



## Stability analysis of seed yield in coriander based on non-parametric methods

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### Abstract

The present study consisted of evaluation of 42 genotypes in two environments –with full irrigations (called irrigated) and with half the number of normal irrigations (called drought) over three years. ANOVA has indicated significant influence of environments on the expression of seed yield. All types of interactions with genotypes were significant indicating non-linear response of genotypes to environments. Stability analysis indicated significant differences among the ranks of stability of the genotypes. Significant positive correlations were noted among the different non parametric statistics and between corrected and uncorrected seed yield. Similarly there was good correspondence between the scatters of the genotypes obtained with  $S_i^{(1)}$ ,  $S_i^{(2)}$ ,  $S_i^{(3)}$  as well as between the scatters of AMMI (mean vs IPCA 1).

**Keywords:** AMMI analysis, coriander, non-parametric tests, seed yield, stability

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### Introduction

Coriander is an important spice crop of India. It is a cool season crop, although it is raised throughout the year under controlled conditions for leaves which are used for garnishing in cuisine across the country. Change in climate, which is being witnessed in the recent times is affecting cultivation of coriander. Coriander when raised for seed, experiences moisture stress during seed formation and ripening stages, basically because of increase in temperatures thereby increasing the evapotranspiration. In such cases, developing genotypes which can withstand the moisture stress is advocated. Genotype x environment interactions is a major problem for a breeder and it further complicates when genotypes suited to

one environment are used for another environment (Kearsey & Pooni 1996; Giauffret *et al.* 2000; Farshadfar & Sutka 2003).

There are several biometrical methods of detecting the stability statistically. Among these most commonly used are the stability analysis proposed by Eberhart & Russell (1966) and AMMI analysis proposed by Zobelet *et al.* (1988). Lin *et al.* (1986) classified stability into three types- Type I stability also called as static stability by Becker & Léon (1988) relies on small environmental variances exhibited by stable genotypes. The Type II stability also called as dynamic stability by Becker & Léon (1988) relies on response of the genotypes to environments. It is expected that a stable genotype is one which gives higher yield in better environments while

giving not so better performance in poor environments. The Type 3 stability relies on residual mean squares from the regression model which should be smaller for a stable genotype (Kadhem *et al.* 2010). These methods are second degree statistics which rely on distributional assumptions about genotypes, environments and their interactions (Parmar *et al.* 2010) which is seldom achieved, particularly if violations occur because of outliers (Akura & Kaya 2008). Non parametric methods on the other hand are free from such assumptions. The non-parametric method of estimating stability as proposed by Huehn (1990) overcomes the failure of assumptions of second degree statistics. The present study therefore uses the non-parametric method of estimating the stability.

### Materials and methods

The study consisted of evaluation of 42 genotypes of coriander. The genotypes were selected randomly from a collection of germplasm being maintained at SKN College of Agriculture, Jobner. The names of the genotypes are given in Table 2. These genotypes were evaluated at two moisture levels: (i) normal, where the genotypes were given full dose of irrigations, and (ii) stress, where half the number of irrigations as given in comparison to normal moisture level. In each level, all the

42 genotypes were evaluated in a randomized block design with three replications. Each genotype was sown in a plot of 3 m length consisting of two rows separated by 40 cm. Thinning was done 20 days after sowing to maintain a plant to plant distance of 10 cm. The whole set was evaluated over a period of three years. Thus, the experiment consisted of four environments (2 moisture levels x three years). In each environment, a random sample of 5 plants was taken from each genotype in each replication. The seed yield was noted in g per five plants. The data were first subjected to pooled ANOVA using linear model. The results of which are presented in Table 1.

The non-parametric method of stability analysis as proposed by Huehn (1990) and Nassar & Huehn (1987) was applied. The method is described in brief here.

The mean seed yield of each genotype in each environment was tabulated. The means were then ranked such that the highest yielding genotype had the lowest rank and the lowest yielder the highest rank. The corrected genotypic means  $y_{ij}^c$  in each environment were also corrected using the following formula:

$$y_{ij}^c = y_{ij} - (\bar{y}_r - \bar{y}.)$$

**Table 1.** Pooled ANOVA for seed yield in coriander for seed yield

Source	df	MSS	Percent of total sum of squares
Environment	5	1023.483**	29.82
Year	2	785.937**	9.16
Moisture level (ML)	1	3046.201**	17.75
Year × ML	2	249.669**	2.91
Reps/Environment	12	43.295**	3.03
Genotypes	41	22.53**	5.38
Genotype × Environment	205	27.44**	32.78
Genotype × Year	82	39.557**	18.9
Genotype × ML	41	16.798**	4.01
Genotype × Year × ML	82	20.645**	9.87
Error	492	10.106	

\*\* Significant at P<0.01

Where  $y_{ij}$  represents the seed yield of  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  environment and the  $\bar{y}_i$  represents the mean yield of a genotype over all locations and  $\bar{y}..$  represents the mean seed yield of all genotypes over all locations. The corrected values of seed yield of each genotype were also ranked in each environment using the same procedure for uncorrected values. For both the uncorrected and corrected seed yield values the following parameters were estimated.

Mean of the absolute rank differences ( $S_i^{(1)}$ ) of a genotype was estimated by the following formula:

$$S_i^{(1)} = \frac{2 \sum_{j=1}^{q-1} \sum_{j'=j+1}^q (|r_{ij} - r_{ij'}|)}{q(q-1)}$$

Where,  $r_{ij}$  represents the rank of the genotype in each environment based on  $(y_{ij} = y_{ij} - (\bar{y}_i - \bar{y}..))$  ranks are assigned highest to the lowest,  $q$  represents the number of environments.

Variance among the ranks over  $q$  environments ( $S_i^{(2)}$ ) was estimated as per the following formula:

$$S_i^{(2)} = \frac{\sum_{j=1}^q (r_{ij} - \bar{r}_i)^2}{q-1}$$

The significance of these statistics was done through  $X^2$  tests designated as  $Z^{(1)}$  and  $Z^{(2)}$  tests to test the  $S_i^{(1)}$  and  $S_i^{(2)}$ , respectively. The details are given by Singh & Pawar (2005).

Two other statistics namely  $S_i^{(3)}$  and  $S_i^{(6)}$  were also estimated.  $S_i^{(2)}$  represents mean of the absolute rank differences of a genotype and was estimated as per the following formula:

$$S_i^{(3)} = \frac{\sum_{j=1}^q |r^{ij} - \bar{r}_i|}{\bar{r}_i}$$

And  $S_i^{(6)}$  represents variance among the ranks over the  $q$  environments and is estimated as per the following formula:

$$S_i^{(6)} = \frac{\sum_{j=1}^q (r^{ij} - \bar{r}_i)^2}{\bar{r}_i}$$

## Results and discussion

As a first step, pooled ANOVA was done for the data of seed yield over all environments and replications and genotypes. The analysis was done with linear model using GLM procedures on SAS software package. The results obtained are presented in Table 1. Significant differences among the genotypes and the environments was noted. Partitioning of the environments into years and moisture stress levels also indicated significant differences in the effects of years, moisture levels and their interaction on the expression of seed yield indicating the sensitivity of this character to environmental influences. Further, significant sum of squares of the interactions of genotypes with the years, moisture levels and their combinations indicated that genotypes exhibited non linear response to these environments, thereby indicating that differential stability responses are exhibited by the genotypes. The estimation of sum squares as percentage of total sum of squares indicated that no single component dominated, even though the environments played a greater role (nearly 30%) followed by genotypes. Partitioning of the environment sum of squares indicated that moisture levels (17.75%) influenced more than the years (9.16%) or their interactions (9.87%). This is in contrast to the reports of Parmer *et al.* (2012).

The non parametric stability parameters  $S_i^{(1)}$  and  $S_i^{(2)}$  as well as two other parameters  $S_i^{(3)}$  and  $S_i^{(6)}$  were also estimated for both corrected and uncorrected seed yield of the genotypes over the environments. Simple correlations were worked out between all the parameters, and it was found that the values based on corrected values correlated with the values based on uncorrected values. Hence, for the sake of brevity, presentation of the results based on uncorrected values are only presented. Stable genotypes are expected to have lower  $S_i^{(1)}$  values ( $S_i^{(1)} = 0$ ).  $S_i^{(2)}$  gives the variance among the ranks over environments. Hence, a lower value ( $S_i^{(2)} \cong 0$ ) of a genotype indicates its stability. An ideal genotype is one which has lower  $S_i^{(1)}$  with higher mean, in other words, genotypes with less variation among the ranks is expected to be stable. Since  $S_i^{(2)}$  represents the variance of the

ranks of each genotype over environment, a lower value of  $S_i^{(2)}$  will indicate stability of the genotype. Based on  $S_i^{(1)}$  values, RCr 436 followed by UD 10 and UD 173 were the stable ones, while UD 481 followed by UD 493 and UD 510 were the most unstable ones. Similar conclusions can be drawn from  $S_i^{(2)}$ . In fact, good correspondence between  $S_i^{(1)}$  and  $S_i^{(2)}$  were observed and is expected because of the high positive correlation between the two values. The same can be inferred by comparing Figs. 1 & 2. Similarly, comparison of means over the environments indicated that Local was the top yielder (15.56 g) followed by RCr 684 (14.28 g) and RCr 480 (14.22 g), while UD 10 (10.25 g), UD 42 (10.62 g) and UD 51 (10.75 g) occupied the bottom positions in yield. Thus perusal of the data indicated that while lower yielding genotypes were stable, higher yielding genotypes were unstable.

For each genotype,  $Z_i^{(1)}$  and  $Z_i^{(2)}$  values were calculated based on the ranks of the corrected data and summed over genotypes. The cumulative  $Z_i$  values ( $\Sigma Z_i^{(1)}$ ) and ( $\Sigma Z_i^{(2)}$ ) were 53.40 and 48.01, respectively. These values were significant compared to Table  $X^2$  values (df=42 and  $p=0.01$ ). These values indicated significant differences among the ranks of stability of the genotypes. Among the  $Z$  values of the genotypes, only UD 493 exhibited value greater than the Table  $X^2$  value, thus this genotype was significantly unstable relative to other genotypes.

Perusal of Table 2, Figs. 1 & 2, indicated that there was good correspondence with regard to scattering of parental points. Each of the figures has four sections in it. The Section I represents genotypes which have lower  $S_i^{(1)}$  and  $S_i^{(2)}$  high mean are stable and desirable ones which are expected to perform better in all the environments. Of all the genotypes in this quarter, UD 493 is the most desirable one followed by RCr 446, UD 119, UD 490. The Section II represents genotypes which are good for better management conditions in the present case as they have higher  $S_i^{(1)}$  and  $S_i^{(2)}$  and higher mean yield. Among the genotypes in this section RCr 684, local, UD 258 and UD 42 are the most prominent ones. Section III has genotypes which

are poorly adapted to the environments or in other words genotypes which are unstable. The most prominent ones are RCr 20, UD 486 and UD 277, UD 157. Section IV contains genotypes with lower  $S_i^{(1)}$  and  $S_i^{(2)}$  and lesser seed yield are better suited to poor environments like drought conditions. Among the genotypes in this category are UD 324 followed by UD 194, UD 483 and RCr 41. Since higher mean is desirable even in drought conditions, UD 483 followed by UD 51 is the most desirable for seed yield in drought conditions.

Nonparametric tests are less powerful than their parametric counterpart. Raiger (1997) and Raiger & Prabhakaran (2000) have shown that when a number of genotypes is fairly large, the power efficiency of the nonparametric measures will be quite close to those of parametric measures if the evaluated genotypes is fairly large. The risk of selecting inferior genotypes with the use of non parametric tests will be minimal if the genotypes tested is large and the number of evaluating environments is more (Rao & Prabhakaran 2000).

Two other statistics  $S_i^{(3)}$  and  $S_i^{(6)}$  were also proposed by Huehn (1966), a good correlation existed between the values of  $S_i^{(3)}$  and  $S_i^{(6)}$ . Simple correlations worked out between different stability parameters and the seed yield of genotypes were very low. This is similar to the observation of Kadhem *et al.* (2010) and supports the view that stability parameters provide information that cannot be gleaned from average yield alone (Kaya & Taner 2003). However, among themselves they were positively and significantly correlated suggesting that use of any one parameter should give desired classification of genotypes. Perusal of Fig. 3 indicated similar conclusions as reached from Figs. 1 & 2.

In order to compare the sensitivity of the non-parametric tests with parametric tests AMMI analysis was performed following the SAS code available at [http://apps.cimmyt.org/biometrics/ammi\\_&\\_pls\\_sas\\_program](http://apps.cimmyt.org/biometrics/ammi_&_pls_sas_program). The results of the plot between mean of the genotypes and IPCA 1 is presented in Fig. 4. Good correlation was seen between the scattering of the genotypes based on AMMI biplot and  $S_i^{(1)}$ .

**Table 2.** Mean absolute rank differences ( $S_i^{(1)}$ ) and variance ranks ( $S_i^{(2)}$ ) for different genotypes over environments

Genotype	Mean	$S_i^{(1)}$	$Z_1$	Rank	$S_i^{(2)}$	$Z_2$	Rank	$S_i^{(3)}$
UD-10	11.79	16.00	0.34	28	171.20	0.14	16	2.78
UD-42	13.30	18.73	1.91	41	250.57	2.49	2	4.32
UD-51	11.94	9.20	1.95	9	55.07	1.96	35	1.34
UD-115	13.31	16.60	0.58	31	194.97	0.54	12	3.91
UD-119	13.17	8.07	2.99	5	43.90	2.46	38	1.88
UD-141	12.65	13.93	0.00	18	126.17	0.10	28	2.67
UD-143	13.56	17.20	0.88	36	203.47	0.74	11	3.96
UD-157	12.06	17.00	0.77	34	208.17	0.87	10	2.94
UD-160	11.77	9.33	1.85	10	64.27	1.59	33	1.34
UD-173	11.73	16.20	0.41	29	174.17	0.17	15	2.67
UD-194	11.93	6.53	4.74	3	36.67	2.82	40	1.12
UD-258	12.74	20.80	3.94	42	314.67	6.53	1	4.65
UD-274	13.00	14.93	0.08	22	162.67	0.06	21	3.20
UD-277	10.62	16.73	0.64	32	211.77	0.98	7	2.54
UD-324	10.26	6.07	5.35	2	29.90	3.18	41	0.81
UD-374	12.72	16.80	0.67	33	183.87	0.32	13	2.78
UD-450	13.61	14.27	0.01	19	165.87	0.08	20	3.28
UD-457	13.10	15.93	0.32	27	167.77	0.10	19	3.29
UD-460	12.67	13.33	0.04	15	140.00	0.01	25	3.16
UD-467	14.28	14.33	0.01	20	145.77	0.00	24	4.51
UD-476	13.92	13.60	0.01	16	129.20	0.07	26	3.33
UD-479	13.78	17.07	0.80	35	208.67	0.88	9	4.08
UD-481	12.51	11.87	0.38	11	97.87	0.56	31	2.48
UD-483	12.37	7.40	3.70	4	41.90	2.56	39	1.56
UD-485	11.93	17.60	1.11	37	236.27	1.85	3	2.68
UD-488	12.88	13.60	0.01	16	126.27	0.10	27	2.61
UD-490	13.49	8.33	2.73	6	47.50	2.29	37	1.88
UD-491	12.90	8.67	2.41	8	56.80	1.88	34	2.00
UD-493	13.98	5.13	6.68**	1	18.57	3.82	42	1.64
UD-503	13.49	18.07	1.41	40	225.50	1.43	4	4.55
UD-505	11.61	15.07	0.10	24	153.60	0.01	22	2.38
UD-509	12.57	16.20	0.41	29	177.77	0.22	14	3.12
UD-510	12.30	15.27	0.14	25	152.30	0.01	23	2.88
UD-512	13.37	12.73	0.13	14	112.17	0.28	29	2.88
RCr-20	12.29	17.80	1.23	39	224.17	1.38	5	3.62
RCr-41	10.78	8.40	2.66	7	49.07	2.22	36	1.15
RCr-435	10.75	14.40	0.01	21	209.07	0.90	8	1.80
RCr-436	10.91	12.07	0.32	12	98.17	0.55	30	1.58
RCr-446	15.57	12.07	0.32	12	96.97	0.58	32	2.74
RCr-480	12.55	15.00	0.09	23	170.57	0.13	17	2.55
RCr-684	14.22	15.33	0.15	26	169.47	0.12	18	3.78
Local	14.11	17.60	1.11	37	213.20	1.02	6	2.75

\*\*significant at  $P < 0.01$



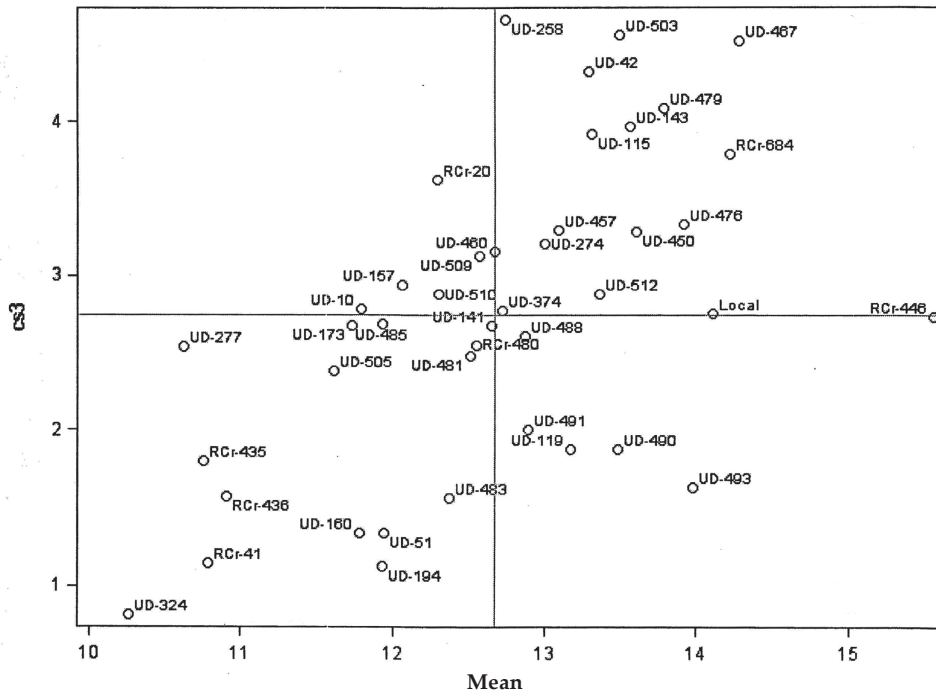


Fig. 3. Scatter plot of  $S_i^{(3)}$  vs. mean seed yield coriander genotypes over environment

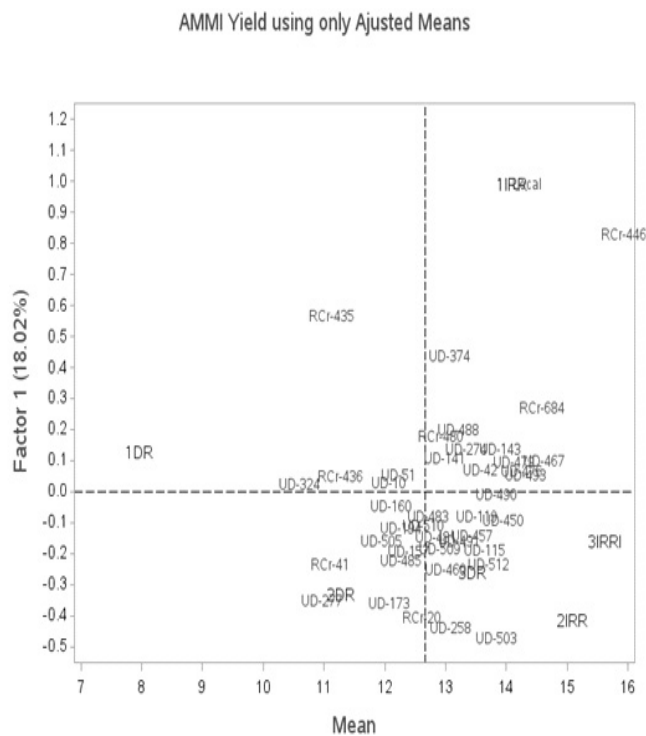


Fig. 4. AMMI biplot between mean seed yield and IPCA1 (1IRRI and 1DR represent the irrigated and drought environments in the first year and 2IRRI and 2DR represent the irrigated and drought environments in the second year and 3IRRI and 3DR represent the irrigated and drought environments in the third year, respectively).

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