**Supporting Information**

Table S1. Fossil sites/drill–well samples used in this study. See also Table S2. Ages are presented in the form: midpoint (minimum–maximum). Sources for age determinations are indicated by footnotes. Ages based on palynostratigraphy were based on regional stratigraphic schemes [1, 2]

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Site | Lat (°S) | Long (°E) | region | Site/core sample age | Age |
| Anglesea | 38.40 | 144.16 | Victoria | late Middle Eocene1 | 38.7 (38–39.4) |
| Ayers Rock Basin, RN10598 | 25.18 | 130.54 | Northern Territory | latest Maastrichtian2 | 67.0 (66.0–68.0) |
| Bell Bay | 41.15 | 146.85 | Tasmania | late Thanetian2 | 56.4 (55.8–57.0) |
| Berwick Quarry | 38.03 | 145.35 | Victoria | Late Oligocene–earliest Miocene3 | 23.7 (19.0–28.4) |
| Biloela Formation, Monto 5 | 24.04 | 150.29 | Queensland | Late Eocene4,5 | 39.5 (33.9–45.0) |
| Brooker Highway | 42.79 | 147.25 | Tasmania | Early Eocene6 | 51.9 (50.5–53.2) |
| Bundey Basin, Huckitta 11 | 22.76 | 135.15 | Northern Territory | late Campanian–early Maastrichtian7 | 70.8 (66.0–75.5) |
| Cethana | 41.48 | 146.14 | Tasmania | Early Oligocene8 | 31.2 (28.4–33.9) |
| Deans Marsh | 38.34 | 143.98 | Victoria | Early Eocene9 | 51.9 (50.5–53.2) |
| Eyre Formation, Peachawarinna 2 | 29.04 | 138.31 | South Australia | Early Eocene10 | 51.9 (50.5–53.2) |
| Eyre Formation, Skeleton 2 | 30.07 | 140.06 | South Australia | latest Paleocene–Early Eocene11 | 53.5 (54.3–57.0) |
| Foulden | 45.52 | 170.13 | New Zealand | Early Miocene12,13 | 22.5 (21.7–23.2) |
| Golden Fleece | 41.31 | 148.17 | Tasmania | late Oligocene–late Early Miocene2 | 25.3 (19.0–31.5) |
| Golden Grove | 34.79 | 138.73 | South Australia | Middle Eocene14 | 39.5 (38.5–40.5) |
| Hyde | 45.30 | 170.25 | New Zealand | Early Miocene2 | 17.5 (16.0–19.0) |
| Kiandra, Golden Crown | 36.00 | 148.43 | New South Wales | early Miocene15 | 13.2 (7.3–19.0) |
| Lake Bungarby | 36.68 | 149.01 | New South Wales | Late Paleocene16 | 56.4 (55.8–57.0) |
| Lea River | 41.51 | 145.99 | Tasmania | Early Oligocene17 | 31.2 (28.4–33.9) |
| Lefroy Palaeodrainage, CD2999 | 31.29 | 121.74 | Western Australia | Middle Eocene18 | 37.2 (33.9–40.4) |
| Lefroy Palaeodrainage, DWT495 | 31.20 | 122.02 | Western Australia | late Middle Eocene18 | 41.7 (38.4–45.0) |
| Lemonthyme | 41.62 | 146.15 | Tasmania | earliest Early Oligocene19 | 32.7 (31.5–33.9) |
| Leven River | 41.46 | 145.83 | Tasmania | Early Oligocene20 | 31.2 (28.4–33.9) |
| Little Bay | 33.98 | 151.25 | New South Wales | late Early–early Late Miocene21 | 13.8 (11.6–16.0) |
| Lowana Rd | 42.17 | 145.36 | Tasmania | Early Eocene22 | 51.9 (50.5–53.2) |
| Maslin Bay | 35.22 | 138.48 | South Australia | Middle Eocene14 | 39.5 (38.5–40.5) |
| Mt Hotham | 36.99 | 147.16 | Victoria | Early–Middle Eocene boundary2 | 47.8 (45.0–50.5) |
| Mulga Rocks, CD-1-1, CD-1-763 | 29.75 | 123.73 | Western Australia | Late Eocene26 | 39.5 (33.9–45.0) |
| Nelly Creek | 29.31 | 137.66 | South Australia | Middle Eocene23 | 43.0 (37.0–49.0) |
| Nerriga | 35.10 | 150.09 | New South Wales | early Middle Eocene24 | 44.5 (44.0–45.0) |
| New Norfolk | 42.73 | 146.95 | Tasmania | Oligocene19 | 28.5 (23.0–33.9) |
| Newvale | 46.15 | 168.75 | New Zealand | Late Oligocene–Early Miocene25 | 23.5 (21.7–25.2) |
| Wilson's Creek | 42.32 | 146.45 | Tasmania | latest Eocene–earliest Oligocene20 | 35.0 (31.5–38.4) |
| Yallourn Formation | 38.20 | 146.34 | Victoria | Middle Miocene27 | 15.4 (14.8–16.0) |

**Footnotes**

1 Christophel, Harris [3]

2 Details given in Table S3

3 Pole, Hill [4]

4 Foster and Harris [5]

5 Macphail [6]

6 Jordan, Carpenter [7]

7 Carpenter, Macphail [8]

8 Macphail, Alley [9]

9 Greenwood, Moss [10]

10 Sluiter [11]

11 Callen, Sheard [12]

12 Lindqvist and Lee [13]

13 Mildenhall, Kennedy [14]

14 Alley [15]

15 Owen [16]

16 Taylor, Truswell [17]

17 Hill and Scriven [18]

18 Carpenter and Pole [19]

19 Macphail, Colhoun [20]

20 Jordan and Hill [21]

21 Pickett, Macphail [22]

22 Carpenter, Jordan [23]

23 Alley, Krieg [24]

24 Hill [25]

25 Lee, Bannister [26]

26 Mack and Milne [27]

27 Holdgate, Cartwright [28]

Table S2. Fossil cuticles used in this study. Source publications for the fossils are given in superscript after the taxon identifier. See Table S1 for details on sites. The nearest living affinity is given to the narrowest taxonomic resolution.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Site** | **Taxon identifier** | **Nearest living affinity** | **Guard cell length****(μm)** | **Stomatal density (mm–2)** | **Pavement cell area (μm2)** | **Stomatal index** | **gs max****(mmol m–2s–1)** |
| Anglesea | ‘lobed Proteaceae’3 | Grevilleoideae (*Megahertzia*) | 24.2 | 355.0 | 272.3 | 10.9 | 0.0780 |
| Anglesea | Anglesea 12 | Proteaceae (probably Grevilleoideae) | 27.7 | 157.0 | 756.3 | 11.9 | 0.0395 |
| Anglesea | Anglesea 22 | Grevilleoideae (cf. *Athertonia*) | 17.9 | 267.0 | 750.8 | 17.7 | 0.0385 |
| Anglesea | Anglesea 32 | Proteaceae (probably Grevilleoideae) | 30.1 | 125.0 | 846.8 | 10.7 | 0.0342 |
| Anglesea | Anglesea 42 | Proteaceae (indet.) | 20.4 | 327.0 | 225.0 | 7.8 | 0.0606 |
| Anglesea | *Banksieaefolia cuneata*1 | Grevilleoideae (Banksieae) | 20.6 | 356.0 |  |  | 0.0666 |
| Ayers Rock Basin, RN10598 | Ayers Rock 12 | probably Grevilleoideae | 25.1 | 55.7 | 614.2 | 3.4 | 0.0353 |
| Ayers Rock Basin, RN10598 | Ayers Rock 22 | probably Proteoideae | 28.4 | 52.9 | 785.7 | 4.2 | 0.0385 |
| Bell Bay | Bell Bay 12 | probably Grevilleoideae | 26.3 | 274.0 | 409.0 | 12.1 | 0.0654 |
| Bell Bay | Bell Bay 22 | probably Grevilleoideae | 24.2 | 450.0 | 353.4 | 17.8 | 0.0989 |
| Bell Bay | Bell Bay 32 | probably Grevilleoideae | 26.2 | 178.0 | 487.3 | 9.0 | 0.0423 |
| Bell Bay | Bell Bay 42 | probably Grevilleoideae | 24.0 | 264.0 | 513.5 | 13.8 | 0.0575 |
| Berwick Quarry | Proteaceae gen. et sp. indet.4 | probably Grevilleoideae | 27.5 | 140.0 | 353.4 | 5.2 | 0.0349 |
| Biloela Formation | Biloela 12 | Proteaceae (probably Grevilleoideae) | 24.6 | 446.0 | 196.0 | 10.7 | 0.0996 |
| Brooker Highway | *Euproteaciphyllum brookerensis*5 | probably Grevilleoideae | 23.1 | 282.0 | 285.6 | 8.7 | 0.0591 |
| Brooker Highway | *E. tasmanicum*5 | probably Grevilleoideae | 21.6 | 316.0 | 388.1 | 12.6 | 0.0620 |
| Bundey Basin, Huckitta 11 | taxon 16 | Proteoideae (cf. *Conospermum*) | 18.2 | 214.0 | 412.1 | 8.7 | 0.0354 |
| Bundey Basin, Huckitta 11 | taxon 26 | Proteoideae (cf. *Stirlingia*) | 23.4 | 232.0 | 531.4 | 12.4 | 0.0493 |
| Bundey Basin, Huckitta 11 | taxon 46 | Proteoideae (cf. *Isopogon*) | 22.2 | 208.0 | 486.0 | 10.1 | 0.0419 |
| Bundey Basin, Huckitta 11 | taxon 56 | Proteaceae (?Proteoideae) | 26.1 | 288.0 | 614.5 | 18.0 | 0.0682 |
| Bundey Basin, Huckitta 11 | taxon 76 | Proteaceae (?Proteoideae) | 30.3 | 180.0 | 632.8 | 12.0 | 0.0495 |
| Bundey Basin, Huckitta 11 | taxon 86 | Grevilleoideae (cf. *Banksia*) | 29.4 | 128.0 | 582.3 | 7.7 | 0.0342 |
| Bundey Basin, Huckitta 11 | taxon 96 | Proteaceae (?Grevilleoideae) | 22.4 | 190.0 | 479.6 | 9.2 | 0.0386 |
| Bundey Basin, Huckitta 11 | taxon 106 | Proteaceae (probably Grevilleoideae) | 25.7 | 175.0 | 706.3 | 12.3 | 0.0408 |
| Bundey Basin, Huckitta 11 | taxon 116 | Proteaceae (?Grevilleoideae) | 27.4 | 200.0 | 814.1 | 16.1 | 0.0497 |
| Bundey Basin, Huckitta 11 | taxon 126 | Proteaceae (?Persoonieae) | 59.7 | 42.0 | 1877.4 | 8.5 | 0.0228 |
| Cethana | *Banksia linearis*1 | Grevilleoideae (*Banksia*) | 20.2 | 473.0 | 219.0 | 11.4 | 0.0867 |
| Cethana | *E. attenuatum*7 | Proteaceae (probably Grevilleoideae) | 37.7 |  |  |  |  |
| Cethana | *E. cethanicum*7 | Proteaceae (probably Grevilleoideae) | 45.3 | 116.0 | 864.4 | 11.6 | 0.0477 |
| Cethana | *E. gevuinoides*7 | Grevilleoideae (cf. Gevuininae) | 26.9 |  |  |  |  |
| Cethana | *E. integrifolium*7 | Proteaceae (probably Grevilleoideae) | 28.7 |  |  |  |  |
| Cethana | *E. linearis*7 | Proteaceae (probably Grevilleoideae) | 44.6 | 125.0 | 585.6 | 8.9 | 0.0506 |
| Cethana | *E. lomatioides*7 | Proteaceae (probably Grevilleoideae) | 35.2 | 132.0 | 309.8 | 4.7 | 0.0422 |
| Cethana | *E. microphyllum*7 | Proteaceae (probably Grevilleoideae) | 66.5 | 50.0 | 1030.4 | 6.2 | 0.0302 |
| Cethana | *E. ornamentalis*7 | Proteaceae (probably Grevilleoideae) | 39.0 | 136.0 | 285.6 | 4.7 | 0.0481 |
| Cethana | *E. rugulatum*7 | Proteaceae (probably Grevilleoideae) | 34.8 |  |  |  |  |
| Cethana | *E. tridacnoides*7 | Proteaceae (probably Grevilleoideae) | 25.0 | 246.0 | 259.2 | 7.0 | 0.0558 |
| Cethana | *Lomatia fraxinifolia*3 | Grevilleoideae (?crown *Lomatia*) | 28.3 | 264.0 | 497.3 | 14.3 | 0.0678 |
| Cethana | *L. xeromorpha*3 | Grevilleoideae (?crown *Lomatia*) | 32.6 | 149.0 | 416.2 | 6.9 | 0.0441 |
| Cethana | *Telopea truncata*3 | Grevilleoideae (crown *Telopea*) | 26.9 | 182.0 | 718.2 | 13.1 | 0.0444 |
| Deans Marsh | Museum Victoria cuticle slide P2465702 | Proteaceae (probably Grevilleoideae) | 25.8 | 210.0 | 624.0 | 13.2 | 0.0492 |
| Eyre Formation, Peachawarinna 2 | Peachawarinna 12 | Grevilleoideae (cf. *Gevuina*) | 15.6 | 380.0 | 338.6 | 12.4 | 0.0538 |
| Eyre Formation, Skeleton 2 | Skeleton 12 | Proteaceae (probably Grevilleoideae) | 23.0 | 356.0 | 275.6 | 10.8 | 0.0743 |
| Eyre Formation, Skeleton 2 | Skeleton 22 | Proteaceae (probably Grevilleoideae) | 23.0 | 121.0 | 979.7 | 11.2 | 0.0253 |
| Eyre Formation, Skeleton 2 | Skeleton 32 | Grevilleoideae (Banksieae) | 17.1 | 350.0 | 198.8 | 7.2 | 0.0543 |
| Eyre Formation, Skeleton 2 | Skeleton 42 | Proteaceae (probably Grevilleoideae) | 15.8 |  |  |  |  |
| Eyre Formation, Skeleton 2 | Skeleton 52 | Proteaceae (probably Grevilleoideae) | 17.7 |  |  |  |  |
| Foulden | *E. alloxylonoides*3 | Grevilleoideae (cf. *Alloxylon*) | 31.5 |  |  |  |  |
| Golden Fleece | Golden Fleece 12 | Proteaceae (probably Grevilleoideae) | 24.5 | 127.0 | 1047.0 | 12.6 | 0.0282 |
| Golden Fleece | *Orites excelsoides*3 | Grevilleoideae (*O. excelsa* R.Br.) | 19.3 | 228.0 | 375.0 | 8.5 | 0.0399 |
| Golden Grove | *Banksieaefolia cuneata*1 | Grevilleoideae (Banksieae) | 21.7 | 356.0 |  |  | 0.0701 |
| Golden Grove | leaf specimen GG27172 | Grevilleoideae | 21.6 | 351.0 | 364.8 | 13.3 | 0.0688 |
| Hyde | Hyde 12 | Proteaceae (probably Grevilleoideae) | 17.4 | 479.0 | 171.6 | 8.8 | 0.0757 |
| Kiandra, Golden Crown | Museum Victoria specimen 28/2/19542 | Proteaceae (probably Grevilleoideae) | 28.2 | 206.0 | 266.5 |  | 0.0527 |
| Lake Bungarby | *Banksia taylorii*1 | Grevilleoideae (*Banksia*) | 19.2 | 628.0 | 285.6 | 18.9 | 0.1094 |
| Lake Bungarby | leaf specimen LB0382 | Proteaceae (probably Grevilleoideae) | 24.8 | 361.0 | 275.6 | 11.3 | 0.0813 |
| Lake Bungarby | leaf specimen LB3022 | Proteaceae (probably Grevilleoideae) | 23.5 | 434.0 | 408.0 | 18.9 | 0.0926 |
| Lea River | *Orites milliganoides*3 | Grevilleoideae (*Orites milliganii*) | 54.3 | 57.0 | 278.9 | 1.9 | 0.0281 |
| Lea River | *O. scleromorpha*3 | Grevilleoideae (*Orites milliganii*) | 57.7 | 77.0 | 408.0 | 4.1 | 0.0403 |
| Lefroy Palaeodrainage, CD2999 | Banksieae (CUT-P-002)1 | Grevilleoideae (Banksieae) | 22.3 | 306.0 | 243.4 | 8.1 | 0.0619 |
| Lefroy Palaeodrainage, CD2999 | CUT–P–0063 | Proteaceae (probably Grevilleoideae) | 26.9 | 197.0 | 368.6 | 7.8 | 0.0481 |
| Lefroy Palaeodrainage, CD2999 | CUT–P–0078 | Proteaceae (probably Grevilleoideae) | 19.9 |  |  |  |  |
| Lefroy Palaeodrainage, CD2999 | CUT–P–0128 | Proteaceae (probably Grevilleoideae) | 25.2 | 178.0 | 590.5 | 10.6 | 0.0407 |
| Lefroy Palaeodrainage, CD2999 | *Darlingia* cf. *ferruginea* (CUT–P–001)3 | Grevilleoideae (cf. *Darlingia*) | 27.4 | 281.0 | 529.0 | 15.9 | 0.0699 |
| Lefroy Palaeodrainage, CD2999 | *Lomatia fraxinifolia* (CUT–P–005)8 | Proteaceae (probably Grevilleoideae) | 24.9 | 217.0 | 506.3 | 11.3 | 0.0490 |
| Lefroy Palaeodrainage, CD2999 | Gevuininae/*Hicksbeachia* (CUT–P–003)8 | Grevilleoideae (cf. Gevuininae/*Hicksbeachia*) | 23.9 | 121.0 | 1176.5 | 13.3 | 0.0263 |
| Lefroy Palaeodrainage, CD2999 | Lefroy new 12 | Grevilleoideae (cf. *Athertonia*) | 18.6 |  |  |  |  |
| Lefroy Palaeodrainage, CD2999 | Lefroy new 22 | Proteaceae (?Proteoideae) | 25.0 |  |  |  |  |
| Lefroy Palaeodrainage, CD2999 | Lefroy new 32 | Proteaceae (?Grevilleoideae) | 27.1 | 238.0 | 630.0 | 15.4 | 0.0585 |
| Lefroy Palaeodrainage, DWT495 | Proteaceae sp.8 | Proteaceae (indet.) | 23.7 | 141.0 | 272.3 | 4.0 | 0.0303 |
| Lemonthyme | *E. falcatum*5 | Proteaceae (probably Grevilleoideae) | 38.9 | 140.3 | 303.5 | 5.0 | 0.0495 |
| Lemonthyme | *E. microlobium*5 | Proteaceae (probably Grevilleoideae) | 39.1 | 109.6 | 778.2 | 9.3 | 0.0389 |
| Lemonthyme | *E. polymorphum*5 | Proteaceae (probably Grevilleoideae) | 35.6 | 182.4 | 382.1 | 8.1 | 0.0589 |
| Lemonthyme | *E. serratum*5 | Proteaceae (probably Grevilleoideae) | 48.0 | 94.7 | 835.9 | 9.2 | 0.0413 |
| Leven River | *O. excelsoides*3 | Grevilleoideae (*O. excelsa*) | 23.4 | 198.0 | 484.0 | 9.7 | 0.0421 |
| Little Bay | Little Bay 12 | Proteaceae (indet.) | 28.9 | 418.0 | 262.4 | 14.4 | 0.1097 |
| Lowana Rd | leaf specimen LR252 | Proteaceae (probably Grevilleoideae) | 24.0 | 198.0 | 823.7 | 15.5 | 0.0431 |
| Maslin Bay | Museum Victoria leaf specimen S31592 | Proteaceae (probably Grevilleoideae) | 30.5 | 32.0 | 547.6 | 1.8 | 0.0089 |
| Maslin Bay | Museum Victoria leaf specimens S1950, S25122 | Proteaceae (indet.) | 26.1 | 333.0 | 185.0 | 7.2 | 0.0759 |
| Maslin Bay | Museum Victoria leaf specimens S810, S8112 | Proteaceae (probably Grevilleoideae) | 39.8 | 112.0 | 676.0 | 8.4 | 0.0405 |
| Maslin Bay | *Parafatsia subpeltata*9 | Proteaceae (probably Grevilleoideae) | 21.0 | 307.0 |  |  | 0.0585 |
| Mt Hotham | Proteaceae sp. 1, Banksieae sp.10 | Grevilleoideae (?Banksieae) | 17.3 | 350.0 | 182.0 | 6.6 | 0.0550 |
| Mt Hotham | Proteaceae sp. 2, *Darlingia* sp.10 | Grevilleoideae | 20.9 | 289.0 | 253.0 | 7.7 | 0.0548 |
| Mt Hotham | Proteaceae sp. 7 10 | Grevilleoideae (cf. *Megahertzia*) | 31.1 | 194.0 | 525.0 | 11.1 | 0.0548 |
| Mulga Rocks, CD–1–1 | Mulga Rocks 12 | Proteaceae (?Proteoideae) | 27.9 | 72.0 | 751.4 | 5.1 | 0.0182 |
| Mulga Rocks, CD–1–763 | Mulga Rocks 22 | Proteaceae (probably Grevilleoideae) | 30.7 | 157.0 | 361.0 | 6.2 | 0.0438 |
| Mulga Rocks, CD–1–763 | Mulga Rocks 32 | Grevilleoideae (cf. *Darlingia*) | 26.7 | 528.0 | 380.3 | 24.4 | 0.1280 |
| Mulga Rocks, CD–1–763 | Mulga Rocks 42 | Proteaceae (probably Grevilleoideae) | 27.8 | 174.0 | 552.3 | 10.0 | 0.0439 |
| Mulga Rocks, CD–1–763 | Mulga Rocks 52 | Proteaceae (probably Grevilleoideae) | 26.6 | 70.0 | 1747.2 | 11.4 | 0.0169 |
| Mulga Rocks | Mulga Rocks 62 | Persoonioideae (Persoonieae) | 53.0 | 46.0 | 3047.0 | 13.9 | 0.0221 |
| Nelly Creek | Nelly 12 | Proteaceae (indet.) | 21.0 | 252.0 | 248.6 | 6.6 | 0.0480 |
| Nelly Creek | *Persoonieaephyllum blackburnii*14 | Persoonioideae (Persoonieae) | 63.2 | 41.0 | 3665.4 | 15.2 | 0.0235 |
| Nelly Creek | Nelly 32 | Proteaceae (probably Grevilleoideae) | 26.8 | 135.0 | 415.1 | 5.8 | 0.0328 |
| Nelly Creek | Nelly 42 | Grevilleoideae (cf. *Telopea*) | 26.2 | 235.0 | 380.9 | 9.6 | 0.0559 |
| Nelly Creek | Nelly 52 | Grevilleoideae (cf. *Darlingia*) | 29.0 | 99.0 | 1049.9 | 10.2 | 0.0261 |
| Nelly Creek | Parataxon 2 (Proteaceae)11 | Grevilleoideae | 22.9 |  |  |  |  |
| Nerriga | Nerriga 12 | Proteaceae (probably Grevilleoideae) | 21.8 |  |  |  |  |
| Nerriga | Nerriga 22 | Proteaceae (probably Grevilleoideae) | 22.8 |  |  |  |  |
| Nerriga | Nerriga 32 | Proteaceae (probably Grevilleoideae) | 23.1 |  |  |  |  |
| Nerriga | Nerriga 42 | Grevilleoideae (f. *Athertonia*) | 20.8 |  |  |  |  |
| Nerriga | Nerriga 52 | Grevilleoideae (cf. Gevuininae) | 17.6 | 388.0 | 334.9 | 12.9 | 0.0620 |
| New Norfolk | New Norfolk 12 | Proteaceae (probably Grevilleoideae) | 26.0 | 149.0 | 625.0 | 9.4 | 0.0352 |
| Newvale | *Banksia novae–zelandiae*12 | Grevilleoideae (*Banksia*) | 24.0 | 438.0 | 299.3 | 14.9 | 0.0954 |
| Newvale | cf. *Beauprea* sp. 3 | Proteoideae (probably *Beauprea*) | 32.3 | 136.0 | 625.0 | 9.0 | 0.0399 |
| Newvale | *E. amphistomaticum*3 | Proteoideae (cf. *Adenanthos*) | 33.4 | 153.0 | 552.3 | 9.2 | 0.0464 |
| Newvale | *E. pinnatum*3 | Proteaceae (indet.) | 23.3 | 277.0 | 392.0 | 11.3 | 0.0586 |
| Newvale | Newvale new 12 | Proteaceae (probably Grevilleoideae) | 50.4 | 79.0 | 1303.2 | 11.4 | 0.0361 |
| Newvale | Newvale new 22 | Proteaceae (probably Grevilleoideae) | 30.5 | 95.0 | 605.2 | 5.9 | 0.0263 |
| Newvale | Newvale new 32 | Proteaceae (probably Grevilleoideae) | 30.8 | 78.0 | 506.3 | 4.1 | 0.0218 |
| Newvale | *Persoonieaephyllum ornatum*13 | Persoonioideae (Persoonieae) | 53.7 | 37.0 | 4435.6 | 15.5 | 0.0180 |
| Newvale | *Persoonieaephyllum villosum*13 | Persoonioideae (Persoonieae) | 74.3 | 41.0 | 4462.2 | 19.1 | 0.0277 |
| Newvale | Proteaceae sp.3 | Proteaceae (probably Grevilleoideae) | 30.7 | 104.0 | 829.4 | 8.7 | 0.0290 |
| Wilson's Creek | leaf specimen WC252 | Proteaceae (probably Grevilleoideae) | 23.2 | 152.0 |  |  | 0.0320 |
| Wilson's Creek | leaf specimen WC3102 | Proteaceae (probably Grevilleoideae) | 28.2 | 152.0 | 497.3 | 7.9 | 0.0389 |
| Yallourn Formation | *Banksia cooksoniae*1 | Grevilleoideae (*Banksia*) | 22.7 | 467.0 | 320.4 | 16.5 | 0.0962 |
| Yallourn Formation | *Banksia laevis*1 | Grevilleoideae (*Banksia*) | 26.1 |   | 265.7 |  |  |

**Footnotes**

1 Carpenter, Jordan [29]

2 This study

3 Carpenter [30]

4 Pole, Hill [4]

5 Jordan, Carpenter [7]

6 Carpenter, Macphail [8]

7 Carpenter and Jordan [31]

8 Carpenter and Pole [19]

9 Carpenter, Hill [32]

10 Carpenter, Hill [33]

11 Christophel, Scriven [34]

12 Carpenter, Jordan [35]

13 Carpenter, Bannister [36]

14 Carpenter, Tarran [37]

Table S3. Justification of additional age determinations for fossil sites.

|  |  |
| --- | --- |
| **Site** | **Justification** |
| **Ayers Rock Basin, Northern Territory** | Core sample sediments from the Ayers Rock Basin included palynotaxa indicative of latest Cretaceous age [38]. Further study of these sediments (from borehole RN10598) yielded a date within the late Maastrichtian Upper *Forcipites longus* Zone Equivalent for the Gippsland Basin [39]. This date is based on the presence of *Quadraplanus brossus* and *Tricolporites lilliei* (which are diagnostic of the *Forcipites longus* Zone Equivalent time) and the presence of *Stereisporites* (al. *Tripunctisporis*) *maastrichtiensis*, which is indicative of the upper part of this zone. Information provided by consultant palynologist Michael Macphail. |
| **Bell Bay, Tasmania** | Samples at 285.8, 287 and 288.4 m depth are assigned to the Late Thanetian Upper *Lygistepollenites balmei* Zone Equivalent for the Gippsland Basin [39]. Important taxa characteristic of the *L. balmei* Zone include the nominate species, *Gambierina rudata*, *Propylipollis annularis*, *Tetracolporites textus* and *Peninsulapollis gillii*. There is also absence of indicator taxa for the overlying *Malvacipollis diversus* Zone. Information provided by consultant palynologist Michael Macphail. |
| **Golden Fleece, Tasmania** | Samples yielded moderately confident late Early Oligocene to late Early Miocene *Proteacidites tuberculatus* Zone Equivalent [39] microfloras. A minimum age of late Early Miocene is based on *Dryadopollis retequetrus* and *Proteacidites rectomarginis*, and a maximum age of Early Oligocene is based on *Cyatheacidites annulatus* and absence of *Granodiporites nebulosus*. Information provided by consultant palynologist Michael Macphail. |
| **Mt Hotham, Victoria** | There is uncertainty in dating this material. The published record [33] proposed an Early Eocene age, in part based on low incidences of *Nothofagus* pollen. However, the minimum age was not constrained by any indicator taxa, and a Late Eocene age, within the Middle *N. asperus* Zone has been proposed [40], although without detailed substantiation. Here, based on a new assessment of the sediment samples from which the fossils used in this paper were obtained, the flora is inferred to fall within the Middle to Late Eocene. A minimum age of Late Eocene is based on the last occurrences of *Proteacidites crassus*, *P. nasus* and *P. pachypolus* in the Gippsland Basin, and a maximum age of Middle Eocene *Proteacidites asperopolus* Zone Equivalent is based on a *Myrtaceidites* specimen resembling *Myrtaceidites tenuis* [39]. Information provided by consultant palynologist Michael Macphail. |
| **Hyde, New Zealand** | The samples from Hyde are Early Miocene in age based on a number of taxa not known to be older than Otaian or younger than Lilburnian on the New Zealand Geological Timescale [41]. Key taxa include *Ilexpollenites anguloclavatus,* *Anisotricolporites truncatus*, *Rhoipites titokioides, Tricolpites patulus* and especially *Nuxpollenites varicosus* [42]. Information provided by consultant palynologist Dallas Mildenhall. |

Table S4. Data of epidermal characteristics from extant Proteaceae species in this study. The terminal represents which tip of the phylogeny to which the species was allocated.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Terminal** | **Species** | **Guard cell length** **(mm)** | **Stomatal density (mm–2)** | **Stomatal index**  | **Pavement cell area (μm2)** |
| *Acidonia* | *Acidonia microcarpa* | 16.00 | 98.44 | 16.60 | 10512.6 |
| *Adenanthos* | *Adenanthos sericeus* | 10.81 | 31.72 | 87.38 | 1269.0 |
| *Agastachys* | *Agastachys odorata* | 6.85 | 61.89 | 46.14 | 1594.0 |
| *Alloxylon* | *Alloxylon flammeum* | 12.88 | 29.30 | 170.03 | 946.1 |
| *Alloxylon* | *Alloxylon pinnatum* | 11.16 | 46.32 | 98.20 | 1278.7 |
| *Athertonia* | *Athertonia diversifolia* | 16.84 | 22.01 | 266.85 | 579.0 |
| *Aulax* | *Aulax cancellata* | 15.44 | 46.79 | 53.60 | 2645.5 |
| *Austromuellera* | *Austromuellera trinervia* | 14.37 | 22.03 | 520.87 | 281.4 |
| *Banksia* | *Banksia grandis* | 6.43 | 30.05 | 170.03 | 327.3 |
| *Beauprea* | *Beauprea montana* | 21.98 | 29.59 | 250.85 | 873.0 |
| *Beaupreopsis* | *Beaupreopsis paniculata* | 22.27 | 30.82 | 219.62 | 1031.9 |
| *Bellendena* | *Bellendena montana* | 12.73 | 43.33 | 127.52 | 900.8 |
| *Bleasdalea* | *Bleasdalea bleasdalei* | 17.90 | 25.74 | 224.35 | 1348.9 |
| *Brabejum* | *Brabejum stellatifolium* | 12.38 | 29.57 | 278.66 | 508.4 |
| *Buckinghamia* | *Buckinghamia celsissima* | 16.51 | 23.47 | 311.72 | 634.2 |
| *Buckinghamia* | *Buckinghamia ferruginiflora* | 14.35 | 25.30 | 299.91 | 563.3 |
| *Cardwellia* | *Cardwellia sublimis* | 8.36 | 25.80 | 247.96 | 408.8 |
| *Carnarvonia* | *Carnarvonia araliifolia* | 15.95 | 38.79 | 144.53 | 963.6 |
| *Catalepidia* | *Catalepidia heyana* | 18.63 | 24.71 | 340.06 | 612.5 |
| *Cenarrhenes* | *Cenarrhenes nitida* | 11.35 | 33.90 | 210.18 | 609.1 |
| *Conospermum* | *Conospermum longifolium* | 29.13 | 30.02 | 292.23 | 1406.4 |
| *Conospermum* | *Conospermum taxifolium* | 15.22 | 35.68 | 93.61 | 1234.8 |
| *Darlingia* | *Darlingia darlingiana* | 10.65 | 35.49 | 126.89 | 569.8 |
| *Darlingia* | *Darlingia ferruginea* | 10.44 | 37.08 | 177.11 | 657.9 |
| *Eidothea* | *Eidothea hardeniana* | 11.73 | 31.94 | 158.99 | 775.1 |
| *Eidothea* | *Eidothea zoexylocarya* | 8.80 | 27.90 | 121.85 | 605.4 |
| *Embothrium* | *Embothrium coccineum* | 11.55 | 30.67 | 160.58 | 806.1 |
| *Floydia* | *Floydia praealta* | 9.28 | 25.93 | 325.89 | 313.8 |
| *Franklandia* | *Franklandia fucifolia* | 9.70 | 50.89 | 90.51 | 908.2 |
| *Garnieria* | *Garnieria spathuliifolia* | 9.89 | 61.60 | 45.55 | 2003.2 |
| *Gevuina* | *Gevuina avellana* | 8.37 | 32.33 | 128.94 | 730.7 |
| *Grevillea* | *Grevillea australis* | 16.31 | 28.62 | 304.64 | 639.8 |
| *Grevillea* | *Grevillea hilliana* | 9.42 | 26.13 | 245.60 | 352.4 |
| *Hakea* | *Hakea lissosperma* | 4.95 | 42.44 | 65.07 | 376.8 |
| *Hakea* | *Hakea salicifolia* | 10.78 | 40.60 | 71.58 | 1368.9 |
| *Helicia* | *Helicia australasica* | 10.77 | 28.64 | 231.43 | 521.5 |
| *Helicia* | *Helicia cochinchinensis* | 15.66 | 27.30 | 155.86 | 822.1 |
| *Helicia* | *Helicia nortoniana* | 15.33 | 24.82 | 278.66 | 666.1 |
| *Hicksbeachia* | *Hicksbeachia pilosa* | 15.72 | 30.22 | 106.48 | 1752.3 |
| *Hicksbeachia* | *Hicksbeachia pinnatifolia* | 16.05 | 34.01 | 101.16 | 1889.7 |
| *Hollandaea* | *Hollandaea riparia* | 12.68 | 33.92 | 189.89 | 629.5 |
| *Hollandaea* | *Hollandaea sayeriana* | 12.88 | 27.12 | 188.92 | 782.9 |
| *Isopogon* | *Isopogon ceratophyllus* | 13.99 | 31.41 | 131.33 | 929.5 |
| *Isopogon* | *Isopogon cuneatus* | 16.68 | 35.82 | 169.48 | 1045.0 |
| *Isopogon* | *Isopogon fletcheri* | 19.44 | 41.32 | 108.61 | 1809.4 |
| *Knightia* | *Knightia excelsa* | 12.00 | 29.72 | 154.40 | 640.3 |
| *Lambertia* | *Lambertia formosa* | 22.74 | 35.24 | 233.79 | 717.9 |
| *Lambertia* | *Lambertia inermis* | 9.31 | 40.86 | 95.64 | 828.9 |
| *Lasjia* | *Lasjia grandis* | 9.48 | 27.04 | 143.75 | 580.8 |
| *Lasjia* | *Lasjia whelanii* | 22.34 | 24.61 | 358.95 | 801.2 |
| *Leucadendron* | *Leucadendron pubescens* | 11.04 | 31.35 | 130.14 | 953.5 |
| *Leucadendron* | *Leucadendron salignum* | 21.03 | 31.57 | 105.59 | 2255.0 |
| *Leucospermum* | *Leucospermum cordifolium* | 17.66 | 40.48 | 102.93 | 1732.8 |
| *Lomatia* | *Lomatia fraxinifolia* | 23.94 | 28.40 | 181.02 | 1448.7 |
| *Lomatia* | *Lomatia polymorpha* | 6.41 | 31.79 | 152.32 | 449.6 |
| *Lomatia* | *Lomatia tinctoria* | 12.51 | 27.99 | 160.58 | 890.7 |
| *Macadamia* | *Macadamia integrifolia* | 7.01 | 25.62 | 227.88 | 422.7 |
| *Megahertzia* | *Megahertzia amplexicaulis* | 9.64 | 24.37 | 302.87 | 289.1 |
| *Musgravea* | *Musgravea heterophylla* | 10.40 | 20.56 | 443.97 | 261.3 |
| *Musgravea* | *Musgravea stenostachya* | 15.49 | 22.50 | 542.60 | 245.2 |
| *Neorites* | *Neorites kevedianus* | 8.28 | 33.48 | 196.01 | 460.6 |
| *Nothorites* | *Nothorites megacarpus* | 22.37 | 29.08 | 406.30 | 465.7 |
| *Opisthiolepis* | *Opisthiolepis heterophylla* | 11.87 | 21.69 | 250.32 | 539.3 |
| *Oreocallis* | *Oreocallis mucronata* | 9.08 | 29.20 | 177.11 | 478.9 |
| *Orites* | *Orites acicularis* | 1.89 | 55.57 | 59.01 | 325.6 |
| *Orites* | *Orites diversifolius* | 8.93 | 24.27 | 304.64 | 321.9 |
| *Orites* | *Orites excelsus* | 17.08 | 24.74 | 292.83 | 630.4 |
| *Orites* | *Orites milliganii* | 4.16 | 52.85 | 95.83 | 453.5 |
| *Panopsis* | *Panopsis metcalfi* | 7.60 | 29.60 | 302.08 | 200.2 |
| *Persoonia* | *Persoonia gunnii* | 7.77 | 69.01 | 18.25 | 4542.1 |
| *Persoonia* | *Persoonia lanceolata* | 19.17 | 79.67 | 26.70 | 7378.4 |
| *Persoonia* | *Persoonia laurina* | 17.79 | 60.51 | 36.45 | 3643.5 |
| *Persoonia* | *Persoonia linifolia* | 14.05 | 56.87 | 58.56 | 2447.8 |
| *Persoonia* | *Persoonia muelleri* | 10.87 | 67.73 | 27.33 | 3901.0 |
| *Petrophile* | *Petrophile shirleyae* | 13.96 | 39.21 | 107.66 | 1128.3 |
| *Placospermum* | *Placospermum coriaceum* | 22.55 | 66.51 | 43.18 | 6743.5 |
| *Protea* | *Protea cynaroides* | 10.96 | 74.40 | 33.42 | 3681.0 |
| *Protea1* | *Protea gaguedii* | 11.70 | 38.61 | 120.68 | 1118.5 |
| *Protea1* | *Protea neriifolia* | 7.82 | 65.62 | 36.38 | 1997.5 |
| *Protea1* | *Protea nitida* | 9.42 | 38.92 | 124.00 | 839.0 |
| *Roupala* | *Roupala pseudocordata* | 7.61 | 38.65 | 131.33 | 298.8 |
| *Sphalmium* | *Sphalmium racemosum* | 16.40 | 43.68 | 129.60 | 1394.9 |
| *Stenocarpus* | *Stenocarpus sinuatus* | 9.76 | 31.73 | 196.01 | 552.8 |
| *Stenocarpus* | *Stenocarpus verticis* | 12.34 | 35.88 | 229.82 | 437.6 |
| *Stirlingia* | *Stirlingia latifolia* | 12.35 | 31.73 | 119.50 | 1025.6 |
| *Strangea* | *Strangea linearis* | 13.47 | 55.85 | 57.38 | 2333.0 |
| *Strangea* | *Strangea stenocarpoides* | 11.62 | 61.89 | 43.94 | 2488.6 |
| *Symphionema* | *Symphionema montanum* | 24.12 | 41.32 | 196.10 | 1145.6 |
| *Symphionema* | *Symphionema paludosum* | 23.96 | 44.58 | 89.62 | 2445.1 |
| *Synaphea* | *Synaphea petiolaris* | 8.69 | 45.87 | 47.92 | 1985.9 |
| *Synaphea* | *Synaphea pinnata* | 13.88 | 26.83 | 204.92 | 670.2 |
| *Telopea* | *Telopea speciossisima* | 23.05 | 36.95 | 170.03 | 1249.9 |
| *Telopea* | *Telopea truncata* | 5.43 | 27.79 | 128.96 | 444.9 |
| *Toronia* | *Toronia toru* | 13.40 | 74.11 | 32.56 | 4752.5 |
| *Triunia* | *Triunia montana* | 11.53 | 33.12 | 137.44 | 948.4 |
| *Triunia* | *Triunia youngiana* | 13.79 | 32.42 | 235.56 | 637.5 |
| *Virotia* | *Virotia leptophylla* | 15.99 | 27.68 | 330.61 | 435.0 |
| *Xylomelum* | *Xylomelum occidentalis* | 4.15 | 42.02 | 68.05 | 559.8 |
| *Xylomelum* | *Xylomelum pyriforme* | 9.91 | 34.70 | 226.71 | 485.1 |
| *Xylomelum* | *Xylomelum salicinum* | 14.32 | 35.94 | 214.63 | 496.5 |
| *Mimetes* | *Mimetes saxatilis* | 9.02 | 39.07 | 57.70 | 1567.3 |
| *Spatalla* | *Spatalla confusa* | 9.95 | 36.57 | 63.60 | 1588.7 |
| *Dilobeia* | *Dilobeia thouarsii* | 15.90 | 27.10 | 222.52 | 710.6 |
| *Eucarpha* | *Eucarpha deplanchei* | 14.95 | 32.02 | 222.52 | 609.5 |
| *Eucarpha* | *Eucarpha strobilina* | 24.22 | 36.01 | 311.53 | 618.9 |
| *Faurea* | *Faurea arborea* | 9.35 | 35.53 | 133.51 | 642.2 |
| *Faurea* | *Faurea delavoyi* | 15.16 | 33.59 | 169.93 | 850.1 |
| *Heliciopsis* | *Heliciopsis terminalis* | 10.46 | 22.63 | 165.88 | 644.4 |
| *Serruria* | *Serruria adscendens* | 12.46 | 35.64 | 94.09 | 1332.3 |

Table S5. Epidermal characteristics considered.

|  |  |  |  |
| --- | --- | --- | --- |
| **Trait** | **definition** | **trans–formation** | **how measured** |
| guard cell length |  | log | ≥ 30 stomata, sampled from multiple regions of cuticle where possible |
| stomatal density | n(stomata) mm–2 | log | counts from at four fields of view, totalling at least 100 stomata. For fragmentary fossil cuticles, incomplete fields of view were sometimes used. |
| pavement cell area | mm2 | log | total area divided by total number of pavement cells, for at least four regions of cuticle with no stomata |
| stomatal index | 100 \* n(stomata)/(n(stomata) + n(epidermal cells)) | none | counts from areas measured for stomatal density |
| maximum stomatal conductance (gs max) |  | log | based on Parlange and Waggoner [43]. See methods for details. |

Table S6. Comparison of traits simulated by fasttree and rTrait under Ornstein-Uhlenbeck (OU) models with parameters equivalent to the five traits investigated here (Table S5) on trees simulated under a range of relative extinction rate (μ/λ). The OU trait parameters for these simulated were then estimated using phylolm. The table presents the percentage differences between the estimated parameters simulated by fasttree and those simulated using rTrait, and also the percentage errors in those estimates (i.e. estimated value versus true value). Note, the estimated values of σ and α differed by less than 0.5%.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **True σ** | **True α** | **μ/λ** | **Difference in estimates** |  | **Error in σ** | **Error in α** |
|  |  |  | **σ** | **α** | **fasttree** | **rTrait** | **fasttree** | **rTrait** |
| 0.382 | 0.073 | 0.909 | 0.01% | 0.30% | 0.13% | 0.15% | 1.40% | 1.70% |
|  |  | 0.667 | 0.00% | 0.04% | 0.17% | 0.17% | 0.98% | 1.02% |
|  |  | 0.5 | 0.02% | -0.02% | 0.20% | 0.23% | 1.09% | 1.08% |
|  |  | 0.2 | 0.01% | -0.25% | 0.16% | 0.17% | 0.98% | 0.73% |
|  |  | 0.1 | 0.07% | 0.15% | 0.16% | 0.22% | 0.79% | 0.94% |
|  |  | 0.05 | -0.03% | -0.14% | 0.28% | 0.25% | 1.13% | 0.99% |
|  |  | 0.02 | 0.08% | -0.09% | 0.16% | 0.23% | 0.97% | 0.87% |
|  |  | 0.01 | -0.01% | 0.00% | 0.23% | 0.21% | 0.92% | 0.92% |
| 0.370 | 0.070 | 0.909 | 0.02% | 0.34% | 0.13% | 0.15% | 1.45% | 1.79% |
|  |  | 0.667 | 0.00% | 0.04% | 0.17% | 0.18% | 1.03% | 1.07% |
|  |  | 0.5 | 0.02% | 0.00% | 0.21% | 0.23% | 1.13% | 1.12% |
|  |  | 0.2 | 0.01% | -0.26% | 0.16% | 0.18% | 1.02% | 0.76% |
|  |  | 0.1 | 0.07% | 0.16% | 0.16% | 0.23% | 0.82% | 0.98% |
|  |  | 0.05 | -0.03% | -0.16% | 0.28% | 0.25% | 1.18% | 1.02% |
|  |  | 0.02 | 0.08% | -0.09% | 0.16% | 0.24% | 0.99% | 0.90% |
|  |  | 0.01 | -0.01% | 0.01% | 0.23% | 0.22% | 0.94% | 0.95% |
| 0.579 | 0.169 | 0.909 | -0.03% | -0.08% | 0.14% | 0.11% | 0.96% | 0.88% |
|  |  | 0.667 | 0.02% | 0.11% | 0.12% | 0.14% | 0.53% | 0.64% |
|  |  | 0.5 | 0.04% | 0.03% | 0.17% | 0.20% | 0.70% | 0.73% |
|  |  | 0.2 | 0.07% | -0.03% | 0.08% | 0.15% | 0.59% | 0.56% |
|  |  | 0.1 | 0.14% | 0.27% | 0.05% | 0.19% | 0.44% | 0.71% |
|  |  | 0.05 | 0.05% | 0.11% | 0.20% | 0.25% | 0.72% | 0.84% |
|  |  | 0.02 | 0.12% | -0.02% | 0.09% | 0.21% | 0.70% | 0.68% |
|  |  | 0.01 | -0.06% | -0.11% | 0.27% | 0.21% | 0.90% | 0.79% |
| 0.451 | 0.104 | 0.909 | -0.01% | 0.06% | 0.13% | 0.12% | 1.16% | 1.22% |
|  |  | 0.667 | 0.01% | 0.09% | 0.14% | 0.15% | 0.69% | 0.78% |
|  |  | 0.5 | 0.01% | -0.05% | 0.19% | 0.21% | 0.91% | 0.86% |
|  |  | 0.2 | 0.02% | -0.18% | 0.13% | 0.16% | 0.80% | 0.61% |
|  |  | 0.1 | 0.08% | 0.14% | 0.12% | 0.20% | 0.65% | 0.79% |
|  |  | 0.05 | 0.00% | -0.03% | 0.23% | 0.23% | 0.87% | 0.84% |
|  |  | 0.02 | 0.09% | -0.09% | 0.13% | 0.22% | 0.83% | 0.75% |
|  |  | 0.01 | -0.03% | -0.06% | 0.23% | 0.20% | 0.85% | 0.79% |
| 0.812 | 0.330 | 0.909 | -0.06% | -0.17% | 0.16% | 0.10% | 0.80% | 0.63% |
|  |  | 0.667 | 0.02% | 0.07% | 0.14% | 0.15% | 0.56% | 0.63% |
|  |  | 0.5 | 0.03% | 0.00% | 0.22% | 0.25% | 0.80% | 0.80% |
|  |  | 0.2 | 0.17% | 0.23% | 0.01% | 0.19% | 0.44% | 0.68% |
|  |  | 0.1 | 0.21% | 0.37% | 0.03% | 0.24% | 0.47% | 0.85% |
|  |  | 0.05 | 0.18% | 0.44% | 0.20% | 0.39% | 0.77% | 1.21% |
|  |  | 0.02 | 0.06% | -0.18% | 0.17% | 0.23% | 0.97% | 0.79% |
|  |  | 0.01 | -0.04% | -0.02% | 0.31% | 0.27% | 0.98% | 0.96% |

Table S7. Pearson’s product–moment correlation coefficients between epidermal traits and paleoenvironmental variables, with simulation–based probabilities of tests of difference from zero in parentheses and probabilities not allowing for phylogeny in square brackets.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Deep ocean temperature; n=104** 1 | **CO2; n=104** 2 | **CO2; n=60** 3 |
| Log of guard cell length | **–0.50 (*P* < 0.01)** [<< 0.001] | –0.20 (*P* > 0.05)[<0.05] | –0.42 (*P* > 0.05)[<0.01] |
| Log of pavement cell area | –0.13 (*P* > 0.05) [0.18] | –0.04 (*P* > 0.05)[0.69] | –0.07 (*P* > 0.05)[0.64] |
| Log of stomatal density | **0.33 (*P* < 0.05)**[<0.001] | 0.02 (*P* > 0.05)[0.84] | 0.22 (*P* > 0.05)[0.13] |
| Stomatal index | 0.22 (*P* > 0.05)[<0.05] | –0.14 (*P* > 0.05)[0.15] | 0.20 (*P* > 0.05)[0.17] |
| Log of gs max | 0.17 (*P* > 0.05)[0.08] | –0.07 (*P* > 0.05)[0.63] | 0.08 (*P* > 0.05)[0.59] |

Footnotes

1 Hansen, Sato [44]

2 Beerling and Royer [45]

3 Anagnostou, John [46]

Table S8. AICc scores for alternative models predicting fossil epidermal traits in Proteaceae from palaeo-environmental estimates, with lowest (best) values in bold text. The best model (i.e. lowest AICc) is shown in bold. The best model for log of guard cell length was log guard cell length = 1.3 - 0.0254\*temperature + 0.00035\*CO2 (Beerling) (multiple r2 = 0.28). The best model for log of stomatal density was log of stomatal density = 1.972 + 0.00035\* CO2 (Anagnostou) (multiple r2 = 0.06).

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| model | null | temperature | CO2 (Anagnostou) | CO2 (Beerling) | temperature + CO2 (Anagnostou) | temperature + CO2 (Beerling) | CO2 (Anagnostou) + CO2 (Beerling) | temperature + CO2 (Anagnostou) + CO2 (Beerling) |
| log of guard cell length | -58.8 | -67.7 | -64.6 | -57.1 | -65.8 | **-68.9** | -62.6 | -66.4 |
| stomatal index | **261.1** | 263.2 | 261.6 | 261.6 | 263.5 | 263.2 | 262.4 | 264.9 |
| log of stomatal density | 16.3 | 15.6 | **15.5** | 17.7 | 17.5 | 15.9 | 17.3 | 18.4 |
| log of pavement cell area | **21.3** | 22.6 | 23.4 | 23.6 | 24.8 | 25.0 | 25.7 | 27.3 |
| gs max | **-9.8** | -7.7 | -8.0 | -8.1 | -5.6 | -6.0 | -6.1 | -3.6 |

Table S9. Code for running simulations and analysing them

1. Introduction

This code is broken into five sections.

The first (section 2 of this table) is r code (e.g. <https://cran.r-project.org/bin/windows/base/>) that runs the simulations. To do this you will need to access the fasttree function, which is currently available within the fasttree2019 package on GitHub (<https://github.com/MichaelWoodhams/stomata>), but is in process of being incorporated into the TreeSim package [47].

The second component (section 3 of this table) is Perl code that compiles the output of the simulations into a single large file

The third component (section 4 of this table) is r code that reads the compiled simulations data and calculates probabilities from them.

The fourth component (section 5 of this table) is r code for simulating traits under both fasttree and rTrait on trees simulated by fasttree under a range of conditions.

The fifth component (section 6 of this table) is r code for summarising the results from section 5.

1. r code for running simulations

library(ape)

library(TreeSim)

library(fasttree2019) #note, this package will be incorporated into the TreeSim package.

measure.stats <- read.csv("OU\_parameters\_full\_data.csv")

measurement.names <- substr(measure.stats[seq(2,10,2),1],7,100) # "GCL" "SI" "SD" "EA" "Gsmax"

measurement.sigma <- sqrt(measure.stats[seq(1,9,2),"mean"])

measurement.alpha <- measure.stats[seq(2,10,2),"mean"]

args <- commandArgs(trailingOnly = TRUE)

if (length(args)==0) {

 print("No command line args - using debugging defaults")

 args <- c("GCL",1.5,1,10)

}

measure\_name <- args[[1]]

measurement <- which(measure\_name==measurement.names)

if (length(measurement)!=1) {

 stop(paste(c("First arg must be one of",measurement.names)))

}

bdratio <- as.numeric(args[[2]])

REPS = 10000

REP.START = 1

climate = as.numeric(args[[3]])

if (! climate %in% 1:6) {

 stop(paste(c("Climate must be in 1:6",climate)))

}

if (length(args)>=4) {

 REPS=as.numeric(args[[4]])

}

if (length(args)>=5) {

 REP.START=as.numeric(args[[5]])

}

sigma <- measurement.sigma[measurement]

alpha <- measurement.alpha[measurement]

root.value = 0 #starting value for the trait arbitrarily set to zero

numtips = 1700 #this is set to match what is known about Proteaceae

data = read.csv('zachos\_correl\_and\_calc\_gsmax1.csv')

clim.vec = data[,c(3:6, 5:6)[climate]]

ages = data[,2]

if (climate <= 4)

{

 keep = which(!is.na(clim.vec) & data$delete == 0)

} else {

 keep = which(!is.na(clim.vec))

}

clim.vec = clim.vec[keep]

ages = ages[keep]

#real sample times (assume sorted)

tab = table(ages)

fossil.ages <- as.numeric(rownames(tab)) #c(15, 18, 20, 24, 30, 32, 33, 34, 40, 43, 45, 47, 49, 50, 51, 56)

fossil.ages <- 93 - sort(fossil.ages, decreasing=TRUE)

numSamplePoints = length(fossil.ages)

#number of fossils at each time point

numfossils = as.integer(tab) #c(2, 2, 2, 13, 1 , 17, 4, 2, 20, 7, 13, 5, 4, 3, 2, 12)

numfossils <- numfossils[length(numfossils):1]

print(sprintf("Simulating measurement %s with sigma=%f, alpha=%f. BD ratio=%f, climate=%d, reps %d..%d",

 measure\_name,sigma,alpha,bdratio,climate,REP.START,REPS))

print("Fossil sample times:")

print(fossil.ages)

 print(sprintf("BD ratio=%f, sigma=%f, alpha=%f",bdratio,sigma,alpha))

 rand.correlations = matrix(0, REPS, 5)

 rand.sds = matrix(0, REPS, 5)

 rand.sigma2 = numeric(REPS)

 rand.ace.sigma2 = numeric(REPS)

 rand.ace.se = numeric(REPS)

 tree.depth = numeric(REPS)

 for (reps in REP.START:REPS){

 # RNG is used for initial trait value, and for sampling from fossil trait values

 # at a given fossil age.

 set.seed(reps+100\*bdratio+10000\*alpha)

 if (reps%%100 == 0) print(reps)

 if (alpha!=0) {

 # For OU process, equilibrium distribution of trait is Gaussian with mean 0 and variance sigma^2/(2 alpha)

 startTrait = rnorm(1,mean=0,sd=sigma/sqrt(2\*alpha))

 } else {

 # alpha=0 is Brownian motion case for trait. There is no equilibrium distribution.

 startTrait = 0

 }

 #print(reps)

 res = fasttree(n = numtips, lambda = bdratio, mu = 1, alpha = alpha, frac = 1,

 sigma = sigma, sampleTimes = fossil.ages / 93, traits = TRUE, seed=reps)

 # output names: tree, samples, n.leaves, sampleTimes

 tree.depth[reps] <- max(node.depth.edgelength(res$tree))

 node.trait = numeric(max(res$tree$edge[,2]))

 node.trait[res$tree$edge[,2]] = res$tree$edge.trait

 for (j in 1:5) # different data

 {

 data.vec = data[keep, 10 + j]

 ij = which(!is.na(data.vec))

 #real sample times (assume sorted)

 tab = table(ages[ij])

 # assume fossil ages will be the same!!!

 # fossil.ages <- as.numeric(rownames(tab)) #c(15, 18, 20, 24, 30, 32, 33, 34, 40, 43, 45, 47, 49, 50, 51, 56)

 #fossil.ages <- 93 - sort(fossil.ages, decreasing=TRUE)

 #numSamplePoints = length(fossil.ages)

 #number of fossils at each time point

 numfossils = as.integer(tab) #c(2, 2, 2, 13, 1 , 17, 4, 2, 20, 7, 13, 5, 4, 3, 2, 12)

 numfossils <- numfossils[length(numfossils):1]

 #set up a list of lists to store the samples in

 df <- NULL #this data frame will store samples ages and trait values

 for (i in 1:numSamplePoints) {

 theseSamples <- res$samples[1:res$n.leaves[i], i] #all the species at this time slice

 theseFossils <- sample(theseSamples, numfossils[i], replace=TRUE) #replacement or not?

 df <- rbind(df, cbind(theseFossils, res$sampleTimes[i]))

 }

 #data frame containing the correlation between random values and zachos

 #each row corresponds to an individual sample

 rand.correlations[reps, j] = cor(df[ ,1], clim.vec[ij])

 rand.sds[reps, j] = sd(df[,1])

 # normalised sigma = tree length / sd@tips

 # scale = max(node.depth.edgelength(res$tree))/sd(node.trait[1:numtips])^2

 # rand.sigma2[reps] = scale

 }

 # TRIM TREE FOR ASR

 res$tree$node.label = paste('n', 1:res$tree$Nnode, sep='')

 drop = (numtips+1):length(res$tree$tip.label)

 old.edge.label = c(res$tree$tip.label, res$tree$node.label)

 old.edge.label = old.edge.label[res$tree$edge[,2]]

 bush = drop.tip(res$tree, drop)

 new.edge.label = c(bush$tip.label, bush$node.label)

 new.edge.label = new.edge.label[bush$edge[,2]]

 all(old.edge.label[old.edge.label %in% new.edge.label] == new.edge.label)

 bush$edge.trait = res$tree$edge.trait[which(old.edge.label %in% new.edge.label)]

 ltt = ltt.plot.coords(bush, backward = FALSE)

 ii = min(which(ltt[,2] == 71))

 #plot(bush, show.tip.label = FALSE); axis(1); abline(v = ltt[ii,1], lty=2, col='grey')

 babies = phytools::treeSlice(bush, slice = mean(ltt[(ii-1):ii,1]), trivial = TRUE)

 tokill = NULL

 for (i in 1:71)

 tokill = c(tokill, setdiff(babies[[i]]$tip.label, sample(babies[[i]]$tip.label, 1)))

 old.edge.label = new.edge.label

 old.edge.trait = bush$edge.trait

 bush = drop.tip(bush, tokill)

 new.edge.label = c(bush$tip.label, bush$node.label)

 new.edge.label = new.edge.label[bush$edge[,2]]

 all(old.edge.label[old.edge.label %in% new.edge.label] == new.edge.label)

 bush$edge.trait = old.edge.trait[which(old.edge.label %in% new.edge.label)]

 node.trait = numeric(max(bush$edge[,2]))

 node.trait[bush$edge[,2]] = bush$edge.trait

 asr = ace(node.trait[1:(bush$Nnode+1)], bush, type="continuous")

 # normalised sigma = tree length / sd@tips

 scale = max(node.depth.edgelength(res$tree))/sd(node.trait[1:71])^2

 rand.sigma2[reps] = sigma \* scale

 rand.ace.sigma2[reps] = asr$sigma2[1] \* scale

 rand.ace.se[reps] = asr$sigma2[2] \* scale

 }

 results <- data.frame(rep=1:reps,

 depth=tree.depth,

 rand.corr1 = rand.correlations[,1],

 rand.corr2 = rand.correlations[,2],

 rand.corr3 = rand.correlations[,3],

 rand.corr4 = rand.correlations[,4],

 rand.corr5 = rand.correlations[,5],

 rand.sd1 = rand.sds[,1],

 rand.sd2 = rand.sds[,2],

 rand.sd3 = rand.sds[,3],

 rand.sd4 = rand.sds[,4],

 rand.sd5 = rand.sds[,5],

 rand.sigma2 = rand.sigma2,

 rand.ace.sigma2 = rand.ace.sigma2,

 rand.ace.se = rand.ace.se)

 filename = paste("results/results", measure\_name, bdratio ,REPS, "climate", climate, ".txt", sep="\_")

 write.table(results, file = filename, quote=FALSE, row.names=FALSE)

# }

#}

1. Perl code for compiling output files. If needed, install Perl (e.g. https://www.perl.org/get.html).

#!/usr/bin/env perl

use strict;

use warnings;

# This is a post-hoc fix to a problem which

# will get a proper fix elsewhere, so is not needed long term.

# I did a bunch of runs of runSim.R, output many text files.

# These text files do not record in their body which

# measurement, climate or bdratio they ran on.

# This code will create a combined table which includes this information.

open(OUT,">combined.txt") or die;

print OUT "measure bdratio climate rep depth rand.corr1 rand.corr2 rand.corr3 rand.corr4 rand.corr5 rand.sd1 rand.sd2 rand.sd3 rand.sd4 rand.sd5 rand.sigma2 rand.ace.sigma2 rand.ace.se\n";

my @files = glob("results/results\*txt");

for my $file (@files) {

 my @parse = split("\_",$file);

 my $measure = $parse[1];

 my $bdratio = $parse[2];

 my $climate = $parse[5];

 open(IN,$file) or die;

 my $header = <IN>; # throw away header

 my @lines = <IN>;

 close(IN);

 for my $line (@lines) {

 print OUT "$measure $bdratio $climate $line";

 }

}

close(OUT);

1. r code for calculating probabilities from the simulation outputs

library(plyr)

library(doBy)

#add line to set working directory

correls=data.frame(c(rep(1,5),rep(2,5),rep(4,5)),

 c(rep("Beerling.CO2",5),rep("Anag.CO2",5),rep("Hansen",5)), (rep(c("SI","GCL","EA","SD","Gsmax"),3)),

 (c(-0.143083,-0.201605,-0.039522,0.021195,-0.072471,0.196907,-0.424963,

 -0.06725,0.215795,0.078833,0.22372,-0.49242,-0.1312,0.3369,0.1726)),

 (rep(c(2.4308543, 1.18148, 1.14046, 0.69834, 1.71374),3)))

names(correls)=c("climate","climate\_name","measure","r","real.sigma2")

p <- read.csv("combined.txt", sep="")

#create function to calculate probabilities for r

probs=function(measure1,climate1){

 p1=p[which(p$measure==measure1 & p$climate==climate1),]

 c1=correls[which(correls$measure==measure1 &correls$climate==climate1),]

 px1=summaryBy(rand.corr1~measure+bdratio+climate,data=p1,FUN=length)

 pv=data.frame(measure=character(),bdratio=double(),climate=double(),p=double())

 for(var in 6:10){

 p2=p1[which(abs(p1[var])>abs(c1$r)),]

 p2=p2[c(1,2,3,var)]

 names(p2)=c("measure","bdratio","climate","rand.corr")

 py1=summaryBy(rand.corr~measure+bdratio+climate,data=p2,FUN=length)

 py1=merge(py1,px1,by=c("measure","bdratio","climate"),all=TRUE)

 py1[is.na(py1)]=0

 py1$p=py1[[4]]/py1[[5]]

 py1=py1[-4]

 py1=py1[-4]

 pv=rbind(pv,py1)

 }

return(pv)

}

#calculate probabilities for each scenario, could be looped but I couldn't be bothered

x=probs("EA",1)

x1=rbind(x,probs("EA",2))

x1=rbind(x1,probs("EA",4))

x1=rbind(x1,probs("GCL",1))

x1=rbind(x1,probs("GCL",2))

x1=rbind(x1,probs("GCL",4))

x1=rbind(x1,probs("Gsmax",1))

x1=rbind(x1,probs("Gsmax",2))

x1=rbind(x1,probs("Gsmax",4))

x1=rbind(x1,probs("SD",1))

x1=rbind(x1,probs("SD",2))

x1=rbind(x1,probs("SD",4))

x1=rbind(x1,probs("SI",1))

x1=rbind(x1,probs("SI",2))

x1=rbind(x1,probs("SI",4))

pvalues=summaryBy(p~measure+bdratio+climate,data=x1,FUN=mean)

pvalues$climate\_name=ifelse(pvalues$climate==1,"Beerling.CO2",pvalues$climate)

pvalues$climate\_name=ifelse(pvalues$climate\_name==2,"Anag.CO2",pvalues$climate\_name)

pvalues$climate\_name=ifelse(pvalues$climate\_name==4,"Hansen",pvalues$climate\_name)

pvalues$mu\_on\_lambda=1/pvalues$bdratio

write.csv(pvalues,"new.probs.csv")

1. r code for run simulations to compare traits simulated by fasttree with those simulated under rTrait under the same OU parameters. The comparisons are made by comparing estimates the parameters made using phylolm.

# Compare our OU simulations with those of phylolm

# command line usage: measure\_name bdratio numsims comparison\_per\_sim

# Where measure\_name is one of "GCL" "SI" "SD" "EA" "Gsmax"

# bdratio = birth/death ratio

# numsims = number of times to run our sim (defaults to 100)

# comparisons\_per\_sim = number of times to run phylolm sim for each of our sims

# (defaults to 5)

library(ape)

library(phylolm)

library(TreeSim)

library(fasttree2019)

measure.stats <- read.csv("OU\_parameters\_full\_data.csv")

measurement.names <- substr(measure.stats[seq(2,10,2),1],7,100) # "GCL" "SI" "SD" "EA" "Gsmax"

measurement.sigma <- sqrt(measure.stats[seq(1,9,2),"mean"])

measurement.alpha <- measure.stats[seq(2,10,2),"mean"]

args <- commandArgs(trailingOnly = TRUE)

if (length(args)==0) {

 print("No command line args - using debugging defaults")

 args <- c("GCL",1.5,10,5)

}

measure\_name <- args[[1]]

measurement <- which(measure\_name==measurement.names)

if (length(measurement)!=1) {

 stop(paste(c("First arg must be one of",measurement.names)))

}

bdratio <- as.numeric(args[[2]])

REPS = 100

REP.START = 1

if (length(args)>=3) {

 REPS=as.numeric(args[[3]])

}

COMPS = 5

if (length(args)>=4) {

 COMPS=as.numeric(args[[4]])

}

if (length(args)>=5) {

 REP.START=as.numeric(args[[5]])

}

sigma <- measurement.sigma[measurement]

alpha <- measurement.alpha[measurement]

print(sprintf("Simulating measurement %s with sigma=%f, alpha=%f",measure\_name,sigma,alpha))

n <- 1700; lambda <- bdratio; mu <- 1; sampleTimes <- c(50); treeDepth <- 93; upper.bound <- 1

# Don't care about sample times, just give one time to avoid potential errors.

# TO DO: try with zero times.

results <- NULL

warnings <- data.frame(rep=integer(),comp=integer(),sigma=double(),alpha=double())

for (rep in REP.START:REPS) {

 res = fasttree(n = n, lambda = lambda, mu = mu, alpha = alpha, sigma = sigma,

 sampleTimes = sampleTimes, treeDepth = treeDepth, traits = TRUE, seed=rep)

 # Trait measurements on the extant tips

 trait <- res$tree$edge.trait[n>=res$tree$edge[,2]]

 #restrict to extant tips only

 tree=keep.tip(res$tree,seq(1:1700))

 #phylolm requires no root edge or root edge of zero

 tree$root.edge=0

 traits <- data.frame(trait,row.names=tree$tip.label)

 OU=phylolm(trait ~ 1, data = traits, phy = tree, model = "OUrandomRoot", upper.bound = 1)

 OU.sigma=OU[[2]]^0.5

 OU.alpha=OU[[3]]

 row <- data.frame(rep,sigma=OU.sigma,alpha=OU.alpha)

 #comp.fits <- c()

 for (comp in 1:COMPS) {

 #simulate new trait on the tree using rTrait

 set.seed(rep\*1000000+comp)

 new.trait=rTrait(n=1,tree,model="OU",parameters=list(optimal.value=0, sigma2=sigma^2, 3,alpha=alpha))

 #avoids warning regarding mismatched labels. Be careful that the order of the trait and the tree are the same

 traits$new.trait <- new.trait

 #calculates OU parameters

 #be careful to look for warnings. phylolm often gets lost and can't find the parameter.

 #print(sprintf("rep=%d, comp=%d",rep,comp))

 sigAlpha <- tryCatch(

 expr={

 OU.newtrait<-NULL

 OU.newtrait=phylolm(new.trait ~ 1, data = traits, phy = tree, model = "OUrandomRoot",upper.bound=1)

 c(OU.newtrait[[2]]^0.5,OU.newtrait.alpha=OU.newtrait[[3]])

 },

 warning = function(w){

 print(sprintf("Caught warning rep=%d,comp=%d",rep,comp))

 return(c(NA,NA))

 })

 row[paste("sigma",comp,sep="")] = sigAlpha[1]

 row[paste("alpha",comp,sep="")] = sigAlpha[2]

 # Debugging: if got a warning, what value do we get when we ignore the warning?

 if (is.na(sigAlpha[1])) {

 OU.newtrait=phylolm(new.trait ~ 1, data = traits, phy = tree, model = "OUrandomRoot")

 newwarning <- data.frame(rep,comp,OU.newtrait[[2]]^0.5,OU.newtrait.alpha=OU.newtrait[[3]])

 names(newwarning)<-names(warnings)

 warnings <- rbind(warnings,newwarning)

 }

 #comp.fits <- c(comp.fits,OU.newtrait.sigma,OU.newtrait.alpha)

 #print(comp.fits)

 }

 if (is.null(results)) {

 results <- row

 } else {

 results <- rbind(results,row)

 }

}

# For each sim, count how many rTrait values are less than the fasttree value.

# If all is good, this should be distributed uniformly in the range 0:COMPS.

results$orderFastSigma = -1

results$orderFastAlpha = -1

results$orderTrueSigma = -1

results$orderTrueAlpha = -1

for (rep in 1:REPS) {

 fastSigma <- results[rep,"sigma"]

 fastAlpha <- results[rep,"alpha"]

 sigmas = results[rep,seq(4,2+2\*COMPS,2)]

 alphas = results[rep,seq(5,3+2\*COMPS,2)]

 results$orderFastSigma[rep]<-sum(sigmas<fastSigma)

 results$orderFastAlpha[rep]<-sum(alphas<fastAlpha)

 results$orderTrueSigma[rep]<-sum(sigmas<sigma)

 results$orderTrueAlpha[rep]<-sum(alphas<alpha)

}

write.csv(results,file=sprintf("results/compare\_%s\_%f.csv",measure\_name,bdratio))

# results <- read.csv(file="../results/compare\_GCL\_1.500000.csv")

print("Order fast alpha vs rTrait alpha")

print(table(results$orderFastAlpha))

print("Order fast sigma vs rTrait sigma")

print(table(results$orderFastSigma))

print("Order true alpha vs rTrait alpha")

print(table(results$orderTrueAlpha))

print("Order true sigma vs rTrait sigma")

print(table(results$orderTrueSigma))

1. r code for analysing the results of the comparisons of traits simulated by fasttree and rTrait.

setwd("results")

measure.stats <- read.csv("../OU\_parameters\_full\_data.csv")

measurement.names <- substr(measure.stats[seq(2,10,2),1],7,100) # "GCL" "SI" "SD" "EA" "Gsmax"

measurement.sigma <- sqrt(measure.stats[seq(1,9,2),"mean"])

measurement.alpha <- measure.stats[seq(2,10,2),"mean"]

files <- list.files(pattern="compare.\*csv")

all.data <- NULL

for (file in files) {

 data <- read.csv(file)

 measurement <- strsplit(file,"\_")[[1]][2]

 index <- which(measurement==measurement.names)

 data$measurement <- measurement

 data$true.sigma <- measurement.sigma[index]

 data$true.alpha <- measurement.alpha[index]

 bdratio <- strsplit(file,"\_")[[1]][3] # looks like "1.100000.csv" currently

 data$bdratio <- as.numeric(substring(bdratio,1,nchar(bdratio)-4)) # looks like 1.1

 print(sprintf("%d %s %s %s %s",index,measurement,measurement.sigma[index],measurement.alpha[index],data$bdratio[1]))

 if (is.null(all.data)) {

 all.data <- data

 } else {

 all.data <- rbind(all.data,data)

 }

}

# Need to name this file so it doesn't get caught by list.files() above if we rerun.

write.csv(all.data,file="CompareAll.csv")

# Check there are no NAs

all.data[is.na(all.data$orderFastAlpha),]

good.data <- all.data[!is.na(all.data$orderFastAlpha),] # No NAs, so not needed

err.sigma <- (good.data$true.sigma-good.data$sigma )/good.data$true.sigma

err.alpha <- (good.data$true.alpha-good.data$alpha )/good.data$true.alpha

err.sigma1 <- (good.data$true.sigma-good.data$sigma1)/good.data$true.sigma

err.alpha1 <- (good.data$true.alpha-good.data$alpha1)/good.data$true.alpha

sderr <- sd(err.sigma )/sqrt(length(err.sigma ))

print(sprintf("%s mean=%f, sd=%f, sderr=%f, mean/sderr=%f","sigma", mean(err.sigma ),sd(err.sigma ),sderr,mean(err.sigma )/sderr))

sderr <- sd(err.sigma1)/sqrt(length(err.sigma1))

print(sprintf("%s mean=%f, sd=%f, sderr=%f, mean/sderr=%f","sigma1",mean(err.sigma1),sd(err.sigma1),sderr,mean(err.sigma1)/sderr))

sderr <- sd(err.alpha )/sqrt(length(err.alpha ))

print(sprintf("%s mean=%f, sd=%f, sderr=%f, mean/sderr=%f","alpha", mean(err.alpha ),sd(err.alpha ),sderr,mean(err.alpha )/sderr))

sderr <- sd(err.alpha1)/sqrt(length(err.alpha1))

print(sprintf("%s mean=%f, sd=%f, sderr=%f, mean/sderr=%f","alpha1",mean(err.alpha1),sd(err.alpha1),sderr,mean(err.alpha1)/sderr)**)**



Figure S1. A cuticle preparation of a Proteaceae species (Isopogon fletcheri) showing epidermal cells in paradermal (i.e. parallel to the leaf surface) view. Note that the guard cells occur in pairs, with each pair with a pore (the stoma) between them. The parameters used in this paper are guard cell length (in the horizontal dimension in this image); stomatal density, which is the number of pairs of guard cells per unit leaf area; pavement cell area, which is the mean area of the pavement cells in paradermal view; stomatal index, which is the number of stomata divided by the total number of epidermal cells observed in paradermal view; and anatomically estimated maximum stomatal conductance, which is a theoretical estimate of diffusional conductance for the leaf based on the number and dimensions of the guard cells. The latter estimate assumes a consistent relationship between stomatal pore size and guard cell length, which is the case for Proteaceae stomata.

****

Figure S2. Tests of correlations between epidermal traits and aspects of paleoenvironment (deep sea temperature [44], and atmospheric CO2 [45, 46]). Each plot represents probability values of tests based on trees simulated under different ratios of extinction rate (µ) to speciation rate (λ). The circles represent tests of the Pearson’s product moment correlation coefficient. Shaded areas represent significant (*p* < 0.05) tests.

****

Figure S3. Within– (a) and among–age (b) correlations among epidermal traits observed on fossils. Line thickness represents relative strength of correlations. Data excluded Cretaceous fossils to allow comparisons with the tests of correlations between epidermal traits and environment. Inclusion of all data produced very similar results. Correlations with Gs max are not shown because they are derived from the other metrics. The within– and among–age correlations were calculated using the *statsBy.boot* function in the *psych* package of R [48], which decomposes the observed correlation into the pooled correlation within groups and the weighted correlation of the means between group [49].

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