3. MATERIALS AND METHODS

3.1. Plant materials

Sixty-four (64) varieties of chilli (Table 3.1) of exotic and local origin representing varying quality determining factors and other agronomic characters were evaluated in MARDI Station, Jalan Kebun, Klang from 1990-1991. The trial was conducted in a randomised complete block design (RCBD) with four replications. Each plot consisted of 10 plants, planted in single row bed of 6 metres long. The plants were spaced at 100 cm between rows and 60 cm within rows.

Based on the performance of this preliminary evaluation trial, 22 varieties were of chilli selected for G x E studies. Factors determining dried chilli quality were the main selection criteria. Hence the following characteristics were measured.

1) Fruit with long, slim and thin mesocarp or varieties whose mesocarp has big pores.
2) Capsaicin level and colour
3) Upright and determinate fruiting habit.
4) Varieties with conversion rate of more than 15 %
<table>
<thead>
<tr>
<th>Varieties</th>
<th>Source</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Ch 291 P (VI)*</td>
<td>Korea</td>
<td>Fresh market, dark green unripe, long fat fruits, pendent, SPH.</td>
</tr>
<tr>
<td>2. Ch 221</td>
<td>Sarawak</td>
<td>Fresh, green, long big fruit, pendent, NPH.</td>
</tr>
<tr>
<td>3. Hong Il pun</td>
<td>Korea</td>
<td>Double purpose, light green/green, medium size fruit, upright, SPH.</td>
</tr>
<tr>
<td>4. Ch 272</td>
<td>AGASIA</td>
<td>Long, fat fruit, light green/green unripe, low pungency.</td>
</tr>
<tr>
<td>5. Ch 274</td>
<td>AGASIA</td>
<td>Long, slim fruit, pungent.</td>
</tr>
<tr>
<td>6. Ch 278</td>
<td>AGASIA</td>
<td>Long, slim fruit, very pungent.</td>
</tr>
<tr>
<td>7. Ch 279</td>
<td>AGASIA</td>
<td>Big fruit type, flat shoulder, dark green unripe, less pungent.</td>
</tr>
<tr>
<td>8. Ch 204</td>
<td>Local</td>
<td>Dark red when mature, long, medium size fruit, light green/green unripe.</td>
</tr>
<tr>
<td>9. Ch 254*</td>
<td>Johor</td>
<td>Fresh market, dark green unripe, slim fruit, fruit in tiers, small leaves, NPH.</td>
</tr>
<tr>
<td>10. R1-20-P4-31</td>
<td>Local</td>
<td>Green unripe, normal size fruit, pendent.</td>
</tr>
<tr>
<td>11. Ch 234-1</td>
<td>Langkap</td>
<td>Long and slightly flattened fruit, straight shoulder, pendent.</td>
</tr>
<tr>
<td>12. Ch 284-4</td>
<td>Lombok</td>
<td>Long fruit, pendent, big plant.</td>
</tr>
<tr>
<td>13. Ch 234-11</td>
<td>Langkap</td>
<td>Long slightly flattened fruits, flattened shoulder, pendent, broad leaves, TPH.</td>
</tr>
<tr>
<td>14. Ch 234-13</td>
<td>Langkap</td>
<td>Long slightly flattened fruits, flattened shoulder, pendent, TPH.</td>
</tr>
<tr>
<td>15. Ch 284-6*</td>
<td>Lombok selection</td>
<td>Fresh market, long wrinkled fruit, pendent, NPH.</td>
</tr>
<tr>
<td>16. Purple Chilli*</td>
<td>Estirico (Exotic)</td>
<td>Dried, slim, purple when unripe fruit, purplish stem, pubescent stem, purple flower, big plant.</td>
</tr>
<tr>
<td>17. 901-166-3.</td>
<td>Local seed Co.</td>
<td>Long fruit, pendent.</td>
</tr>
<tr>
<td>18. Ch 248 (901)</td>
<td>Local seed Co.</td>
<td>Internode purple, presence of pubescence, green unripe.</td>
</tr>
<tr>
<td>20. Junsol</td>
<td>Korea</td>
<td>Medium size fruit.</td>
</tr>
<tr>
<td>21. Chilli 3109</td>
<td>Local seed Co.</td>
<td>Long fruit, upright fruiting habit.</td>
</tr>
<tr>
<td>22. Chilli 3110</td>
<td>Local seed Co.</td>
<td>Upright fruiting habit.</td>
</tr>
<tr>
<td>24. Ch 258 XIAN</td>
<td>China</td>
<td>Dried chilli, small fruits, upright fruiting.</td>
</tr>
<tr>
<td>25. Ch 257 XIAN*</td>
<td>China</td>
<td>Dried chilli, long fruits, pendent.</td>
</tr>
<tr>
<td>27. Ch 260 B</td>
<td>China</td>
<td>Slim, wrinkled fruit, small plant.</td>
</tr>
<tr>
<td>28. Ch 252-C*</td>
<td>Thailand</td>
<td>Dried chilli, quite long fruit, upright, big plant.</td>
</tr>
<tr>
<td>29. Ch 252-A</td>
<td>Thailand</td>
<td>Dried chilli, cili padi like, upright, big plant, upright fruiting, fruits in cluster.</td>
</tr>
<tr>
<td>31. Ch 286*</td>
<td>Sri Lanka</td>
<td>Dried chilli, small fruit, pendent, small leaves, bushy plant, SBP.</td>
</tr>
<tr>
<td>32. Ch 291</td>
<td>Korea</td>
<td>Double purpose, big fleshy fruits, light green unripe, pendent, SPH.</td>
</tr>
<tr>
<td>33. Ch 256</td>
<td>Korea</td>
<td>Glossy fruits, light green/green, upright and single.</td>
</tr>
<tr>
<td>34. Cili Akar</td>
<td>Indonesia</td>
<td>Long, very slim wrinkled fruit, big plant, narrow leaves.</td>
</tr>
<tr>
<td>Varieties</td>
<td>Origin</td>
<td>Description</td>
</tr>
<tr>
<td>---------------------------------</td>
<td>---------</td>
<td>-----------------------------------------------------------------------------</td>
</tr>
<tr>
<td>35. Local Japan</td>
<td>Japan</td>
<td>Dried, small conical, upright, cluster, SPH.</td>
</tr>
<tr>
<td>36. Ch 3811 Hantaka*</td>
<td>Japan</td>
<td>Dried, small fruit, cluster, upright, SPH.</td>
</tr>
<tr>
<td>37. Ch 287</td>
<td>Thailand</td>
<td>For powder, small leaves, fruit <em>cili padi</em> like, upright, shrubby.</td>
</tr>
<tr>
<td>38. CK #17*</td>
<td>Taiwan</td>
<td>Dried chilli, upright fruiting, single, small fruit type, TPH.</td>
</tr>
<tr>
<td>39. Huey Si Thon *</td>
<td>Thailand</td>
<td>Dried chilli, small fruit, upright fruiting, wavy leaf margin, TPH.</td>
</tr>
<tr>
<td>40. Kulai*</td>
<td>Local</td>
<td>Fresh market, long fruit, pointed end, erect plant type, internode purple.</td>
</tr>
<tr>
<td>41. Langkap*</td>
<td>Local</td>
<td>Fresh market, flat shoulder, slightly wrinkled surface, slightly flattened.</td>
</tr>
<tr>
<td>42. Tanjong Minyak</td>
<td>Local</td>
<td>Fresh, fleshy big fruit, erect plant type.</td>
</tr>
<tr>
<td>43. Ch 290 (1-3-18)</td>
<td>Local</td>
<td>Dried chilli, light green almost yellow unripe.</td>
</tr>
<tr>
<td>44. Cabe Berebes*</td>
<td>Indonesia</td>
<td>Dried chilli, long slim fruit, dark green unripe, pendant, narrow leaves, short shrubby, flat top (determinate).</td>
</tr>
<tr>
<td>45. TIT super</td>
<td>Indonesia</td>
<td>Fresh market, big compact, table top plant type, long, dark green, unripe, purplish stem.</td>
</tr>
<tr>
<td>46. Ch 234-14*</td>
<td>Local selection</td>
<td>Double purpose, long fruit, wrinkled surface, slightly flattened, NPH.</td>
</tr>
<tr>
<td>47. Ch 280</td>
<td>AGASIA</td>
<td>Dried chilli, wrinkled and twisted fruit.</td>
</tr>
<tr>
<td>48. Ch 291 (1-4-18)</td>
<td>Korea</td>
<td>Dried chilli, fat fruit, green unripe, medium table, flat top.</td>
</tr>
<tr>
<td>49. Ch 252-C(1-5-15)*</td>
<td>Thailand</td>
<td>Dried chilli, small slim fruit, upright, TPH.</td>
</tr>
<tr>
<td>50. Jatilaba</td>
<td>Indonesia</td>
<td>Fresh market, pendant, dark green leaves.</td>
</tr>
<tr>
<td>51. Ch 382 (MC-CH1)</td>
<td>Local</td>
<td>Fresh market, pendant, light/green unripe.</td>
</tr>
<tr>
<td>52. Ch 383 MC-CH2</td>
<td>Local</td>
<td>Fresh market, pendant, long fruit.</td>
</tr>
<tr>
<td>53. Ch 384 (MC-CH3)</td>
<td>Local</td>
<td>Fresh, pendant, long good size fruit, green unripe, wrinkled surface, pubescent stem, purple internode.</td>
</tr>
<tr>
<td>54. Ch 385 (MC)*</td>
<td>Japan</td>
<td>Dried, small fruit upright, in cluster.</td>
</tr>
<tr>
<td>55. Ch 386 (MC)</td>
<td>Exotic</td>
<td>Dried chilli, medium size fruit.</td>
</tr>
<tr>
<td>56. 01110-1 (MC)*</td>
<td>Exotic</td>
<td>Dried, chilli, dried on plants.</td>
</tr>
<tr>
<td>57. Ch 388 (MC)*</td>
<td>Local</td>
<td>Fresh market, long fruit pendant, light green unripe.</td>
</tr>
<tr>
<td>58. Ch 389 (MC)*</td>
<td>Local</td>
<td>Fresh market, pendant medium size fruit, purple stem.</td>
</tr>
<tr>
<td>59. Ch 391 (MC)</td>
<td>Local</td>
<td>Fresh market, pendant.</td>
</tr>
<tr>
<td>60. Ch 392 (MC)</td>
<td>Sekincan</td>
<td>Fresh market, pendant.</td>
</tr>
<tr>
<td>61. Ch 393 (MC)*</td>
<td>Menglembu</td>
<td>Fresh market, pendant, dark green unripe, normal size, fat fruit.</td>
</tr>
<tr>
<td>62. Chili No 40-1</td>
<td>Local</td>
<td>Fresh market, pendant fruiting habit.</td>
</tr>
<tr>
<td>63. MC 4*</td>
<td>MARDI</td>
<td>Fresh market, pendant, medium size fruit, flat shoulder, synchronised fruiting, NPH.</td>
</tr>
<tr>
<td>64. Indian Sanam*</td>
<td>India</td>
<td>Dried, small size chilli, pendant, NPH.</td>
</tr>
</tbody>
</table>

* = Selected for G x E study
P  = pendent
SPH = short plant height
NPH = normal plant height
TPH = tall plant height
SBP = short bushy plant
3.2. Multilocalional trials

Seven locations namely Jalan Kebun, Klang (Selangor), Cameron Highlands (Pahang), Kuala Linggi (Melaka), Bertam (Penang), Telong (Kelantan), Gajah Mati (Kedah) and Kundang (Selangor) were chosen to provide a range of environmental conditions varying in agro-ecological zone including temperature regime, rainfall pattern and soil types. The locations are illustrated in Figure 3.1. The planting dates and the agro-ecological features such as soil types, effective rainfall for each of the test environments are given in Table 3.2. At each location the trials were carried out for two seasons differing in rainfall distribution. The planting dates (Table 3.2) were staggered to accommodate different distribution of rainfall and to facilitate management and data collection.

The experimental design, number of replications, plot size, spacing and management practices adopted were similar in all environments. The experimental design used was randomised complete block design (RCBD) with four replications. Each plot planted with 20 plants in a single-row bed at 100 cm between rows and 60 cm within rows. The seedlings were raised, one plant per cell in multi-cellular seedling trays, commonly known as Speeding Trays after the inventor, in the nursery and they were transplanted when they were about 4 weeks old. Chicken dung was applied as top dressing at the rates depending on soil types, 20 t/ha, 40 t/ha, 6 t/ha and 4 t/ha for bris, acid sulphate, mineral and peat, respectively. Peat and acid sulphate soils at Jalan Kebun and Kuala Linggi respectively were limed to a pH of about 5.0 to 5.5. Compound NPK fertilizer (12:12:17:2) was applied at the rate 2.5 t/ha in four split applications. With the exception of Telong (bris), reflective plastic mulching was applied on the bed. Inter row weeding was carried out manually.
TL - Telong (Kelantan) in Agricultural Zone 1; GM-Gajah Mati (Kedah) in Agricultural Zone 1
BT - Bertam (Penang) in Agricultural Zone 2; KL - Kuala Linggi (Malacca) in Agricultural Zone 2;
KD - Kundang (Selangor) in Agricultural Zone 4; JK - Jalan Kebun (Selangor) in Agricultural Zone 4
CH - Cameron Highlands (Pahang) in Agricultural Zone 4.

Figure 3.1. Location of the trial sites.
Table 3.2. Meteorological data and soil conditions of selected sites for G x E study

<table>
<thead>
<tr>
<th>Location</th>
<th>Code</th>
<th>Soil Type</th>
<th>Soil pH</th>
<th>Planting-season</th>
<th>Temperature (°C)</th>
<th>Mean Monthly Rainfall (mm)</th>
<th>Agriculture zone*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Jalan Kebun</td>
<td>JK1</td>
<td>Peat</td>
<td>3.5-4.7</td>
<td>Mac 91 - Sept. 91</td>
<td>35.7</td>
<td>23.3</td>
<td>154.5</td>
</tr>
<tr>
<td></td>
<td>JK2</td>
<td></td>
<td></td>
<td>Sept. 92 - Mac 93</td>
<td>32.7</td>
<td>22.4</td>
<td>200.8</td>
</tr>
<tr>
<td>Kuala Linggi</td>
<td>LG1</td>
<td>Acid sulphate</td>
<td>2.8-3.5</td>
<td>Oct.91 - Apr.92</td>
<td>31.2</td>
<td>22.7</td>
<td>137.0</td>
</tr>
<tr>
<td></td>
<td>LG2</td>
<td></td>
<td></td>
<td>May.93 - Dec. 93</td>
<td>31.3</td>
<td>24.0</td>
<td>164.0</td>
</tr>
<tr>
<td>Cameron Highlands</td>
<td>CH1</td>
<td>Mineral</td>
<td>4.8-5.2</td>
<td>Feb. 92 - Dec. 92</td>
<td>22.6</td>
<td>15.2</td>
<td>204.0</td>
</tr>
<tr>
<td></td>
<td>CH2</td>
<td></td>
<td></td>
<td>Aug. 93 - Jan. 94</td>
<td>22.1</td>
<td>15.2</td>
<td>270.0</td>
</tr>
<tr>
<td>Bertam</td>
<td>BM1</td>
<td>Mineral</td>
<td>4.5-5.2</td>
<td>Oct. 91 - Mar. 92</td>
<td>32.9</td>
<td>23.1</td>
<td>99.0</td>
</tr>
<tr>
<td></td>
<td>BM2</td>
<td></td>
<td></td>
<td>Feb.93 - Aug. 93</td>
<td>33.1</td>
<td>23.5</td>
<td>127.8</td>
</tr>
<tr>
<td>Gajah Mati</td>
<td>GM1</td>
<td>Mineral</td>
<td>4.5-5.0</td>
<td>May 92 - Sept. 92</td>
<td>32.5</td>
<td>23.4</td>
<td>170.4</td>
</tr>
<tr>
<td></td>
<td>GM2</td>
<td></td>
<td></td>
<td>Aug. 93 - Dec.93</td>
<td>31.5</td>
<td>23.0</td>
<td>163.2</td>
</tr>
<tr>
<td>Telong</td>
<td>TL1</td>
<td>Bris</td>
<td>4.5-5.5</td>
<td>Aug.91 - Dec. 91</td>
<td>30.7</td>
<td>23.7</td>
<td>229.7</td>
</tr>
<tr>
<td></td>
<td>TL2</td>
<td></td>
<td></td>
<td>June.92 - Nov.92</td>
<td>31.7</td>
<td>23.7</td>
<td>206</td>
</tr>
<tr>
<td>Kundang</td>
<td>KD1</td>
<td>Sand tailing</td>
<td>4.5-5.0</td>
<td>Dec.93 - May 94</td>
<td>32.8</td>
<td>22.5</td>
<td>218.0</td>
</tr>
<tr>
<td></td>
<td>KD2</td>
<td></td>
<td></td>
<td>Aug.94 - Mar.95</td>
<td>32.4</td>
<td>22.5</td>
<td>222.0</td>
</tr>
</tbody>
</table>

* @ 1, 2, 4, denotes areas with 3-5 months agriculture drought; areas with 1-2 months agriculture drought; areas with no agriculture drought, respectively (Nieuwolt 1982)
Insecticides namely dicofol (Keltane*), profenofos (Selecron*), methiocarb (Miserol*) and copper fungicides such as Kocide* were sprayed on the chilli plants when the symptom of the attack by insects or the diseases appeared. Dicofol was used for controlling mites, while profenofos and methiocarb were used to control insects such as aphids and thrips, respectively. To control Choanephora leaf blight and anthracnose fruit rot copper hydroxide and mancozeb (Dithane M-45) were used.

The fruits were harvested when they were fully ripe and only 10 randomly selected plants per plot were harvested. Samples of 200 g of fruits per plot were solar dried. The weight of each sample was recorded every alternate day for the first week and daily recording for the subsequent weeks until constant weight was reached. The dried sample with 9-12 % moisture level was ground using centrifugal grinder with 0.5 mm mesh size.

3.3 Data Collection

The following data were collected from 10 randomly selected plants/plot.

1) Yield per plant (g): Accumulated fresh weight of fully ripe fruits harvested per plot divided by number of plants.

2) Number of fruits per plant: Accumulated number of fruits harvested per plant divided by number of plants.

3) Fruit length (cm): The length from the tip of fruit to the apex of calyx was measured by callipers. The measurements were taken from 10 fruits from harvested at peak period for each plot.

4) Number of seeds/fruit: The accumulated number of seeds from 10 selected fruits divided by 10.
5) Plant height at harvest (cm): Height was measured by a metre ruler from the soil level to the apical bud of the main stem at first harvest.

6) Days to dry (DTD): Number of days to take for fruit to dry till constant weight (at moisture content of about 12%). Samples of 200 g of fruits per plot were solar dried (described in 3.5). The weight of each sample was recorded every alternate day for the first week and daily recording for the subsequent weeks until constant weight.

7) Conversion rate (%): The ratio of dry weight to initial fresh weight of 200 g. Here, conversion rate was calculated based on the dry weight of the 200 g fruit sample.

\[
\text{Conversion rate (\%)} = \frac{\text{Dry weight (g)}}{200 \text{ (g)}} \times 100 \%
\]

8) Percentage of bleaching (%): Bleaching is discolouration of fruit on drying. Percentage of bleaching is the % of discolouration of the individual fruit. It was calculated as an accumulative % of the discoloured portion of the fruit over total number of fruits.

9) Colour: The fully ripe fruits were first dried until constant weight. The dried sample with 9-12 % moisture level was ground using centrifugal grinder with 0.5 mm mesh size. To calibrate standard colour curve, the method by Lease and Lease (1962) was used. Ten ml of acetone (lab grade) and 40 ml of hexane were added to 0.5 g of dried ground sample of chilli in a 100-ml conical flask. The content of the flask was subjected to 5 hours shaking at 1000 rpm. The light transmission was determined colorimetrically at wave length 490 nm, respectively. The
sample of extract is placed in the vial and placed in the colorimeter. The light transmission was expressed in percentage.

10) Capsaicin content (mg/g): The fully ripe fruits were dried to 9-12 % moisture and then ground using centrifugal grinder with 0.5 mm mesh size. Fifty samples of varying range of capsaicin levels were determined to calibrate capsaicin standard. Ten g of dried ground chillies were extracted using 50 ml of acetone (A.R. grade) according to Sankarikutty et al. (1978). The extract was then made up to 100 ml with acetone and analysed using gas chromatography technique as described by Todd et al. (1977). The capsaicin content was expressed in mg/g. The capsaicin contents of samples from the multilocational trials, were measured using computerised Near Infrared spectrophotometer (Perstorp Analytical Co., USA) according to Casciero et al. 1985.

**Meteorological data:**

Data on a) temperature and b) rainfall were collected per month from the nearest meteorological stations over the growing period for each location. The relative humidity (R.H.) for each location was calculated by comparing the difference between the dry bulb and wet bulb against the scale of Mason’s Hygrometer.

For acidity test, about 50 points soil samples were collected at random per site. All the samples were analysed for pH by a pH meter.

Distribution of temperature, rainfall, solar radiation and R.H for each location as in Figures 3.2.1-3.2.7.
Figure 3.2.1. Distribution of temperature, rainfall and sunshine at Cameron Highlands
Figure 3.2.2. Distribution of temperature, rainfall and sunshine at Bertam
Figure 3.2.3. Distribution of temperature, rainfall and sunshine at Gajah Mati
Figure 3.2.4  Distribution of temperature, rainfall and sunshine at Jalan Kebun
Figure 3.2.5 Distribution of temperature, rainfall and sunshine at Kuala Linggi
Figure 3.2.6  Distribution of temperature, rainfall and sunshine at Telong
Figure 3.2.7  Distribution of temperature, rainfall and sunshine at Kundang
3.5 Drying method

A solar dryer which is a modification of two dryers, namely solar dryer used for drying persimmons in Pakistan (Marden and Schoemaker 1992) and solar dryer for vitamin A (Linehan et al. 1993), was adopted. The dryer consisting of a rectangular raised tray of black plastic insulated wire netting on a metal frame supported at a height of 1 m (to allow free air circulation) above concrete ground by four angular iron beams. The tray was covered with UV treated clear plastic mounted on semi-circular steel frame. The temperature inside the unit was indicated by thermometer, which was hanged inside the unit. All the samples were put out to dry during the day while at night the trays were placed under shelter. The hottest temperature attainable was 44 °C, which is about as high as the drying temperature recommended by Misra (1972).

Under this solar dryer, the temperature rises rapidly to about 40 °C at noon and reaching the hottest point about 44 °C around 2 to 4 PM under normal day. The temperature in the dryer is about 5 - 9 °C higher than the external surrounding. Daily recording of the sample weight was carried out every evening before the trays were placed under shelter until constant weight (the equilibrium moisture) was obtained. During rainy days, the dryer together with the product were kept under shelter and normal heater (hot air blower) was used to raise the temperature of the air under the trolleys so that the drying process continued. The number of days to reach the constant reading reflects the number days taken for the drying process.
3.6. Statistical analysis

3.6.1 Analyses of variance

Analysis of variance was conducted first for each character within each environment, where an environment was defined as one particular planting in a particular location and season and determined by using PROC ANOVA of the SAS Package. Homogeneity of error variances obtained from individual environments was checked by Bartlett’s test (Snedecor and Cochran 1980).

The following illustrates the expected mean squares and tests of significant difference for ANOVA in each environment.

<table>
<thead>
<tr>
<th>Source</th>
<th>df</th>
<th>MS</th>
<th>Expected mean Square</th>
<th>F-tests</th>
</tr>
</thead>
<tbody>
<tr>
<td>Replicate</td>
<td>r-1</td>
<td>M₁</td>
<td>σ² + gσ²_r</td>
<td>M₁/M₃</td>
</tr>
<tr>
<td>Genotype</td>
<td>g-1</td>
<td>M₂</td>
<td>σ² + rσ²_g</td>
<td>M₂/M₃</td>
</tr>
<tr>
<td>Error</td>
<td>(r-1)(g-1)</td>
<td>M₃</td>
<td>σ²</td>
<td></td>
</tr>
</tbody>
</table>

3.6.2. G x E interaction

3.6.2.1. Combined analyses of variance

After analyses of variance by environment, combined analyses of variance over seven locations, each for two planting-seasons were computed. All the traits recorded were each subjected to two methods of analyses. Genotypes, environments (planting-season and location combined) were assumed to be random, normally and independently distributed variables with means of zero and generating variances of corresponding designations.
a) Method A (With Planting-season and location effects combined)

\[ Y_{grt} = \mu + G_g + E_t + R_{rt0} + e_{grt} \]

where, \( Y_{grt} \) = the value of the character for the \( g^{th} \) genotype in the \( t^{th} \) environment, in the \( r^{th} \) replication

\( G_g \) = effect of the \( g^{th} \) genotype

\( \mu \) = the mean value across all genotypes and environments.

\( E_t \) = the effect of the \( t^{th} \) environment

\( R_{rt0} \) = the effect of \( r^{th} \) replication within \( t^{th} \) environment

\( e_{grt} \) = the error associated with the \( g^{th} \) genotype in the \( t^{th} \) environment and \( r^{th} \) replication

and, \( r = 1 \) to \( 4 \); \( t = 1 \) to \( 14 \); \( g = 1 \) to \( 22 \).

Test of significance for method A were as follows:

\[
F(\text{Genotype}) = \frac{M_3}{M_4}
\]

\[
F(\text{G x E}) = \frac{M_4}{M_5}
\]

\[
F(\text{Environments}) = \frac{(M_1 + M_2)/(M_4 + M_4)}{\text{degrees of freedom as Satherth Waite's approximation.}}
\]

Approximate degree of freedom for \( (M_1 + M_3) \) and \( (M_2 + M_4) \), degree calculate according to Satherth Waite's

\[
\text{Approximate } df_{nl} \ (M_1 + M_5) = \frac{(M_1 + M_4)^2}{\frac{M_1^2}{df[(e-1)]} + \frac{M_4^2}{df[e(r-1)(g-1)]}}
\]

Similarly for \( (M_2 + M_4) \),

\[
\text{Approximate } df_{nl} = \frac{(M_2 + M_4)^2}{\frac{M_2^2}{df[e(r-1)]} + \frac{M_4^2}{df[(g-1)(e-1)]}}
\]
The estimates of variance component through Method A, were estimated from the appropriate linear functions of mean squares as indicated in Table 3.3 and were calculated as follows:

\[
\begin{align*}
\sigma^2 & = M_1 \\
\sigma^2_{GE} & = (M_4 - M_5)/r \\
\sigma^2_0 & = (M_3 - M_4)/rt \\
\sigma^2_E & = (M_1 - M_2 - M_4 + M_5)/rg
\end{align*}
\]

Thus the phenotypic variance, \( \sigma^2_P = \sigma^2_G + \sigma^2_E / rg + \sigma^2_{GE} / r \)

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>df</th>
<th>MS</th>
<th>Expected Mean squares</th>
<th>F-tests</th>
</tr>
</thead>
<tbody>
<tr>
<td>Environments (E)</td>
<td>e-1</td>
<td>M_1</td>
<td>( \sigma^2 + \sigma^2_{GE} + g\sigma^2_{r(E)} + r\sigma^2_E )</td>
<td>( (M_1 + M_5)/(M_2 + M_4) )</td>
</tr>
<tr>
<td>Reps within Environments r(E)</td>
<td>e(r-1)</td>
<td>M_2</td>
<td>( \sigma^2 + g\sigma^2_{r(E)} )</td>
<td>( M_3/M_5 )</td>
</tr>
<tr>
<td>Genotypes (G)</td>
<td>g-1</td>
<td>M_3</td>
<td>( \sigma^2 + \sigma^2_{GE} )</td>
<td>( M_3/M_4 )</td>
</tr>
<tr>
<td>G x E</td>
<td>(g-1)(e-1)</td>
<td>M_4</td>
<td>( \sigma^2 + r\sigma^2_{GE} )</td>
<td>( M_4/M_5 )</td>
</tr>
<tr>
<td>Pool Error</td>
<td>e(g-1) (r-1)</td>
<td>M_5</td>
<td>( \sigma^2 )</td>
<td>-</td>
</tr>
</tbody>
</table>

\( e, r, g \) are numbers of environments, replications, genotypes, respectively.

\( \sigma^2 \) = error variance

\( \sigma^2_G \) = genotype variance

\( \sigma^2_{GE} \) = genotype x environment interaction variance

\( \sigma^2_E \) = Environment variance.

\( \sigma^2_{r(E)} \) = replicate within environment variance
b) Method B (With planting-season and location effects separated)

The environmental components are partitioned into locations, planting-seasons, location x planting-seasons. Similarly, the genotype interactions are partitioned into genotype and location, genotype and planting-season and genotype x planting-season x location interactions.

\[ Y_{gls} = \mu + G_g + L_l + S_s + R_{r(l,s)} + (GS)_{gs} + (GL)_{gl} + (GSL)_{gsl} + e_{gls} \]

where,

\( Y_{gls} \) = the value for the character \( g^{th} \) genotype in the \( s^{th} \) planting-season, the \( l^{th} \) location, and the \( r^{th} \) replicate

\( \mu \) = the population mean

\( G_g \) = the effect of the \( g^{th} \) genotype

\( L_l \) = the effect of the \( l^{th} \) location

\( S_s \) = the effect of the \( s^{th} \) planting-season

\( R_{r(l,s)} \) = the effect of \( r^{th} \) replicate in the \( s^{th} \) planting-season and the \( l^{th} \) location

\( (GS)_{gs} \) = the effect of the interaction between the \( g^{th} \) genotype and the \( s^{th} \) planting-season

\( (GL)_{gl} \) = the effect of the interaction between the \( g^{th} \) genotype and the \( l^{th} \) location

\( (GSL)_{gsl} \) = the effect of the interaction between the \( g^{th} \) genotype in the \( s^{th} \) planting-season and the \( l^{th} \) location.

\( e_{gls} \) = the error associated with the genotype in the \( s^{th} \) planting-season, \( l^{th} \) location, and \( r^{th} \) replication

and , \( r = 1 \) to \( 4; \ s = 1 \) to \( 2; \ l = 1 \) to \( 7; \ g = 1 \) to \( 22; \)

Similarly, the genotypes, planting-seasons, and locations were assumed to be random, normally and independently distributed variable with means of zero and generating variances of corresponding designations (Table 3.4).
Table 3.4. Analysis of variance and expected mean squares for the analysis of Method B: over planting-season and location effects separated

<table>
<thead>
<tr>
<th>Source of variation</th>
<th>Degree of Freedom</th>
<th>Mean squares</th>
<th>Expected Mean squares</th>
<th>F-tests</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotypes (G)</td>
<td>(g-1)</td>
<td>M&lt;sub&gt;1&lt;/sub&gt;</td>
<td>( \sigma^2 + r \sigma^2_{GL} + r \sigma^2_{OS} + r \sigma^2_{SL} + r \sigma^2_{OL} )</td>
<td>(M&lt;sub&gt;1&lt;/sub&gt;+M&lt;sub&gt;8&lt;/sub&gt;)/(M&lt;sub&gt;6&lt;/sub&gt;+M&lt;sub&gt;7&lt;/sub&gt;)</td>
</tr>
<tr>
<td>Location (L)</td>
<td>(l-1)</td>
<td>M&lt;sub&gt;2&lt;/sub&gt;</td>
<td>( \sigma^2 + r \sigma^2_{GL} + r \sigma^2_{OS} + r \sigma^2_{SL} + r \sigma^2_{OL} + g \sigma^2_{L} )</td>
<td>(M&lt;sub&gt;2&lt;/sub&gt;+M&lt;sub&gt;8&lt;/sub&gt;)/(M&lt;sub&gt;4&lt;/sub&gt;+M&lt;sub&gt;6&lt;/sub&gt;)</td>
</tr>
<tr>
<td>Planting-season (S)</td>
<td>(s-1)</td>
<td>M&lt;sub&gt;3&lt;/sub&gt;</td>
<td>( \sigma^2 + r \sigma^2_{GL} + r \sigma^2_{OS} + r \sigma^2_{SL} + r \sigma^2_{OL} + s \sigma^2 + g \sigma^2_{L} )</td>
<td>(M&lt;sub&gt;3&lt;/sub&gt;+M&lt;sub&gt;8&lt;/sub&gt;)/(M&lt;sub&gt;4&lt;/sub&gt;+M&lt;sub&gt;7&lt;/sub&gt;)</td>
</tr>
<tr>
<td>S x L</td>
<td>(s-1) (l-1)</td>
<td>M&lt;sub&gt;4&lt;/sub&gt;</td>
<td>( \sigma^2 + r \sigma^2_{GL} + r \sigma^2_{OS} + r \sigma^2_{SL} + r \sigma^2_{OL} + s \sigma^2 + g \sigma^2 )</td>
<td>(M&lt;sub&gt;4&lt;/sub&gt;+M&lt;sub&gt;7&lt;/sub&gt;)/(M&lt;sub&gt;5&lt;/sub&gt;+M&lt;sub&gt;8&lt;/sub&gt;)</td>
</tr>
<tr>
<td>Reps in Environments (R x L x S)</td>
<td>s / (r-1)</td>
<td>M&lt;sub&gt;5&lt;/sub&gt;</td>
<td>( \sigma^2 + g \sigma^2 )</td>
<td>-</td>
</tr>
<tr>
<td>G x L</td>
<td>(g-1) (l-1)</td>
<td>M&lt;sub&gt;6&lt;/sub&gt;</td>
<td>( \sigma^2 + r \sigma^2_{GL} + r \sigma^2_{OS} )</td>
<td>(M&lt;sub&gt;6&lt;/sub&gt;+M&lt;sub&gt;8&lt;/sub&gt;)</td>
</tr>
<tr>
<td>G x S</td>
<td>(g-1) (s-1)</td>
<td>M&lt;sub&gt;7&lt;/sub&gt;</td>
<td>( \sigma^2 + r \sigma^2_{GL} + r \sigma^2_{OS} )</td>
<td>(M&lt;sub&gt;7&lt;/sub&gt;+M&lt;sub&gt;8&lt;/sub&gt;)</td>
</tr>
<tr>
<td>G x S x L</td>
<td>(g-1) (s-1) (l-1)</td>
<td>M&lt;sub&gt;8&lt;/sub&gt;</td>
<td>( \sigma^2 + r \sigma^2_{OS} )</td>
<td>(M&lt;sub&gt;8&lt;/sub&gt;+M&lt;sub&gt;9&lt;/sub&gt;)</td>
</tr>
<tr>
<td>Pooled Error</td>
<td>s / (g-1) (r-1)</td>
<td>M&lt;sub&gt;9&lt;/sub&gt;</td>
<td>( \sigma^2 )</td>
<td>-</td>
</tr>
</tbody>
</table>

\( l, s, r, \text{and } g \) are numbers of locations, planting-seasons, replications, genotypes, respectively.

\( \sigma^2 = \text{error variance} \); \( \sigma^2_{G} = \text{genotype variance} \); \( \sigma^2_{L} = \text{location variance} \); \( \sigma^2_{S} = \text{planting-season variance} \);

\( \sigma^2_{LS} = \text{location x planting-season interaction variance} \); \( \sigma^2_{r(LS)} = \text{replicate within environment variance} \);

\( \sigma^2_{GL} = \text{genotype x location interaction variance} \); \( \sigma^2_{GS} = \text{genotype x planting-season interaction variance} \);

\( \sigma^2_{GLS} = \text{genotype x location x planting-season interaction variance} \).
For Method B, the variation among environment effects is expressed in terms of averages of each location (L) and for each planting-season (S), as well as residual location x planting-season (L x S) interaction. Similarly, the genotype environment interaction (G x E) component is subdivided into three components, namely, G x L, G x S and residual G x L x S. The expectations of mean squares assume all factors are random. The various effect were then tested by the appropriate F-ratios.

The F-ratios were calculated based on the given expression:

Genotypes: (tested against genotype interactions) \( F = \frac{(M_1 + M_8)/(M_6 + M_7)}{M_6} \)

Locations: (tested against location interactions) \( F = \frac{(M_2 + M_4)/(M_4 + M_7)}{M_4} \)

Planting-seasons: (tested against season interactions) \( F = \frac{(M_3 + M_5)/(M_4 + M_7)}{M_4} \)

Genotype x location: (tested against 3-factor interaction) \( F = \frac{(M_6 + M_8)}{M_6} \)

Genotype x planting-season: (tested against 3-factor interaction) \( F = \frac{(M_7 + M_8)}{M_7} \)

Planting-seasons x locations: \( F = \frac{(M_3 + M_7)/(M_5 + M_8)}{M_5} \)

Genotypes x planting-seasons x locations: (tested against Pool error) \( F = \frac{M_e}{M_y} \)

Degree of freedom for respective test on the composite F-ratio was calculated according to Satherth Waite's.

Variance component estimates for Method B: were calculated based on linear functions of mean squares as indicated in Table 3.4 as follows:

\[
\begin{align*}
\sigma^2 & = M_0 \\
\sigma^2_G & = \frac{(M_1-M_6-M_7+M_8)/rsl}{M_1} \\
\sigma^2_L & = \frac{(M_2-M_4-M_6+M_8)/rgs}{M_2} \\
\sigma^2_S & = \frac{(M_3-M_4-M_7+M_8)/rgl}{M_3} \\
\sigma^2_{GL} & = \frac{(M_5-M_6)/rs}{M_5} \\
\sigma^2_{GS} & = \frac{(M_7-M_8)/rl}{M_7} \\
\sigma^2_{GSL} & = \frac{(M_8-M_9)/r}{M_8}
\end{align*}
\]
Small negative estimates were assumed to be the result of sampling errors, i.e.,
sampling errors of similar magnitude but in the opposite direction. However, if the
magnitude of the values were big, they could be due to the antagonistic effects of the
environmental factors. Consequently, negative values were considered in the
variance components estimates.

The standard error of these estimates $\sigma_{(s^2)}$ was estimated by fitting in the
equation (Anderson & Bancroft, 1952):

$$
\sigma_{(s^2)} = \sqrt{\frac{2/c^2}{\sum \left( V_i^2 / f_i + 2 \right)}}
$$

where

- $c_j$ = The coefficient of the $j$th variance component
- $V_i$ = the $i$th mean square in the linear function providing the estimate of the $j$th variance component
- $f_i$ = the degrees of freedom associated with the $i$th mean square

As an example of the above computation, consider the derivation of the standard
error for the genotype x location interaction variance component estimate $\sigma_{(GL)}$

Given that $r=4$, $s=2$, $l=7$ and $g=22$

df for $M_s=21 \times 6 =126$

df for $M_s 21 \times 1 \times 6=126$

Therefore,

Standard error for $\sigma^2_{(GL)},$

$$
\sigma (\sigma^2_{(GL)}) = \frac{2/c^2}{M_s^2/\{((g-1)(l-1) +2) +M_s^2/\{(g-1)(l-1)(s-1)+2\}}
$$

$$
\sigma_{(GL)} = \sqrt{\frac{2/c^2}{M_s^2/128} +M_s^2/128}}
$$

Thus, the phenotypic variance, $\sigma^2_P = \sigma^2_G + \sigma^2_{GL}/I + \sigma^2_{GS}/S + \sigma^2_{GLS}/I/S + \sigma^2/i/tls$

-92-
3.6.3 *Genotypic coefficient of variation*

The genotypic coefficient of variation (GCV) was calculated for each character in turns from the following.

\[
GCV = \frac{\sqrt{\sigma^2_G}}{\bar{x}} \times 100
\]

Where \( \bar{x} \) is the grand mean of the particular parameter

3.6.4 *Heritability*

From the variance components calculated using PROC VARCOMP of the SAS Package, heritability estimates for each agronomic character were computed from the ratio of genotypic variance over phenotypic variance:

\[
h^2 = \frac{\sigma^2_G}{\sigma^2_p}
\]

From the combined ANOVA analyses, genotypic variance is equal to \( \sigma^2_G \), phenotypic variance is derived as follows;

\[
\sigma^2_p = \sigma^2_G + \frac{\sigma^2_{GE}}{e} + \frac{\sigma^2}{re}
\]

Where \( e \) is = number of macro-environments
where \( r \) is = number of replications.

or \[
\sigma^2_p = \sigma^2_G + \frac{\sigma^2_{GL}}{l} + \frac{\sigma^2_{GS}}{s} + \frac{\sigma^2_{GLS}}{ls} + \frac{\sigma^2}{rls}
\]

Where \( l \) is = number of locations
\( s \) is = number of planting-seasons
\( r \) is = number of replications

-93-
3.6.5. Correlation among characters

Linear correlations were determined among all the possible combinations of the parameters over four replications of the preliminary trial and of 14 environments of the multilocational trials using PROC CORR of the SAS Package.

3.6.6. Cross-over interactions

Genotype-environment interaction (G x E) exists in two forms, showing cross-over effects or without cross-over effect. When there is cross-over effect, there is a change in ranking order among the genotypes for a particular characters in different environments. If no cross-over effect, the ranking remains unchanged but there are changes in the magnitudes of the character value.

To detect whether the interactions are of cross-over type or otherwise, the individual regression lines of all the genotypes were plotted on a single graph for each characters in turns. This graphical presentation also enables identification of genotypes having similar response to the environmental variations.

3.6.7. Stability analyses

Significance G x E interaction indicating that the genotype performance is environment dependent. Under such circumstances, selection cannot be based on values alone. Stability of performance has to be considered. Several methods can be used in the analysis of G x E and stability.
3.6.7.1 Genotype-grouping using means and coefficient of variance (CV)

In Francis and Kennenberg's (1978) genotype clustering characterises the stability of genotypes on group basis based on two statistics, coefficient of variance and mean values over environments. In this model, both means and CVs were computed by SAS package. Genotypic means were computered using PROC MEANS, while the coefficient of variance of each macro-environment as well as micro-environment for each genotype were obtained using PROC ANOVA (by genotype) of the SAS Package.

The simple coefficients of variations (CV) on X-axis, were plotted against the corresponding genotype means on Y-axis. The four quadrants are delimitated by the intercepting lines defined by the mean CV and the grand genotype mean after Francis and Kennenberg (1978). The quadrants were labelled in the following manner:

Quadrant I: area with above average means and below average CV
Quadrant II: area with above average means and above average CV
Quadrant III: area with below average means and below average CV
Quadrant IV: area with below average means and above average CV

Therefore, genotypes that fall in Quadrant I were most desirable and those that fall in Quadrant IV were the least desired. 'Above average' here means more preferable. Thus, for negative characters (higher preference for smaller mean values) such as percentage of bleaching, number of days to dry (DTD) and days to harvest are preferred. The position of the quadrant of these characters will then be shifted accordingly. In this case Quadrant III would be most desirable.
3.6.7.2. Regression and deviation

Another method used to measure the stability of the varietal performance was simple regression and deviation from linear regression \((S^2_d)\), of Eberhart and Russell (1966). These stability parameters \((b_i)\) and \((S^2_d)\), could be defined by the following model:

\[ Y_{ij} = \mu_i + b_i I_j + \delta_{ij} \]

Where, \(Y_{ij}\) is the variety mean of the \(i^{th}\) variety at the \(j^{th}\) environment,

\(\mu_i\) is the mean of the \(i^{th}\) variety over all environments,

\(b_i\) is the regression coefficient that measures the response of the \(i^{th}\) variety to varying environments,

\(\delta_{ij}\) is the deviation from regression of the \(i^{th}\) variety at the \(j^{th}\) environment, and \(I_j\) is the environment index, mean of all varieties at the \(j^{th}\) environment minus the grand mean.

The first stability parameter is a regression coefficient,

\[ b_i = (\Sigma X.Y - (\Sigma X.\Sigma Y)/n)/(\Sigma X^2 - (\Sigma X)^2/n), \]

was obtained by using PROC REG of the SAS Package. Here, the observed values \((Y_{ij})\) were regressed on environmental indices \((X_j)\) which was obtained by the difference between the marginal mean of the environments and the overall means (means of all varieties at the particular environment minus the grand mean). The form of this analysis is shown in Table 3.5 The residual mean squares (MS) of deviation from the regression is the measure of stability for each genotype.
Table 3.5. Partition of the G x E interaction for each genotype into regression and deviation components.

<table>
<thead>
<tr>
<th>items</th>
<th>df</th>
<th>Sum of squares</th>
<th>Mean squares</th>
</tr>
</thead>
<tbody>
<tr>
<td>Regression</td>
<td>1</td>
<td>$b_i ^2 \sum_j (E_{ij})^2$</td>
<td>$b_i 2 \sum_j (E_{ij})^2$</td>
</tr>
<tr>
<td>Deviation</td>
<td>e-2</td>
<td>$\sum_i \sigma_{ij}^2$</td>
<td>$\sum_i \sigma_{ij}^2/(e-2)$</td>
</tr>
</tbody>
</table>

\[
\sigma_{ij}^2 = \text{the deviation of the } i^{th} \text{ genotype from the regression in the } j^{th} \text{ environment}
\]
\[
e = \text{the number of environments}
\]
\[
E_{ij} = \text{the additive environment component of the } j^{th} \text{ environment.}
\]
\[
b_i = \text{the regression coefficient for the } i^{th} \text{ genotype}
\]

The ratio of the regression and deviation mean square was used to test the significance of the regression coefficient for each genotype.

Here the above average genotype would be those with $b_i = 0$ (Finlay and Wilkinson 1963) or Type I stability by Lin et al. (1986) or biological concept of Becker (1981), would be the desired goal. However in reality, $b_i$ and yield is often positively correlated (Finlay and Wilkinson 1963, Gray 1982), thus most desirable group is the first group ($b_i=1$) which refer to genotypes with average adaptability/stability which is analogous to Type II stability by Lin et al. (1986), or agronomical concept (Becker 1981) or dynamic (Kang 1990). The second group ($b_i > 1$) usually has mean below the grand mean or below average adaptability and the third group ($b_i < 1$) above average adaptability.
In cases where variance are heterogeneous such as the present study, regression coefficient b, 's would have different precision, additional stability parameter is suggested. Another stability variance, i.e. deviation from regression, was incorporated as a second stability parameter. A small deviation from regression was considered more stable (Type III stability). Based on this assumption, the most desirable variety would be the one that performs above average in all environments, i.e. the variety with $b_i = 1.0$ and $(S_d^2) = 0$ (Eberhart and Russell, 1966).

$(S_d^2)$ was estimated by squaring and then summing the deviation ($\delta_{ij} = Y_{ij} - \bar{Y}_{ij}$). This stability parameter for each variety was obtained by fitting the values in the following equation of Eberhart and Russell (1966).

$$(S_d^2)_i = [\sum_j \delta_{ij}^2 / (n-2)] - s^2 / r$$

where,

$$[\sum_j \delta_{ij}^2 / (n-2)] = \text{MS deviation.}$$

$s^2 / r$ is the estimate of the pooled error (or the variance of a variety mean at the $j^{th}$ location). Pooled error for the respective characters previously obtained by the ANOVA were used in the estimation of the respective stability variance. Likewise, the F-ratios for the respective stability variance were calculated based on

$$F \text{ ratio } = [\sum_j \delta_{ij}^2 / (n-2)] / s^2 / r$$

3.6.7.3. Rank - sum index

Modification of rank-sum index of Kang (1991a) was adopted. Two sets of ranks (stability parameters) were required. The first set of rank was based on the mean performance of the genotypes and another parameter, stability variance ($\sigma^2_i$), which measure Type II stability was calculated based on Shukla's model (Shukla 1972).
Stability variances were calculated for each genotype and for each trait using Shukla's method:

$$\sigma^2_{i} = \frac{1}{(g-1)(e-1)(e-2)} e(e-1) \sum_j (\bar{Y}_{ij} - \bar{Y}_i - \bar{Y}_j + \bar{Y}.)^2 - \sum_i \sum_j (\bar{Y}_{ij} - \bar{Y}_i - \bar{Y}_j + \bar{Y}.)^2$$

$$\sigma^2_{i} = \frac{1}{(g-1)(e-1)(e-2)} e(e-1) \sum_j (u_{ij} - \bar{u}_i)^2 - \sum_i \sum_j (u_{ij} - \bar{u}_i)^2$$

with $u_{ij} = Y_{ij} - \bar{Y}_j$ and $\bar{u}_i = \sum_i u_{ij}/e$

where, $\sigma^2_{i}$ = the estimate of the stability variance for the $i^{th}$ genotype.

$g$ = number of genotypes

e = number of environments

Each stability variance was multiplied by 4 (the number of replicate to convert to a single plot basis) to be in the same unit as the pooled error. If the values of $\sigma^2_{i}$ is large (testing against $\sigma^2_{0}$ or the pooled error), the genotype is considered unstable.

When the variance ($\sigma^2_{i}$) is negative or less than $\sigma^2_{0}$, then the variance were taken as equal to zero (Shukla 1972). The significance of the variance was tested by

$$F = \frac{\sigma^2_{i}}{\text{pooled error obtained in the ANOVA}}$$

Weights were given to means and stability variance statistics ($\sigma^2_{i}$). Genotype with the highest mean receiving the rank of 1 and consequently the lowest mean received the biggest rank value. Stability ratings were assigned for $\sigma^2_{i}$ based on its F test. Stability rating of '0' for non-significant $\sigma^2_{i}$, value of '4' for significant at 5% probability, and '8' was given for $\sigma^2_{i}$ significant at 1% probability. These ratings are added to the mean rank of a genotype, and selection is based on the sum of the genotypic mean rank and the rank of the stability variance. Genotypes with the lowest sum are selected. For each characters, varieties are ranked in accordance with preferability. This method is mean oriented.