Table1 Descriptive statistics for maternal haploid induction rate (mhir) of DH population across four environments

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Environment | Mean | Min | Max | Median | SD | Skewness | Kurtosis | *H*2 |
| Shunyi | 12.29 | 8.13 | 16.86 | 12.22 | 1.58 | 0.54 | 0.36 | 0.49 |
| Jinan | 12.07 | 8.90 | 16.65 | 11.85 | 1.65 | 0.51 | -0.05 | 0.44 |
| SJZ | 12.40 | 8.43 | 17.36 | 12.30 | 1.77 | 0.43 | 0.05 | 0.46 |
| Hainan | 14.57 | 10.16 | 19.04 | 14.53 | 1.75 | 0.05 | -0.16 | 0.53 |

Table2 SNP characteristics of the DH population

|  |  |  |
| --- | --- | --- |
|  | Mean ± SD | Range |
| High-quality SNP number | 5124 |  |
| SNP missing rate (%) | 1.08±1.17 | 0-10.34 |
| MAF of SNPs | 0.42±0.06 | 0.16-0.50 |
| SNP missing rate in each line (%) | 0.54±1.44 | 0-8.62 |
| SNP heterozygosity in each line (%) | 0.80±2.17 | 0-10.12 |



Fig.1 Maternal Haploid Induction Rate across four environments. By the violin plots, the first and third quartiles of the DHs’ mhir were represented with black bar inside. The medians were shown with white points. The shape of each plot represents probability density of the population at different values



Fig.2 Variation of maternal haploid induction rate across four environments in DHs. Mean of the parents are indicated at top of the histogram with arrows respectively.



Fig.3 Principal component analysis (PCA) bioplot of four environments in DH populations. The results revealed differences in response to maternal haploid induction rate (MHIR) in different environments (environmental grouping)

Fig.4 Genotype map of the DH population. Red: Chang7-2, Blue: Q319

Table4 No. of markers and map length of the linkage map, crossover and recombination per chromosome in DH population

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | chr1 | chr2 | chr3 | chr4 | chr5 | chr6 | chr7 | chr8 | chr9 | chr10 |
| No. of markers | 280 | 263 | 315 | 225 | 231 | 183 | 224 | 168 | 149 | 126 |
| map length (cM) | 234.86 | 185.49 | 162.35 | 183.17 | 161.89 | 167.65 | 117.99 | 180.89 | 163.50 | 151.87 |
| No. of crossovers | 1.64 | 2.52 | 1.98 | 2.29 | 1.97 | 1.15 | 1.96 | 1.42 | 1.59 | 1.12 |
| Frequency of no recombinations | 0.45 | 0.42 | 0.53 | 0.13 | 0.64 | 0.53 | 0.50 | 0.48 | 0.50 | 0.61 |

Table 5 QTLs of maternal haploid induction in DH population

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Environment | QTL | Chromosome | Peak(cM) | Flanking Markers | | Genetic interval (cM) | Physical Position(Mb) | LOD | A | R2(%) |
| Shunyi | *qMHI3-1* | 3 | 100.0 | PZE-103118170 | PZE-103126743 | 88.9-103.2 | 176.8-184.1 | 2.88 | 0.42 | 7.16 |
| Shunyi | *qMHI9-1* | 9 | 21.6 | PHM11946.19 | PZE-109016384 | 9.1-31.1 | 10.0-16.5 | 2.98 | 0.43 | 7.71 |
| Shunyi | *qMHI10-1* | 10 | 142.9 | PZA-002969009 | PZE-110111368 | 132.6-150.0 | 144.1-150.0 | 3.35 | -0.47 | 8.42 |
| Jinan | *qMHI4-1* | 4 | 43.5 | PZE-104019928 | PZE-104029115 | 39.7-51.1 | 20.9-35.2 | 3.83 | 0.55 | 10.42 |
| Jinan | *qMHI9-2* | 9 | 31.1 | PZE-109013421 | PZE-109021565 | 23.1-46.4 | 13.7-21.9 | 3.11 | 0.48 | 8.26 |
| Jinan | *qMHI10-2* | 10 | 78.3 | PZE-110050659 | PZE-110052323 | 77.5-79.7 | 95.4-99.0 | 2.95 | 0.49 | 8.03 |
| SJZ | *qMHI2-1* | 2 | 17.0 | SYN6306 | PZE-102015152 | 5.5-25.1 | 2.8-6.5 | 3.54 | 0.56 | 8.67 |
| SJZ | *qMHI4-2* | 4 | 103.7 | PZE-104099837 | PZE-104103734 | 101.6-106.8 | 176.9-180.0 | 4.38 | 0.60 | 11.40 |
| SJZ | *qMHI5-1* | 5 | 49.8 | SYN19685 | PZE-105047654 | 39-51.1 | 13.7-37.2 | 2.75 | -0.48 | 6.63 |
| SJZ | *qMHI10-3* | 10 | 67.8 | SYN12506 | PZE-110023112 | 62.6-69 | 10.3-34.1 | 6.68 | 0.79 | 17.44 |
| SJZ | *qMHI10-4* | 10 | 144.9 | PZA-002969009 | PZE-110111368 | 132.5-150.0 | 144.1-150.0 | 3.25 | -0.55 | 8.40 |
| Sanya | *qMHI1-1* | 1 | 232.8 | SYN15622 | PZE-101257184 | 221.1-233.8 | 293.8-300.7 | 2.81 | 0.49 | 7.38 |
| Sanya | *qMHI9-3* | 9 | 21.8 | SYN33212 | PZE-109013421 | 15.7-23.3 | 11.7-13.7 | 7.60 | 0.84 | 22.14 |
| Combine | *qMHI1-2* | 1 | 232.8 | SYN15622 | PZE-101257184 | 221.1-233.8 | 293.8-300.7 | 2.56 | 0.43 | 6.39 |
| Combine | *qMHI10-5* | 10 | 144.9 | PZA-002969009 | PZE-110111368 | 132.7-150 | 144.1-150.0 | 2.96 | -0.49 | 8.00 |

Combine: traits of four environments were combined with BLUP.



Fig. 5 QTLs located at 10 chromosomes. Positions of 2164 SNPs used as genetic markers are indicated by horizontal lines spaced proportionally according to their genetic distance on the linkage map. Arrow heads indicate LOD peak locations of the QTL. Grey arrow heads are QTLs detected in single environment, black arrow head QTLs with combined environmets. QTL abbreviations can be found in Table 1.



Fig.6 Major QTLs on chromosome 9 and 10