**Supplementary materials**

**Table S1: Details of the germplasm collected from different places of Mizoram and Manipur**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Sl No.** | **Genotypes** | **Place of collection** | **District** | **State** | **Kernel colour/ unique trait** |
| 1 | MZ 44 (c) | Serkawn | Lunglei | Mizoram | Purple |
| 2 | MZ 13(a) | Chekawn | Serchhip | Mizoram | White |
| 3 | MZ 34 (a) | Hauruang | Lunglei | Mizoram | White |
| 4 | GP(H) 1 | Imphal | Imphal west | Manipur | Purple |
| 5 | GP(H) 6 | Imphal | Imphal west | Manipur | Orange, stay green |
| 6 | MZ 45 (A) | Thualthu | Lunglei | Mizoram | Deep red |
| 7 | MZ 21 (a) | Hnanthial | Lunglei | Mizoram | Orange, stay green |
| 8 | MN 17 | Andro | Imphal east | Manipur | Light purple |
| 9 | GP(H)-2 | Imphal | Imphal west | Manipur | Yellow |
| 10 | MZ 41 ( A) | Serkawn | Lunglei | Mizoram | Purple |
| 11 | MZ 46 (B ) | Tawipui | Lunglei | Mizoram | Creamy white, mucous producing brace roots |
| 12 | GP (H) 38 | Imphal | Imphal east | Manipur | Yellow |
| 13 | Kolasib1(2) | Kolasib | Kolasib | Mizoram | White |
| 14 | MN 30 | Bishnupur bazar | Bishnupur | Manipur | Purple |
| 15 | MN 12 | Andro | Imphal east | Manipur | Purple |
| 16 | MZ 42 | Tawipui | Lunglei | Mizoram | White |
| 17 | MZ 40 | Serkawn | Lunglei | Mizoram | White |
| 18 | MZ 70 | Niawthlang -II | Saiha | Mizoram | Orange, stay green |
| 19 | MZ 24 | Hnanthial | Lunglei | Mizoram | White |
| 20 | MZ 2 | Tlungvel | Aizawl | Mizoram | Orange |
| 21 | MN 29 | Bishnupur awang leikai | Bishnupur | Manipur | Dark purple |
| 22 | MN 1 | Andro | Imphal east | Manipur | Light yellow, stay green |
| 23 | SCM 15/9LC | Imphal | Imphal west | Manipur | Orange |
| 24 | MZ 56 (a) | Tawipui | Lunglei | Mizoram | Orange |
| 25 | MZ 48 | Tawipui | Lunglei | Mizoram | Orange |
| 26 | MZ 29 | Tuipui- D | Lunglei | Mizoram | Yellow |
| 27 | MN 13 | Andro | Imphal east | Manipur | Multicob bearing, mucous producing brace roots |
| 28 | MN 3 | Bishnupur | Bishnupur | Manipur | Orange, stay green, mucous producing brace roots |
| 29 | GP(H) 28 | Imphal | Imphal west | Manipur | Yellow |
| 30 | MZ 22 | Hnanthial | Lunglei | Mizoram | White |

**Table S2: Genetic diversity analysis for 52 SSR markers in 30 genotypes**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sl No.** | **Locus** | **Bin location** | **K** | **HObs** | **HExp** | **PIC** |
| 1 | umc 1354 | 1.00 | 6 | 0.89 | 0.71 | 0.66 |
| 2 | umc 1685 | 1.01 | 2 | 0.03 | 0.50 | 0.37 |
| 3 | umc 2225 | 1.02 | 4 | 0.07 | 0.59 | 0.50 |
| 4 | bnlg 2238 | 1.04 | 5 | 0.07 | 0.66 | 0.59 |
| 5 | umc 2064 | 1.07 | 4 | 0.57 | 0.75 | 0.69 |
| 6 | umc 1622 | 1.12 | 3 | 0 | 0.19 | 0.17 |
| 7 | bnlg 1064 | 2.03 | 3 | 0.2 | 0.56 | 0.47 |
| 8 | umc 2007 | 2.04 | 5 | 0.03 | 0.68 | 0.61 |
| 9 | umc 2252 | 2.05 | 3 | 0.33 | 0.44 | 0.37 |
| 10 | bnlg 2077 | 2.07 | 4 | 0.15 | 0.75 | 0.69 |
| 11 | umc 2085 | 2.08 | 2 | 0 | 0.51 | 0.37 |
| 12 | P 101049 | 2.10 | 5 | 0.07 | 0.68 | 0.61 |
| 13 | phi 036 | 3.04 | 5 | 0.21 | 0.74 | 0.67 |
| 14 | bnlg 1601 | 3.05 | 4 | 0.27 | 0.72 | 0.66 |
| 15 | umc 2050 | 3.07 | 2 | 0.14 | 0.46 | 0.35 |
| 16 | umc2174 | 3.08 | 2 | 0.05 | 0.34 | 0.28 |
| 17 | bnlg 1496 | 3.09 | 6 | 0.29 | 0.74 | 0.68 |
| 18 | umc 1008 | 4.00 | 2 | 0 | 0.51 | 0.37 |
| 19 | umc 2410 | 4.02 | 3 | 0.03 | 0.62 | 0.54 |
| 20 | umc 1117 | 4.04 | 3 | 0 | 0.67 | 0.58 |
| 21 | bnlg 2291 | 4.06 | 3 | 0.34 | 0.52 | 0.45 |
| 22 | bnlg2162 | 4.08 | 5 | 0.79 | 0.77 | 0.71 |
| 23 | umc 2289 | 4.10 | 5 | 0.13 | 0.64 | 0.56 |
| 24 | umc 1305 | 5.00 | 4 | 0.07 | 0.35 | 0.32 |
| 25 | bnlg 565 | 5.02 | 5 | 0.39 | 0.76 | 0.71 |
| 26 | umc 2304 | 5.05 | 4 | 0.18 | 0.47 | 0.41 |
| 27 | umc 1225 | 5.08 | 5 | 0.1 | 0.79 | 0.74 |
| 28 | umc 1686 | 5.03 | 2 | 0 | 0.50 | 0.37 |
| 29 | umc 1153 | 5.09 | 6 | 0 | 0.80 | 0.76 |
| 30 | umc 1002 | 6.00 | 2 | 0 | 0.49 | 0.36 |
| 31 | umc 2318 | 6.05 | 2 | 0 | 0.44 | 0.34 |
| 32 | umc 1257 | 6.02 | 3 | 0 | 0.55 | 0.45 |
| 33 | umc 1912 | 6.06 | 5 | 0 | 0.70 | 0.64 |
| 34 | bnlg 1740 | 6.07 | 5 | 0.22 | 0.63 | 0.58 |
| 35 | umc 1642 | 7.00 | 4 | 0 | 0.61 | 0.51 |
| 36 | umc 2325 | 7.01 | 2 | 0 | 0.48 | 0.36 |
| 37 | mmc 0411 | 7.03 | 3 | 0.22 | 0.56 | 0.45 |
| 38 | umc 1154 | 7.05 | 2 | 0.04 | 0.40 | 0.31 |
| 39 | umc 1543 | 7.04 | 2 | 0 | 0.34 | 0.27 |
| 40 | umc 1932 | 7.02 | 2 | 0 | 0.46 | 0.35 |
| 41 | umc 2042 | 8.01 | 2 | 0 | 0.50 | 0.37 |
| 42 | bnlg 1194 | 8.02 | 4 | 0.36 | 0.72 | 0.65 |
| 43 | bnlg 1031 | 8.06 | 8 | 0.30 | 0.73 | 0.68 |
| 44 | umc 1607 | 8.07 | 2 | 0 | 0.41 | 0.32 |
| 45 | bnlg 1012 | 9.04 | 3 | 0 | 0.58 | 0.49 |
| 46 | bnlg 1091 | 9.05 | 4 | 0.12 | 0.58 | 0.49 |
| 47 | umc 1380 | 10.00 | 3 | 0.13 | 0.56 | 0.46 |
| 48 | umc 1576 | 10.02 | 2 | 0 | 0.47 | 0.36 |
| 49 | umc 1962 | 10.03 | 5 | 0.23 | 0.44 | 0.40 |
| 50 | umc 1506 | 10.05 | 4 | 0 | 0.62 | 0.54 |
| 51 | bnlg2190 | 10.06 | 5 | 0.07 | 0.65 | 0.58 |
| 52 | umc 2021 | 10.07 | 3 | 0.17 | 0.55 | 0.46 |
| Mean ± SD | |  | 3.634±1.428 | 0.139±0.193 | 0.574±0.137 | 0.493±0.146 |

**Table S3**: **Population structure group and heterozygosity (%) of 30 early inbred lines**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Sl No.** | **Genotypes** | **Heterozygosity (%)** | **Q1** | **Q2** | **Q3** | **Structure groups** |
| 1 | MZ 44 (c) | 14.28 | 0.006 0 | 0.042 0 | 0.952 | G3 |
| 2 | MZ 13(a) | 8.0 | 0.144 | 0.011 | 0.845 | G3 |
| 3 | MZ 34 (a) | 13.04 | 0.196 | 0.006 | 0.798 | G3 |
| 4 | GP(H) 1 | 14.58 | 0.024 | 0.017 | 0.959 | G3 |
| 5 | GP(H) 6 | 27.45 | 0.112 | 0.036 | 0.852 | G3 |
| 6 | MZ 45 (A) | 10.20 | 0.947 | 0.018 | 0.035 | G1 |
| 7 | MZ 21 (a) | 8.51 | 0.077 | 0.009 | 0.914 | G3 |
| 8 | MN 17 | 8.69 | 0.609 | 0.344 | 0.046 | AD |
| 9 | GP(H)-2 | 5.12 | 0.036 | 0.009 | 0.956 | G3 |
| 10 | MZ 41 ( A) | 6.60 | 0.986 | 0.006 | 0.008 | G1 |
| 11 | MZ 46 (B ) | 16.67 | 0.905 | 0.011 | 0.084 | G1 |
| 12 | GP (H)38 | 4.25 | 0.988 | 0.004 | 0.008 | G1 |
| 13 | Kolasib1(2) | 20.41 | 0.961 | 0.029 | 0.01 | G1 |
| 14 | MN 30 | 6.12 | 0.022 | 0.003 | 0.975 | G3 |
| 15 | MN 12 | 6.52 | 0.988 | 0.008 | 0.004 | G1 |
| 16 | MZ 42 | 8.33 | 0.956 | 0.007 | 0.037 | G1 |
| 17 | MZ 40 | 14.00 | 0.956 | 0.006 | 0.038 | G1 |
| 18 | MZ 70 | 20.41 | 0.983 | 0.004 | 0.013 | G1 |
| 19 | MZ 24 | 10.41 | 0.965 | 0.028 | 0.007 | G1 |
| 20 | MZ 2 | 11.53 | 0.991 | 0.005 | 0.004 | G1 |
| 21 | MN 29 | 10.0 | 0.005 | 0.902 | 0.092 | G2 |
| 22 | MN 1 | 3.92 | 0.005 | 0.992 | 0.003 | G2 |
| 23 | SCM 15/9LC | 0 | 0.012 | 0.948 | 0.039 | G2 |
| 24 | MZ 56 (a) | 6.38 | 0.022 | 0.972 | 0.006 | G2 |
| 25 | MZ 48 | 14.89 | 0.006 | 0.986 | 0.007 | G2 |
| 26 | MZ 29 | 8.33 | 0.003 | 0.017 | 0.981 | G3 |
| 27 | MN 13 | 12.76 | 0.01 | 0.951 | 0.038 | G2 |
| 28 | MN 3 | 14.0 | 0.003 | 0.994 | 0.003 | G2 |
| 29 | GP(H) 28 | 7.84 | 0.008 | 0.931 | 0.061 | G2 |
| 30 | MZ 22 | 6.38 | 0.207 | 0.759 | 0.034 | G2 |

AD: Admixture

**Table S4: Results of analysis of molecular variance (AMOVA) between the two populations**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Source** | **df** | **SS** | **MS** | **Est. Var.** | **Percentage of variation** |
| **Among Pops** | 1 | 0.316 | 0.316 | 0.010 | 6 |
| **Within Pops** | 28 | 4.751 | 0.170 | 0.170 | 94 |
| **Total** | 29 | 5.067 |  | 0.180 | 100 |

df: degree of freedom; SS: sum of squares; MS: mean squares; Est. Var. = estimated variance (*P* value > 0.001)

**Table S5: Mean Allelic Patterns Across Populations**

|  |  |  |
| --- | --- | --- |
| **Mean values** |  |  |
| **Population** | **MAN** | **MIZ** |
| **Na** | 3.000 | 6.000 |
| **Na Freq. >= 5%** | 3.000 | 6.000 |
| **Ne** | 2.305 | 3.986 |
| **I** | 0.958 | 1.575 |
| **No. Private Alleles** | 0.000 | 3.000 |
| **He** | 0.566 | 0.749 |
| **uHe** | 0.593 | 0.772 |

Na= No. of Different Alleles

Na (Freq>= 5%) = No. of Different Alleles with a Frequency >= 5%

Ne = No. of Effective Alleles = 1 / (Sum pi^2)

I = Shannon's Information Index = -1\* Sum (pi \* Ln (pi)

No. Private Alleles = No. of Alleles Unique to a Single Population

No. LComm Alleles (<=25%) = No. of Locally Common Alleles (Freq. >= 5%) Found in 25% or Fewer Populations

No. LComm Alleles (<=50%) = No. of Locally Common Alleles (Freq. >= 5%) Found in 50% or Fewer Populations

He = Expected Heterozygosity = 1 - Sum pi^2

uHe = Unbiased Expected Heterozygosity = (2N / (2N-1)) \* He

**Table S6: Mean phenotypic data of the 30 lines used in the present study**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Sl.no.** | **Genotype** | **PH (cm)** | **EH (cm)** | **KRPE** | **KPR** | **CL (cm)** | **CD (cm)** | **KW (g)** |
| 1 | MZ 44 (C) | 224.33 | 83.42 | 9.75 | 12.88 | 11.99 | 2.57 | 24.38 |
| 2 | MZ 13(a) | 278.78 | 134.33 | 12.33 | 19.50 | 13.00 | 2.15 | 16.72 |
| 3 | MZ 34 (a) | 223.56 | 120.17 | 13.42 | 17.34 | 15.33 | 2.34 | 14.62 |
| 4 | GP (H) 1 | 266.10 | 138.03 | 12.57 | 23.17 | 15.64 | 3.32 | 31.19 |
| 5 | GP (H) 6 | 247.33 | 117.83 | 12.50 | 28.25 | 17.00 | 3.00 | 31.53 |
| 6 | MZ 45 (A) | 206.22 | 111.00 | 14.00 | 54.72 | 12.17 | 2.21 | 16.23 |
| 7 | MZ 21 (a) | 212.95 | 94.11 | 11.50 | 25.00 | 14.91 | 2.45 | 25.60 |
| 8 | MN 17 | 285.00 | 170.00 | 14.00 | 26.00 | 15.00 | 2.10 | 17.61 |
| 9 | GP (H) 2 | 238.33 | 92.03 | 12.23 | 15.60 | 16.83 | 2.22 | 22.55 |
| 10 | MZ 41 ( A) | 172.00 | 76.77 | 12.00 | 18.80 | 10.07 | 2.56 | 16.45 |
| 11 | MZ 46 (B ) | 258.17 | 116.83 | 12.67 | 23.17 | 15.75 | 2.38 | 25.43 |
| 12 | GP (H) 38 | 199.08 | 69.04 | 17.00 | 27.75 | 15.77 | 2.79 | 22.32 |
| 13 | Kolasib 1 (2) | 223.75 | 81.88 | 12.00 | 22.00 | 13.00 | 2.00 | 18.44 |
| 14 | MN 30 | 217.50 | 130.00 | 12.17 | 13.00 | 13.00 | 1.50 | 22.06 |
| 15 | MN 12 | 253.00 | 155.00 | 17.00 | 14.00 | 9.50 | 2.30 | 23.59 |
| 16 | MZ 42 | 234.00 | 115.33 | 12.75 | 20.75 | 14.88 | 3.32 | 22.38 |
| 17 | MZ 40 | 209.67 | 99.33 | 12.50 | 19.00 | 9.69 | 2.52 | 20.30 |
| 18 | MZ 70 | 273.00 | 132.75 | 11.56 | 19.00 | 12.42 | 2.72 | 32.15 |
| 19 | MZ 24 | 212.83 | 105.20 | 11.37 | 16.03 | 13.22 | 2.36 | 22.53 |
| 20 | MZ 2 | 212.50 | 46.50 | 9.50 | 10.50 | 12.50 | 1.40 | 17.42 |
| 21 | MN 29 | 181.42 | 72.51 | 12.75 | 15.79 | 10.51 | 2.24 | 22.81 |
| 22 | MN 1 | 176.27 | 82.13 | 12.67 | 22.11 | 10.08 | 1.93 | 16.82 |
| 23 | SCM 15/9LC | 189.29 | 81.51 | 11.40 | 22.10 | 11.10 | 2.42 | 23.16 |
| 24 | MZ 56 (A) | 197.17 | 77.79 | 10.75 | 18.25 | 14.17 | 2.24 | 21.85 |
| 25 | MZ 48 | 244.20 | 100.78 | 9.33 | 22.50 | 13.53 | 2.45 | 27.27 |
| 26 | MZ 29 | 225.44 | 112.62 | 14.00 | 18.50 | 10.17 | 2.65 | 22.41 |
| 27 | MN 13 | 241.50 | 131.58 | 14.00 | 9.75 | 9.13 | 2.58 | 17.08 |
| 28 | MN 3 | 218.50 | 71.25 | 11.93 | 25.53 | 14.57 | 3.17 | 22.19 |
| 29 | GP (H) 28 | 238.17 | 98.00 | 15.67 | 16.83 | 12.61 | 2.91 | 19.44 |
| 30 | MZ 22 | 237.17 | 109.83 | 13.00 | 29.38 | 14.89 | 2.94 | 24.36 |
| **Mean** | | **226.57** | **104.25** | **12.61** | **20.91** | **12.91** | **2.46** | **22.03** |
| **SD** | | **29.34** | **27.81** | **1.81** | **8.18** | **2.29** | **0.45** | **4.58** |