**Table II.** Results of the identification simulations from “All sequences” datasets using Best Close Match (BCM) and BOLD ID criteria based on SPIDER and tree-based comparison of efficiency among the studied barcoding markers using the percentage of monophyletic groups recovered from the neighbor-joining phylogenetic reconstructions.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  | Distance-based evaluation | | | | | | | | | | | | | | | | | | | |  |  |  |  | Tree-based evaluation | |
|  |  |  | threshVal | | | | LocalMinima | | | | 1.00% | | | | 3.00% | | | | 6.00% | | | |  | 10.00 |  |  | Monophyly | |
| All sequences |  |  | Correct (%) | Incorrect (%) | Ambiguous (%) | No ID (%) | Correct (%) | Incorrect (%) | Ambiguous (%) | No ID (%) | Correct (%) | Incorrect (%) | Ambiguous (%) | No ID (%) | Correct (%) | Incorrect (%) | Ambiguous (%) | No ID (%) | Correct (%) | Incorrect (%) | Ambiguous (%) | No ID (%) | Correct (%) | Incorrect (%) | Ambiguous (%) | No ID (%) | Correct (%) | Incorrect (%) |
| 12s  (259 sp;  1690 spm) | Threshold value | 0.30% | | | | 0.66% | | | | 1.00% | | | | 3.00% | | | | 6.00% | | | | 10.00% | | | | 71.43 | 28.57 |
| BCM | 73.49 | 2.13 | 4.02 | 20.36 | 81.24 | 2.78 | 4.32 | 11.66 | 84.50 | 3.02 | 4.38 | 8.11 | 89.41 | 3.85 | 4.44 | 2.31 | 90.59 | 4.32 | 4.44 | 0.65 | 90.77 | 4.73 | 4.44 | 0.06 |
| BOLD ID | 65.56 | 1.54 | 12.54 | 20.36 | 64.32 | 1.24 | 22.78 | 11.66 | 62.31 | 1.18 | 28.40 | 8.11 | 38.17 | 0.95 | 58.58 | 2.31 | 15.44 | 0.65 | 83.25 | 0.65 | 4.73 | 0.30 | 94.91 | 0.06 |
| 16s  (276 sp;  2712 spm) | ThreshID value | 0.50% | | | | 0.37% | | | | 1.00% | | | | 3.00% | | | | 6.00% | | | | 10.00% | | | | 68.12 | 31.88 |
| BCM | 82.45 | 1.92 | 4.54 | 11.10 | 80.64 | 1.70 | 4.42 | 13.24 | 87.72 | 2.36 | 4.61 | 5.31 | 90.63 | 2.69 | 4.65 | 2.03 | 91.78 | 2.91 | 4.65 | 0.66 | 92.00 | 3.20 | 4.65 | 0.15 |
| BOLD ID | 76.51 | 1.11 | 11.28 | 11.10 | 76.00 | 0.92 | 9.85 | 13.24 | 68.73 | 1.18 | 24.78 | 5.31 | 49.37 | 0.44 | 48.16 | 2.03 | 24.19 | 0.37 | 74.78 | 0.66 | 5.53 | 0.29 | 94.03 | 0.15 |
| COI  (156 sp;  1737 spm) | ThreshID value | 1.15% | | | | 0.91% | | | | 1.00% | | | | 3.00% | | | | 6.00% | | | | 10.00% | | | | 75.00 | 25.00 |
| BCM | 90.39 | 0.86 | 0.12 | 8.64 | 88.72 | 0.86 | 0.12 | 10.31 | 89.23 | 0.86 | 0.12 | 9.79 | 94.13 | 1.09 | 0.12 | 4.66 | 96.03 | 1.21 | 0.12 | 2.65 | 97.47 | 1.21 | 0.11 | 1.21 |
| BOLD ID | 85.26 | 0.46 | 5.64 | 8.64 | 84.80 | 0.46 | 4.43 | 10.31 | 85.20 | 0.46 | 4.55 | 9.79 | 81.81 | 0.46 | 13.07 | 4.66 | 77.14 | 0.46 | 19.75 | 2.65 | 69.77 | 0.29 | 28.73 | 1.21 |
| CytB  (53 sp;  2425 spm) | ThreshID value | 0.70% | | | | 1.25% | | | | 1.00% | | | | 3.00% | | | | 6.00% | | | | 10.00% | | | | 67.92 | 32.08 |
| BCM | 96.08 | 0.83 | 3.01 | 0.08 | 94.72 | 0.66 | 3.01 | 1.61 | 94.56 | 0.58 | 3.01 | 1.85 | 95.71 | 0.78 | 3.01 | 0.50 | 96.04 | 0.78 | 3.01 | 0.17 | 96.12 | 4.87 | 3.01 | 0.00 |
| BOLD ID | 62.43 | 0.17 | 37.32 | 0.08 | 82.84 | 0.29 | 15.26 | 1.61 | 83.05 | 0.25 | 14.85 | 1.85 | 81.77 | 0.25 | 17.48 | 0.50 | 68.48 | 0.16 | 31.19 | 0.17 | 54.64 | 0.12 | 45.24 | 0.00 |