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# An Integrated Approach for Simultaneous Selection of Stable and High Yielding Genotypes in Lentil (*Lens culinaris* Medikus)

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## ABSTRACT

**Background:** Lentil is a major *rabi* pulse crop and is known for its protein rich grains. It is important to develop area-specific high yielding varieties of lentil.

**Methods:** The present study was conducted with 24 lentil genotypes grown at three different locations of Uttarakhand for two consecutive years 2018-19 and 2019-20. The average of sum of ranks (ASR) of parametric and non-parametric measures along with yield stability index was used in present study to identify the high yielding and stable lentil genotypes.

**Result:** The pooled ANOVA revealed the presence of significant differences among genotypes, environments and G × E interaction effects. The ASR method in combination with YSI was found to be effective in identifying high yielding as well as stable genotypes. The genotypes PL 8, IPL 315, DPL 15 and PL 7 were found as most stable and high yielding genotypes.

**Key words:** AMMI, Lentil, Non-parametric, Parametric, Stability.

## INTRODUCTION

Lentil (*Lens culinaris* Medikus sub sp. *culinaris*) is an autogamous annual pulse crop cultivated mainly in Indian subcontinent, West Asia, North Africa, North America, South America and Australia. In India, it is cultivated on approximately 1.5 million hectare area with an annual production of 1.5 million tons and with an average productivity of around 1000 kg/ha during 2018-19 (Anonymous, 2018). In order to make it popular among farming community, it is very important to increase its productivity by developing area-specific high yielding varieties. Stable and high yielding genotypes in any crop species are must for enhanced production and productivity (Pal *et al.,* 2018; Gaur *et al.,* 2020). For estimation of G × E interaction several parametric and non-parametric stability methods has been proposed by different workers however, each method has its own strengths and weaknesses for the selection of stable genotypes (Gauch, 2006). These traditional statistical methods are either based on Analysis of Variance (ANOVA) or Principal Component Analysis (PCA). The additive main effects and multiplicative interaction (AMMI) model used the ANOVA for estimation of main effects (genotype and environment) while the interaction effects (G × E) was estimated by using PCA (Zobel *et al.,* 1988). The G × E interaction pattern can be easily diagnosed by using the AMMI biplots and these biplots provide a visual inspection and interpretation of the G × E interaction (Gabriel, 1971). Several workers recommended the use of average of sum ranks (ASR) of parametric and non-parametric measures for estimation of G × E effects (Mohammadi and Amri, 2008; Vaezi *et al.,* 2019). The Yield Stability Index (YSI) can be effectively used for simultaneous selection of stable and high yielding genotypes (Bajpai and Prabhakaran, 2000). Therefore, present study was conducted with an aim to identify stable and high yielding lentil genotypes for variable environmental conditions by integrating ASR method with YSI.

## MATERIALS AND METHODS

### Plant materials and field evaluation

The present study was conducted at three different locations *i.e.* Norman E. Borlaug Crop Research Centre, Pantnagar, Krishi Vigyan Kendra, *Dhakrani* and Agricultural Research Station, Majhera in Uttarakhand. The experimental material was sown in all three studied environments for two consecutive years 2018-19 and 2019-20. Thus in present study six environments *i.e.* Pantnagar-2018 (Environment I), Dhakrani-2018 (Environment II), Majhera-2018 (Environment III), Pantnagar-2019 (Environment IV), Dhakrani-2019 (Environment V) and Majhera-2019 (Environment VI) were used to estimate the G × E interaction pattern. In these environments climatic condition remains highly variable. The field trials consisting of 24 lentil genotypes were laid down in randomized block design during

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both the years (Table 1). At harvest, seed yield data was collected for each plot and converted to kg/ha.

**Statistical analysis and procedures**

The parametric measures used in present study includes regression coefficient ($b_i$) and deviation from regression ($S^2d_i$) parameters of Eberhart and Russell (1966) and additive main effects and multiplicative interaction (AMMI) model based stability parameters such as ASV (AMMI stability value) and YSI (yield stability index) (Purchase *et al.*, 2000; Bajpai and Prabhakaran, 2000). The non-parametric methods includes $S^{(i)}$ measures of Huehn's (1990) and Nassar and Huehn's (1987), $NP^{(i)}$ measures of Thennarasu's (1995). The Eberhart and Russell (1966) parameters were estimated by using PBSTAT-GE 2.3 software. The AMMI analysis and biplot construction were performed on GEA-R (2017) Version 4.1 software available at www.cimmyt. org. AMMI stability values (ASV) were calculated as per method suggested by Purchase *et al.*(2000). The Yield Stability Index (YSI) was also calculated to identify both high yielding and stable genotypes (Kang, 1993; Bajpai and Prabhakaran, 2000; Bose *et al.,* 2014) The non-parametric stability measures were calculated by using an online program, STABILITYSOFT (Pour-Aboughadareh *et al.,* 2019).

## RESULTS AND DISCUSSION

The mean seed yield over all the environments ranged from 310.56 kg/ha (Kota Massor-1) to 723.33 kg/ha (PL 8) (Table 1). The Environment I (690.97 kg/ha) was found to be the best performing environment while Environment VI (405.00) was found to be poorest. A critical insight of Table 2 indicated that under all the studied environments the genotypic differences were significant and hence for pooled analysis data obtained from all six environments were used. The results of pooled ANOVA indicated that mean sum of squares for genotype, environment and G × E interaction were highly significant ($p<0.01$) (Table 3). The significant genotypic differences for seed yield indicated sufficient genetic variability among the genotypes included in the study. The significant differences among different environments indicated that these environments were different in their climatic conditions. The significant G × E interaction indicated that genotypes performed differently under different environments. The significance of genotype, environment and G × E interaction effects for seed yield in lentil was reported earlier by several researchers (Yadav *et al.,* 2016; Sellami *et al.,* 2021). As the G × E interaction was found significant, the analysis was proceeded further to estimate stability parameters by different models.

**Stability analysis by using Non-parametric models**

Huehn (1990) and Nassar and Huehn (1987) developed four parameters for stability analysis *i.e.* $S^{(1)}$, $S^{(2)}$, $S^{(3)}$ and $S^{(6)}$. The lowest value of these parameters corresponds to high stability of the genotype. The parameter $S^{(1)}$ (mean of absolute rank differences of a genotype over all tested environments) indicated that genotype Kota Masoor-1 ($S^{(1)}$ =0.333, rank=1) followed by Kota Masoor-2 ($S^{(1)}$ =0.933, rank=2), KLS 218 ($S^{(1)}$ =1.467, rank=3) PL 8 ($S^{(1)}$ =1.867, rank=4) and IPL 315 ($S^{(1)}$=2.133, rank=5) were most stable genotypes across studied environments (Table 4). The parameter $S^{(2)}$ (the variance among the ranks over all tested environments) indicated that genotype Kota Masoor-1 ($S^{(2)}$ =0.167, rank=1) followed by Kota Masoor-2 ($S^{(2)}$ =0.667, rank=2), KLS 218 ($S^{(2)}$ =1.467, rank=3), IPL 315 ($S^{(2)}$=3.2, rank= 4) and PL 8 ($S^{(2)}$ =4, rank=5) were most stable genotypes. The parameter $S^{(3)}$ (the sum of the absolute deviations for each genotype relative to the mean of ranks) indicated that the most stable genotype were Kota Masoor-1 ($S^{(3)}$ =0.714, rank=1) followed by PL 8 ($S^{(3)}$=0.87, rank= 2), IPL 315 ($S^{(3)}$ =0.889, rank=3), Kota Masoor-2 ($S^{(3)}$ =1.25, rank=4) and PL 7 ($S^{(3)}$ =1.384 , rank=5). In case of stability parameters $S^{(6)}$ (the sum of squares of rank for each genotype relative to the mean of ranks) the most stable genotype was PL 8 ($S^{(6)}$=0.348, rank =1), followed by IPL 315 ($S^{(6)}$ =0.449, rank=2), PL 7 ($S^{(6)}$ =0.554 , rank=3), PL 9 ($S^{(6)}$ =0.651, rank=4) and DPL 15 ($S^{(6)}$ =0.928 , rank=5). The use of $S^{(1-6)}$ models suggested that two genotypes PL 8 and IPL 315 were found to be most stable in all four statistics. Thennarasu (1995) developed four non-parametric stability statistics *i.e.* $NP^{(1-4)}$ on basis of the ranks of adjusted means of the genotypes in each environment. The low values of each of parameters correspond to high stability. The stability parameter $NP^{(1)}$ revealed variety DPL 15 ($NP^{(1)}$ =3.333, rank=1) followed by KLS 218 ($NP^{(1)}$ =3.667 , rank=2), IPL 315 ($NP^{(1)}$ =3.833, rank=3), Kota Massor-1 ($NP^{(1)}$ =3.833, rank=3) and LL 864 ($NP^{(1)}$ = 3.833, rank=3) as most stable. The stability parameter $NP^{(2)}$ revealed L 4147 ($NP^{(2)}$ =0.156, rank=1), DPL 15 ($NP^{(2)}$ = 0.196, rank=2), PL 9 ($NP^{(2)}$= 0.274, rank =3), PL 6 ($NP^{(2)}$ =0.283, rank=4) and PL 234 ($NP^{(2)}$=0.308, rank=5) as most stable. The stability parameter $NP^{(3)}$ revealed DPL 15 ($NP^{(3)}$ =0.257, rank=1), IPL 315 ($NP^{(3)}$=0.267, rank=2), PL 9 ($NP^{(3)}$=0.271 , rank=3), PL 8 ($NP^{(3)}$=0.283, rank= 4) and PL 7 ($NP^{(3)}$ =0.29, rank=5) as most stable varieties. The stability parameter $NP^{(4)}$ revealed PL 8 ($NP^{(4)}$=0.081, rank=1), IPL 315 ($NP^{(4)}$= 0.119, rank= 2), PL 7 ($NP^{(4)}$=0.138, rank=3), PL 9 ($NP^{(4)}$=0.171 , rank=4) and DPL 15 ($NP^{(4)}$=0.227, rank=5) as most stable varieties. The use of four $NP^{(1-4)}$ statistics suggested that only a single genotype DPL 15 was found to be most stable across all environments in all four statistics. The above results indicated that each non-parametric models produces differential ranking of genotypes in terms of stability. Sabaghnia *et al.* (2006) also used non parametric stability methods to estimate for G × E interaction in 11 lentil genotypes and reported that each one of the non parametric methods produced a unique genotype ranking.

**Stability analysis by using parametric models**

In Eberhart and Russell (1966) model, the stable genotypes were identified on basis of regression coefficient (bi) around unity and mean square deviations from regression ($s^2di$) non-significant from zero. The results indicated that genotypes *i.e.* KLS 218 ($b_i$=1, rank=1), DPL 62 ($b_i$=0.98, rank=2), PL 8

**Table 1:** Mean seed yield of lentil genotypes across different environments.

| Genotypes | Seed yield (Kg/ha) | | | | | | |
|---|---|---|---|---|---|---|---|
| | E I | E II | E III | E IV | E V | E VI | Mean |
| DPL 15 | 750.00 | 683.33 | 480.00 | 550.00 | 596.67 | 466.67 | 587.78 |
| DPL 62 | 726.67 | 533.33 | 433.33 | 540.00 | 570.00 | 426.67 | 538.33 |
| HUL 57 | 576.67 | 543.33 | 630.00 | 526.67 | 503.33 | 513.33 | 548.89 |
| IPL 315 | 743.33 | 746.67 | 576.67 | 610.00 | 600.00 | 453.33 | 621.67 |
| IPL 406 | 643.33 | 556.67 | 520.00 | 430.00 | 496.67 | 433.33 | 513.33 |
| K-75 | 661.67 | 576.67 | 356.67 | 550.00 | 396.67 | 320.00 | 476.94 |
| KLS 218 | 610.00 | 493.33 | 376.67 | 380.00 | 460.00 | 320.00 | 440.00 |
| Kota Massor-1 | 436.67 | 366.67 | 203.33 | 320.00 | 286.67 | 250.00 | 310.56 |
| Kota Massor-2 | 453.33 | 420.00 | 330.00 | 346.67 | 406.67 | 263.33 | 370.00 |
| L 4076 | 736.67 | 620.00 | 390.00 | 403.33 | 486.67 | 256.67 | 482.22 |
| L 4147 | 733.33 | 676.67 | 513.33 | 600.00 | 526.67 | 356.67 | 567.78 |
| L 4188 | 820.00 | 500.00 | 470.00 | 606.67 | 440.00 | 426.67 | 543.89 |
| LL 864 | 670.00 | 623.33 | 423.33 | 476.67 | 490.00 | 316.67 | 500.00 |
| LL 931 | 626.67 | 540.00 | 470.00 | 436.67 | 463.33 | 426.67 | 493.89 |
| LM 84-8 | 721.67 | 593.33 | 343.33 | 603.33 | 463.33 | 336.67 | 510.28 |
| PL 4 | 640.00 | 650.00 | 650.00 | 580.00 | 606.67 | 543.33 | 611.67 |
| PL 5 | 623.33 | 640.00 | 606.67 | 416.67 | 553.33 | 580.00 | 570.00 |
| PL 6 | 663.33 | 690.00 | 646.67 | 373.33 | 623.33 | 556.67 | 592.22 |
| PL 7 | 833.33 | 820.00 | 580.00 | 680.00 | 706.67 | 493.33 | 685.56 |
| PL 8 | 860.00 | 856.67 | 690.00 | 736.67 | 613.33 | 583.33 | 723.33 |
| PL 9 | 913.33 | 783.33 | 640.00 | 716.67 | 710.00 | 430.00 | 698.89 |
| PL 234 | 700.00 | 566.67 | 610.00 | 596.67 | 546.67 | 423.33 | 573.89 |
| PL 406 | 790.00 | 666.67 | 470.00 | 693.33 | 673.33 | 320.00 | 602.22 |
| PL 639 | 650.00 | 630.00 | 300.00 | 640.00 | 630.00 | 223.33 | 512.22 |
| Mean | 690.97 | 615.69 | 487.92 | 533.89 | 535.42 | 405.00 | 544.81 |

E I, E II, E III, E IV, E V and E VI refers to Pantnagar-2018, *Dhakrani-2018,* Majhera-2018 Pantnagar-2019, *Dhakrani-2019* and Majhera-2019 respectively.

**Table 2:** ANOVA of different environments for seed yield.

| Source of variation | d.f. | Mean sum of square for seed yield | | | | | |
|---|---|---|---|---|---|---|---|
| | | E I | E II | E III | E IV | E V | E VI |
| Replication | 2 | 13533.50 | 1101.50 | 2866.50 | 2218.00 | 3150.00 | 2450.10 |
| Genotypes | 23 | 38507.91** | 41459.35** | 51153.09** | 44880.17** | 32107.70** | 35086.97** |
| Error | 46 | 6144.19 | 5417.32 | 5911.58 | 7475.58 | 6770.28 | 4493.47 |

**Table 3:** Pooled ANOVA for seed yield across environments.

| Source of Variation | d.f. | Mean sum of squares |
|---|---|---|
| Replication/E | 12 | 4220.01 |
| Environment (E) | 5 | 711060.40** |
| Genotype (G) | 23 | 162815.70** |
| G × E | 115 | 16075.71** |
| Error | 276 | 6035.24 |

* and ** refers to significant at 0.05 and 0.01 probability levels, respectively.

($b_i$=1.05, rank=3), IPL 315 ($b_i$=1.07, rank=4) and DPL 15 ($b_i$=1.09, rank=5) performed better across all studied environments and hence considered as most stable (Table 5). The ANOVA of AMMI revealed that for grain yield, the environment, genotype and G × E interaction was found to be significant (Table 6). This indicated that seed yield was influenced by both, main effects as well as their interactions. An insight of Table 6 indicated that for seed yield, 40.93% of total sum of square (TSS) was attributable to genotypic effects, 38.86% to environment effect and 20.20% to G × E effects. The major portion of total sum of squares (TSS) was contributed by both genotypic and environment effects indicating the preponderance of genetic diversity in the genotypes under study and also indicated that the environments under study were variable. The significance of G × E interaction suggested the differential response of environments towards genotypes. The sum of squares due to G × E interaction were further partitioned into five principal component axis accounting for 100 per cent of the G × E interaction sum of squares. In present study, AMMI having two principle components axis was found as the best

**Table 4:** Ranking of different genotypes of lentil according to non-parametric models.

| Genotype | $S^{(1)}$ | $S^{(1)}$ rank | $S^{(2)}$ | $S^{(2)}$ rank | $S^{(3)}$ | $S^{(3)}$ rank | $S^{(6)}$ | $S^{(6)}$ rank | $NP^{(1)}$ | $NP^{(1)}$ rank | $NP^{(2)}$ | $NP^{(2)}$ rank | $NP^{(3)}$ | $NP^{(3)}$ rank | $NP^{(4)}$ | $NP^{(4)}$ rank |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DPL 15 | 3.667 | 10 | 9.367 | 10 | 2.897 | 8 | 0.928 | 5 | 3.333 | 1 | 0.196 | 2 | 0.257 | 1 | 0.227 | 5 |
| DPL 62 | 4.600 | 14 | 14.567 | 14 | 6.522 | 13 | 1.522 | 14 | 5.167 | 10 | 0.333 | 9 | 0.548 | 12 | 0.412 | 13 |
| HUL 57 | 8.333 | 20 | 47.767 | 20 | 20.183 | 22 | 2.761 | 22 | 8.000 | 22 | 0.556 | 18 | 0.764 | 17 | 0.704 | 21 |
| IPL 315 | 2.133 | 5 | 3.200 | 4 | 0.889 | 3 | 0.444 | 2 | 3.833 | 3 | 0.400 | 14 | 0.267 | 2 | 0.119 | 2 |
| IPL 406 | 4.533 | 13 | 15.067 | 15 | 7.063 | 14 | 1.813 | 15 | 5.167 | 10 | 0.352 | 10 | 0.550 | 13 | 0.425 | 15 |
| K-75 | 4.600 | 14 | 14.300 | 13 | 9.533 | 15 | 2.533 | 20 | 6.500 | 15 | 0.750 | 21 | 0.928 | 20 | 0.613 | 19 |
| KLS 218 | 1.467 | 3 | 1.467 | 3 | 1.571 | 6 | 1.286 | 8 | 3.667 | 2 | 1.852 | 22 | 0.931 | 21 | 0.314 | 9 |
| Kota Massor-1 | 0.333 | 1 | 0.167 | 1 | 0.714 | 1 | 1.429 | 10 | 3.833 | 3 | 8.333 | 24 | 4.335 | 24 | 0.286 | 7 |
| Kota Massor-2 | 0.933 | 2 | 0.667 | 2 | 1.250 | 4 | 1.500 | 11 | 5.500 | 14 | 3.933 | 23 | 2.223 | 23 | 0.350 | 10 |
| L 4076 | 6.133 | 17 | 25.867 | 17 | 14.923 | 19 | 2.692 | 21 | 7.500 | 19 | 0.667 | 19 | 0.945 | 22 | 0.708 | 22 |
| L 4147 | 3.600 | 9 | 8.667 | 9 | 3.023 | 9 | 0.977 | 6 | 4.500 | 7 | 0.156 | 1 | 0.381 | 6 | 0.251 | 6 |
| L 4188 | 8.600 | 23 | 49.500 | 22 | 21.522 | 23 | 2.870 | 23 | 7.500 | 19 | 0.530 | 17 | 0.744 | 16 | 0.748 | 23 |
| LL 864 | 3.467 | 8 | 8.267 | 8 | 4.429 | 11 | 1.357 | 9 | 3.833 | 3 | 0.315 | 7 | 0.474 | 9 | 0.371 | 12 |
| LL 931 | 2.933 | 7 | 6.400 | 7 | 4.000 | 10 | 1.500 | 11 | 4.667 | 8 | 0.310 | 6 | 0.698 | 15 | 0.367 | 11 |
| LM 84-8 | 6.067 | 16 | 23.767 | 16 | 11.689 | 17 | 2.262 | 17 | 7.167 | 18 | 0.383 | 13 | 0.786 | 18 | 0.597 | 18 |
| PL 4 | 6.867 | 18 | 32.300 | 18 | 9.788 | 16 | 1.515 | 13 | 6.667 | 16 | 0.402 | 15 | 0.441 | 7 | 0.416 | 14 |
| PL 5 | 8.467 | 21 | 48.300 | 21 | 17.889 | 20 | 2.370 | 19 | 6.833 | 17 | 0.414 | 16 | 0.610 | 14 | 0.627 | 20 |
| PL 6 | 8.533 | 22 | 59.467 | 23 | 18.204 | 21 | 2.286 | 18 | 7.500 | 19 | 0.283 | 4 | 0.542 | 11 | 0.522 | 17 |
| PL 7 | 2.867 | 6 | 5.767 | 6 | 1.384 | 5 | 0.544 | 3 | 4.833 | 9 | 0.364 | 11 | 0.290 | 5 | 0.138 | 3 |
| PL 8 | 1.867 | 4 | 4.000 | 5 | 0.870 | 2 | 0.348 | 1 | 5.167 | 10 | 0.375 | 12 | 0.283 | 4 | 0.081 | 1 |
| PL 9 | 3.667 | 10 | 11.500 | 11 | 2.674 | 7 | 0.651 | 4 | 4.333 | 6 | 0.274 | 3 | 0.271 | 3 | 0.171 | 4 |
| PL 234 | 4.133 | 12 | 11.867 | 12 | 4.450 | 12 | 1.100 | 7 | 5.333 | 13 | 0.308 | 5 | 0.470 | 8 | 0.310 | 8 |
| PL 406 | 7.933 | 19 | 44.967 | 19 | 13.907 | 18 | 2.021 | 16 | 8.000 | 22 | 0.315 | 8 | 0.531 | 10 | 0.491 | 16 |
| PL 639 | 10.600 | 24 | 74.967 | 24 | 33.567 | 24 | 3.851 | 24 | 8.833 | 24 | 0.667 | 19 | 0.869 | 19 | 0.949 | 24 |

Where, $S^{(1)}$ and $S^{(2)}$ (Nassar and Huehn's 1987); $S^{(3)}$ and $S^{(6)}$ (Huehn's 1990); $NP^{(i)}$ (Thennarasu's 1995).

**Table 5:** Ranking of different genotypes of lentil according to parametric models.

| Genotype | $b_i$ | $b_i$ Rank | $s^2di$ | ASV value | ASV rank | SR | ASR |
|---|---|---|---|---|---|---|---|
| DPL 15 | 1.09 | 5 | -898.95 | 0.259093 | 3 | 50 | 5 |
| DPL 62 | 0.98 | 2 | 1105.70 | 0.412838 | 6 | 107 | 10.7 |
| HUL 57 | 0.10 | 24 | 680.44 | 2.856395 | 21 | 207 | 20.7 |
| IPL 315 | 1.07 | 4 | -922.01 | 0.215902 | 2 | 41 | 4.1 |
| IPL 406 | 0.69 | 14 | 265.65 | 1.661073 | 16 | 135 | 13.5 |
| K-75 | 1.27 | 9 | 1751.60 | 1.449199 | 15 | 161 | 16.1 |
| KLS 218 | 1.00 | 1 | -866.07 | 0.363495 | 4 | 79 | 7.9 |
| Kota Massor-1 | 0.75 | 7 | -260.53 | 0.367806 | 5 | 83 | 8.3 |
| Kota Massor-2 | 0.66 | 15 | -1388.64 | 0.82157 | 9 | 113 | 11.3 |
| L 4076 | 1.71 | 22 | -874.47 | 1.29988 | 12 | 190 | 19 |
| L 4147 | 1.31 | 13 | -734.68 | 1.029687 | 10 | 76 | 7.6 |
| L 4188 | 1.18 | 6 | 8905.56** | 1.304372 | 13 | 185 | 18.5 |
| LL 864 | 1.29 | 11 | -1644.34 | 0.692641 | 7 | 85 | 8.5 |
| LL 931 | 0.70 | 12 | -720.39 | 1.34964 | 14 | 101 | 10.1 |
| LM 84-8 | 1.42 | 16 | 3309.08* | 2.226913 | 19 | 168 | 16.8 |
| PL 4 | 0.30 | 21 | -734.79 | 2.160545 | 18 | 156 | 15.6 |
| PL 5 | 0.22 | 23 | 5608.43** | 3.522774 | 22 | 193 | 19.3 |
| PL 6 | 0.43 | 18 | 12623.53** | 3.598648 | 23 | 176 | 17.6 |
| PL 7 | 1.29 | 10 | -545.93 | 1.080004 | 11 | 69 | 6.9 |
| PL 8 | 1.05 | 3 | 1772.75 | 0.19619 | 1 | 43 | 4.3 |
| PL 9 | 1.58 | 19 | -462.73 | 1.734178 | 17 | 84 | 8.4 |
| PL 234 | 0.75 | 8 | 1383.01 | 0.748726 | 8 | 93 | 9.3 |
| PL 406 | 1.57 | 17 | 5187.71** | 2.833168 | 20 | 165 | 16.5 |
| PL 639 | 1.59 | 20 | 14717.75** | 3.679111 | 24 | 226 | 22.6 |

Where, bi (regression coefficient and $S^2di$ (deviation from regression) (Eberhart and Russell (1966), ASV (AMMI stability value); SR Sum of parametric and non parametric parameters; ASR= Average sum of rank.

**Table 6:** ANOVA of AMMI model showing IPCA components along with per cent variation.

| Source of variation | df | MSS | Variation explained (%) |
|---|---|---|---|
| Environment | 5 | 711060.40** | 38.86 |
| Genotype | 23 | 162815.70** | 40.93 |
| Genotype × Environment | 115 | 16075.71** | 20.20 |
| IPCA I | 27 | 40977.04** | 59.84 |
| IPCA II | 25 | 11784.32** | 15.93 |
| IPCA III | 23 | 8491.12 | 10.56391 |
| IPCA IV | 21 | 6446.667 | 7.32296 |
| IPCA V | 19 | 6160.142 | 6.33106 |
| Error | 288 | 5959.60 | |

* and ** refers to significant at 0.05 and 0.01 probability levels, respectively.

predictive model. Jeberson *et al.* (2019) also reported that the first two IPCA components explained about 90% variability of G × E interaction in lentil genotypes grown in north hill zones of India and hence AMMI with two IPCA components is best predictive model. On the basis of AMMI biplot I and II, ASV (AMMI stability value), variety PL 8 (IPCA I 0.0172; IPCA II -0.1853; ASV rank=1) was identified as most stable genotype followed by IPL 315 (IPCA I -0.0261; IPCA II 0.1925; ASV rank=2), DPL 15 (IPCA I -0.0499; IPCA II 0.1786; ASV rank=3), KLS 218 (IPCA I 0.0915; IPCA II 0.1189; ASV rank=4) and Kota Massor-1(IPCA I 0.0770; IPCA II -0.2269; ASV rank=5) (Table 7 and Fig 1-2). These results indicated that separate application of parametric and non-parametric models results in differential ranking of genotypes which creates an ambiguity in selection of stable genotype. Instead of using a single stability parameter the average of sum of ranks (ASR) of all measures can be used to select stable genotypes and genotypes with low ASR values was considered as stable (Vaezi *et al.,* 2019). The perusal of Table 5 indicated that the genotypes IPL 315, PL 8, DPL 15, PL 7 and L 4147 were most stable genotypes as they had lowest ASR value of 4.1, 4.3, 5, 6.9 and 7.6 respectively. It is not necessary that a stable genotype also possess high yield and hence the stability *per se* should not

**Table 7:** The ASV and YSI value of different lentil genotypes.

| Genotypes | Genotype code no. | Mean yield | Yield rank | IPCA I | IPCA II | ASV value | ASV rank | YSI value | YSI rank |
|---|---|---|---|---|---|---|---|---|---|
| DPL 15 | 1 | 587.78 | 8 | -0.0499 | 0.1786 | 0.2590 | 3 | 11 | 3 |
| DPL 62 | 2 | 538.33 | 14 | -0.0952 | -0.2059 | 0.4128 | 6 | 20 | 7 |
| HUL 57 | 3 | 548.89 | 12 | 0.7529 | -0.4038 | 2.8563 | 21 | 33 | 20 |
| IPL 315 | 4 | 621.67 | 4 | -0.0261 | 0.1925 | 0.2159 | 2 | 6 | 2 |
| IPL 406 | 5 | 513.33 | 15 | 0.4423 | -0.0076 | 1.6610 | 16 | 31 | 16 |
| K-75 | 6 | 476.94 | 21 | -0.3745 | -0.3486 | 1.4491 | 15 | 36 | 22 |
| KLS 218 | 7 | 440.00 | 22 | 0.0915 | 0.1189 | 0.3634 | 4 | 26 | 11 |
| Kota Massor-1 | 8 | 310.56 | 24 | 0.0770 | -0.2269 | 0.3678 | 5 | 29 | 14 |
| Kota Massor-2 | 9 | 370.00 | 23 | 0.2164 | 0.1189 | 0.8215 | 9 | 32 | 17 |
| L 4076 | 10 | 482.22 | 20 | -0.3231 | 0.4655 | 1.2998 | 12 | 32 | 18 |
| L 4147 | 11 | 567.78 | 11 | -0.2741 | -0.0114 | 1.0296 | 10 | 21 | 8 |
| L 4188 | 12 | 543.89 | 13 | -0.2230 | -1.0000 | 1.3043 | 13 | 26 | 12 |
| LL 864 | 13 | 500.00 | 18 | -0.1729 | 0.2409 | 0.6926 | 7 | 25 | 10 |
| LL 931 | 14 | 493.89 | 19 | 0.3578 | -0.1240 | 1.3496 | 14 | 33 | 21 |
| LM 84-8 | 15 | 510.28 | 17 | -0.5862 | -0.3351 | 2.2269 | 19 | 36 | 23 |
| PL 4 | 16 | 611.67 | 5 | 0.5751 | -0.0543 | 2.1605 | 18 | 23 | 9 |
| PL 5 | 17 | 570.00 | 10 | 0.9366 | 0.1928 | 3.5227 | 22 | 32 | 19 |
| PL 6 | 18 | 592.22 | 7 | 0.9425 | 0.6479 | 3.5986 | 23 | 30 | 15 |
| PL 7 | 19 | 685.56 | 3 | -0.2702 | 0.3690 | 1.0800 | 11 | 14 | 4 |
| PL 8 | 20 | 723.33 | 1 | 0.0172 | -0.1853 | 0.1961 | 1 | 2 | 1 |
| PL 9 | 21 | 698.89 | 2 | -0.4599 | 0.1550 | 1.7341 | 17 | 19 | 6 |
| PL 234 | 22 | 573.89 | 9 | 0.1714 | -0.3819 | 0.7487 | 8 | 17 | 5 |
| PL 406 | 23 | 602.22 | 6 | -0.7533 | 0.1541 | 2.8331 | 20 | 26 | 13 |
| PL 639 | 24 | 512.22 | 16 | -0.9723 | 0.4507 | 3.6791 | 24 | 40 | 24 |

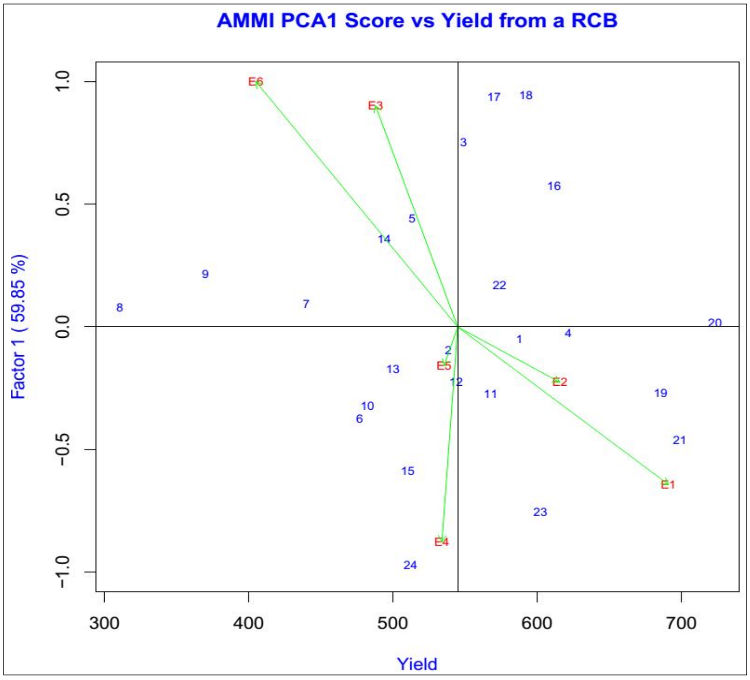

**Fig 1:** AMMI I biplot.

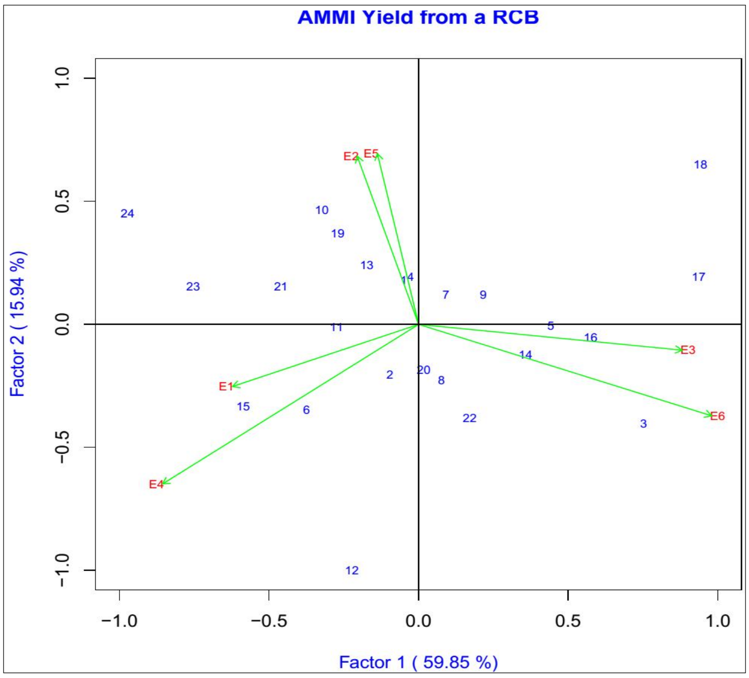

Fig 2: AMMI II biplot.

be used as the sole selection criteria (Mohammadi *et al.,* 2007).

The yield stability index (YSI) is an integrated approach based on both mean performance and stability and hence effective for simultaneous selection of high yielding and stable genotypes (Kang, 1993; Bajpai and Prabhakaran, 2000). On basis of yield stability index (YSI) scores, the genotype PL 8 (YSI rank=1) followed by IPL 315 (YSI rank=2), DPL 15 (YSI rank= 3), PL 7 (YSI rank= 4), PL 234 (YSI rank= 5) were identified as most stable and high yielding genotypes (Table 7). The genotypes PL 8, IPL 315, DPL 15 and PL 7 were also found as most stable by using ASR method, however, this method do not provide idea about the yield of these genotypes and hence, ASR method in combination with YSI was found to be effective in identifying high yielding as well as stable genotypes.

## CONCLUSION

The pooled ANOVA indicated significant MSS for genotype, environment and G × E interaction indicating that prevailing climatic conditions influenced the seed yield to a large extent and genotypes performed differently under different environments. The parametric and non-parametric models generates differential ranking of genotypes in terms of stability. The ASR method in combination with YSI was found to be effective in identifying high yielding as well as stable genotypes. The genotypes PL 8, IPL 315, DPL 15 and PL 7 were found as most stable and high yielding genotypes.

**Conflict of interest:** None.

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