Supplementary Table 2. Pairwise estimates of genetic differentiation (*F*ST) (below the diagonal) between *S. furcifera* populations (2012), and gene flow (*Nem* = (1- *F*ST)/4*F*ST) inferred from each estimate (above diagonal).

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Country | Population | B1 | B2 | B3 | B4 | V | TH | NE | SA1 | LA |
| Bangladesh | B1 | - | 1.0651 | 1.5964 | 1.5256 | 0.7717 | 0.9069 | 1.4909 | 1.3253 | 1.4873 |
|  | B2 | 0.1901\*1 | - | 2.6071 | 1.0798 | 1.5669 | 1.2267 | 1.4946 | 1.7694 | 1.9449 |
|  | B3 | 0.1354\* | 0.0875\* | - | 2.4793 | 1.8669 | 1.5977 | 2.3247 | 3.7246 | 4.4848 |
|  | B4 | 0.1408\* | 0.1880\* | 0.0916\* | - | 0.9204 | 1.0453 | 1.7436 | 1.7645 | 2.4411 |
| Vietnam | V | 0.2447\* | 0.1376\* | 0.1181\* | 0.2136\* | - | 0.7593 | 1.4958 | 1.5486 | 1.5682 |
| Thailand | TH | 0.2161\* | 0.1693\* | 0.1353\* | 0.1930\* | 0.2477\* | - | 1.1506 | 2.0145 | 1.2542 |
| Nepal | NE | 0.1436\* | 0.1433\* | 0.0971\* | 0.1254\* | 0.1432\* | 0.1785\* | - | 2.3733 | 2.7584 |
| Korea | SA1 | 0.1587\* | 0.1238\* | 0.0629\* | 0.1241\* | 0.1390\* | 0.1104\* | 0.0953\* | - | 2.5340 |
| Laos | LA | 0.1439\* | 0.1139\* | 0.0528\* | 0.0929\* | 0.1375\* | 0.1662\* | 0.0831\* | 0.0898\* | - |

1Probability of being different from zero following correction for multiple comparison. \*P<0.05. The adjusted nominal level (5%) for multiple comparisons was 0.000055.