**Table S1.** Details of *P. kurroa* tissues chosen for SSRs mining in transcriptomes

|  |  |  |  |
| --- | --- | --- | --- |
| **Tissue** | **Description** | **P-I (%)** | **P-II (%)** |
| **PKS-25** | Tissue cultured shoots grown at 25°C | 0.001 | - |
| **PKR-25** | Tissue cultured roots grown at 25°C | - | - |
| **PKS-15** | Tissue cultured shoots grown at 15°C | 0.6 | - |
| **PKSS** | Field grown shoot | 2.7 | - |
| **PKSR** | Field grown root | - | 0.4 |
| **PKSTS** | Field grown stolon | 1.77 | 0.99 |

**Table S2.** P-I contents in field grown and green house grown shoots of different accessions of *P. kurroa* (High- 1.50%-2.70%%, Intermediate-0.70%-1.50%, Low- 0.38%-0.70%)

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ***P. kurroa* accession code** | **Altitude (in meters)** | **P-I content (%) in field grown shoots (Mean±S.D.)** | **P-I content (%) in green house grown shoots (Mean±S.D.)** | **Categorization on the basis of P-I content in field grown shoots** |
| PKS-1 | 3620 | 2.70 ± 0.07 | 2.15 ± 0.24 | High |
| PKS-2 | 3330 | 1.80 ± 0.13 | 1.54 ± 0.14 | High |
| PKS-3 | 3597 | 1.51 ± 0.20 | 1.91 ± 0.10 | High |
| PKS-5 | 3354 | 1.50 ± 0.55 | 1.71 ± 0.02 | High |
| PKS-26 | 3307 | 1.60 ± 0.15 | 1.66 ± 0.03 | High |
| PKS-6 | 3144 | 0.87 ± 0.41 | 0.83 ± 0.06 | Intermediate |
| PKS-7 | 3645 | 1.14 ± 0.88 | 1.42 ± 0.06 | Intermediate |
| PKS-8 | 3200 | 1.06 ± 0.44 | 1.04 ± 0.11 | Intermediate |
| PKS-9 | 3435 | 0.98 ± 0.32 | 0.82 ± 0.11 | Intermediate |
| PKS-10 | 2703 | 0.95 ± 0.12 | 0.98 ± 0.15 | Intermediate |
| PKS-11 | 3979 | 0.87 ± 0.25 | 0.88 ± 0.15 | Intermediate |
| PKS-12 | 3064 | 0.90 ± 0.45 | 1.15 ± 0.14 | Intermediate |
| PKS-13 | 3671 | 0.81 ± 0.60 | 1.14 ± 0.05 | Intermediate |
| PKS-17 | 2354 | 0.90 ± 0.41 | 1.09 ± 0.07 | Intermediate |
| PKS-19 | 2866 | 0.92 ± 0.37 | 0.99 ± 0.03 | Intermediate |
| PKS-20 | 3115 | 0.86 ± 0.43 | 1.13 ± 0.11 | Intermediate |
| PKS-22 | 3238 | 0.88 ± 0.50 | 1.18 ± 0.03 | Intermediate |
| PKS-23 | 3100 | 0.95 ± 0.18 | 0.87 ± 0.17 | Intermediate |
| PKS-24 | 3100 | 0.79 ± 0.24 | 0.75 ± 0.14 | Intermediate |
| PKS-25 | 4170 | 0.76 ± 0.35 | 0.62 ± 0.02 | Intermediate |
| PKS-4 | 2560 | 0.38 ± 0.10 | 0.38 ± 0.07 | Low |
| PKS-14 | 3435 | 0.55 ± 0.43 | 0.77 ± 0.08 | Low |
| PKS-15 | 2135 | 0.70 ± 0.42 | 0.89 ± 0.11 | Low |
| PKS-16 | 3440 | 0.55 ± 0.28 | 0.66 ± 0.14 | Low |
| PKS-18 | 3323 | 0.48 ± 0.21 | 0.59 ± 0.03 | Low |
| PKS-21 | 3245 | 0.51 ± 0.08 | 0.54 ± 0.05 | Low |

**Table** **S3.** Distribution of SSRs mined in six different transcriptomes of *P. kurroa*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sample Name** | **Motif Length** | **Repeat Number** | **Total** | **%** |
| **4** | **5** | **6** | **7** | **8** | **9** | **10** | **11** | **>11** |  |  |
| **PKR-25** | **Mono** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2000 | 2000 | 38.9 |
| **Di** | 0 | 0 | 0 | 103 | 62 | 42 | 31 | 35 | 20 | 293 | 5.7 |
| **Tri** | 0 | 774 | 296 | 207 | 124 | 65 | 61 | 200 | 290 | 2017 | 39.3 |
| **Tetra** | 210 | 43 | 21 | 11 | 3 | 6 | 2 | 5 | 30 | 331 | 6.4 |
| **Penta** | 153 | 37 | 14 | 5 | 6 | 3 | 0 | 1 | 0 | 219 | 4.3 |
| **Hexa** | 172 | 65 | 22 | 7 | 1 | 7 | 1 | 1 | 0 | 276 | 5.4 |
| **Total** | 535 | 919 | 353 | 333 | 196 | 123 | 95 | 242 | 2340 |  **5136** |  |
| **%** | 10.4 | 17.9 | 6.9 | 6.5 | 3.8 | 2.4 | 1.8 | 4.7 | 45.6 |  |  |
|  |
| **PKS-15** | **Mono** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 741 | 741 | 17.4 |
| **Di** | 0 | 0 | 0 | 214 | 137 | 99 | 57 | 46 | 100 | 653 | 15.4 |
| **Tri** | 0 | 1224 | 524 | 211 | 110 | 76 | 37 | 28 | 140 | 2350 | 55.3 |
| **Tetra** | 194 | 29 | 7 | 8 | 0 | 0 | 0 | 5 | 7 | 250 | 5.9 |
| **Penta** | 67 | 21 | 19 | 0 | 1 | 0 | 0 | 1 | 0 | 109 | 2.6 |
| **Hexa** | 97 | 41 | 4 | 3 | 0 | 0 | 0 | 0 | 0 | 145 | 3.4 |
| **Total** | 358 | 1315 | 554 | 436 | 248 | 175 | 94 | 80 | 988 | **4248** |  |
| **%** | 8.4 | 31.0 | 13.0 | 10.3 | 5.8 | 4.1 | 2.2 | 1.9 | 23.3 |  |  |
|  |
| **PKS-25** | **Mono** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1452 | 1452 | 25.2 |
| **Di** | 0 | 0 | 0 | 270 | 200 | 129 | 66 | 72 | 101 | 838 | 14.6 |
| **Tri** | 0 | 1476 | 630 | 281 | 107 | 49 | 51 | 90 | 103 | 2787 | 48.4 |
| **Tetra** | 233 | 32 | 2 | 3 | 4 | 4 | 1 | 2 | 4 | 285 | 5.0 |
| **Penta** | 68 | 27 | 20 | 1 | 0 | 0 | 1 | 0 | 0 | 117 | 2.0 |
| **Hexa** | 193 | 63 | 9 | 9 | 1 | 0 | 0 | 0 | 0 | 275 | 4.8 |
| **Total** | 494 | 1598 | 661 | 564 | 312 | 182 | 119 | 164 | 1660 | **5754** |  |
| **%** | 8.6 | 27.8 | 11.5 | 9.8 | 5.4 | 3.2 | 2.1 | 2.9 | 28.8 |  |  |
|  |
| **PKSR** | **Mono** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 262 | 262 | 14.8 |
| **Di** | 0 | 0 | 0 | 95 | 62 | 31 | 19 | 11 | 15 | 233 | 13.2 |
| **Tri** | 0 | 554 | 246 | 116 | 32 | 25 | 9 | 20 | 24 | 1026 | 58.0 |
| **Tetra** | 77 | 24 | 5 | 3 | 3 | 1 | 0 | 1 | 2 | 116 | 6.6 |
| **Penta** | 33 | 3 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 39 | 2.2 |
| **Hexa** | 62 | 24 | 5 | 1 | 1 | 0 | 0 | 0 | 0 | 93 | 5.3 |
| **Total** | 172 | 605 | 259 | 215 | 98 | 57 | 28 | 32 | 303 | **1769** |  |
| **%** | 9.7 | 34.2 | 14.6 | 12.2 | 5.5 | 3.2 | 1.6 | 1.8 | 17.1 |  |  |
|  |
| **PKSS** | **Mono** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 392 | 392 | 18.8 |
| **Di** | 0 | 0 | 0 | 93 | 87 | 47 | 25 | 21 | 37 | 310 | 14.9 |
| **Tri** | 0 | 559 | 225 | 118 | 52 | 52 | 17 | 18 | 33 | 1074 | 51.6 |
| **Tetra** | 68 | 37 | 4 | 5 | 2 | 1 | 0 | 15 | 2 | 134 | 6.4 |
| **Penta** | 36 | 9 | 7 | 0 | 1 | 0 | 0 | 0 | 0 | 53 | 2.5 |
| **Hexa** | 82 | 20 | 3 | 7 | 7 | 0 | 0 | 0 | 0 | 119 | 5.7 |
| **Total** | 186 | 625 | 239 | 223 | 149 | 100 | 42 | 54 | 464 | **2082** |  |
| **%** | 8.9 | 30.0 | 11.5 | 10.7 | 7.2 | 4.8 | 2.0 | 2.6 | 22.3 |  |  |
|  |
| **PKSTS** | **Mono** | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 441 | 441 | 16.0 |
| **Di** | 0 | 0 | 0 | 136 | 90 | 48 | 35 | 40 | 34 | 383 | 13.9 |
| **Tri** | 0 | 841 | 383 | 142 | 87 | 67 | 24 | 31 | 34 | 1609 | 58.3 |
| **Tetra** | 109 | 20 | 5 | 1 | 3 | 3 | 0 | 3 | 1 | 145 | 5.3 |
| **Penta** | 49 | 13 | 6 | 1 | 0 | 0 | 0 | 2 | 0 | 71 | 2.6 |
| **Hexa** | 74 | 21 | 5 | 3 | 3 | 0 | 4 | 0 | 0 | 110 | 4.0 |
| **Total** | 232 | 895 | 399 | 283 | 183 | 118 | 63 | 76 | 510 | **2759** |  |
| **%** | 8.4 | 32.4 | 14.5 | 10.3 | 6.6 | 4.3 | 2.3 | 2.8 | 18.5 |   |  |

**Table S4.** Genic annotation for SSRs polymorphic among accessions of *P. kurroa*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **SSR locus** | **SSR Motif** | **Target locus annotation in transcriptome** | **Primer Sequence** | **Annealing temperature (°C)** |
| PKSTS-D1 | (CT)20 | lrr receptor-like serine threonine-protein kinase fls2-like | 5’-AATGTAGCTTGCTTTGGTGT-3’5’-TTGAGTCATGAGTCATGGAA-3’ | 52 |
| PKSTS-T2 | (TTC)11 | lrr receptor-like serine threonine-protein kinase fls2-like | 5’-GGTAATTTCCCCTTCTGTTT-3’5’-TATCCAAATCGAAAGGAAGA-3’ | 49 |
| PKSTS-TT2 | (ACTC)3 | Hypothetical chloroplast rf68 | 5’-TACGCTAATGCAGTTCTTCA-3’5’-CGTATTGGTACAACTACGCA-3’ | 53 |
| PKSTS-TT13 | (CCAA)3 | Bel1-like homeodomain protein 1-like | 5’CCTAAGAGAAGAACGAGCAA3’3’TTTTTCCTAGTTTTCCTGCA5’ | 51 |
| PKSTS-P1 | (TTATT)4 | lrr receptor-like serine threonine-protein kinase fls2-like | 5’-ACGAGTTTTCTGCAGATGAT-3’5’-AACCAAATTGAACACACACA-3’ | 51 |
| PKSTS-H8 | (CTCCAG)4 | e3 ubiquitin-protein ligase upl1-like | 5’-GTTTTATTCGTGTTTACCGG-3’5’-TAACATACCGACCAGGATTC-3’ | 50 |
| PKSTS-H11 | (TCGAGC)3 | PREDICTED: uncharacterized protein LOC100267936 [Vitis vinifera] | 5’-TCGTCATACCTAGAGCCTTC-3’5’-TCTCACACAACACACACACA-3’ | 54 |
| PKR25-H7 | (AAAAAT)3 | Retroelement pol poly | 5’-GTGTCGACGTCTCCTACAAT-3’5’-TTACTTGTCGACCGTGTACA-3’ | 54 |
| PKR25-H11 | (TAAAAA)3 | fin and gill-specific type-1 keratin | 5’-TCAGCAAACGGATTTTAGAT-3’5’-CCCAAAAAGTCTGAAACAAC-3’ | 50 |
| PKSS-M15 | (A)14 | s-adenosylmethionine synthase-like isoform 1 | 5’-TCAACTCCTGAAGATCAGCT-3’5’-GGTAGACTCGTGCACCATAT-3’ | 52 |
| PKSS-D5 | (AG)10 | wrky transcription factor | 5’-AAAGGAGTTTGGCTCTAGCT-3’5’-TACCCAGTACTACGGAAAGG-3’ | 51 |
| PKS15-D14 | (CT)14 | No blast hit | 5’-ACACAAGGTATGCAAGCTTT-3’5’-GTTCATTGATCCATGACATG-3’ | 51 |
| PKSTS-M1 | (A)14 | Glutamine synthetase | 5’-CTTTCAAGATTTATCGACCG-3’5’-ACGACAAAAAGAACTCCTGA-3’ | 50 |
| PKSTS-M4 | (A)12 | Cytochrome c oxidase subunit 2 | 5’-AGAGAATAGGCCTGTCACCT-3’5’-TAGAACCACGATGATTCACA-3’ | 53 |
| PKSTS-M7 | (A)12 | Cation-transporting atpaseprotein binding | 5’-TTAACTTTCAATACCCCCAA-3’5’-AGAAGCTGATACAGCGAAAG-3’ | 51 |
| PKSTS-M8 | (T)12 | Translational initiation factor eif-4a | 5’-TTGATGCACACAAGAGTGAT-3’5’-CTATTCGGTTGAGCATAAGC-3’ | 52 |
| PKSTS-M10 | (T)12 | Calcium-transporting atpase plasma membrane-type-like | 5’-TTTAGACTTGATAGCTGCCC-3’5’-ACTGATAGAGCGTGAGAGGA-3’ | 53 |
| PKSTS-M13 | (T)12 | f-box protein skip14-like | 5’-TTTTCTTGGGTTTAGTTGGA-3’5’-AAGATGTGAGGTAGGTGGTG-3’ | 51 |
| PKSTS-D3 | (AC)9 | rna-dependent rna polymerase | 5’-GGACCTTAGCTCCTCAAACT-3’5’-GTTTTCCGTGGTGTGTTTAT-3’ | 52 |
| PKSTS-TT15 | (TGGT)3 | Nucleolar protein 14-like | 5’CTCATTATGCAGTTGGTGTG3’3’CAGCTAAGCATATGGAATCC5’ | 51 |
| PKSTS-P9 | (TGGTG)4 | Probable histone-lysine n-methyltransferase atxr3-like | 5’-TGCTTTCGACTAGCTTCTTC-3’5’-CGTCTATCAGAATAATCGGC-3’ | 51 |
| PKSTS-H5 | (CGGGAA)8 | p30 dbc | 5’-AAGGTCTTCTTTACGCTCCT-3’5’-CTATCTCTTTCCCGTACCCT-3’ | 53 |
| PKSTS-H12 | (AAATCC)4 | Methyltransferase pmt3 | 5’-TTCATTTTGGCACATGAGTA-3’5’-TGCAAACACTCAAACTTTAACT-3’ | 49 |
| PKSTS-H15 | (GGTGGA)3 | Zinc finger ccch domain-containing protein | 5’-GAATTCGCTTGACGAATTAC-3’5’-TTTGATTCCTTAAACAGGGA-3’ | 49 |
| PKR25-D4 | (AT)7 | Photosystem ii reaction center protein m | 5’-TTTTTCAATGAAATATCGTGAA-3’5’-GGATTTGAACCGATGACTTA-3’ | 48 |
| PKR25-D13 | (AT)8 | Reverse transcriptase | 5’-TTTAGAGGATTTGGTGCAAT-3’5’-TTGGGTAAGAGTTGCAAGTT-3’ | 51 |
| PKR25-T1 | (AAT)5 | Tetracycline resistance protein | 5’-CAAATATTGGGACGATATGC-3’5’-CCCGTCAAGTCTCTCTACAT-3’ | 51 |
| PKR25-TT2 | (GTTT)3 | Ribosomal protein l20 | 5’-ATCGTTGTTGTTTCAAGGTC-3’5’-TCCTTTCCTTGAACTTGAAA-3’ | 50 |
| PKR25-P12 | (AGAAA)3 | Copia protein | 5’-TGGGAATGATCGAAATAAAC-3’5’-TCCTGATATCCACTTCTGCT-3’ | 50 |
| PKR25-H8 | (TTTCTT)3 | Response regulator receiver protein | 5’-AGAGGCCGTAAGAGAGTTCT-3’5’-CTCCAATTCAACCATTGATT-3’ | 52 |
| PKS15-M1 | (T)48 | Photosystem ii 47 kda protein | 5’-TCAATAGACTGCTAAAGCCC-3’5’-TCGTCTTTTTGGTCTCATTT-3’ | 53 |
| PKS15-M15 | (T)12 | No blast hit | 5’-ATCACTTATTTTGTCGCGTT-3’5’-CGCCCAAAAAGAAAATTATA-3’ | 50 |
| PKS15-TT1 | (CAAT)3 | ycf1 protein | 5’-GTGGATTGATGACGAGAGAT-3’5’-AATTCTTCTCTTTACCTTACCAAA-3’ | 51 |
| PKSR-D5 | (AT)8 | 6-phosphofructokinase 3 like | 5’-CAAATTTCGAAGTACTTGGG-3’5’-CAAAAGCTCCCATCTAAATG-3’ | 52 |
| PKSTS-D2 | (TG)8 | lrr receptor-like serine threonine-protein kinase fls2-like | 5’-AATGTAGCTTGCTTTGGTGT-3’5’-AAGAGAAGTTTTGCGTCAAC-3’ | 52 |

**Table S5.** Summary of genetic variation statistics for all polymorphic SSR markers\*

|  |  |  |  |
| --- | --- | --- | --- |
| **Locus** | **Sample size**  | **h** | **I** |
| PKSTS-D1 | 26 | 0.355 | 0.5402 |
| PKSTS-T2 | 26 | 0.3935 | 0.5825 |
| PKSTS-TT2 | 26 | 0.2604 | 0.4293 |
| PKSTS-TT13 | 26 | 0.4734 | 0.6663 |
| PKSTS-P1 | 26 | 0.4527 | 0.645 |
| PKSTS-H8 | 26 | 0.497 | 0.6902 |
| PKSTS-H11 | 26 | 0.3107 | 0.4896 |
| PKR25-H7 | 26 | 0.4527 | 0.645 |
| PKR25-H11 | 26 | 0.3107 | 0.4896 |
| PKSS-M15 | 26 | 0.500 | 0.6931 |
| PKSS-D5 | 26 | 0.3935 | 0.5825 |
| PKS15-D14 | 26 | 0.4527 | 0.645 |
| PKSTS-M1 | 26 | 0.4734 | 0.6663 |
| PKSTS-M4 | 26 | 0.2604 | 0.4293 |
| PKSTS-M7 | 26 | 0.4882 | 0.6813 |
| PKSTS-M8 | 26 | 0.355 | 0.5402 |
| PKSTS-M10 | 26 | 0.500 | 0.6931 |
| PKSTS-M13 | 26 | 0.074 | 0.163 |
| PKSTS-D3 | 26 | 0.3935 | 0.5825 |
| PKSTS-TT15 | 26 | 0.3935 | 0.5825 |
| PKSTS-P9 | 26 | 0.4527 | 0.645 |
| PKSTS-H5 | 26 | 0.426 | 0.6172 |
| PKSTS-H12 | 26 | 0.4882 | 0.6813 |
| PKSTS-H15 | 26 | 0.2604 | 0.4293 |
| PKR25-D4 | 26 | 0.4734 | 0.6663 |
| PKR25-D13 | 26 | 0.426 | 0.6172 |
| PKR25-T1 | 26 | 0.3935 | 0.5825 |
| PKR25-TT2 | 26 | 0.4882 | 0.6813 |
| PKR25-P12 | 26 | 0.2604 | 0.4293 |
| PKR25-H8 | 26 | 0.3935 | 0.5825 |
| PKS15-M1 | 26 | 0.355 | 0.5402 |
| PKS15-M15 | 26 | 0.426 | 0.6172 |
| PKS15-TT1 | 26 | 0.426 | 0.6172 |
| PKSR-D5 | 26 | 0.3935 | 0.5825 |
| PKSTS-D2 | 26 | 0.4527 | 0.645 |
| Mean |  | **0.3973** | **0.582** |
| St. Dev. |  | **0.0926** | **0.1089** |

\*POPGENE was used to calculate Nei’s genetic diversity (h) and Shannon’s information index (I)

**Table S6.** Genetic variation among high, intermediate and low picrosides content accessions

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Accession** | **Sample Size** | **H (Avg.±S.D.)** | **I (Avg.±S.D.)** | **No. of Polymorphic Loci** | **PPL\*** |
| High  | 5 | 0.3383 (±0.1725)  | 0.4935 (±0.2412) | 29 | 82.86 |
| Intermediate | 15 | 0.3967 (±0.1079) | 0.5783 (±0.1361) | 34 | 97.14 |
| Low  | 6 | 0.3238 (±0.1835)  | 0.4727 (±0.2561) | 28 | 80.00 |

 \* PPL: Percentage of polymorphic loci

**Table S7.** PIC values, Hobs and Hexp at each SSR locus

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **S. No.** | **SSR locus** | **Sample size** | **No. of alleles** | **Hobs** | **Hexp** | **PIC** |
| 1 | PKSTS-D1 | 26 | 3 | 0.538 | 0.411 | 0.336 |
| 2 | PKSTS-T2 | 26 | 3 | 0.654 | 0.480 | 0.402 |
| 3 | PKSTS-TT2 | 26 | 2 | 0.154 | 0.145 | 0.132 |
| 4 | PKSTS-TT13 | 26 | 3 | 0.885 | 0.603 | 0.525 |
| 5 | PKSTS-P1 | 26 | 3 | 0.115 | 0.112 | 0.107 |
| 6 | PKSTS-H8 | 26 | 3 | 0.769 | 0.562 | 0.472 |
| 7 | PKSTS-H11 | 26 | 3 | 0.269 | 0.245 | 0.224 |
| 8 | PKR25-H7 | 26 | 3 | 0.346 | 0.302 | 0.270 |
| 9 | PKR25-H11 | 26 | 3 | 0.462 | 0.388 | 0.348 |
| 10 | PKSS-M15 | 26 | 3 | 0.385 | 0.335 | 0.303 |
| 11 | PKSS-D5 | 26 | 3 | 0.923 | 0.540 | 0.424 |
| 12 | PKS15-D14 | 26 | 3 | 0.692 | 0.509 | 0.420 |
| 13 | PKSTS-M1 | 26 | 3 | 0.500 | 0.539 | 0.472 |
| 14 | PKSTS-M4 | 26 | 3 | 0.231 | 0.212 | 0.193 |
| 15 | PKSTS-M7 | 26 | 3 | 0.72 | 0.571 | 0.498 |
| 16 | PKSTS-M8 | 26 | 3 | 0.654 | 0.504 | 0.426 |
| 17 | PKSTS-M10 | 26 | 3 | 0.731 | 0.582 | 0.504 |
| 18 | PKSTS-M13 | 26 | 3 | 0.615 | 0.482 | 0.425 |
| 19 | PKSTS-D3 | 26 | 3 | 0.269 | 0.242 | 0.217 |
| 20 | PKSTS-TT15 | 26 | 3 | 0.962 | 0.627 | 0.546 |
| 21 | PKSTS-P9 | 26 | 3 | 1.000 | 0.634 | 0.551 |
| 22 | PKSTS-H5 | 26 | 3 | 0.577 | 0.461 | 0.409 |
| 23 | PKSTS-H12 | 26 | 3 | 0.423 | 0.363 | 0.327 |
| 24 | PKSTS-H15 | 26 | 3 | 0.923 | 0.578 | 0.482 |
| 25 | PKR25-D4 | 26 | 3 | 0.962 | 0.612 | 0.524 |
| 26 | PKR25-D13 | 26 | 3 | 0.808 | 0.542 | 0.450 |
| 27 | PKR25-T1 | 26 | 3 | 0.385 | 0.435 | 0.384 |
| 28 | PKR25-TT2 | 26 | 3 | 0.885 | 0.603 | 0.525 |
| 29 | PKR25-P12 | 26 | 3 | 0.538 | 0.426 | 0.366 |
| 30 | PKR25-H8 | 26 | 3 | 0.615 | 0.456 | 0.376 |
| 31 | PKS15-M1 | 26 | 3 | 0.500 | 0.405 | 0.352 |
| 32 | PKS15-M15 | 26 | 3 | 0.654 | 0.555 | 0.484 |
| 33 | PKS15-TT1 | 26 | 3 | 0.846 | 0.586 | 0.509 |
| 34 | PKSR-D5 | 26 | 3 | 0.462 | 0.386 | 0.343 |
| 35 | PKSTS-D2 | 26 | 3 | 0.462 | 0.386 | 0.343 |
| Mean |  |  | **2.97** | **0.597** | **0.452** | **0.391** |



**Figure S1.** **(A)** The relationship between number of clusters (K) and the estimated likelihood of data (LnP(D)). A model based clustering of 26 accessions using STRUCTURE without prior knowledge about the populations and under an admixed model calculated that LnP(D) was greatest when K = 2. **(B)** The relationship between K and ΔK., i.e. ΔK is reaches its maximum when K =2, suggesting that all accessions fall into one of the 2 clusters **(C)** Population structure analysis of 26 accessions using STRUCTURE. The accessions were grouped into two clusters