**Table S1.** Diversity indices obtained with ISSR study

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| ***Na*** a **(SD)**\* | ***Ne*** b **(SD)** | ***h*** c **(SD)** | ***I*** d **(SD)** | ***HT*** e **(SD)** | ***HS*** f **(SD)** | ***GST*** g | ***Nm*** h |
| 1.81 (0.38) | 1.50 (0.35) | 0.28 (0.18) | 0.43 (0.25) | 0.28 (0.03) | 0.20 (0.01) | 0.29 | 1.22 |

a observed number of alleles per locus; b effective number of alleles per locus; c Nei’s (1972) gene diversity; d Shannon’s index; e total diversity; f average within population diversity; g coefficient of genetic differentiation; h gene flow; \* Standard deviation

**Table S2.** Analysis of molecular variance (AMOVA) in Khasi mandarin populations

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Source** | ***Df*** *a* | ***SS*** *b* | ***MS c*** | ***Est. Var*** *d* | ***%*** *e* |
| **Considering Kamrup**  |  |  |  |  |  |
| Among population | 5 | 420.163 | 84.033 | 6.349 | 20 |
| Within population | 50 | 1269.694 | 25.394 | 25.394 | 80 |
| Total | 55 | 1689.857 |  | 31.744 | 100 |
| **Considering Kamrup (M)**  |  |  |  |  |  |
| Among population | 3 | 270.689 | 90.230 | 7.300 | 22 |
| Within population | 32 | 810.867 | 25.340 | 25.340 | 78 |
| Total | 35 | 1081.556 |  | 32.640 | 100 |
| **Considering two regions [Kamrup and Kamrup (M)]** |  |  |  |  |  |
| Among regions | 1 | 107.544 | 107.544 | 0.419 | 1 |
| Among population | 8 | 690.852 | 86.356 | 6.697 | 21 |
| Within population | 82 | 2080.561 | 25.373 | 25.373 | 78 |
| Total | 91 | 2878.957 |  | 32.490 | 100 |

*a* degrees of freedom; *b* sum of squared deviation; *c*mean squared deviation; *d* estimated variance; *e* percentage of total variance.



**Figure S1.** Correlation among ten Khasi mandarin populations based on Mantel’s test (matrix A: geographic distance; matrix B: genetic distance)



**Figure S2.** Negative correlation found between based geographic distance and genetic distance based on Mantel’s test which has been calculated using the distribution of *r (AB)* estimated from 10000 permutations (*p*-value 0.001 < 0.05)