|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Locus name | Na | HE | HO | *F*IS | *F*ST(1) | P(1) | *F*ST(2) | P(2) | |
| CVRL4D | 9 | 0.665 | 0.632\*\* | 0.199 | 0.01 | 0.12 | 0.01 | 0.18 |
| CVRL5D | 13 | 0.684 | 0.625 | 0.086\*\* | 0.02 | 0.01 | 0.02 | 0.00 |
| CMS121 | 12 | 0.723 | 0.722\*\* | 0.002 | 0.01 | 0.04 | 0.01 | 0.01 |
| CVRL6D | 4 | 0.342 | 0.332 | 0.029 | 0.01 | 0.15 | 0.01 | 0.04 |
| LCA66 | 9 | 0.731 | 0.769 | 0.052 | 0.01 | 0.08 | 0.00 | 0.20 |
| CVRL1D | 24 | 0.849 | 0.819 | 0.036\* | 0.01 | 0.02 | 0.00 | 0.08 |
| YWLL44 | 8 | 0.572 | 0.557\* | 0.026 | 0.02 | 0.00 | 0.03 | 0.00 |
| YWLL59 | 4 | 0.501 | 0.433\*\* | 0.136\* | 0.03 | 0.01 | 0.03 | 0.00 |
| CMS50 | 14 | 0.837 | 0.830 | 0.007 | 0.01 | 0.02 | 0.01 | 0.01 |
| CVRL8 | 2 | 0.380 | 0.363 | 0.043 | 0.00 | 0.62 | 0.00 | 0.57 |
| CMS9 | 11 | 0.812 | 0.636\*\* | 0.217\*\* | 0.04 | 0.00 | 0.05 | 0.00 |
| VOLP10 | 13 | 0.803 | 0.739\*\* | 0.080\*\* | 0.00 | 0.63 | 0.01 | 0.06 |
| CVRL7 | 16 | 0.807 | 0.758\* | 0.061\*\* | 0.02 | 0.00 | 0.02 | 0.00 |
| CMS25 | 6 | 0.618 | 0.625 | 0.010 | 0.01 | 0.02 | 0.01 | 0.10 |
| CMS15 | 11 | 0.782 | 0.751 | 0.039 | 0.01 | 0.02 | 0.01 | 0.02 |
| CMS18 | 6 | 0.404 | 0.425\*\* | 0.052 | 0.01 | 0.05 | 0.01 | 0.09 |
| CMS32 | 8 | 0.656 | 0.580\*\* | 0.116\*\* | 0.01 | 0.16 | 0.01 | 0.03 |
| CMS13 | 13 | 0.773 | 0.732\*\* | 0.053\* | 0.01 | 0.01 | 0.01 | 0.00 |
| VOLP32 | 3 | 0.355 | 0.284\*\* | 0.199\*\* | 0.09 | 0.00 | 0.07 | 0.00 |
| Mean | 9.79 | 0.647 | 0.611 | 0.074 | 0.02 |  | 0.02 |  |
| S. D | 5.31 | 0.173 | 0.169 | 0.068 | 0.02 |  | 0.02 |  |

**Table S3.** Locus-by-locus genetic diversity parameters for the total sample (N = 331).

Na, Number of alleles. HE, expected heterozygosity. HO, observed heterozygosity. *F*IS, inbreeding coefficient. \* P<0.05; \*\*P<0.01. 1Total sample arranged in six populations. 2Total sample arranged in thirteen geographic regions.The monomorphic CMS17 locus is not shown.