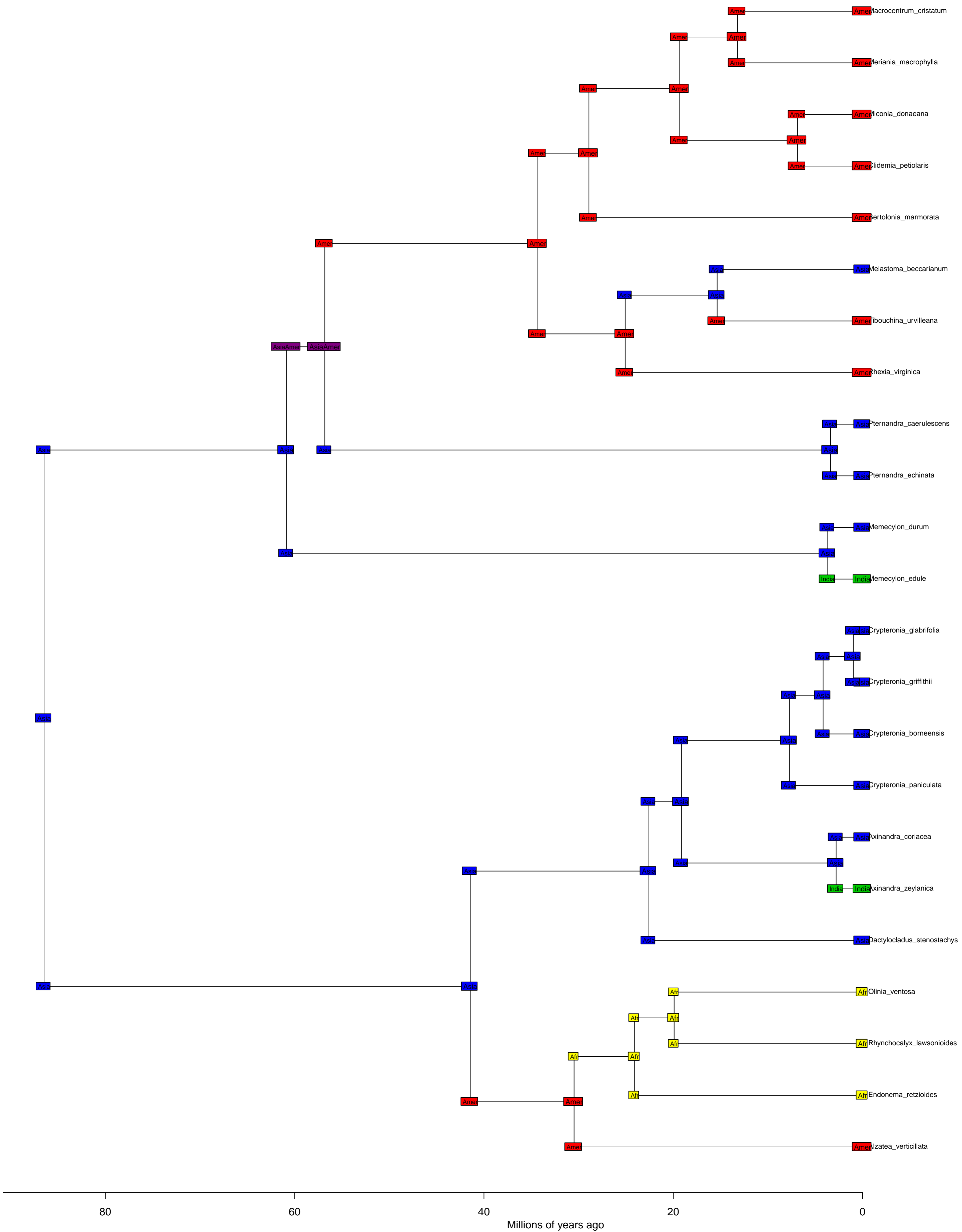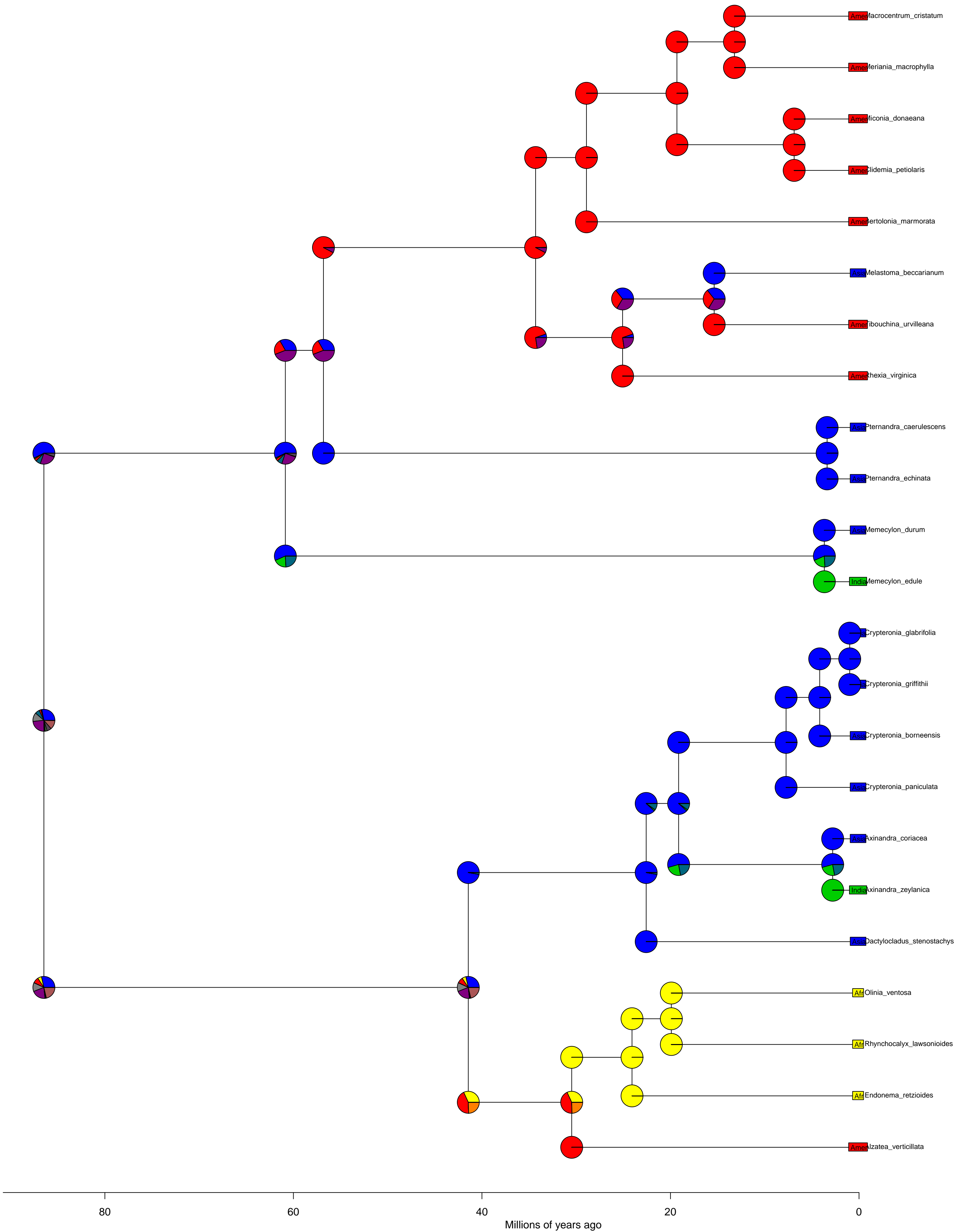# Supplementary Figure 1

Suppl. Fig. 1 | Time calibrated phylogenetic trees with annotated biogeographical range estimates used to infer dispersal events between the Indian subcontinent and mainland Asia. The 37 phylogenies are shown once with the best range estimate and once with the relative probability for the respective areas/ranges; annotated with the model used (DEC or DEC+j), the maximum number of areas allowed within a range, the resulting extinction rate (e), dispersal rate (d), founder-event weight (j), and the log likelihood (lnL).

Crypteroniacae BioGeoBEARS DEC+J
ancstates: global optim, 3 areas max. d=0; e=0; j=0.0635; LnL=−21.29

Macrocentrum_cristatum
Meriania_macrophylla
Miconia_donaeana
Clidemia_petiolaris
Bertolonia_marmorata
Melastoma_beccarianum
Tibouchina_urvilleana
Rhexia_virginica
Pternandra_caerulescens
Pternandra_echinata
Memecylon_durum
Memecylon_edule
Crypteronia_glabrifolia
Crypteronia_griffithii
Crypteronia_borneensis
Crypteronia_paniculata
Axinandra_coriacea
Axinandra_zeylanica
Dactylocladus_stenostachys
Olinia_ventosa
Rhynchocalyx_lawsonioides
Endonema_retzioides
Alzatea_verticillata

Millions of years ago

Crypteroniaceae BioGeoBEARS DEC+J
ancstates: global optim, 3 areas max. d=0; e=0; j=0.0635; LnL=−21.29

Amer Macrocentrum_cristatum
Amer Meriania_macrophylla
Amer Miconia_donaeana
Amer Clidemia_petiolaris
Amer Bertolonia_marmorata
Asia Melastoma_beccarianum
Amer Tibouchina_urvilleana
Amer Rhexia_virginica
Asia Pternandra_caerulescens
Asia Pternandra_echinata
Asia Memecylon_durum
India Memecylon_edule
Asia Crypteronia_glabrifolia
Asia Crypteronia_griffithii
Asia Crypteronia_borneensis
Asia Crypteronia_paniculata
Asia Axinandra_coriacea
India Axinandra_zeylanica
Asia Dactylocladus_stenostachys
Afr Olinia_ventosa
Afr Rhynchocalyx_lawsonioides
Afr Endonema_retzioides
Amer Alzatea_verticillata

Millions of years ago

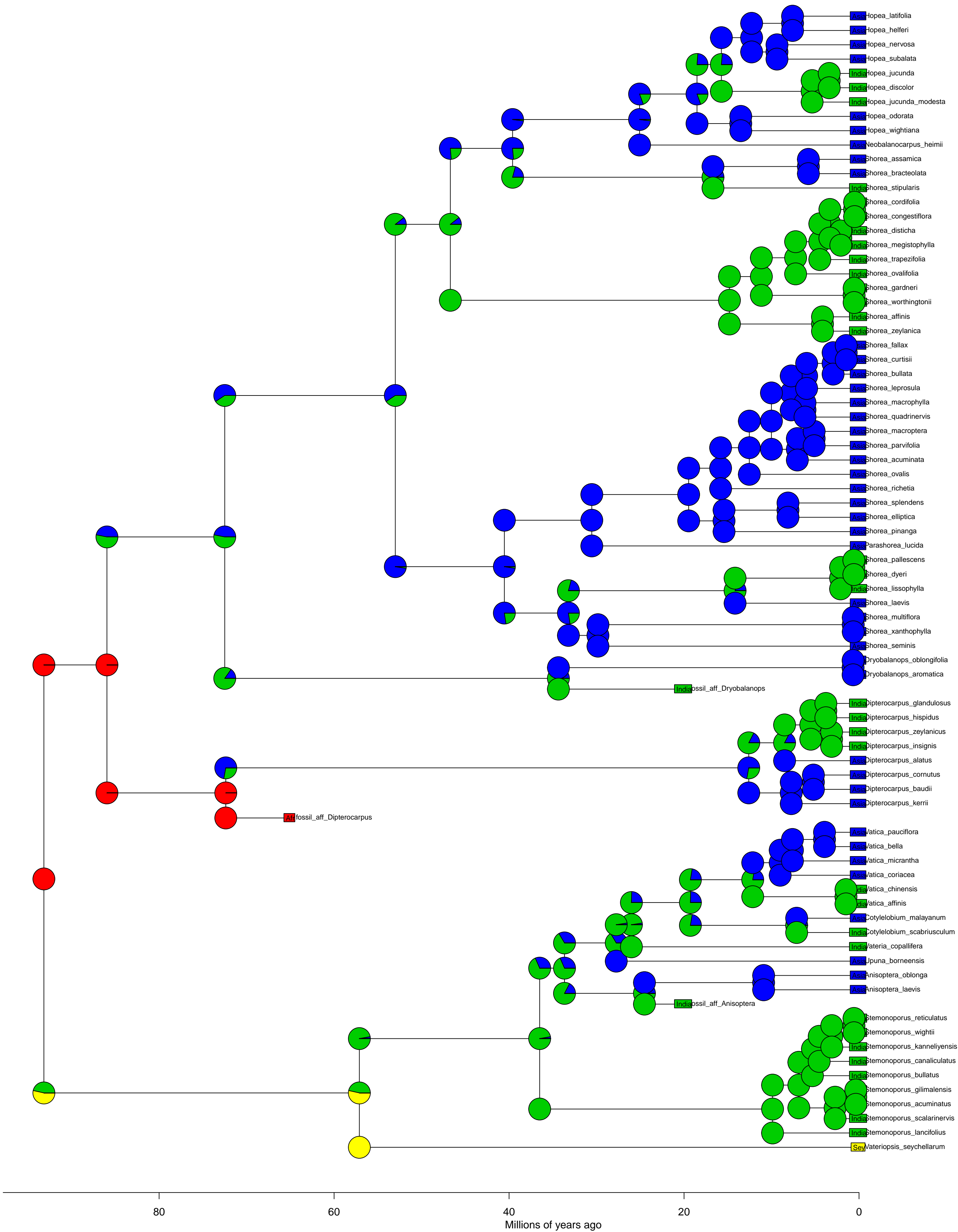Dipterocarpaceae BioGeoBEARS DEC+J
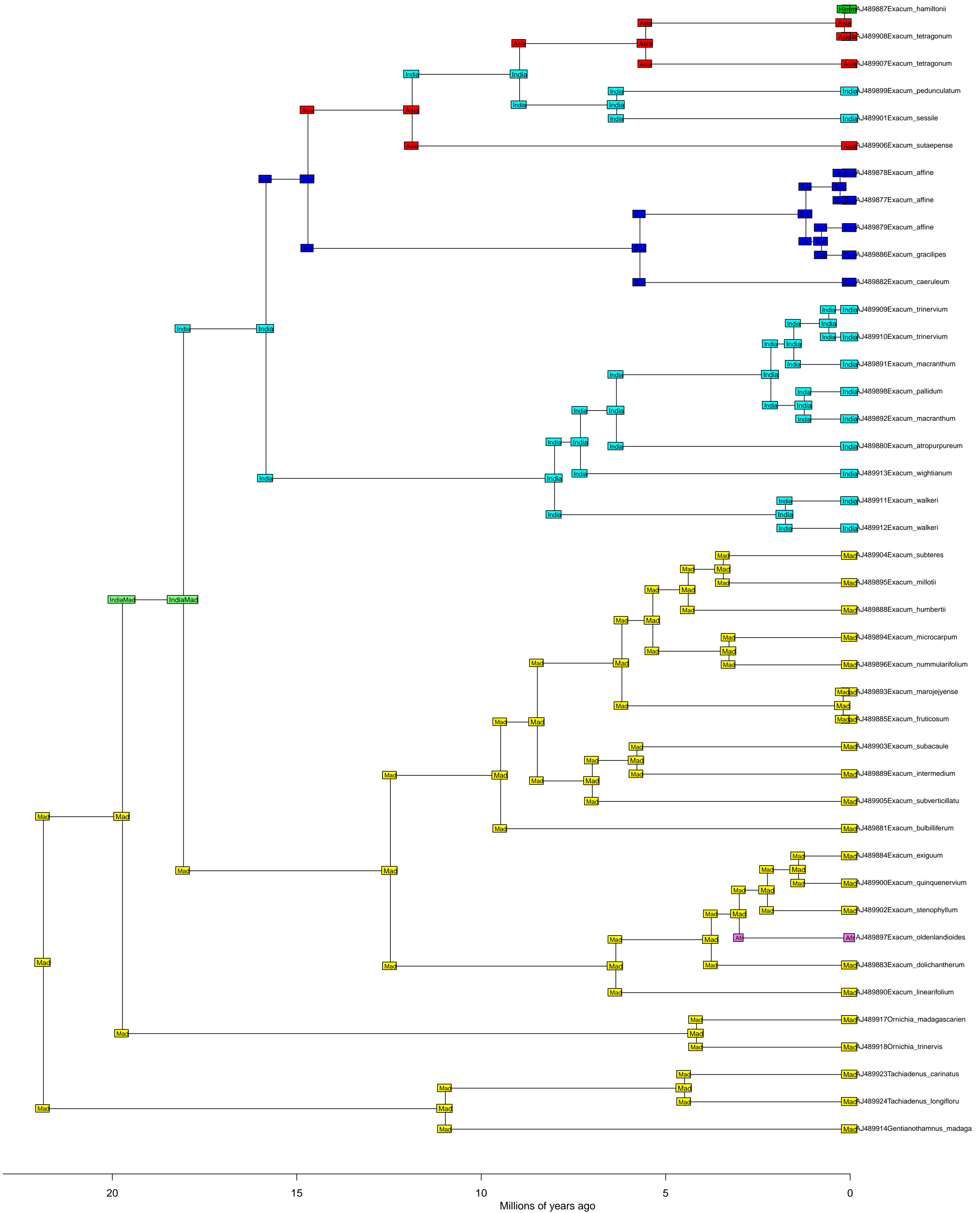ancstates: global optim, 2 areas max. d=0; e=0; j=0.0823; LnL=−53.72

Dipterocarpaceae BioGeoBEARS DEC+J
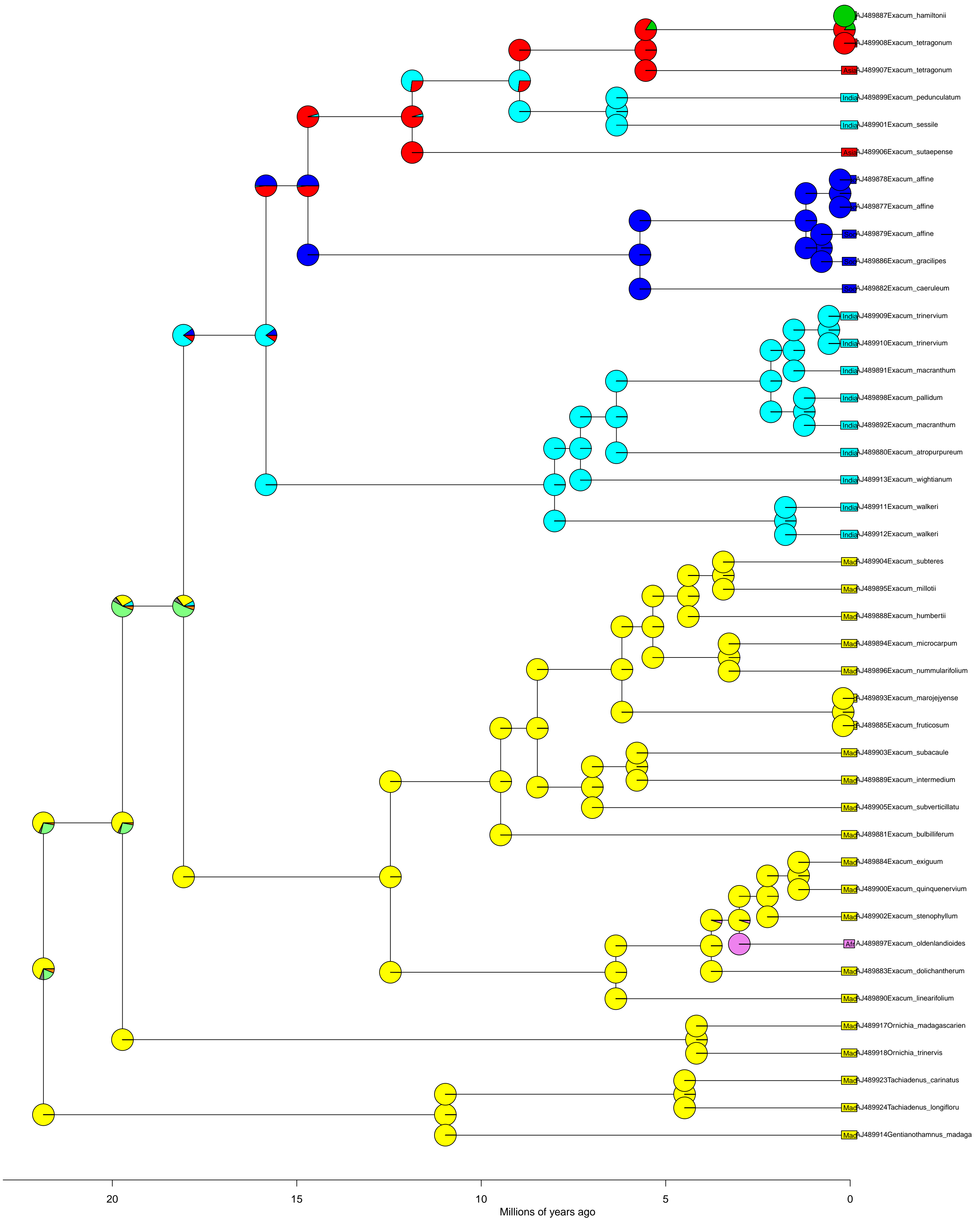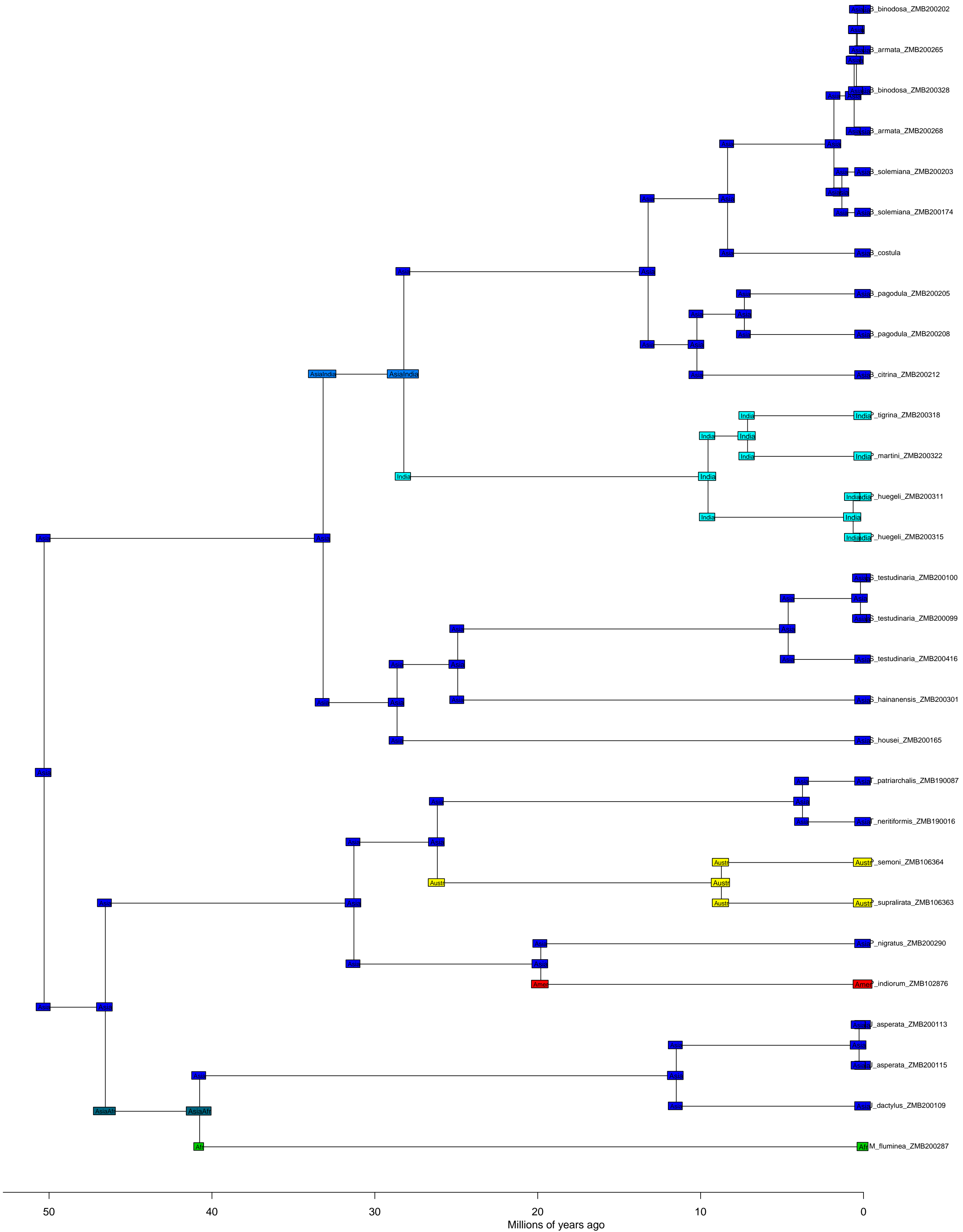ancstates: global optim, 2 areas max. d=0; e=0; j=0.0823; LnL=−53.72

Exacum BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0167; LnL=−28.83

AJ489887Exacum_hamiltonii
AJ489908Exacum_tetragonum
AJ489907Exacum_tetragonum
AJ489899Exacum_pedunculatum
AJ489901Exacum_sessile
AJ489906Exacum_sutaepense
AJ489878Exacum_affine
AJ489877Exacum_affine
AJ489879Exacum_affine
AJ489886Exacum_gracilipes
AJ489882Exacum_caeruleum
AJ489909Exacum_trinervium
AJ489910Exacum_trinervium
AJ489891Exacum_macranthum
AJ489898Exacum_pallidum
AJ489892Exacum_macranthum
AJ489880Exacum_atropurpureum
AJ489913Exacum_wightianum
AJ489911Exacum_walkeri
AJ489912Exacum_walkeri
AJ489904Exacum_subteres
AJ489895Exacum_millotii
AJ489888Exacum_humbertii
AJ489894Exacum_microcarpum
AJ489896Exacum_nummularifolium
AJ489893Exacum_marojejyense
AJ489885Exacum_fruticosum
AJ489903Exacum_subacaule
AJ489889Exacum_intermedium
AJ489905Exacum_subverticillatu
AJ489881Exacum_bulbilliferum
AJ489884Exacum_exiguum
AJ489900Exacum_quinquenervium
AJ489902Exacum_stenophyllum
AJ489897Exacum_oldenlandioides
AJ489883Exacum_dolichantherum
AJ489890Exacum_linearifolium
AJ489917Ornichia_madagascarien
AJ489918Ornichia_trinervis
AJ489923Tachiadenus_carinatus
AJ489924Tachiadenus_longifloru
AJ489914Gentianothamnus_madaga

Millions of years ago

Exacum BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0167; LnL=−28.83

AJ489887Exacum_hamiltonii
AJ489908Exacum_tetragonum
Asia AJ489907Exacum_tetragonum
India AJ489899Exacum_pedunculatum
India AJ489901Exacum_sessile
Asia AJ489906Exacum_sutaepense
AJ489878Exacum_affine
AJ489877Exacum_affine
Sril AJ489879Exacum_affine
Sril AJ489886Exacum_gracilipes
Sril AJ489882Exacum_caeruleum
India AJ489909Exacum_trinervium
India AJ489910Exacum_trinervium
India AJ489891Exacum_macranthum
India AJ489898Exacum_pallidum
India AJ489892Exacum_macranthum
India AJ489880Exacum_atropurpureum
India AJ489913Exacum_wightianum
India AJ489911Exacum_walkeri
India AJ489912Exacum_walkeri
Mad AJ489904Exacum_subteres
Mad AJ489895Exacum_millotii
Mad AJ489888Exacum_humbertii
Mad AJ489894Exacum_microcarpum
Mad AJ489896Exacum_nummularifolium
AJ489893Exacum_marojejyense
AJ489885Exacum_fruticosum
Mad AJ489903Exacum_subacaule
Mad AJ489889Exacum_intermedium
Mad AJ489905Exacum_subverticillatu
Mad AJ489881Exacum_bulbilliferum
Mad AJ489884Exacum_exiguum
Mad AJ489900Exacum_quinquenervium
Mad AJ489902Exacum_stenophyllum
Afr AJ489897Exacum_oldenlandioides
Mad AJ489883Exacum_dolichantherum
Mad AJ489890Exacum_linearifolium
Mad AJ489917Ornichia_madagascarien
Mad AJ489918Ornichia_trinervis
Mad AJ489923Tachiadenus_carinatus
Mad AJ489924Tachiadenus_longifloru
Mad AJ489914Gentianothamnus_madaga

20   15   10   5   0
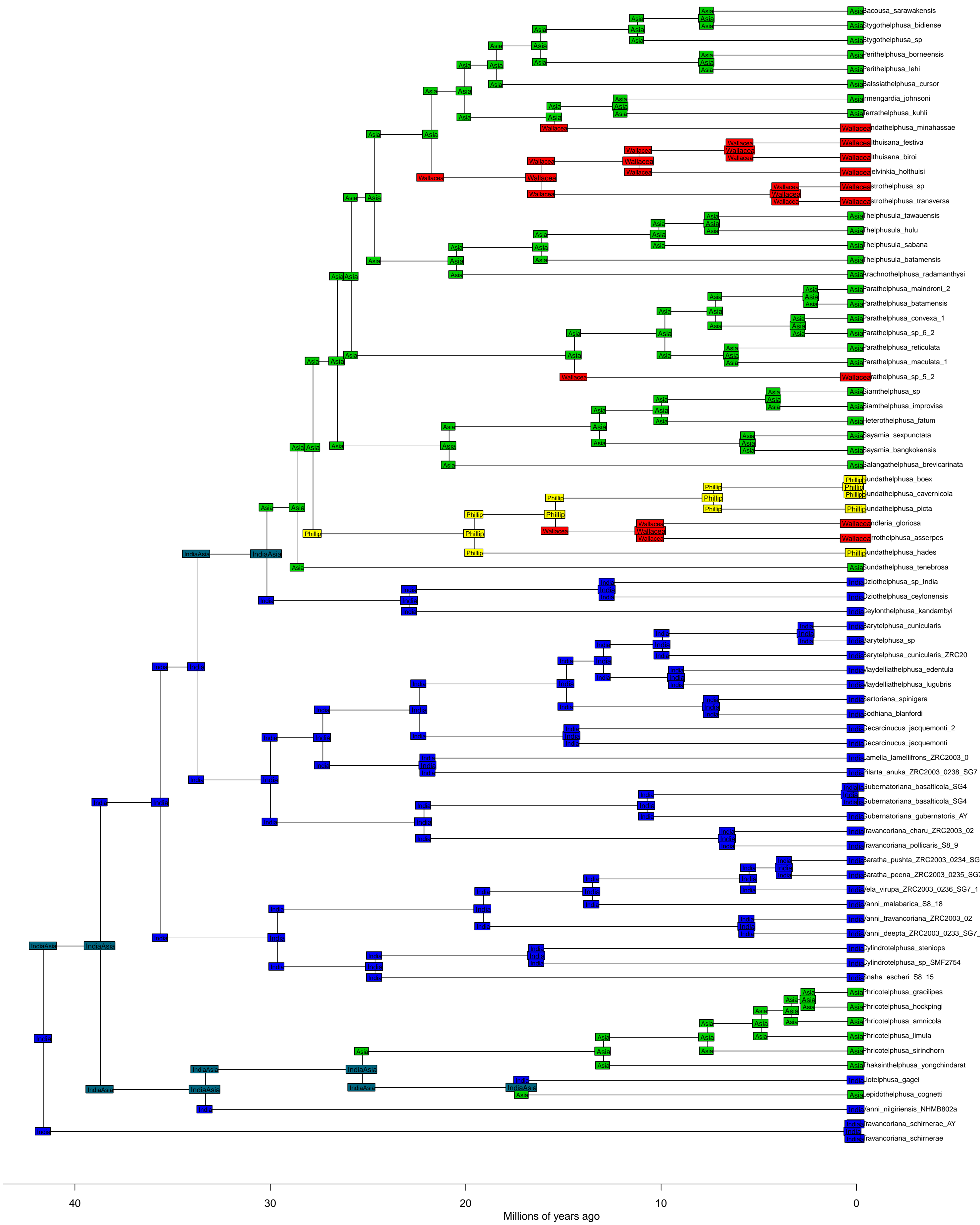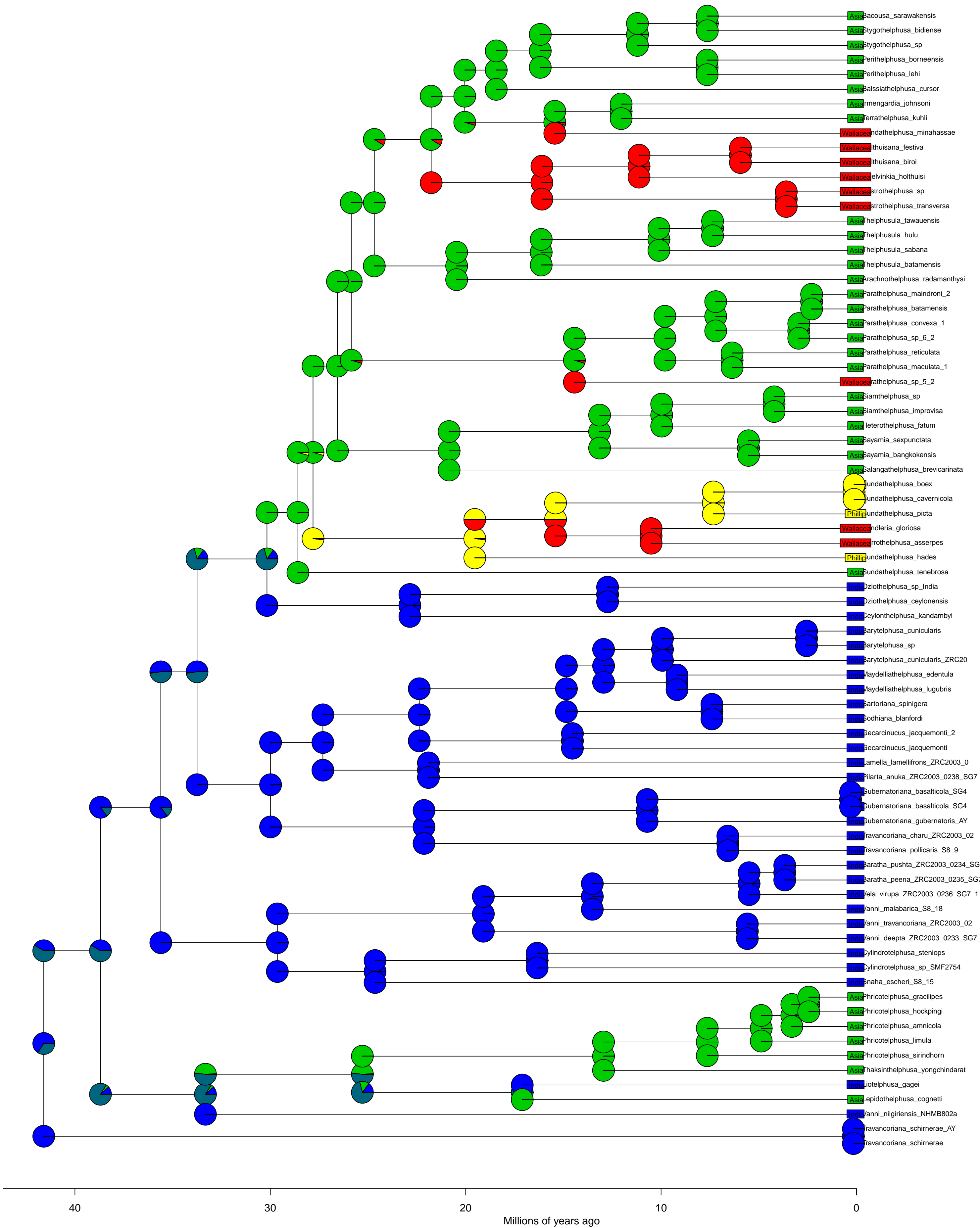
Millions of years ago

Pachychilidae BioGeoBEARS DEC+J
ancstates: global optim, 3 areas max. d=0; e=0; j=0.0197; LnL=−19.05

B_binodosa_ZMB200202
B_armata_ZMB200265
B_binodosa_ZMB200328
B_armata_ZMB200268
B_solemiana_ZMB200203
B_solemiana_ZMB200174
B_costula
B_pagodula_ZMB200205
B_pagodula_ZMB200208
B_citrina_ZMB200212
P_tigrina_ZMB200318
P_martini_ZMB200322
P_huegeli_ZMB200311
P_huegeli_ZMB200315
S_testudinaria_ZMB200100
S_testudinaria_ZMB200099
S_testudinaria_ZMB200416
S_hainanensis_ZMB200301
S_housei_ZMB200165
P_patriarchalis_ZMB190087
P_neritiformis_ZMB190016
P_semoni_ZMB106364
P_supralirata_ZMB106363
P_nigratus_ZMB200290
P_indiorum_ZMB102876
J_asperata_ZMB200113
J_asperata_ZMB200115
J_dactylus_ZMB200109
M_fluminea_ZMB200287

50   40   30   20   10   0

Millions of years ago

Pachychilidae BioGeoBEARS DEC+J
ancstates: global optim, 3 areas max. d=0; e=0; j=0.0197; LnL=−19.05

B_binodosa_ZMB200202
B_armata_ZMB200265
B_binodosa_ZMB200328
B_armata_ZMB200268
B_solemiana_ZMB200203
B_solemiana_ZMB200174
B_costula
B_pagodula_ZMB200205
B_pagodula_ZMB200208
B_citrina_ZMB200212
India P_tigrina_ZMB200318
India P_martini_ZMB200322
a P_huegeli_ZMB200311
a P_huegeli_ZMB200315
S_testudinaria_ZMB200100
S_testudinaria_ZMB200099
S_testudinaria_ZMB200416
S_hainanensis_ZMB200301
S_housei_ZMB200165
T_patriarchalis_ZMB190087
T_neritiformis_ZMB190016
Austr P_semoni_ZMB106364
Austr P_supralirata_ZMB106363
P_nigratus_ZMB200290
Amer P_indiorum_ZMB102876
J_asperata_ZMB200113
J_asperata_ZMB200115
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Afr M_fluminea_ZMB200287

Millions of years ago

50   40   30   20   10   0

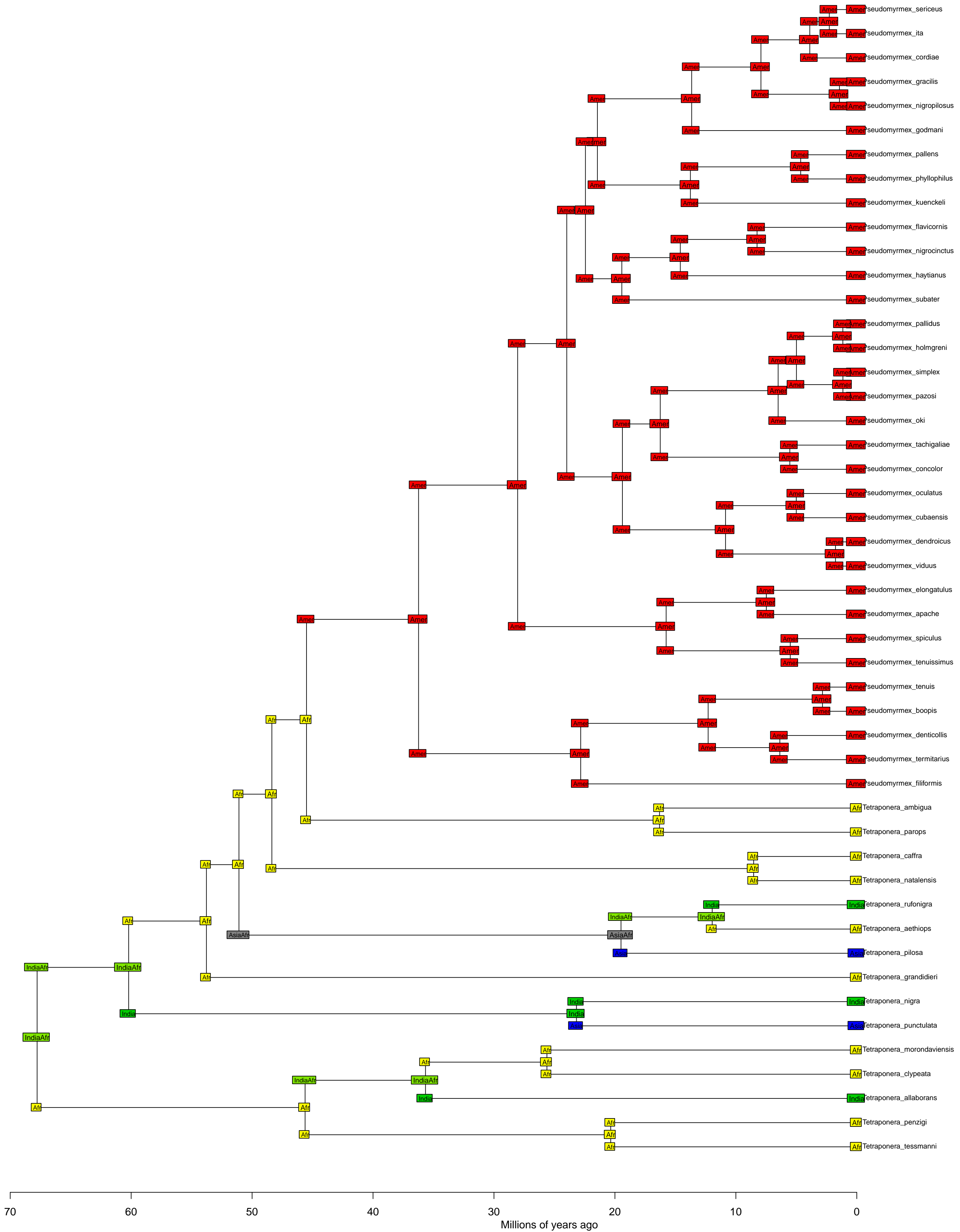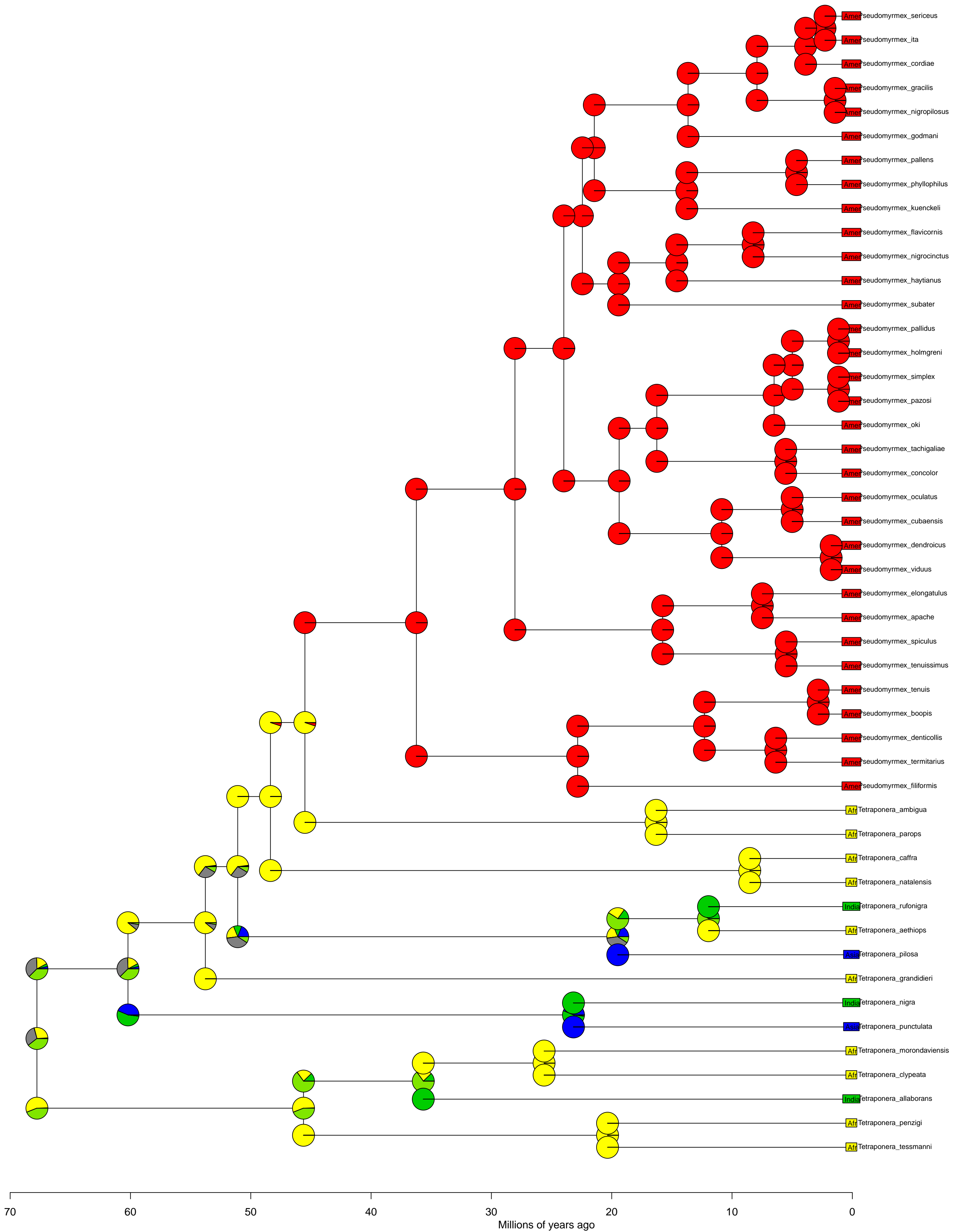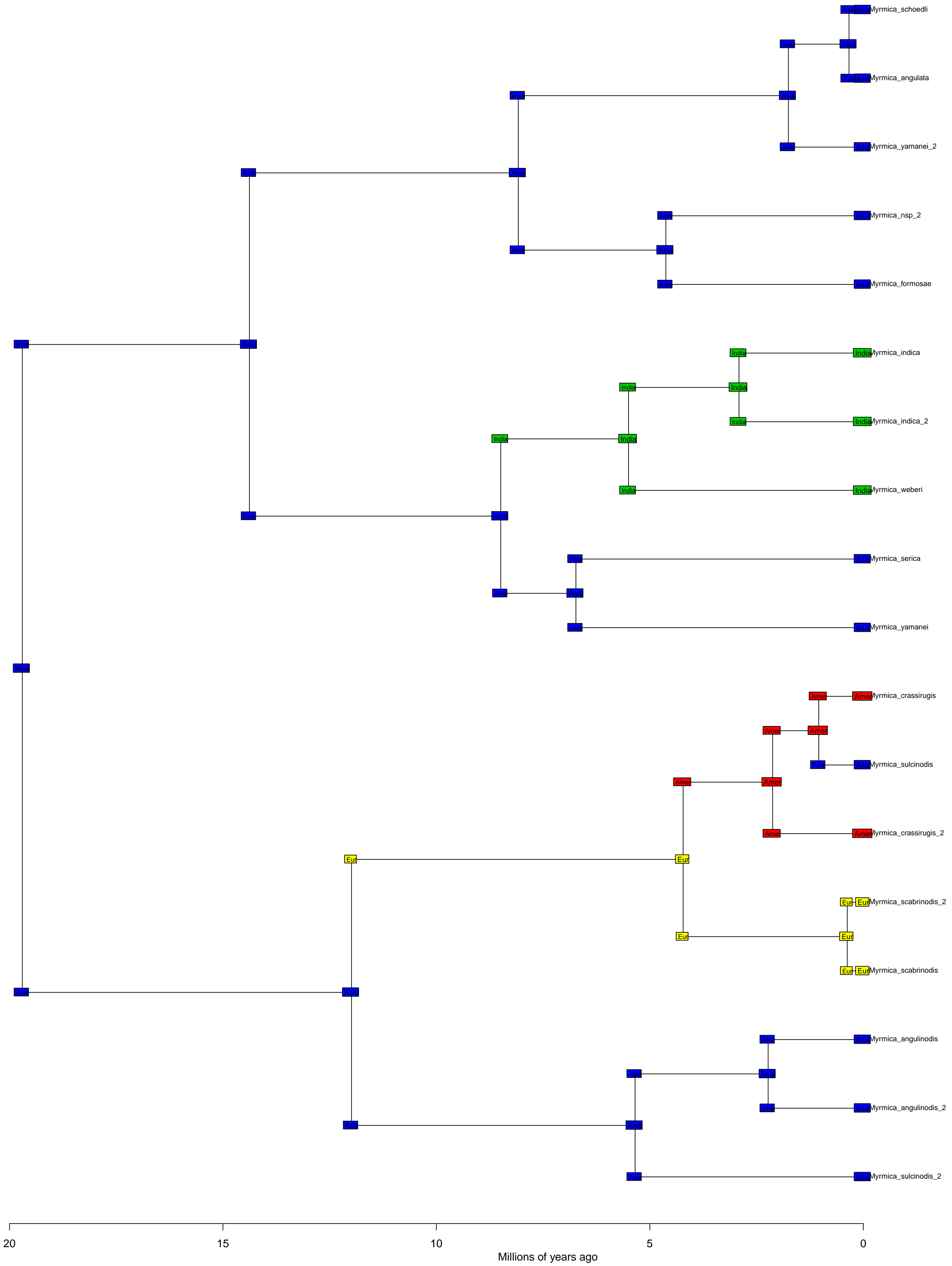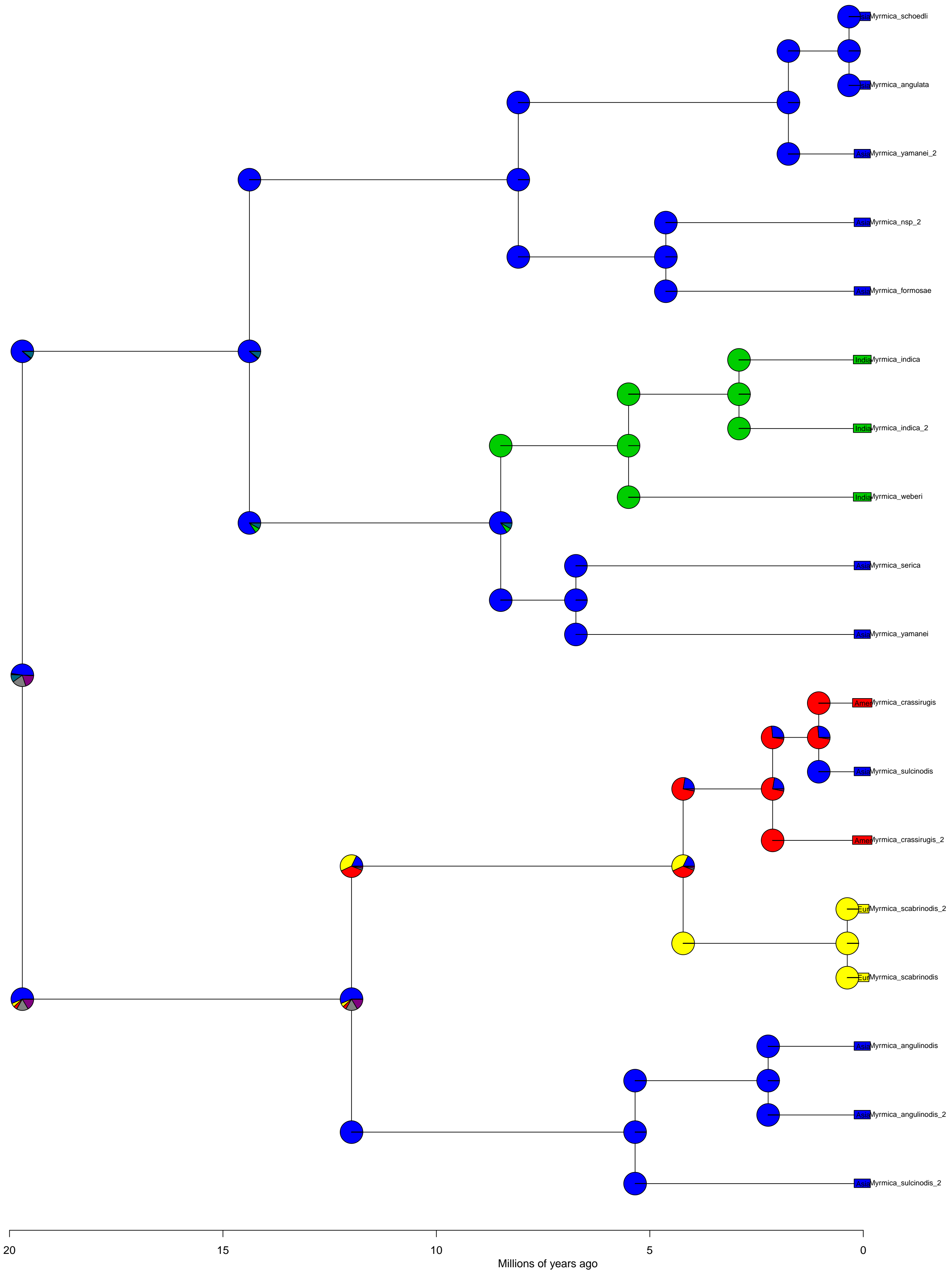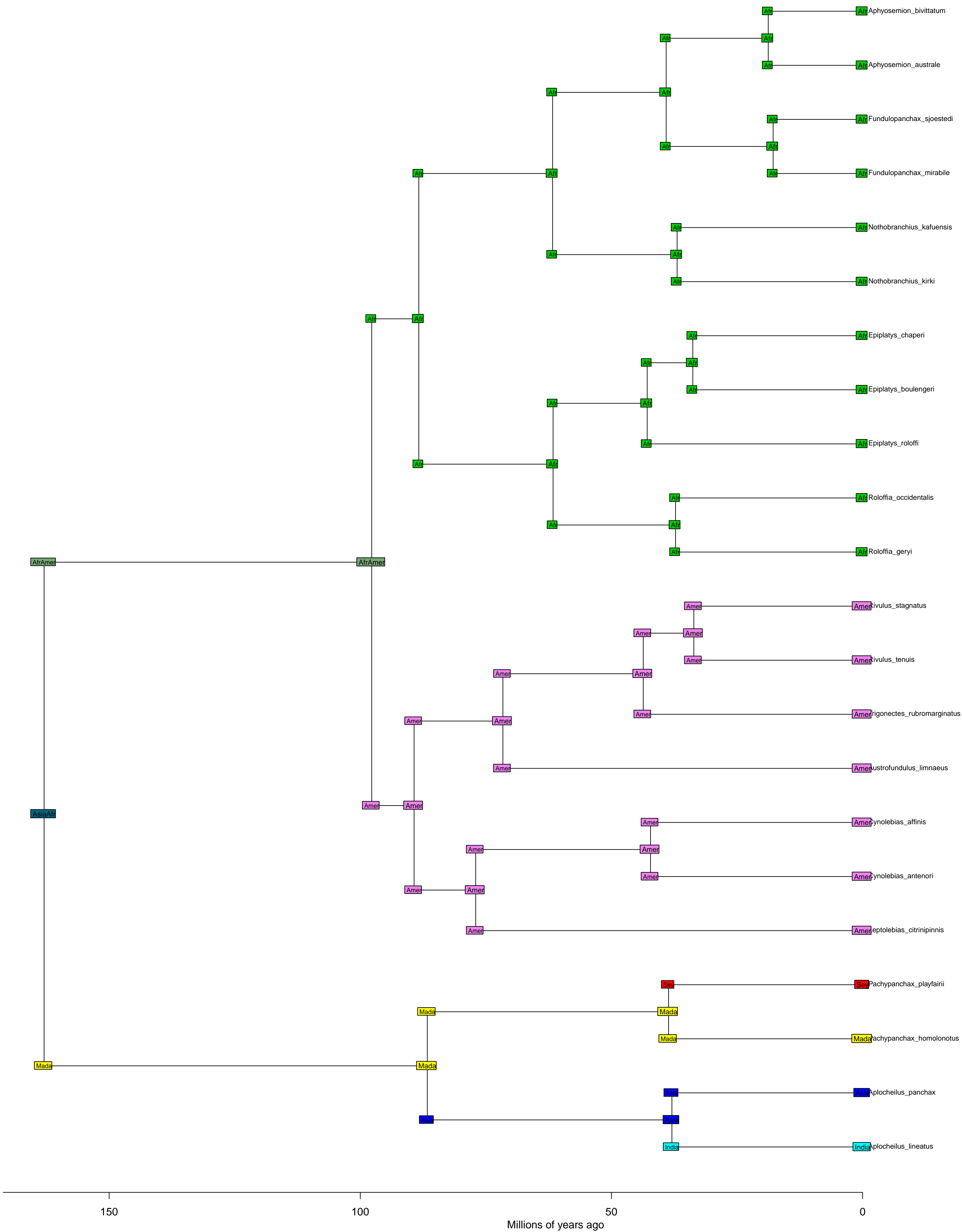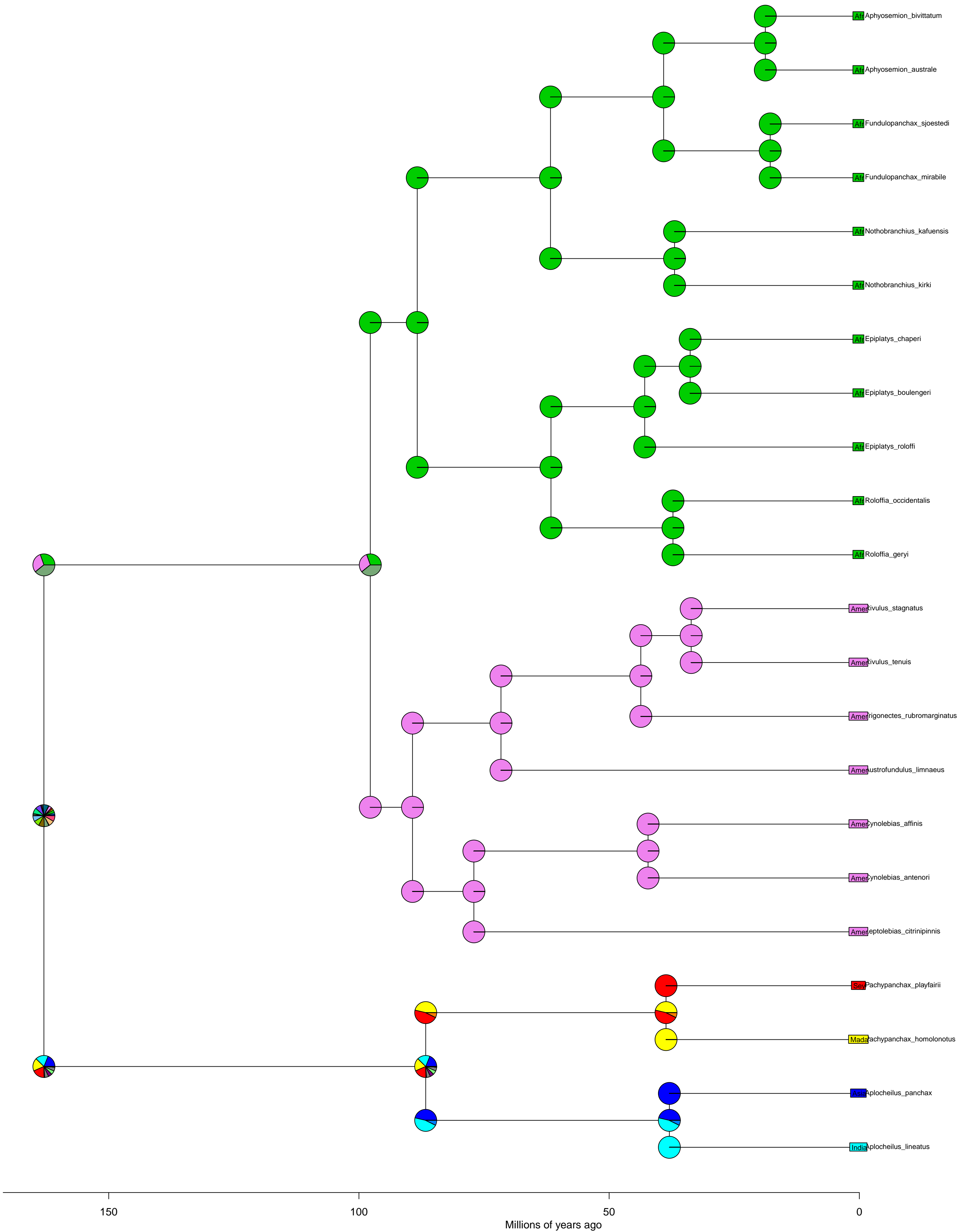Gecarcinucidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0187; LnL=−38.72

Gecarcinucidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0187; LnL=−38.72

Asia Bacousa_sarawakensis
Asia Stygothelphusa_bidiense
Asia Stygothelphusa_sp
Asia Perithelphusa_borneensis
Asia Perithelphusa_lehi
Asia Balssiathelphusa_cursor
Asia Irmengardia_johnsoni
Asia Terrathelphusa_kuhli
Wallacea Sundathelphusa_minahassae
Wallacea Ikthuisana_festiva
Wallacea Ikthuisana_biroi
Wallacea Nelvinkia_holthuisi
Wallacea Nautilothelphusa_sp
Wallacea Nautilothelphusa_transversa
Asia Thelphusula_tawauensis
Asia Thelphusula_hulu
Asia Thelphusula_sabana
Asia Thelphusula_batamensis
Asia Arachnothelphusa_radamanthysi
Asia Parathelphusa_maindroni_2
Asia Parathelphusa_batamensis
Asia Parathelphusa_convexa_1
Asia Parathelphusa_sp_6_2
Asia Parathelphusa_reticulata
Asia Parathelphusa_maculata_1
Wallacea Parathelphusa_sp_5_2
Asia Siamthelphusa_sp
Asia Siamthelphusa_improvisa
Asia Heterothelphusa_fatum
Asia Sayamia_sexpunctata
Asia Sayamia_bangkokensis
Asia Salangathelphusa_brevicarinata
Phillip Sundathelphusa_boex
Phillip Sundathelphusa_cavernicola
Phillip Sundathelphusa_picta
Wallacea Candleria_gloriosa
Wallacea Parrothelphusa_asserpes
Phillip Sundathelphusa_hades
Asia Sundathelphusa_tenebrosa
India Oziothelphusa_sp_India
India Oziothelphusa_ceylonensis
India Ceylonthelphusa_kandambyi
India Barytelphusa_cunicularis
India Barytelphusa_sp
India Barytelphusa_cunicularis_ZRC20
India Maydelliathelphusa_edentula
India Maydelliathelphusa_lugubris
India Sartoriana_spinigera
India Sodhiana_blanfordi
India Gecarcinucus_jacquemonti_2
India Gecarcinucus_jacquemonti
India Lamella_lamellifrons_ZRC2003_0
India Pilarta_anuka_ZRC2003_0238_SG7
India Gubernatoriana_basalticola_SG4
India Gubernatoriana_basalticola_SG4
India Gubernatoriana_gubernatoris_AY
India Travancoriana_charu_ZRC2003_02
India Travancoriana_pollicaris_S8_9
India Baratha_pushta_ZRC2003_0234_SG
India Baratha_peena_ZRC2003_0235_SG7
India Vela_virupa_ZRC2003_0236_SG7_1
India Vanni_malabarica_S8_18
India Vanni_travancoriana_ZRC2003_02
India Vanni_deepta_ZRC2003_0233_SG7_
India Cylindrotelphusa_steniops
India Cylindrotelphusa_sp_SMF2754
India Snaha_escheri_S8_15
Asia Phricotelphusa_gracilipes
Asia Phricotelphusa_hockpingi
Asia Phricotelphusa_amnicola
Asia Phricotelphusa_limula
Asia Phricotelphusa_sirindhorn
Asia Thaksinthelphusa_yongchindarat
India Liotelphusa_gagei
Asia Lepidothelphusa_cognetti
India Vanni_nilgiriensis_NHMB802a
India Travancoriana_schirnerae_AY
India Travancoriana_schirnerae

40   30   20   10   0

Millions of years ago

Papilionidae BioGeoBEARS DEC+J
ancstates: global optim, 4 areas max. d=0.0029; e=0; j=0.0105; LnL=−384.97

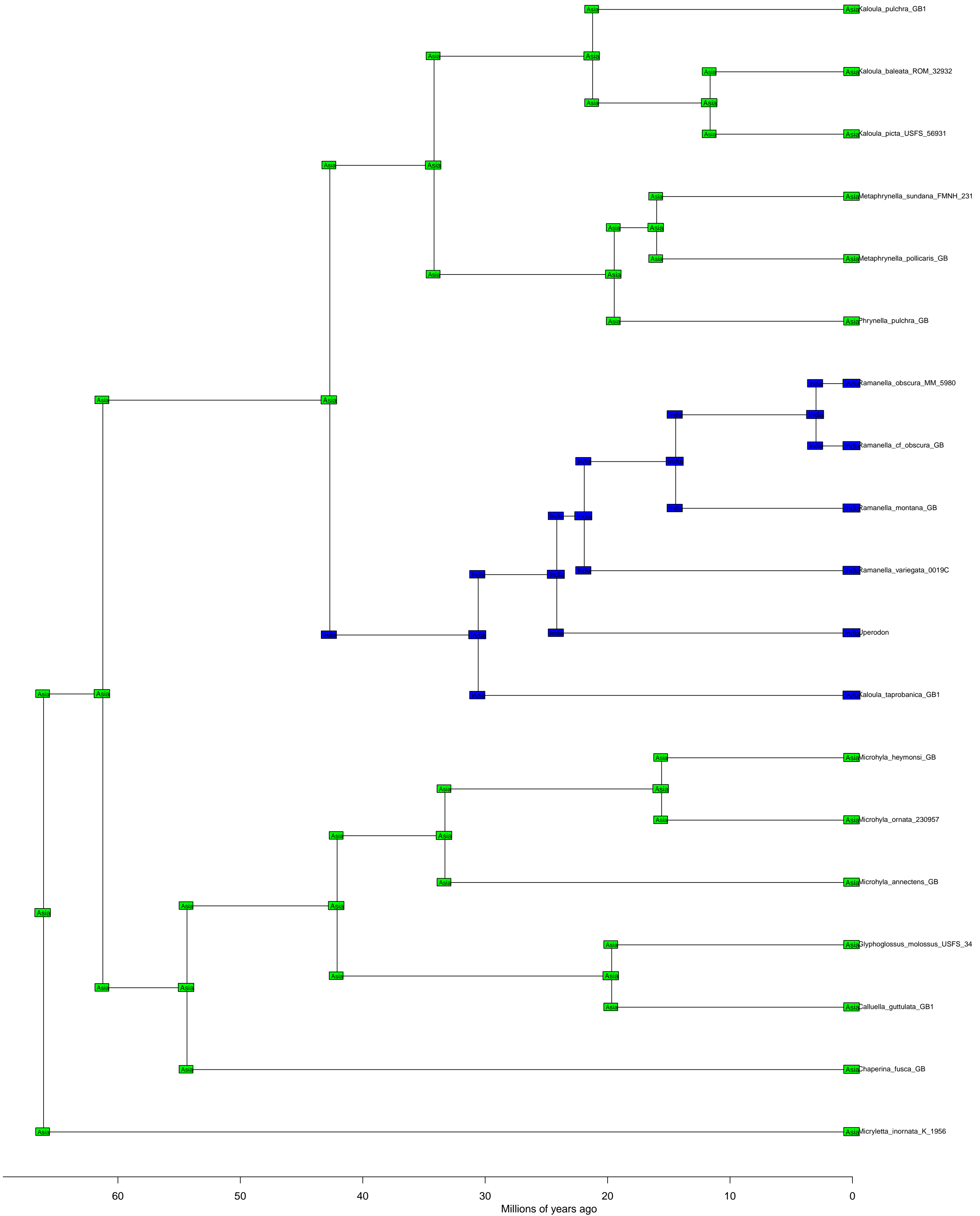**Papilionidae BioGeoBEARS DEC+J**
ancstates: global optim, 4 areas max. d=0.0029; e=0; j=0.0105; LnL=−384.97

Papilio_aegeus
Papilio_gambrisius2
Papilio_gambrisius1
Papilio_bridgei_hecataeus
Papilio_tydeus
Papilio_heringi
Papilio_albinus
Papilio_hipponous
Papilio_pitmani
Papilio_enganius
Papilio_elenus
Papilio_amynthor
Papilio_memnon
Papilio_oenomanus
Papilio_deiphobus
Papilio_rumanzovia
Papilio_thaiwanus
Papilio_forbesi
Papilio_macilentus
Papilio_protenor
Papilio_polytes
Papilio_nephelus
Papilio_mahadeva
Papilio_erithonioides
Papilio_demodocus
Papilio_grossmithi
Papilio_morondavana
Papilio_bianor
Papilio_maackii
Papilio_paris
Papilio_lorquinianus
Papilio_ulysses
Papilio_montrouzieri
Papilio_epiphorbas
Papilio_oribazus
Papilio_nobilis
Papilio_machaon
Papilio_arregonius
Papilio_hippocrates
Papilio_hospiton
Papilio_polyxenes
Papilio_zelicaon
Papilio_indra
Papilio_xuthus
Papilio_meriones
Papilio_dardanus
Papilio_constantinus
Papilio_phorcas
Papilio_rex
Papilio_lormieri
Papilio_delalandei
Papilio_noblei
Papilio_demolion
Papilio_gigon
Papilio_aristacus
Papilio_troilus
Papilio_palamedes
Papilio_pilumnus
Papilio_esperanza
Papilio_clytia
Papilio_epycides
Papilio_alexanor
Papilio_glaucus
Papilio_canadensis
Papilio_rutulus
Papilio_multicaudatus
Papilio_birchalli
Papilio_scamander
Papilio_garamas
Papilio_torquatus
Papilio_hectorides
Papilio_anchisiades
Papilio_erostratus
Papilio_astyalus
Papilio_thoas
Papilio_cresphontes
Meandrusa_sciron
Meandrusa_payeni
Teinopalpus_aureus
Teinopalpus_imperialis
Parides_panthonus
Parides_burchellanus
Parides_lysander
Parides_zacynthus
Parides_eurimedes
Parides_neophilus
Parides_aeneas
Parides_tros
Parides_anchises
Parides_vertumnus
Parides_sesostris
Parides_photinus
Parides_childrenae
Parides_chabrias
Parides_proneus
Parides_agavus
Parides_ascanius
Parides_burichus
Euryades_corethrus
Euryades_duponchelii
Ornithoptera_goliath
Ornithoptera_rothschildi
Ornithoptera_tithonus
Ornithoptera_paradisea
Ornithoptera_euphorion
Ornithoptera_aesacus
Ornithoptera_croesus
Trogonoptera_helena
Troides_aeacus
Troides_prattorum
Troides_staudingeri
Troides_haliphron
Troides_amphrysus
Troides_hypolitus
Atrophaneura_neptunus
Pachliopta_aristolochiae
Atrophaneura_alcinous
Atrophaneura_horishana
Cressida_cressida
Trogonoptera_brookiana
Pharmacophagus_antenor
Battus_crassus
Battus_belus
Battus_polystictus
Battus_polydamas
Battus_philenor
Parnassius_stenosemus
Parnassius_stoliczkanus
Parnassius_staudingeri
Parnassius_cardinal
Parnassius_delphius
Parnassius_maximinus
Parnassius_patricius
Parnassius_imperator
Parnassius_acdestis
Parnassius_inopinatus
Parnassius_charltonius
Parnassius_autocrator
Parnassius_loxias
Parnassius_bremeri
Parnassius_sacerdos
Parnassius_smintheus
Parnassius_behri
Parnassius_phoebus
Parnassius_apollo
Parnassius_actius
Parnassius_tianschanicus
Parnassius_jacquemontii
Parnassius_epaphus
Parnassius_nomion
Parnassius_honrathi
Parnassius_apollonius
Parnassius_mnemosyne
Parnassius_ariadne
Parnassius_eversmanni
Parnassius_clodius
Parnassius_glacialis
Parnassius_stubbendorfii
Parnassius_nordmanni
Parnassius_orleans
Parnassius_simo
Parnassius_andreji
Parnassius_simonius
Parnassius_boedromius
Parnassius_acco
Parnassius_hannyngtoni
Parnassius_maharaja
Parnassius_schultei
Parnassius_cephalus
Parnassius_szechenyii
Parnassius_hardwickii
Parnassius_arcticus
Parnassius_tenedius
Hypermnestra_helios
Allancastria_caucasica
Allancastria_cerisyi
Allancastria_cretica
Allancastria_deyrollei
Allancastria_louristana
Zerynthia_polyxena
Zerynthia_rumina
Bhutanitis_marsfieldi
Bhutanitis_lidderdalii
Bhutanitis_thaidina
Sericinus_montela
Luehdorfia_taibai
Luehdorfia_chinensis
Luehdorfia_japonica
Luehdorfia_puziloi
Archon_apollinaris
Archon_apollinus
Eurytides_marcellus
Mimoides_branchus
Eurytides_serville
Protesilaus_glaucolaus
Graphium_sarpedon
Graphium_agamemnon
Graphium_doson
Lamproptera_meges
Lamproptera_curius
Iphiclides_podalirius
Baronia_brevicornis

Millions of years ago

Ceratinini BioGeoBEARS DEC+J
ancstates: global optim, 3 areas max. d=4e−04; e=0; j=0.0317; LnL=−70.21

Ceratina_moderata
Ceratina_hieroglyphica
Ceratina_bowringi
Ceratina_japonica
Ceratina_okinawana
Ceratina_papuana
Ceratina_nigrolateralis
Ceratina_bryanti
Ceratina_cognata
Ceratina_accusator
Ceratina_nasalis
Ceratina_waini
Ceratina_Pithitis_sp_Kenya
Ceratina_fastigiata
Ceratina_tarsata
Ceratina_citriphila
Ceratina_unimaculata
Ceratina_binghami
Ceratina_smaragdula
Ceratina_sp_SMR_2010
Ceratina_calcarata
Ceratina_strenua
Ceratina_dupla_floridana
Ceratina_dupla
Ceratina_cyaniventris
Ceratina_cockerelli
Ceratina_Ceratinula_sp_paragua
Ceratina_breviceps
Ceratina_Calloceratina_sp_Pana
Ceratina_Calloceratina_sp_blue
Ceratina_chrysomalla
Ceratina_chalcites
Ceratina_tibialis
Ceratina_mandibulari
Ceratina_azurea
Ceratina_rufigastra
Ceratina_penicillata
Ceratina_sp_Kenya
Ceratina_ericia
Ceratina_penicilligera
Ceratina_malindae
Ceratina_lunata
Ceratina_moerenhouti
Ceratina_tanganyicensis
Ceratina_Hirashima_sp_Zambia_1
Ceratina_Hirashima_sp_Zambia_2
Ceratina_Hirashima_sp_SAfrica_
Ceratina_Hirashima_sp_SAfrica_
Ceratina_lativentris
Ceratina_Hirashima_sp_Malagasy
Ceratina_Hirashima_sp_Malagasy
Ceratina_dentipes_isolate_MAU
Ceratina_dentipes_isolate_MAL
Ceratina_satoi
Ceratina_Neoceratina_sp_Solomo
Ceratina_bispinosa
Ceratina_propinqua
Ceratina_australensis
Ceratina_lineola
Ceratina_Ctenoceratina_sp_Zamb
Ceratina_bilobata
Ceratina_flavolateralis
Ceratina_sculpturata
Ceratina_braunsi
Ceratina_subquadrata
Ceratina_speculifrons
Ceratina_minutula
Ceratina_minuta
Ceratina_perpolita
Ceratina_aloes
Ceratina_rhodura

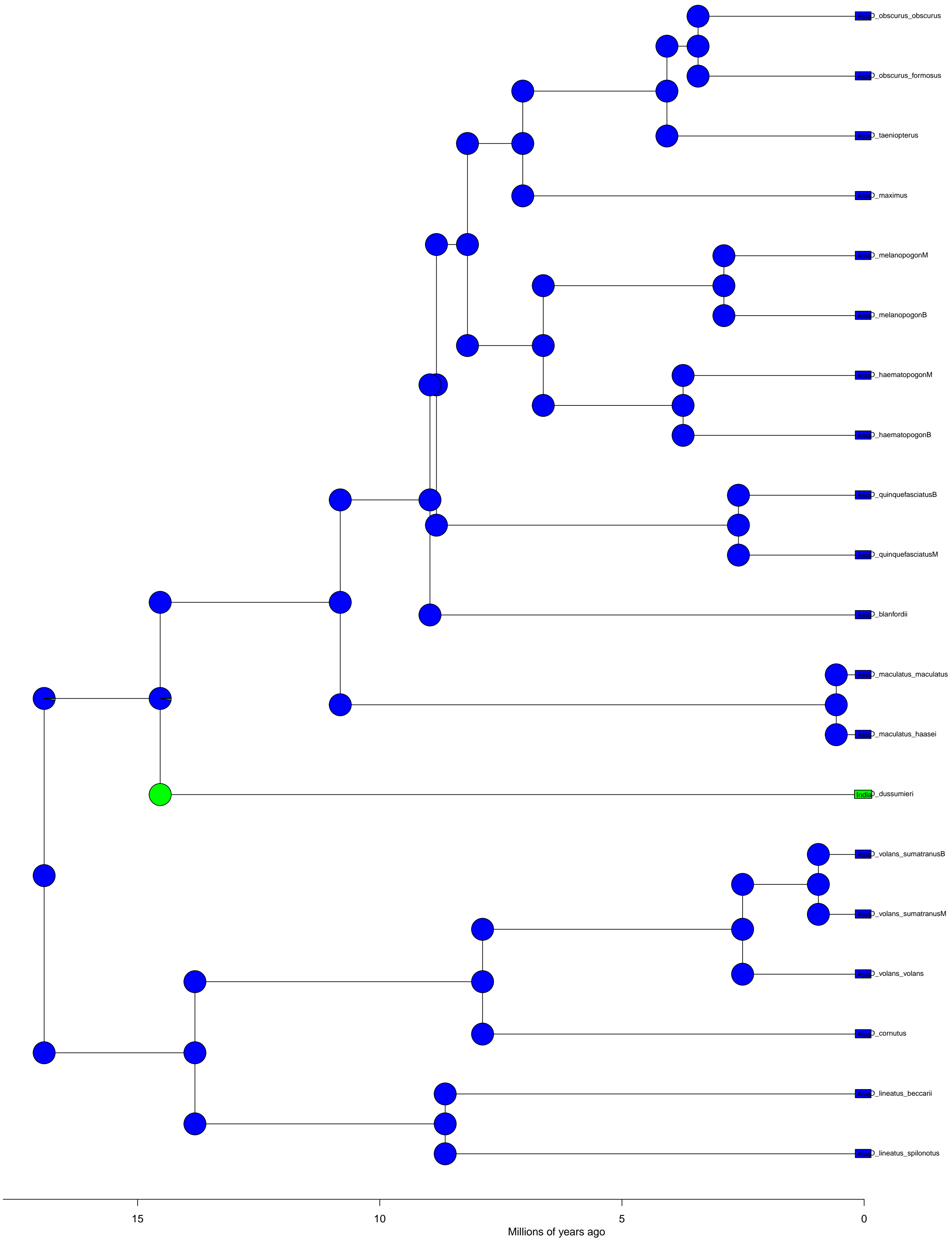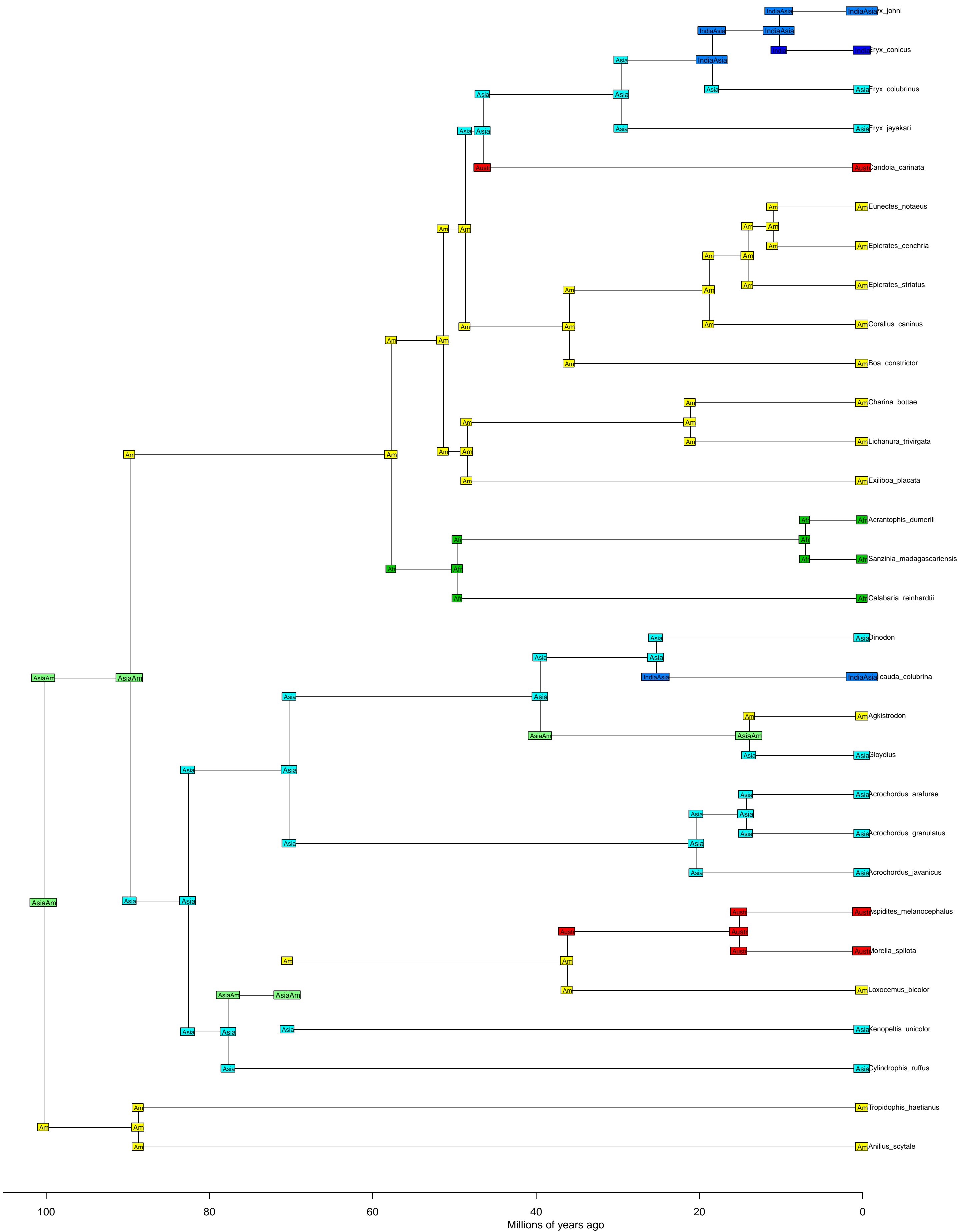30   20   10   0

Millions of years ago

Ceratinini BioGeoBEARS DEC+J
ancstates: global optim, 3 areas max. d=4e−04; e=0; j=0.0317; LnL=−70.21

India Ceratina_moderata
India Ceratina_hieroglyphica
India Ceratina_bowringi
Asia Ceratina_japonica
Asia Ceratina_okinawana
Aust Ceratina_papuana
Asia Ceratina_nigrolateralis
Asia Ceratina_bryanti
Asia Ceratina_cognata
Asia Ceratina_accusator
Afr Ceratina_nasalis
Afr Ceratina_waini
Afr Ceratina_Pithitis_sp_Kenya
Afr Ceratina_fastigiata
Afr Ceratina_tarsata
Afr Ceratina_citriphila
Asia Ceratina_unimaculata
India Ceratina_binghami
Asia Ceratina_smaragdula
Afr Ceratina_sp_SMR_2010
Amer Ceratina_calcarata
Amer Ceratina_strenua
Amer Ceratina_dupla_floridana
Amer Ceratina_dupla
Amer Ceratina_cyaniventris
Amer Ceratina_cockerelli
Amer Ceratina_Ceratinula_sp_paragua
Amer Ceratina_breviceps
Amer Ceratina_Calloceratina_sp_Pana
Amer Ceratina_Calloceratina_sp_blue
Asia Ceratina_chrysomalla
Afr Ceratina_chalcites
Asia Ceratina_tibialis
Asia Ceratina_mandibulari
Afr Ceratina_azurea
Afr Ceratina_rufigastra
Afr Ceratina_penicillata
Afr Ceratina_sp_Kenya
Afr Ceratina_ericia
Afr Ceratina_penicilligera
Afr Ceratina_malindae
Afr Ceratina_lunata
Afr Ceratina_moerenhouti
Afr Ceratina_tanganyicensis
Afr Ceratina_Hirashima_sp_Zambia_1
Afr Ceratina_Hirashima_sp_Zambia_2
Afr Ceratina_Hirashima_sp_SAfrica_
Afr Ceratina_Hirashima_sp_SAfrica_
Afr Ceratina_lativentris
Afr Ceratina_Hirashima_sp_Malagasy
Afr Ceratina_Hirashima_sp_Malagasy
Asia Ceratina_dentipes_isolate_MAU
Asia Ceratina_dentipes_isolate_MAL
Asia Ceratina_satoi
Aust Ceratina_Neoceratina_sp_Solomo
Asia Ceratina_bispinosa
India Ceratina_propinqua
Aust Ceratina_australensis
Afr Ceratina_lineola
Afr Ceratina_Ctenoceratina_sp_Zamb
Afr Ceratina_bilobata
Asia Ceratina_flavolateralis
Afr Ceratina_sculpturata
Afr Ceratina_braunsi
Afr Ceratina_subquadrata
Afr Ceratina_speculifrons
Asia Ceratina_minutula
Afr Ceratina_minuta
Afr Ceratina_perpolita
Afr Ceratina_aloes
Afr Ceratina_rhodura

30   20   10   0
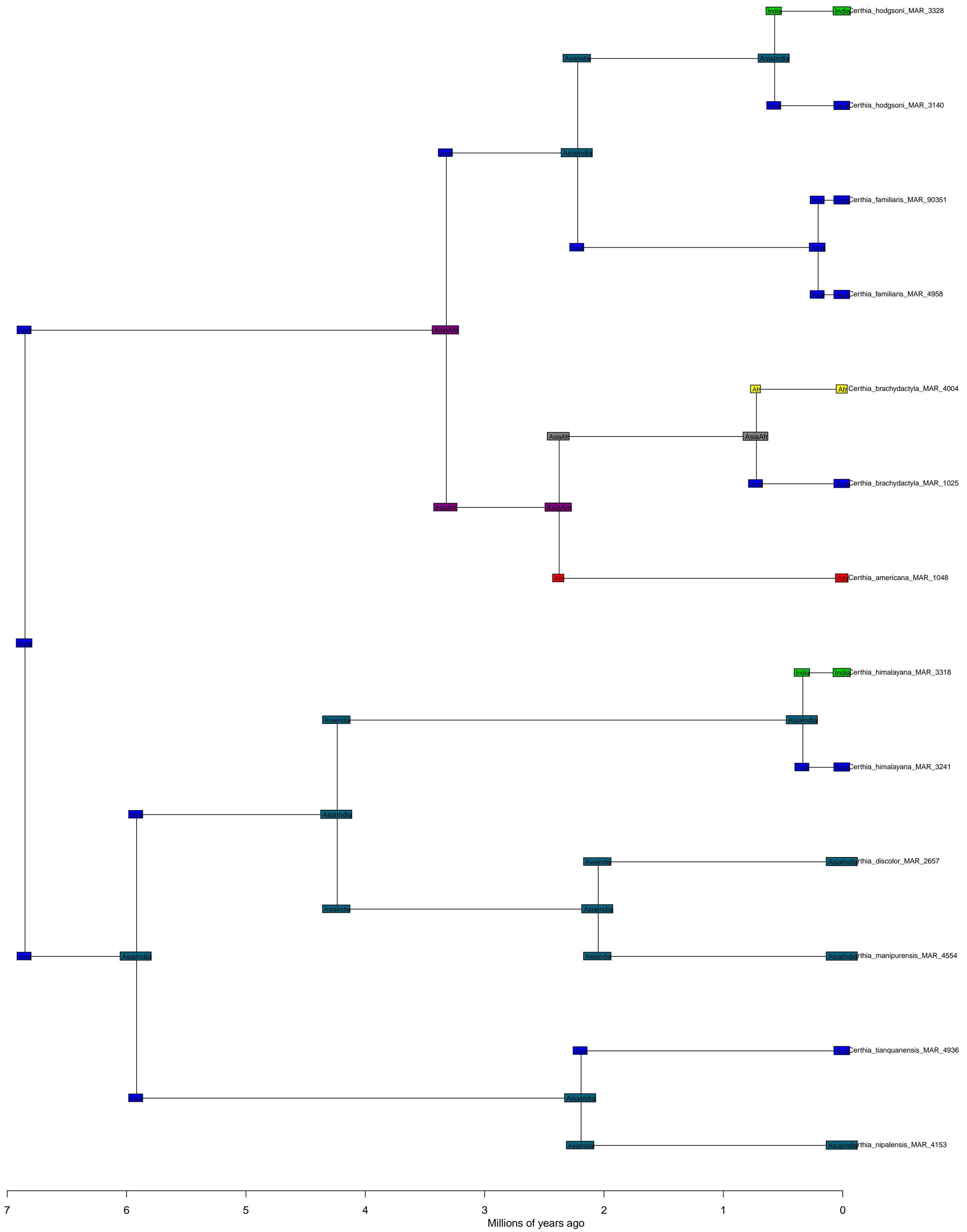
Millions of years ago

Pseudomyrmecinae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0224; LnL=−26.62

Pseudomyrmecinae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0224; LnL=−26.62

Amer Pseudomyrmex_sericeus
Amer Pseudomyrmex_ita
Amer Pseudomyrmex_cordiae
Amer Pseudomyrmex_gracilis
Amer Pseudomyrmex_nigropilosus
Amer Pseudomyrmex_godmani
Amer Pseudomyrmex_pallens
Amer Pseudomyrmex_phyllophilus
Amer Pseudomyrmex_kuenckeli
Amer Pseudomyrmex_flavicornis
Amer Pseudomyrmex_nigrocinctus
Amer Pseudomyrmex_haytianus
Amer Pseudomyrmex_subater
Amer Pseudomyrmex_pallidus
Amer Pseudomyrmex_holmgreni
Amer Pseudomyrmex_simplex
Amer Pseudomyrmex_pazosi
Amer Pseudomyrmex_oki
Amer Pseudomyrmex_tachigaliae
Amer Pseudomyrmex_concolor
Amer Pseudomyrmex_oculatus
Amer Pseudomyrmex_cubaensis
Amer Pseudomyrmex_dendroicus
Amer Pseudomyrmex_viduus
Amer Pseudomyrmex_elongatulus
Amer Pseudomyrmex_apache
Amer Pseudomyrmex_spiculus
Amer Pseudomyrmex_tenuissimus
Amer Pseudomyrmex_tenuis
Amer Pseudomyrmex_boopis
Amer Pseudomyrmex_denticollis
Amer Pseudomyrmex_termitarius
Amer Pseudomyrmex_filiformis
Afr Tetraponera_ambigua
Afr Tetraponera_parops
Afr Tetraponera_caffra
Afr Tetraponera_natalensis
India Tetraponera_rufonigra
Afr Tetraponera_aethiops
Afr Tetraponera_pilosa
Afr Tetraponera_grandidieri
India Tetraponera_nigra
Afr Tetraponera_punctulata
Afr Tetraponera_morondaviensis
Afr Tetraponera_clypeata
India Tetraponera_allaborans
Afr Tetraponera_penzigi
Afr Tetraponera_tessmanni

70   60   50   40   30   20   10   0
Millions of years ago

Myrmica BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0494; LnL=−14.46

Myrmica_schoedli
Myrmica_angulata
Myrmica_yamanei_2
Myrmica_nsp_2
Myrmica_formosae
Myrmica_indica
Myrmica_indica_2
Myrmica_weberi
Myrmica_serica
Myrmica_yamanei
Myrmica_crassirugis
Myrmica_sulcinodis
Myrmica_crassirugis_2
Myrmica_scabrinodis_2
Myrmica_scabrinodis
Myrmica_angulinodis
Myrmica_angulinodis_2
Myrmica_sulcinodis_2

20   15   10   5   0

Millions of years ago

Myrmica BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0494; LnL=−14.46

Millions of years ago

Aplocheiloidei BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0259; LnL=−17.88

Afr		Aphyosemion_bivittatum
Afr	Afr	Aphyosemion_australe
Afr	Afr	Fundulopanchax_sjoestedi
Afr	Afr	Fundulopanchax_mirabile
Afr	Afr	Nothobranchius_kafuensis
Afr	Afr	Nothobranchius_kirki
Afr	Afr	Epiplatys_chaperi
Afr	Afr	Epiplatys_boulengeri
Afr	Afr	Epiplatys_roloffi
Afr	Afr	Roloffia_occidentalis
Afr	Afr	Roloffia_geryi
Amer	Amer	Rivulus_stagnatus
Amer	Amer	Rivulus_tenuis
Amer	Amer	Trigonectes_rubromarginatus
Amer	Amer	Austrofundulus_limnaeus
Amer	Amer	Cynolebias_affinis
Amer	Amer	Cynolebias_antenori
Amer	Amer	Leptolebias_citrinipinnis
Sau	Sau	Pachypanchax_playfairii
Mada	Mada	Pachypanchax_homolonotus
Asia	Asia	Aplocheilus_panchax
India	India	Aplocheilus_lineatus

Millions of years ago
150   100   50   0

Aplocheiloidei BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0259; LnL=−17.88

Aphyosemion_bivittatum
Aphyosemion_australe
Fundulopanchax_sjoestedi
Fundulopanchax_mirabile
Nothobranchius_kafuensis
Nothobranchius_kirki
Epiplatys_chaperi
Epiplatys_boulengeri
Epiplatys_roloffi
Roloffia_occidentalis
Roloffia_geryi
Rivulus_stagnatus
Rivulus_tenuis
Trigonectes_rubromarginatus
Austrofundulus_limnaeus
Cynolebias_affinis
Cynolebias_antenori
Leptolebias_citrinipinnis
Pachypanchax_playfairii
Pachypanchax_homolonotus
Aplocheilus_panchax
Aplocheilus_lineatus

Millions of years ago

Channna BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.3815; LnL=−9.44

Channa_striata_TanjungKarang
Channa_striata_Lampung
Channa_striata_Kerala
Channa_striata_Vientiane
Channa_cf_marulius_StungTreng1
Channa_marulia
Channa_gachua_KongJeam
Channa_gachua_VangVien
Channa_bleheri
Channa_maculata
Channa_micropeltes_TienBien
Channa_diplogramme
Channa_lucius_Kratie
Channa_lucius_sumatera

35   30   25   20   15   10   5   0

Millions of years ago

Channa BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.3815; LnL=−9.44

Channa_striata_TanjungKarang
Channa_striata_Lampung
Channa_striata_Kerala
Channa_striata_Vientiane
Channa_cf_marulius_StungTreng1
Channa_marulia
Channa_gachua_KongJeam
Channa_gachua_VangVien
Channa_bleheri
Channa_maculata
Channa_micropeltes_TienBien
Channa_diplogramme
Channa_lucius_Kratie
Channa_lucius_sumatera

35   30   25   20   15   10   5   0
Millions of years ago

Anabantoidei, Osphronemidae BioGeoBEARS DEC+J
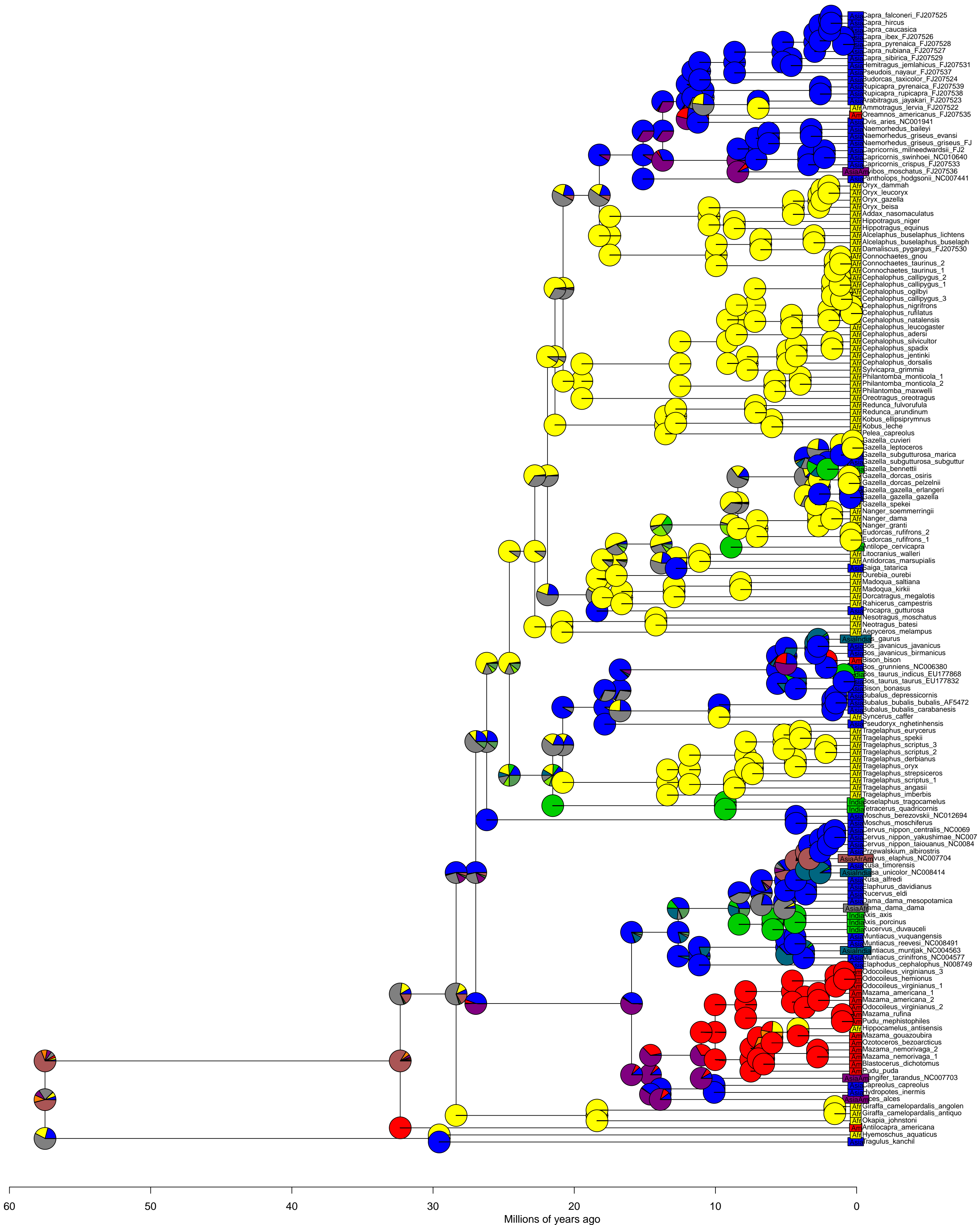ancstates: global optim, 2 areas max. d=0.0019; e=0; j=0.0207; LnL=−35.48

Betta_dimidiata
Betta_albimarginata
Betta_foerschi
Betta_coccina
Betta_splendens
Betta_macrostoma
Betta_unimaculata
Parosphromenus_deissneri
Parosphromenus_anjunganensis
Parosphromenus_paludicola
Parosphromenus_ornaticauda
Trichopsis_schalleri
Trichopsis_pumila
Trichopsis_vittata
Pseudosphromenus_cupanus
Pseudosphromenus_dayi
Malpulutta_kretseri
Macropodus_opercularis
Macropodus_spechti
Trichogaster_trichopterus
Trichogaster_pectoralis
Trichogaster_microlepis
Trichogaster_leerii
Colisa_chuna
Colisa_lalia
Colisa_labiosa
Colisa_fasciata
Sphaerichthys_osphromenoides
Sphaerichthys_selatanensis
Sphaerichthys_acrostoma
Sphaerichthys_vaillanti
Luciocephalus_sp
Luciocephalus_pulcher
Parasphaerichthys_ocellatus
Parasphaerichthys_lineatus
Ctenops_nobilis
Osphronemus_gouramy
Osphronemus_septemfasciatus
Osphronemus_exodon
Belontia_hasselti
Belontia_signata
Microctenopoma_sp_Mai_Ndombe
Microctenopoma_damasi
Microctenopoma_nanum
Microctenopoma_ansorgii
Microctenopoma_fasciolatum
Ctenopoma_muriei
Ctenopoma_acutirostre
Ctenopoma_ocellatum
Ctenopoma_petherici
Ctenopoma_kingsleyae
Ctenopoma_nebulosum
Ctenopoma_pellegrini
Ctenopoma_nigropannosum
Sandelia_capensis
Anabas_testudineus
Helostoma_temminkii

30   20   10   0

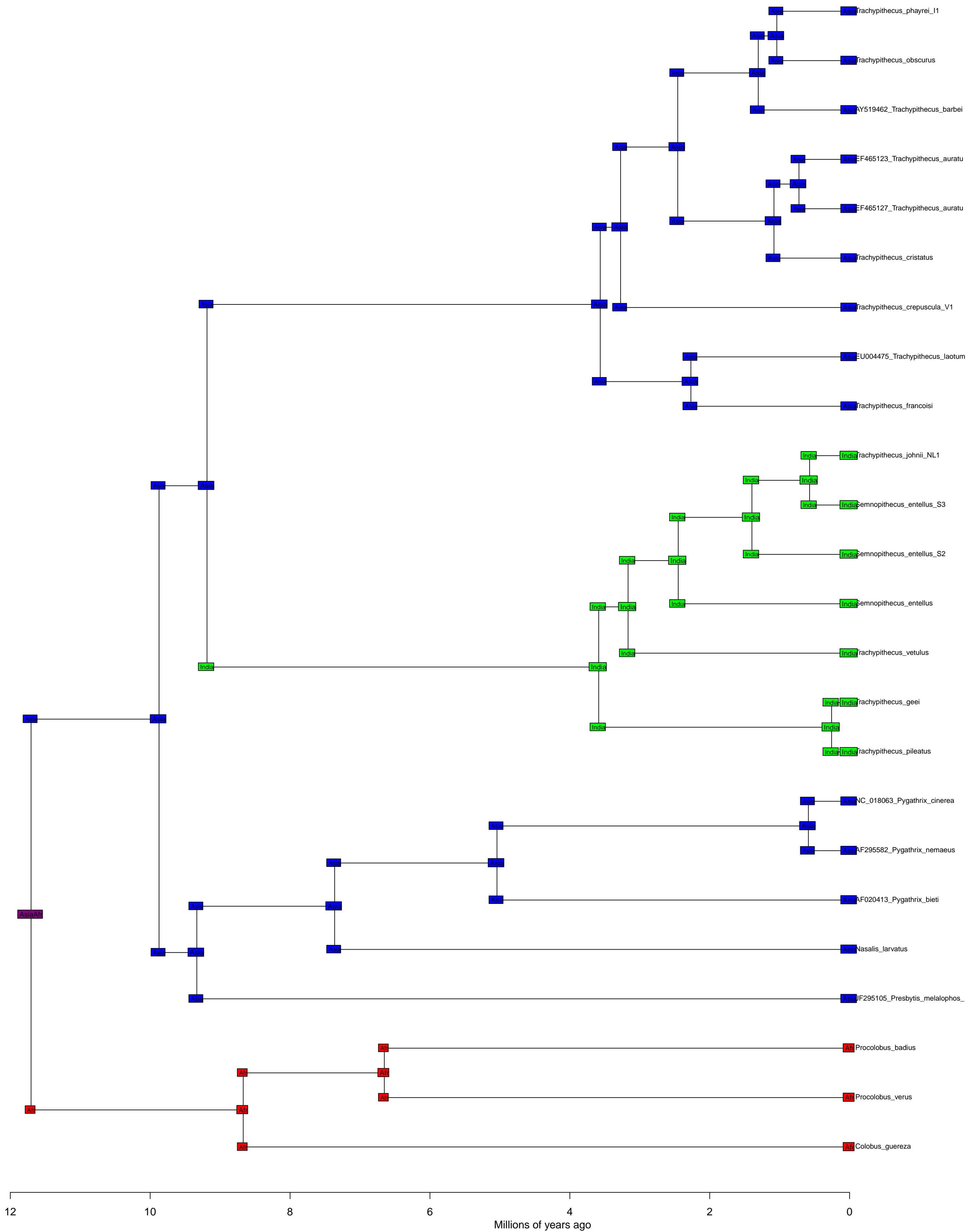Millions of years ago

Anabantoidei, Osphronemidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.0019; e=0; j=0.0207; LnL=−35.48

Betta_dimidiata
Betta_albimarginata
Betta_foerschi
Betta_coccina
Betta_splendens
Betta_macrostoma
Betta_unimaculata
Parosphromenus_deissneri
Parosphromenus_anjunganensis
Parosphromenus_paludicola
Parosphromenus_ornaticauda
Trichopsis_schalleri
Trichopsis_pumila
Trichopsis_vittata
Pseudosphromenus_cupanus
Pseudosphromenus_dayi
Malpulutta_kretseri
Macropodus_opercularis
Macropodus_spechti
Trichogaster_trichopterus
Trichogaster_pectoralis
Trichogaster_microlepis
Trichogaster_leerii
Colisa_chuna
Colisa_lalia
Colisa_labiosa
Colisa_fasciata
Sphaerichthys_osphromenoides
Sphaerichthys_selatanensis
Sphaerichthys_acrostoma
Sphaerichthys_vaillanti
Luciocephalus_sp
Luciocephalus_pulcher
Parasphaerichthys_ocellatus
Parasphaerichthys_lineatus
Ctenops_nobilis
Osphronemus_gouramy
Osphronemus_septemfasciatus
Osphronemus_exodon
Belontia_hasselti
Belontia_signata
Microctenopoma_sp_Mai_Ndombe
Microctenopoma_damasi
Microctenopoma_nanum
Microctenopoma_ansorgii
Microctenopoma_fasciolatum
Ctenopoma_muriei
Ctenopoma_acutirostre
Ctenopoma_ocellatum
Ctenopoma_petherici
Ctenopoma_kingsleyae
Ctenopoma_nebulosum
Ctenopoma_pellegrini
Ctenopoma_nigropannosum
Sandelia_capensis
Anabas_testudineus
Helostoma_temminkii

30   20   10   0

Millions of years ago

Heteropneustes fossilis BioGeoBEARS DEC+J
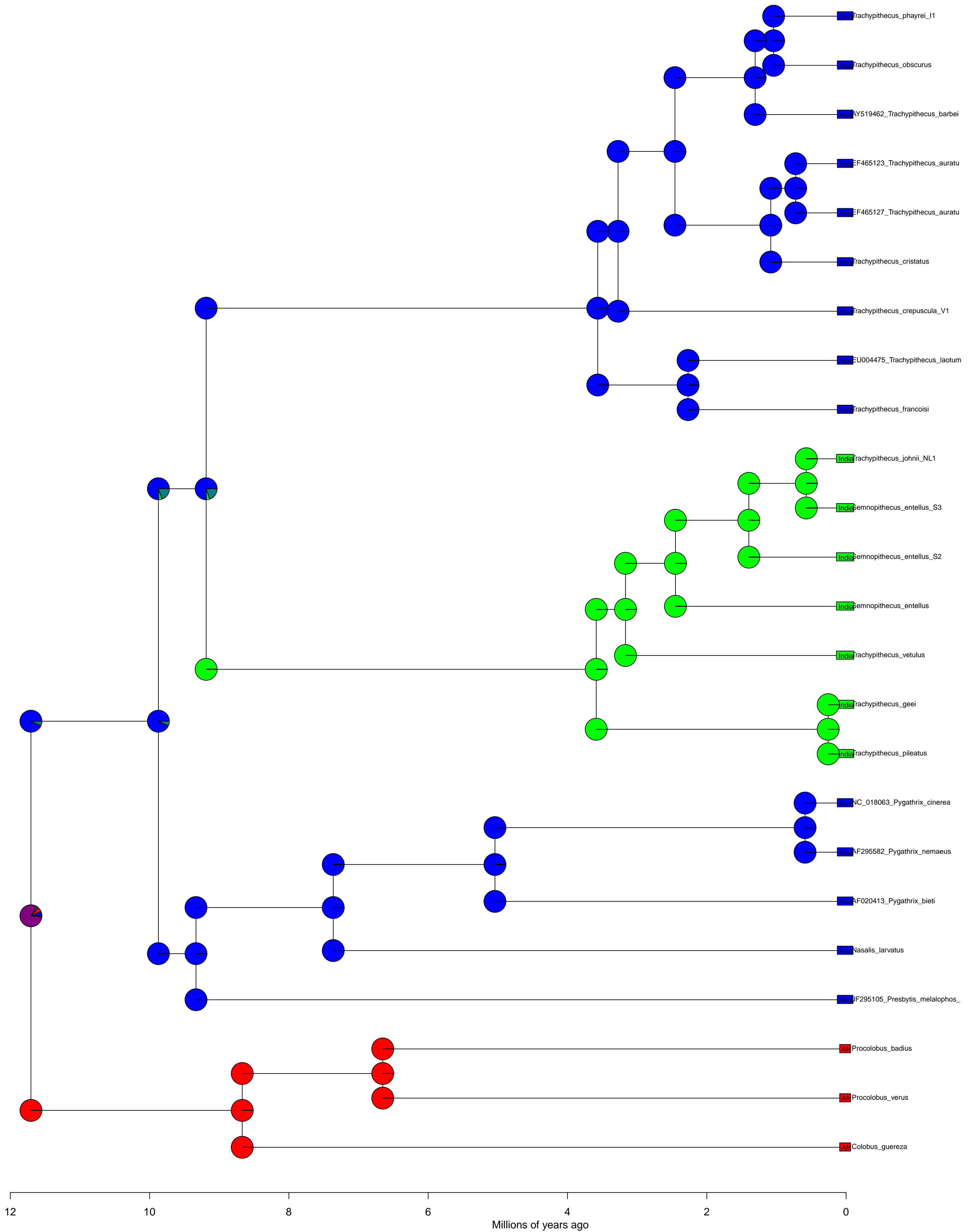**ancstates: global optim, 2 areas max. d=0; e=0; j=0.071; LnL=−2.96**

Millions of years ago

Heteropneustes fossilis BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.071; LnL=−2.96

India Heteropneustes_fossilis_Hky2

India Heteropneustes_fossilis_Has1

India Heteropneustes_fossilis_Hwb1

Asia Heteropneustes_fossilis_Hcp1

Asia Heteropneustes_fossilis_Hkc2

Asia Heteropneustes_fossilis_Hyg1

Asia Heteropneustes_fossilis_Hbg2

Asia Heteropneustes_fossilis_Hrk2

25   20   15   10   5   0

Millions of years ago

Cobitidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0252; LnL=−14.02

Misgurnus_mohoity_A1114
Misgurnus_bipartitus_haplotype
Misgurnus_sp_3_A1879
Misgurnus_sp_2_A1958
Misgurnus_anguillicaudatus_A40
Niwaella_multciata_A1907
Kichulchoia_brevciata_A1936
ksookimia_yongdokensis_A1896
ksookimia_longicorpa_A1918
Cobitis_taenia
Cobitis_vettonica_A1862
Cobitis_elazigensis_A2094
Niwaella_cf_laterimaculata_IHC
Cobitis_bilineata_A1069
Cobitis_elongata
Cobitis_lutheri_A1930
Cobitis_rara_A2019
ksookimia_koreensis_A1868
ksookimia_pumila_A1928
Cobitis_pacifica_A1889
Niwaella_delicata_A2177
Cobitis_biwae_A2237
Cobitis_striata
Cobitis_cf_sibirica
Cobitis_melanoleuca_A1068
Cobitis_choii_A2029
Misgurnus_fossilis_A081
Misgurnus_sp_1_A212
Misgurnus_anguillicaudatus_A40
Paramisgurnus_dabryanus_A409
Koreocobitis_rotundicauda_A188
Koreocobitis_naktongensis_A197
Cobitis_misgurnoides_A301
Sabanejewia_balcanica_A457
Sabanejewia_romanica_G23
Sabanejewia_larvata_A1859
Somileptus_gongota_A175
Neoeucirrhichthys_maydelli_A50
Lepidocephalus_macrochir_A866
Lepidocephalichthys_hasselti_A
Lepidocephalichthys_guntea_A03
Lepidocephalichthys_guntea_A49
Lepidocephalichthys_guntea_A49
Lepidocephalichthys_berdmorei_
Lepidocephalichthys_berdmorei_
Lepidocephalus_thermalis_A280
Pangio_cf_kuhlii_A1553
Pangio_cuneovirgata_A550
Pangio_oblonga_A1778
Pangio_pangia_A2181
Pangio_doriae_A1583
Pangio_anguillaris_A1061
Kottelatlimia_pristes_A239
Kottelatlimia_katik_A1855
Acanthopsoides_robertsi_A1580
Acanthopsoides_robertsi_A1613
Acanthopsoides_robertsi_A1720
Acanthopsoides_gracilentus_A97
Acanthopsoides_gracilentus_A65
Acanthopsoides_hapalias_A634
Acantopsis_sp_1_A1714
Acantopsis_sp_2_A624
Acantopsis_sp_3_A222
Acantopsis_sp_4_A090

40   30   20   10   0

Millions of years ago

Cobitidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0252; LnL=−14.02

Misgurnus_mohoity_A1114
Misgurnus_bipartitus_haplotype
Misgurnus_sp_3_A1879
Misgurnus_sp_2_A1958
Misgurnus_anguillicaudatus_A40
Niwaella_multciata_A1907
Kichulchoia_brevciata_A1936
ksookimia_yongdokensis_A1896
ksookimia_longicorpa_A1918
Cobitis_taenia
Cobitis_vettonica_A1862
Cobitis_elazigensis_A2094
Niwaella_cf_laterimaculata_IHC
Cobitis_bilineata_A1069
Cobitis_elongata
Cobitis_lutheri_A1930
Cobitis_rara_A2019
ksookimia_koreensis_A1868
ksookimia_pumila_A1928
Cobitis_pacifica_A1889
Niwaella_delicata_A2177
Cobitis_biwae_A2237
Cobitis_striata
Cobitis_cf_sibirica
Cobitis_melanoleuca_A1068
Cobitis_choii_A2029
Misgurnus_fossilis_A081
Misgurnus_sp_1_A212
Misgurnus_anguillicaudatus_A40
Paramisgurnus_dabryanus_A409
Koreocobitis_rotundicauda_A188
Koreocobitis_naktongensis_A197
Cobitis_misgurnoides_A301
Sabanejewia_balcanica_A457
Sabanejewia_romanica_G23
Sabanejewia_larvata_A1859
Somileptus_gongota_A175
Neoeucirrhichthys_maydelli_A50
Lepidocephalus_macrochir_A866
Lepidocephalichthys_hasselti_A
Lepidocephalichthys_guntea_A03
Lepidocephalichthys_guntea_A49
Lepidocephalichthys_guntea_A49
Lepidocephalichthys_berdmorei_
Lepidocephalichthys_berdmorei_
Lepidocephalus_thermalis_A280
Pangio_cf_kuhlii_A1553
Pangio_cuneovirgata_A550
Pangio_oblonga_A1778
Pangio_pangia_A2181
Pangio_doriae_A1583
Pangio_anguillaris_A1061
Kottelatlimia_pristes_A239
Kottelatlimia_katik_A1855
Acanthopsoides_robertsi_A1580
Acanthopsoides_robertsi_A1613
Acanthopsoides_robertsi_A1720
Acanthopsoides_gracilentus_A97
Acanthopsoides_gracilentus_A65
Acanthopsoides_hapalias_A634
Acantopsis_sp_1_A1714
Acantopsis_sp_2_A624
Acantopsis_sp_3_A222
Acantopsis_sp_4_A090

Millions of years ago

Microhylidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0258; LnL=−4.32

Asia Kaloula_pulchra_GB1
Asia Kaloula_baleata_ROM_32932
Asia Kaloula_picta_USFS_56931
Asia Metaphrynella_sundana_FMNH_231
Asia Metaphrynella_pollicaris_GB
Asia Phrynella_pulchra_GB
India Ramanella_obscura_MM_5980
India Ramanella_cf_obscura_GB
India Ramanella_montana_GB
India Ramanella_variegata_0019C
India Uperodon
India Kaloula_taprobanica_GB1
Asia Microhyla_heymonsi_GB
Asia Microhyla_ornata_230957
Asia Microhyla_annectens_GB
Asia Glyphoglossus_molossus_USFS_34
Asia Calluella_guttulata_GB1
Asia Chaperina_fusca_GB
Asia Micryletta_inornata_K_1956

Millions of years ago

Microhylidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0258; LnL=−4.32

Asia Kaloula_pulchra_GB1
Asia Kaloula_baleata_ROM_32932
Asia Kaloula_picta_USFS_56931
Asia Metaphrynella_sundana_FMNH_231
Asia Metaphrynella_pollicaris_GB
Asia Phrynella_pulchra_GB
India Ramanella_obscura_MM_5980
India Ramanella_cf_obscura_GB
India Ramanella_montana_GB
India Ramanella_variegata_0019C
India Uperodon
India Kaloula_taprobanica_GB1
Asia Microhyla_heymonsi_GB
Asia Microhyla_ornata_230957
Asia Microhyla_annectens_GB
Asia Glyphoglossus_molossus_USFS_34
Asia Calluella_guttulata_GB1
Asia Chaperina_fusca_GB
Asia Micryletta_inornata_K_1956

Millions of years ago

Dicroglossidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0324; LnL=−39.67

Dicroglossidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0324; LnL=−39.67

Limnonectes_magnus
Limnonectes_heinrichi
Limnonectes_modestus
Limnonectes_macrocephalus
Limnonectes_woodworthi
Limnonectes_visayanus
Limnonectes_microtympanum
Limnonectes_arathooni
Limnonectes_acanthi
Limnonectes_leytensis
Limnonectes_finchi
Limnonectes_malesianus
Limnonectes_poilani
Limnonectes_parvus
Limnonectes_grunniens
Limnonectes_leporinus
Limnonectes_bannaensis
Limnonectes_kuhlii
Limnonectes_fujianensis
Limnonectes_fragilis
Limnonectes_microdiscus
Limnonectes_kadarsani
Limnonectes_dabanus
Limnonectes_gyldenstolpei
Paa_arnoldi
Paa_chayuensis
Paa_maculosa
Paa_medogensis
Paa_conaensis
Nanorana_pleskei
Nanorana_ventripunctata
Nanorana_parkeri
Paa_bourreti
Paa_yunnanensis
Paa_taihangnicus
Paa_liebigii
Paa_exilispinosa
Paa_spinosa
Paa_jiulongensis
Paa_robertingeri
Paa_boulengeri
Paa_shini
Paa_fasciculispina
Fejervarya_pierrei
Fejervarya_granosa
Fejervarya_syhadrensis
Fejervarya_caperata
Fejervarya_kudremukhensis
Fejervarya_rufescens
Fejervarya_kirtisinghei
Fejervarya_greenii
Fejervarya_hp6
Fejervarya_hp3
Fejervarya_mudduraja
Fejervarya_limnocharis
Fejervarya_hp2
Fejervarya_sakishimensis
Fejervarya_orissaensis
Fejervarya_iskandari
Fejervarya_triora
Fejervarya_vittigera
Fejervarya_cancrivora
Sphaerotheca_breviceps
Sphaerotheca_dobsonii
Hoplobatrachus_rugulosus
Hoplobatrachus_tigerinus
Hoplobatrachus_occipitalis
Euphlyctis_ehrenbergii
Euphlyctis_cyanophlyctis
Euphlyctis_hexadactylus
Nannophrys_marmorata
Nannophrys_ceylonensis
Occidozyga_martensii
Occidozyga_magnapustulosa
Occidozyga_lima
Occidozyga_baluensis
Occidozyga_laevis
Ingerana_tenasserimensis
Occidozyga_borealis
Ingerana_baluensis
Indirana_semipalmata
Indirana_beddomii

Millions of years ago

Rhacophoridae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.0067; e=0; j=0.0019; LnL=−307.04

Millions of years ago

Rhacophoridae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.0067; e=0; j=0.0019; LnL=−307.04

Millions of years ago

Bufonidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0229; LnL=−57.14

Bufonidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0229; LnL=−57.14

Mannophryne_variegata_SA
Mannophryne_cophotis_SA
Rhaebo_nascicus_SA
Rhaebo_haematiticus_SA
Incilius_luetkenii_SA
Incilius_alvarius_NA
Anaxyrus_boreas_NA
Anaxyrus_californicus_NA
Anaxyrus_americanus_NA
Anaxyrus_terrestris_NA
Rhinella_vellardi_SA
Rhinella_atacamensis_SA
Rhinella_granulosa_SA
Rhinella_marina_SA
Rhinella_schneideri_SA
Rhinella_veraguensis_SA
Rhinella_cf_margaritifera_SA
Rhinella_nesiotes_SA
Rhamphophryne_festae_SA
Mertensophryne_uzunguensis_Af
Mertensophryne_taitana_Af
Mertensophryne_micranotis_Af
Mertensophryne_lindneri_Af
Mertensophryne_loveridgei_Af
Amietophrynus_mauritanicus_Af
Amietophrynus_garmani_Af
Amietophrynus_gracilipes_Af
Amietophrynus_gutturalis_Af
Amietophrynus_steindachneri_Af
Amietophrynus_poweri_Af
Amietophrynus_brauni_Af
Wolterstorffina_parvipalmata_A
Werneria_mertensi_Af
Schismaderma_carens_Af
Churamiti_maridadi_Af
Nectophrynoides_viviparus_Af
Nectophrynoides_minutus_Af
Nectophrynoides_tornieri_Af
Ingerophrynus_divergens_A
Ingerophrynus_macrotis_A
Ingerophrynus_galeatus_A
Pedostibes_hosii_A
Phrenoides_juxtasper_A
Pseudepidalea_brongersmai_Af
Pseudepidalea_cf_surda_A
Pseudepidalea_viridis_Eu
Pseudepidalea_cf_variabilis_A
Pseudepidalea_cf_pewzowi_A
Epidalea_calamita_Eu
Bufo_gargarizans_A
Bufo_andrewsi_A
Bufo_spinosus_Eu
Bufo_verrucosissimus_A
Bufo_bufo_Eu
Ansonia_ornata_I
Pelophryne_misera_A
Pelophryne_signata_A
Ansonia_hanitschi_A
Ansonia_spinulifer_A
Ansonia_leptopus_A
Ansonia_longidigita_A
Leptophryne_borbonica_A
Pedostibes_tuberculosus_I
Adenomus_kelaartii_I
Bufo_koynayensis_I
Bufo_sp_I
Duttaphrynus_dhufarensis_A
Duttaphrynus_stomaticus_I
Duttaphrynus_hololius_I
Duttaphrynus_crocus_A
Duttaphrynus_stuarti_A
Duttaphrynus_himalayanus_I
Duttaphrynus_atukoralei_I
Duttaphrynus_scaber_I
Duttaphrynus_sp_b_I
Duttaphrynus_sp_c_A
Duttaphrynus_brevirostris_I
Duttaphrynus_sp_a_I
Duttaphrynus_parietalis_I
Duttaphrynus_melanostictus_I

40   30   20   10   0
Millions of years ago

Crocodylia BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.002; e=0; j=0.0797; LnL=−21.48

Crocodylia BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.002; e=0; j=0.0797; LnL=−21.48

Tomistoma_schlegelii
Gavialis_gangeticus
Mecistops_cataphractus
Osteolaemus_tetraspis_1
Osteolaemus_tetraspis_2
Crocodylus_johnstoni
Crocodylus_novaeguineae
Crocodylus_mindorensis
Crocodylus_porosus
Crocodylus_palustris
Crocodylus_siamensis
Crocodylus_niloticus_2
Crocodylus_niloticus_1
Crocodylus_acutus
Crocodylus_intermedius
Crocodylus_rhombifer
Crocodylus_moreletii

Millions of years ago

Cyrtodactylus BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0501; LnL=−31.94

Cyrtodactylus_quadrivirgatus_L
Cyrtodactylus_sworderi_LSUHC76
Cyrtodactylus_tuberculatus_CJS
Cyrtodactylus_semenanjungensis
Cyrtodactylus_pantiensis_LSUHC
Cyrtodactylus_seribuatensis_LS
Cyrtodactylus_batucolus_LSUHC8
Cyrtodactylus_kimberleyensis
Cyrtodactylus_sp_Timor
Cyrtodactylus_marmoratus_TNHC5
Cyrtodactylus_jellesmae_MVZ239
Cyrtodactylus_darmandvillei_WA
Cyrtodactylus_grismeri_LSUHC86
Cyrtodactylus_eisenmanae_LSUHC
Cyrtodactylus_cf_condorensis_L
Cyrtodactylus_paradoxus_LSUHC8
Cyrtodactylus_consobrinus_LLG4
Cyrtodactylus_malayanus_ID8424
Cyrtodactylus_philippinicus
Cyrtodactylus_pubisulcus_LSUHC
Cyrtodactylus_irregularis
Cyrtodactylus_interdigitalis
Cyrtodactylus_elok_LSUHC6471
Cyrtodactylus_pulchellus_LSUHC
Geckoella_collegalensis_CES_11
Geckoella_deccanensis_JB7
Cyrtodactylus_intermedius_FMNH
Geckoella_triedrus_ADS35
Cyrtodactylus_salomonensis_AMS
Cyrtodactylus_epiroticus_BPBM1
Cyrtodactylus_robustus_BPBM197
Cyrtodactylus_sermowaiensis_BP
Cyrtodactylus_novaeguineae_FK1
Cyrtodactylus_loriae_FK_7709
Cyrtodactylus_tiomanensis_LSUH
Cyrtodactylus_yoshii_ZRC24851
Cyrtodactylus_tigroides_IRSNB2
Cyrtodactylus_oldhami_JB126
Cyrtodactylus_angularis
Cyrtodactylus_chanhomeae_CUMZ2
Cyrtodactylus_jarujini_FMNH_HE
Cyrtodactylus_ayeyarwadyensis
Cyrtodactylus_gansi_CAS222412
Cyrtodactylus_chrysopylos_CAS2
Cyrtodactylus_brevidactylus_CA
Cyrtodactylus_gubernatoris_CES
Cyrtodactylus_feae_USNM559805
Cyrtodactylus_annandalei_CAS21
Cyrtodactylus_fasciolatum_CES0
Cyrtodactylus_russelli_CAS2261
Cyrtodactylus_slowinskii_CAS21

30   20   10   0
Millions of years ago

Cyrtodactylus BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0501; LnL=−31.94

Cyrtodactylus_quadrivirgatus_L
Cyrtodactylus_sworderi_LSUHC76
Cyrtodactylus_tuberculatus_CJS
Cyrtodactylus_semenanjungensis
Cyrtodactylus_pantiensis_LSUHC
Cyrtodactylus_seribuatensis_LS
Cyrtodactylus_batucolus_LSUHC8
Cyrtodactylus_kimberleyensis
Cyrtodactylus_sp_Timor
Cyrtodactylus_marmoratus_TNHC5
Cyrtodactylus_jellesmae_MVZ239
Cyrtodactylus_darmandvillei_WA
Cyrtodactylus_grismeri_LSUHC86
Cyrtodactylus_eisenmanae_LSUHC
Cyrtodactylus_cf_condorensis_L
Cyrtodactylus_paradoxus_LSUHC8
Cyrtodactylus_consobrinus_LLG4
Cyrtodactylus_malayanus_ID8424
Cyrtodactylus_philippinicus
Cyrtodactylus_pubisulcus_LSUHC
Cyrtodactylus_irregularis
Cyrtodactylus_interdigitalis
Cyrtodactylus_elok_LSUHC6471
Cyrtodactylus_pulchellus_LSUHC
Geckoella_collegalensis_CES_11
Geckoella_deccanensis_JB7
Cyrtodactylus_intermedius_FMNH
Geckoella_triedrus_ADS35
Cyrtodactylus_salomonensis_AMS
Cyrtodactylus_epiroticus_BPBM1
Cyrtodactylus_robustus_BPBM197
Cyrtodactylus_sermowaiensis_BP
Cyrtodactylus_novaeguineae_FK1
Cyrtodactylus_loriae_FK_7709
Cyrtodactylus_tiomanensis_LSUH
Cyrtodactylus_yoshii_ZRC24851
Cyrtodactylus_tigroides_IRSNB2
Cyrtodactylus_oldhami_JB126
Cyrtodactylus_angularis
Cyrtodactylus_chanhomeae_CUMZ2
Cyrtodactylus_jarujini_FMNH_HE
Cyrtodactylus_ayeyarwadyensis
Cyrtodactylus_gansi_CAS222412
Cyrtodactylus_chrysopylos_CAS2
Cyrtodactylus_brevidactylus_CA
Cyrtodactylus_gubernatoris_CES
Cyrtodactylus_feae_USNM559805
Cyrtodactylus_annandalei_CAS21
Cyrtodactylus_fasciolatum_CES0
Cyrtodactylus_russelli_CAS2261
Cyrtodactylus_slowinskii_CAS21

30   20   10   0

Millions of years ago

Scincidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0232; LnL=−47.68

Eutropis_macularia_1
Eutropis_macularia_3
Eutropis_macularia_2
Eutropis_macularia_4
Eutropis_allapallensis_3
Eutropis_allapallensis_2
Eutropis_allapallensis_1
Eutropis_clivicola_CESL089
Eutropis_madaraszi_ZFMK15976
Eutropis_quadricarinata_USNM52
Eutropis_bibronii
Eutropis_indeprensa
Eutropis_cumingi
Eutropis_multicarinata_boreali
Eutropis_carinata_CES09_879
Eutropis_carinata_CES09_849
Eutropis_carinata_CES08_809
Eutropis_carinata_CES08_808
Eutropis_nagarjuni
Eutropis_trivittata_CES09_976
Eutropis_beddomii_CES09_943
Eutropis_rugifera
Eutropis_rugifera_2
Eutropis_tytleri
Eutropis_multifasciata_1
Eutropis_multifasciata
Eutropis_macrophtalma
Eutropis_rudis
Dasia_vittata
Dasia_gricea
Dasia_olivacea
Eutropis_dissimilis
Trachylepis_aureopunctata
Trachylepis_elegans
Trachylepis_quinquetaeniata
Trachylepis_perrotetii
Trachylepis_albilabris
Trachylepis_striata
Trachylepis_spilogaster
Trachylepis_hoeschi
Mabuya_wrightii
Trachylepis_polytropis
Mabuya_macrorhyncha
Mabuya_nigropunctata
Mabuya_agilis
Mabuya_heathi
Mabuya_unimarginata
Chioninia_stangeri
Chioninia_spinalis_salensis

Millions of years ago

Scincidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0232; LnL=−47.68

India	Eutropis_macularia_1
India	Eutropis_macularia_3
India	Eutropis_macularia_2
Asia	Eutropis_macularia_4
India	Eutropis_allapallensis_3
India	Eutropis_allapallensis_2
India	Eutropis_allapallensis_1
India	Eutropis_clivicola_CESL089
India	Eutropis_madaraszi_ZFMK15976
Asia	Eutropis_quadricarinata_USNM52
India	Eutropis_bibronii
Asia	Eutropis_indeprensa
Asia	Eutropis_cumingi
Asia	Eutropis_multicarinata_boreali
India	Eutropis_carinata_CES09_879
India	Eutropis_carinata_CES09_849
India	Eutropis_carinata_CES08_809
India	Eutropis_carinata_CES08_808
India	Eutropis_nagarjuni
India	Eutropis_trivittata_CES09_976
India	Eutropis_beddomii_CES09_943
Asia	Eutropis_rugifera
Asia	Eutropis_rugifera_2
India	Eutropis_tytleri
Asia	Eutropis_multifasciata_1
Asia	Eutropis_multifasciata
Asia	Eutropis_macrophtalma
Asia	Eutropis_rudis
Asia	Dasia_vittata
Asia	Dasia_gricea
Asia	Dasia_olivacea
Asia	Eutropis_dissimilis
Mad	Trachylepis_aureopunctata
Mad	Trachylepis_elegans
Afr	Trachylepis_quinquetaeniata
Afr	Trachylepis_perrotetii
Afr	Trachylepis_albilabris
Afr	Trachylepis_striata
Afr	Trachylepis_spilogaster
Afr	Trachylepis_hoeschi
Sey	Mabuya_wrightii
Afr	Trachylepis_polytropis
Amer	Mabuya_macrorhyncha
Amer	Mabuya_nigropunctata
Amer	Mabuya_agilis
Amer	Mabuya_heathi
Amer	Mabuya_unimarginata
CVerde	Chioninia_stangeri
CVerde	Chioninia_spinalis_salensis

60   50   40   30   20   10   0

Millions of years ago

Acrodonta BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.0024; e=0; j=0.038; LnL=−44.36

Acrodonta BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.0024; e=0; j=0.038; LnL=−44.36

Draco_blanfordii
Japalura_variegata
Japalura_tricarinata
Otocryptis_wiegmanni
Sitana_ponticeriana
Calotes_mystaceus
Calotes_emma
Calotes_versicolor
Calotes_ceylonensis
Calotes_liocephalus
Calotes_nigrilabris
Calotes_liolepis
Calotes_calotes
Acanthosaura_lepidogastra
Acanthosaura_capra
Japalura_flaviceps
Japalura_splendida
Pseudocalotes_flavigula
Pseudocalotes_brevipes
Salea_horsfieldii
Cophotis_ceylanica
Lyriocephalus_scutatus
Ceratophora_stoddartii
Ceratophora_aspera
Gonocephalus_grandis
Aphaniotis_fusca
Bronchocela_cristatella
Hydrosaurus_sp
Laudakia_lehmanni
Laudakia_microlepis
Laudakia_caucasia
Laudakia_erythrogastra
Laudakia_stoliczkana
Laudakia_himalayana
Laudakia_stellio
Laudakia_nupta
Laudakia_tuberculata
Laudakia_sacra
Phrynocephalus_mystaceus
Phrynocephalus_raddei
Phrynocephalus_interscapularis
Agama_agama
Agama_bibroni
Agama_atra
Trapelus_agilis
Trapelus_savignii
Trapelus_sanguinolentus
Trapelus_persicus
Trapelus_ruderatus
Pseudotrapelus_sinaitus

Millions of years ago

Agamidae−2 BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0283; LnL=−4.58

D_obscurus_obscurus
D_obscurus_formosus
D_taeniopterus
D_maximus
D_melanopogonM
D_melanopogonB
D_haematopogonM
D_haematopogonB
D_quinefasciatusB
D_quinefasciatusM
D_blanfordii
D_maculatus_maculatus
D_maculatus_haasei
D_dussumieri
D_volans_sumatranusB
D_volans_sumatranusM
D_volans_volans
D_cornutus
D_lineatus_beccarii
D_lineatus_spilonotus

15   10   5   0

Millions of years ago

Agamidae−2 BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0283; LnL=−4.58

D_obscurus_obscurus
D_obscurus_formosus
D_taeniopterus
D_maximus
D_melanopogonM
D_melanopogonB
D_haematopogonM
D_haematopogonB
D_quinquefasciatusB
D_quinquefasciatusM
D_blanfordii
D_maculatus_maculatus
D_maculatus_haasei
D_dussumieri
D_volans_sumatranusB
D_volans_sumatranusM
D_volans_volans
D_cornutus
D_lineatus_beccarii
D_lineatus_spilonotus

15   10   5   0
Millions of years ago

Boidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=5e−04; e=0; j=0.0422; LnL=−40.40

Boidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=5e−04; e=0; j=0.0422; LnL=−40.40

India Asia Eryx_johni
India Eryx_conicus
Asia Eryx_colubrinus
Asia Eryx_jayakari
Aust Candoia_carinata
Am Eunectes_notaeus
Am Epicrates_cenchria
Am Epicrates_striatus
Am Corallus_caninus
Am Boa_constrictor
Am Charina_bottae
Am Lichanura_trivirgata
Am Exiliboa_placata
Afr Acrantophis_dumerili
Afr Sanzinia_madagascariensis
Afr Calabaria_reinhardtii
Asia Dinodon
India Asia Enicauda_colubrina
Am Agkistrodon
Asia Gloydius
Asia Acrochordus_arafurae
Asia Acrochordus_granulatus
Asia Acrochordus_javanicus
Aust Aspidites_melanocephalus
Aust Morelia_spilota
Am Loxocemus_bicolor
Asia Xenopeltis_unicolor
Asia Cylindrophis_ruffus
Am Tropidophis_haetianus
Am Anilius_scytale

100   80   60   40   20   0
Millions of years ago

Viperidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=7e−04; e=0; j=0.0211; LnL=−101.90

Porthidium_arcosae
Porthidium_nasutum
Porthidium_lansbergii
Porthidium_ophryomegas
Atropoides_picadoi
Atropoides_olmec
Cerrophidion_godmani
Bothriechis_nigroviridis
Bothriechis_aurifer
Bothriechis_schlegelii
Bothriopsis_taeniata
Bothrops_asper
Bothrops_diporus
Bothrops_alternatus
Porthidium_hyoprora
Crotalus_adamanteus
Crotalus_tigris
Crotalus_durissus
Sistrurus_ravus
Sistrurus_miliarius
Sistrurus_catenatus
Agkistrodon_contortrix
Agkistrodon_piscivorus
Lachesis_muta
Lachesis_stenophrys
Ophryacus_melanurus
Trimeresurus_gracilis
Dvophis_okinavensis
Gloydius_strauchii
Gloydius_shedaoensis
Dvophis_monticola
Protobothrops_flavoviridis
Protobothrops_mucrosquamatus
Protobothrops_cornutus
Ermia_mangshanensis
Triceratolepidophis_sieversoru
Trimeresurus_stejnegeri
Trimeresurus_insularis
Trimeresurus_medoensis
Trimeresurus_macrops
Trimeresurus_hageni
Trimeresurus_flavomaculatus
Trimeresurus_tibetanus
Trimeresurus_popeorum
Trimeresurus_borneensis
Trimeresurus_trigonocephalus
Deinagkistrodon_acutus
Dvophis_chaseni
Tropidolaemus_wagleri
Hypnale_hypnale
Calloselasma_rhodostoma
Azemiops_feae
Bitis_rubida
Bitis_cornuta
Bitis_atropos
Bitis_xeropaga
Bitis_caudalis
Bitis_peringueyi
Bitis_gabonica
Bitis_rhinoceros
Bitis_nasicornis
Bitis_worthingtoni
Bitis_arietans
Atheris_nitschei
Atheris_chlorechis
Atheris_ceratophora
Atheris_squamigera
Proatheris_superciliaris
Causus_resimus
Causus_rhombeatus
Causus_defilippi
Cerastes_cerastes
Echis_coloratus
Echis_pyramidum
Echis_ocellatus
Echis_carinatus
Vipera_xanthina
Vipera_albizona
Macrovipera_lebetina
Macrovipera_schweizeri
Macrovipera_mauritanica
Daboia_russellii
Vipera_ammodytes
Pseudocerastes_fieldi
Eristicophis_macmahoni
Hemorrhois_hippocrepis
Hemorrhois_algirus
Hemorrhois_nummifer
Macroprotodon_brevis
Eirenis_modestus
Macroprotodon_cucullatus
Coronella_girondica
Elaphe_quatuorlineata
Farancia_abacura
Diadophis_punctatus
Contia_tenuis
Natrix_natrix
Naja_kaouthia
Naja_naja
Naja_nigricollis
Naja_nivea
Bungarus_fasciatus
Ophiophagus_hannah
Lamprophis_fuliginosus
Mimophis_mahfalensis
Psammophis_condanarus
Malpolon_monspessulanus
Leioheterodon_madagascariensis
Cerberus_rhynchops
Alsophis_portoricensis

Millions of years ago

Viperidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=7e−04; e=0; j=0.0211; LnL=−101.90

Porthidium_arcosae
Porthidium_nasutum
Porthidium_lansbergii
Porthidium_ophryomegas
Atropoides_picadoi
Atropoides_olmec
Cerrophidion_godmani
Bothriechis_nigroviridis
Bothriechis_aurifer
Bothriechis_schlegelii
Bothriopsis_taeniata
Bothrops_asper
Bothrops_diporus
Bothrops_alternatus
Porthidium_hyoprora
Crotalus_adamanteus
Crotalus_tigris
Crotalus_durissus
Sistrurus_ravus
Sistrurus_miliarius
Sistrurus_catenatus
Agkistrodon_contortrix
Agkistrodon_piscivorus
Lachesis_muta
Lachesis_stenophrys
Ophryacus_melanurus
Trimeresurus_gracilis
Ovophis_okinavensis
Gloydius_strauchii
Gloydius_shedaoensis
Ovophis_monticola
Protobothrops_flavoviridis
Protobothrops_mucrosquamatus
Protobothrops_cornutus
Ermia_mangshanensis
Triceratolepidophis_sieversoru
Trimeresurus_stejnegeri
Trimeresurus_insularis
Trimeresurus_medoensis
Trimeresurus_macrops
Trimeresurus_hageni
Trimeresurus_flavomaculatus
Trimeresurus_tibetanus
Trimeresurus_popeorum
Trimeresurus_borneensis
Trimeresurus_trigonocephalus
Deinagkistrodon_acutus
Ovophis_chaseni
Tropidolaemus_wagleri
Hypnale_hypnale
Calloselasma_rhodostoma
Azemiops_feae
Bitis_rubida
Bitis_cornuta
Bitis_atropos
Bitis_xeropaga
Bitis_caudalis
Bitis_peringueyi
Bitis_gabonica
Bitis_rhinoceros
Bitis_nasicornis
Bitis_worthingtoni
Bitis_arietans
Atheris_nitschei
Atheris_chlorechis
Atheris_ceratophora
Atheris_squamigera
Proatheris_superciliaris
Causus_resimus
Causus_rhombeatus
Causus_defilippi
Cerastes_cerastes
Echis_coloratus
Echis_pyramidum
Echis_ocellatus
Echis_carinatus
Vipera_xanthina
Vipera_albizona
Macrovipera_lebetina
Macrovipera_schweizeri
Macrovipera_mauritanica
Daboia_russellii
Vipera_ammodytes
Pseudocerastes_fieldi
Eristicophis_macmahoni
Hemorrhois_hippocrepis
Hemorrhois_algirus
Hemorrhois_nummifer
Macroprotodon_brevis
Eirenis_modestus
Macroprotodon_cucullatus
Coronella_girondica
Elaphe_quatuorlineata
Farancia_abacura
Diadophis_punctatus
Contia_tenuis
Natrix_natrix
Naja_kaouthia
Naja_naja
Naja_nigricollis
Naja_nivea
Bungarus_fasciatus
Ophiophagus_hannah
Lamprophis_fuliginosus
Mimophis_mahfalensis
Psammophis_condanarus
Malpolon_monspessulanus
Leioheterodon_madagascariensis
Cerberus_rhynchops
Alsophis_portoricensis

Millions of years ago

Certhiidae BioGeoBEARS DEC
ancstates: global optim, 2 areas max. d=0.1046; e=0; j=0; LnL=−23.68

Certhiidae BioGeoBEARS DEC
ancstates: global optim, 2 areas max. d=0.1046; e=0; j=0; LnL=−23.68

India Certhia_hodgsoni_MAR_3328
Asia Certhia_hodgsoni_MAR_3140
Asia Certhia_familiaris_MAR_90351
Asia Certhia_familiaris_MAR_4958
Afr Certhia_brachydactyla_MAR_4004
Asia Certhia_brachydactyla_MAR_1025
Am Certhia_americana_MAR_1048
India Certhia_himalayana_MAR_3318
Asia Certhia_himalayana_MAR_3241
AsiaIndia Certhia_discolor_MAR_2657
AsiaIndia Certhia_manipurensis_MAR_4554
Asia Certhia_tianquanensis_MAR_4936
AsiaIndia Certhia_nipalensis_MAR_4153

Millions of years ago

Aegithalidae BioGeoBEARS DEC
ancstates: global optim, 2 areas max. d=0.0344; e=0.0097; j=0; LnL=−21.85

Aegithalidae BioGeoBEARS DEC
ancstates: global optim, 2 areas max. d=0.0344; e=0.0097; j=0; LnL=−21.85

Aegithalos_bonvaloti_bonv31_03

Aegithalos_fuliginosus_809

India Aegithalos_iouschistos_iouschi

Aegithalos_sharpei_shar33_5088

India Aegithalos_niveogularis_nive35

Asia Aegithalos_glaucogularis_MAR_7

Asia Aegithalos_caudatus_taiti_caud

AsiaIndia Aegithalos_concinnus_iredalei_

AsiaIndia Aegithalos_concinnus_manipuren

Asia Aegithalos_concinnus_voucher_M

India Aegithalos_leucogenys_leuc37_0

Am Psaltriparus_minimus_minimus_p

Am Psaltriparus_minimus_plumbeus_

Asia Leptopoecile_sophiae_soph43_02

Asia Leptopoecile_elegans_eleg42_05

Millions of years ago

20   15   10   5   0

Paridae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.0493; e=0; j=0.0566; LnL=−19.27

Periparus_ater_ptilosus
Periparus_ater_eckodedicatus_M
Periparus_ater_aemodius
Periparus_ater_ater_MAR_692
Periparus_ater_melanolophus_MA
Periparus_ater_atlas_MAR_4008
Periparus_ater_abietum_MAR_267
Parus_rubidiventris_beavani_MA
Parus_rubidiventris_rubidivent
Parus_rubidiventris_whistleri_
Parus_rufonuchalis_MAR_90131
Periparus_elegans_Philippines
Parus_venustulus_MAR_2033
Parus_amabilis_MCZ_94997
Parus_elegans_mindanensis_FMNH

Millions of years ago

Paridae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.0493; e=0; j=0.0566; LnL=−19.27

Peripararus_ater_ptilosus
Peripararus_ater_eckodedicatus_M
Peripararus_ater_aemodius
Peripararus_ater_ater_MAR_692
Peripararus_ater_melanolophus_MA
Peripararus_ater_atlas_MAR_4008
Peripararus_ater_abietum_MAR_267
Parus_rubidiventris_beavani_MA
Parus_rubidiventris_rubidivent
Parus_rubidiventris_whistleri_
Parus_rufonuchalis_MAR_90131
Peripararus_elegans_Philippines
Parus_venustulus_MAR_2033
Parus_amabilis_MCZ_94997
Parus_elegans_mindanensis_FMNH

Millions of years ago

Timaliidae BioGeoBEARS DEC
ancstates: global optim, 2 areas max. d=0.0345; e=0; j=0; LnL=−50.67

Taxon
Garrulax_poecilorhynchus_berth
Garrulax_poecilorhynchus_1840
Garrulax_caerulatus_4531
Garrulax_albogularis_ruficeps
Garrulax_albogularis_eous
Garrulax_lanceolatus_2230
Garrulax_davidi_389
Garrulax_pectoralis_picticolli
Garrulax_perspicillatus
Garrulax_sannio_sannio
Garrulax_courtoisi_1771
Garrulax_chinensis_1753
Garrulax_leucolophus
Garrulax_leucolophus_549
Garrulax_milleti
Garrulax_strepitans_3756
Garrulax_canorus_owstoni_T951
Garrulax_canorus_762
Garrulax_canorus_taewanus_T079
Garrulax_monileger_1780
Garrulax_maximus_2828
Garrulax_ocellatus_90049
Garrulax_lunulatus_lunulatus
Garrulax_sukatschewi_5828
Garrulax_cineraceus_4921
Turdoides_reinwardtii_1744
Turdoides_bicolor
Turdoides_squamiceps_2245
Garrulax_morrisonianus_92006
Garrulax_elliotii_804
Garrulax_affinis_1860
Garrulax_variegatus_4113
Garrulax_erythrocephalus_5495
Garrulax_formosus_2240
Garrulax_erythrocephalus_2654
Garrulax_milnei_1757
Garrulax_lineatus_90145
Garrulax_squamatus_GLGS1833
Garrulax_subunicolor_T0289
Garrulax_striatus_3670

Millions of years ago

Timaliidae BioGeoBEARS DEC
ancstates: global optim, 2 areas max. d=0.0345; e=0; j=0; LnL=−50.67

Asia Garrulax_poecilorhynchus_berth
Asia Garrulax_poecilorhynchus_1840
AsiaIndia Garrulax_caerulatus_4531
Asia Garrulax_albogularis_ruficeps
AsiaIndia Garrulax_albogularis_eous
AsiaIndia Ianthocincla_lanceolatus_2230
Asia Garrulax_davidi_389
AsiaIndia Garrulax_pectoralis_picticolli
Asia Garrulax_perspicillatus
AsiaIndia Garrulax_sannio_sannio
Asia Garrulax_courtoisi_1771
Asia Garrulax_chinensis_1753
Asia Garrulax_leucolophus
AsiaIndia Garrulax_leucolophus_549
Asia Garrulax_milleti
Asia Garrulax_strepitans_3756
Asia Garrulax_canorus_owstoni_T951
Asia Garrulax_canorus_762
Asia Garrulax_canorus_taewanus_T079
AsiaIndia Garrulax_monileger_1780
Asia Garrulax_maximus_2828
AsiaIndia Garrulax_ocellatus_90049
Asia Garrulax_lunulatus_lunulatus
Asia Garrulax_sukatschewi_5828
Asia Garrulax_cineraceus_4921
Af1 Turdoides_reinwardtii_1744
Af1 Turdoides_bicolor
Asia Turdoides_squamiceps_2245
Asia Garrulax_morrisonianus_92006
AsiaIndia Garrulax_elliotii_804
AsiaIndia Garrulax_affinis_1860
India Garrulax_variegatus_4113
India Garrulax_erythrocephalus_5495
Asia Garrulax_formosus_2240
India Garrulax_erythrocephalus_2654
Asia Garrulax_milnei_1757
AsiaIndia Garrulax_lineatus_90145
AsiaIndia Garrulax_squamatus_GLGS1833
AsiaIndia Garrulax_subunicolor_T0289
AsiaIndia Garrulax_striatus_3670

Millions of years ago

15   10   5   0

Pyrrhula BioGeoBEARS DEC
ancstates: global optim, 2 areas max. d=0.1031; e=0; j=0; LnL=−18.59

Millions of years ago

Pyrrhula BioGeoBEARS DEC
ancstates: global optim, 2 areas max. d=0.1031; e=0; j=0; LnL=−18.59

Pinicola_enucleator_enucleator

Pyrrhula_nipalensis_ricketti_P

Pyrrhula_leucogenis_leucogenis

Pyrrhula_leucogenis_steerei_Pl

Pyrrhula_aurantiaca_Paur6

Pyrrhula_erythaca_owstoni_Pery

Pyrrhula_erythrocephala_Perc3

Pyrrhula_erythaca_erythaca_Per

Pyrrhula_murina_Pmur1

Pyrrhula_pyrrhula_griseiventri

Pyrrhula_pyrrhula_europoea_Ppy

Pyrrhula_pyrrhula_cineracea_Pc

Millions of years ago

6   4   2   0

Psittacula BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.0707; e=0; j=0.1075; LnL=−28.60

Millions of years ago

Psittacula BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.0707; e=0; j=0.1075; LnL=−28.60

Psittacula_krameri_manillensis
Psittacula_krameri_manillensis
Psittacula_krameri_manillensis
Psittacula_krameri_borealis
Psittacula_echo
Psittacula_krameri_1
Psittacula_krameri_krameri_2
Psittacula_alexandri_2
Psittacula_alexandri_1
Psittacula_derbiana
Psittacula_longicauda
Psittacula_columboides
Psittacula_eupatria
Psittacula_himalayana
Psittacula_cyanocephala
Psittacula_roseata
Eclectus_roratus_roratus

Millions of years ago

Nisaetus (Accipitridae) BioGeoBEARS DEC
ancstates: global optim, 2 areas max. d=0.3846; e=0; j=0; LnL=−11.51

Nisaetus (Accipitridae) BioGeoBEARS DEC
ancstates: global optim, 2 areas max. d=0.3846; e=0; j=0; LnL=−11.51

AsiaIndia Nisaetus_cirrhatus_limnaeetus_

Nisaetus_cirrhatus_vanheurni_S

AsiaIndia Nisaetus_cirrhatus_limnaeetus_

AsiaIndia Nisaetus_cirrhatus_limnaeetus_

Nisaetus_cirrhatus_andamanensi

Nisaetus_cirrhatus_floris_Scir

India Nisaetus_cirrhatus_cirrhatus_S

India Nisaetus_cirrhatus_ceylanensis

Nisaetus_pinskeri_Sphipin8

Asia Nisaetus_philippensis_Sphiphi2

Asia Nisaetus_lanceolatus_Slan1

Millions of years ago

2   1.5   1   0.5   0

Sciuridae, Pteromyini BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.0048; e=0; j=0.1439; LnL=−32.24

Millions of years ago

Sciuridae, Pteromyini BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0.0048; e=0; j=0.1439; LnL=−32.24

Label	Taxon
AsiaPalArk	Aeretes_melanopterus
AsiaPalArk	opterus_xanthipes
AsiaIndia	omys_pearsonii
Asia	Pteromyscus_pulverulentus
Asia	Aeromys_tephromelas
India	Eupetaurus_cinereus
PalArk	teromys_volans
AsiaIndia	aurista_petaurista
Ark	Petaurista_alborufus
PalArk	etaurista_leucogenys
Asia	Hylopetes_phayrei
Asia	Petaurillus_kinlochii
Asia	Petinomys_setosus
Asia	omys_horsfieldi
Amer	Glaucomys_volans
India	Eoglaucomys_fimbriatus

Millions of years ago

Ruminantia BioGeoBEARS DEC+J
ancstates: global optim, 3 areas max. d=0.0027; e=0; j=0.022; LnL=−142.23

Ruminantia BioGeoBEARS DEC+J
ancstates: global optim, 3 areas max. d=0.0027; e=0; j=0.022; LnL=−142.23

Capra_falconeri_FJ207525
Capra_hircus
Capra_caucasica
Capra_ibex_FJ207526
Capra_pyrenaica_FJ207528
Capra_nubiana_FJ207527
Capra_sibirica_FJ207529
Hemitragus_jemlahicus_FJ207531
Pseudois_nayaur_FJ207537
Budorcas_taxicolor_FJ207524
Rupicapra_pyrenaica_FJ207539
Rupicapra_rupicapra_FJ207538
Arrabitragus_jayakari_FJ207523
Ammotragus_lervia_FJ207522
Oreamnos_americanus_FJ207535
Ovis_aries_NC001941
Naemorhedus_baileyi
Naemorhedus_griseus_evansi
Naemorhedus_griseus_griseus_FJ
Capricornis_milneedwardsii_FJ2
Capricornis_swinhoei_NC010640
Capricornis_crispus_FJ207533
Ovibos_moschatus_FJ207536
Pantholops_hodgsonii_NC007441
Oryx_dammah
Oryx_leucoryx
Oryx_gazella
Oryx_beisa
Addax_nasomaculatus
Hippotragus_niger
Hippotragus_equinus
Alcelaphus_buselaphus_lichtens
Alcelaphus_buselaphus_buselaph
Damaliscus_pygargus_FJ207530
Connochaetes_gnou
Connochaetes_taurinus_2
Connochaetes_taurinus_1
Cephalophus_callipygus_2
Cephalophus_callipygus_1
Cephalophus_ogilbyi
Cephalophus_callipygus_3
Cephalophus_nigrifrons
Cephalophus_rufilatus
Cephalophus_natalensis
Cephalophus_leucogaster
Cephalophus_adersi
Cephalophus_silvicultor
Cephalophus_spadix
Cephalophus_jentinki
Cephalophus_dorsalis
Sylvicapra_grimmia
Philantomba_monticola_1
Philantomba_monticola_2
Philantomba_maxwelli
Oreotragus_oreotragus
Redunca_fulvorufula
Redunca_arundinum
Kobus_ellipsiprymnus
Kobus_leche
Pelea_capreolus
Gazella_cuvieri
Gazella_leptoceros
Gazella_subgutturosa_marica
Gazella_subgutturosa_subguttur
Gazella_bennettii
Gazella_dorcas_osiris
Gazella_dorcas_pelzelnii
Gazella_gazella_erlangeri
Gazella_gazella_gazella
Gazella_spekei
Nanger_soemmerringii
Nanger_dama
Nanger_granti
Eudorcas_rufifrons_2
Eudorcas_rufifrons_1
Antilope_cervicapra
Litocranius_walleri
Antidorcas_marsupialis
Saiga_tatarica
Ourebia_ourebi
Madoqua_saltiana
Madoqua_kirkii
Dorcatragus_megalotis
Raphicerus_campestris
Procapra_gutturosa
Nesotragus_moschatus
Neotragus_batesi
Aepyceros_melampus
Bos_gaurus
Bos_javanicus_javanicus
Bos_javanicus_birmanicus
Bison_bison
Bos_grunniens_NC006380
Bos_taurus_indicus_EU177868
Bos_taurus_taurus_EU177832
Bison_bonasus
Bubalus_depressicornis
Bubalus_bubalis_bubalis_AF5472
Bubalus_bubalis_carabanesis
Syncerus_caffer
Pseudoryx_nghetinhensis
Tragelaphus_eurycerus
Tragelaphus_spekii
Tragelaphus_scriptus_3
Tragelaphus_scriptus_2
Tragelaphus_derbianus
Tragelaphus_oryx
Tragelaphus_strepsiceros
Tragelaphus_scriptus_1
Tragelaphus_angasii
Tragelaphus_imberbis
Boselaphus_tragocamelus
Tetracerus_quadricornis
Moschus_berezovskii_NC012694
Moschus_moschiferus
Cervus_nippon_centralis_NC0069
Cervus_nippon_yakushimae_NC007
Cervus_nippon_taiouanus_NC0084
Przewalskium_albirostris
Cervus_elaphus_NC007704
Rusa_timorensis
Rusa_unicolor_NC008414
Rusa_alfredi
Elaphurus_davidianus
Rucervus_eldi
Dama_dama_mesopotamica
Dama_dama_dama
Axis_axis
Axis_porcinus
Rucervus_duvauceli
Muntiacus_vuquangensis
Muntiacus_reevesi_NC008491
Muntiacus_muntjak_NC004563
Muntiacus_crinifrons_NC004577
Elaphodus_cephalophus_N008749
Odocoileus_virginianus_3
Odocoileus_hemionus
Odocoileus_virginianus_1
Mazama_americana_1
Mazama_americana_2
Odocoileus_virginianus_2
Mazama_rufina
Pudu_mephistophiles
Hippocamelus_antisensis
Mazama_gouazoubira
Ozotoceros_bezoarcticus
Mazama_nemorivaga_2
Mazama_nemorivaga_1
Blastocerus_dichotomus
Pudu_puda
Rangifer_tarandus_NC007703
Capreolus_capreolus
Hydropotes_inermis
Alces_alces
Giraffa_camelopardalis_angolen
Giraffa_camelopardalis_antiquo
Okapia_johnstoni
Antilocapra_americana
Hyemoschus_aquaticus
Tragulus_kanchil

60   50   40   30   20   10   0
Millions of years ago

Herpestidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0555; LnL=−22.79

Herpestes_javanicus_MNHN_TC472
Herpestes_auropunctatus_MNHN_T
Herpestes_edwardsii_MNHN_TC144
Herpestes_fuscus_AMNH217678
Herpestes_urva_FMNH_39355
Herpestes_vitticollis
Herpestes_smithii_AMNH_163179
Herpestes_brachyurus_MNHN_TC42
Atilax_paludinosus
Herpestes_naso
Bdeogale_nigripes
Bdeogale_crassicauda
Rhynchogale_melleri
Paracynictis_selousi
Cynictis_penicillata
Ichneumia_albicauda
Galerella_pulverulenta
Galerella_sanguinea
Herpestes_ichneumon
Helogale_hirtula
Helogale_parvula
Crossarchus_alexandri
Crossarchus_obscurus
Mungos_mungo
Liberiictis_kuhni
Suricata_suricatta

20   15   10   5   0
Millions of years ago

Herpestidae BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0555; LnL=−22.79

Asia Herpestes_javanicus_MNHN_TC472
Asia Herpestes_auropunctatus_MNHN_T
Asia Herpestes_edwardsii_MNHN_TC144
India Herpestes_fuscus_AMNH217678
Asia Herpestes_urva_FMNH_39355
India Herpestes_vitticollis
India Herpestes_smithii_AMNH_163179
Asia Herpestes_brachyurus_MNHN_TC42
Afr Atilax_paludinosus
Afr Herpestes_naso
Afr Bdeogale_nigripes
Afr Bdeogale_crassicauda
Afr Rhynchogale_melleri
Afr Paracynictis_selousi
Afr Cynictis_penicillata
Asia Ichneumia_albicauda
Afr Galerella_pulverulenta
Afr Galerella_sanguinea
Eur Herpestes_ichneumon
Afr Helogale_hirtula
Afr Helogale_parvula
Afr Crossarchus_alexandri
Afr Crossarchus_obscurus
Afr Mungos_mungo
Afr Liberiictis_kuhni
Afr Suricata_suricatta

20   15   10   5   0
Millions of years ago

Scandentia BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0421; LnL=−12.45

Tupaia_belangeri_b
Tupaia_belangeri_c
Tupaia_glis_a
Tupaia_belangeri_g
Tupaia_longipes
Tupaia_chrysogaster
Urogale_everetti
Tupaia_splendidula_a
Tupaia_montana
Tupaia_picta
Tupaia_tana_a
Tupaia_minor_a
Tupaia_palawanensis
Tupaia_moellendorffi
Tupaia_nicobarica
Tupaia_javanica
Tupaia_dorsalis_a
Tupaia_gracilis
Anathana_ellioti
Dendrogale_murina_a
Dendrogale_melanura
Ptilocercus_lowii_a

Millions of years ago

Scandentia BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0421; LnL=−12.45

Tupaia_belangeri_b
Tupaia_belangeri_c
Tupaia_glis_a
Tupaia_belangeri_g
Tupaia_longipes
Tupaia_chrysogaster
Urogale_everetti
Tupaia_splendidula_a
Tupaia_montana
Tupaia_picta
Tupaia_tana_a
Tupaia_minor_a
Tupaia_palawanensis
Tupaia_moellendorffi
Tupaia_nicobarica
Tupaia_javanica
Tupaia_dorsalis_a
Tupaia_gracilis
Anathana_ellioti
Dendrogale_murina_a
Dendrogale_melanura
Ptilocercus_lowii_a

40   30   20   10   0

Millions of years ago

Cercopithecidae (Colobinae) BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0138; LnL=−7.06

Trachypithecus_phayrei_I1
Trachypithecus_obscurus
AY519462_Trachypithecus_barbei
EF465123_Trachypithecus_auratu
EF465127_Trachypithecus_auratu
Trachypithecus_cristatus
Trachypithecus_crepuscula_V1
EU004475_Trachypithecus_laotum
Trachypithecus_francoisi
Trachypithecus_johnii_NL1
Semnopithecus_entellus_S3
Semnopithecus_entellus_S2
Semnopithecus_entellus
Trachypithecus_vetulus
Trachypithecus_geei
Trachypithecus_pileatus
NC_018063_Pygathrix_cinerea
AF295582_Pygathrix_nemaeus
AF020413_Pygathrix_bieti
Nasalis_larvatus
JF295105_Presbytis_melalophos_
Procolobus_badius
Procolobus_verus
Colobus_guereza

Millions of years ago

Cercopithecidae (Colobinae) BioGeoBEARS DEC+J
ancstates: global optim, 2 areas max. d=0; e=0; j=0.0138; LnL=−7.06

Asia Trachypithecus_phayrei_I1
Asia Trachypithecus_obscurus
Asia AY519462_Trachypithecus_barbei
Asia EF465123_Trachypithecus_auratu
Asia EF465127_Trachypithecus_auratu
Asia Trachypithecus_cristatus
Asia Trachypithecus_crepuscula_V1
Asia EU004475_Trachypithecus_laotum
Asia Trachypithecus_francoisi
India Trachypithecus_johnii_NL1
India Semnopithecus_entellus_S3
India Semnopithecus_entellus_S2
India Semnopithecus_entellus
India Trachypithecus_vetulus
India Trachypithecus_geei
India Trachypithecus_pileatus
Asia NC_018063_Pygathrix_cinerea
Asia AF295582_Pygathrix_nemaeus
Asia AF020413_Pygathrix_bieti
Asia Nasalis_larvatus
Asia JF295105_Presbytis_melalophos_
Afr Procolobus_badius
Afr Procolobus_verus
Afr Colobus_guereza

Millions of years ago

Supplementary Figure 2

Suppl. Fig. 2 | Example for the translation of credibility intervals of dispersal time estimation into the maximal number of observed dispersal events per Ma. The credibility intervals for the time points of dispersal for three events overlap such that the MDE increases from one to two between 0 and 2 Ma, peaks between 2 and 3 Ma and drops down to one after 3 Ma.

Supplementary Figure 3

Suppl. Fig. 3 | Raw maximal dispersal events (MDE) before smoothing: Dispersal from mainland Asia to India (orange), from India to mainland Asia (blue), and in both directions (black).

Supplementary Figure 4

Suppl. Fig. 4 | Influence of taxon sampling on maximal dispersal rate. To account for a bias against more recent dispersal events due to increasing incomplete taxon sampling towards the present, we removed maximal dispersal events (MDE) with an age <7 Ma from the subsequent analyses based on the comparison of MDE between birds and other taxon groups (plants, arthropods, teleosts, amphibians, non-avian reptiles and mammals) with a less complete sampling (data not smoothed, dispersal rates for non-avian taxa not cumulative).

Supplementary Table 1

Taxon	95% HPD		Dispersal direction
	upper bound	lower bound	
Crypteroniaceae (Rosids, Myrtales)	5	1	A → I
Dipterocarpaceae (Rosids, Malvales)	79	36	A → I
Dipterocarpaceae (Rosids, Malvales)	59	26	A → I
Dipterocarpaceae (Rosids, Malvales)	54	18	A → I
Dipterocarpaceae (Rosids, Malvales)	28	13	A → I
Dipterocarpaceae (Rosids, Malvales)	108	50	I → A
Dipterocarpaceae (Rosids, Malvales)	70	31	I → A
Dipterocarpaceae (Rosids, Malvales)	44	18	I → A
Dipterocarpaceae (Rosids, Malvales)	29	7	I → A
Dipterocarpaceae (Rosids, Malvales)	27	5	I → A
Dipterocarpaceae (Rosids, Malvales)	24	10	I → A
Dipterocarpaceae (Rosids, Malvales)	20	6	I → A
Dipterocarpaceae (Rosids, Malvales)	16	4	I → A
Dipterocarpaceae (Rosids, Malvales)	14	2	I → A
Gentianaceae (Asterids, Gentianales)	17	8	A → I
Gentianaceae (Asterids, Gentianales)	13	6	I → A
Pachychilidae (Mollusca: Gastropoda)	65	12	A → I
Gecarcinucidae (Crustacea, Brachyura)	58	30	I → A
Gecarcinucidae (Crustacea, Brachyura)	47	24	I → A

Papilionidae (Insecta, Lepidoptera)	54	32	A → I
Papilionidae (Insecta, Lepidoptera)	30	11	A → I
Papilionidae (Insecta, Lepidoptera)	26	15	A → I
Papilionidae (Insecta, Lepidoptera)	26	15	A → I
Papilionidae (Insecta, Lepidoptera)	22	13	A → I
Papilionidae (Insecta, Lepidoptera)	22	11	A → I
Papilionidae (Insecta, Lepidoptera)	10	5	A → I
Papilionidae (Insecta, Lepidoptera)	20	12	I → A
Papilionidae (Insecta, Lepidoptera)	19	11	I → A
Papilionidae (Insecta, Lepidoptera)	16	9	I → A
Papilionidae (Insecta, Lepidoptera)	12	6	I → A
Apidae (Insecta, Hymenoptera)	27	11	A → I
Apidae (Insecta, Hymenoptera)	11	4	A → I
Apidae (Insecta, Hymenoptera)	14	4	A → I
Formicidae (Insecta, Hymenoptera, *Myrmica* spp.)	11	5	A → I
Formicidae (Insecta, Hymenoptera, *Tetraponera* spp.)	44	7	A → I
Aplocheiloidei (Teleostei, Cyprinodontiformes)	46	30	I → A
Channidae (Teleostei, Perciformes)	7	3	A → I
Channidae (Teleostei, Perciformes)	20	7	A → I
Channidae (Teleostei, Perciformes)	19	8	A → I
Channidae (Teleostei, Perciformes)	16	5	A → I
Osphronemidae (Teleostei: Perciformes)	35	23	A → I
Osphronemidae (Teleostei: Perciformes)	30	17	A → I
Osphronemidae (Teleostei: Perciformes)	33	20	A → I

Osphronemidae (Teleostei: Perciformes)	38	28	A → I
Osphronemidae (Teleostei: Perciformes)	38	22	A → I
Osphronemidae (Teleostei: Perciformes)	21	11	I → A
Cobitidae (Teleostei, Cypriniformes)	19	8	A → I
Cobitidae (Teleostei, Cypriniformes)	24	10	A → I
Cobitidae (Teleostei, Cypriniformes)	52	27	A → I
Heteropneustes fossilis (Teleostei, Siluriformes)	48	11	I → A
Dicroglossidae (Amphibia, Anura)	49	28	I → A
Dicroglossidae (Amphibia, Anura)	26	14	I → A
Dicroglossidae (Amphibia, Anura)	19	7	A → I
Dicroglossidae (Amphibia, Anura)	19	3	I → A
Dicroglossidae (Amphibia, Anura)	13	3	I → A
Microhylidae (Amphibia, Anura)	58	30	A → I
Rhacophoridae (Amphibia, Anura)	32	23	I → A
Rhacophoridae (Amphibia, Anura)	41	31	A → I
Rhacophoridae (Amphibia, Anura)	28	19	A → I
Rhacophoridae (Amphibia, Anura)	29	19	A → I
Rhacophoridae (Amphibia, Anura)	40	29	A → I
Bufonidae (Amphibia, Anura)	24	14	I → A
Bufonidae (Amphibia, Anura)	11	6	I → A
Bufonidae (Amphibia, Anura)	30	18	A → I
Bufonidae (Amphibia, Anura)	32	20	A → I
Bufonidae (Amphibia, Anura)	12	6	A → I
Bufonidae (Amphibia, Anura)	18	10	A → I

Bufonidae (Amphibia, Anura)	9	4	A → I
Geckonidae (Reptilia, Squamata, *Cyrtodactylus* spp.)	33	18	A → I
Geckonidae (Reptilia, Squamata, *Cyrtodactylus* spp.)	30	14	A → I
Geckonidae (Reptilia, Squamata, *Cyrtodactylus* spp.)	28	14	A → I
Geckonidae (Reptilia, Squamata, *Cyrtodactylus* spp.)	18	7	A → I
Geckonidae (Reptilia, Squamata, *Cyrtodactylus* spp.)	31	16	I → A
Scincidae (Reptilia: Squamata)	40	15	A → I
Scincidae (Reptilia: Squamata)	35	13	A → I
Scincidae (Reptilia: Squamata)	41	14	A → I
Scincidae (Reptilia: Squamata)	52	20	A → I
Scincidae (Reptilia: Squamata)	58	19	A → I
Scincidae (Reptilia: Squamata)	1	0	A → I
Scincidae (Reptilia: Squamata)	69	28	A → I
Agamidae 1 (Reptilia, Squamata)	46	32	A → I
Agamidae 1 (Reptilia, Squamata)	38	25	A → I
Agamidae 1 (Reptilia, Squamata)	27	17	I → A
Agamidae 1 (Reptilia, Squamata)	41	29	I → A
Agamidae 2 (Reptilia, Squamata)	10	20	A → I
Boidae (Reptilia, Squamata)	25	12	A → I
Viperidae (Reptilia, Squamata)	27	14	A → I
Viperidae (Reptilia, Squamata)	22	11	A → I
Crocodylidae (Reptilia, Crocodylia)	8	4	A → I
Crocodylidae (Reptilia, Crocodylia)	64	40	A → I
Timaliidae (Reptilia, Aves)	12	6	A → I

Timaliidae (Reptilia, Aves)	1	0	A → I
Timaliidae (Reptilia, Aves)	2	1	A → I
Timaliidae (Reptilia, Aves)	4	1	A → I
Timaliidae (Reptilia, Aves)	4	2	A → I
Timaliidae (Reptilia, Aves)	13	7	A → I
Paridae (Reptilia, Aves)	1	0	A → I
Paridae (Reptilia, Aves)	3	1	A → I
Paridae (Reptilia, Aves)	6	0	A → I
Aegithalidae (Reptilia, Aves)	1	0	A → I
Aegithalidae (Reptilia, Aves)	6	3	A → I
Aegithalidae (Reptilia, Aves)	7	4	A → I
Aegithalidae (Reptilia, Aves)	21	11	A → I
Fringillidae (Reptilia, Aves)	3	1	I → A
Fringillidae (Reptilia, Aves)	3	1	A → I
Fringillidae (Reptilia, Aves)	4	2	A → I
Certhiidae (Reptilia, Aves)	3	1	A → I
Certhiidae (Reptilia, Aves)	3	1	A → I
Certhiidae (Reptilia, Aves)	6	3	A → I
Certhiidae (Reptilia, Aves)	8	4	A → I
Psittacidae (Reptilia, Aves)	5	1	A → I
Psittacidae (Reptilia, Aves)	6	2	I → A
Psittacidae (Reptilia, Aves)	5	1	A → I
Nisaetus spp. (Reptilia, Aves, Accipitridae)	2	1	A → I
Bovidae (Mammalia, Ruminantia)	23	26	A → I

Cervidae (Mammalia, Ruminantia)	8	9	A → I
Bovidae (Mammalia, Ruminantia)	8	10	A → I
Bovidae (Mammalia, Ruminantia)	0	2	A → I
Herpestidae (Mammalia, Carnivora)	12	4	I → A
Herpestidae (Mammalia, Carnivora)	9	2	A → I
Herpestidae (Mammalia, Carnivora)	15	7	A → I
Herpestidae (Mammalia, Carnivora)	14	7	A → I
Sciuridae (Mammalia, Rodentia)	26	15	A → I
Sciuridae (Mammalia, Rodentia)	19	12	A → I
Sciuridae (Mammalia, Rodentia)	18	5	A → I
Tupaiidae (Mammalia, Scandentia)	34	25	A → I
Colobinae (Mammalia, Primates)	13	6	A → I

Suppl. Table 1 | Inferred dispersal events between mainland Asia and the Indian subcontinent. Given are the respective taxon, upper and lower bounds of the 95% highest posterior density intervals (HPD) for the age of range shifts/dispersal events in million years before present (Ma) as used for the calculation of the maximal number of dispersal events (MDE) per Ma between the Indian subcontinent (I) and mainland Asia (A).

Supplementary Note 1

Crypteroniaceae (Rosids, Myrtales): We re-analysed the data set of Rutschmann *et al.*[1], reduced to 44 taxa to estimate the divergence time between *Axinandra zeylanica* and SE-Asian *A. coriacea*. The data set included the *rbcL, ndhF, rpl16-intron, 18S,* and *26S rRNA* genes (5,421 bp total alignment length). We initially applied the best calibration scheme as suggested by the authors of the original study[1]. However, we had severe difficulties in implementing all suggested calibration points as this dropped the initial likelihood to 'infinity'. Therefore, we could reduce the data set, omitting the families Myrtaceae *s. lat.*, Vochysiaceae, and Onagraceae. We kept a log-normal calibration density for the MRCA of *Rhexia virginica* and *Melastoma beccarianum* (minimum age = 23 Ma; 5–95% interquantile range = 23.9–46.2 Ma), and the MRCA of *Pternandra echinata* and *M. beccarianum* (minimum age = 53 Ma; 5–95% interquantile range = 53.9–76.2 Ma). Resulting mean rates were 0.1% per Ma (95% CI = 0.08–0.13% per Ma) for *ndhF*; 0.04% per Ma (95% CI = 0.03–0.05% per Ma) for *rbcL*; 0.1% per Ma (95% CI = 0.07–0.12% per Ma) for *rpl16*; 0.02% per Ma (95% CI = 0.01–0.02% per Ma) for *18S rRNA*; and 0.05% per Ma (95% CI = 0.04–0.06% per Ma) for *26S rRNA*. We defined as ranges India, mainland Asia, Africa and the New World.

Dipterocarpaceae (Rosids, Malvales): The phylogeny of the dipterocarp subfamily Dipterocarpoideae published by Gamage *et al.*[2] is based on the *trnL-intron*, t*rnL-trnF* spacer region and the *matK* gene (3,926 bp total alignment length). To calibrate the phylogeny, we applied the approach described by Gunasekara[3] and constrained the MRCA of the genus *Hopea* to a minimum of 12 Ma (log-normal calibration density, 5–95% interquantile range = 13.4–50.3),

and that of the genus *Vatica* to 3.6 Ma (lognormal calibration density, 5–95% interquantile range = 5.0–41.9 Ma) based on the fossil record. Additionally, we included (as 'empty sequences') dated fossils that are closely related to the genera *Dipterocarpus* (estimated age: 65 Ma[4]), *Dryobalanops* (estimated age: 20 Ma[5]) and *Anisoptera* (estimated age: 20 Ma[5]). We applied a broad exponential distribution as prior for the uncorrelated relaxed clock rate, with a mean of 0.2% per Ma (5–95% interquantile range = 0.01–0.60% per Ma). The resulting mean substitution rates were 0.03 % per Ma (95% CI = 0.02–0.05% per Ma) for *matK*; 0.1% per Ma (95% CI = 0.05–0.15% per Ma) for the *trnL*-intron; and 0.06 % per Ma (95% CI = 0.04–0.08% per Ma) for the *trnL-trnF* spacer region. We defined as ranges India, mainland Asia, Africa and the Seychelles. The subfamily Dipterocarpoideae is an example *par excellence* of a taxonomic group which—based on the biogeographical distribution of extant taxa and the fossil record—was formerly widespread in Africa, on the Indian Plate and associated continental fragments (such as the Seychelles). It subsequently diversified explosively in SE-Asia, but later became extinct in Africa and severely retracted its range in India. African fossils, including the genus *Dipterocarpus*[4], and pre-collision (i.e., Early Eocene) Indian macrofossils and geochemical biomarkers have been reported by Dutta *et al.*[5]. To reflect this prior knowledge, we constrained the range of the MRCA of Dipterocarpaceae to Africa for our biogeographical estimation and adjusted the dispersal multiplier (dm) for dispersal into Africa (dm = 0.0001; thus setting Africa as origin), from mainland Asia to the Seychelles (dm = 0.01), and from Africa and the Seychelles to mainland Asia (dm = 0.01), while we kept dm = 1.00 for all other dispersal directions.

Gentianaceae (Asterids, Gentianales): Yuan *et al.*[6] based their study on the genus *Exacum* on the nuclear encoded ribosomal *ITS-1* and *ITS-2* regions, the *5.8S rRNA*

gene, and the chloroplast *trnL*(UAA) intron sequence. Four independent fossil-based calibration points (minimum ages) were introduced in a phylogeny of the family Gentianaceae; resulting time estimates for the divergence between the outgroup (*Gentianothamnus–Tachiadenus* clade) and the ingroup (*Exacum–Ornichia* clade) were then used to calibrate the *Exacum* tree: tMRCA of Gentianales (60 Ma), tMRCA of *Lisianthius* (40 Ma), tMRCA of the subtribe Swertiinae (15 Ma), and tMRCA of *Gentiana* (5 Ma). We re-analysed the data set using an *ITS* rate of 0.452% per Ma (SD = 0.1)[7,8], and an exponential prior distribution for *5.8S rRNA* and *trnL* with a mean of 1% per Ma (5–95% interquantile range = 0.05–3.00% per Ma). We applied a normally distributed calibration density for the tMRCA of *Exacum* (mean = 22 Ma, SD = 8.3 Ma, 5–95% interquantile range = 8.3–35.7 Ma) following the study published by Yuan *et al.*[6]. The resulting mean rates for the unconstrained gene partitions were 0.05% per Ma (95% CI = 0.02–0.08% per Ma) for *5.8S rRNA* and 0.07% per Ma (95% CI = 0.04–0.10% per Ma) for *trnL*. We defined as ranges India, mainland Asia, the Himalayas, Africa, Madagascar and the island of Socotra.

Pachychilidae (Mollusca, Caenogastropoda): Unfortunately, fossil Pachychilidae have not been described that could be used for calibration, nor are reliable external rates for freshwater snails available. Therefore, we applied a broad external rate based on the data set presented by Köhler and Glaubrecht[9] (*16S rRNA*, and the *CO1* gene; 1,511 bp total alignment length) for dating the split between the genera *Brotia* and *Paracrostoma*. After an initial series of test runs, we used a fixed strict rate with a normal prior of 1% per Ma (SD = 1.25), truncated at 5% per Ma for both partitions (5–95% interquantile range = 0.0–20.7% per Ma). This broadly covers mitochondrial substitution rates of marine gastropods that have been calibrated using the closure of the Isthmus of Panama

as a geological calibration point[10,11]. We defined as ranges India, mainland Asia, Australia, Africa and the Americas.

Gecarcinucidae (Crustacea, Brachyura): Klaus *et al.*[12,13] based their phylogeny of Asian freshwater crabs on the nuclear-encoded histone *H3* (318 bp) gene and the mitochondrial *16S rRNA* gene (558 bp; 876 bp total alignment length. The phylogeny was calibrated using three fossil calibration points that were translated into a gamma-distributed calibration density: fossil *Potamonautes niloticus* (node *P. niloticus–Platythelphusa armata*: 6 Ma), fossil *Potamon quenstedti* (node *P. fluviatile–P. persicum*: 16.5 Ma), and fossil *Sartoriana* sp. (node *S. spinigera–S. blanfordi*: 2.5 Ma). According to a recent phylogeny of the family Potamonautidae[14], we corrected the first calibration point to comprise the MRCA of *Potamonautes niloticus* and *P. stanleyensis*. The analysis was run for 80 M iterations, and the first 30 M were discarded as burn-in. We applied a uniform distribution as prior for the substitution rates (0.1–10.0% per Ma for *16S rRNA* and 0.01–1.00% per Ma for histone *H3*). The resulting mean rates were 0.28% per Ma (95% CI = 0.18–0.37% per Ma) for *H3* and 0.41% per Ma (95% CI = 0.28–0.53% per Ma) for the *16S rRNA* gene. Especially the *16S rRNA* rate differs from previous studies (16S rRNA 0.64–1.42% per Ma; mean 1.02%; histone *H3* 0.12–0.26% per Ma, mean 0.19%)[12]. We used the same area coding as given in Klaus *et al.*[12] (India, East-/Southest Asia, Philippines and Wallacea).

Papilionidae (Insecta, Lepidoptera): Condamine *et al.*[15] based their phylogeny of papilionid butterflies on ~2.3 kb of mitochondrial *CO1* and *CO2* genes and ~1.0 kb of the nuclear *EF-1a* gene. We followed their calibration scheme and translated the following age estimates into log-normally distributed calibration densities: the MRCA of the family Papilionidae was set to a minimum age of 48 Ma (fossil *Praepapilio*; mean = 2.945 Ma, SD = 1.0, offset = 15 Ma, 5–95%

interquantile range = 51.7–146.5 Ma); 30 Ma was assumed as the minimum age for the subfamily Parnassiinae (mean = 3.0708 Ma, SD = 1.0, offset = 30 Ma, 5–95% interquantile range = 34.2–141.7 Ma); and the MRCA of the tribe Luehdorfiini was set to a minimum age of 15 Ma (mean = 3.164 Ma, SD = 1.0, offset = 15 Ma, 5–95% interquantile range = 19.6–137.6 Ma). The MRCA of family Pieridae was confined to a minimum age of 34 Ma (fossil *Stolopsyche libytheoides*), as was the MRCA of the family Nymphalidae (both mean = 3.044 Ma, SD = 1.0, offset = 34 Ma, 5–95% interquantile range = 38.1–142.7 Ma). We applied a broad exponential prior for the substitution rates of the partitions (*CO1* and *CO2*: mean = 3.0% per Ma, 5–95% interquantile range = 0.15–9.00% per Ma; *EF-1a*: mean = 1.0% per Ma, 5–95% interquantile range = 0.05–3.00% per Ma). We did not constrain the root age of the phylogeny as done in the original study (183 Ma, origin of angiosperms), as this resulted in an 'infinite negative' initial likelihood and abortion of the analysis. 8 M iterations were discarded as burn-in. The resulting mean rates were 0.71% per Ma (95% CI = 0.55–0.86% per Ma) for the combined *CO1/CO2* partition and 0.15% per Ma (95% CI = 0.12–0.18% per Ma) for *EF-1a*. The area coding was the following: India, SE Asia, Australia, the Palearctic, the Americas, Africa, and Madagascar

Apidae (Insecta, Hymenoptera): To retrieve credibility intervals we re-analysed a subset of data from the study by Rehan *et al.*[16] on the phylogeny of carpenter bees (subfamily Xylocopinae, tribe Ceratinini; 74 taxa) using the mitochondrially-encoded *CO1* and *Cytb*, and the nuclear *EF-1a* (2,807 bp total alignment length) that includes three dispersal events from mainland Asia to the Indian subcontinent (at the divergence nodes of *Ceratina propinqua* and *C. binghami*, and at the MRCA of *C. japonica*, *C. okinawana*, *C. bowringi*, *C. hieroglyphica* and *C. moderata*). We used the three calibration points as suggested by the authors with a

log-normal calibration density: a minimum divergence between the tribes Ceratinini and Allodapini of 45 Ma (5–95% interquantile range = 45.2–50.2 Ma); a minimum divergence between *Apis mellifera* from the genus *Liotrigona* of 65 Ma (5–95% interquantile range = 65.3–73.5 Ma); and 90 Ma (5–95% interquantile range = 91.4–128.3 Ma) for the MRCA of the Xylocopinae and Apinae. The resulting mean rates were 3.14% per Ma (95% CI = 1.32–7.07% per Ma) for *Cytb*, 0.28% per Ma (95% CI = 0.21–0.34% per Ma) for *EF-1a*, and 2.08% per Ma (95% CI = 1.66–2.54% per Ma) for *CO1*. We defined as ranges India, mainland Asia, Australia, Africa and the Americas.

Formicidae (Insecta, Hymenoptera): We combined partial sequence information of the *28S rRNA* and *LWRh* genes (1,388 bp total) obtained from the studies of Ward and Downie[17] on the subfamily Pseudomyrmecinae and Jansen *et al.*[18] on the genus *Myrmica*. Thereby, we could employ the calibration points provided by Jansen *et al.*[18], i.e., the split between the subfamilies Formicinae and Myrmicinae, calibrated with fossil *Kyromyrma* (92 Ma, 5–95% interquantile range = 92.2–124.0 Ma) and the MRCA of the genus *Myrmica*, calibrated based on baltic amber fossils (44.1 Ma; 5–95% interquantile range = 41.3–73.2 Ma). We inferred dispersal times to the Indian subcontinent for *Myrmica indica* and *T. rufonigra*, with separate biogeographical analyses for the subfamily Pseudomyrmecinae and the genus *Myrmica*. The resulting mean rates were 0.08% per Ma (95% CI = 0.07–0.10% per Ma) for *28S rRNA*; and 0.34% per Ma (95% CI = 0.26–0.42% per Ma) for *LWRh*. For the biogeographical analysis we split the resulting phylogeny and used different area coding for *Pseudomyrmex–Tetraponera* (India, mainland Asia, Africa and the Americas) and for *Myrmica* (India, East/Southeast Asia, western Eurasia/Europe and the Americas.

Aplocheiloidei (Teleostei, Cyprinodontiformes): We used the mitochondrial data set of Murphy and Collier[19] to calibrate the split between SE-Asian *Aplocheilus panchax* and Indian *A. lineatus*, consisting of partial sequences of *12S rRNA* (333 bp), *16S rRNA* (520 bp), and *Cytb* (360 bp) genes. We applied a normally distributed divergence density for the calibrations of the following splits: the split between American and African taxa (tectonic break up of western Gondwana, 5–95% interquantile range = 81.7–88.3 Ma); the split between Asian and Madagascan species (tectonic separation of Madagascar and India, 5–95% interquantile range = 85.4–88.6 Ma); and the age of the separation of Afrotropical/Neotropical and Asian/Madagascan taxa (break up of Western and Eastern Gondwana, 5–95% interquantile range = 166.7–173.3 Ma). The resulting mean rates were 0.30% per Ma (95% CI = 0.23–0.38% per Ma) for *16S rRNA*; 0.21% per Ma (95% CI = 0.17–0.26% per Ma) for *12S rRNA*; and 1.45% per Ma (95% CI = 1.07–1.89% per Ma) for *Cytb*. For the biogeographical inference, we used mainland Asia, India, Africa, Madagascar, the Seychelles and the Americas as area coding.

Channidae (Teleostei, Perciformes): We re-calculated the phylogeny published by Adamson *et al.*[20] that was based on the mitochondrially encoded *Cytb* (809 bp) and nuclear *RAG-1* (1,484 bp) genes. We followed their calibration scheme and constrained the MRCA of the genera *Channa* and *Parachanna* with the first occurrence date of *Channa* (5–95% interquantile range = 40.9–63.2 Ma); and the divergence of the family Channidae from other members of the order Perciformes (5–95% interquantile range = 48.6–103.3 Ma). We applied broad normally distributed rate priors for *Cytb* (2.0% per Ma, SD = 1.0, 5–95% interquantile range = 0.54–3.66% per Ma) and *RAG-1* (0.1% per Ma, SD = 0.1, 5–95% interquantile range = 0.02–0.27% per Ma) Resulting mean rates were 0.51% per

Ma (95% CI = 0.43–0.61% per Ma) for *Cytb* and 0.15% per Ma (95% CI = 0.12–0.20% per Ma) for the *RAG-1* gene. For the biogeographical inference, we used mainland Asia and India as area coding. The distribution range at the root node was constrained to Asia[20].

Heteropneustidae (Teleostei: Siluriformes): We re-analysed data from the phylogenetic study by Ratmuangkhwang *et al.*[21] on heteropneustid catfishes which are currently described as one species (*Heteropneustes fossilis*), based on *RAG-1* sequence information of 1,494 bp length. We followed the calibration scheme of the original study by incorporating six calibration points as normally distributed calibration densities within the outgroup taxa. These were derived as secondary calibration points from the study of Nakatani *et al.*[22] (phylogeny of the teleost group Otophysi; the calibration was based on 23 fossil and three biogeographical constraints), such that the 5–95% interquantile ranges correspond to the node age credibility intervals of the latter study. The resulting mean substitution rate was 0.96% per Ma (95% CI = 0.59–1.34% per Ma). The mutation rate under the calibration scheme of Ratmuangkhwang *et al.*[21] is thus extremely fast compared to the mutation rates of *RAG-1* inferred for the Channidae (see above) and Osphronemidae (see below), and might point to an underestimation of divergence dates. However, the resulting credibility intervals for the estimates of node ages were large (spanning >30 Ma) and thus, most likely still captured the actual divergence times. For the biogeographical inference, we used mainland Asia and India as area coding.

Osphronemidae (Teleostei: Perciformes): We re-analysed the data from the study of Rüber *et al.*[23] on the phylogeny of fishes in the family Osphronemidae. We used the complete data set comprising 60 taxa (*RAG-1* gene, complete *Cytb*, partial *12S rRNA, Val-tRNA* and partial *16S rRNA* genes; 4,258 bp total alignment

length). We followed the authors' calibration scheme by calibrating with fossil *Osphronemus* from Sumatra of Late Eocene/Early Oligocene age, applying the suggested crown group calibration. We translated this information into a log-normally distributed calibration density with an offset at 28 Ma (5–95% interquantile range = 29–54 Ma). Resulting rates were 0.34% per Ma for *RAG-1* (95% CI = 0.26–0.40% per Ma), 3.01% per Ma for *Cytb* (95% CI = 2.31–3.65% per Ma), and 0.47% per Ma (95% CI = 0.36–0.57% per Ma) for the combined non-protein coding mitochondrial tRNA and rRNA genes. For the biogeographical inference, we used mainland Asia, India and Africa as area coding.

Cobitidae (Teleostei, Cypriniformes): We re-analysed the data set on which the phylogenetic study by Šlechtová *et al.*[24] builds (mitochondrial *Cytb* and nuclear *RAG-1* sequences; 2,016 bp total alignment length) using an external rate for *Cytb* (normally distributed, with a mean rate of 0.68% per Ma; 5–95% interquantile range = 0.52–0.84% per Ma). A calibration for the genus *Cobitis* was available using the opening of the Strait of Gibraltar, as cobitids are primary freshwater fish and thus, incapable of dispersing through marine habitats[25]. We assumed three dispersal events from Southeast Asia to the Indian subcontinent (Bangladesh and N-Bengal) at the divergence of *Pangio pangia* and *P. doriae*; *Lepidocephalichtys guntea* and *L. hasselti*; and *Neoeucirrichthys maydelli* and *Somileptus gongota*. The resulting mean mutation rate of the *RAG-1* gene was 0.17% per Ma (95% CI = 0.12–0.23% per Ma). For the biogeographical inference, we used mainland Asia and India as area coding.

Dicroglossidae (Amphibia, Anura): In case of the anuran family Dicroglossidae we re-analysed the respective subset of data from the amphibian phylogeny published by Pyron and Wiens[26], including the genera *Indirana* (outgroup),

Occidozyga, *Nannophrys*, *Hoplobatrachus*, *Euphlyctis*, *Sphaerotheca*, *Fejervarya*, *Paa*, and *Limnonectes*), while we included three additional specimens of the genus *Fejervarya*[27]. The data consist of seven partitions, three mitochondrial (*12S* and *16S rRNA* genes, *Cytb*) and four nuclear genes (*CXCR4*, *NCX1*, *RHOD*, *TYR*). We assigned a GTR+G model of sequence evolution to all partitions except for the *12S rRNA* and *CXCR4* partitions, in which case a HKY+G model was applied. We ran the analysis for 50 M generations, sampling every 2,000[th] generation, discarding 10% of the samples as burn-in. We constrained the tMRCA of dicroglossids with a normally distributed calibration density with a mean of 63 Ma (SD = 9.7 Ma; 5–95% interquantile range = 47–79 Ma). This secondary calibration point is based on the study of Van Bocxlaer *et al.*[28], as the different calibration schemes employed by the authors cover a range of 47–79 Ma for this split. For the biogeographical inference, we used mainland Asia, Africa and India as area coding. Although not unequivocal in our analysis, we assumed an Indian origin of the family Dicroglossidae, and thus initial dispersal from the Indian subcontinent to East-/SE-Asia at the deepest split within the subfamily Dicroglossinae[28]. The resulting mean rates were 0.74% per Ma (95% CI = 0.56–0.95% per Ma) for *12 rRNA*; 0.87% per Ma (95% CI = 0.64–1.10% per Ma) for *16S rRNA*; 3.70% per Ma (95% CI = 2.27–5.48% per Ma) for *Cytb*; 0.07% per Ma (95% CI = 0.04–0.12% per Ma) for *CXCR4*; 0.06% per Ma (95% CI = 0.04–0.08% per Ma) for *NCX1*; 0.08% per Ma (95% CI = 0.05–0.12% per Ma) for *RHOD*; and 0.12% per Ma (95% CI = 0.09–0.16% per Ma) for *TYR*.

Microhylidae (Amphibia, Anura): For the family Microhylidae we re-analysed a part of the data set published by de Sá *et al.*[29], in which three nuclear (*TYR*, *BDNF*, and the *28S rRNA* gene) and one mitochondrial marker (*16S rRNA* gene) were employed. We ran the analysis for 100 M iterations, sampling every 10,000[th]

iteration, discarding 10% as burn-in. We applied a HKY+G model of sequence evolution for all partitions. According to the original study[29] we constrained (using a normally distributed calibration density) the tMRCA of the subfamily Otophryninae to 60.4 Ma (SD = 5); the tMRCA of subfamily Gastrophryninae to 79.1 Ma (SD = 5); and the tMRCA of the genus *Gastrophryne* to 1.7 Ma (SD = 0.5). The resulting mean rates were 0.06% per Ma (95% CI = 0.05–0.07% per Ma) for *BDNF*; 0.19% per Ma (95% CI = 0.15–0.25% per Ma) for *TYR*; 0.017% per Ma (95% CI = 0.01–0.02% per Ma) for *28S rRNA*; and 0.89% per Ma (95% CI = 0.69–1.11% per Ma) for *16S rRNA*. For the biogeographical inference, we used mainland Asia and India as area coding.

Rhacophoridae (Amphibia, Anura): The study on rhacophorid tree frogs[30] was based on five nuclear gene fragments (*BDNF*, 614 bp; *POMC*, 601 bp; *RAG-1*, 1,164 bp; *RHOD*, 315 bp; *TYR*, 531 bp) and 2,041 bp of mitochondrial DNA covering the *12S* and *16S rRNA* genes as well as the complete *tRNA Val* (5,266 bp total alignment length). The authors calibrated the age of the most recent common ancestor of the Rhacophoridae with fossil *Indorana prasadi* from Early Eocene sediments of India, and constrained the split between *Boophis tephraeomystax* from the Comoro island of Mayotte and its sister species *Boophis doulioti* to a maximum age of 15 Ma. We did not re-analyse this data set but used the original chronogram to calculate the biogeographic estimates. For the biogeographical inference, we used mainland Asia, India, insular SE Asia and Africa as area coding.

Bufonidae (Amphibia, Anura): We re-analysed the data set of Van Bocxlaer *et al.*[31], which included nuclear (1,970 bp; *NCX1*, *CXCR4*) and mitochondrial genes (4,339 bp; *12S rRNA*, *tRNA Val*, *16S rRNA*, *tRNA Leu*, *ND1*, *tRNA Ile*, *tRNA Gln*, *tRNA Met*, *ND2*; 6,309 bp total alignment length), to infer the phylogeny and

divergence time estimates of toads, with the focus on the Asian subfamily Adenominae. We translated the following calibration points based on minimum ages of fossils into log-normally distributed calibration densities (SD = 1.0 in all cases): 18 Ma for the MRCA of the *Bufo viridis* group (mean = 1.7 Ma, offset = 18.0 Ma, 5–95% interquantile range = 19.1–46.7 Ma), 11 Ma for the origin of the genus *Rhinellamarina* (mean = 1.88 Ma, offset = 11.0 Ma, 5–95% interquantile range = 12.3–44.8 Ma), 9.6 Ma for the MRCA of the *Bufo bufo* group (mean = 1.905 Ma, offset = 9.6 Ma, 5–95% interquantile range = 10.9–44.4 Ma), and a minimum age of 15 Ma for the MRCA of the subgenus *Eleutherodactylus* (mean = 2.17 Ma, offset = 15.0 Ma, 5–95% interquantile range = 16.7–60.3 Ma). Divergence time analysis was run as described under "Phylogenetic methods and divergence time estimations" with the exception that we discarded 2,500 samples as burn-in. The resulting mean rates were 0.09% per Ma (95% CI = 0.07–0.11% per Ma) for the nuclear and 0.88% per Ma (95% CI = 0.65–1.10% per Ma) for the mitochondrial partition. For the biogeographical inference, we used East/SE Asia, India, Africa, and western Eurasia as area coding.

Crocodylidae (Reptilia, Crocodylia): Oaks[32] presents a phylogeny of the family Crocodylidae based on two partitions: 7,282 bp of mitochondrial *Cytb, tRNA Glu, tRNA Thr, ND2, tRNA Met, tRNA Trp, ND3, tRNA Gly, tRNA Arg*), the D-loop of the control region and *tRNAPhe*, and nuclear encoded *c-mos, EPIC, ACTC* Exon 4–5, *aTROP* Exon 5–6, *ACTB* Exon 3–4, *AChR* Exon 7–8, *GAPDH* Exon 11–12, *LDH-B* Exon 6–7, *LDH-A* Exon 7–8, and *RHO* Exon 2–3. This phylogeny was calibrated with the tMRCA of the subfamilies Alligatorinae and Caimaninae (5–95% interquantile range of a lognormal calibration density = 71–64 Ma; upper bound of the tMRCA of the order Crocodylia = 90 Ma). The *BEAST[33] minimum credibility tree was kindly provided by the first author of this study and used for

our biogeographical inference. For the biogeographical inference, we used mainland Asia, India, Africa and the Americas as area coding. We assumed dispersal from SE-Asia to the Indian subcontinent at the divergence of *Crocodylus siamensis* and *C. palustris*, and – more arbitrary in light of the fossil record[34] – at the MRCA of the genera *Tomistoma* and *Crocodylus*.

Geckonidae (Reptilia, Squamata): Based on the study of Wood *et al.*[35], including additional outgroup taxa from Bansal and Karanth[36], we calculated a phylogeny of the gekkonid genus *Cyrtodactylus* based on the partial nuclear *RAG-1* and *PDC* genes (1,454 bp total alignment length). Substitution schemes were not partitioned between both genes. We calibrated the divergence between *Sphaerodactylus roosevelti* and *S. torrei* based on fossil *Sphaerodactylus* from Hispaniola, dated 15–20 Ma (exponential calibration density, mean = 3.0 Ma, offset = 15 Ma, 5–95% interquantile range = 15–24 Ma), the divergence between the genera *Oedura* and *Woodworthia* with fossil "*Hoplodactylus* sp." from New Zealand, dated to 16–19 Ma (exponential calibration density, mean = 17 Ma, offset = 16 Ma, 5–95% interquantile range = 17–67 Ma). Fossil *Primaderma nessovi* served to constrain the MRCA of the split between the families Helodermatidae and Anguidae (exponential calibration density, mean = 3.0, offset = 99 Ma, 5–95% interquantile range = 99–108 Ma), and the split between *Teratoscincus scincus* and *T. roborowskii* was constrained biogeographically to 10 Ma (mean = 10 Ma, SD = 0.5, 5–95% interquantile range = 9–11 Ma). The resulting mean substitution rates were 0.08% per Ma for both partitions (95% CI = 0.06–0.09% per Ma for *RAG-1* and 0.06–0.1% per Ma for *PDC*). For the biogeographical inference, we used mainland Asia, India and Australia as area coding.

Scincidae (Reptilia: Squamata): We re-analysed the data used for the phylogenetic analyses published by Datta-Roy *et al.*[37] based on partial

mitochondrial *12S* and *16S rRNA* genes and the nuclear *c-mos* gene (1,641 bp total alignment length). We added the species *Coprucia zebrata*, *Tiliqua adelaidensis* and *Egernia whitii* from the study of Honda *et al*[38] and calibrated the split between the latter two based on fossil *Proegernia palankarinnensis* from the Late Oligocene[39]. We used a lognormal calibration density with 25 Ma as a hard younger bound, resulting in a 5–95% interquantile range of 25.52–39.08 Ma for that split. The resulting rates were 0.33% per Ma (95% CI 0.19–0.47% per Ma) for *16S rRNA*, 0.30% per Ma (95% CI 0.18–0.43% per Ma) for *12S rRNA*, and 0.04% per Ma (95% CI 0.02–0.06% per Ma) for *c-mos*. For the biogeographical inference, we used mainland Asia, India, Africa, Madagascar, the Seychelles, teh Cape Verde silands and the Americas as area coding.

Agamidae 1 (Reptilia, Squamata): We re-analysed the data set of Macey *et al.*[40], based on the mitochondrial *ND1*, *tRNA Gln*, *tRNA Ile*, *tRNA Met*, *ND2*, *tRNA Trp*, *tRNA Ala*, *tRNA Asn*, *tRNA Cys*, *tRNA Tyr*, and *CO1* genes (1,551 bp total alignment length). We used three fossil calibration points with a lognormal distributed calibration density[41] and calibrated the MRCA of crown Acrodonta (families Chamaeleonidae and Agamidae; 5–95% interquantile range = 46.4–134.0 Ma), the MRCA of crown Agamidae (5–95% interquantile range = 32.3–124.4 Ma), and the MRCA of *Istiurus lesuseurii* and *Pogona vitticeps* (5–95% interquantile range = 20.4–56.7 Ma). The resulting rates were 2.20% per Ma (95% CI 1.20–3.20% per Ma) for *CX1*, 1.90% per Ma (95% CI 1.10–2.51 per Ma) for *ND1*, 1.32% per Ma (95% CI 1.08–1.56 per Ma) for *ND2*, 0.95% per Ma (95% CI 0.68–1.23 per Ma) for *tRNA Ala*, 0.87% per Ma (95% CI 0.49–1.24 per Ma) for *tRNA Asn*, 1.50% per Ma (95% CI 1.09–1.95 per Ma) for *tRNA Cys*, 0.61% per Ma (95% CI 0.42–0.82 per Ma) for *tRNA Gln*, 0.66% per Ma (95% CI 0.37–0.97 per Ma) for *tRNA Ile*, 1.50% per Ma (95% CI 0.94–2.15 per Ma) for *tRNA Met*,

1.53% per Ma (95% CI 1.14–1.94 per Ma) for *tRNA Trp*, and 1.46% per Ma (95% CI 1.08–1.86 per Ma) for *tRNA Tyr*. For the biogeographical inference, we used mainland Asia, India, and Africa as area coding.

Agamidae 2 (Reptilia, Squamata): The aforementioned data set on agamids included only one Asian specimen of *Draco*; however, there are also Indian representatives this genus. Therefore, we re-analysed the data set of Honda *et al.*[42] based on mitochondrial *12S* and *16S rRNA* gene fragments (780 bp total alignment length). To estimate the divergence of Indian *D. dussumieri*, we calibrated the root of the tree (tMRCA [*Draco + Aphaniotis fusca*] with a secondary calibration point based on the previous analysis ('Agamidae 1'; normal calibration density with 5–95% interquantile range of 32–45 Ma). The resulting rates were 1.30% per Ma (95% CI = 0.91–1.74 per Ma) for *12S*; and 0.71% per Ma (95% CI = 0.48–0.96 per Ma) for the *16S rRNA* gene. For the biogeographical inference, we used mainland Asia and India as area coding.

Boidae (Reptilia, Squamata): We reanalysed the phylogeny of the family Boidae by Noonan and Chippindale[43] based on the nuclear *RAG-1*, *c-mos*, *NT3*, *ODC*, and *BDNF* genes and the mitochondrial *Cyt-b* gene (~4.3 kb total alignment length). We followed the suggestions for calibrating snake phylogenies provided by Sanders *et al*[44].: the MRCA of *Acrochordus javanicus* and the clade including *A. granulatus and A. arafurae* (5–95% interquantile range = 18.7–25.0 Ma), the split between the genus *Acrochordus* and the superfamily Colubroidea (5–95% interquantile range = 51.0–69.9 Ma), the MRCA of Boidae (5–95% interquantile range = 57.3–83.7 Ma), the split between the families Colubridae and Elapidae (5–95% interquantile range = 21.7–35.1 Ma), and the most basal split in extant snakes (uniform calibration density = 85.0–140.0 Ma). We assumed dispersal from SE Asia to India to have occurred between the MRCA of *Eryx colubrinus*

and the clade comprising *E. johni* and *E. conicus*, and the MRCA of *E. johni* and *E. conicus*, resulting in a time range of the combined 95% credibility intervals of 25–5 Ma. The resulting rates were 0.07% per Ma (95% CI = 0.05–0.09% per Ma) for *ODC*, 0.03% per Ma (95% CI = 0.02–0.04% per Ma) for *BDNF*, 0.05% per Ma (95% CI = 0.03–0.06% per Ma) for *RAG-1*, 0.05% per Ma (95% CI = 0.04–0.06% per Ma) for *c-mos*, and 0.07% per Ma (95% CI = 0.05–0.1% per Ma) for *NT3*. For the biogeographical inference, we used mainland Asia, India, Australia, Africa and the Americas as area coding.

Viperidae (Reptilia, Squamata): We re-analysed the mitochondrial data set used in the study of Wüster *et al.*[45] on the phylogeny of viperid snakes (based on *Cytb*, *ND4*, *12S* and *16S rRNA* genes; 2,962 bp total alignment length) that—following biogeographical inference—includes two dispersal events from SE-Asia to India, namely, at the split nodes between *Hypnale hypnale* and *Calloselasma rhodostoma*, and between *Trimeresurus borneensis* and *T. trigonocephalus*. We incorporated five calibrations points: the divergence of South American populations of the Neotropical pitviper genus *Porthidium* with the uplift of the Isthmus of Panama (mean = 3.5 Ma, SD = 0.51, 5–95% interquantile range = 2.7–4.4 Ma), minimum divergence of the Eurasian viper clade (excluding *Pseudocerastes* and *Eristicophis*) at 20 Ma (lognormal calibration density, mean = 1.0 Ma, SD = 1.0, offset = 20.0 Ma, 5–95% interquantile range = 20.5–34.1 Ma), a minimum age of 16 Ma for the divergence between the Asian clade of the genus *Naja* and its African sister clade (lognormal calibration density, mean = 1.0 Ma, SD = 1.0, offset = 16.0 Ma, 5–95% interquantile range = 16.5–30.1 Ma), the divergence between *Crotalus* and *Sistrurus* before 9 Ma (lognormal calibration density, mean = 0.0 Ma, SD = 1.0, offset = 9.0 Ma, 5–95% interquantile range = 9.2–14.2 Ma), and the tMRCA of the genus *Hemorrhois* (normal calibration

density, mean = 18.0 Ma, SD = 2.04, offset = 9.0 Ma, 5–95% interquantile range = 14.6–21.4 Ma). The resulting mean substitution rates were 1.64% per Ma (95% CI = 1.41–1.87% per Ma) for *ND4*, 2.12% per Ma (95% CI = 1.82–2.42% per Ma) for *Cytb*, 0.75% per Ma (95% CI = 0.60–0.92% per Ma) for *16S*, and 1.39% per Ma (95% CI = 0.95–1.89% per Ma) for *12S rRNA*. For the biogeographical inference, we used mainland Asia, India, Australia, Africa and the Americas as area coding.

Passeriform birds (Reptilia, Aves): Päckert *et al.*[46] presented a study on the biogeography of Himalayan and SE Asian songbirds (order Passeriformes) that included time-calibrated phylogenies (Bayesian approach in BEAST 1.4.8) and biogeographical reconstructions (parsimony approach) of several genera belonging to the families Phylloscopidae (*Cytb*, *12S rRNA* gene, *myoglobin* intron 2; 1,899 bp total alignment length), Timaliidae (*Cytb*; 861 bp; external rate 2.1% per Ma), Paridae (*Cytb*, *16S rRNA* gene, control region, and *fib7*; 2,527 bp total alignment length), Aegithalidae (*Cytb*, *16S rRNA* gene, *ND2*, *fib7*, *GAPDH11*, *ODC6*, and *TGFB2*; 3,995 bp total alignment length), Fringillidae (genus *Pyrrhula*; *Cytb*, *16S rRNA* gene, *fib7*, and *GAPDH11*; 2,357 bp total alignment length) and Certhiidae (*Cytb*, *16S rRNA* gene, *myo2*, and *GAPDH11*; 2,019 bp total alignment length) that we re-analysed for the present study. They calibrated these trees with various biogeographic events, i.e., the opening of the Bering Strait (uniform calibration density = 10.0–4.8 Ma and 14.0–4.8 Ma, respectively), the Messinian salinity Crisis (5.96 Ma), Pleistocene glaciations (2.4–0.18 Ma), the age of lava flows to calibrate splits between Africa and the Canary Islands (5.96–1.22 Ma), within the Canary Islands (1.77–0.00 Ma, 1.22–0.00 Ma), between Africa and the Azores (0.88–0.00 Ma), and within the Azores (0.2–0.0 Ma). However, we were not able to run the analyses under these calibration schemes, as

these priors resulted in extremely low initial model likelihoods. Therefore, we applied an external substitution rate for the *Cytb* partition of 1.35 % per Ma (SD = 0.4; 5–95% interquantile range = 0.7–2.3% per Ma). This broadly covers previously suggested avian *Cytb* substitution rates[47,48]. The resulting divergence times are considerably younger than in the original study (except for the Timaliidae), indicating that Päckert *et al.*[46] used pairwise divergence instead of substitution rates. We included those splits that separated west-Himalayan endemics (the authors' 'bioregion F04a') from their eastern relatives.

Psittacidae (Reptilia, Aves): We re-analysed the phylogeny by Groombridge *et al.*[49] of the genus *Psittacula* (*Cytb*, 800 bp), applying the above-mentioned external rate of 1.35 % per Ma (SD = 0.4; 5–95% interquantile range = 0.7–2.3% per Ma). We inferred a shift from SE-Asia to India at the divergence of *P. cyanocephala* and *P. longicauda*, and for the other dispersal direction at the divergence of *P. columboides*. For the biogeographical inference, we used mainland Asia, India, and Africa as area coding.

Accipitridae (Reptilia, Aves): We re-analysed the phylogeny of Asian hawk-eagles of the genus *Nisaetus* published by Gamauf *et al.*[50] that used mitochondrial *Cytb* and control region sequences (502 bp total alignment length). We applied an external rate of 1.35 % per Ma (SD = 0.4; 5–95% interquantile range = 0.7–2.3% per Ma) under an uncorrelated relaxed lognormal clock prior. For the biogeographical inference, we used mainland Asia and India as area coding. We inferred dispersal from Asia to India along the branch leading to the MRCA of the subspecies of *Nissaetus cirrhatus*.

Bovidae (Mammalia, Ruminantia): We re-analysed parts of the data set from the study by Hassanin *et al.*[51], who presented a phylogeny of the Cetartiodactyla

based on partial mitochondrial genome sequences (14,904 bp total alignment length). We followed their approach and calibrated (with normally distributed prior densities) the tMRCA of whales (Cetacea) to 35 Ma (SD = 1), the tMRCA of the Cetacea and *Hippopotamus* to 55 Ma (SD = 5), the tMRCA of Hippopotamus to 8 Ma (SD = 1), the divergence between the tribes Muntiacini and Cervini to 9 Ma (SD = 1), the tMRCA of the tribe Odocoileini to 5 Ma (SD = 1), and the tMRCA of the family Bovidae to 20 Ma (SD = 2). We removed 1,300 samples of the Bayesian analysis as burn-in. The resulting rates were 0.38% per Ma (95% CI = 0.35–0.42% per Ma) for the tRNAs, 0.35% per Ma (95% CI = 0.32–0.31% per Ma) for *12S rRNA*, 0.4% per Ma (95% CI = 0.37–0.44% per Ma) for *16S rRNA*, 0.80% per Ma (95% CI = 0.74–0.85% per Ma) for *ND1*, 0.96% per Ma (95% CI = 0.90–1.02% per Ma) for *ND2*, 0.75% per Ma (95% CI = 0.70–0.80% per Ma) for *CO1*, 0.69% per Ma (95% CI = 0.64–0.73% per Ma) for *CO2*, 0.75% per Ma (95% CI = 0.70–0.80% per Ma) for A8A6, 0.82% per Ma (95% CI = 0.76–0.88% per Ma) for *CO3*, 0.81% per Ma (95% CI = 0.75–0.89% per Ma) for *ND3*, 0.85% per Ma (95% CI = 0.79–0.90% per Ma) for *ND4*, 0.85% per Ma (95% CI = 0.79–0.90% per Ma) for *ND5*, 1.10% per Ma (95% CI = 1.00–1.20% per Ma) for *ND6*, and 0.90% per Ma (95% CI = 0.84–0.96% per Ma) for *CBP*. For the biogeographical inference, we used mainland Asia, India, Australia, Africa and the Americas as area coding.

Herpestidae (Mammalia, Carnivora): We re-analysed the data from the phylogenetic study by Patou *et al.*[52] on mongooses (family Herpestidae) based on the mitochondrial *Cytb* and *ND2* genes, and nuclear *FGBi7* sequences (2,770 bp total alignment length). We followed the authors' approach and calibrated the minimum age of the MRCA of the Herpestidae with fossil *Leptoplesictis* (uniform calibration density = 18–66 Ma), and of the MRCA of the genus *Galerella* based

on fossil evidence (7–66 Ma). The resulting mean substitution rates were 0.69% per Ma (95% CI = 0.50–0.87% per Ma) for *Cytb*, 0.56% per Ma (95% CI = 0.41–0.70% per Ma) for *ND2*, and 0.12% per Ma (95% CI = 0.08–0.16% per Ma) for *FGBi7*. For the biogeographical inference, we used SE Asia, India, Africa, Europe and the Americas as area coding.

Sciuridae (Mammalia, Rodentia): We re-analysed the data set of Lu *et al.*[53] on flying squirrels (subfamily Pteromyinae), including the *IRBP* gene, and partial *12S* and *16S rRNA* gene sequences; 2,584 bp total alignment length). We calibrated the MRCA of the tribe Pteromyini with the first appearance date of the pteromyine fossil *Oligopetes* spp. from southern Germany in the Early Oligocene (MP21, 33.9–32.6 Ma)[54]. We translated this date into a lognormal calibration density with an offset of 32.6 Ma and a 5–95% interquantile range of 33.1–46.7 Ma. The resulting rates were 0.45% per Ma (95% CI = 0.34–0.56% per Ma) for the *12S rRNA*, 0.39% per Ma (95% CI = 0.29–0.50% per Ma) for the *16S rRNA*, and 0.08% per Ma (95% CI = 0.06–0.09% per Ma) for the *IRBP* gene. For the biogeographical inference, we used East/SE Asia, the Palearctic, India and the Americas as area coding.

Tupaiidae (Mammalia, Scandentia): We re-analysed the data set of Roberts *et al.*[55] using the alignment provided by the authors and also applied the fossil calibration points as suggested by the authors. However, we were unable to run the analysis using all suggested calibration points. Therefore, we reduced the number of calibration points to the two ingroup calibrations (lognormal calibration densities with mean and SD = 1.0; tMRCA [*Tupaia*, *Urogale* and *Anathana*] = 18.0 Ma, and tMRCA of the order Scandentia = 38.2 Ma as offset points), and also used a re-aligned data set without excluding the more variable parts of the sequences (*12S rRNA*, *16S rRNA*, *tRNA Leu*, *tRNA Val* and *tRNA Phe*

genes; 2,849 bp total alignment length). Credibility intervals of divergence events overlap with those given by Roberts *et al.*[55], but the retrieved mean values were considerably younger. The resulting rates were 0.86% per Ma (95% CI = 0.70–1.02% per Ma) for the *12S rRNA* gene, 1.18% per Ma (95% CI = 0.99–1.38% per Ma) for the *16S rRNA* gene, 0.85% per Ma (95% CI = 0.07–3.0% per Ma) for the *tRNA Leu* gene, 1.28% per Ma (95% CI = 0.49–2.09% per Ma) for the *tRNA Phe* gene, and 1.62% per Ma (95% CI = 0.96–2.36% per Ma) for the *tRNA Val* gene. For the biogeographical inference, we used mainland Asia, India, and the Philippines as area coding. Dispersal to the Indian subcontinent was inferred at the MRCA of the genera *Dendrogale* and *Tupaia*.

Colobinae (Mammalia, Primates): We re-analysed the phylogeny by He *et al.*[56] that used 1,140 bp sequence information of *Cytb* and 376 bp of the nuclear *PRM1* gene to infer the phylogeny and divergence times for the genus *Trachypithecus* in the subfamily Colubinae. To calibrate the phylogeny, we applied a secondary calibration point based on the study of He *et al.*[56] for the MRCA of Colobinae using a normal calibration density (mean = 12.28 Ma, SD = 1.74, 5–95% interquantile range = 9.4–15.1 Ma). Resulting mean substitution rates were 1.74% per Ma (95% CI = 1.17–2.36% per Ma) for *Cytb*, and 0.16% per Ma (95% CI = 0.05–0.35% per Ma) for *PRM1*. For the biogeographical inference, we used mainland Asia, India, and Africa as area coding.

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