triangle, Himalayas and adjacent mountains of S. W. China; open rectangle, S. Asia and mainland S. E. Asia (S. W. India and Sri Lanka, Indo-Burma); open five-pointed star, S. China, Taiwan, Ryukyu and Kyushu islands, S. Japan (subtropical); open circle, Philippines; open hexagon, Sundaland; closed hexagon, Wallacea; closed circle, New Guinea; closed upside-down triangle, Melanesia and New Caledonia; closed ten-pointed star, Polynesian islands; closed sevenpointed star, Australia.

- Fig. 4. *Hoya* phylogeny, Clade V and VI and related taxa (Group 2). Detail of the best-known ML tree based on the combined plastid (*trnT-trnL* and *trnH-psbA* intergenic spacers) and nuclear data set (ITS region, and 5'-ETS; matrix 3). Numbers denote bootstrap support values under ML (BS<sub>ML</sub>). Symbols left of species names show the distribution of each species: Open triangle, Himalayas and adjacent mountains of S. W. China; open rectangle, S. Asia and mainland S. E. Asia (S. W. India and Sri Lanka, Indo-Burma); open five-pointed star, S. China, Taiwan, Ryukyu and Kyushu islands, S. Japan (subtropical); open circle, Philippines; open hexagon, Sundaland; closed hexagon, Wallacea; closed circle, New Guinea; closed upside-down triangle, Melanesia and New Caledonia; closed tenpointed star, (outer) Polynesian islands; closed seven-pointed star, Australia.
- Fig. 5. Best-known ML tree showing putative phylogenetic relationships between major clades of *Hoya* after all phylogenetically ambiguous taxa were excluded from the data set (matrix 4). Numbers at branches indicate ML-BS support based on 400 replicates (BS<sub>ML</sub>).

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Note the general increase in backbone support and the shift within Group 1 regarding the putative sister clade of Clade IV. Terminal subtrees have been collapsed for better visibility, the triangles reflect the dimensions of the collapsed subtrees. For branches with  $BS_{ML} < 95$ , competing splits are shown in the inlets; only such splits are shown that occurred at least in 15% of BS replicates. Taxa inflicting ambiguous signal regarding basal relationships within Clade V abbreviated by first three letters: KUH = H. *kuhlii*; OBS = H. *obscura*; SIP = H. *sipitangensis*; PUS = H. *pusilla*.

- Fig. 6. Phylogenetic relationships based on a matrix with as comprehensive as possible gene sampling, strongly limited taxon sampling, and adding further outgroup taxa from the Marsdenieae. A. Best-known ML tree, BS support (based on 1000 replicates) annotated along branches. B. Bipartition network based on the BS replicate sample, only bipartitions are shown that were found in >20% of the BS replicates. Note that even this most optimal dimensioned matrix (few taxa, many nucleotides) failed to resolve basal relationships in *Hoya* (grey-shadowed circles) and to unambiguously place *H. serpens* (pink-shadowed circle)
- Fig. 7. Competing and additive signals from nuclear and plastid data, illustrated using bipartition networks. A. Based on the combined *trnH-psbA* and *trnT-trnL* data (matrix 1);
  B. Based on the combined 5'-ETS and ITS data (matrix 2). Edge lengths are proportional to the number of BS replicates showing the respective phylogenetic split. For selected splits (coloured), absolute BS support values are given. Species clustering outside major and minor clades are abbreviated by the three first letters of their names.

- Fig. 8. Schematized median-joining networks illustrating general differentiation pathways in *Hoya*. A–C. Relatively variable/informative partitions. A. 5'-ETS. B. ITS1. C. *trn*T-*trn*L.
  D–E. Conserved/rather uninformative partitions. D. ITS2. E. *trnH-psbA* (only unambiguously alignable nucleotides considered).
- Fig. 9. Hoya biogeography. A. Distribution of Clade I-III. Dotted line shows the widespread distribution of *H. multiflora*; B. Distribution of Clade IV. Purple, distribution range of phylogenetically ambiguous species with affinities to Clade V and VI; C-D. Distribution of Clade V and VI in the IAA and adjacent areas of continental Asia and Australia. Arrows indicate potential migration routes.

















