**Table S1: Agro-meteorological details of the test locations viz. Medziphema (MDZ), Palampur (PLM), Dharwad (DWD), Jabalpur (JBL) and Indore (IND) in three consecutive years namely, 2017 (17), 2018 (18) and 2019 (19). masl-** **metres above sea level,** RF-Rainfall, RH-Relative Humidity and RD-Number of Rainy Days.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Environment | Location | Latitude  (°N) | Longitude  (°E) | Altitude (masl) | Agro-ecosystem | RF  (mm) | RH (%) | RD |
| MDZ17 | Medziphema | 25.753717 | 93.857852 | 449.07 | Hot sub-humid (moist) to humid eco-region | 1476.4 | 83.72 | 61 |
| MDZ18 | 993.8 | 81.54 | 52 |
| MDZ19 | 850.4 | 85.54 | 63 |
| PLM17 | Palampur | 32.100048 | 76.546847 | 1270 | Sub-humid mid-hill | 2302.6 | 74.89 | 84 |
| PLM18 | 2606.7 | 78.15 | 76 |
| PLM19 | 1450.3 | 73.85 | 84 |
| DWD17 | Dharwad | 15.498779 | 74.985373 | 678 | Sub-humid hot-dry | 143.1 | 86.50 | 24 |
| DWD18 | 131.1 | 78.60 | 11 |
| DWD19 | 204.2 | 86.35 | 72 |
| JBL17 | Jabalpur | 23.215343 | 79.945885 | 390.4 | Hot sub-humid (Dry) | 839.1 | 70.54 | 56 |
| JBL18 | 1115.1 | 79.54 | 47 |
| JBL19 | 1639.2 | 76.02 | 56 |
| IND17 | Indore | 22.679201 | 75.873164 | 550 | Semi arid | 736.2 | 78.11 | 67 |
| IND18 | 642.2 | 79.66 | 58 |
| IND19 | 1249.9 | 79.54 | 56 |

**Table S2: Location-wise mean performance of genotypes.** MDS(G)-Genotypic Mean Disease Score and MDS(L)-Location Mean Disease Score

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Genotype(Genotype Code) | Medziphema | Palampur | Dharwad | Jabalpur | Indore | MDS(G) |
| AMS 100-39(G1) | 2.55 | 3.66 | 4.11 | 2.66 | 7.44 | 4.08 |
| AMS 2014-1(G2) | 0.66 | 2.33 | 4.33 | 2.66 | 5.22 | 3.04 |
| BAUS 102(G3) | 2.44 | 7.44 | 4.33 | 2.11 | 0.55 | 3.37 |
| DS 3108(G4) | 2.22 | 1.66 | 5.00 | 2.00 | 2.33 | 2.64 |
| DSb 34(G5) | 0.00 | 3.66 | 3.66 | 2.11 | 8.11 | 3.51 |
| KDS 992(G6) | 4.55 | 2.11 | 4.77 | 4.00 | 8.33 | 4.75 |
| MACS 1493(G7) | 0.88 | 0.88 | 4.77 | 1.66 | 7.00 | 3.04 |
| NRC 128(G8) | 0.44 | 0.00 | 5.00 | 0.22 | 1.77 | 1.48 |
| NRC 131(G9) | 3.11 | 4.33 | 5.66 | 1.22 | 5.88 | 4.04 |
| NRC 132(G10) | 1.00 | 0.77 | 3.88 | 2.44 | 7.66 | 3.15 |
| NRC 136(G11) | 3.55 | 0.11 | 4.77 | 2.33 | 7.44 | 3.64 |
| NRC 137(G12) | 1.00 | 0.66 | 5.22 | 3.44 | 7.88 | 3.64 |
| NRCSL 1(G13) | 2.55 | 2.55 | 5.44 | 3.44 | 7.88 | 4.37 |
| PS 1611(G14) | 0.22 | 2.11 | 4.55 | 0.22 | 4.77 | 2.37 |
| PS 1613(G15) | 1.00 | 0.55 | 5.22 | 1.22 | 7.22 | 3.04 |
| RSC 11-03(G16) | 1.00 | 2.77 | 4.33 | 0.66 | 2.77 | 2.31 |
| RSC 11-07(G17) | 1.00 | 2.55 | 3.66 | 2.44 | 3.00 | 2.53 |
| SKF-SPS-11(G18) | 6.55 | 0.66 | 4.11 | 2.55 | 0.77 | 2.93 |
| JS 335(G19) | 8.55 | 7.00 | 6.33 | 5.22 | 7.66 | 6.95 |
| MDS(L) | 2.28 | 2.41 | 4.69 | 2.24 | 5.46 | - |

**Table S3 : BLUP values for the anthracnose disease scores in genotypes under study.** BLUPg-Best Linear Unbiased Prediction for genotype effect, LL-Lower Limit and UL-Upper Limit

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genotype(Genotype Code) | **BLUPg** | **Predicted** | **LL** | **UL** |
| AMS 100-39(G1) | 0.56 | 3.98 | 3.00 | 4.96 |
| AMS 2014-1(G2) | -0.31 | 3.10 | 2.12 | 4.09 |
| BAUS 102(G3) | -0.03 | 3.38 | 2.40 | 4.37 |
| DS 3108(G4) | -0.65 | 2.77 | 1.79 | 3.75 |
| DSb 34(G5) | 0.07 | 3.50 | 2.51 | 4.48 |
| KDS 992(G6) | 1.12 | 4.54 | 3.56 | 5.52 |
| MACS 1493(G7) | -0.31 | 3.10 | 2.12 | 4.09 |
| NRC 128(G8) | -1.62 | 1.80 | 0.81 | 2.78 |
| NRC 131(G9) | 0.52 | 3.94 | 2.96 | 4.93 |
| NRC 132(G10) | -0.22 | 3.20 | 2.22 | 4.18 |
| NRC 136(G11) | 0.18 | 3.61 | 2.63 | 4.59 |
| NRC 137(G12) | 0.18 | 3.61 | 2.63 | 4.59 |
| NRCSL 1(G13) | 0.80 | 4.22 | 3.24 | 5.21 |
| PS 1611(G14) | -0.87 | 2.55 | 1.56 | 3.53 |
| PS 1613(G15) | -0.31 | 3.10 | 2.12 | 4.09 |
| RSC 11-03(G16) | -0.93 | 2.49 | 1.51 | 3.47 |
| RSC 11-07(G17) | -0.74 | 2.68 | 1.69 | 3.66 |
| SKF-SPS-11(G18) | -0.40 | 3.01 | 2.03 | 3.99 |
| JS 335(G19) | 2.97 | 6.39 | 5.41 | 7.37 |

**Table S4 : WAASB and WAASBY based ranking of genotypes: MDS- Mean Disease Score, OrWAASB-ranking based on WAASB index, OrWAASBY- ranking based on WAASBY index**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Genotype(Genotype Code) | **MDS** | **WAASB** | **OrWAASB** | **WAASBY** | **OrWAASBY** |
| AMS 100-39(G1) | 4.08 | 0.41 | 4 | 66.72 | 11 |
| AMS 2014-1(G2) | 3.04 | 0.34 | 2 | 81.14 | 5 |
| BAUS 102(G3) | 3.37 | 1.61 | 19 | 42.54 | 18 |
| DS 3108(G4) | 2.64 | 0.68 | 12 | 76.73 | 6 |
| DSb 34(G5) | 3.51 | 0.83 | 16 | 62.14 | 13 |
| KDS 992(G6) | 4.75 | 0.69 | 13 | 51.39 | 17 |
| MACS 1493(G7) | 3.04 | 0.58 | 8 | 74.62 | 7 |
| NRC 128(G8) | 1.48 | 0.50 | 7 | 94.31 | 1 |
| NRC 131(G9) | 4.04 | 0.42 | 6 | 67.00 | 10 |
| NRC 132(G10) | 3.15 | 0.62 | 10 | 72.07 | 9 |
| NRC 136(G11) | 3.64 | 0.86 | 17 | 59.89 | 15 |
| NRC 137(G12) | 3.64 | 0.80 | 15 | 61.60 | 14 |
| NRCSL 1(G13) | 4.37 | 0.42 | 5 | 63.19 | 12 |
| PS 1611(G14) | 2.37 | 0.33 | 1 | 89.43 | 2 |
| PS 1613(G15) | 3.04 | 0.64 | 11 | 73.05 | 8 |
| RSC 11-03(G16) | 2.31 | 0.60 | 9 | 82.73 | 4 |
| RSC 11-07(G17) | 2.53 | 0.38 | 3 | 86.00 | 3 |
| SKF-SPS-11(G18) | 2.93 | 1.29 | 18 | 56.61 | 16 |
| JS 335(G19) | 6.95 | 0.76 | 14 | 23.19 | 19 |