Table S1: Mean sum of squares captured for various traits in selected wheat genotypes

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Source of Variation | DF | DH | DM | GFD | PHT | PTL | TGW | CTD1 | CTD2 | BM | GY2 | GN | GW | HI | CMS |
| Genotype | 29 | 82.79\*\* | 35.49\*\* | 12.90 | 157.55\*\* | 642.25 | 129.63\*\* | 1.47 | 0.49 | 94773\*\* | 12819.2\*\* | 195.14\*\* | 0.32\*\* | 111.48 | 223.6 |
| Rreplication (REP) | 1 | 9.63 | 2.41 | 20.01 | 411.93\*\* | 3015.02 | 5.94 | 38.53\*\* | 1.32 | 270750\*\* | 227157\*\* | 90.06 | 0.17 | 454.45\*\* |  |
| Condition (COND) | 1 | 2842.13\*\* | 8892.41\*\* | 1340.01\*\* | 541.88\*\* | 77140.10\*\* | 1219.05\*\* | 83.33\*\* | 20.01\*\* | 1610080\*\* | 83582.4\*\* | 1675.22\*\* | 10.96\*\* | 66.95 | 420.6 |
| Genotype\*REP | 29 | 3.91 | 4.13 | 9.11 | 37.28 | 404.71 | 41.79 | 0.97 | 0.31 | 67991.4\* | 2966.44 | 45.18 | 0.18 | 74.26 |  |
| Genotype\*COND | 29 | 10.03 | 7.44282\* | 16.87\* | 82.65 | 582.50 | 26.16 | 1.64 | 0.50 | 75945.4\* | 3109.63 | 50.24 | 0.16 | 64.04 | 16.7 |
| Residual | 30 | 5.90 | 3.54 | 8.21 | 58.91 | 991.82 | 28.44 | 1.41 | 0.95 | 33750.00 | 2496.03 | 36.92 | 0.13 | 64.42 |  |
| Total (Corrected) | 119 | 49.03 | 87.11 | 22.97 | 90.49 | 1320.70 | 65.37 | 2.38 | 0.74 | 82486.70 | 7845.24 | 94.64 | 0.28 | 81.49 | 125.2 |

*Note= \*P< 0.05; \*\*P< 0.01 ; DF= days to filling; DH= days to heading; DM= dates to maturity; GFD= grain filling days; PHT= plant height; PTL= ; GN grain number; GN=grain number; HI= harvest index*

Table S2: Mean values calculated for number of traits under non-stressed and stressed conditions and per cent reduction

|  |  |  |  |
| --- | --- | --- | --- |
| Trait | Non- stressed |  Stressed | Reduction (%) |
| DH | 91.4 | 81.6 | 10.7 |
| DA | 97.3 | 86.7 | 10.8 |
| DM | 137.8 | 120.6 | 12.5 |
| GFD | 40.5 | 33.8 | 16.5 |
| PHT | 98.9 | 94.7 | 4.3 |
| PTL | 148.6 | 97.9 | 34.1 |
| TGW | 36.7 | 30.4 | 17.3 |
| CTD1 | 5.7 | 7.4 | -29.0 |
| CTD2 | 4.7 | 3.9 | 17.5 |
| BM | 1005.0 | 773.3 | 23.1 |
| GY2 | 232.4 | 179.6 | 22.7 |
| GN | 53.5 | 46.0 | 14.0 |
| GW | 2.0 | 1.4 | 30.6 |
| HI | 24.3 | 22.8 | 6.1 |
| CMS | 40.1 | 33.9 | 15.5 |

Table S3 : Genetic diversity across 41 loci and phenotypic traits captured in values for 30 wheat genotypes divided into three heat tolerance levels.

|  |  |  |  |
| --- | --- | --- | --- |
| Category | HHT | MHT | LHT |
| Number of Genotypes | 10 | 10 | 10 |
| Total number of alleles | 138 | 118 | 99 |
| Mean alleles per loci | 5.52 | 4.72 | 3.96 |
| CMS-NS | 41 | 39.6 | 39.7 |
| GY-NS | 225 | 227 | 246 |
| CTD2-NS | 4.5 | 4.9 | 4.6 |
| BM-NS | 935 | 980 | 1100 |
| CMS-S | 36.8 | 35.9 | 29.7 |
| GY-S | 208 | 178 | 153 |
| CTD2-S | 3.9 | 3.8 | 3.9 |
| BM-S | 840 | 755 | 725 |

 *Note: NS= non-stressed; S= stressed; HHT= high heat tolerance; MHT= medium heat tolerance; LHT= low heat tolerance*

|  |  |  |
| --- | --- | --- |
|  | ISSR | SSR |
| Source of Variation | d.f | Sum of square | Variance of components | % of variance | Sum of square | Variance of components | % of variance |
| among pop | 2 | 63.678 | 0.62716 | 2.36 | 88.800 | 2.88667 | 8.79 |
| within pop | 25 | 649.822 | 25.99289 | 97.64 | 359.600 | 29.96667 | 91.21 |
| Total | 27 | 713.5 | 26.62005 |  | 448.400 | 32.85333 |  |

Table S4: Analysis of molecular variance (AMOVA) for molecular markers

Table S5: Nei's unbiased genetic diversity (Above diagonal) and genetic distance (below diagonal) among wheat populations revealed by markers

|  |  |  |
| --- | --- | --- |
|  | ISSR | SSR |
| pop ID | 1 | 2 | 3 | 1 | 2 | 3 |
| 1 | \*\*\*\* | 0.9834 | 0.9911 | \*\*\*\* | 0.9815 | 0.9775 |
| 2 | 0.0167 | \*\*\*\* | 0.9805 | 0.0186 | \*\*\*\* | 0.9701 |
| 3 | 0.0089 | 0.0197 | \*\*\*\* | 0.0228 | 0.0304 | \*\*\*\* |