**Table S1:** Grouping of genotypes from two Indian subcontinent landrace collections into Mesoamerican and Andean genepool subgroups based on microsatellite marker analysis.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **HPK Collection****(Set I)** |   |   | **FAO Collection (Set II)** |  |  |  |
| **M1** | **M2** | **A1** | **A2** | **A3** | **M1** | **M2** | **M2** | **M3** | **A1** | **A1** |
| KR-201 | KR-216 | KR-157 | KR-257 | KR-260 | G14204 | G13114 | G13110 | G14211 | G20602 | G13113 |
| KR-248 | KR-133 | KR-227 | KR-39 | KR-45 | G14205 | G20575 | G486 | G20618 | G20626 | G13892 |
| KR-197 | KR-131 | KR-94 | KR-158 |  | G20659 | G20577 | G183 | G20690 | G20632 | G14200 |
| KR-24 | KR-172 | KR-221 | KR-90 |  | G20667 | G20579 | G183A | G464 | G474 | G20568 |
| KR-64 | KR-117 | KR-43 | KR-82 |  | G20668 | G20586 | G183B |  | G13886 | G20603 |
| KR-62-2 | KR-240 | KR-9 | KR-293 |  | G20669 | G20590 | G449 |  | G13894 | G20604 |
| KR-95 | KR-190 | KR-130 | KRC-1 |  | G20669A | G20601 | G467 |  | G20653 | G20622 |
| KR-246 | KR-166 | KR-62 | KRC-2 |  | G20682 | G20605 | G16830 |  | G20654 | G20640 |
| Kullu-3 | KR-84 | KR-256 | KRC-22 |  | G20683 | G20629 | G7223 |  | G20655 | G20692 |
| Kullu-5 | IC-415517 | Kullu-7 | KRC-6 |  | G20690A | G20630 |  |  | G146 |  |
| Sirmour-4 | Hans | Kullu-8 | KRC-7 |  | G5773\* | G20633 |  |  | G1380 |  |
| IC-448907 | IC-423495 | Kullu-9 | KRC-9 |  | DOR364\* | G20644 |  |  | G1382 |  |
| IC-415334 | IC-421101 | Nichar | Kullu-2 |  |  | G13100 |  |  | G13106 |  |
| IC-329505 | IC-415408 | Sirmour-1 | Lari-1 |  |  | G14202 |  |  | G13107 |  |
|   | IC-319370 | Sirmour-5-II | Contender |  |  | G14203 |  |  | G13898 |  |
|   | ICAPIJAO | Jwala | Baspa |  |  | G20656 |  |  | G13899 |  |
|   | DOR364 | KRC5 |  |  |  | G20657 |  |  | G13900 |  |
|   |  | Him-1 |  |  |  | G20658 |  |  | G463 |  |
|   |  | IC-311080 |  |  |  | G20660 |  |  | G448 |  |
|   |  | IC-329499 |  |  |  | G20670 |  |  | G468 |  |
|   |  | G4494 |  |  |  | G20671 |  |  | G469 |  |
|   |  | G19833 |  |  |  | G20681 |  |  | G470 |  |
|   |  |  |  |  |  | G20691 |  |  | G20698 |  |
|   |  |  |  |  |  | G145 |  |  | IJR |  |
|   |  |  |  |  |  | G1379 |  |  | G4494\* |  |
|   |  |  |  |  |  | G711 |  |  | G19833\* |  |

**Table S2.** Allele size, number, heterozygosity and polymorphism information contents (PIC) based on evaluation of 157 common bean collections, analysis in germplasm set I from the HPK collection, germplasm set II from the FAO collection and for the total germplasm set with genomic and gene-based microsatellite markers.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | **Set I (HPK collection)** | **Set II (FAO collection)** | **Total**  |
|  | **Allele size (bp)** | **na** | **He** | **Ho** | **PIC** | **na** | **He** | **Ho** | **PIC** | **na** | **He** | **Ho** | **PIC** |
| **Marker** | **Min**  | **Max**  | **Range**  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **Genomic** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| AG1 | 124 | 142 | 22 | 4 | 0.134 | 0.000 | 0.130 | 5 | 0.133 | 0.000 | 0.130 | 5 | 0.113 | 0.000 | 0.110 |
| BM139 | 84 | 118 | 34 | 7 | 0.716 | 0.000 | 0.674 | 7 | 0.635 | 0.000 | 0.601 | 8 | 0.684 | 0.000 | 0.647 |
| BM140 | 160 | 200 | 40 | 3 | 0.378 | 0.000 | 0.317 | 4 | 0.465 | 0.000 | 0.423 | 4 | 0.434 | 0.000 | 0.403 |
| BM143 | 150 | 174 | 24 | 10 | 0.744 | 0.083 | 0.708 | 7 | 0.778 | 0.145 | 0.746 | 12 | 0.772 | 0.121 | 0.740 |
| BM151 | 144 | 155 | 11 | 3 | 0.430 | 0.015 | 0.368 | 3 | 0.663 | 0.000 | 0.588 | 3 | 0.606 | 0.007 | 0.533 |
| BM155 | 105 | 120 | 15 | 2 | 0.466 | 0.014 | 0.357 | 2 | 0.499 | 0.000 | 0.374 | 2 | 0.496 | 0.007 | 0.373 |
| BM157 | 100 | 118 | 18 | 3 | 0.574 | 0.042 | 0.494 | 3 | 0.490 | 0.023 | 0.390 | 3 | 0.528 | 0.033 | 0.442 |
| BM160 | 180 | 255 | 75 | 6 | 0.731 | 0.085 | 0.685 | 8 | 0.703 | 0.013 | 0.659 | 10 | 0.733 | 0.041 | 0.694 |
| BM181 | 178 | 200 | 22 | 4 | 0.637 | 0.029 | 0.566 | 3 | 0.535 | 0.023 | 0.449 | 5 | 0.602 | 0.026 | 0.524 |
| BM197 | 196 | 202 | 6 | 4 | 0.654 | 0.014 | 0.584 | 3 | 0.611 | 0.000 | 0.530 | 4 | 0.653 | 0.007 | 0.580 |
| BM210 | 165 | 190 | 25 | 7 | 0.675 | 0.014 | 0.641 | 6 | 0.774 | 0.012 | 0.738 | 9 | 0.757 | 0.013 | 0.723 |
| BMd33 | 98 | 114 | 16 | 4 | 0.598 | 0.014 | 0.539 | 4 | 0.691 | 0.000 | 0.634 | 4 | 0.660 | 0.007 | 0.597 |
| BMd36 | 164 | 188 | 24 | 5 | 0.566 | 0.028 | 0.497 | 5 | 0.612 | 0.000 | 0.535 | 6 | 0.601 | 0.013 | 0.526 |
| **Gene based** |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| BMd15 | 165 | 204 | 39 | 2 | 0.271 | 0.000 | 0.234 | 2 | 0.242 | 0.000 | 0.213 | 2 | 0.242 | 0.000 | 0.213 |
| BMd20 | 113 | 130 | 17 | 4 | 0.577 | 0.014 | 0.499 | 3 | 0.552 | 0.035 | 0.451 | 4 | 0.567 | 0.020 | 0.478 |
| BMd26 | 132 | 142 | 10 | 2 | 0.498 | 0.000 | 0.374 | 3 | 0.483 | 0.000 | 0.377 | 3 | 0.494 | 0.000 | 0.378 |
| BMd45 | 92 | 130 | 38 | 2 | 0.499 | 0.000 | 0.375 | 2 | 0.498 | 0.000 | 0.374 | 2 | 0.499 | 0.000 | 0.374 |
| BMd46 | 320 | 325 | 5 | 2 | 0.438 | 0.000 | 0.342 | 2 | 0.311 | 0.000 | 0.263 | 2 | 0.487 | 0.000 | 0.369 |
| BMd53 | 106 | 110 | 4 | 2 | 0.499 | 0.000 | 0.375 | 2 | 0.483 | 0.000 | 0.366 | 2 | 0.492 | 0.000 | 0.371 |
| Pv-ctt1 | 150 | 178 | 28 | 5 | 0.714 | 0.043 | 0.673 | 4 | 0.670 | 0.000 | 0.599 | 5 | 0.706 | 0.020 | 0.654 |
| Pv-ag1 | 148 | 158 | 10 | 3 | 0.133 | 0.000 | 0.127 | 4 | 0.509 | 0.012 | 0.402 | 4 | 0.400 | 0.007 | 0.343 |
| Pv-gaa1 | 158 | 168 | 10 | 2 | 0.473 | 0.000 | 0.361 | 3 | 0.506 | 0.023 | 0.389 | 3 | 0.493 | 0.014 | 0.378 |
| Pv-ag003 | 165 | 168 | 3 | 2 | 0.041 | 0.014 | 0.041 | 2 | 0.090 | 0.000 | 0.086 | 2 | 0.070 | 0.007 | 0.067 |
| Pv-gaat001 | 135 | 145 | 10 | 3 | 0.514 | 0.042 | 0.395 | 2 | 0.483 | 0.000 | 0.366 | 3 | 0.502 | 0.020 | 0.382 |
| **Mean** | 147  | 168  |  21 | 3.8 | 0.498 | 0.019 | 0.431 | 3.7 | 0.517 | 0.012 | 0.445 | 4.5 | 0.525 | 0.015 | 0.454 |

na = Observed number of alleles, He= Expected heterozygosity Nei's (1976), Ho = Observed heterozygosity, PIC polymorphism information contents.

**Figure S1**. Geographic distribution of common bean land races from India that were used in the diversity analysis. Round dots represent the FAO (set I) genotypes and triangles represent the HPK (set II) genotypes.