Table S2. Genetic differentiation (*FST*) estimated based on the two nuclear genes between all pairs of geographic populations of the *R. virescens* species complex in Yunnan, southwestern China

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| JN\_Km | SM\_Km | NH\_Cx | YM\_Yx | SZ\_Qj | GJ\_Hh | 84\_Xs | LC\_Lc | Yx\_Lc | BS\_Bs | YP\_Yp | DL\_Dl |  |
| 0.037 |  |  |  |  |  |  |  |  |  |  |  | SM\_Km |
| 0.088\*\* | 0.043\*\* |  |  |  |  |  |  |  |  |  |  | NH\_Cx |
| 0.041\* | 0.015 | 0.024 |  |  |  |  |  |  |  |  |  | YM\_Yx |
| 0.100\*\* | 0.064\*\* | 0.025 | 0.039\*\* |  |  |  |  |  |  |  |  | SZ\_Qj |
| 0.045\* | 0.023 | 0.028\* | 0.012 | 0.045\*\* |  |  |  |  |  |  |  | GJ\_Hh |
| 0.039 | 0.034 | 0.079\*\* | 0.033\* | 0.088\*\* | 0.031\* |  |  |  |  |  |  | 84\_Xs |
| 0.036 | 0.029 | 0.074\*\* | 0.036 | 0.086\*\* | 0.031 | 0.030 |  |  |  |  |  | LC\_Lc |
| 0.030 | 0.020 | 0.065\*\* | 0.027 | 0.085\*\* | 0.027 | 0.028 | 0.024 |  |  |  |  | YX\_Lc |
| 0.024 | 0.048\* | 0.113\*\* | 0.057\*\* | 0.124\*\* | 0.062\*\* | 0.044 | 0.035 | 0.041 |  |  |  | BS\_Bs |
| 0.051\* | 0.026 | 0.080\*\* | 0.036 | 0.097\*\* | 0.037\* | 0.042 | 0.028 | 0.022 | 0.051\* |  |  | YP\_Dl |
| 0.028 | 0.020 | 0.028\*\* | 0.013 | 0.040\*\* | 0.011 | 0.027\* | 0.029 | 0.025\* | 0.047\*\* | 0.038\*\* |  | DL\_Dl |
| 0.106\*\* | 0.052\* | 0.036 | 0.033 | 0.051\* | 0.039 | 0.085\*\* | 0.079\*\* | 0.071\*\* | 0.119\*\* | 0.068\*\* | 0.046\* | SG\_Dl |

\*,0.01 ≤ *P* ≤ 0.05; \*\*, *P* ≤ 0.01