

Diversity assessment and population structure analysis of mango (*Mangifera indica* L.) germplasm based on microsatellite (SSR) markers

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Supplementary Table 1. *Mangifera indica* accessions used in this study.

| No | Plant ID | Number of Individual | No | Plant ID | Number of Individual |
|----|-----------|----------------------|----|------------|----------------------|
| 1 | A_RUMANIA | 4 | 59 | MARDI_6 | 2 |
| 2 | A_MERAH | 2 | 60 | M_PILLAI | 3 |
| 3 | ALFONSO | 1 | 61 | M_SURI | 3 |
| 4 | ALIMALI | 1 | 62 | M_TAN | 1 |
| 5 | M_ANSON | 2 | 63 | MADAPALI | 4 |
| 6 | BANGKOK1 | 1 | 64 | MANALAGI | 2 |
| 7 | BANGKOK2 | 1 | 65 | MANGOVERT | 4 |
| 8 | BANGKOK4 | 2 | 66 | MAS_HITAM4 | 4 |
| 9 | BANGKOK5 | 2 | 67 | MAS_HITAM5 | 3 |
| 10 | BANTAL | 1 | 68 | MAS_HITAM | 2 |
| 11 | BEMBAN | 1 | 69 | MAS_HITAM6 | 3 |
| 12 | BERSELERA | 3 | 70 | MELELE | 1 |
| 13 | BOBBY | 1 | 71 | MINI | 2 |
| 14 | CAMEL | 2 | 72 | MOMI_K | 2 |
| 15 | CARIBOU | 3 | 73 | NDM1 | 3 |
| 16 | CARRIE | 2 | 74 | NDM2 | 2 |
| 17 | CETI | 4 | 75 | NDM_TWAI | 2 |
| 18 | CHOKANAN | 2 | 76 | NAM_PUTRI | 4 |
| 19 | COBRA | 2 | 77 | OKRONG | 1 |
| 20 | DAGING | 2 | 78 | ORANGE | 3 |
| 21 | EARLYGOLD | 2 | 79 | P_KUNING | 2 |
| 22 | EDWARD | 2 | 80 | PAHERI | 2 |
| 23 | EMILIE | 3 | 81 | PAUH AIR | 1 |
| 24 | FAIRCHILD | 2 | 82 | PAUHWAN | 1 |
| 25 | GP_TERAP | 3 | 83 | PIRIE | 2 |
| 26 | GADUNG | 1 | 84 | PISANG | 1 |
| 27 | GLENN | 1 | 85 | POPE | 1 |
| 28 | GOUVIA | 1 | 86 | SG_SIPUT | 2 |
| 29 | GRAHAM | 4 | 87 | S1 | 3 |
| 30 | H_KUNING | 3 | 88 | S_FIELD | 2 |

| | | | | | |
|----|------------|---|-----|-------------|---|
| 31 | HADEN | 4 | 89 | S_PUTIH | 3 |
| 32 | HADYAI | 1 | 90 | SAIHOAN | 1 |
| 33 | HARUMANIS | 1 | 91 | ALA_MERAH | 2 |
| 34 | HAWAI1 | 2 | 92 | SAM_SENG | 2 |
| 35 | HAWAI2 | 2 | 93 | SEPAM | 4 |
| 36 | HJYUSUF | 1 | 94 | SERDANG | 1 |
| 37 | IND_MAYU | 1 | 95 | SG_CHUA | 2 |
| 38 | IR_TAIWAN | 2 | 96 | SIAM_LAMA | 1 |
| 39 | JULIE | 2 | 97 | SIKU_RAJA | 1 |
| 40 | K_SELANGOR | 2 | 98 | SONGKLA | 2 |
| 41 | K_TEMBAGA | 4 | 99 | SPG_4 | 3 |
| 42 | K_SAPROY | 2 | 100 | SPG_GETI | 1 |
| 43 | KANDANG | 2 | 101 | SPG_GETI2 | 3 |
| 44 | KARTHA | 2 | 102 | SRI_SIAM | 1 |
| 45 | KEITT | 4 | 103 | STRAWBERRY | 2 |
| 46 | KENSINGTON | 2 | 104 | T_ATKIN | 4 |
| 47 | KENT | 1 | 105 | TANDUK | 2 |
| 48 | SG_DAUN | 1 | 106 | TELOR | 3 |
| 49 | KUDUS | 1 | 107 | TETENENE | 1 |
| 50 | L_MOHD | 3 | 108 | THAI_B | 3 |
| 51 | LENGGONG | 1 | 109 | TOKMAN | 2 |
| 52 | LIN_BULAN | 2 | 110 | TONY_B | 2 |
| 53 | LUZOU | 3 | 111 | TONY_C | 1 |
| 54 | MA199 | 1 | 112 | TRENGGANU | 2 |
| 55 | MA3 | 3 | 113 | VAL_Pride | 2 |
| 56 | MDKOU | 3 | 114 | VAN_DYKE | 2 |
| 57 | M_LOOI | 3 | 115 | YTM_PANJANG | 2 |
| 58 | MARDI_1 | 1 | 116 | ZILL | 3 |

Supplementary Table 2. List and information of SSR markers initially used in this study (Ravishankar et al, 2011).

| SSR ID | SSR ID | PRIMER (5'-3') | REPEAT MOTIF | T _a |
|--------|----------|--|--|----------------|
| 1 | MiiIHR01 | F: GGATGCACAACAACAAGCAC R: TCAGCAAGCAATCCCTTCTT | (GAA) ₄ CAG(CAA) ₂ (TA) ₂ | |
| 2 | MiiIHR02 | F: CCCCAACATTTTCATAAACACA R: CCTCCTTACATGCCTCCTTG | (CA) ₂ A(CA) ₇ AG(CA) ₅ | |
| 3 | MiiIHR03 | F: GTCGATGCCTGGAATGAAGT R: AAGCATCGAACAGCTCCAAT | (CTT) ₆ (CA) ₂ | |
| 4 | MiiIHR04 | F: CGTTTTTGACCCTCTTGAGC R: CCGCATACTTCCCTTCACAT | (CA) ₁₁ | |
| 5 | MiiIHR05 | F: CTCTCCCTCACTTGCTCCAC R: AGACCACGACAACGAAAAC | (CT) ₈ C(CT) ₂ TTTT(CT) ₄ | |
| 6 | MiiIHR06 | F: CGCCGAGCCTATAACCTCTA R: ATCATGCCCTAAACGACGAC | (CA) ₇ CG(CA) ₅ | |
| 7 | MiiIHR07 | F: GCCACTCAGCTAAATAGCCTCT R: TGCAGTCGGTAAAGTGATGG | (GA) ₁₁ | |
| 8 | MiiIHR08 | F: TGCTCTCTACTGCCCGTAT R: GTCACACCAATCGGGAATCT | (GAA) ₂ GTA(GAA) ₄ | |
| 9 | MiiIHR09 | F: GTTGTGACCGAGGCTTAAA R: CTTTGACATCGCTGATCTGG | (CT) ₃ TTGC(CT) ₂ GT(CT) ₄ TC(GT) ₂ (CT) ₂ | |
| 10 | MiiIHR10 | F: CGATTCAAGACGGAAGGAA R: TTCAAGCACAGACGACCAAC | (GTT) ₆ | |
| 11 | MiiIHR11 | F: CAGTGAACCACAGGTCAA | (CT) ₂ TT(CTT) ₅ | |

| | | | |
|----|---------|--|---|
| 12 | MiIHR12 | R: TGGCCAGCTGATACCTTCTT F: GCCCCATCAATACGATTGTC | (GA) ₁₁ |
| 13 | MiIHR13 | R: ATTTCCACCATTGTCGTTG F: CCCAGTTCCAACATCATCAG | (CCCTTT) ₃ (CTCTTT) ₆ |
| 14 | MiIHR14 | R: TTCCTCTGGAAGAGGGAAGA F: CCGAAACAACCTTTCCTCCA | (GAA) ₃ (AG) ₂ A(AAG) ₃ AG(GAA) ₂ G GA(GAAA) ₂ AA(GAA) ₃ |
| 15 | MiIHR15 | R: TCTGTGATAGAATGGCAAAGAA F: CTAACCATTGCGCATCCTCT | (CTT) ₁₁ CTA(CTT) ₅ (CTGCTT) ₂ CTA(CTT) ₆ |
| 16 | MiIHR16 | R: TCTGTGATAGAATGGCAAAGAA F: TTCACTTGTTCTGGATTGC | (GA) ₁₀ |
| 17 | MiIHR17 | R: ATTTCCACCATTGTCGTTG F: GCTTGCTTCCAACGAGACC | (GT) ₁₃ GAGT(GA) ₁₀ |
| 18 | MiIHR18 | R: GCAAAATGCTCGGAGAAGAC F: TCTGACGTCACCTCCTTCA | (GT) ₁₂ |
| 19 | MiIHR19 | R: ATACTCGTGCCTCGCTCTGT F: TGATATTTTCAGGGCCCAAG | (AC) ₁₁ |
| 20 | MiIHR20 | R: AAATGGCACAAGTGGGAAAG F: CCTAACGCGCAAGAAACATA | (AT) ₂ (GT) ₈ |
| 21 | MiIHR21 | R: ACCCACCTTCCAATCTTTT F: TTTGGCTGGGTGATTTAGC | (GTTT) ₃ (GT) ₂ TTTTGTG(TG) ₄ (AAT GA) ₂ |
| 22 | MiIHR22 | R: TTAATTGCAGGACTGGAGCA F: TGGCCGAAGTACAACTCT | (GTCTC) ₂ (TGTCTC) ₃ T(CTC) ₂ |
| 23 | MiIHR23 | R: CCCCATTTGAGAAAATTCC F: TCTGACCCAACAAGAACCA | (GA) ₁₇ GG(GA) ₆ |
| 24 | MiIHR24 | R: TCCTCCTCGTCCTCATCATC F: GCTCAACGAACCAACTGAT | (CA) ₉ TACC(CATA) ₆ |
| 25 | MiIHR25 | R: TCCAGATTCAATGAAGAAGTT F: TGTGAGTCTCCGTTTGTGCT | (GTTT) ₃ ATTTG(ATT) ₂ |
| 26 | MiIHR26 | R: CCCTCTATTTCCAGTCA F: GCGAAAGAGGAGAGTGCAAG | (GA) ₁₄ GGA(GAA) ₂ |
| 27 | MiIHR27 | R: TCTATAAGTGCCCCCTCACG F: TGGGGATTCATCGGAGATAG | (GT) ₈ AT(AG) ₂ |
| 28 | MiIHR28 | R: TGGAAGACCCATTCTCATGC F: GCGGTGCGAGACAAATTCTATAT | (GA) ₁₂ |
| 29 | MiIHR29 | R: ACAACTCGAGATTGTCACATCTTT F: CGATGAGGATGGTTGGTTTT | (GT) ₁₀ |
| 30 | MiIHR30 | R: CATCAACAGTCGCCATCAAT F: AGCTATCGCCACAGCAAATC | (CT) ₁₃ |
| 31 | MiIHR31 | R: GTCTTCTTCTGGCTGCCAAC F: TTCTGTTAGTGGCGGTGTTG | (GAC) ₆ |
| 32 | MiIHR32 | R: CACCTCCTCCTCCTCCTT F: TGGTGGTGTGTTGTTGCAAG | (GA) ₁₂ |
| | | R: ACCACCCGAGTATTGAAAG | |
