**Appendix S10 Dispersal sinks and sources**

Number of dispersal (range expansion and jump dispersal) events for the three time slices (Figure 3) from the DEC+TS+j model (Table 3). Counts of events were averaged across the 100 biogeographic stochastic mappings (BSMs) with standard deviations in parentheses. Rows represent source ranges; columns represent dispersal sinks. Darker shades indicate a higher frequency of dispersal events. The sum and percent of events in each row and column are given on the margins. Regions are abbreviated as follows: A = Andean-Argentinian, B = Neotropical, C = Southern Africa, D = African, E = Madagascan, F = Northern Australia, G = Malesian, H = Indian-Indochinese, I = Neozealandic-Patagonian and J = Eurasiatic

**TS1** 80-40 Ma - ALL dispersal (mean of all observed anagenetic 'a', 'd' and cladogenetic ‘j’ dispersals):

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **A** | **B** | **C** | **D** | **E** | **F** | **G** | **H** | **I** | **J** |  |
| **A** | - | 0.01 (0.1) | 0  (0) | 0.01 (0.1) | 0  (0) | 0  (0) | 0.02 (0.14) | 0 (0) | 0.06 (0.28) | 0  (0) | 0.1  2% |
| **B** | 0  (0) | - | 0  (0) | 0.02 (0.14) | 0  (0) | 0  (0) | 0  (0) | 0 (0) | 0  (0) | 0  (0) | 0.02  0% |
| **C** | 0  (0) | 0.03 (0.17) | - | 0  (0) | 0.01 (0.01) | 0  (0) | 0.03 (0.22) | 0  (0) | 0  (0) | 0  (0) | 0.07  0% |
| **D** | 0.01 (0.1) | 0.12 (0.33) | 0  (0) | - | 0.03 (0.17) | 0.01 (0.1) | 0.07 (0.26) | 0.01  (0.1) | 0  (0) | 0  (0) | 0.25  6% |
| **E** | 0  (0) | 0  (0) | 0  (0) | 0  (0) | - | 0.01 (0.1) | 0.21 (0.43) | 0.02 (0.14) | 0.01 (0.1) | 0  (0) | 0.25  6% |
| **F** | 0.03 (0.17) | 0.01 (0.1) | 0.01 (0.1) | 0.05 (0.22) | 0.06 (0.24) | - | 0.54 (0.67) | 0  (0) | 0.49 (0.58) | 0  (0) | 1.19  30% |
| **G** | 0.37 (0.51) | 0.04 (0.2) | 0.08 (0.27) | 0.28 (0.49) | 0.33 (0.7) | 0.6 (0.7) | - | 0.03 (0.17) | 0.02 (0.14) | 0  (0) | 1.75  44% |
| **H** | 0  (0) | 0  (0) | 0  (0) | 0.01 (0.1) | 0.01 (0.1) | 0  (0) | 0  (0) | - | 0  (0) | 0  (0) | 0.02  0% |
| **I** | 0.08 (0.27) | 0  (0) | 0  (0) | 0.02 (0.14) | 0.01 (0.1) | 0.24 (0.53) | 0.02 (0.14) | 0  (0) | - | 0  (0) | 0.37  9% |
| **J** | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | - | 0  0% |
|  | 0.49  12% | 0.21  5% | 0.09  2% | 0.39  10% | 0.45  11% | 0.86  21% | 0.89  22% | 0.06  1% | 0.58  14% | 0  0% | 4.02  100% |

**TS2** 40-20 Ma: ALL dispersal (mean of all observed anagenetic 'a', 'd' and cladogenetic ‘j’ dispersals):

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **A** | **B** | **C** | **D** | **E** | **F** | **G** | **H** | **I** | **J** |  |
| **A** | - | 0.38 (0.55) | 0  (0) | 0.01 (0.1) | 0  (0) | 0  (0) | 0  (0) | 0.65 (0.59) | 0.44 (0.59) | 0  (0) | 1.48  15% |
| **B** | 0.06  (0.24) | - | 0  (0) | 0.04 (0.2) | 0  (0) | 0  (0) | 0.08  (0.27) | 0.22  (0.42) | 0  (0) | 0  (0) | 0.4  4% |
| **C** | 0  (0) | 0  (0) | - | 0.08  (0.27) | 0.09 (0.29) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0.17  2% |
| **D** | 0.02 (0.14) | 0.07 (0.26) | 0.26  (0.46) | - | 0.96 (0.72) | 0.04 (0.2) | 0  (0) | 0  (0) | 0.01  (0.1) | 0  (0) | 1.36  13% |
| **E** | 0  (0) | 0  (0) | 0.06  (0.24) | 0.75  (0.64) | - | 0.03 (0.17) | 0.06 (0.24) | 0.01 (0.1) | 0.04 (0.2) | 0  (0) | 0.95  9% |
| **F** | 0.01 (0.1) | 0  (0) | 0  (0) | 0.37 (0.49) | 0.25 (0.44) | - | 0.87 (0.46) | 0.03 (0.2) | 0.73 (0.69) | 0  (0) | 2.26  0.22 |
| **G** | 0  (0) | 0.69 (0.46) | 0.01 (0.1) | 0.03 (0.17) | 0.27 (0.45) | 0.27  (0.57) | - | 0.46 (0.69) | 0.01 (0.1) | 0  (0) | 1.74  17% |
| **H** | 0.01  (0.1) | 0.02  (0.14) | 0  (0) | 0.01 (0.1) | 0  (0) | 0  (0) | 0.04  (0.2) | - | 0  (0) | 0  (0) | 0.08  0% |
| **I** | 1.22 (0.7) | 0.1  (0.3) | 0  (0) | 0.05 (0.22) | 0.07 (0.26) | 0.23 (0.49) | 0.04 (0.2) | 0.01  (0.1) | - | 0  (0) | 1.72  17% |
| **J** | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | - | 0  0% |
|  | 2.22  22% | 1.26  12% | 0.33  3% | 1.34  13% | 1.64  16% | 0.57  5% | 1.09  11% | 1.38  14% | 1.23  12% | 0  0% | 10.16  100% |

**TS1** 20-0 Ma: ALL dispersal (mean of all observed anagenetic 'a', 'd' and cladogenetic ‘j’ dispersals):

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **A** | **B** | **C** | **D** | **E** | **F** | **G** | **H** | **I** | **J** |  |
| **A** | - | 2.23 (1.22) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0.03 (0.17) | 0.05 (0.22) | 0  (0) | 2.31  10% |
| **B** | 4.01  (1.07) | - | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0.07  (0.26) | 0  (0) | 0  (0) | 4.08  17% |
| **C** | 0  (0) | 0  (0) | - | 0.45  (0.77) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0.45  2% |
| **D** | 0  (0) | 0  (0) | 2.28  (0.87) | - | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 2.28  10% |
| **E** | 0  (0) | 0  (0) | 0  (0) | 0  (0) | - | 0  (0) | 0.01 (0.1) | 0.07 (0.26) | 0  (0) | 0  (0) | 0.08  0% |
| **F** | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | - | 1.06 (0.4) | 0.1 (0.3) | 0.9 (0.61) | 0.05  (0.22) | 2.11  9% |
| **G** | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0.74 (0.44) | 1.09  (0.74) | - | 5.92 (1.35) | 0  (0) | 0.92  (0.27) | 8.67  37% |
| **H** | 0.01  (0.1) | 0.05  (0.22) | 0  (0) | 0  (0) | 0.25  (0.44) | 0.23  (0.42) | 2.68  (1.25) | - | 0  (0) | 0  (0) | 3.22  14% |
| **I** | 0.1 (0.3) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0.32 (0.51) | 0  (0) | 0  (0) | - | 0  (0) | 0.42  2% |
| **J** | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0  (0) | 0.08  (0.31) | 0  (0) | - | 0.08  0% |
|  | 4.12  17% | 2.28  10% | 2.28  10% | 0.45  2% | 0.99  4% | 1.64  7% | 3.75  16% | 6.27  26% | 0.95  4% | 0.97 | 23.7  100% |