SUPPLEMENTARY DATA

Article title: Time-calibrated phylogenies reveal mediterranean and pre-mediterranean origin of the thermophilous vegetation of the Canary Islands

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The following Supplementary data are available for this article:

Figs. S1-S13. Majority rule consensus trees of the 13 plant groups analysed in this study resulting from applying Bayesian Inference in MrBayes and using previously published phylogenetic datasets (see Table 1) in combination with newly generated sequences (see Table S2).

Figs. S14-S26. Time-calibrated phylogenies of the 13 plant groups analysed in this study obtained in BEAST using previously published phylogenetic datasets (see Table 1) in combination with newly generated sequences (see Table S2).

Figs. S27-S39. Biogeographic reconstructions of ancestral ranges of the 13 plant groups analysed in this study resulting from applying dispersal–extinction–cladogenesis (DEC) analyses using the BioGeoBEARS R package.

Table S1. Information extracted from the literature and obtained in this study for the 43 plant lineages including thermophilous species from the Canary Islands (Macaronesia) for hypothesis testing.

Table S2. Studied taxa and their corresponding collection code, voucher information, island (archipelado or country), locality, collection date, collector's name (leg), DNA sequenced regions and GenBank accesion numbers.

Table S3. Primers and PCR cycles used for sequencing DNA regions of the 13 plant groups analyzed in this study (genera, seldom families).

Table S4. Detailed information (phylogenetic relationships and colonization times) of the 16 lineages with thermophilous species recovered by BEAST analyses of the 13 plant groups of this study.

Table S5. Results of the ancestral area reconstruction under the dispersal-extinction-cladogenesis (DEC) analyses performed on the 13 newly generated time-calibrated phylogenies including thermophilous species in the Canary Islands analysed in this study.

Methods S1. Details of the maximum likelihood phylogenetic analyses performed in this study.

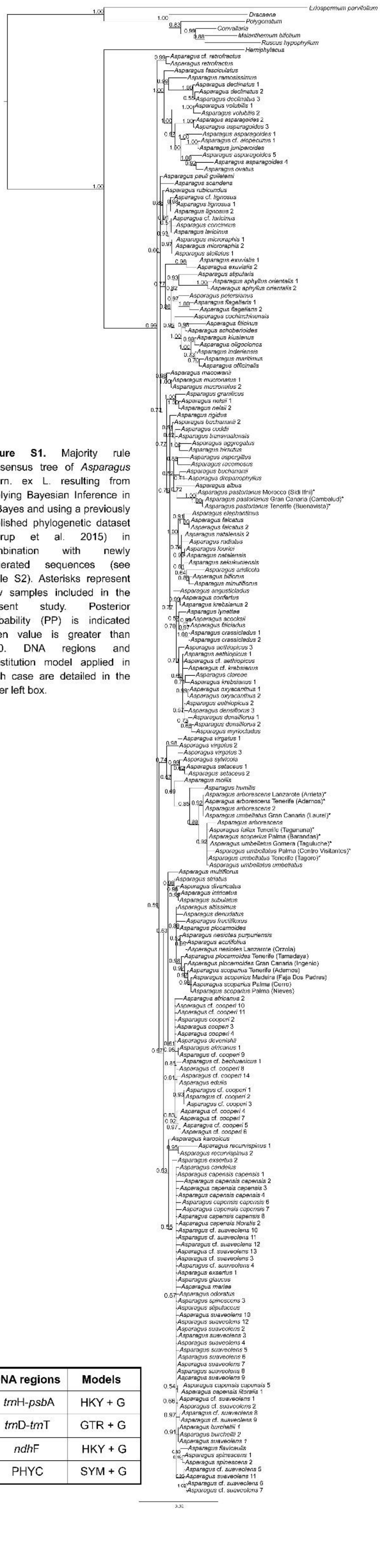


Figure S1. Majority rule consensus tree of *Asparagus* Tourn. ex L. resulting from applying Bayesian Inference in MrBayes and using a previously published phylogenetic dataset (Norup et al. 2015) in combination with newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA regions	Models
*trn*H-*psb*A	HKY + G
*trn*D-*trn*T	GTR + G
*ndh*F	HKY + G
PHYC	SYM + G

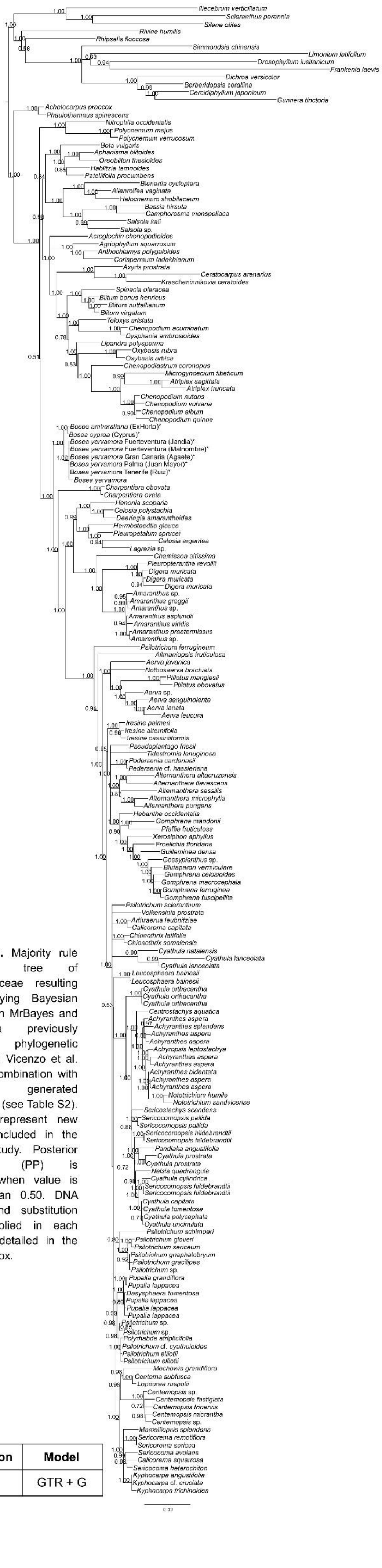


Figure S2. Majority rule consensus tree of Amaranthaceae resulting from applying Bayesian Inference in MrBayes and using a previously published phylogenetic dataset (Di Vicenzo et al. 2018) in combination with newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA region	Model
*mat*K	GTR + G

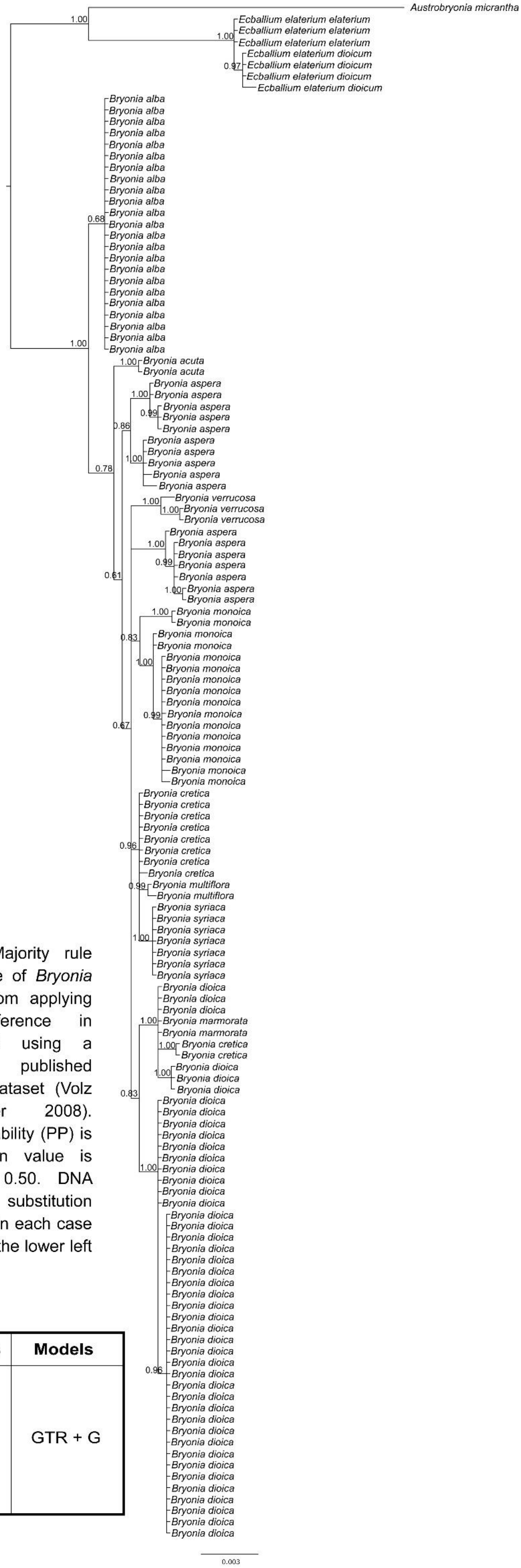


Figure S3. Majority rule consensus tree of *Bryonia* L. resulting from applying Bayesian Inference in MrBayes and using a previously published phylogenetic dataset (Volz and Renner 2008). Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA regions	Models
ITS LFY *trn*L *trn*L-*trn*F *psb*A-*trn*H *trn*H2 *trn*R-*atp*A	GTR + G

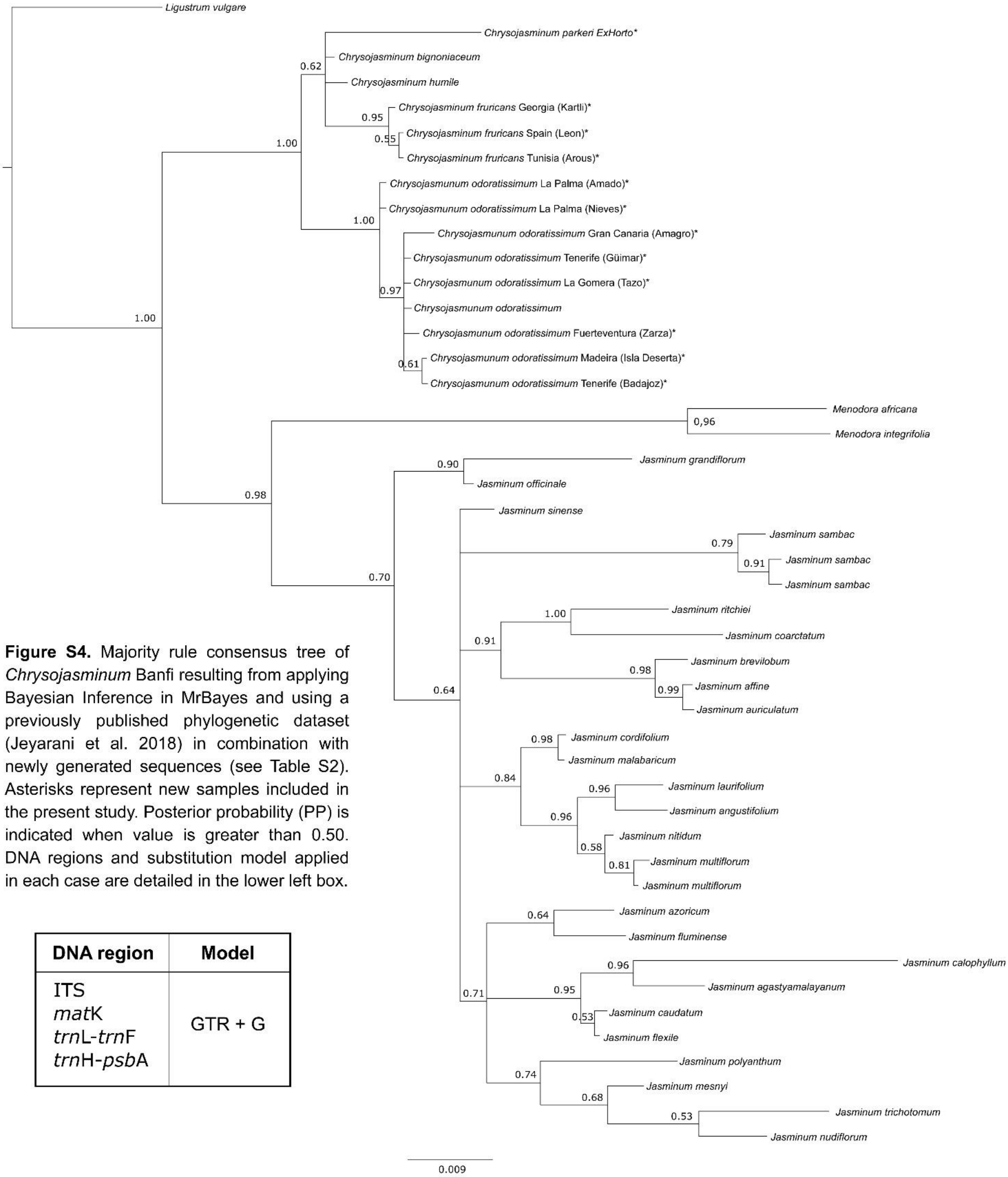


Figure S4. Majority rule consensus tree of *Chrysojasminum* Banfi resulting from applying Bayesian Inference in MrBayes and using a previously published phylogenetic dataset (Jeyarani et al. 2018) in combination with newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA region	Model
ITS *mat*K *trn*L-*trn*F *trn*H-*psb*A	GTR + G

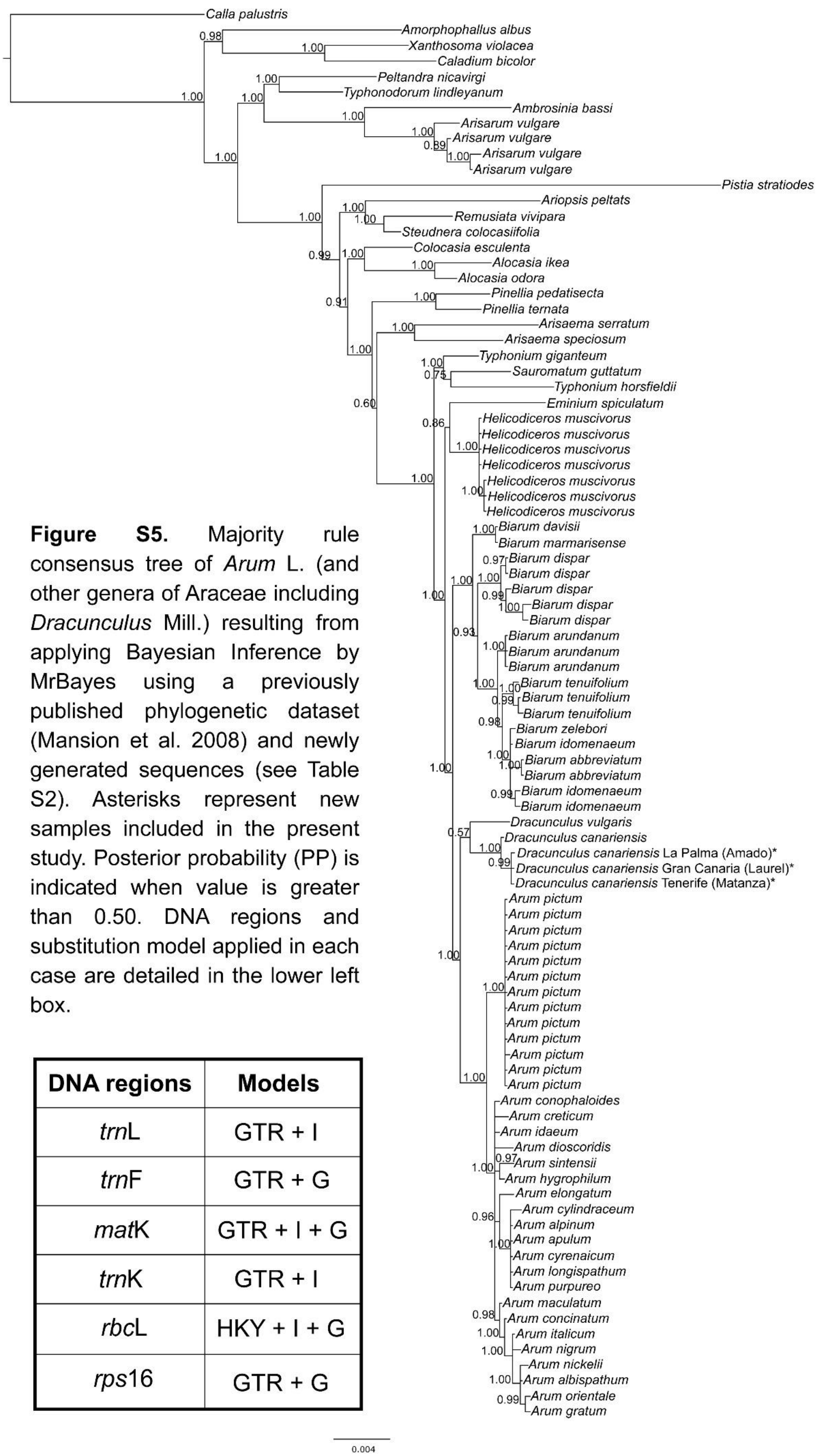


Figure S5. Majority rule consensus tree of *Arum* L. (and other genera of Araceae including *Dracunculus* Mill.) resulting from applying Bayesian Inference by MrBayes using a previously published phylogenetic dataset (Mansion et al. 2008) and newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA regions	Models
*trn*L	GTR + I
*trn*F	GTR + G
*mat*K	GTR + I + G
*trn*K	GTR + I
*rbc*L	HKY + I + G
*rps*16	GTR + G

Figure S6. Majority rule consensus tree of *Ephedra* Tourn. ex L. resulting from applying Bayesian Inference by MrBayes using a previously published phylogenetic dataset (Ickert-Bond et al. 2009) and newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower right box.

DNA regions	**Model**
26S 18S ITS *atp*B *rbc*L *mat*K *rps*4 *psb*A-*trn*H *trn*L *trn*L–*trn*F	GTR + G

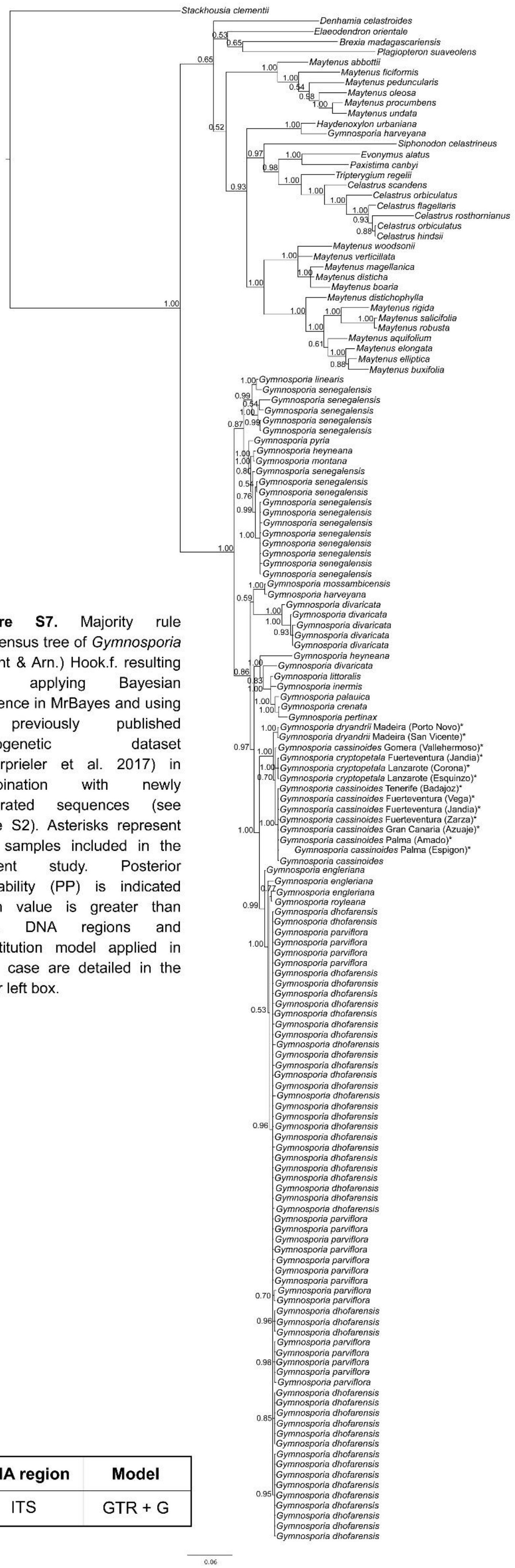


Figure S7. Majority rule consensus tree of *Gymnosporia* (Wight & Arn.) Hook.f. resulting from applying Bayesian Inference in MrBayes and using a previously published phylogenetic dataset (Oberprieler et al. 2017) in combination with newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA region	Model
ITS	GTR + G

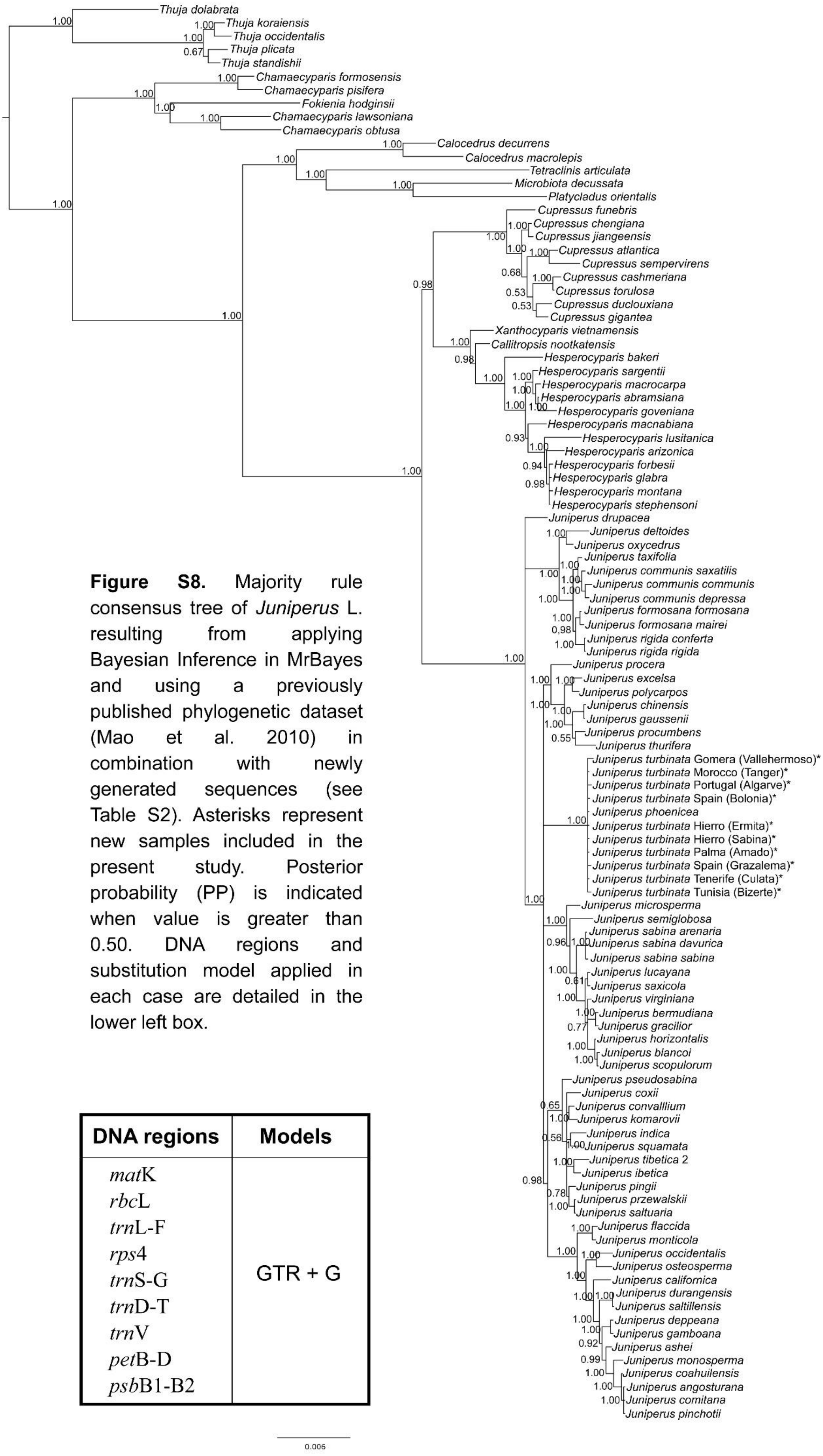


Figure S8. Majority rule consensus tree of *Juniperus* L. resulting from applying Bayesian Inference in MrBayes and using a previously published phylogenetic dataset (Mao et al. 2010) in combination with newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA regions	Models
*mat*K *rbc*L *trn*L-F *rps*4 *trn*S-G *trn*D-T *trn*V *pet*B-D *psb*B1-B2	GTR + G

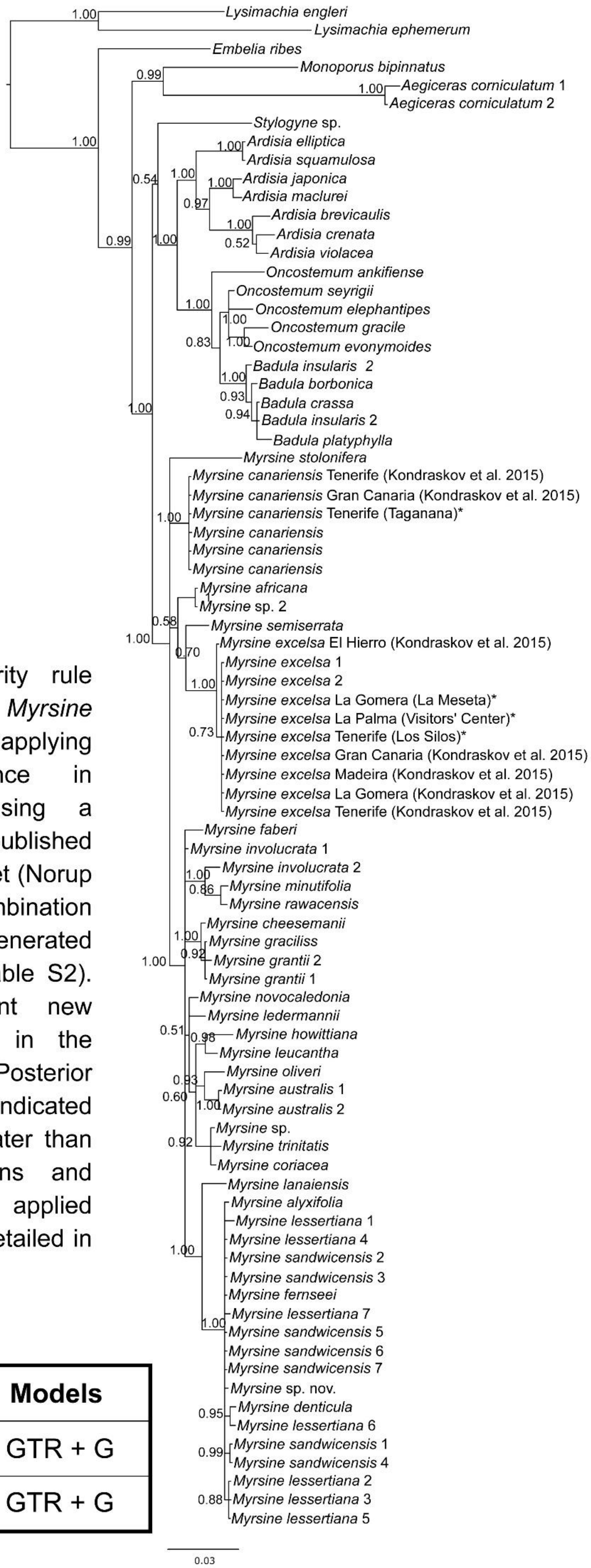


Figure S9. Majority rule consensus tree of *Myrsine* L. resulting from applying Bayesian Inference in MrBayes and using a previously published phylogenetic dataset (Norup et al. 2015) in combination with newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA regions	Models
ITS	GTR + G
ETS	GTR + G

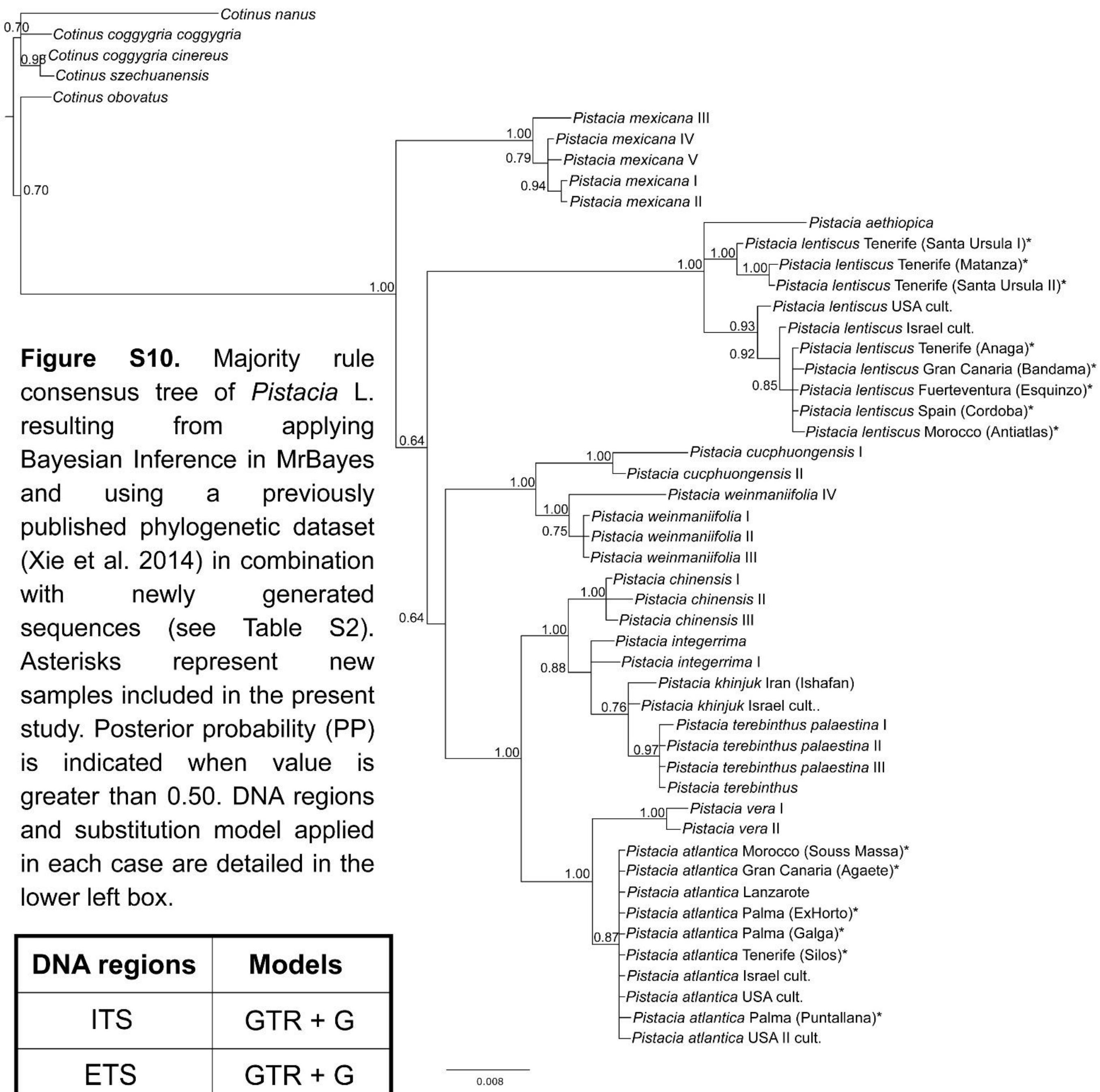
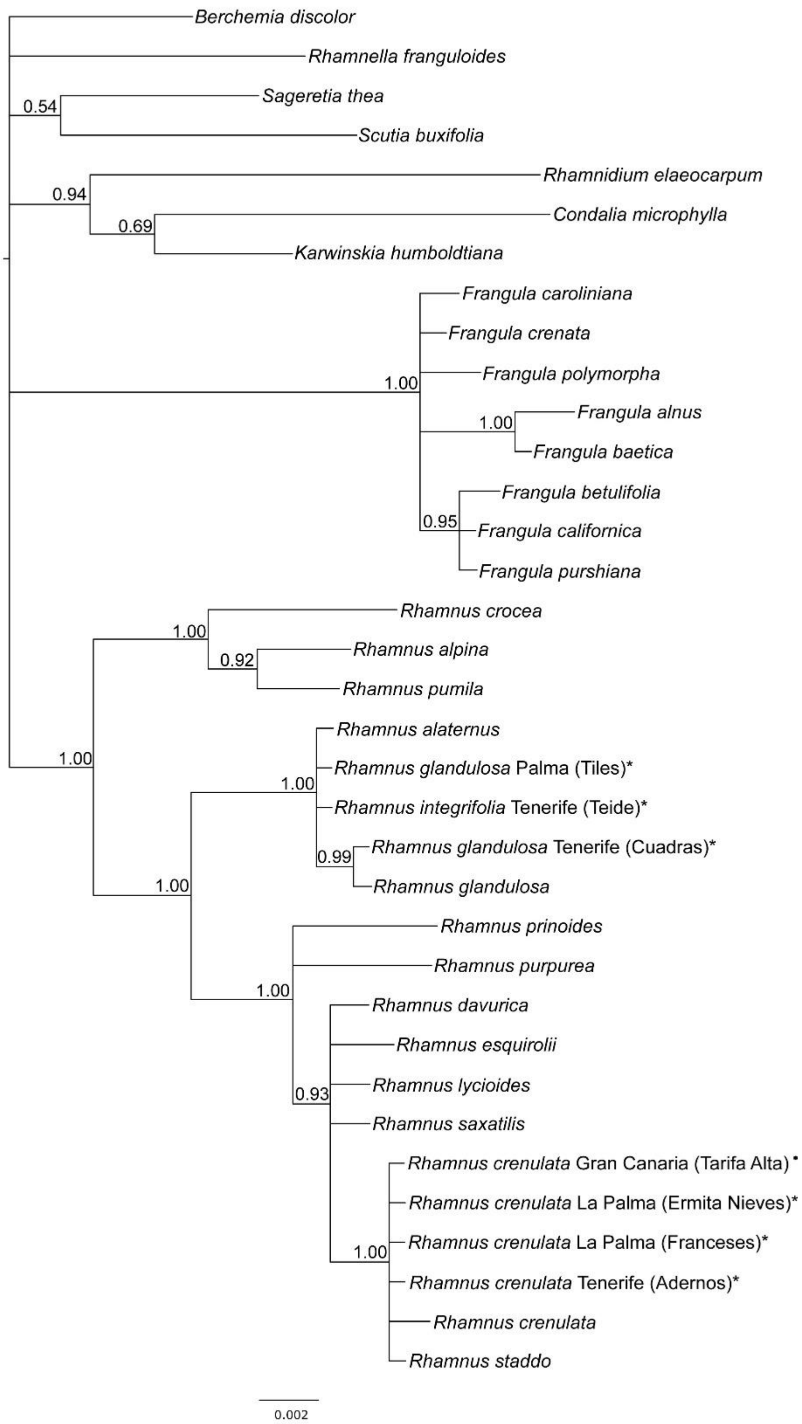


Figure S10. Majority rule consensus tree of *Pistacia* L. resulting from applying Bayesian Inference in MrBayes and using a previously published phylogenetic dataset (Xie et al. 2014) in combination with newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA regions	Models
ITS	GTR + G
ETS	GTR + G

Figure S11. Majority rule consensus tree of *Rhamnus* L. resulting from applying Bayesian Inference in MrBayes and using a previously published phylogenetic dataset (Bolmgren and Oxelman 2004) in combination with newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower left box.



DNA regions	Models
ITS	GTR + G
*trn*L-*trn*F	GTR + G

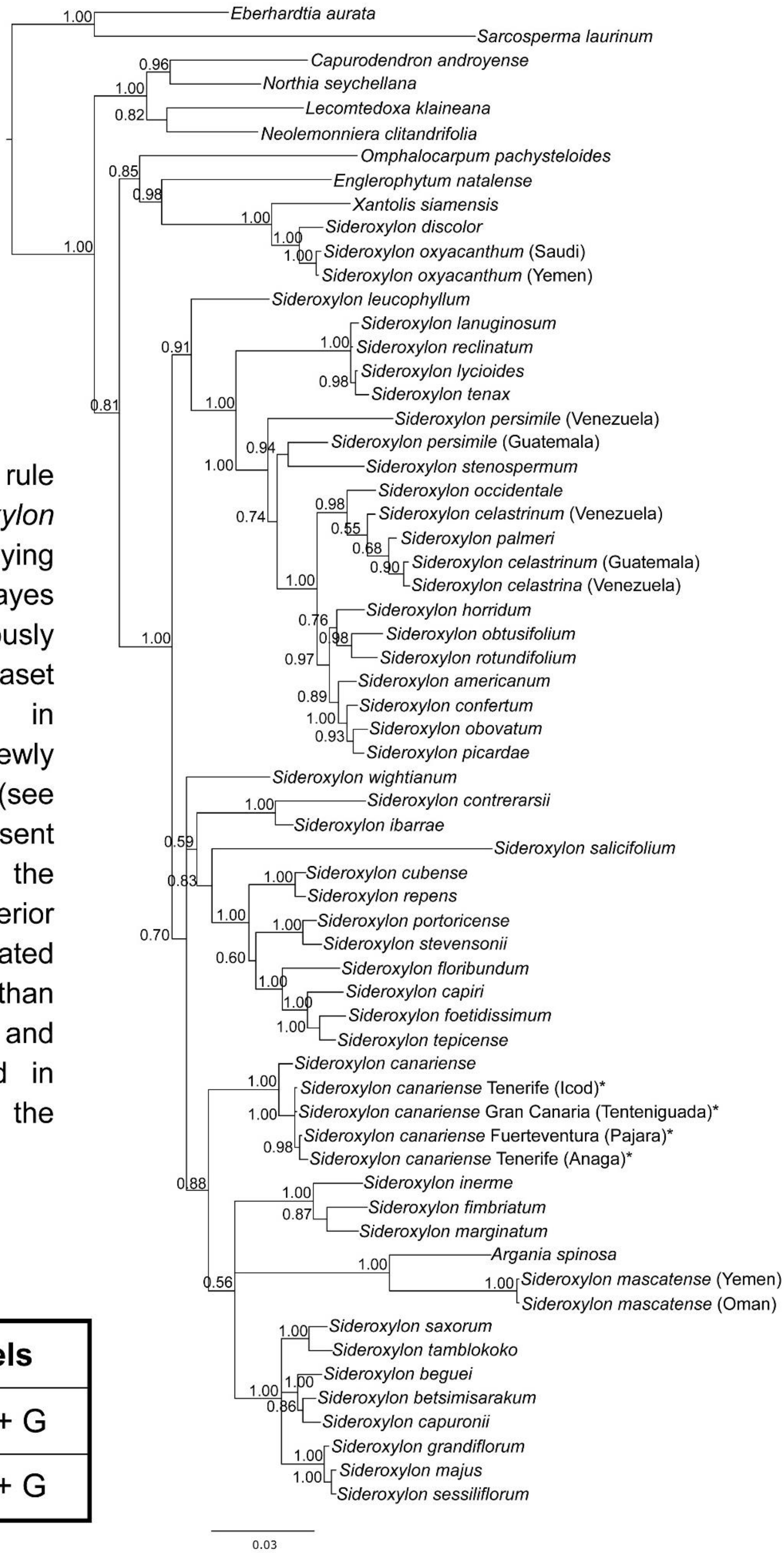


Figure S12. Majority rule consensus tree of *Sideroxylon* L. resulting from applying Bayesian Inference in MrBayes and using a previously published phylogenetic dataset (Stride et al. 2014) in combination with newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA regions	Models
ITS	GTR + G
*trn*H-*psb*A	GTR + G

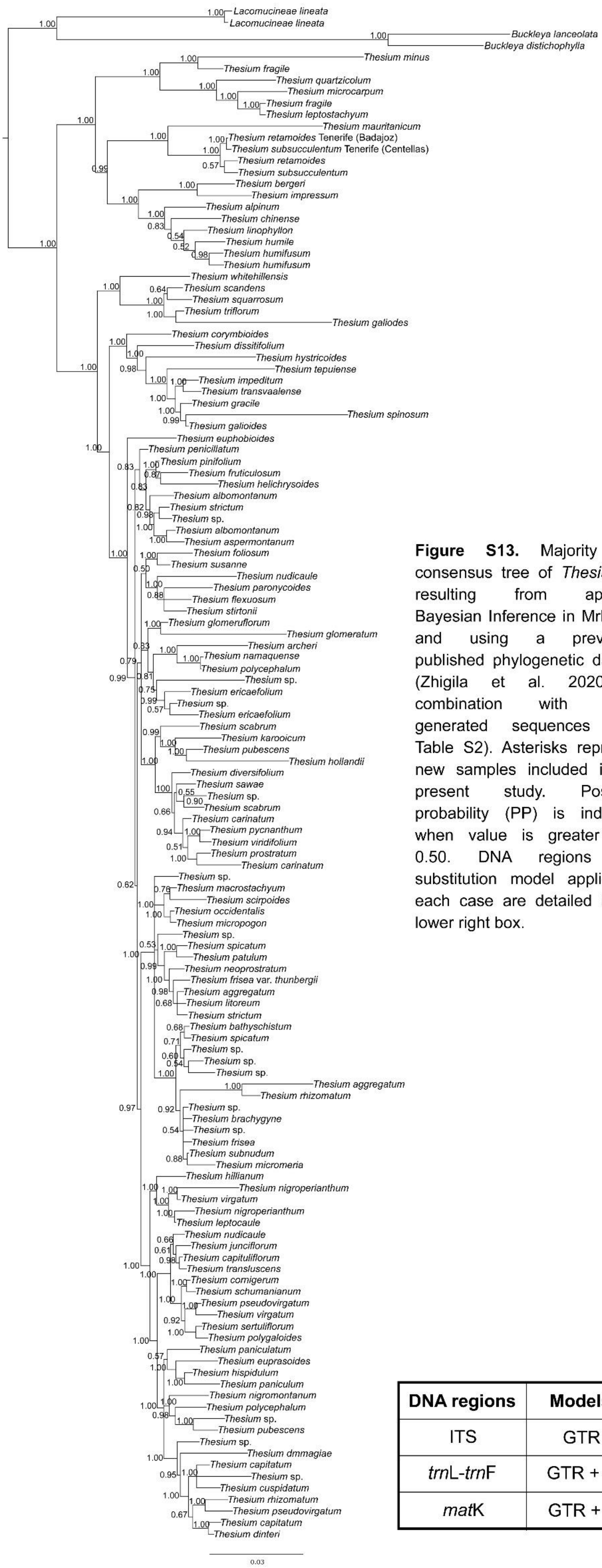


Figure S13. Majority rule consensus tree of *Thesium* L. resulting from applying Bayesian Inference in MrBayes and using a previously published phylogenetic dataset (Zhigila et al. 2020) in combination with newly generated sequences (see Table S2). Asterisks represent new samples included in the present study. Posterior probability (PP) is indicated when value is greater than 0.50. DNA regions and substitution model applied in each case are detailed in the lower right box.

DNA regions	Models
ITS	GTR
*trn*L-*trn*F	GTR + G
*mat*K	GTR + G

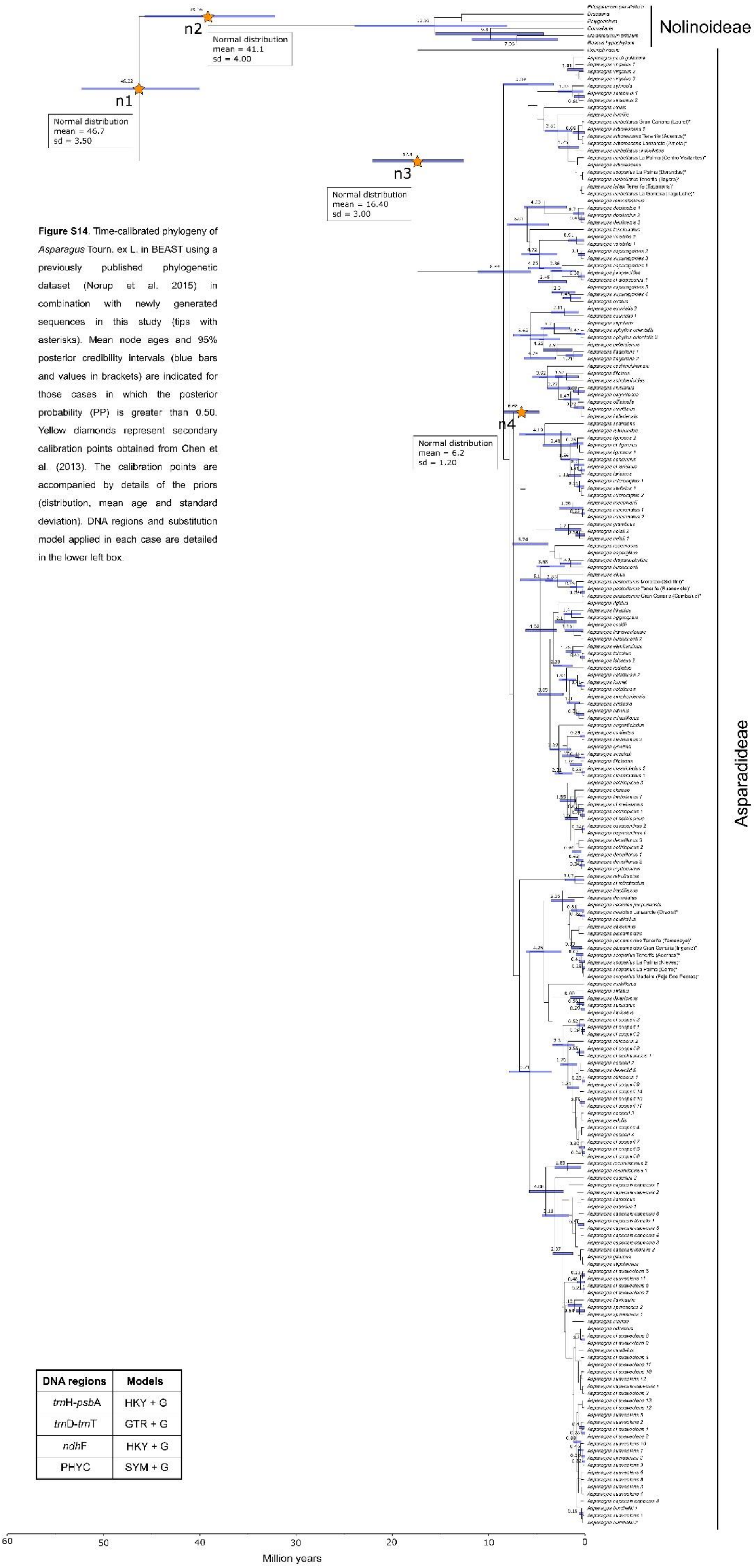


Figure S14. Time-calibrated phylogeny of *Asparagus* Tourn. ex L. in BEAST using a previously published phylogenetic dataset (Norup et al. 2015) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Yellow diamonds represent secondary calibration points obtained from Chen et al. (2013). The calibration points are accompanied by details of the priors (distribution, mean age and standard deviation). DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA regions	Models
*trn*H-*psb*A	HKY + G
*trn*D-*trn*T	GTR + G
*ndh*F	HKY + G
PHYC	SYM + G

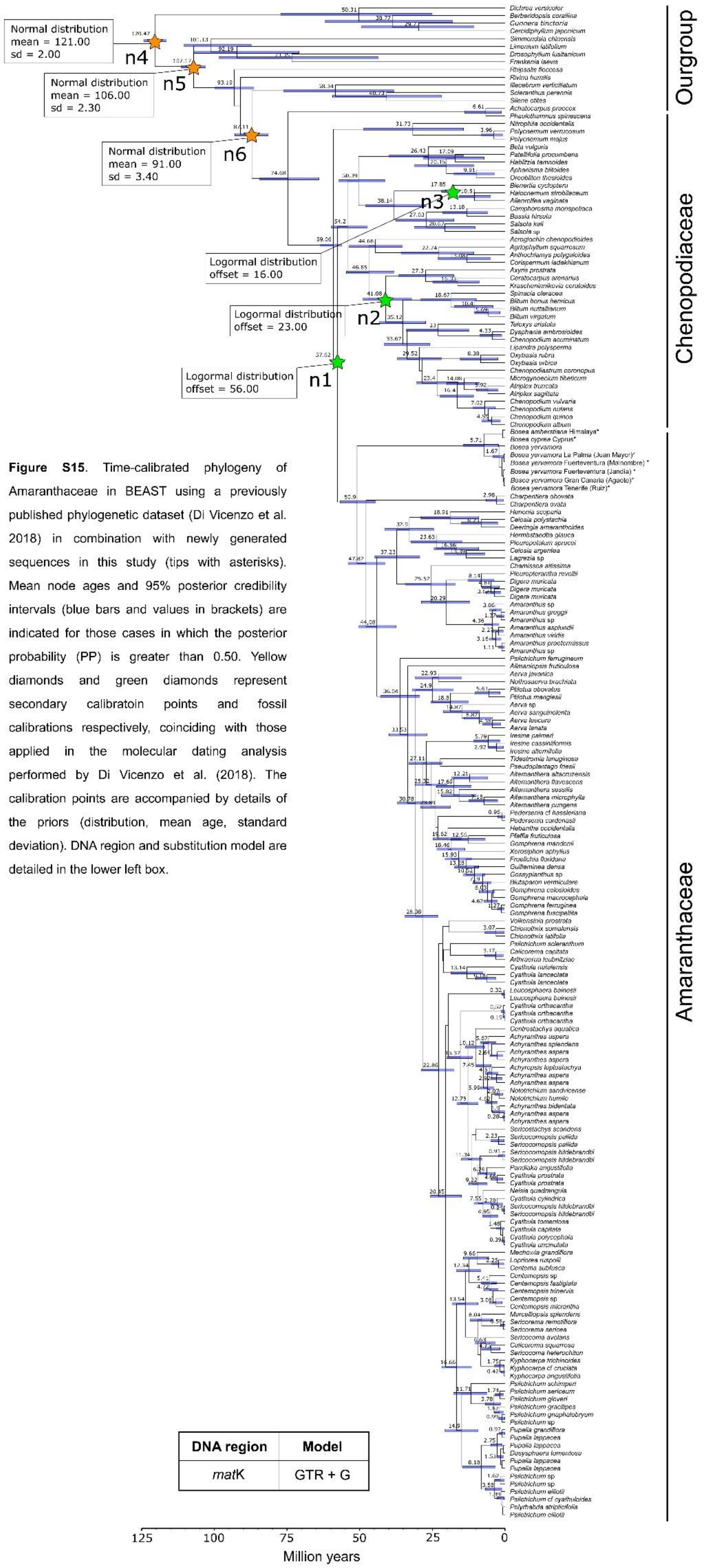


Figure S15. Time-calibrated phylogeny of Amaranthaceae in BEAST using a previously published phylogenetic dataset (Di Vicenzo et al. 2018) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Yellow diamonds and green diamonds represent secondary calibratoin points and fossil calibrations respectively, coinciding with those applied in the molecular dating analysis performed by Di Vicenzo et al. (2018). The calibration points are accompanied by details of the priors (distribution, mean age, standard deviation). DNA region and substitution model are detailed in the lower left box.

DNA region	Model
*mat*K	GTR + G

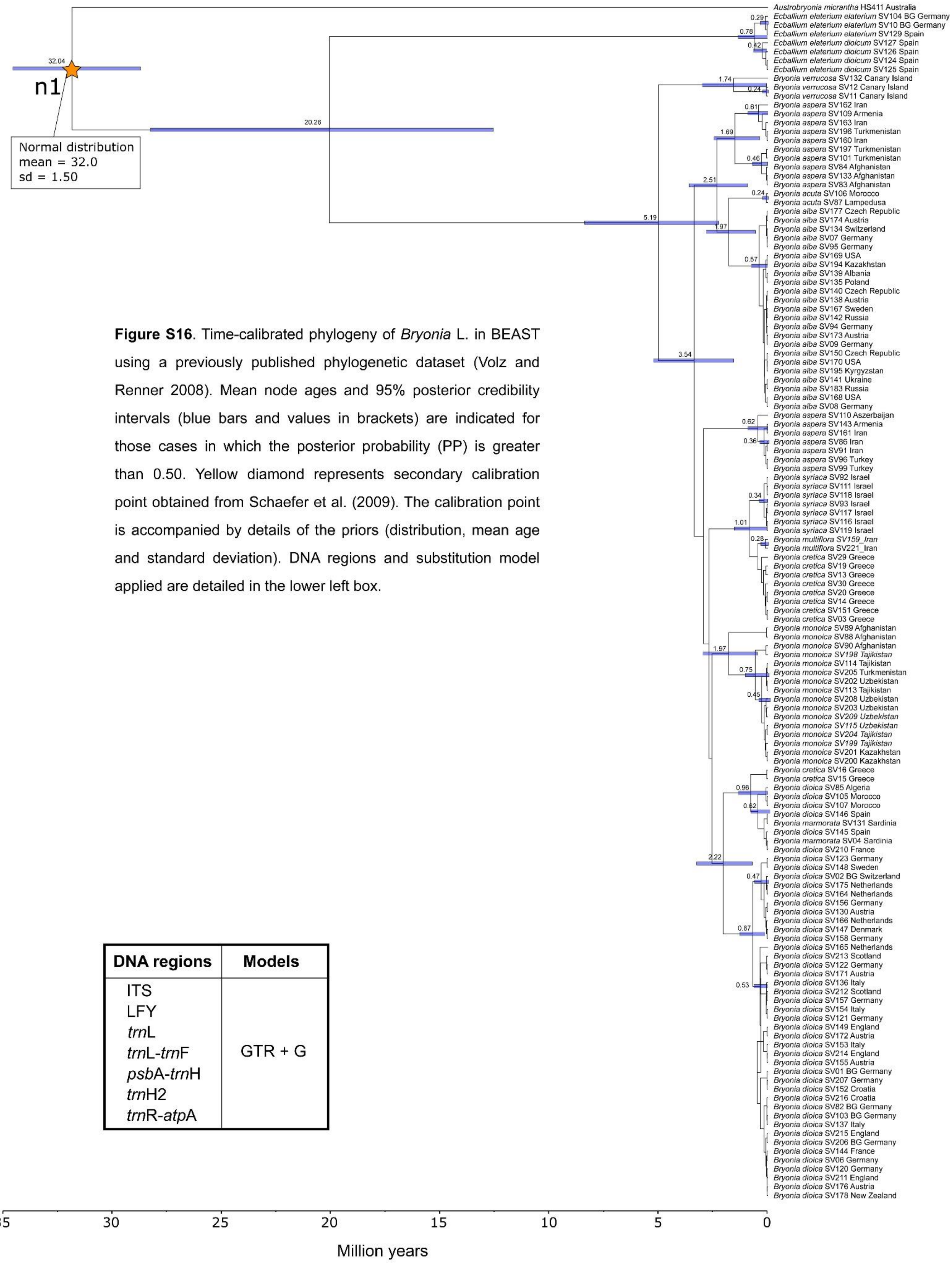
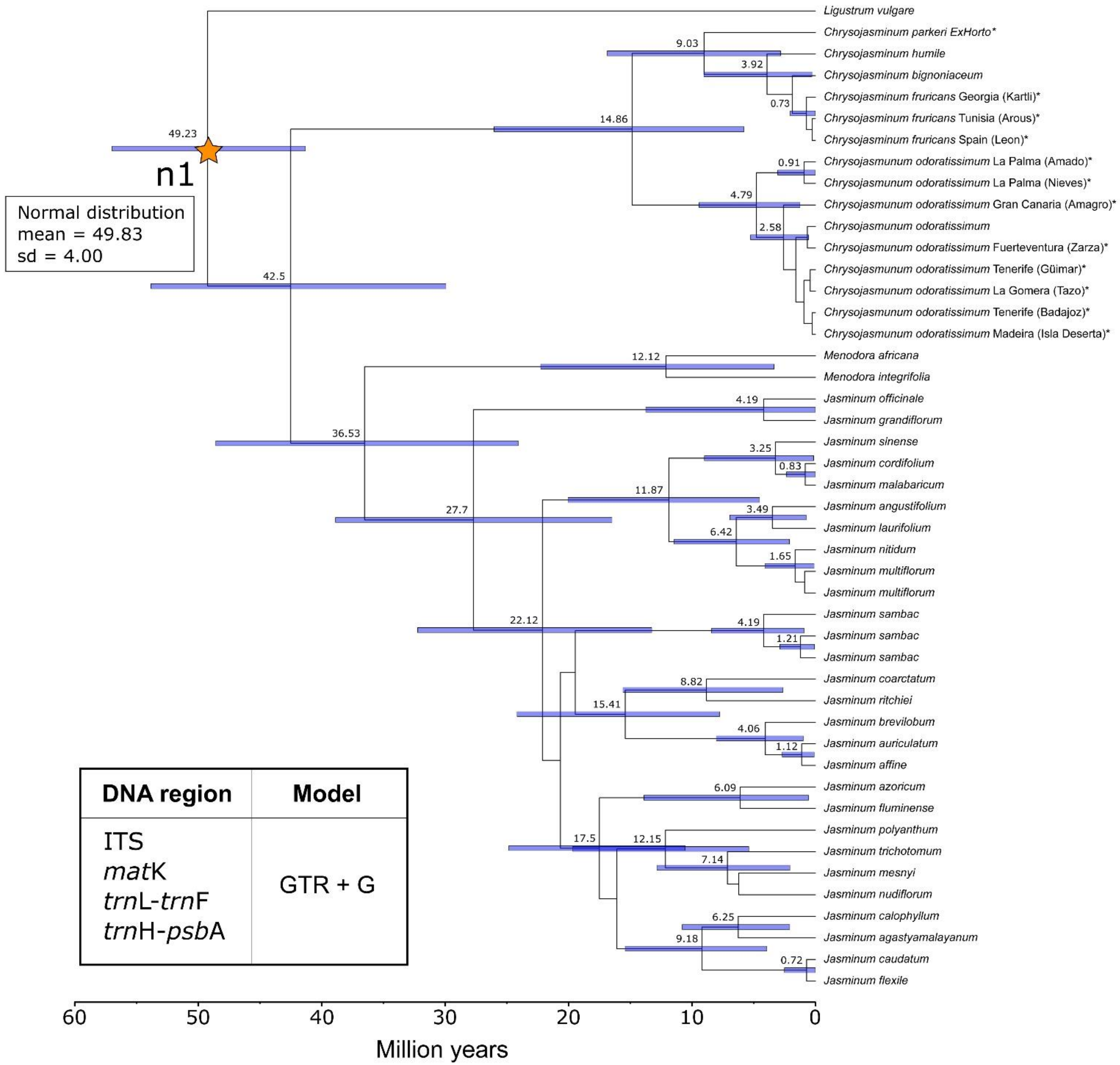


Figure S16. Time-calibrated phylogeny of *Bryonia* L. in BEAST using a previously published phylogenetic dataset (Volz and Renner 2008). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Yellow diamond represents secondary calibration point obtained from Schaefer et al. (2009). The calibration point is accompanied by details of the priors (distribution, mean age and standard deviation). DNA regions and substitution model applied are detailed in the lower left box.

DNA regions	Models
ITS	GTR + G
LFY	
*trn*L	
*trn*L-*trn*F	
*psb*A-*trn*H	
*trn*H2	
*trn*R-*atp*A	

Figure S17. Time-calibrated phylogeny of *Chrysojasminum* Banfi in BEAST using a previously published phylogenetic dataset (Jeyarani et al. 2018) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Yellow diamond represents secondary calibration point obtained from Vargas et al. (2014). The calibration point are accompanied by details of the priors (distribution, mean age and standard deviation). DNA region and substitution model are detailed in the lower left box.



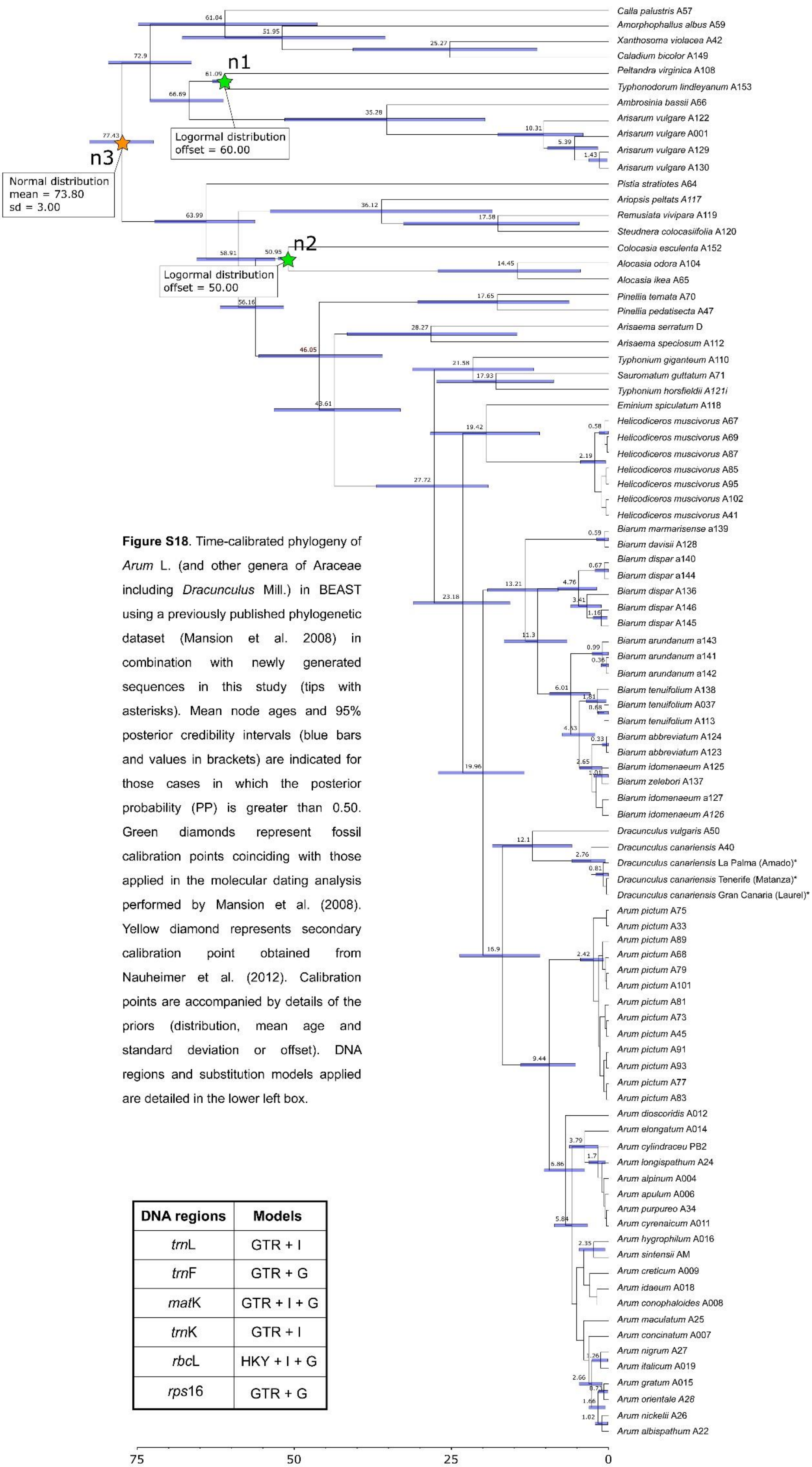
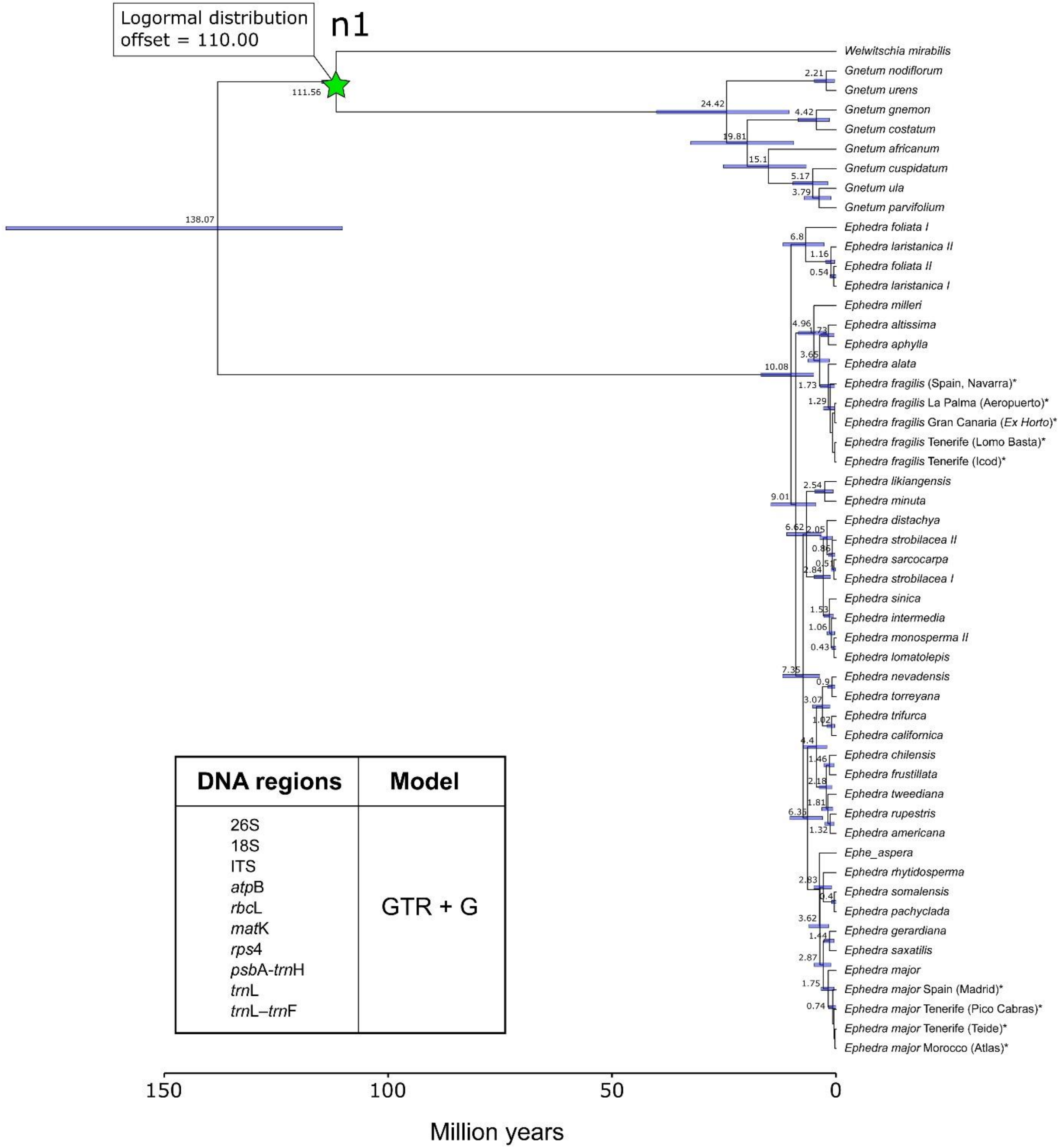


Figure S18. Time-calibrated phylogeny of *Arum* L. (and other genera of Araceae including *Dracunculus* Mill.) in BEAST using a previously published phylogenetic dataset (Mansion et al. 2008) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Green diamonds represent fossil calibration points coinciding with those applied in the molecular dating analysis performed by Mansion et al. (2008). Yellow diamond represents secondary calibration point obtained from Nauheimer et al. (2012). Calibration points are accompanied by details of the priors (distribution, mean age and standard deviation or offset). DNA regions and substitution models applied are detailed in the lower left box.

DNA regions	Models
*trn*L	GTR + I
*trn*F	GTR + G
*mat*K	GTR + I + G
*trn*K	GTR + I
*rbc*L	HKY + I + G
*rps*16	GTR + G

Figure S19. Time-calibrated phylogeny of *Ephedra* Tourn. ex L. in BEAST using a previously published phylogenetic dataset (Ickert-Bond et al. 2009) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Green diamond represents a fossil calibration point coinciding with those applied in the molecular dating analysis performed by Ickert-Bond et al. (2009). The calibration point are accompanied by details of the priors (distribution, offset). DNA regions and substitution model are detailed in the lower left box.



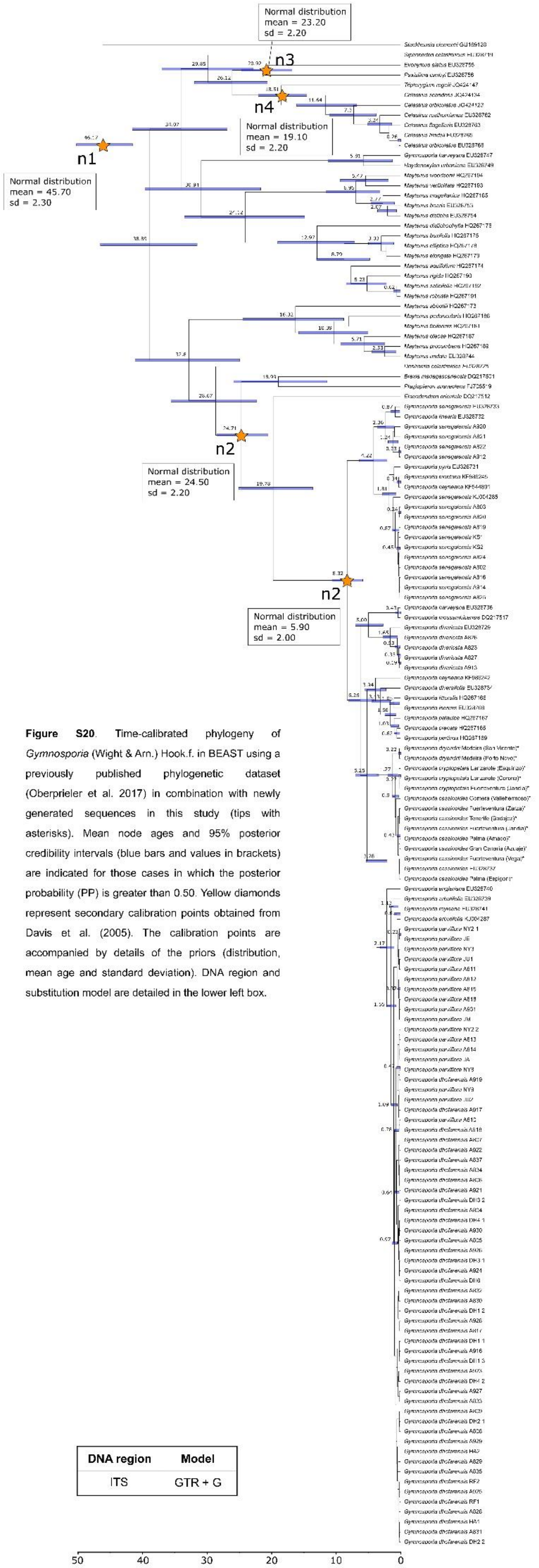


Figure S20. Time-calibrated phylogeny of *Gymnosporia* (Wight & Arn.) Hook.f. in BEAST using a previously published phylogenetic dataset (Oberprieler et al. 2017) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Yellow diamonds represent secondary calibration points obtained from Davis et al. (2005). The calibration points are accompanied by details of the priors (distribution, mean age and standard deviation). DNA region and substitution model are detailed in the lower left box.

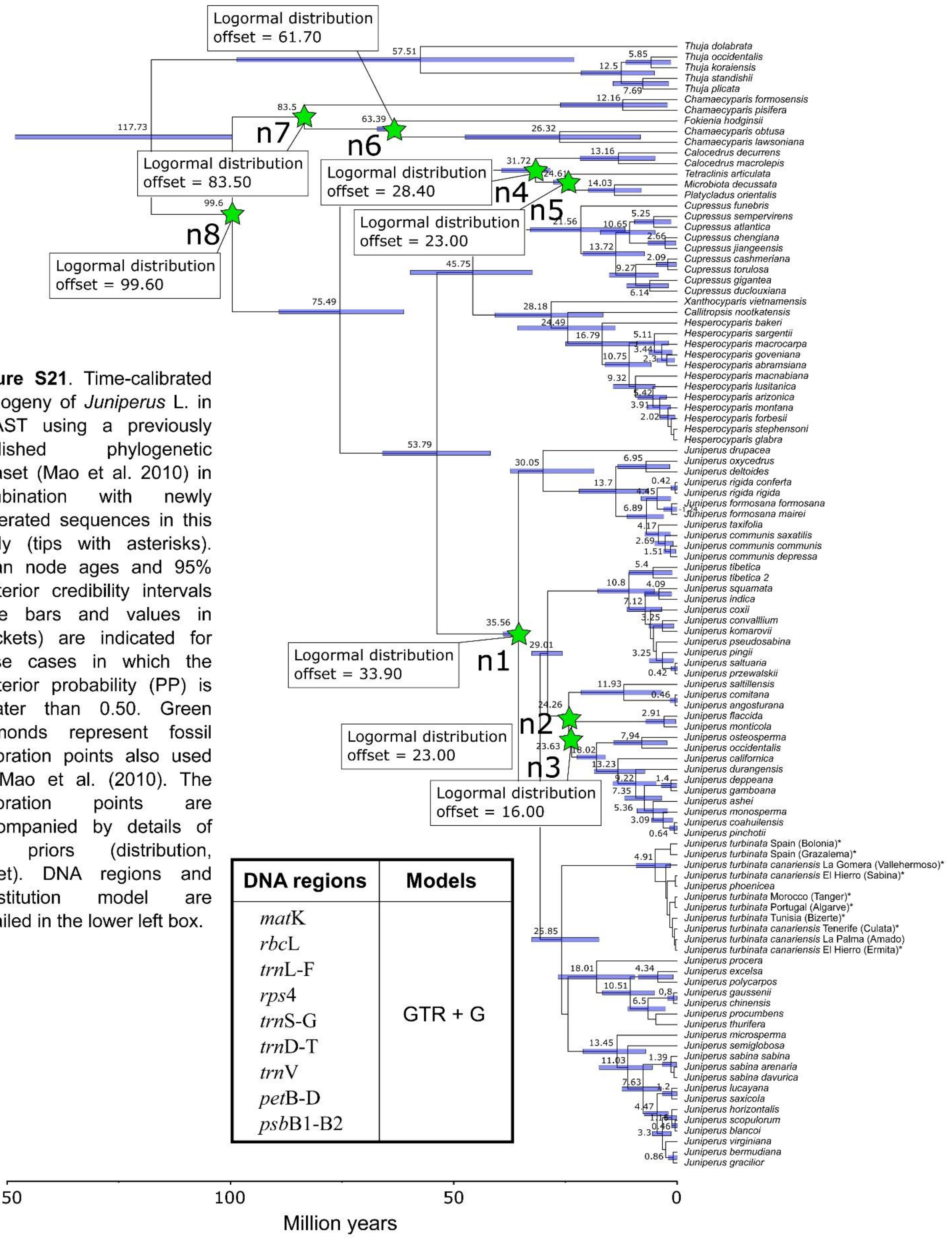


Figure S21. Time-calibrated phylogeny of *Juniperus* L. in BEAST using a previously published phylogenetic dataset (Mao et al. 2010) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Green diamonds represent fossil calibration points also used by Mao et al. (2010). The calibration points are accompanied by details of the priors (distribution, offset). DNA regions and substitution model are detailed in the lower left box.

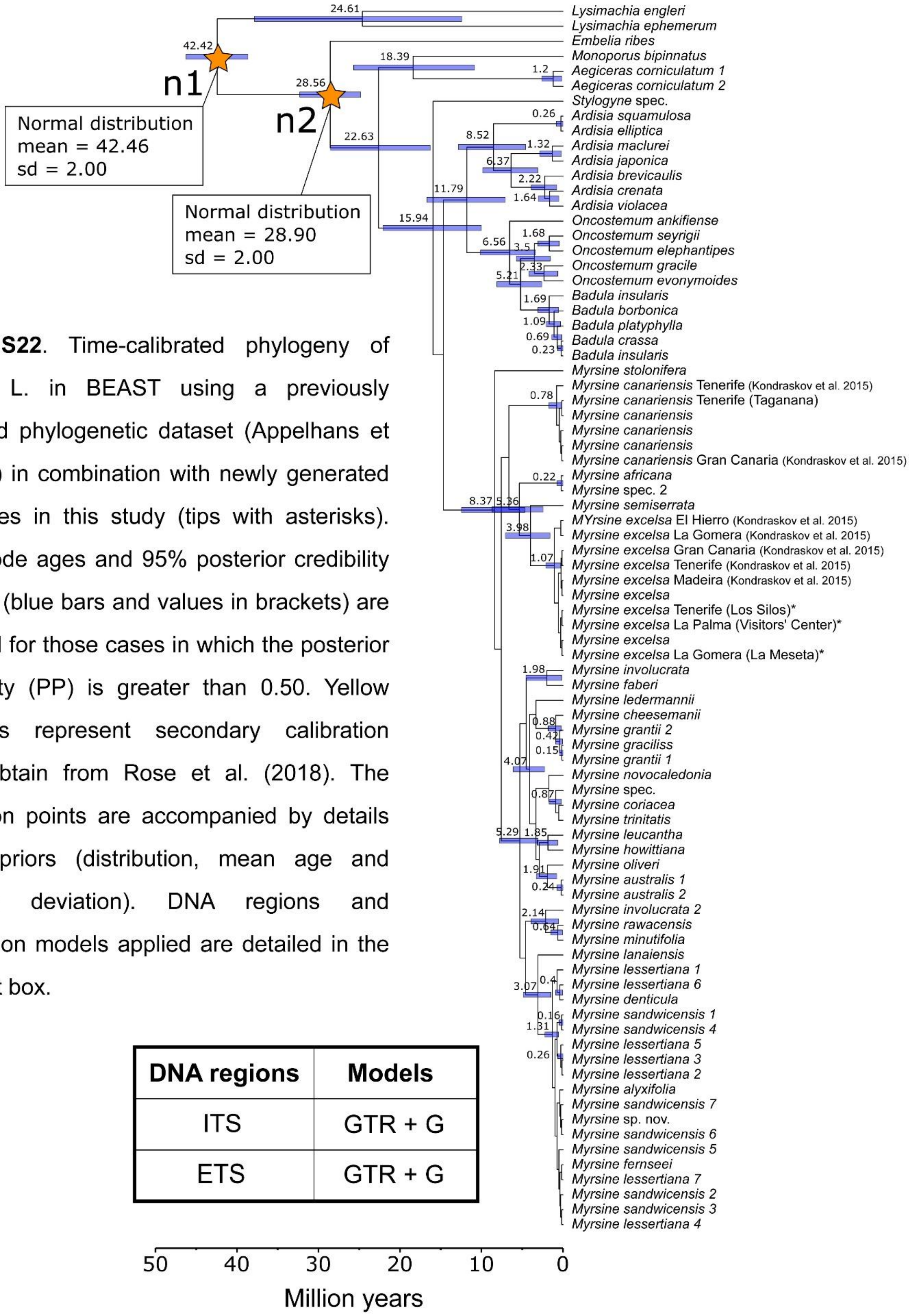
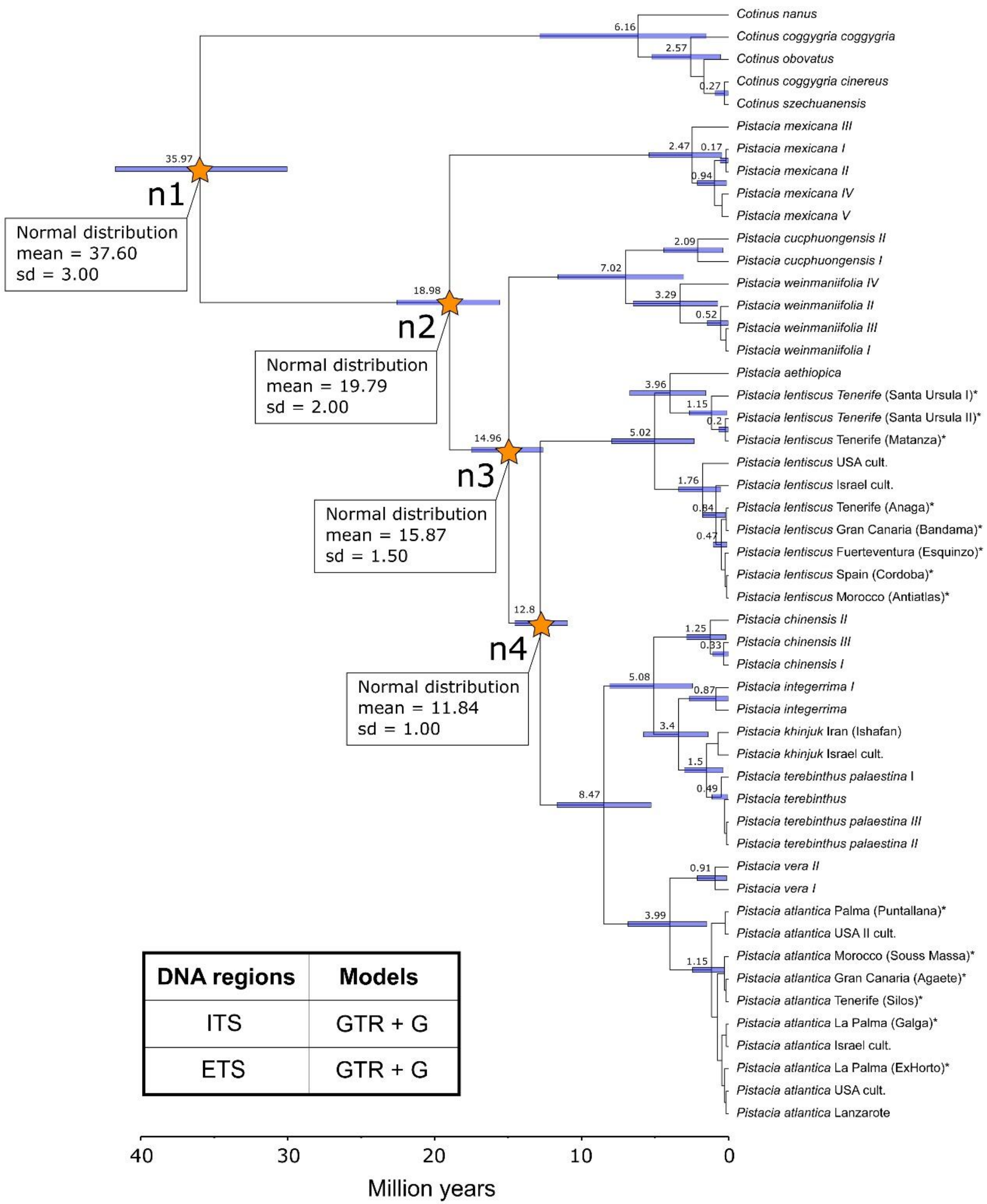


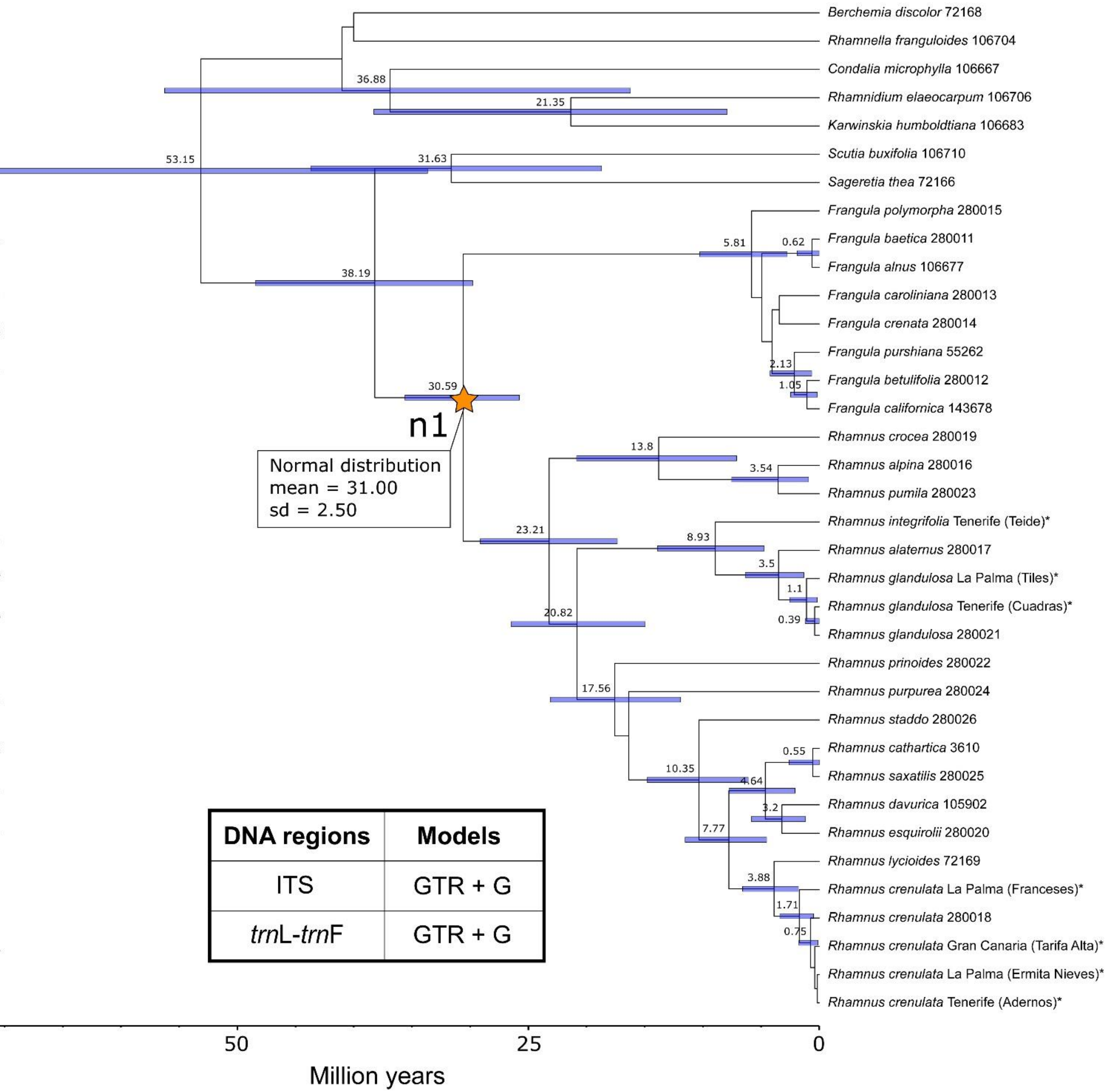
Figure S22. Time-calibrated phylogeny of *Myrsine* L. in BEAST using a previously published phylogenetic dataset (Appelhans et al. 2020) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Yellow diamonds represent secondary calibration points obtain from Rose et al. (2018). The calibration points are accompanied by details of the priors (distribution, mean age and standard deviation). DNA regions and substitution models applied are detailed in the lower left box.

DNA regions	Models
ITS	GTR + G
ETS	GTR + G



DNA regions	Models
ITS	GTR + G
ETS	GTR + G

Figure S23. Time-calibrated phylogeny of *Pistacia* L. in BEAST using a previously published phylogenetic dataset (Xie et al. 2014) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Yellow diamonds represent secondary calibration points, coinciding with those applied in the molecular dating analysis performed by Xie et al. (2014). The calibration points are accompanied by details of the priors (distribution, mean age and standard deviation). DNA regions and substitution models applied are detailed in the lower left box.

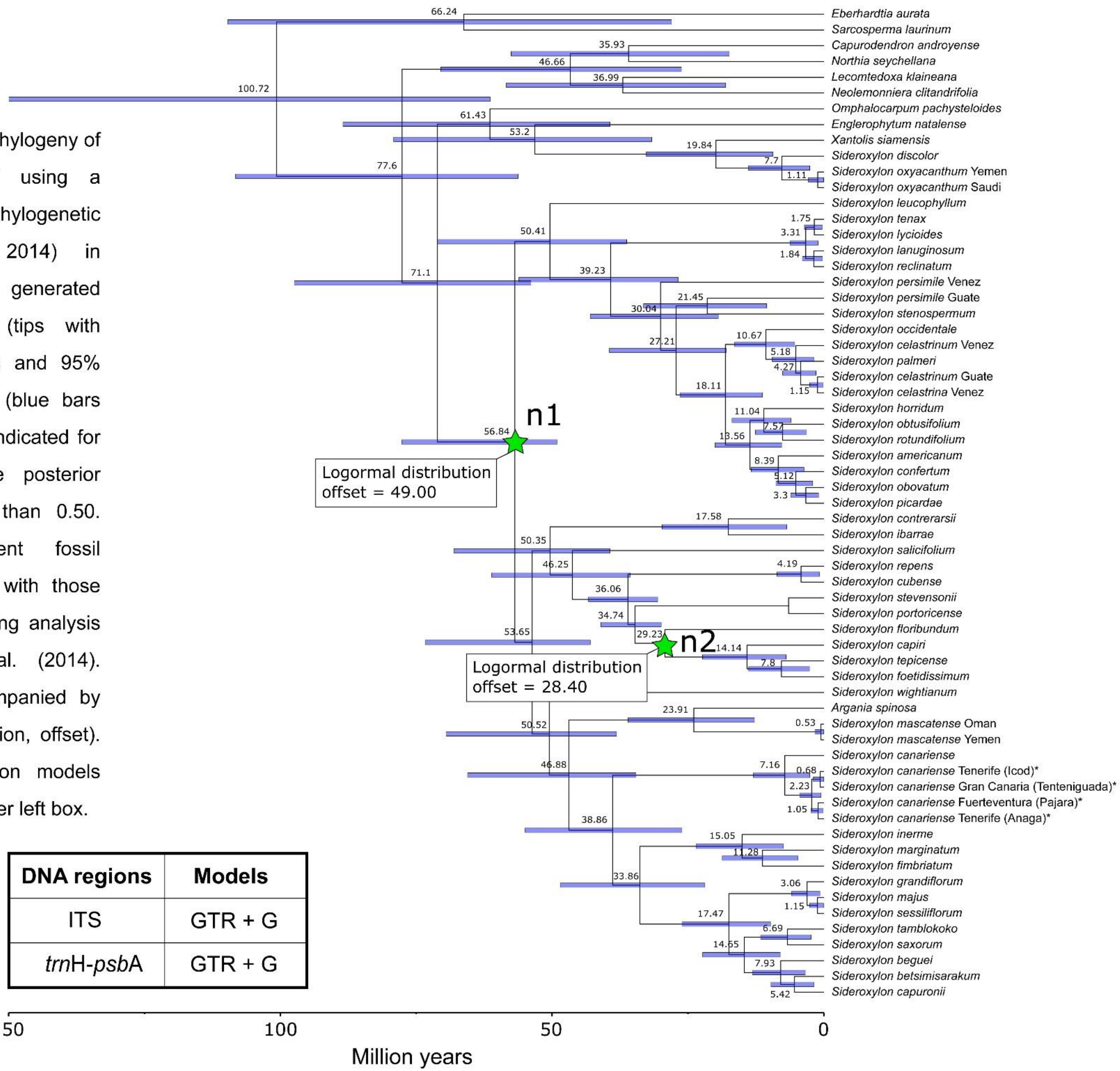


DNA regions	Models
ITS	GTR + G
*trn*L-*trn*F	GTR + G

Figure S24. Time-calibrated phylogeny of *Rhamnus* L. in BEAST using a previously published phylogenetic dataset (Bolmgren and Oxelman 2004) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Yellow diamond represents secondary calibration point obtained from Onstein et al. (2015). The calibration point is accompanied by details of the priors (distribution, mean age and standard deviation). DNA regions and substitution models applied are detailed in the lower left box.

Figure S25. Time-calibrated phylogeny of *Sideroxylon* L. in BEAST using a previously published phylogenetic dataset (Stride et al. 2014) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Green diamonds represent fossil calibration points coinciding with those applied in the molecular dating analysis performed by Stride et al. (2014). Calibration points are accompanied by details of the priors (distribution, offset). DNA regions and substitution models applied are detailed in the lower left box.

DNA regions	Models
ITS	GTR + G
*trn*H-*psb*A	GTR + G



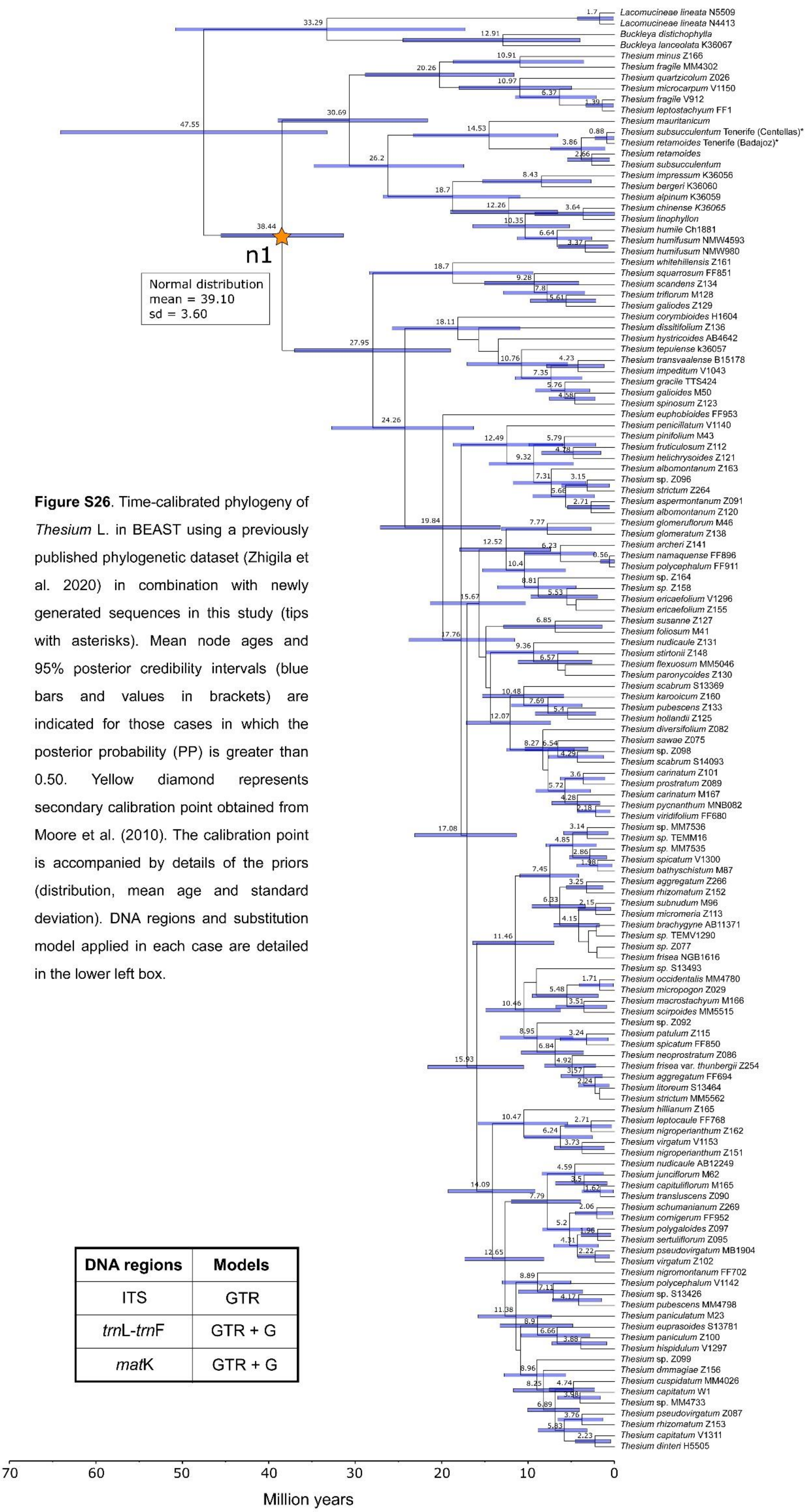


Figure S26. Time-calibrated phylogeny of *Thesium* L. in BEAST using a previously published phylogenetic dataset (Zhigila et al. 2020) in combination with newly generated sequences in this study (tips with asterisks). Mean node ages and 95% posterior credibility intervals (blue bars and values in brackets) are indicated for those cases in which the posterior probability (PP) is greater than 0.50. Yellow diamond represents secondary calibration point obtained from Moore et al. (2010). The calibration point is accompanied by details of the priors (distribution, mean age and standard deviation). DNA regions and substitution model applied in each case are detailed in the lower left box.

DNA regions	Models
ITS	GTR
*trn*L-*trn*F	GTR + G
*mat*K	GTR + G

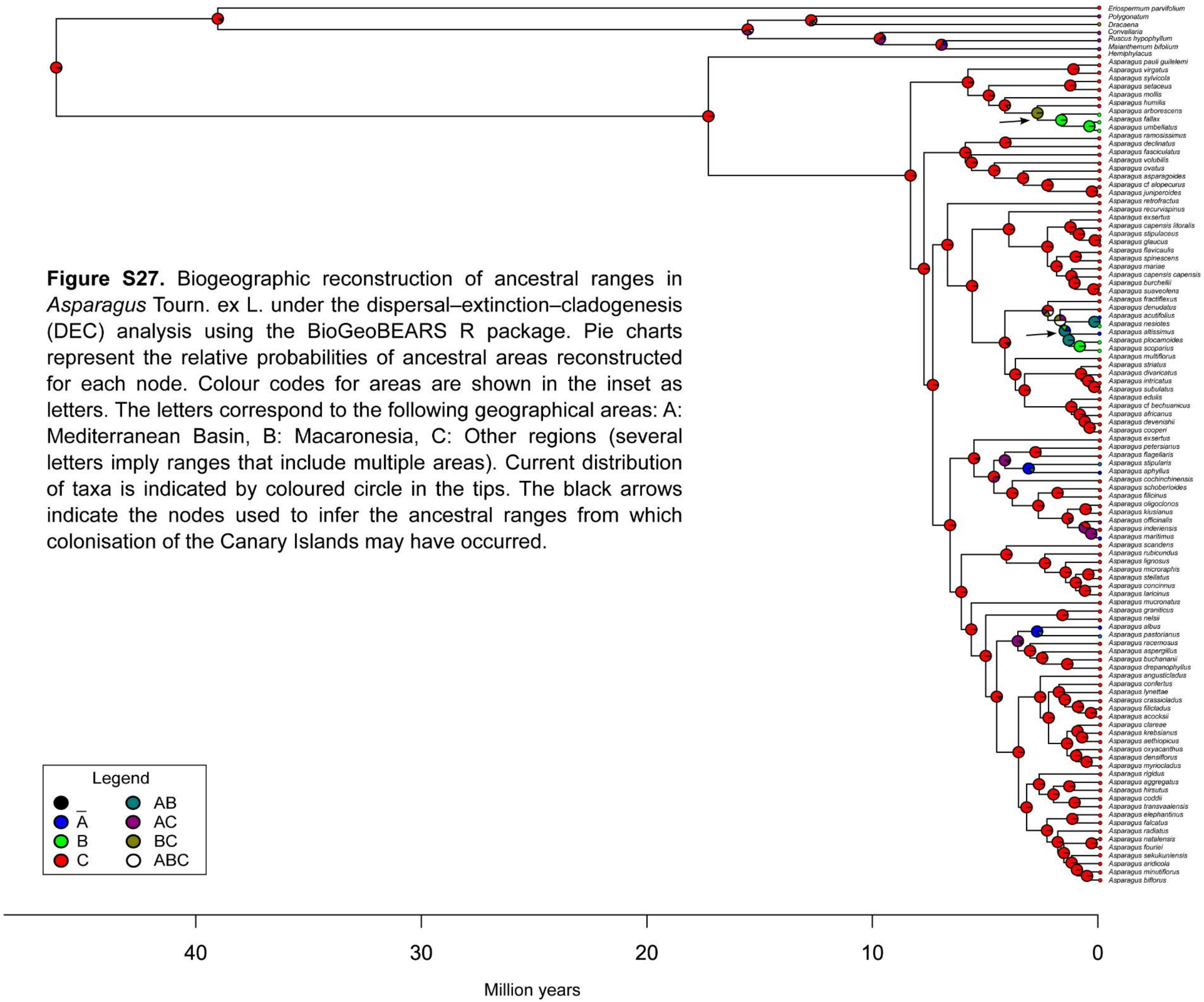


Figure S27. Biogeographic reconstruction of ancestral ranges in *Asparagus* Tourn. ex L. under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

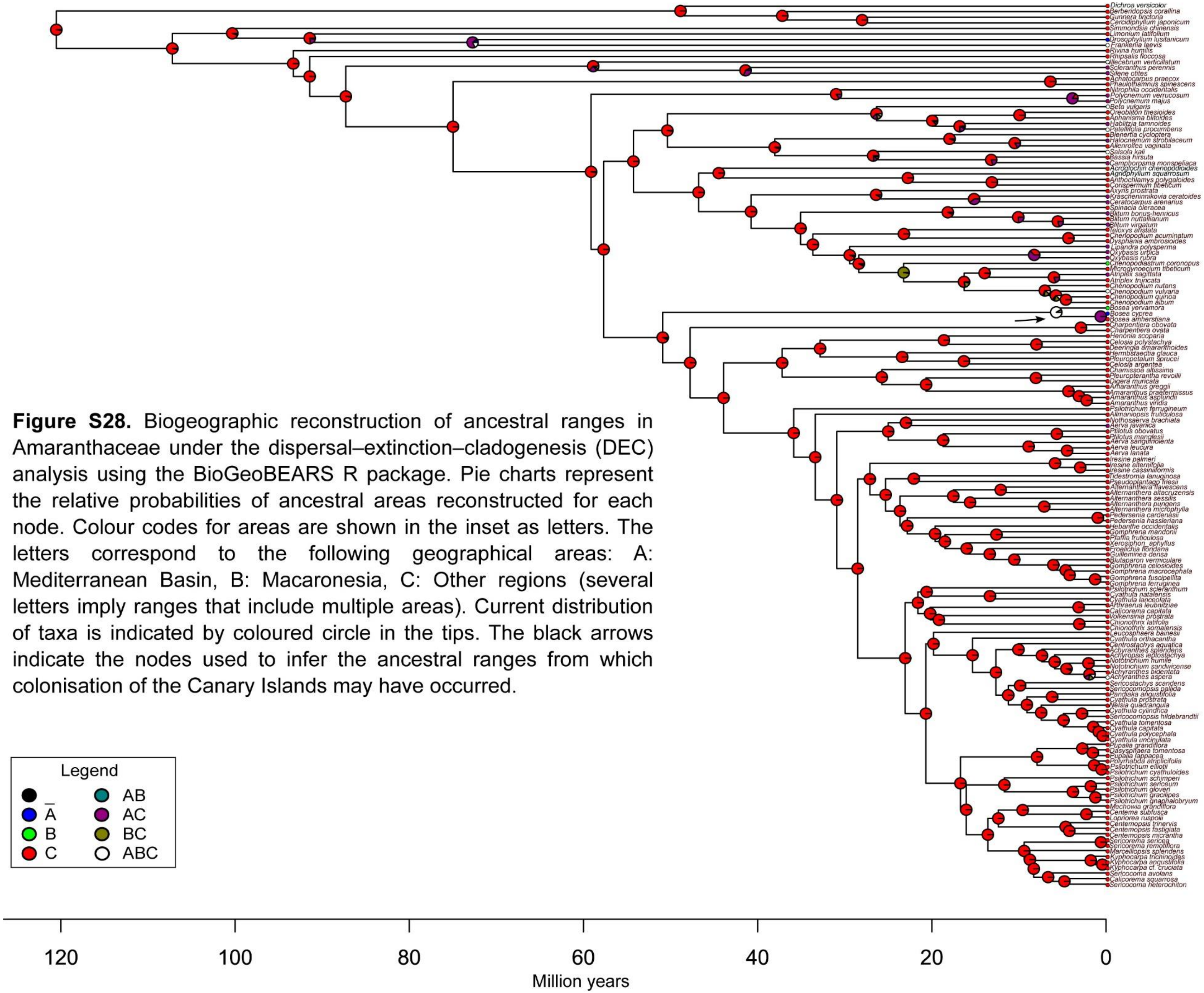


Figure S28. Biogeographic reconstruction of ancestral ranges in Amaranthaceae under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

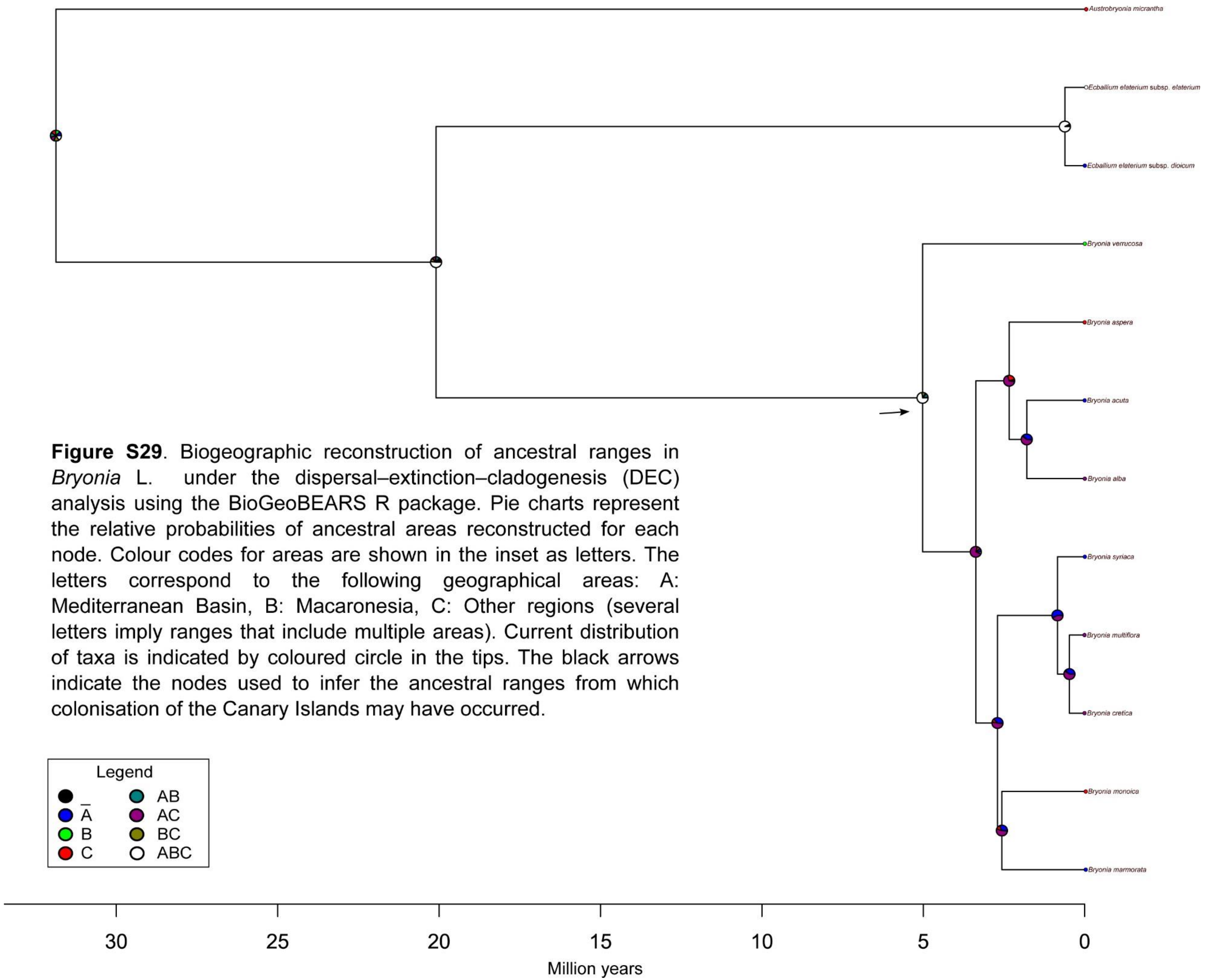


Figure S29. Biogeographic reconstruction of ancestral ranges in *Bryonia* L. under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

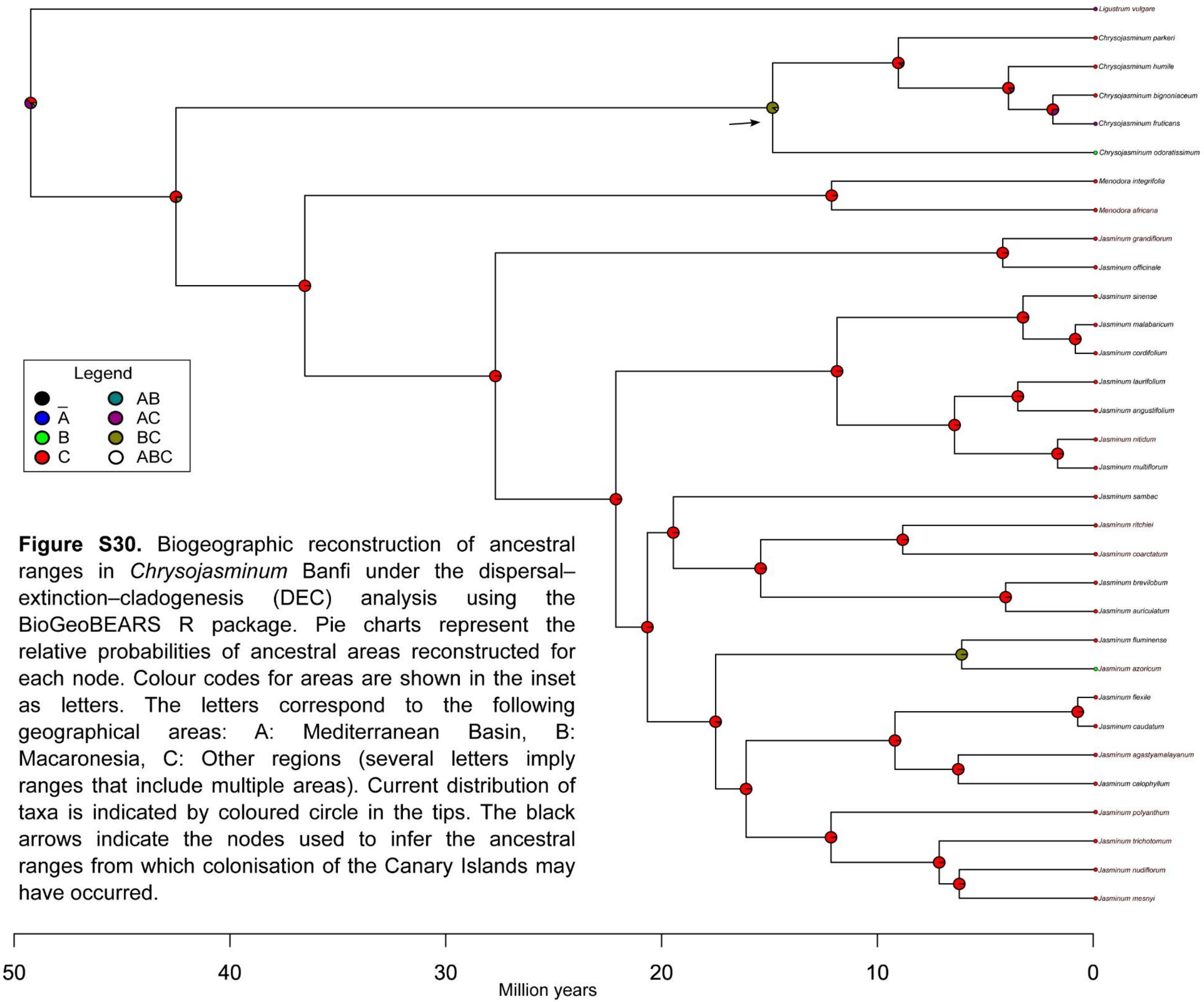


Figure S30. Biogeographic reconstruction of ancestral ranges in *Chrysojasminum* Banfi under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

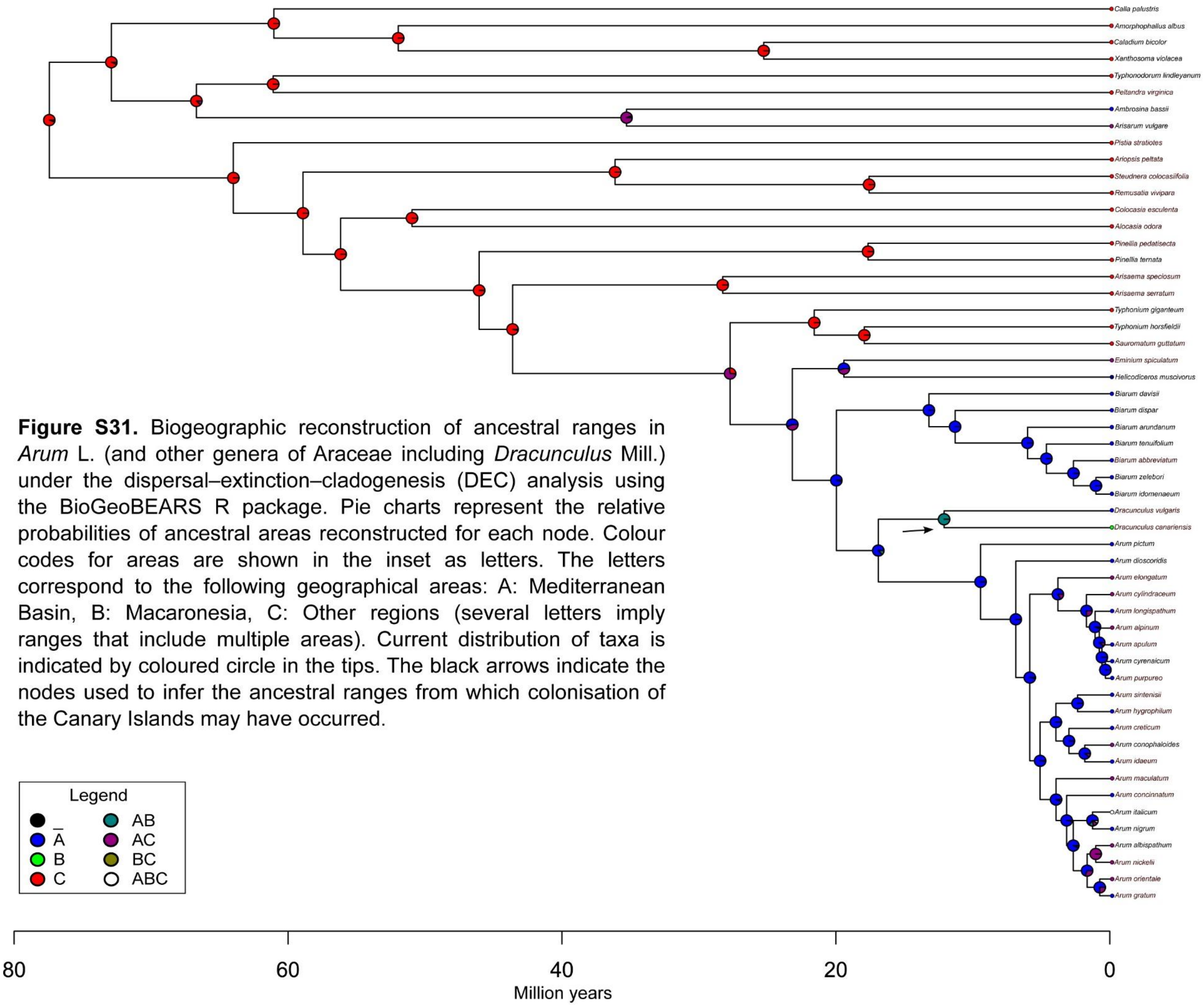


Figure S31. Biogeographic reconstruction of ancestral ranges in *Arum* L. (and other genera of Araceae including *Dracunculus* Mill.) under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

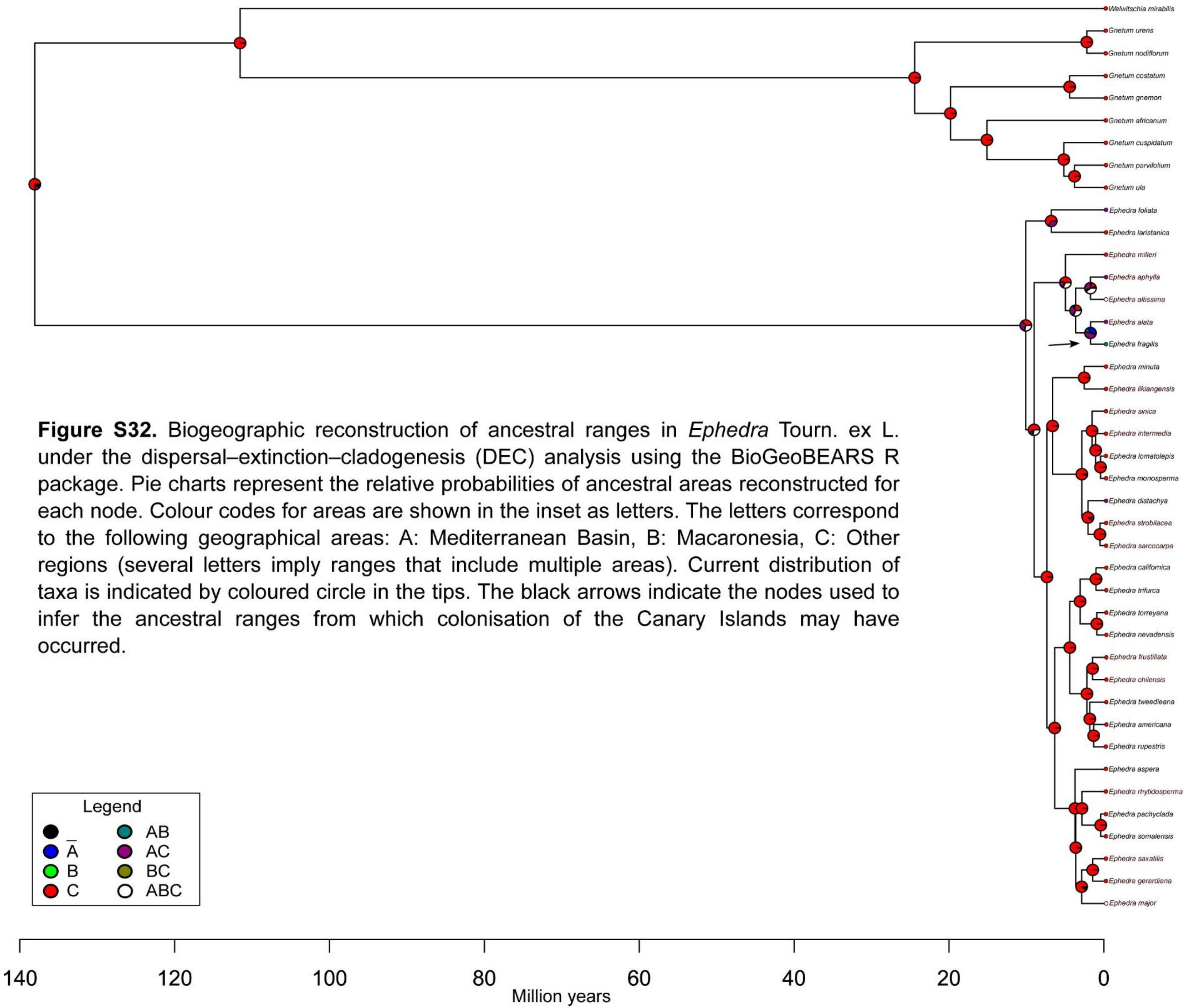


Figure S32. Biogeographic reconstruction of ancestral ranges in *Ephedra* Tourn. ex L. under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

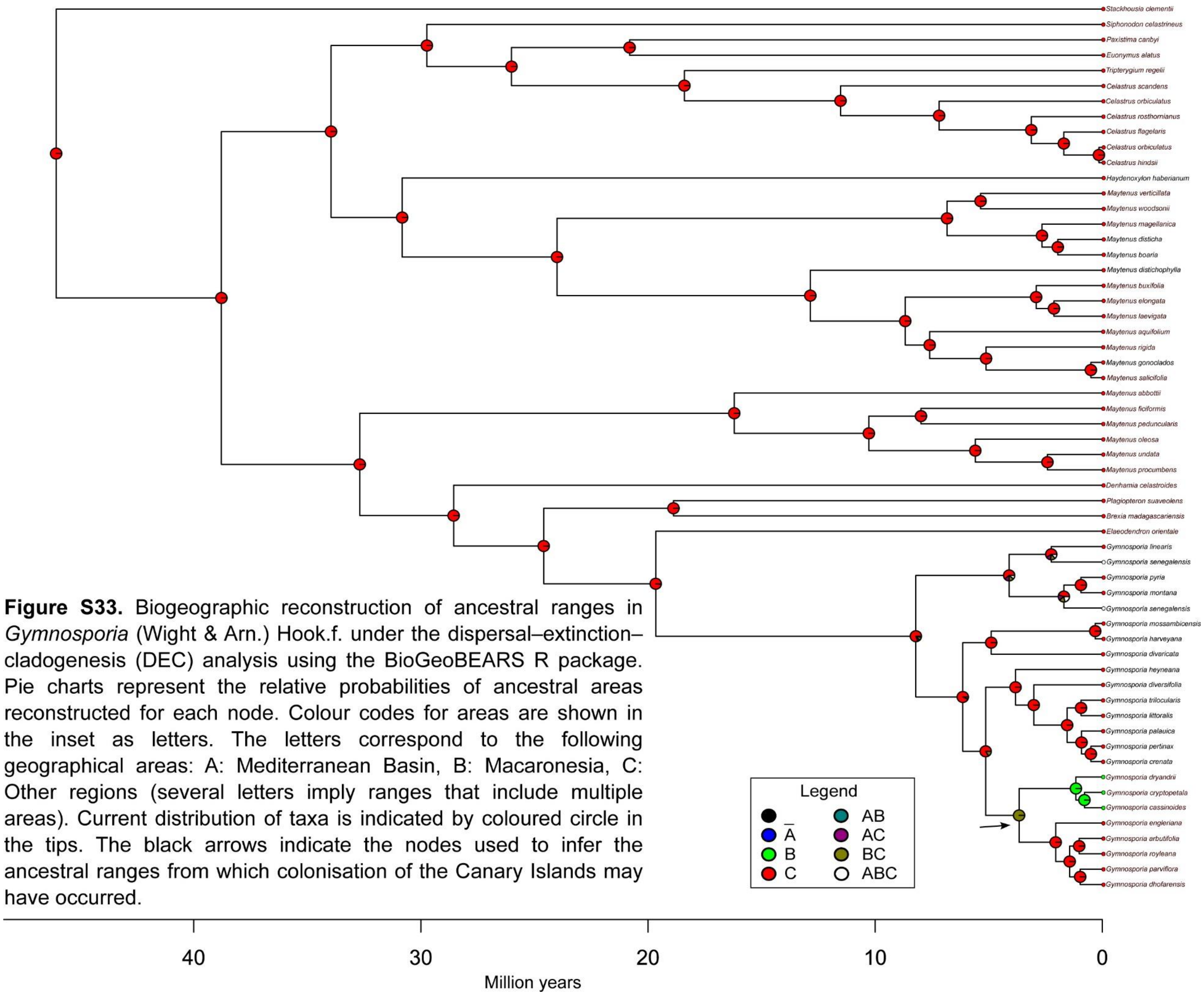


Figure S33. Biogeographic reconstruction of ancestral ranges in *Gymnosporia* (Wight & Arn.) Hook.f. under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

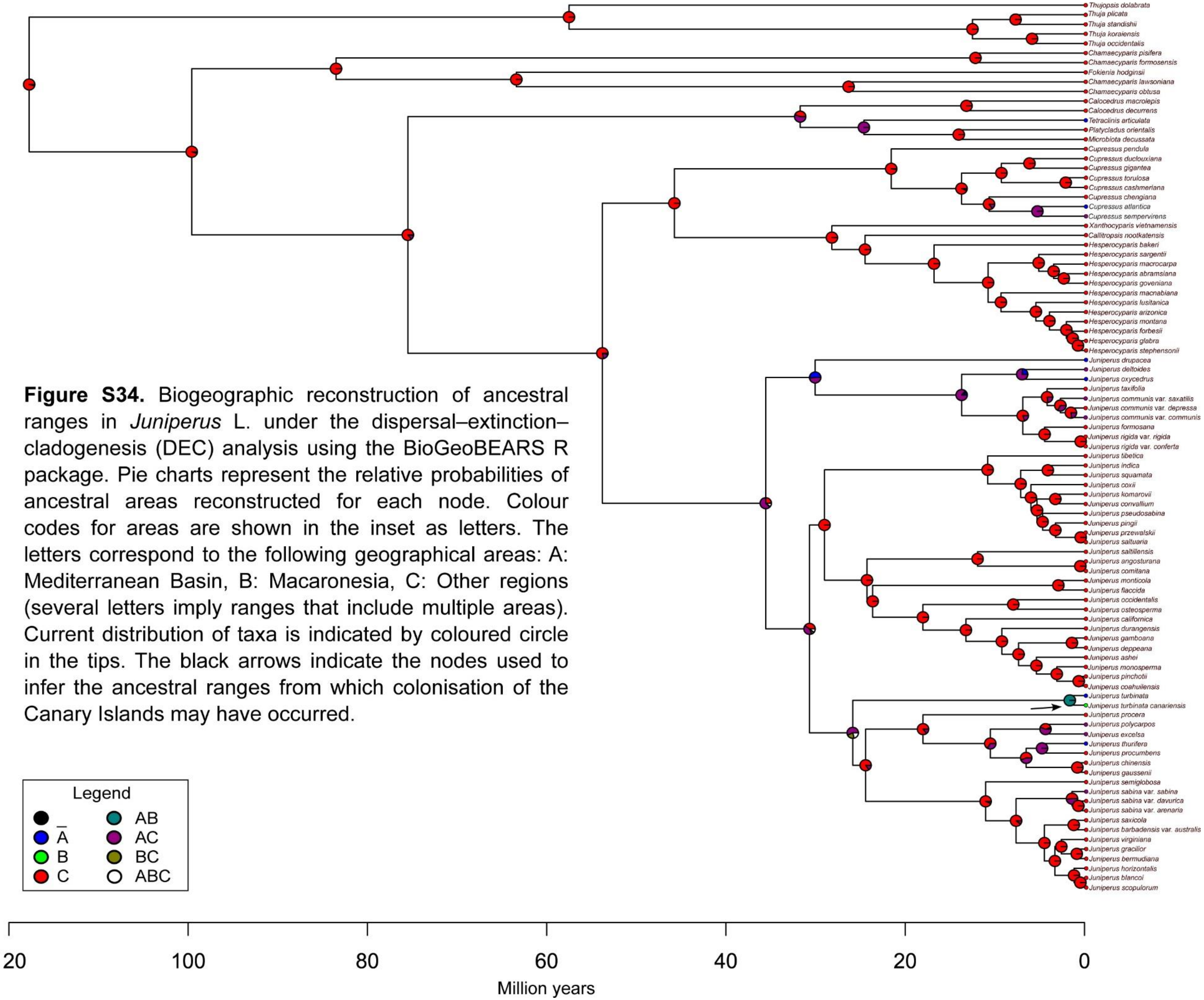


Figure S34. Biogeographic reconstruction of ancestral ranges in *Juniperus* L. under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

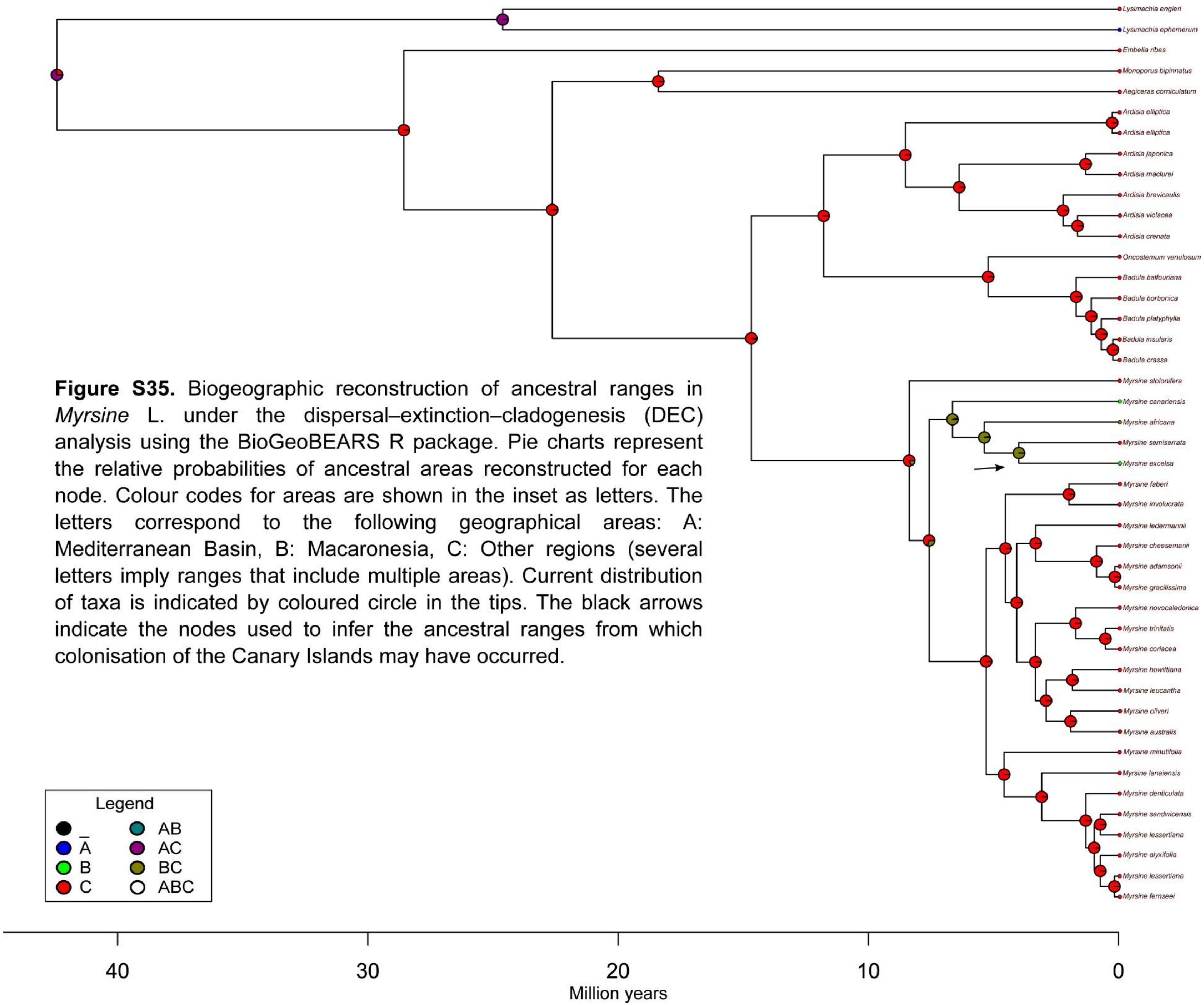


Figure S35. Biogeographic reconstruction of ancestral ranges in *Myrsine* L. under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

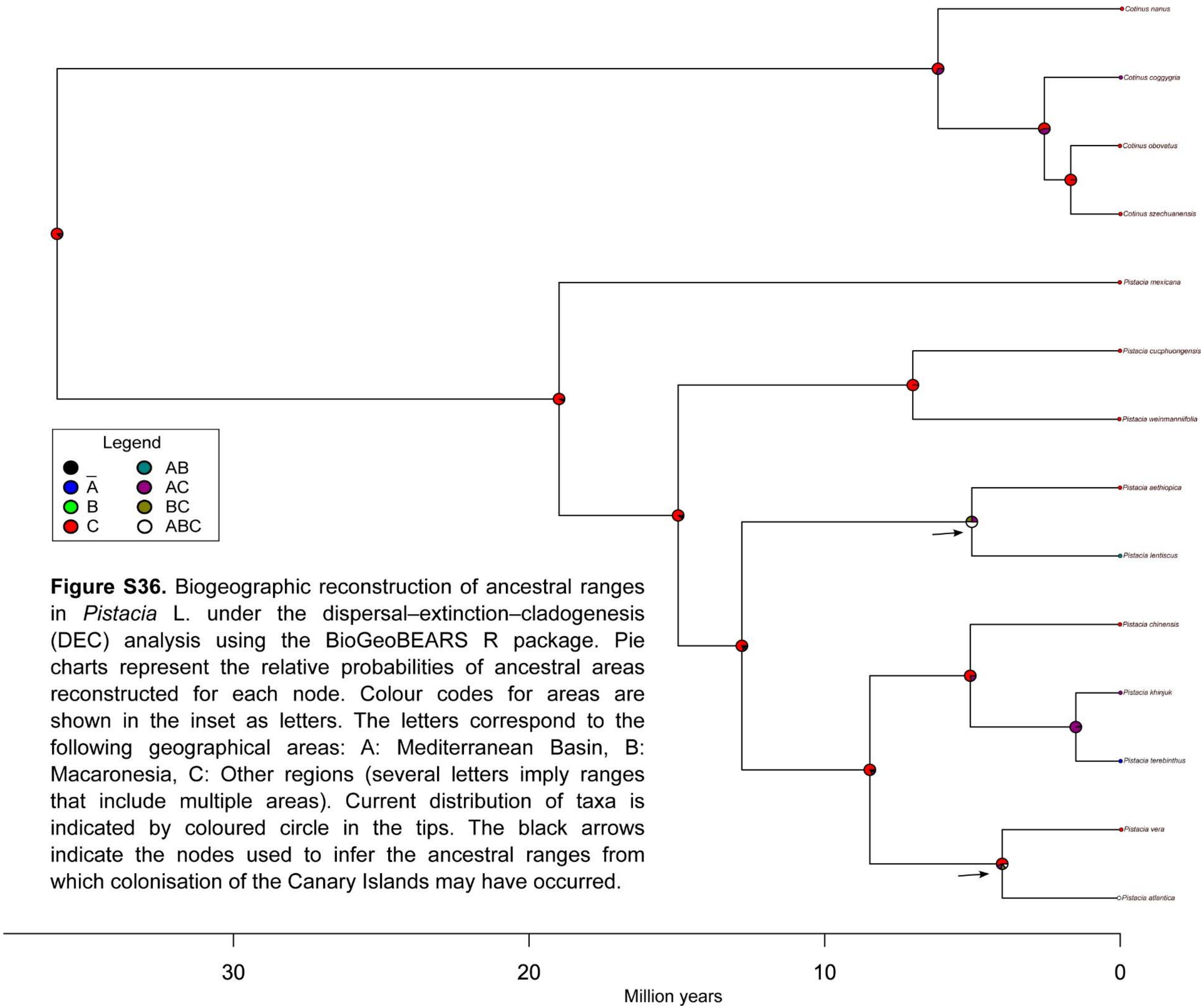


Figure S36. Biogeographic reconstruction of ancestral ranges in *Pistacia* L. under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

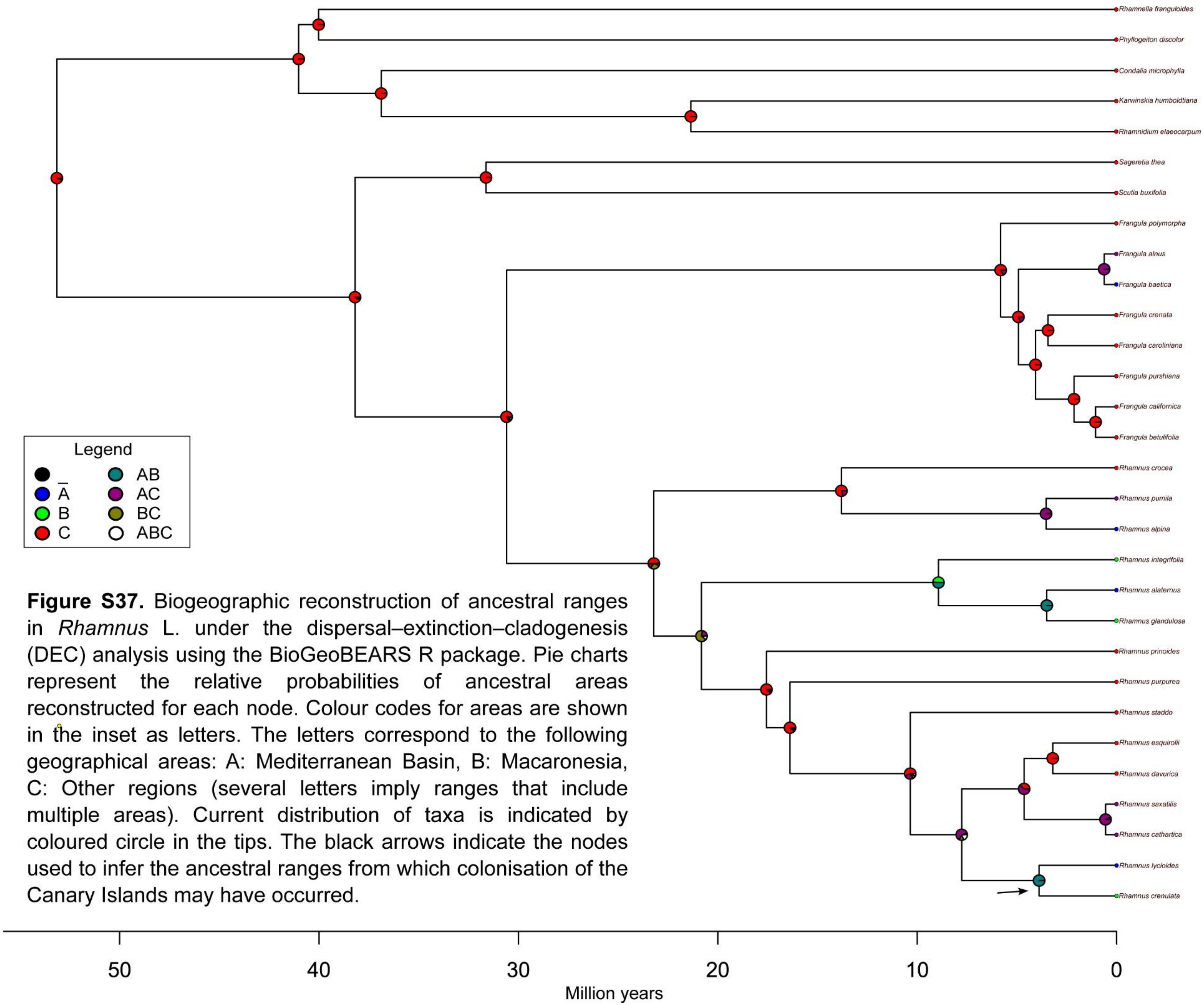


Figure S37. Biogeographic reconstruction of ancestral ranges in *Rhamnus* L. under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

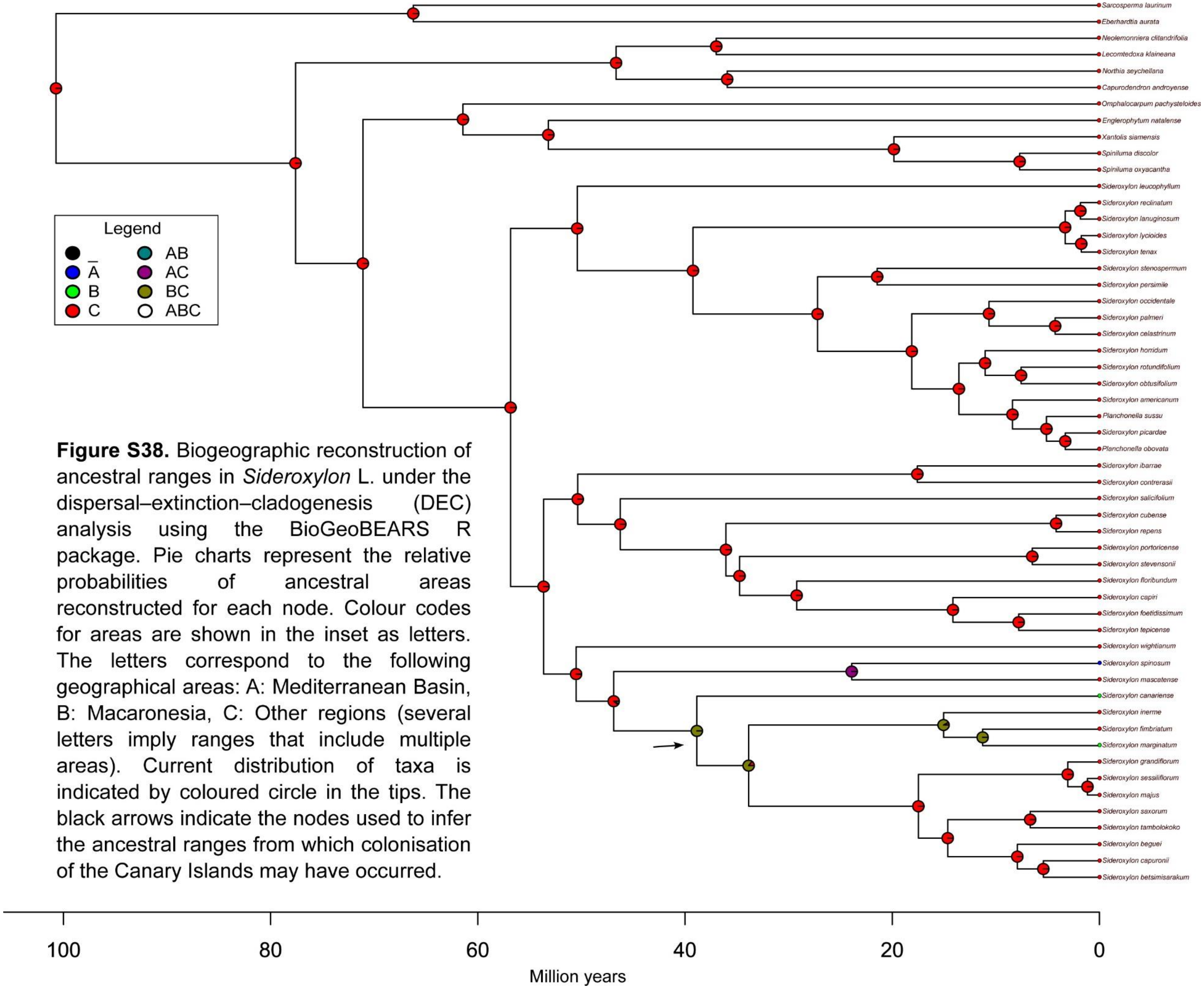


Figure S38. Biogeographic reconstruction of ancestral ranges in *Sideroxylon* L. under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

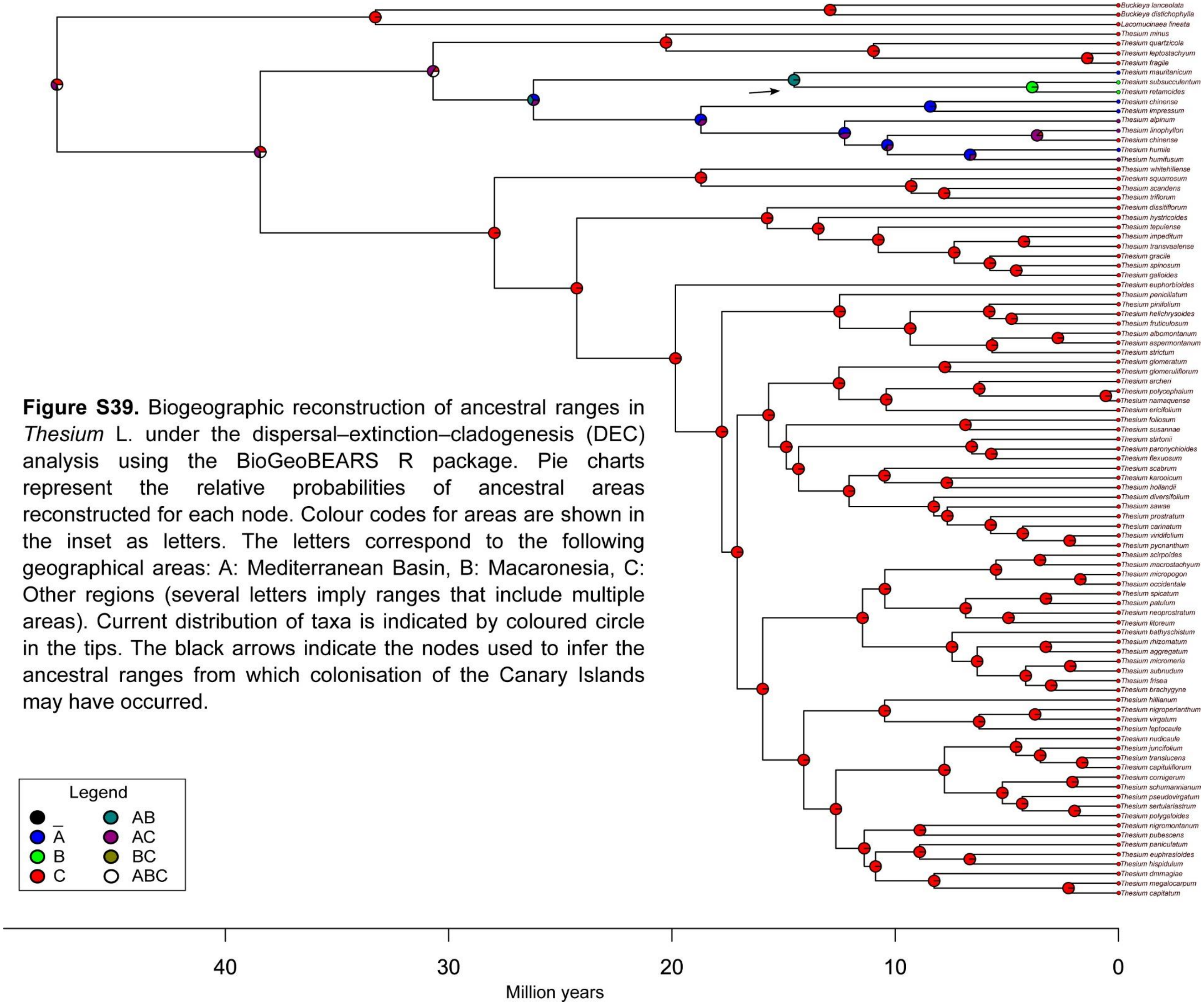


Figure S39. Biogeographic reconstruction of ancestral ranges in *Thesium* L. under the dispersal–extinction–cladogenesis (DEC) analysis using the BioGeoBEARS R package. Pie charts represent the relative probabilities of ancestral areas reconstructed for each node. Colour codes for areas are shown in the inset as letters. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). Current distribution of taxa is indicated by coloured circle in the tips. The black arrows indicate the nodes used to infer the ancestral ranges from which colonisation of the Canary Islands may have occurred.

Table S1. Information extracted from the literature and obtained in this study for the 43 plant lineages including thermophilous species from the Canary Islands (Macaronesia) for hypothesis testing. This information include: number of species in the lineage (when more than one the species name are shown with red names highlighting thermophilous ones), sister group species names, phylogenetic support values (bootstrap support: BS; posterior probability: PP) for crown and stem nodes, distribution of the sister group (for non-endemics, distribution of the species in mainland), stem and crown ages, classification of lineages according to divergence times for the Canarian thermophilous plant community following the methodology proposed in this paper (i.e., mediterranean, pre-mediterranean and undetermined) and references (next page).

Canarian (macaronesian) lineage including termophilous species	Number of species in the lineage	Sister group	Well-supported canarian monophyletic lineage ML (BS > 70)	Well-supported thermophilous monophyletic lineage BI (PP > 0.90)	Well-supported sister-group relationship ML (BS > 70)	Well-supported sister-group relationship BI (PP > 0.90)	Sister group distribution / Non-endemic species distribution	Stem age	Crown age	Type	References
Anagyris latifolia Brouss. ex Willd.	1 spp	*Anagyris foetida* Lour.	YES (100)	YES (1.00)	YES (92)	YES (1.00)	Mediterranean (Circunmenditerranean)	8.20 (3.70-12.70)	1.9 (0.00-4.00)	Undetermined	Ortega-Olivencia and Catalan 2009 (phylogeny, molecular dating)
Argyranthemum lineage	32 spp in the lineage	*Glebionis* Cass., *Heteranthemis* Schott, and *Ismelia* Cass.	_	_	_	_	Mediterranean, Southern Iberia and Morocco, respectively	2.20 (1.50–3.00) - *Argyranthemum* spp. Francisco-Ortega et al 1997	2.48 (1.84-3.04) - White et al 2020	Mediterranean	Francisco-Ortega et al. 1997 (phylogeny, molecular dating); White et al. 2020 (phylogeny, molecular dating)
Artemisia lineage	3 spp in Macaronesia: *Artemisia thuscula* Cav. (Canary Islands), *Artemisia gorgonum* Webb (Cape Verde), *Artemisia argentea* Seb. & Maur. ex Willk. & Lange (Madeira) [also including the mainland *Artemisia arborescens* L.]	Close to *Artemisia arborescens*, *Artemisia sieversiana* Ehrh. ex Willd., *Artemisia absinthium* L.	_	NO (0.43)	_	YES (1.00)	*A. arborescens*: Mediterranean and Yemen; *A. sieversiana*: Asia, *A. absinthium*: Palearctic	3.84 (0.04-6.20) - TMRCA	?	Undetermined	Malik et al. 2017 (phylogeny, molecular dating)
Asparagus lineage I	3 spp - *Asparagus umbellatus* Link, *Asparagus arborescens* Willd. ex Schult. & Schult.f., *Asparagus fallax* Svent.	*Asparagus humilis* Engl.	YES (86)	NO (0.54)	YES (91)	NO (0.46)	E Africa	2.80 (1.39-4.17)	1.75 (0.62-2.70)	Mediterranean*	Norup et al. 2015 (phylogeny), Chen et al. 2013 (calibration points), **this study** (molecular dating)
Asparagus lineage II	3 spp - *Asparagus nesiotes* Svent., *Asparagus scoparius* Lowe, *Asparagus plocamoides* Webb ex Svent. [also including the mainland *Asparagus altissimus* Munby and *Asparagus acutifolius* L.]	Close to *A. altissimus*, *A. acutifolius*, *A. denudatus* (Kunth) Baker, *A. fractiflexus* (Oberm.) Fellingham & N.L.Mey.	NO (51)	NO (0.10)	YES (79)	NO (0.87)	*A. altissimus*: NW Africa; *A. acutifolius*: circunmenditerranean; *A. denudatus*: E and S Africa; *A. fractiflexus*: S Africa	1.60 (0.72-2.38) - TMRCA	?	Mediterranean	Norup et al. 2015 (phylogeny), Chen et al. 2013 (calibration points), **this study** (molecular dating)
Bosea yervamora L.	1 spp	*Bosea cypria* Boiss. ex Hook.f., *Bosea amherstiana* (Moq.) Hook.f.	YES (94)	YES (1.00)	YES (100)	YES (1.00)	E Med, C Asia	5.71 (1.75-11.61)	1.67 (0.37-3.35)	Undetermined	Di Vincenzo et al. 2018 (phylogeny, calibration points), **this study** (molecular dating)
Brachypodium arbuscula Gay ex Knoche	1 spp	*Brachypodium retusum* (Pers.) P.Beauv.	_	_	YES (> 80 BS)	_	Circunmediterranean + Arabia	0.80 (1.47–0.14)	?	Mediterranean	Díaz-Pérez et al. 2018 (phylogeny, molecular dating)
Bryonia verrucosa Aiton	1 spp	Rest of *Bryonia* spp.	YES (89)	NO (polytomy)	YES (1.00)	YES (1.00)	Palearctic (N. Africa, Europe to Central Asia and W. Himalaya)	5.19 (2.41-8.56)	1.74 (0.23-3.17)	Undetermined	Volz and Renner 2008 (phylogeny), Schaefer et al. 2009 (calibration points), **this study** (molecular dating)
Cheirolophus lineage	17 spp in the lineage	*Cheirolophus uliginosus* (Brot.) Dostál	_	YES (1.00)	_	YES (1.00)	Mediterranean (Iberian Peninsula)	8.50 (4.70–12.50)	1.70 (0.80–2.90)	Undetermined	Vitales et al. 2014 (phylogeny, molecular dating)
Chrysojasminum odoratissimum (L.) Banfi	1 spp	Rest of *Chrysojasminum* spp.	YES (98)	YES (1.00)	YES (74) but clade as a whole, not species relationships)	YES (1.00)	*Chrysojasminum bignoniaceum* (Wall. ex G.Don) Banfi: India, *C. parkeri* (Dunn) Banfi: West Himalaya, *C. humile* (L.) Banfi: S. Iran to Central China and N. Myanmar, *C. fruticans* (L.) Banfi: Medit. to N. Iran	14.86 (5.79-26.03)	4.79 (1.25-9.44)	Pre-mediterranean	Jeyarani et al. 2018 (phylogeny), Vargas et al. 2014 (calibration points), **this study** (molecular dating)
Cistus monspeliensis L.	1 spp	Non-endemic	_	YES (> 0.95)	_	YES (0.90)	Mediterranean	0.50 (0.20–0.90)	0.23 (0.05-0.52)	Mediterranean	Fernández-Mazuecos and Vargas 2010 (phylogeny, molecular dating - stem node estimation); Coello et al. 2021 (molecular dating - Crown node)
Convolvulus lineage II	3 spp - *Convolvulus floridus* L.f., *Convolvulus scoparius* L.f., *Convolvulus caput-medusae* Lowe	*C. cneorum*, *C. lanuginosus*, *C. dorycnium*	YES (100, MP)	_	YES (100, MP)	_	E Mediterranean, W Asia	1.50 (0.35–2.65)	0.59 (0.07–1.11)	Mediterranean	Carine et al. 2004 (phylogeny); Carine 2005 (molecular dating)
Crambe lineage	14 spp in the lineage, 9 spp in the thermophilous (*Crambe arborea* Webb ex Christ, *Crambe laevigata* DC. ex Christ, *Crambe scaberrima* Webb ex Bramwell, *Crambe gomeraea* Webb ex Christ, *Crambe wildpretii* Prina & Bramwell, *Crambe pritzelii* Bolle, *Crambe scoparia* Svent., *Crambe tamadabensis* Prina & Marrero Rodr., *Crambe sventenii* Pett. ex Bramwell & Sunding)	Sister to *Crambe kralikii*	YES (90)	_	YES (98)	_	Mediterranean (Magrheb)	14.90 (9.30–20.30)	8.20 (3.90–12.50)	Pre-mediterranean	Francisco-Ortega et al. 2002 (phylogeny); Kim et al. 2008 (molecular dating)
Dioscorea edulis (Lowe) Campos, Wilkin & Viruel	1 spp	Sister to *Dioscorea communis* (L.) Caddick & Wilkin *and Dioscorea cretica* (L.) Campos, Wilkin & Viruel	_	_	YES (100)	NO (1.00)	W, N, E Mediterranean	13.48 (5.20-22.00)	?	Undetermined	Viruel et al. 2016 (phylogeny, molecular dating), Campos et al. in prep (phylogeny, molecular dating)
Dracaena lineage	2 spp - *Dracaena draco* (L.) L., *Dracaena tamaranae* Marrero Rodr., R.S.Almeira & M.Gonzáles-Martin	*Dracaena cochinchinensis* (Lour.) S.C.Chen	YES (100)	YES (1.00)	NO (56)	NO (0.60)	SE Asia	11.80 (4.90-16.30)	2.30 (0.70–5.80)	Undetermined*	Durán et al. 2020 (phylogeny, molecular dating)
Dracunculus canariensis Kunth	1 spp	*Dracunculus vulgaris* Schott	YES (100)	YES (1.00)	NO (56)	NO (0.80)	Mediterranean (Southern Europe, Argelia)	12.10 (5.82-18.49)	2.76 (0.48-5.82)	Undetermined	Mansion et al. 2008 (Phylogeny), Mansion et al. 2008, Nauheimer et al 2012 (calibration points), **this study** (molecular dating)
Echium lineage	27 Macaronesian spp in the lineage. *Echium handiense* Svent., *Echium giganteum* L.f. and *Echium strictum* L.f. in the thermophilous	*Echium parviflorum* St.-Lag. and *Echium sabulicola* Pomel (Böhle et al. 1996), *Echium tenue* Roth, *Echium sabulicola* Pomel (García-Maroto et al 2009)	YES (100)	YES (1.00)	YES (98, MP)	_	Mediterranean (Circunmenditerranean)	7.90 (4.30–11.10) - Kim et al 2008, 21.00 (Calibration point, García-Maroto et al 2009)	3.70 (1.50–5.90) - Kim et al 2008, 6.95 (3.04-10.86) - García-Maroto et al 2009	Pre-mediterranean	Böhle et al. 1996 (phylogeny); Kim et al. 2008 (molecular dating), García-Maroto et al. 2009 (phylogeny + molecular dating)
Ephedra fragilis Desf.	1 spp	Non-endemic	NO (polytomy)	NO (0.14)	NO (polytomy)	NO (0.59)	Mediterranean (Western Mediterranean - *E. fragilis* distribution)	1.29 (0.25-2.78) - TMRCA	?	Mediterranean	Ickert-Bond et al. 2009 (phylogeny, calibration points), **this study** (molecular dating)
Erysimum lineage	4 Macaronesian in the linage: *Erysimum bicolor* (Hornem.) DC., *Erysimum caboverdeanum* (A.Chev.) Sunding, *Erysimum scoparium* (Brouss. ex Willd.) Wettst. and *Erysimum arbuscula* (Lowe) Snogerup	*Erysimum ehrendorferi* Polatschek, *Erysimum nervosum* Pomel, *Erysimum gramineum* Pomel	_	NO (0.70)	_	NO (0.55)	Mediterranean (Magrehb)	0.80 (0.50–1.10) - *Erysimum* spp.	<1.00 - *Erysimum* spp.	Mediterranean	Moazzeni et al. 2014 (phylogeny, molecular dating)
Euphorbia sect. *Aphyllis* subsect. *Macaronesicae* Molero & Barres	11 species nearly endemic to Macaronesia. *Euphorbia regis-jubae* J.Gay, *Euphorbia lamarckii* Sweet and *Euphorbia bourgeana* J.Gay ex Boiss. are xerophilous and thermophilous specie	Sister to *Euphorbia* sect. *Aphyllis* subsect. *Africanae* Molero & Barres (see Su et al 2016)	_	YES (1.00)	_	YES (1.00)	E, C and S Africa	9.81 (8.76–10.86)	6.92 (5.37–8.47)	Pre-mediterranean*	Barres et al. 2011 (phylogeny); Sun et al. 2016 (molecular dating)
Globularia lineage	4 Macaronesian spp: *Globularia amygdalifolia* Webb, *Globularia ascanii* Bramwell & Kunkel, *Globularia salicina* Lam., *Globularia sarcophylla* Svent.	*Globularia arabica* Jaub. & Spach, *Globularia alypum* L.	YES (100)	YES (1.00)	YES (70)	NO (0.80)	N, Africa, Mediterranean	0.30 (0.10–0.60)	0.20	Mediterranean	Affenzeller et al. 2018 (phylogeny, molecular dating)
Gonospermum lineage	7 spp. Two of the species (i.e., *G. elegans* and *G. canariense*) occur primarily in the pine forest. The remaining species of the Gonosperminae are mainly found on northern slopes of the lowland scrub zone (Oleo-Rhamnetea crenulatae A. Santos).	*Tanacetum*, *Matricaria*, *Anthemis*	NO (54, MP)	_	NO (polytomy)	_	Mediterranean	3.10 - *Gonosperum* spp	?	Undetermined	Francisco-Ortega et al. 2002 (phylogeny), Oberprieler 2017 (molecular dating)
Gymnosporia lineage	3 spp - *Gymnosporia cassinoides* (L'Hér.) Masf., *Gymnosporia cryptopetala* Reyes-Bet. & A.Santos, *Gymnosporia dryandrii* (Lowe) Masf	*G. parviflora*, *G. dhofarensis*, *G. arbutifolia*, *G. engleriana* (high support)	YES (100)	YES (1.00)	YES (93)	YES (1.00)	CE Africa, S Asia	3.78 (2.11-5.36)	1.27 (0.46-2.00)	Undetermined*	Oberprieler et al. 2017 (phylogeny and calibration points), **this study** (molecular dating)
Helianthemum Mill. sect. *Helianthemum*	15 spp. *Helianthemum gonzalezferreri* Marrero Rodr. from thermophilous (probably others). Different biomes	*Helianthemum grosii* Pau & Font Quer, *Helianthemum ruficomum* (Viv.) Spreng., *Helianthemum helianthemoides* (Desf.) Grosser, Engler, Pflanzenr, *Helianthemum obtusifolium* Dunal	YES (>75)	YES (>0.95)	YES (>75)	YES (>0.95)	Mediterranean (NW Africa, Cyprus, Turkey)	1.82 (0.61–3.04)	1.09 (0.32–1.90)	Mediterranean	Martín-Hernanz et al. 2019, 2021 (phylogeny); Albaladejo et al. 2021 (molecular dating)
Hypericum canariense L.	1 spp	*Hypericum androsaemum* L., *Hypericum grandifolium* Choisy, *Hypericum hircinum* subsp. *Metroi* (Maire & Sauvage) Sauvage, *Hypericum foliosum* Aiton	NO (> 50)	NO (> 0.5)	YES (79)	YES (0.91)	Mediterranean, Azores	10.8 (5.30–17.40)	1.90 (0.20–3.50)	Undetermined	Dlugosch and Parker 2007 (phylogeny), Meseguer et al. 2013 (phylogeny, molecular dating), Pokorny et al. 2015 (molecular dating)
Juniperus turbinata subsp. *Canariensis* (Guyot & Mathou) Rivas Mart., Wildpret &	1 spp	Non-endemic	NO (polytomy)	NO (polytomy)	NO (polytomy)	NO (polytomy)	_	4.91(1.18-9.19) - TMRCA	?	Undetermined	Mao et al. 2010 (phylogeny, calibration points), **this study** (molecular dating)
Malva canariensis M.F.Ray	1 spp	*Lavatera maritima* Gouan	_	_	_	YES (1.00)	W Mediterranean	2.78 (0.44–5.76)	?	Mediterranean	Fuertes et al. 2002 (phylogeny); Villa et al. 2018 (molecular dating)
Myrsine excelsa D.Don	1 spp	*Myrsine semiserrata* Wall.	YES (100)	YES (1.00)	YES (74)	NO (0.58)	S Asia	3.98 (1.59-7.06) - This study; 4.56 (2.50-5.70) - Kondraskov et al 2015	1.07 (0.28-2.11)	Undetermined*	Appelhans et al. 2020 (phylogeny), Rose et al. 2018 (calibration points); Kondraskov et al. 2015, **this study** (molecular dating)
Navaea phoenicea (Vent.) Webb & Berthel.	1 spp	*Lavatera maritima* + *Malva canariensis*	_	_	_	YES (0.99)	Mediterranean	6.77 (2.67–10.82)	?	Undetermined	Escobar García et al. 2009 (phylogeny); Villa et al. 2018 (molecular dating)
Olea europaea subsp. guanchica P.Vargas, J.Hess, Muñoz Garm. & Kadereit	1 spp	*O. europea* L. subsp. *europaeae*	NO (polytomy)	NO (polytomy)	NO (polytomy)	NO (polytomy)	Mediterranean	2.60 (1.00–3.00)	?	Mediterranean	Besnard et al. 2009
Pistacia atlantica Desf.	1 spp	Non-endemic. Unresolved population relationships	NO (polytomy)	NO (polytomy)	NO (polytomy)	NO (polytomy)	Mediterranean (Southern and Eastern Mediterranean - *P. atlantica* distribution)	1.15 (0.24-2.43) - TMRCA	_	Mediterranean	Xie et al. 2014 (phylogeny + calibration points), **this study** (molecular dating)
Pistacia lentiscus lineage I	Population from Tenerife (Matanza, Santa Ursula)	Non-endemic - Population related to *Pistacia aethiopica* Kokwaro	_	_	NO (polytomy)	NO (polytomy)	E Africa (*P. aethiopica*)	3.96 (1.52-6.71)	1.15 (0.00-1.43)	Undetermined*	Xie et al. 2014 (phylogeny + calibration points), **this study** (molecular dating)
Pistacia lentiscus lineage II	Population from Tenerife (Anaga), Gran Canaria (Bandama) and Fuerteventura (Esquinzo)	Non-endemic - Sister to populations from Spain and Morocco	NO (polytomy)	NO (polytomy)	NO (polytomy)	YES (polytomy)	Mediterranean (Circunmenditerranean + Canary Islands - *P. lentiscus* distribution)	1.76 (0.49-3.37) - TMRCA	_	Mediterranean	Xie et al. 2014 (phylogeny + calibration points), **this study** (molecular dating)
Rhamnus crenulata Aiton	1 spp	*Rhamnus lycioides* Pall.	NO (51)	YES (0.97)	YES (90)	YES (1.00)	Mediterranean (Western and Eastern Mediterranean)	3.88 (1.79-6.59)	1.71 (0.49-3.38)	Undetermined	Bolmgren and Oxelman 2004 (phylogeny), Onstein et al. 2015 (calibration points), **this study** (molecular dating)
Rubia fruticosa Aiton	1 spp	Sister to a clade containing 10 spp	_	YES (1.00)	_	NO (0.84)	Circunmediterranean, Horn of Africa, Azores, Madeira	6.69 (12.40-3.20)	2.10 (5.40-1.10)	Undetermined	Schaefer et al. unpublished (phylogeny and molecular dating)
Ruta lineage	3 spp - *Ruta pinnata* L.f., *Ruta oreojasme* Webb, *Ruta microcarpa* Svent.	*Ruta montana* (L.) L.	YES (100)	YES (1.00)	NO (51)	NO (0.72)	Mediterranean	17.04 (8.14–27.37)	8.10 (2.70–14.90)	Pre-mediterranean	Salvo et al. 2010 (phylogeny and molecular dating)
Sideritis lineage	27 spp. Different biomes	*Sideritis cossoniana* Ball			YES	_	Mediterranean (Morocco)	11.90 (6.00–17.80)	3.30 (1.20–5.40)	Pre-mediterranean	Barber et al. 2007 (phylogeny); Kim et al. 2008 (molecular dating)
Sideroxylon canariense Leyens, Lobin & A.Santos	1 spp	Sister to a clade containing 11 spp	YES (100)	YES (1.00)	NO (36)	YES (1.00)	Cape Verde, Socotra, C+E Asia, Reunion, Madagascar, Mauricio	37.73 (26.07-56.07)	7.99 (3.28-15.08)	Pre-mediterranean*	Stride et al. 2014 (phylogeny and calibration points), **this study** (molecular dating)
Smilax aspera L.	1 spp	Non-endemic	_	_	_	_	Paleartic + Central Europe - Distribution of *S. aspera*	< 0.30 Ma - haplotype 3 (Iberian Peninsula and Canary Islands) - TMRCA	?	Mediterranean	Chen et al. 2014 (phylogeny and molecular dating)
Solanum lineage	2 spp - *Solanum lidii* Sunding, *Solanum vespertilio* Aiton	*S. humile*, *S. tomentosum*, *S. capense*	YES (89) - MP	_	_	_	S Africa	1.70 (0.70–2.20)	0.90 (0.20–1.30)	Mediterranean*	Anderson et al. 2006 (phylogeny), Särkinen et al. 2013 (molecular dating)
Sonchus lineage	32 spp. Different biomes	*S. masguindalii*, *S. fragilis*, *S. pustulatus* (Kim et al 2008) // *S. palustris* (Kim et al 2007)			NO	_	Western Mediterranean	13.20 (7.70–18.70)	8.50 (3.00–13.90)	Pre-mediterranean	Kim et al. 1996 (phylogeny); Kim et al 2007 (phylogeny); Kim et al. 2008 (molecular dating)
Thesium lineage	4 spp - *Thesium retamoides* (A.Santos) J.C.Manning & F.Forest, *Thesium subsucculentum* (Kämmer) J.C.Manning & F.Forest, *Thesium canariense* (Stearn) J.C.Manning & F.Forest (non included in this study), *Thesium palmense* (see Rodríguez-Rodríguez et al. 2022; non included in this study)	*Thesium mauritanicum* Batt.	YES (99)	YES (1.00)	YES (100)	YES (1.00)	Mediterranean (NW Africa)	14.53 (6.56-23.57)	3.86 (1.06-7.39)	Pre-mediterranean	Zhigila et al. 2020, Rodríguez-Rodríguez et al. 2022 (phylogeny), Moore et al. 2010 (calibration points), **this study** (molecular dating)
Visnea mocanera L.f.	1 spp	Sister to all other species of the tribe Freziereae (Theaceae)	_	_	_	NO (<0.90)	Asia and America	27.00 (17.00-41.00)	2.50 (0.10-5.00)	Undetermined*	Schüßler 2020
	In red, thermophilous spp when the lineage is composed of several spp									* Non-mediterranean sister-groups distribution	

Table S2. Studied taxa (thermophilous species in bold) and their corresponding collection code, voucher information (herbarium code), island (archipelado or country), locality, collection date, collector's name (leg), DNA sequenced regions and GenBank accesion numbers.

ASPARAGUS									
Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	PHYC	*trn* H-*psb* A	*trn* D-*trn* T
Asparagus arborescens	3PV21	NA	Tenerife	Los Adernos (Buenavista)	09/11/2020	P Marrero, M Nogales	_	OM418819	OM418837
Asparagus arborescens	AQ1768	MA-01-00750332	Lanzarote	Arrieta, Malpaís de la Corona, La Caleta de las Aulagas	05/04/2006	C Aedo, L Medina, A Quintanar	_	OM418820	OM418838
Asparagus fallax	4PV21	NA	Tenerife	Vueltas de Taganana	27/10/2020	P Marrero, M Nogales	_	OM418821	OM418839
Asparagus nesiotes	26081	MA-01-00628064	Lanzarote	Orzola (Kanarische Inselm), Malpais de la Corona	06/02/1989	Max Nydegger	_	OM418822	OM418840
Asparagus pastorianus	5PV21	NA	Tenerife	Buenavista	09/11/2020	P Marrero, M Nogales	_	OM418823	OM418841
Asparagus pastorianus	s/n	NA	Gran Canaria	Inmediaciones de Cambalud	18/05/2021	María Olangua	OM418807	OM418824	OM418842
Asparagus pastorianus	20448	MA-01-00785968	Morocco	coast road. 28.5 km from Tiznit, N of Mirleft	06/02/2007	TM Upson, Stephen Jury	OM418808	OM418825	OM418843
Asparagus plocamoides	71PV21	NA	Tenerife	Barranco de Tamadaya (Arico)	25/01/2021	P Marrero, M Nogales	OM418809	OM418826	OM418844
Asparagus plocamoides	JC1973	MA-01-00768757	Gran Canaria	Montaña las Tierras	26/02/2008	B Ríos, Joel Calvo, Inés Álvarez	OM4188010	OM418827	OM418845
Asparagus scoparius	53PV21	NA	Tenerife	Los Adernos (Buenavista del Norte)	23/12/2020	P. Marrero/M. Nogales	OM4188011	OM418828	OM418846
Asparagus scoparius	5FP19	NA	La Palma	Sendero Mirador del Topo de las Barandas	19/02/2019	Fernando Pomeda, Daniel Pareja	OM4188012	OM418829	OM418847
Asparagus scoparius	91PV21	NA	La Palma	Lomo del Cerro	29/05/2021	Maria Olangua Corral, Sara Martín Hernanz	OM4188013	OM418830	OM418848
Asparagus scoparius	92PV21	NA	La Palma	Ermita de las Nieves	29/05/2021	Maria Olangua Corral, Sara Martín Hernanz	OM4188014	OM418831	OM418849
Asparagus scoparius	17407	MA-01-00714488	Madeira	Faja dos Padres	28/02/2004	Santiago Castroviejo Bolíbar	OM4188015	OM418832	OM418850
Asparagus umbellatus	81PV21	NA	Tenerife	Tagoro	29/04/2021	S. Martín-Hernanz, M. Nogales, P. Vargas	OM4188016	OM418833	OM418851
Asparagus umbellatus	389	MA-01-00892832	La Gomera	Gomera. Path descending from Arure	07/05/1968	LJG Van der Maesen, ERS Sventenius	OM4188017	OM418834	OM418852
Asparagus umbellatus	111PV21	NA	La Palma	Cerca del Centro de Visitantes de Caldera de Taburiente	30/05/2021	María Olangua, Sara Martín Hernanz	OM4188018	OM418835	OM418853
Asparagus umbellatus	s/n	NA	Gran Canaria	Bco del Laurel	18/05/2021	María Olangua	_	OM418836	OM418854

BOSEA							
Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	*trn* K/*mat* K
Bosea yervamora	73PV21	NA	Tenerife	Bco. de Ruiz, Los Realejos	26/02/2021	P Marrero, M Nogales	OM460770
Bosea yervamora	17239	MA-01-00805386	Gran Canaria	Agaete, pr. Los Berrazales	09/04/2010	Carlos Aedo Pérez	OM460771
Bosea yervamora	98PV21	NA	La Palma	Juan Mayor	29/05/2021	María Olangua, Sara Martín Hernanz	OM460772
Bosea yervamora	141PV21	NA	Fuerteventura	Barranco Malnombre (ExHorto Jardín Botánico Fuerteventura)	06/11/2021	Moritz Albersdörser	OM460773
Bosea yervamora	142PV21	NA	Fuerteventura	Riscos de Jandía	06/11/2021	Stephan Schloz	OM460774
Bosea cypria	16333	MA-01-00748044	Cyprus	Halbinsel Karpasia/Karpas, Dipkarpaz/Rizokarpaso, im Ortsgebiet an der Strrasse nach Agios Filon	08/07/2005	Robert M. Vogt	OM460775
Bosea amherstiana	s/n	BC-956022	Ex Horto Hymalaya	Barcelona, Montjuïc, near cable car	20/06/2016	S. Pyke, N. Ibáñez, J. López-Pujol & P. Farelo	OM460776

CHRYSOJASMINUM									
Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	ITS	*trn* L-*trn* F	*trn* H-*psb* A
Chrysojasminum odoratissimum	21PV21	NA	Tenerife	Bco. Badajoz	22/10/2020	P. Marrero, M. Nogales	OM522958	OM436792	OM436781
Chrysojasminum odoratissimum	CAN 060	MA-01-00848477	Tenerife	au dessus de Güimar en montant vers le Pico del Valle	02/05/1973	Hervé M. Burdet	_	OM436803	OM436791
Chrysojasminum odoratissimum	s/n	ORT-39768	Fuerteventura	Pico de la Zarza ex horto	01/10/2007	S. Scholz	_	OM436793	_
Chrysojasminum odoratissimum	93PV21	NA	La Palma	Ermita de las Nieves	29/05/2021	María Olangua, Sara Martín Hernanz	_	OM436794	OM436782
Chrysojasminum odoratissimum	99PV21	NA	La Palma	Finca Amado	30/05/2021	María Olangua, Sara Martín Hernanz	_	OM436795	OM436783
Chrysojasminum odoratissimum	s/n	NA	Gran Canaria	Mta. De Amagro	01/04/2021	María Olangua	_	OM436796	OM436784
Chrysojasminum odoratissimum	10873MV	MA-01-00757874	Madeira	Isla Deserta Grande, alrededores de la casa de los forestales	22/03/2007	Mauricio Velayos	OM522959	OM436797	OM436785
Chrysojasminum odoratissimum	s/n	NA	La Gomera	Bajada a Tazo	27/03/2021	María Olangua	_	OM436798	OM436786
Chrysojasminum fructicans	s/n	MA-01-00892149	Spain	León, La Balouta	01/07/2012	Carlos Manuel Romero Rodríguez	OM522960	OM436799	OM436787
Chrysojasminum fructicans	620	MA-01-00908856	Tunisia	Gouv. Ben Arous, Jebel Ressas, c. 3.5 km SW of Dawwar at Talib Áli	28/03/2014	E. Vitek, N. Ardenghi	OM522961	OM436800	OM436788
Chrysojasminum fructicans	17	MA-01-00775921	Georgia	Kartli, Mtskheta District (33). Right bank of Mtkvari River. Karsani	29/07/2004	Mukbaniani, D. Mtskhvetadze	_	OM436801	OM436789
Chrysojasminum parkeri	43	MA-01-00884036	Ex Horto	Recinto del Real Jardín Botánico. Plantas cultivadas	13/05/2014	Voluntarios RJB	OM522962	OM436802	OM436790

DRACUNCULUS										
Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	*mat* K	*trn* K	*rbc* L	*rpl* 16
Dracunculus canariensis	79PV21	NA	Tenerife	El Caletón (La Matanza)	07/04/2021	P. Marrero, M. Nogales	OM489535	OM489538	OM460824	OM489541
Dracunculus canariensis	17224	MA-01-00805401	Gran Canaria	pr. Moya, barranco de los Laureles	08/04/2010	Carlos Aedo Pérez	OM489536	OM489539	OM460825	OM489542
Dracunculus canariensis	34FP21	NA	La Palma	Finca Amado	22/06/2021	Fernando Pomeda	OM489537	OM489540	OM460826	_

EPHEDRA										
Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	ITS	*mat* K	*psb* A-*trn* H	*rps* 4
Ephedra fragilis	11PV21	NA	Tenerife	Lomo de Basta (Icod)	12/09/2020	P Marrero, M Nogales	OM478581	_	OM489665	OM541666
Ephedra fragilis	117PV21bis	NA	Tenerife	Icod	05/07/2021	P Marrero, M Nogales	OM478582	OM489662	OM489666	OM541667
Ephedra fragilis	s/n	ORT-37328	La Palma	Bajada a Aeropuerto sobre La Bajita	26/07/2003	A. Santos	OM478583	_	OM489667	_
Ephedra fragilis	s/n	NA	Gran Canaria	Ex horto Jardín Botánico Viera y Clavijo	13/05/2021	María Olangua	OM478584	OM489663	OM489668	OM541668
Ephedra fragilis	VIT 86118	SEV-264317	Spain	Navarra, Andosilla, cerro La Peña, sobre la vega del río Ega	02/07/2010	P.M. Uribe-Echebarria	OM478585	_	OM489669	_
Ephedra major	12PV21	NA	Tenerife	El Teide, Minas de San José	26/10/2020	P Marrero, M Nogales	OM478586	OM489664	OM489670	OM541669
Ephedra major	117PV21	NA	Tenerife	Pico Cabras (El Teide)	15/07/2021	Manuel Nogales	OM478587	_	OM489671	OM541670
Ephedra major	s/n	SEV-90929	Spain	Madrid, Aranjuez. N-400. Cerros del Arroyo Martín	08/06/1982	S. Laorga	OM478588	_	OM489672	OM541671
Ephedra major	17713	SEV-270374	Morocco	High Atlas, El-Ksiba to Tinghir, road from Imilchil to Tinghir, just south of pass	09/07/1997	S.L. Jury, A. Abaouz, M. Ait Lafkih & A.J.K. Griffiths	OM478589	_	_	_

GYMNOSPORIA

Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	ITS
Gymnosporia cassinoides	84PV21	NA	Tenerife	Bco. de Badajoz	29/04/2021	S. Martín-Hernanz, M. Nogales, P. Vargas	OM514992
Gymnosporia cassinoides	28FP19	NA	La Palma	Sendero Espigón Atravesado Zona de La Portada	20/02/2019	Fernando Pomeda, Daniel Pareja	OM514993
Gymnosporia cassinoides	103PV21	NA	La Palma	Finca Amado	30/05/2021	María Olangua, Sara Martín Hernanz	OM514994
Gymnosporia cassinoides	AH 2533	MA-01-00733780	La Gomera	Vallehermoso, meseta de Vallehermoso	16/04/2005	A. Herrero, L. Medina, J. Leralta	OM514995
Gymnosporia cassinoides	s/n	NA	Gran Canaria	Bco de Azuaje	18/05/2021	María Olangua	OM514996
Gymnosporia cassinoides	s/n	ORT-37909	Fuerteventura	Pico de La Zarza, Jandía	12/05/2005	S. Scholz	OM514997
Gymnosporia cassinoides	143PV21	NA	Fuerteventura	Riscos de Jandía	06/11/2021	Stephan Schloz	OM514998
Gymnosporia cassinoides	144PV21	NA	Fuerteventura	Vega del Río Palmas	06/11/2021	Stephan Schloz	OM514999
Gymnosporia cryptopetala	s/n	ORT-41369	Lanzarote	Malpaís de la Corona	07/04/2009	J.A. Reyes-Betancort	OM515000
Gymnosporia cryptopetala	146PV21	NA	Lanzarote	Barranco de Esquinzo	06/11/2021	Stephan Schloz	OM515001
Gymnosporia cryptopetala	148PV21	NA	Fuerteventura	Riscos de Jandía (ExHorto)	06/11/2021	Stephan Schloz	OM515002
Gymnosporia dryandri	13627	MA-01-00757582	Madeira	pr. Porto Novo	17/03/2007	Carlos Aedo Pérez	OM515003
Gymnosporia dryandri	17397	MA-01-00714538	Madeira	San Vicente	27/02/2004	Santiago Castroviejo Bolíbar	OM515004

JUNIPERUS

Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	ITS	*mat* K	*rbc* L	*trn* L-*trn* F	*rps* 4	*trn* S-*trn* G	*trn* V	*psb* B1-*psb* B2
Juniperus turbinata* subsp. *canariensis	68PV21	NA	Tenerife	Acantilados de la Culata (Guarachico)	20/01/2021	P. Marrero, M. Nogales	_	OM801629	OM801646	OM801663	OM801654	OM801672	OM801681	OM801638
Juniperus turbinata* subsp. *canariensis	100PV21	NA	La Palma	Finca Amado	30/05/2021	María Olangua, Sara Martín Hernanz	OM759832	OM801630	OM801647	OM801664	OM801655	OM801673	OM801682	OM801639
Juniperus turbinata* subsp. *canariensis	49FP21	NA	El Hierro	La Sabina	28/06/2021	Fernando Pomeda	OM759833	OM801631	OM801648	OM801665	OM801656	OM801674	OM801683	OM801640
Juniperus turbinata* subsp. *canariensis	19682	MA-01-00866694	El Hierro	Ermita de Nuestra Señora de los Reyes, montaña Tagutanta	03/01/2013	Carlos Aedo Pérez	_	OM801632	OM801649	OM801666	OM801657	OM801675	OM801684	OM801641
Juniperus turbinata	630/14	MA-01-00898926	Spain	Cádiz, Sierra de Grazalema, La Camilla	21/10/2014	F.J. Salgueiro, M. Arsita, P.L. Ortiz	OM759834	OM801633	OM801650	OM801667	OM801658	OM801676	OM801685	OM801642
Juniperus turbinata	s/n	MA-01-00909388	Tunisia	Gouv. Bizerte, coast c. 6.5km NNW Bizerte, near the Roman grottos	29/03/2014	E. Vitek, F. Abdallah	_	OM801634	OM801651	OM801668	OM801659	OM801677	OM801686	OM801643
Juniperus turbinata	JC2621	MA-01-00781962	Morocco	Tánger-Tetouan, Tleta-Oued-Laou, pr. Cap Mazari	25/06/2008	Joel Calvo, Alejandro Quintanar Sánchez	OM759835	OM801637	OM801652	OM801669	OM801660	OM801678	OM801687	OM801644
Juniperus turbinata	484	MA-01-00690874	Portugal	Algarve, Vila do Bispo, Raposeira, praia da Ingrina	06/06/2001	Sara Nisa de Oliveira, L. Medina, M. Pardo de Santayana	_	OM801635	OM801653	OM801670	OM801661	OM801679	OM801688	OM801645
Juniperus turbinata	s/n	MA-01-00779192	Spain	Cádiz, Ensenada de Bolonia	08/04/1992	L.M. Ferrero	_	OM801636	_	OM801671	OM801662	OM801680	OM801689	_

MYRSINE

Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	ITS
Myrsine excelsa	14PV21	NA	Tenerife	Los Silos	19/10/2020	P Marrero, M Nogales	OM522014
Myrsine excelsa	25FP19	NA	La Palma	Alrededores Centro de Visitantes	20/02/2019	Fernando Pomeda, Daniel Pareja	OM522015
Myrsine excelsa	s/n	NA	La Gomera	La Meseta	25/03/2021	María Olangua	OM522016
Myrsine canariensis	30PV21	NA	Tenerife	Vueltas de Taganana	27/10/2020	P. Marrero, M. Nogales	OM522017

PISTACIA								
Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	ITS	ETS
Pistacia atlantica	28PV21	NA	Tenerife	Los Silos	19/10/2020	P. Marrero, M. Nogales	OM746110	OM801613
Pistacia atlantica	s/n	MA-01-00694792	Gran Canaria	Agaete, Los Berrazales, camino al Sao	09/04/2001	Roca, Marrero	OM746111	OM801614
Pistacia atlantica	110PV21	NA	La Palma	Ex horto Centro Visitantes Caldera de Taburiente	30/05/2021	María Olangua, Sara Martín Hernanz	OM746112	OM801615
Pistacia atlantica	2386-08	ORT-40296	La Palma	Puntallana, Bco. sobre Puerto Trigo	09/08/2008	Arnoldo Santos	_	OM801616
Pistacia atlantica	31FP21	NA	La Palma	Cubo de la Galga	19/06/2021	Fernando Pomeda	OM746113	OM801617
Pistacia atlantica	145PV21	NA	Lanzarote	NA	06/11/2021	Stephan Schloz	OM746114	OM801618
Pistacia atlantica	JC3814	MA-01-00799482	Morocco	Souss - Massa - Daraâ Anezi, Agadir-ogjgal, jbel Imzi, ladera norte	06/06/2009	Joel Calvo	OM746115	OM801619
Pistacia khinjuk	s/n	MA-01-00748956	Iran	Isfahan Province/Semirom/Vanak/Cheshme-Naz	12/06/2003	M.R. Parishani	OM746116	OM801620
Pistacia lentiscus	s/n	MA-01-00867153	Spain	Córdoba, Orilla del Arroyo Guadalnuño	11/04/2010	V.R. Invernón, M. de la Estrella	OM746117	OM801621
Pistacia lentiscus	JC0621	MA-01-00758144	Morocco	Antiatlas occidental, Ladera NE Jbel Imzi	15/04/2007	T. Buira, Joel Calvo	_	OM801622
Pistacia lentiscus	78PV21	NA	Tenerife	Barranco de la Matanza	28/03/2021	P. Marrero, M. Nogales	OM746118	OM801623
Pistacia lentiscus	165PV21	NA	Tenerife	Barranco de Santa Úrsula	03/12/2021	P. Marrero, M. Nogales	OM746119	OM801624
Pistacia lentiscus	166PV21	NA	Tenerife	Barranco de Santa Úrsula	03/12/2021	P. Marrero, M. Nogales	OM746120	OM801625
Pistacia lentiscus	167PV21	NA	Tenerife	Anaga	13/12/2021	P. Marrero, Javier Romero	OM746121	OM801626
Pistacia lentiscus	s/n	NA	Gran Canaria	Caldera de Bandama	21/05/2021	María Olangua	OM746122	OM801627
Pistacia lentiscus	147PV21	NA	Fuerteventura	Barranco de Esquinzo	06/11/2021	Stephan Schloz	OM746123	OM801628

RHAMNUS								
Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	ITS	*trn* L-*trn* F
Rhamnus crenulata	33PV21	NA	Tenerife	Los Adernos (Buenavista)	09/11/2020	P. Marrero, M. Nogales	OM522104	OM541906
Rhamnus crenulata	5901	MA-01-00647208	La Palma	Los Franceses	29/07/2000	Carlos Aedo Pérez	OM522105	OM541907
Rhamnus crenulata	94PV21	NA	La Palma	Ermita de las Nieves	29/05/2021	María Olangua, Sara Martín Hernanz	OM522106	OM541908
Rhamnus crenulata	s/n	NA	Gran Canaria	Tarifa Alta	09/04/2021	María Olangua Corral	OM522107	OM541909
Rhamnus glandulosa	46PV21	NA	Tenerife	Las Cuadras (Anaga)	16/12/2020	P. Marrero, M. Nogales	OM522108	OM541910
Rhamnus glandulosa	27FP19	NA	La Palma	Los Tiles, Alrededores Centro de Visitantes	20/02/2019	Fernando Pomeda, Daniel Pareja	OM522109	OM541911
Rhamnus integrifolia	35PV21	NA	Tenerife	El Teide	23/10/2020	P. Marrero, M. Nogales	OM522110	OM541912

SYDEROXYLON								
Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	ITS	*trn* H-*psb* A
Sideroxylon canariense	41PV21	NA	Tenerife	Batán de Arriba (Anaga)	11/11/2020	P. Marrero, M. Nogales	OM522633	OM541945
Sideroxylon canariense	MM299	MA-01-00887516	Tenerife	Las Furnias (Icod)	04/01/2015	Mario Mairal	OM522634	OM541946
Sideroxylon canariense	s/n	NA	Gran Canaria	Tenteniguada	09/04/2021	Marcos Díaz Bertrana, María Olangua Corral	OM522635	OM541947
Sideroxylon canariense	s/n	ORT-39460	Fuerteventura	Barranco de Mal Nombre (Pájara)	05/10/2006	S.Scholz	OM522636	OM541948

THESIUM										
Taxa	Collection code	Voucher information	Island/archipelago/country	Locality	Collection date	Leg	ITS	*mat* K	*rpl* 32-*trn* L	*trn* L-*trn* F
Thesium retamoides	24PV21	NA	Tenerife	Bco. Badajoz	24/10/2020	P. Marrero, M. Nogales	OM730033	OM801607	OM801609	OM801611
Thesium subsucculentum	65PV21	NA	Tenerife	Punta de Juan Centellas	20/01/2021	P. Marrero, M. Nogales	OM730034	OM801608	OM801610	OM801612

Table S3. Primers and PCR cycles used for sequencing DNA regions of the 13 plant groups analyzed in this study (genera, seldom families).

ASPARAGUS				
DNA region	Primers	Reference	Primer sequence	PCR cycle
PHYC	PHYC (Asparagus specific): PHYC-F1/PHYC-R1	Hertweck et al. 2015	5' CAG TTA ACC CTG CTG ATG TAC C 3' / 5' ACC TCG CCA CTT TAC AAC CT 3'	5 min at 94 C followed by 39 cycles of 94 C for 1 min, 55 C for 1 min, and 72 C for 1.5 min followed by a final extension at 72 C for 7 min.
trn H-*psb* A	trnHGUG/psbA	Shaw et al. 2005	5' CGC GCA TGG TGG ATT CAC AAT CC 3' / 5' GTT ATG CAT GAA CGT AAT GCT C 3'	initial 3 min at 94 C, followed by 32 cycles of 94 C for 1 min, 53 C for 1 min, 72 C for 1 min, and a final extension at 72 C for 7 min
trn D-*trn* T	trnDGUC/trnTGGU	Shaw et al. 2005	5' ACC AAT TGA ACT ACA ATC CC 3' / 5' CTA CCA CTG AGT TAA AAG GG 3'	initial 3 min at 94 C, followed by 34 cycles of 94 C for 1 min, 53 C for 1 min, 72 C for 1 min, and a final extension at 72 C for 5 min

BOSEA				
DNA region	Primers	Reference	Primer sequence	PCR cycle
trn K/*mat* K	trnK2R		5' AAC TAG TCG GAT GGA GTA G 3'	34 cycles of 94°C (1 min.) denaturation, 52°C (1 min.) annealing, 72°C (2 min.) extension, and 72°C (15 min.) final extension
	trnKF/ ACmatK1400R	Wicke and Quandt 2009 / Müller and Borsch 2005	5' GGG TTG CTA ACT CAA TGG TAG AG 3' / 5' TTC TTC TTT GCA TTT ATT ACG 3'	
	ACmatK500F / psbA5'R	Müller and Borsch 2005 / Shaw et al. 2005	5' TTC TTC TTT GCA TTT ATT ACG 3' / 5' AAC CAT CCA ATG TAA AGA CGG TTT 3'	

CHRYSOJASMINUM				
DNA region	Primers	Reference	Primer sequence	PCR cycle
ITS	ITS1 / ITS2	White et al. 1990	5' TCC GTA GGT GAA CCT GCG G 3' / 5' GCT GCG TTC TTC ATC GAT GC 3'	35 cycles (denaturation for 1 min at 94◦C, annealing for 1 min at 49◦C and 1 min of extension at 72◦C followed by a last cycle of final extension for 5 min at 72◦C).
trn L-*trn* F	trne / trnf	Taberlet et al. 1991	5' GGT TCA AGT CCC TCT ATC CC 3' / 5' ATT TGA ACT GGT GAC ACG AG 3'	35 cycles (denaturation for 1 min at 94◦C, annealing for 1 min at 49◦C and 1 min of extension at 72◦C followed by a last cycle of final extension for 5 min at 72◦C).
trn H-*psb* A	trnHGUG/psbA	Shaw et al. 2005	5' CGC GCA TGG TGG ATT CAC AAT CC 3' / 5' GTT ATG CAT GAA CGT AAT GCT C 3'	35 cycles (denaturation for 1 min at 94◦C, annealing for 1 min at 49◦C and 1 min of extension at 72◦C followed by a last cycle of final extension for 5 min at 72◦C).

DRACUNCULUS				
DNA region	Primers	Reference	Primer sequence	PCR cycle
mat K	matk-F1/matK-3AR	Sang et al. 1997, Winkworth et al. 2002	5' ACTGTATCGCACTATGTATCA 3' / 5' CGT ACA STA CTT TTG TGT TTM CG 3'	1 cycle of 3 to 5 min denaturation at 94◦C, followed by 30 cycles of 30 s denaturation at 94◦C, 1 min annealing at 52◦C to 56◦C, and 1 to 2 min elongation at 72◦C, finishing with a 5- to 10-min elongation step at 72◦C to complete primer extension
trn K	tk3-MY2F/trnK-2R	Winkworth et al. 2002, Johnson and Soltis 1995	5' CAA TCA AAA TCT TCT GGA ATC 3' / 5' AAC TAG TCG GAT GGA GTA G 3'	
rbc L	rbcL-1F/ rbcL-739R	Asmussen and Chase 2001	5' ATG TCA CCA CAA ACAG AAA C 3' / 5' CCG TTA AGT AGT CGT GCA 3'	
	rbcL-636F / rbcL-Rev	Asmussen and Chase 2001	5' CGA AAT CGG TAG ACG CTA CG 3' / 5' TCC TTT TAG TAA AAG ATT GGG CCG AG 3'	
rpl 16	rps16-F / rps16-R2	Oxelman et al. 1997	5' GTG GTA GAA AGC AAC GTG CGA CTT 3' / 5' TCG GGA TCG AAC ATC AAT TGC AAC 3'	

EPHEDRA				
DNA region	Primers	Reference	Primer sequence	PCR cycle
ITS	ITS1-Ep1S/ITS1-Ep2R	Ickert-Bond and Wojciechowski 2004	5' GGA CGG TCT TTG ACC AGT TTA TA 3' / 5' GCG ACG TAG GAA AGG AAA TAG 3'	initial denaturation (92C, 2 min), followed by 40 cycles of denaturation (92C, 45 sec), annealing (55C, 30 sec), and extension (72C, 30 sec), and concluding with a final extension (72C, 7 min).
mat K	trnK-Ep2/matK-Ep3R	Huang et al. 2005	5' TTC ATG AGT CAG GAG AAC 3' / 5' GTA TAT ACT TCA CAC GAT 3'	40 cycles with an annealing temperature of 47 °C and an extension period of 3min, with 10 s added to each subsequent cycle.
psb A-*trn* H	trnHGUG/psbA	Shaw et al. 2005	5' CGC GCA TGG TGG ATT CAC AAT CC 3' / 5' GTT ATG CAT GAA CGT AAT GCT C 3'	initial 3 min at 94 C, followed by 32 cycles of 94 C for 1 min, 53 C for 1 min, 72 C for 1 min, and a final extension at 72 C for 7 min
rps 4	trnSR2/rps5F	Ickert-Bond and Wojciechowski 2004	5' GCT TAC CGG GGT TCG AAT C 3' / 5' ATG TTC CCG TTA TCG AGG ACC T 3'	initial denaturation (92 C, 2 min), followed by 40 cycles of denaturation (92 C, 45 sec), annealing (55 C, 30 sec), and extension (72 C, 30 sec), and concluding with a final extension (72 C, 7 min).

GYMNOSPORIA				
DNA region	Primers	Reference	Primer sequence	PCR cycle
ITS	ITS5 (P1) / ITS4?	White et al. 1990, Kim and Jansen 1994	5' GGA AGT AAA AGT CGT AAC AAG G 3' / 5' TCC TCC GCT TAT TGA TAT GC 3'	the first cycle used a longer denaturation time (3 min) than the normal cycle (1 min) at 95 °C. Each of the 30 cycles consisted of 1 min at 95 °C to denature template DNA, 1 rain at 55 °C to anneal primers to denatured template DNA, and 45 sec at 72 °C for primer extension. Primer extension time was gradually increased by 3 sec intervals during each cycle. After 30 cycles the PCR reactions were incubated at 72 °C for 7 min to complete primer extension.

JUNIPERUS

DNA region	Primers	Reference	Primer sequence	PCR cycle
ITS	Jun-ITS-F	Little et al. 2004	5' GGA AGG AGA AGT CGT AAC AAG G 3'	94°C, 5min, 37 cycles at 94°C, 1min; 56°C, 45 sec and 72°C, 1 min; finally 72°C, 7min
	Jun-ITS-R	Little et al. 2004	5' CTT TTC CTC CGC TTA TTG ATA TG 3'	
mat K	Jun-matK-F	Kusumi et al. 2000	5' CCA AAT TCG TTC TCT CTG TG 3'	**matK F-R:** 94°C, 5 min, 37 cycles of 94°C, 1 min, 53°C, 45 sec and 72°C, 1min and 20 sec, finally 72°C, 7 min; **matK F-IR2**: 94°C, 5 min, 37 cycles of 94°C, 50 sec, 54°C, 45 sec and 72°C, 1min; finally 72°C, 7 min; **matK IF2-R:** 94°C, 5 min; 37 cycles of 94°C, 50 sec, 54°C, 45 sec and 72°C, 1 min; finally 72°C, 7 min
	Jun-matK-R	Kusumi et al. 2000	5' TAT TCC ATG AGT CAG GAG AG 3'	
	Jun-matK-IF2	Kusumi et al. 2000	5' AAG GGA TCT TTC TCC ATA TC 3'	
	Jun-matK-IF4	Kusumi et al. 2000	5' ATT GCG AAC GAA ACT TCC AA 3'	
	Jun-matK-IR2	Kusumi et al. 2000	5' CTT TGG TTT CAA CCG TAT AG 3'	
	Jun-matK-IR4	Kusumi et al. 2000	5' CAG ATA TAC GAG TGC CCT AC 3'	
rbc L	Jun-rbcL-F	Little et al. 2004	5' ATG TCA CCA CAA ACA GAA ACT AAA GCA A	**rbcL F-R**: 94°C, 5 min, 37 cycles of 94°C, 1 min, 54°C, 45 sec and 72°C, 1 min and 10 sec, , finally 72°C, 7 min. **rbcL F-AR**: 94°C, 5 min, 37 cycles of 94°C, 50 sec, 55°C, 45 sec and 72°C, 1 min; finally 72°C, 7 min. **rbcL DF-R**: 94°C, 5 min; 37 cycles of 94°C, 50 sec, 55°C, 45 sec and 72°C, 1min; finally 72°C, 7 min
	Jun-rbcL-R	Little et al. 2004	5' TCA CAA GCA GCA GCT AGT TCA GGA CTC 3	
	Jun-rbcL-AR	Mao et al. 2010	5' TGA GCC AAC GAA GTA TTT GC 3'	
	Jun-rbcL-BF	Mao et al. 2010	3' GCA AAT ACT TCG TTG GCT CA 3'	
	Jun-rbcL-CR	Mao et al. 2010	5' GAA TAA GCA GGA GGA ATT CG 3'	
	Jun-rbcL-DF	Mao et al. 2010	5' CGA ATT CCT CCT GCT TAT TC 3'	
rps 4	Jun-rps4-F	Souza-Chies et al. 1997	5' ATG TCC CGT TAT CGA GGA CCT 3'	94°C 5M, 37 cicles of 94°C 50S, 56°C 45S, 72°C 1M 72°C, and finally 7M 72°C
	Jun-rps4-R	Souza-Chies et al. 1997	5' TAC CGA GGG TTC GAA TC 3'	
trn L-*trn* F	trne / trne	Taberlet et al. 1991	5' GGT TCA AGT CCC TCT ATC CC 3' / 5' ATT TGA ACT GGT GAC ACG AG 3'	94°C 5M, 37 cycles of 95°C 50S, 56°C 40S, 72°C 1M, and finally 72°C 7M
trn S-*trn* G	Jun-trnSGCU	Shaw et al. 2005	5' GCC GCT TTA GTC CAC TCA GC 3'	94°C 5M, 37 cycles of 94°C 50S, 56°C 45S, 72°C 1M, and finally 72°C 7M
	Jun-trnGUCC	Shaw et al. 2005	5' GAA CGA ATC ACA CTT TTA CCA C 3'	
trn V	Jun-trnV-F	Wang et al. 1999	5' GTA GAG CAC CTC GTT TAC AC 3'	94°C 5M, 37 cycles of 94°C 50S, 56°C 45S, 72°C 50s, and finally 72°C 7M
	Jun-trnV-R	Wang et al. 1999	5' CTC GAA CCG TAG ACC TTC TC 3'	
psb B1-*psb* B2	Jun-psbBB-F	Grivet et al. 2001	5' TGC CTT GGT ATC GTG TTC ATA C 3'	**psbB1-B2 F-R:** 94°C 5M, 37 cycles of 94°C 1M, 53°C 45S, 72°C 1M 15S, and finally 72°C, 7M **psbB1-B2 F-IR:** 94°C 5M, 37 cycles of 94°C 50S, 53°C 45S, 72°C 1M, and finally 72°C, 7M
	Jun-psbBB-R	Grivet et al. 2001	5' CYT GTC TTY TTG TAG TTG GAT 3'	
	Jun-psbBB-IF	Mao et al. 2010	5' GCA GGT CTA TTC CAT CTC AGT G 3'	
	Jun-psbBB-IR	Mao et al. 2010	5' CAC GAA CCC GTC GAT CTA TTT C 3'	

MYRSINE

DNA region	Primers	Reference	Primer sequence	PCR cycle
ITS	ITS4 / ITS5	White et al. 1990	5' TCC TCCG CTT ATT GAT ATG C 3' / 5' GGA AGT AAA AGT CGT AAC AAG G 3'	Initial denaturation of 5 min at 95 °C; 35 cycles of 1 min at 95 °C, 1 min at 52 °C, and 0:40 min at 72 °C; and final elongation of 7 min at 72 °C.

PISTACIA

DNA region	Primers	Reference	Primer sequence	PCR cycle
ITS	ITS4 / ITS5	White et al. 1990	5' TCC TCCG CTT ATT GAT ATG C 3' / 5' GGA AGT AAA AGT CGT AAC AAG G 3'	a 95 C initial hot start for 5 min, 32 cycles of 94 C for 30 s, 50 C for 40 s and 72 C for 60 s, and a final extension of 72 C for 10 min
ETS	ETS1F / 18s-IGS	Weeks et al. 2005 / Baldwin and Markos 1998	5' GAG ACA AGC ATA TGA CTA CTG GCA GGA TCA ACC AG 3' / 5' TTC GGT ATC CTG TGT TGC TTA C 3'	a 95 C initial hot start for 5 min, 32 cycles of 94 C for 30 s, 50 C for 40 s and 72 C for 60 s, and a final extension of 72 C for 10 min

RHAMNUS

DNA region	Primers	Reference	Primer sequence	PCR cycle
ITS	P17 (F)	Popp and Oxelman 2001	5´CTA CCG ATT GAA TGG TCC GGT GAA 3´	The cycling program started with a denaturation step at 95°C for 2 min followed by 38 cycles of: 95°C 30 s, 55°C 1 min, 72°C 2 min. The program was terminated with a 72°C step for 15 min.
	26S-82R (R)	Popp and Oxelman 2001	5´TCC CGG TTC GCT CGC CGT TAC TA 3´	
	P16 (F)	Popp and Oxelman 2001	5´TCA CTG AAC CTT ATC ATT TAG AGG A 3´	
	P25 (R)	Oxelman and Lidén 1995	5´GGG TAG TCC CGC CTG ACC TG 3´	
trn L-*trn* F	TRN C-F	Taberlet et al. 1991	5' CGA AAT CGG TAG ACG CTA CG 3'	The cycling program started with a denaturation step at 95°C for 2 min followed by 38 cycles of: 95°C 30 s, 55°C 1 min, 72°C 2 min. The program was terminated with a 72°C step for 15 min.
	TRN D-R	Taberlet et al. 1991	5' GGG GAT AGA GGG ACT TGA AC 3'	
	trne / trnf	Taberlet et al. 1991	5' GGT TCA AGT CCC TCT ATC CC 3' / 5' ATT TGA ACT GGT GAC ACG AG 3'	

SYDEROXYLON

DNA region	Primers	Reference	Primer sequence	PCR cycle
ITS	ITS5P / ITS4	Möller and Cronk 1997 / White et al. 1990	5' GGA AGG AGA AGT CGT AAC AAG G / 5' TCC TCCG CTT ATT GAT ATG C 3'	2-min denaturation at 95 C, followed by 35 cycles of 95 C denaturation for 30 s, 50 C annealing for 30 s, and 72 C extension for 30 s, followed by a final 8-min extension at 72 C
trn H-*psb* A	psbA3'f / trnHf	Sang et al. 1997 / Tate and Simpson 2003	5' GTT ATG CAT GAA CGT AAT GCTC 3' / 5' GCG CAT GGT GGA TTC ACA ATC C 3'	initial 3-min denaturation at 94 C, followed by two cycles of 94 C denaturation for 45 s, 50 C annealing for 45 s, and 72 C extension for 60 s, then a further 30 cycles with an annealing temperature of 45 C, followed by a final 7-min extension at 72 C

THESIUM

DNA region	Primers	Reference	Primer sequence	PCR cycle
ITS	ITS4 / ITS5	White et al. 1990	5' TCC TCCG CTT ATT GAT ATG C 3' / 5' GGA AGT AAA AGT CGT AAC AAG G 3'	an initial denaturation of 2 min at 94 C; 30 cycles each comprising 94 C for 1 min (denaturation), 48 C for 1 min (annealing) and 72 C for 1.5 min; and a final extension of 4 min at 72 C
mat K	matK-1RKIM-f / matK-3FKIM-r	Kuzmina et al. 2012	5' ACC CAG TCC ATC TGG AAA TCT TGG TTC 3' / 5' CGT ACA GTA CTT TTG TGT TTA CGA G 3'	an initial denaturation of 2 min at 94 C; 30 cycles each comprising 94 C for 1 min (denaturation), 48 C for 1 min (annealing) and 72 C for 1.5 min; and a final extension of 4 min at 72 C
rpl 32-*trn* L	trnL(UAG) / rpl32-F	Shaw et al. 2007	5' CTG CTT CCT AAG AGC AGC GT 3' / 5' CAG TTC CAA AA A AAC GTA CTT C 3'	an initial denaturation of 2 min at 94 C; 30 cycles each comprising 94 C for 1 min (denaturation), 48 C for 1 min (annealing) and 72 C for 1.5 min; and a final extension of 4 min at 72 C
trn L-*trn* F	trnc / trnf	Taberlet et al. 1991	5' CGA AAT CGG TAG ACG CTA CG 3' / 5' ATT TGA ACT GGT GAC ACG AG 3'	an initial denaturation of 2 min at 94 C; 30 cycles each comprising 94 C for 1 min (denaturation), 48 C for 1 min (annealing) and 72 C for 1.5 min; and a final extension of 4 min at 72 C

Table S4. Table S4. Detailed information (phylogenetic relationships and colonization times) of the 16 lineages with thermophilous species recovered from the BEAST analyses of 13 plant groups in this study: species comprising the Canarian (Macaronesian) lineages, continental sister groups, distribution of sister groups, stem age inferred, percentage of trees supporting a mediterranean and pre-Mediterranean stem node, stem node category assigned (i.e., mediterranean, pre-mediterranean, undetermined), crown age inferred, percentage of trees supporting a mediterranean and pre-mediterranean stem node, crown node category assigned and lineage category (next page).

Canarian (Macaronesian) lineages	Sister group	Distribution sister group	Stem age	% TREES	% TREES OUT OF 3	Category Stem node	CROWN	% TREES WITHIN	% TREES OUT OF 3	Category Crown node	Category lineage (Stem + crown)
Asparagus lineage I: ***Asparagus umbellatus***, *A. arborescens* and *A. fallax*	*A. humilis* (low support BI, high support ML)	Kenya, Tanzania, Mozambique	2.80 (1.39-4.17)	**61.24**	38.76	Mediterranean	1.75 (0.62-2.70)	**96.02**	3.98	Mediterranean	Mediterranean
Asparagus lineage II: ***Asparagus scoparius***, *A. nesiotes, A. plocamoides*	Included the mainland *A. altissimus* and *A. acutifolius* (low support). Closely related to to *A. fractiflexus* and *A. denudatus* (low support)	*A. fractiflexus*: South Africa;*A. denudatus*: South Africa; Kenya and Tanzania	1.60 (0.72-2.38) - TMRCA	**89.28**	10.72	Mediterranean	_	_	_	_	Mediterranean
Bosea yervamora	*B. cypria* and *B. amherstiana* (high support)	*B. cypria*: Cyprus; *B. amherstiana*:: Nepal, Pakistan, West Himalaya	5.71 (1.75-11.61)	7.92	**92.08**	Pre-mediterranean	1.64 (0.36-3.45)	**90.59**	9.41	Mediterranean	Undetermined
Bryonia verrucosa	The rest species of *Bryonia* (high support)	N. Africa, Europe to Central Asia and W. Himalaya	5.19 (2.41-8.56)	2.06	**97.94**	Pre-mediterranean	1.74 (0.23-3.17)	**92.11**	7.89	Mediterranean	Undetermined
Chrysojasminum odoratissimum	Polytomy with *C. parkeri*, *C. humile*, *C. bignoniaceum* and *C. fruticans* (clade well-supported but low sampling)	*C. bignoniaceum*: India; *C. parkeri*: West Himalaya; *C. humile*: S. Iran to Central China and N. Myanmar; *C. fruticans*: Medit. to N. Iran	14.86 (5.79-26.03)	0.01	**99.99**	Pre-mediterranean	4.79 (1.25-9.44)	18.08	**81.92**	Pre-mediterranean	Pre-mediterranean
Dracunculus canariensis	*D. vulgaris*	Mediterranean	12.10 (5.82-18.49)	0.01	**99.99**	Pre-mediterranean	2.76 (0.48-5.82)	**60.16**	39.84	Mediterranean	Undetermined
Ephedra fragilis	Unresolved polytomy including *E. alata*, *E. aphylla*, *E. altissima*	N Africa + Arabia	1.29 (0.25-2.78) - TMRCA	**82.16**	17.84	Mediterranean	_	_	_	_	Mediterranean
Gymnosporia lineage: ***Gymnosporia cassinoides***, ***G. cryptosepala*** and *G. dryandrii*	*G. parviflora*, *G. dhofarensis*, *G. arbutifolia*, *G. engleriana* (high support)	*G. parviflora:* Yemen and Eritrea; *G. dhofarensis*: Arabian Peninsula; *G. royleana*: S Asia; *G. arbutifolia*: C+CE Africa	3.78 (2.11-5.36)	15.23	**84.77**	Pre-mediterranean	1.27 (0.46-2.00)	**99.73**	0.27	Mediterranean	Undetermined
Myrsine excelsa	*Myrsine semiserrata* (low support)	SW Asia	3.98 (1.59-7.06)	12.34	**87.66**	Pre-mediterranean	1.07 (0.28-2.11)	**98.92**	1.08	Mediterranean	Undetermined
Juniperus turbinata (non-endemic)	Unresolved	Mediterranean	4.91(1.18-9.19) - TMRCA	13.14	**86.86**	Pre-mediterraneo	_	_	_	_	Undetermined
Pistacia atlantica (non-endemic)	*P. vera*, *P. integerrima*, *P. khinjuk* (low support)	P. atlantica: S + E Med + Macaronesia; P. vera: SW Asia; P. integerrima: E Asia; P. khinjuk: E Med, SW Asia	1.15 (0.24-2.43) - TMRCA	**97.22**	2.78	Mediterranean	_	_	_	_	Mediterranean
***Pistacia lentiscus* lineage I** (non-endemic)	*P. aethiopica* (low support)	P. aethiopica: CE Africa	3.96 (1.52-6.71)	11.04	**88.96**	Pre-mediterranean	1.15 (0.00-1.43)	**96.19**	3.81	Mediterranean	Undetermined
***Pistacia lentiscus* lineage II** (non-endemic)	Populations of *P. lentiscus* from Spain and Morocco	P. lentiscus: circunmed + Macaronesia	1.76 (0.49-3.37) - TMRCA	**89.28**	10.72	Mediterranean	_	_	_	_	Mediterranean
Rhamnus crenulata	*R. lycioides* (High support)	Mediterranean	3.88 (1.79-6.59)	16.05	**83.95**	Pre-mediterranean	1.71 (0.49-3.38)	**87.02**	12.98	Mediterranean	Undetermined
Syderoxylon canariense	Sister to a clade containing 11 spp	Cape Verde, Socotra, C+E Asia, Reunion, Madagascar, Mauricio	38.86 (26.11-55.00)	0.00	**100.00**	Pre-mediterranean	7.16 (2.57-12.99)	1.28	**98.72**	Pre-mediterranean	Pre-mediterranean
Thesium lineage: ***Thesium subsuculentum*** and *T. retamoides*	*T. mauritanicum* (High support)	N Africa	14.53 (6.56-23.57)	0.00	**100.00**	Pre-mediterranean	3.86 (1.06-7.39)	31.11	**68.89**	Pre-mediterranean	Pre-mediterranean

Table S5. Results of the ancestral area reconstruction under the dispersal-extinction-cladogenesis (DEC) analyses performed on the 13 newly generated time-calibrated phylogenies including thermophilous species in the Canary Islands analysed in this study. Log-likelihood (lnL) values corresponding to the stem node (or to the most recent common ancestor when the posterior probability of the stem node was lower than 0.90) of the lineage for each of the possible ancestral ranges (in bold the most likely) are indicated. The letters correspond to the following geographical areas: A: Mediterranean Basin, B: Macaronesia, C: Other regions (several letters imply ranges that include multiple areas). It is also indicated whether or not the Mediterranean Basin is part of the inferred ancestral range for the lineage, and whether the lineage is pre-, post- or undetermined with respect to the establishment of the Mediterranean climate.

Canarian (Macaronesian) lineages	Sister group	Null range	A	B	C	AB	AC	BC	ACB	Mediterranean Basin in the ancestral range	Temporal origin (mediterranean vs. pre-mediterranean)
Asparagus lineage I: ***Asparagus umbellatus***, *A. arborescens* and *A. fallax*	*A. humilis*	0.00	0.00	0.00	0.00	0.00	0.00	**1.00**	0.00	NO	Mediterranean
Asparagus lineage II: ***Asparagus scoparius***, *A. nesiotes, A. plocamoides*	Included the mainland *A. altissimus* and *A. acutifolius* (low support)	0.00	0.18	0.18	0.00	**0.64**	0.00	0.00	0.00	YES	Mediterranean
Bosea yervamora	*B. cypria* and *B. amherstiana*	0.00	0.00	0.00	0.00	0.00	0.00	0.09	**0.91**	YES	Undetermined
Bryonia verrucosa	The rest species of *Bryonia*	0.00	0.01	0.00	0.01	0.12	0.03	0.11	**0.73**	YES	Undetermined
Chrysojasminum odoratissimum	*C. parkeri*, *C. humile*, *C. bignoniaceum* and *C. fruticans*	0.00	0.00	0.00	0.00	0.00	0.00	**0.90**	0.10	NO	Pre-mediterranean
Dracunculus canariensis	*D. vulgaris*	0.00	0.00	0.00	0.00	**1.00**	0.00	0.00	0.00	YES	Undetermined
Ephedra fragilis (non-endemic)	*E. alata* (low support)	0.00	0.32	0.00	0.00	0.14	**0.49**	0.01	0.04	YES	Mediterranean
Gymnosporia lineage: ***Gymnosporia cassinoides***, ***G. cryptosepala*** and *G. dryandrii*	*G. parviflora*, *G. dhofarensis*, *G. arbutifolia*, *G. engleriana*	0.00	0.00	0.00	0.00	0.00	0.00	**1.00**	0.00	NO	Undetermined
Juniperus turbinata (non-endemic)	*J. phoenicea* (low support)	0.00	0.00	0.00	0.00	**1.00**	0.00	0.00	0.00	YES	Undetermined
Myrsine excelsa	*Myrsine semiserrata* (low support)	0.00	0.00	0.00	0.00	0.00	0.00	**1.00**	0.00	NO	Undetermined
Pistacia atlantica (non-endemic)	*P. vera* (low support)	0.00	0.00	0.00	**0.56**	0.00	0.15	0.14	0.15	NO	Mediterranean
Pistacia lentiscus (including P. lentiscus lineages I and II; non-endemic)	*P. aethiopica* (low support)	0.00	0.00	0.00	0.00	0.00	0.25	0.24	**0.51**	YES	Undetermined
Rhamnus crenulata	*R. lycioides*	0.00	0.00	0.00	0.00	**1.00**	0.00	0.00	0.00	YES	Undetermined
Syderoxylon canariense	Sister to a clade containing 11 spp	0.00	0.00	0.00	0.00	0.00	0.00	**1.00**	0.00	NO	Pre-mediterranean
Thesium lineage: ***Thesium subsuculentum*** and *T. retamoides*	*T. mauritanicum*	0.00	0.00	0.00	0.00	**1.00**	0.00	0.00	0.00	YES	Pre-mediterranean

METHODS S1. Details of the maximum likelihood phylogenetic analyses performed in this study

We reconstructed phylogenetic trees including the new DNA sequences and the previously-published DNA datasets using a maximum likelihood (ML) approach implemented in RaxML v.8.2.11 (Stamatakis, 2014) in Geneious. A GTR+GAMMA model and the “Rapid bootstrapping and search for the best-scoring ML tree” algorithm option was selected, and a total of 100 bootstrap replicates were performed.

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