**Table S1.** Sample size, location information, and ADMIXTURE cluster information for each collection site.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Site | No. samples | Latitude | Longitude | K11 | K2 |
| S1 | 15 | 34.38444 | 126.7967 | 7 | 8 |
| S2 | 12 | 34.33806 | 125.9994 | 4 | 8 |
| S3 | 28 | 34.83861 | 126.1436 | 10 | 18 |
| S4 | 14 | 34.84528 | 126.255 | 12 | 2 |
| S5 | 16 | 34.9365 | 126.3241 | 10 | 6 |
| S6 | 11 | 34.28389 | 126.0494 | 7 | 4 |

1 ADMIXTURE clusters

**Table S2**. Analysis of molecular variance (AMOVA) results among and within the population in the six samples and the sub-population, as derived from the ADMIXTURE analysis.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Df | SS | MS | Est. Var. | % | PhiPT | p value |
| CollectionSite | Among population | 5 | 659.7 | 131.9 | 0.7 | 0.60 | 0.0056 | 0.04 |
| Within population | 90 | 10913.1 | 121.3 | 121.3 | 99.40 |  |  |
| Total | 95 | 11572.8 | 121.8 | 121.9 | 100.00 |  |  |
| ADMIXTURE | Among population | 5 | 659.7 | 131.9 | 0.7 | 0.56 | 0.0056 | 0.03 |
| Within population | 90 | 10913.1 | 121.3 | 121.3 | 99.44 |  |  |
| Total | 95 | 11572.8 | 121.8 | 121.9 | 100.00 |  |  |

1 df, degree of freedom; SS, sum of squares; MS, mean squares; Est. Var., estimates of variance; %, percent of variance

**Table S3.** Pairwise Fst values for the *Centella asiatica* samples analyzed in this study.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | S1 | S2 | S3 | S4 | S5 |
| S2 | 0.000031 |  |  |  |  |
| S3 | 0.000448 | -0.00025 |  |  |  |
| S4 | 0.000308 | 0.000451 | 0.00001 |  |  |
| S5 | 0.000368 | 0.000303 | 0.00023 | 0.000672 |  |
| S6 | 0.000306 | 0.000284 | -0.00017 | 0.000385 | 0.00034 |



**Figure S1.** Isolation-by-distance (IBD) patterns for *Centella asiatica* determined using the Mantel test. The regression of the standardized genetic differentiation Fst vs. the geographic distance (km) is not significant.



**Figure S2.** Genetic admixture of the *Centella asiatica* samples analyzed in this study. (A) Optimal clusters as determined using the Bayesian information criterion (BIC). The optimal K value for admixture is two based on 10 replicates of K 1–20, determined using a cross-validation method. (B) Bar plots of the membership probabilities at K = 2.