

Ecography

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Supplementary material

1 **Appendix 1. Supplementary methods**

2 *Supermatrix phylogenetic reconstruction*

3 We first compiled a set list of all native vascular plant genera present in
4 Andalusia and North Morocco, based on specialized regional floras (Valdés et al. 1987,
5 2002; Blanca et al. 2009). Then, we conducted an exhaustive retrieval of DNA
6 sequences available in Genbank [accessed in September 2011]. We downloaded three
7 conserved chloroplastic gene regions (rbcL, matK, ndhF), plus 1 chloroplastic and two
8 nuclear fast-evolving DNA regions (trnL-F intergenic spacer, ITS1 and ITS2,
9 respectively). We selected those regions because they are broadly sampled across
10 plants. We included both conserved and non-conserved regions in order to be able to
11 resolve deep and shallow nodes. Fast-evolving regions were clustered in taxonomic
12 groups in order to avoid saturation problems (see below). In order to avoid overload of
13 missing data in the supermatrix, we only considered fast-evolving regions when at least
14 one of the genera within each family lacked available sequences for rbcL, matK and
15 ndhF markers. Because there was no data in Genbank for all the species of our list, we
16 decided to only recover sequences for one species of each genus, in order to obtain a
17 genus-level phylogeny, and later replace the tip-labels by polytomies of species. When
18 possible, we selected those species native to Andalusia and North Morocco. In the cases
19 where the six regions were not available for the same species, we retrieved sequences of
20 different species of the same genus, following the methodology of Roelants et al.
21 (2011). When several sequences for the same taxon and region were available, we
22 selected the longest and most recent one.

23 All sequences of each region were aligned using four different programs: Clustal
24 X (Thompson et al. 1994; Larkin et al. 2007), MAFFT (Kato et al. 2005), Kalign

25 (Lassmann and Sonnhammer 2005) and MUSCLE (Edgar 2004). We selected the best
26 alignment for each region with the multiple overlap score (MOS) implemented in
27 MUMSA (Lassmann and Sonnhammer, 2006). We also assessed the quality of the
28 obtained alignments computing the average overlap score (AOS) with MUMSA. An
29 AOS score < 0.5 indicates that the alignment is probably saturated by multiple
30 substitutions and thus it may be unreliable. In this case, we compartmentalized the
31 alignment by splitting the sequences in blocks going a step down in the taxonomic
32 hierarchy, and performed the alignment again. The array of taxonomic hierarchies
33 considered was division, order and family. The fast-evolving regions trnL-F, ITS 1 and
34 ITS 2 were clustered at the family level in all cases. When a marker could not be
35 aligned reliably at the family level (e.g. ITS 1 and ITS 2 for Santalaceae) we decided to
36 remove these sequences. For each region, we removed ambiguous or poorly aligned
37 blocks using the software trimAl (Capella-Gutiérrez et al. 2009), and finally
38 concatenated the resulting alignments into a single supermatrix with the software
39 FASconCAT (Kueck and Meusemann 2010).

40 Phylogenetic inference was performed using Maximum Likelihood (ML) with the
41 program RaxML (Stamatakis 2006; Stamatakis et al. 2008) on the CIPRES on-line
42 portal (Miller et al. 2010), applying the GTRCAT model with partitions defined for
43 each region, and a prior tree constraint at the family level based on consensus
44 knowledge (Davies et al. 2004; Moore et al. 2010; Smith et al. 2011). The ML tree that
45 yielded the highest likelihood was then dated (i.e. branch lengths were converted to
46 absolute evolutionary age) using penalized-likelihood as implemented in r8s (Sanderson
47 2003). Node support was estimated using bootstrap values. Nodes with less than 50%
48 support were collapsed into soft polytomies. Multiple fossils were used to calibrate the
49 tree (see the complete list in Table S1).

50 **Table A1.** Summary of the fossil data used for calibration. All fossils were used as
 51 minimum age constraints, except *, which was used as a fixed age.

| Clade | Fossil name | Age (mya) | References |
|---------------------|--|-----------|--|
| Alismatales | Tofieldiaceae/ <i>Dicolpopollis</i> | 69.5 | Chmura, C. A. 1973 |
| Eudicots * | Unnamed | 125 | Friis, E. M. et al. 2006a |
| Apocynaceae | Unnamed | 53.2 | Magallón, S. et al. 1999 |
| Araliaceae | Unnamed | 69.5 | Magallón, S. et al. 1999 |
| Asparagales | <i>Liliacidites</i> cf. <i>intermedius</i> and <i>L.</i> cf. <i>kaitangataensis</i> | 93 | Dettmann, M. E. 1973; Raine, J. I. et al. 2006 |
| Asterales | Menyanthaceae pollen | 29.3 | Magallón, S. et al. 1999 |
| Boraginaceae | Unnamed | 53.2 | Magallón, S. et al. 1999 |
| Brassicales | <i>Dressiantha</i> | 85 | Gandolfo, M. A. et al. 1998 |
| Buxales | Unnamed | 98 | Drinnan, A. N. et al. 1991 |
| Caryophyllales | Unnamed (Caryophyllales) | 83.5 | Collinson, M. E. et al. 1993 |
| Convolvulaceae | Unnamed | 53.2 | Magallón, S. et al. 1999 |
| Cucurbitaceae | Unnamed | 58.5 | Magallón, S. et al. 1999 |
| Cupressaceae | <i>Cupressinocladus interruptus</i> | 99.6 | Stockey, R. A. et al. 2005 |
| Dipsacales | Caprifoliaceae | 53.2 | Magallón, S. et al. 1999 |
| Ericaceae | Ericaceae s. l. | 89.5 | Magallón, S. et al. 1999 |
| Ericales | Unnamed | 91.2 | Nixon, K. C. and Crepet, W. L. 1993 |
| Euphorbiaceae | Euphorbiaceae pollen | 58.5 | Magallón, S. et al. 1999 |
| Euphyllophyta | Unnamed | 365 | Rothwell, G. W. and Scheckler, S. E. 1988 |
| Fabaceae | Unnamed | 56 | Magallón, S. et al. 1999 |
| Fabales | Unnamed (Fabales) | 59.9 | Herendeen, P. S. and Crane, P. R. 1992 |
| Fagales | <i>Tenerina</i> sp. | 96 | Friis, E. M. et al. 2006b |
| <i>Fumana</i> | Unnamed | 28 | Palibin, I. V. 1909 |
| Geraniaceae | Geraniaceae pollen | 7.8 | Magallón, S. et al. 1999 |
| Gymnosperms | <i>Emporia lockardii</i> | 290 | Mapes, G. and Rothwell, G. W. 1984; 1991 |
| <i>Helianthemum</i> | Unnamed | 11 | Menke, B. 1976; Naud, G. and Suc. J. P. 1975 |
| Lamiales | <i>Fraxinus wilcoxiana</i> | 44.3 | Call, V. B. and Dilcher, D. L. 1992 |
| Laurales | Unnamed (Laurales) | 108.8 | Crane, P. R. et al. 1994 |
| Malpighiales | <i>Paleoclusia</i> sp. | 89 | Crepet, W. L. and Nixon, K. C. 1998 |
| Malvales | Unnamed (Malvales) | 69.7 | Wolfe, J. A. 1976 |

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| Myrtales | <i>Esqueiria futabensis</i> | 88.2 | Takahashi, M. et al. 1999 |
| Orchidaceae | <i>Meliorchis caribea</i> | 15 | Ramírez, S. R. et al. 2007 |
| Osmundaceae | <i>Grammatopteris</i> sp., <i>Rastropteris</i> sp. | 299 | Galtier, J. et al. 2001; Miller, C. N. 1971; Phipps, C. J. et al. 1998; Rößler, R. and Galtier, J. 2002 |
| Phyllanthaceae | <i>Phyllanthus</i> type (pollen) | 33.7 | Zaklinskaya, E. D. et al. 1978 |
| <i>Pilularia-Marsilea</i> | <i>Regnellidium upatoensis</i> | 83 | Lupia, R. et al. 2000; Pryer, K. M. 1999 |
| Pinaceae | Unnamed Pinaceae | 225 | Miller, C. N. 1999 |
| Poales | <i>Restio</i> sp. | 68.1 | Muller, J. 1981 |
| Polypodiaceae | <i>Protodrynaria</i> sp. | 34 | Van Uffelen, G. A. 1991 |
| Pteridaceae | <i>Pteris</i> sp. | 93 | Krassilov, V. and Bacchia, F. 2000 |
| Ranunculideae | Menispermaceae | 69.5 | Magallón, S. et al. 1999 |
| Rosaceae | Unnamed | 44.3 | Magallón, S. et al. 1999 |
| Rutaceae | Unnamed (Rutaceae) | 67.2 | Magallón, S. et al. 1999 |
| <i>Salix-Populus</i> | <i>Pseudosalix handleyi</i> | 48 | Boucher, L. D. et al. 2003 |
| Santalales | Olacaceae | 53.2 | Magallón, S. et al. 1999 |
| Sapindales | Unnamed | 65 | Knobloch, E. D. and Mai, D. H. 1986 |
| Saxifragales | <i>Divisestylus</i> sp. | 89.3 | Hermesen, E. J. et al. 2003 |
| <i>Tuberaria</i> | Unnamed | 5.3 | Menke, B. 1976; Naud, G. and Suc, J. P. 1975 |
| Vascular plants | Zosterophyllophytes and <i>Baragwanathia</i> sp. | 421 | Garrat, M. J. and Rickards, R. B. 1987; Hueber, F. M. 1992; Tims, J. D and Chambers, T. C. 1984; |

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