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Joint Regression and AMMI Analysis to Comprehend GE- Interaction for Oilseed Hybrids

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Abstract: Joint Regression Stability Analysis (JRSA) and AMMI analysis were performed on MET data of Helianthus Annuus and Brassica Napus, to evaluate genotypic stability at varying environments. In combined ANOVA, GEI turned out highly significant by contributing 62% in total variation for Helianthus A., while environments effects contributed about 72% in total variation for Brassica Napus which means tested environments are of diverse nature. Also significant GE-interaction means that genotypes performance is dependent on environments. Further Duncan LSD revealed that Helianthus A. genotypes within groups: (LG_55_25, NK_Singi, FSS60, NK_S_278, SMH_0917, T_40318), (Hysun33, FSS_58, SMH_1027, SMH_1007, Golden_1) were found having similar mean yield. Also in context of Brassica Napus, Duncan LSD showed that B. Napus genotypes within each group: (SPS-N7/28, 04K12/13-10-1, NH97-5/2-4, AUP04-10, RM-H/06-1, HYOLA401C, CRH40/10), (AUO-03-11, FBHSR45, FBHSR-36), (AUP05-11, CRH30440/11, CRH257401/11) have similar mean yield. Genotypic stability and their adaptability were also evaluated using JRSA and AMMI stability measures. Based on JRSA, it was concluded that genotypes: (SMH1026, Ausigold4, NKS 278) can be considered as most stable in performance at all tested environments for Helianthus Annuus, while genotypes: (RBN04722, IBGE/AUP/ARBQQ003, FBHSR-18 CRH40/10, KN120-33, IBGE/AUP/ARBQQ001, IBGE/AUP/ARBQQ004, PUNJAB-SARSON-C) can be considered as most stable in performance at all tested environments for Brassica Napus. In AMMI analysis based on AMMI Distance (D_i) and AMMI stability value (ASV), Helianthus genotypes: LG-55-25, NK-Singi, FSS-60, NK-S-278, SMH0917 were found to be high yielding, while genotypes: (Aditya, SMH-1026, AusiGold4, SMH1007, Hysun33) were observed to be more stable in performance. Similarly genotypes: (RBN04722, Gold-Star, KN-120-34, FBHSR-18, KN120-33) can be suggested as high yielding Brassica Napus cultivars while genotypes within group: (CRH30440/11,IBGE/AUP/ARBQQ001, KN120-33, KN-120-34, CRH18140/11) can be declared as stable in performance over tested sites using ASV for Napus.

Keywords: Joint Regression; Stability; AMMI analysis; ASV; GE-Interaction; IPC's scores.

1. INTRODUCTION

In Pakistan *Helianthus Annuus* and *Brassica Napus* are commonly used as source of edible oil. Pakistan lies consistently almost at the bottom due to inconsistent agricultural policies and old farming system as compared to regional countries and as a result, Pakistan has to import edible oil of Rs 20.00 billion per year to fulfill consumption demand which is increasing at the rate of 8% per year, quoted by Arshad *et al.*, 2014. In Pakistan due to favorable seasonal conditions, all major oilseed crops can be easily adjusted in rotation without disturbing major cereal crops. It requires a genetic improvement in varieties to get maximum yield potential. Yield performance of cultivars significantly affected due to random factors: soil fertility rate, rainfall, temperature and other climatic changes so it requires studying the yield stability of cultivars at varying environments in order to recommend cultivar(s) at well adopted environment(s). Agronomists and plant breeders interested in developing hybrids having consistent and genetically potential yield at varying environments specially in presence of statistically significant *GxE* interaction (*GEI*).

Akçura *et al.* (2009) compared the parametric stability measures: (b_j, S^2_{dj}, R_j^2, P_j) and non-parametric stability measures: ($S_j^{(1)}$, $S_j^{(2)}$), to evaluate stability in performance of durum wheat cultivars. Associations among stability measures were computed using rank correlation and in regression analysis b_j was observed significantly negatively correlated with superiority index (P_j). While, $S_j^{(1)}$, $S_j^{(2)}$ and S^2_{dj} were observed to be significantly positively correlated with P_j.

Genotypic yield stability was evaluated by Alwala *et al.* (2010) using *JRA* and *G+GE* biplot analysis. The main aim of study was to compare the effectiveness of two stability approaches that are commonly used in order to identify high yielding and stable in performance genotypes. On the basis of certain measures it was concluded that *G+GE* biplot analysis would serve better platform as compared to *JRA*, to identify stable and high yielding hybrids. Similarly, Mohammadi *et al.* (2007) analyzed non-parametric stability methods to investigate different non-parametric tests for *GE* interactions. Results of non-parametric methods for *GE* interaction and combined *ANOVA* indicated the presence of both crossover and non-crossover interactions. *JRA* and *AMMI* tools were analyzed by Annicchiarico (1997) in which Genotype x Location (*GL*) and Genotype x Environment (*GE*) interaction effects were assessed in terms of estimated variance of heterogeneity of genotype regressions coefficients and sum of the variances of significant interaction principal component (*PC*) axes.

Sabaghnia *et al*, (2006) analyzed *METs* data for eleven Lens culinaris Medik hybrids at twenty

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environments, to evaluate both stability in performance and high yield. For this purpose ten non-parametric stability methods along with application of nonparametric tests for *GxE* interaction were investigated. These methods suggested that FLIP_92_12L as stable while FLIP96_6L as unstable genotypes. In present study, stability in performance of genotypes and their adaptability at suitable environments in the presence of *GEI* is evaluated, to achieve maximum genetic potential yield, using Joint Regression Stability (*JRS*) models and *AMMI* Stability statistics. It also includes comparison among different stability measure based on their recommendations.

2. MATERIALS AND METHODS

Multi Environments Trials (MET) data consists of twenty eight *Brassica Napus* and eighteen *Helianthus Annuus* hybrids were tested at eight and twelve sites respectively. These *ML* trials were conducted by National Uniform Seed Yield Trial (*NUSYT*) throughout in Pakistan using layout of *Randomized Complete Block Design* and seed yield was measured. To access yield stability and adaptability at varying environments, among series of existing Biometrical methods, *Joint Regression Stability Model* and *AMMI* stability statistics were selected and their detailed methodology is given as under:

2.1 Joint Regression Stability Models

In order to evaluate genotypic stability in performance, following regression based stability models: *Eberhart Russell's* and *Freeman Perkins'* were studied. Considering Y_{ij} as the mean yield of i^{th} genotype at j^{th} environment then *Eberhart* and *Russell's* (1966) model to study the genotypic stability and adaptability of genotype at varying environments/ locations can be defined as:

$$Y_{ij} = m + B_i I_j + \delta_{ij}$$
$$where \quad i = 1, 2,3, \dots t \quad and \quad j = 1, 2, 3, \dots s$$

$\boldsymbol{Y_{ij}}$ =Mean yield of i^{th} genotype at j^{th} environment.
$\boldsymbol{m}$ = Grand mean of all genotypes at all environments.
$\boldsymbol{B_i}$ =Regression coefficient of i^{th} genotype on the environmental index I_j, which measures the response of i^{th} genotype at varying environments.
$\boldsymbol{I_j}$ = Environmental index, defined as the deviation of the mean of all genotypes at given location from the grand mean.
$\boldsymbol{\delta_{ij}}$ = Deviation from regression of i^{th} genotype at j^{th} environment.
Two stability parameters based on model stated above can be discussed as under:

a) Regression coefficient (b_i), which is the regression of performance of each genotype under different environments on environmental means over all genotypes, which can be estimated as:

$$b_i = \sum_i Y_{ij} I_j \Big/ \sum_j I_j^2$$

b) Mean square deviation S_d^2 from linear regression which is defined as:

$$S_d^2 = \frac{\sum_j \delta_{ij}}{s-2} - \frac{S_e^2}{r}$$

Where

$$\delta_i^2 = \frac{1}{q-2}\left[\sum_j (y_{ij} - \bar{y}_{i.})^2 - b_i^2 \sum_j (\bar{y}_{.j} - \bar{\bar{y}})^2\right.$$

c) Coefficient of determination is as follows:

$$R_i^2 = b_i^2 \sum_j (\bar{y}_{.j} - \bar{\bar{y}})^2 \Big/ \sum_j (y_{ij} - \bar{y}_{i.})^2$$

But on the other hand, *Freeman and Perkins*' (1971) proposed a slightly different model which is actually modification of *Perkin and Jinks'* (1968) model as:

(i) Divide the replications into two groups, so that one group may be used for measuring the average performance of genotypes in various environments and the other group, averaging over the genotypes is used for estimating the environmental index.

(ii) Use one or more genotypes as check and assess the environmental index on the basis of their performance. *Freeman and Perkins'* model describe $\boldsymbol{Y_{ijk}}$, performance of k^{th} replicate of i^{th} genotype at j^{th} environment in the following way:

$$Y_{ijk} = m + G_i + E_j + GE_{ij} + e_{ijk}$$
$$where \quad i = 1, 2, 3, .. t; \quad j = 1, 2, 3,$$
$$s \ and \ k = 1, 2, 3, \dots r$$

Where

$\boldsymbol{Y_{ijk}}$ = k^{th} replicate of i^{th} genotype at j^{th} environment.
$\boldsymbol{m}$=Grand mean yield of all genotypes at all environments.
$\boldsymbol{G_i}$ = Additive Genotypic effect.
$\boldsymbol{E_j}$ = Additive Environmental effect.
$\boldsymbol{GE_{ij}}$=Genotype x Environmental interaction effect.
$\boldsymbol{e_{ij}}$ = Error associated with k^{th} observation.
Detail about various sum of squares arranged in *ANOVA* can be viewed as described by *Freeman and Perkins'* (1971).

2.2 *AMMI* Stability Statistics

In context of *AMMI* stability analysis, it was decided to use AMMI distance ($\boldsymbol{D_i}$) and AMMI Stability Value (ASV) as measures to evaluate stability in genotypic performance at varying environment. *AMMI* distance "$\boldsymbol{D_i}$" suggested by Zhang *et al.* (1998) can be obtained as:

$$D_i = \sqrt{\sum_{r=1}^{N} \gamma_{ir}^2} \quad i = 1,2,3 \dots n$$

Where $\boldsymbol{D_i}$ is the distance of *IPC* for i^{th} genotype from origin and *N* is the number of statistically significant *IPCs*. So genotype having smaller $\boldsymbol{D_i}$ can be considered as more stable in performance over sites as compared to genotypes having larger $\boldsymbol{D_i}$. Another measure used for measuring stability in performance,

developed by Purchase *et al*. (2000) is known as *AMMI* Stability Value (*ASV*), based on *IPCs* scores of *AMMI* model. *ASV* is actually the distance of genotypes score from origin in two dimensional scatter plot of *IPCs* scores and can be obtained as:

$$ASV = \sqrt{[(\frac{IPCA1_SS}{IPCA2_SS}(IPCA1^2_{Scores})^2 + (IPCA2^2_{Scores})^2]}$$

Where *IPCA1_SS* and *IPCA2_SS* are sum of squares of first two interaction principal components (*IPC*) scores and their fraction is used as weight to balance the contribution of *IPCA1* in interaction sum of squares.

3. RESULTS AND DISCUSSIONS

In order to evaluate genotypic stability and their adaptability at suitable environments: Joint Regression Stability models (given in section 2) and *AMMI* stability measures were applied to analyzed *G x E* data for selected oilseed crops. In section 3.1, regression based *ANOVA* including *Duncan group LSD* test (1955), was performed, while in section 3.2, certain stability and adaptability procedures were analyzed using Joint Regression models and AMMI statistics.

3.1 Regression based analysis of *GEI*

In the first step combined *Analysis of Variance* (*ANOVA*) for *Helianthus Annuus* given in **(Table 3.1),** in which mean squares and percent contribution of main effects, interaction effect and further its partitioning based on regression is shown. It can be observed that both genotypes and environments effect turned out to be significant (with P-value < 0.05). In context of *GE*-Interaction, *ANOVA* revealed that *GEI* effect is observed to be highly significant by contributing 62% in total variation, which mean that *Helianthus Annuus* genotypes' performance is dependent on environments and so evaluation of genotypes with respect to environments is much significant to achieve maximum genetic yield potential of cultivars/genotypes.

Table 3.1 Partitioning of *GE* for *Helianthus A.* yield

SOV	*Helianthus Annuus*		
	Df	***MS***	***%***
Genotypes	**17**	**425619***	**14**
Environments	**11**	**1193960****	**24**
Genotypes X Environments	**187**	**175156****	**62**
Regression	**17**	**230041****	**12**
Deviation	**170**	**169667****	**88**
Total	**215**	**53123200(TSS)**	

*, **Significant at 5% and 1% respectively

Similarly, combined *Analysis of Variance* (ANOVA) for *Brassica Napus* yield, *GE*-interaction was also partitioned using Joint Regression Analysis and resultant mean squares alongwith percent contributions of effects in total variation were listed in **(Table 3.2)**. It can be viewed from Table-3.2 that both genotypes and environments effects for Brassica *Napus* were observed to be significant (P< 0.05) which means that mean yield of all genotypes is not equal for all tested hybrids. Moreover, environment effects were also observed to be highly significant by contributing 72% in total variation for *Brassica Napus*. So it can be concluded that environments under Napus are of diverse nature. In addition to significant *GE*-interaction effect showed that genotypes' performance is dependent over environments. So it further demands to sort out genotypes at well adapted environments.

Table 3.2 Partitioning of *GE* for yield of *B. Napus*

S O V	*Brassica Napus*		
	df	*MS*	*%*
Genotypes	27	584509*	06
Environments	7	26795100**	72
Genotypes X Environments	189	309700**	22
Regression	27	490198**	23
Deviation	162	279617**	77
Total	223	261881000(TSS)	

*, **Significant at 5% and 1% respectively

3.1.1 Duncan Groups LSD Test

In preceding section, test of significance of overall equality of mean response of all genotypes/ environments was statistically rejected (at P<0.05/P<0.01), so such situation further demands to move towards pair wise/multiple comparison among different subsets of genotypes/environments so as to point out possible subsets of genotypes/environments having similar mean response pattern. For this purpose *Duncan groups LSD test* is used on both genotypes and environments mean. So in context of *Helianthus Annuus* genotypes, Duncan LSD revealed that genotypes within groups: (*LG_55_25, NK_Singi, FSS60, NK_S_278, SMH_0917, T_40318*), (*Hysun33, FSS_58, SMH_1027, SMH_1007, Golden_1*), (*Ausigold_4, NK_Tekni*) and (*SMH_1026, Pan-08-101, Ausigold_7*) can be declared as having similar mean yield while the genotypes: *Aditya* and *FH_417* turned out to be individually different. In comparison with suggestions, due to Arshad *et al.* (2014), based on Ward's *clustering algorithm* with *Duncan groups LSD* test, it can be concluded that present suggestions of similar *Helianthus A.* genotypes also validate the recommendation of similar genotypes based on *Ward's agglomerative hierarchical clustering algorithms.* Now *Duncan Group LSD* w. r. t. environments revealed that environment within groups: (*AliAkbar-Multan, ICI-Hyderabad, Dera-Ismail-Khan*), (*RARI-Bahawalpur, ORI-Faisalabad, Four-Brothers*), and (*University of Peshawar, NARC*) were observed to be similar for *Helianthus A.* Also in case of *Helianthus A.*, recommendations based on *Duncan Group LSD Test* and *Ward's clustering* method, due to Arshad *et al.* (2014), agreed that environment such as *University of Peshawar (UAP)* and *NARC* have similar mean response.

In preceding section, test of significance regarding Brassica Napus, revealed that equality of

means yield of all genotypes/environments in case of Brassica Napus were rejected (at P<0.05 and/or P<0.01), so it demands to move towards pair-wise or multiple comparison among genotypes or environments. *Duncan LSD Test* showed that *Brassica Napus* genotypes within each group: (*SPS-N7/28, 04K12/13-10-1, NH97-5/2-4, AUP04-10, RM-H/06-1, HYOLA401C, CRH40/10*), (*AUO-03-11, FBHSR45, FBHSR-36*), (*AUP05-11, CRH30440/11, CRH257401/11*) can be suggested as similar w. r. t. mean response. While in context of environments, environments under *Brassica Napus* within each groups: (*NARC, KANZO-Sheikhupura*), (*Khanpur, NIFA*) and (*Tandojam, Bahawalpur*) can be declared as having similar mean response while *Pioneer-Sahiwal* and *Faisalabad* were observed to be individually different.

3.2 Joint Regression Stability Analysis (JRSA)

In order to obtain maximum genetic potential of genotypes it is important that each genotype should be adapted at its suitable environment. For this purpose, *GE-interaction* effect is further analyzed using *Joint Regression Stability Analysis* (in present section) and *AMMI stability analysis* (in next section). In context of *JRSA*, *Eberhart-Russell's* and *Freeman-Perkins'* regression models were used to partition *GE-Interaction* further into two components: due to regression and deviation from regression as listed in Tables 3.1-3.2 and other stability statistics as a result of *JRSA*: slope regression coefficients (b_i), deviation from regression (δ_i^2) and coefficient of determination (R^2) were arranged in Table 3.3 and Table 3.4. *ANOVA* shown in Table 3.1 revealed that about 12% of *GEI* can be attributed towards heterogeneity among regressions for *Helianthus Annuus* while remaining 82% of *GEI* variation for *Helianthus Annuus* is towards deviation from regression and so such a large percent contribution of *GEI* due to nonlinear component can be regarded as important parameter for selection of stable genotypes. To evaluate stability and adaptability of oilseed genotypes, resulting regression coefficient of each cultivar can be used as a measure of stability i.e. a genotype having unit slope, can be considered as stable in performance. Similarly deviations from the regression ($\boldsymbol{\delta_i^2}$) and coefficient of determination ($\mathbf{R^2}$) can be considered as measures of stability as they provide measure of goodness of fit of model. *Finlay* and *Wilkinson's* (1963) suggested that slope not only provides a measure of stability but also indicates the regions of adaptability for genotypes. Genotypes having slopes significantly greater than unity can be specifically adapted to high yielding environments while genotypes having slope less than unity can be considered as insensitive to change in environment and so better adapted to poor environments.

Resultant stability parameters: slope parameter ($\boldsymbol{b_i}$), deviation from regression parameter and coefficient of determination were listed in Table 3.3 for *Helianthus Annuus.* On the basis of regression coefficient ($\boldsymbol{b_i}$), genotypes can be divided into three mutually exclusive groups. The first group which is categorized as stable group of genotypes having b value close to unity, so genotypes: *SMH1026, Ausigold4,* and *NKS 278* can be considered as most stable group of genotypes in performance at all tested environments for *Helianthus Annuus.* Moreover these genotypes also have low values of deviation from regression ($\boldsymbol{\delta_i^2}$) and high values for both mean yield and coefficient of determination ($\mathbf{R^2}$) as compared to remaining genotypes. The other group which consists of genotypes having significantly greater than unity slopes given as: (*SMH1007, Golden1, FSS60, Pan-08-101, T40318, NK Singi, LG 55 25, FSS 58, FH 417*) for *Helianthus Annuus* and can be better adapted to better environments. While the third group of genotypes: (*NK-Tekni, SMH1027, Ausigold7, Aditya, SMH0917, Hysun33*) comprises those genotypes which have slope less than one and hence can be concluded as insensitive to environmental change. So these genotypes can be better adapted at poor environment.

To view behavior of genotypes graphically, stability statistics given in Table 3.3 were displayed in the form of scatter plots of regression coefficient versus mean yield and deviation from regression versus mean yield and were displayed in **(Fig. 3.1 and Fig. 3.2)** respectively. For ease in interpretation of genotypic stability, scatter plots were divided using horizontal and vertical line which are either passing through b=1 or through average value of measure of interest taken at respective axis. In Fig. 3.1, it can be seen that genotypes: *NKS-278* can be considered as most stable and high yielding (above mean yield) cultivar, while (*SMH1026, Ausigold4*) represent most stable (b close to unity) but have below average yield for *Helianthus Annuus.* Similarly in Fig. 3.2 stability parameters such as deviation from regression and mean yield were plotted and here again genotypes: (*NKS278, Aditya, SMH1026, SMH1007*) seems to have reasonable values of stability parameters for *Helianthus A.*, so can be suggested for wider cultivation.

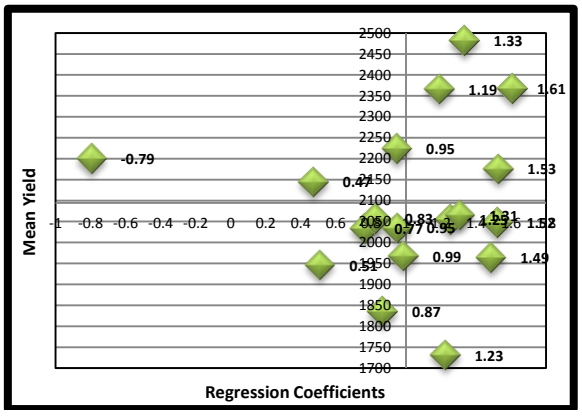


Fig-3.1 Regression Coefficient vs Mean Yield of Helianthus A.

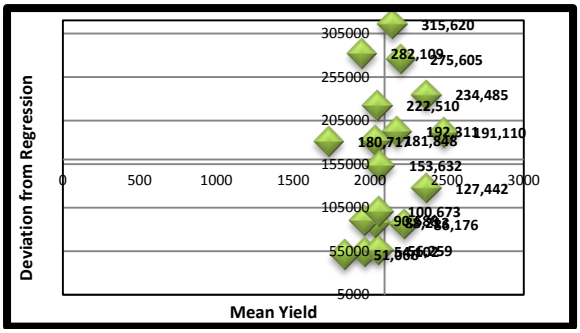


Fig 3.2 Mean Yield vs Deviation from Reg. Helianthus A

Now in context of *Brassica Napus* analysis of variance given in Table 3.2 for *B. Napus*, revealed that high percent contribution of environment effect exists in total variation i.e. 72%, which reflects much wider range of environments were tested under Napus hybrids as compared to genotypes. Also in Table 3.2, *GEI* is further partitioned using *JRA* and it can be seen that about one fourth of *GEI* variance is due to heterogeneity of regressions, while remaining 77% of *GEI* is due to nonlinear component that can be regarded as important parameter for selection of stable *B. Napus* genotypes. Now in order to evaluate genotypic stability of *Napus* cultivars over tested environments, JRSA was performed, and resultant stability parameters were listed in Table 3.4. So based on regression coefficients, genotypes can be divided into three mutually exclusive groups. The first group: which was categorized as stable group of genotypes having b value close to unity contained *Napus* genotypes: (*RBN04722, IBGE/AUP/ ARBQQ003, FBHSR-18 CRH40/10, KN120-33, IBGE/AUP/ ARBQQ001, IBGE/AUP/ARBQQ004, PUNJAB-SARSON-C*) can be considered as most stable in performance over all tested environments. Moreover these genotypes also small deviation from regression parameter ($\boldsymbol{\delta_i^2}$) and larger values for coefficient of determination as measure of goodness of fit ($\mathbf{R^2}$), as compared to remaining *B. Napus* genotypes. The other group of genotypes, which has significantly greater than unity slope includes: (*FBHSR45, KHC139, FBHSR-36, SPS N7/28, KN-120-34, IBGE/ AUPARBQQ002, GOLD STAR, OR-04, SPS-N11/62*) and can be better adapted to better environment. While third group contains genotypes: (*AUP05-11, RM-H/06-1, AUO-03-11, 04K12/13-10-1, NH97-5/2-4, HYOLA401-C, CRH18140/11, AUP04-10, AUP06-10, CRH257401/11, CRH30440/11*), comprises those *Napus* genotypes , which have slope less than one and hence suggested as insensitive to environmental change and hence can be better adapted at poor environments. To view behavior of *B. Napus* genotypes graphically, stability statistics given in Table 3.4 were displayed in the form of scatter plots of regression coefficients versus mean yield and deviation from regression versus mean yield which were shown in **(Fig. 3.3 and Fig. 3.4)** respectively. In Fig. 3.3, it can be seen that that genotypes: (*RBN04722, FBHSR-18, KN120-33*) can be considered as most stable and high yielding genotypes for *Brassica Napus*. While (*IBGE/AUP/ARBQQ003, CRH40/10, IBGE/AUP/ARBQQ001, IBGE/AUP/ ARBQQ004, PUNJAB-SARSON-C*) appeared to be most stable ("b" close to unity) but have equal to or below average yield for *Napus*. Similarly in Fig. 3.4 stability parameters: deviation from regression stability statistics and mean yield for Napus were plotted and here again genotypes: (*PAC437, SPS-J185*) can be considered as having reasonable values of stability parameters for *Brassica Napus* and can be suggested for wider cultivation.

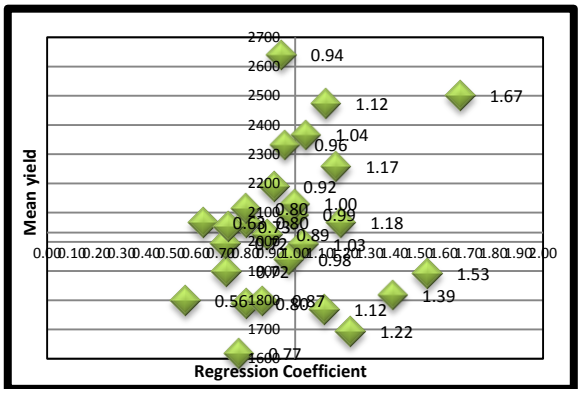


Fig 3.3 Regression Coefficient vs Mean Yield of B. Napus

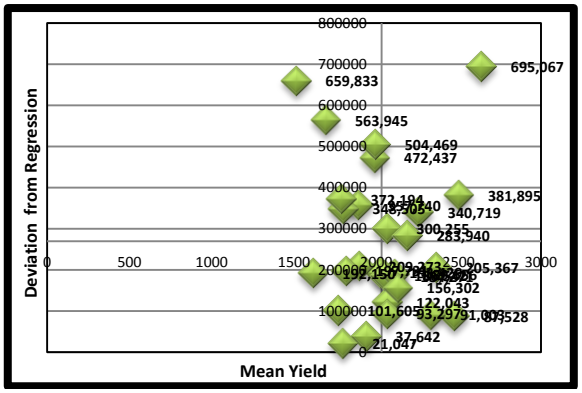


Fig 3.4 Mean Yield vs Deviation from Regression for B. Napus

3.3 AMMI Stability Statistics

Two stability measures: *AMMI* Distance (D_i) and AMMI stability value (*ASV*) discussed in section-3.2 were also computed and listed in stability statistics tables, in order to identify cultivars having high and stable yield performance over tested environments. It can be seen in **(Table 3.3)** that top five (in order) *Helianthus A.* genotypes: *LG-55-25, NK-Singi, FSS-60, NK-S-278, SMH0917* were found to be high yielding, while genotypes: (*Aditya, SMH-1026, AusiGold4, SMH1007, Hysun33*) and (*SMH-1026, Aditya, NK-S-278, AusiGold4, SMH1007*) were observed to be more stable in performance because of having smaller values of stability measure $\boldsymbol{D_i}$ and ***ASV*** respectively. As *Helianthus A.* genotypes: *NK-S-278* has both qualities of high mean yield and low *ASV*, so can be declared as stable in performance and high yielding cultivar and can be recommended for wider cultivation over tested environments. But on the other

hand, *FH417* and *AuisGold7* were observed as low yielding with relatively unstable cultivars, so cannot be suggested for wider cultivation.

In preceding sections joint regression based stability for *Brassica Napus* genotypes was discussed and now AMMI based stability statistics for *B. Napus* were listed in Table 3.4. It can be seen that genotypes such as: (*RBN04722, Gold-Star, KN-120-34, FBHSR-18, KN120-33*) can be suggested as high yielding cultivars. While based on AMMI stability statistics listed in **Table 3.4** genotypes within groups: (*IBGE/AUP/ARBQQ001, CRH30440/11, KN120-33, KN-120-34, SPS-N11/62*) can be declared as stable in performance over tested sites using *AMMI* distance (as stability measure). Similarly genotypes within group: (*CRH30440/11, IBGE/AUP/ARBQQ001, KN120-33, KN-120-34, CRH18140/11*) can be declared as stable in performance over tested sites using *ASV* for *Brassica Napus*. Finally being most commonly selected, using all stability statistics, genotypes such as: (*KN-120-34, KN120-33*) can be suggested as stable in performance over tested environments and high yielding cultivars for *Brassica Napus*

Table 3.3 *AMMI* and *JRA* Stability Statistics for *Helianthus Annuus* genotypes

Genotypes	STABILITY STATISTICS						
	AMMI			*Eberhart and Russell*			*Freeman Perkin*
	SY	D_i	*ASV*	B	δ_i^2	R^2	B
SMH1026	1968	9	6	0.99	54102.03	0.57	0.90
SMH1007	2055	13	9	1.25	56258.76	0.67	1.16
NK Tekni	2034	16	14	0.77	181847.54	0.19	0.69
Ausigold 4	2035	10	9	0.95	88213.05	0.43	0.87
Golden1	2048	26	18	1.52	222509.85	0.43	1.38
FSS60	2366	31	15	1.19	234485.13	0.31	1.10
Pan-08-101	1964	17	16	1.49	90588.10	0.64	1.38
T40318	2176	26	18	1.53	192310.53	0.47	1.45
NK Singi	2367	21	22	1.61	127441.84	0.60	1.51
LG 55 25	2482	26	17	1.33	191109.54	0.40	1.23
FSS 58	2065	25	11	1.31	153631.58	0.45	1.19
FH 417	1732	24	19	1.23	180717.15	0.38	1.16
SMH1027	2057	14	10	0.83	100672.66	0.33	0.76
Ausigold7	1946	32	28	0.51	282109.35	0.06	0.43
Aditya	1835	7	7	0.87	51066.28	0.52	0.78
SMH0917	2201	42	40	-0.79*	275604.96	0.14	-0.74
Hysun33	2145	34	34	0.47	315619.63	0.05	0.45
NK S 278	2224	14	8	0.95	86176.00	0.43	0.85

Table 3.4 *AMMI* and *JRA* Stability Statistics for *Brassica Napus* genotypes

Genotypes	*Stability Statistics*						
	AMMI			*Eberhart and Russell*			*Freeman Perkins*
	SY	D_i	*ASV*	B	δ_i^2	R^2	B
RBN04722	2640	33	25	0.94	695066.70	0.59	0.93
FBHSR45	1892	29	33	1.53	357740.10	0.88	1.50
KHC139	1694	29	30	1.22	563945.24	0.75	1.20
AUP05-11	1799	30	23	0.56	348504.90	0.50	0.54
IBGE/AUP/ARBQQ003	2092	17	15	0.99	184270.51	0.86	0.98
RM-H/06-1	2024	18	14	0.89	193428.64	0.82	0.87
AUO-03-11	1899	19	21	0.72	209272.85	0.74	0.71
FBHSR-36	1818	24	21	1.39	197731.10	0.92	1.37
04K12/13-10-1	2067	22	18	0.80	300254.84	0.71	0.79
SPS N7/28	2067	16	12	1.18	122042.60	0.93	1.16
KN-120-34	2474	12	10	1.12	87528.02	0.94	1.10
FBHSR-18	2366	21	12	1.04	205366.71	0.86	1.02
NH97-5/2-4	2066	17	18	0.63	93297.16	0.83	0.62
IBGE/AUPARBQQ002	2257	25	16	1.17	340719.10	0.82	1.15
GOLD STAR	2502	35	34	1.67	381895.29	0.89	1.63
CRH40/10	1992	26	25	1.03	472436.99	0.72	1.01
HYOLA401 C	1995	31	26	0.72	504469.23	0.53	0.70
CRH18140/11	1618	21	11	0.77	192149.64	0.78	0.75
KN120-33	2332	11	7	0.96	91002.70	0.92	0.94
AUP04-10	2053	19	19	0.73	186542.23	0.76	0.71
IBGE/AUP/ARBQQ001	1939	9	3	0.98	37641.63	0.97	0.95
OR-04	1514	34	34	1.42	659832.91	0.77	1.39
SPS-N11/62	1769	14	11	1.12	101604.92	0.93	1.09
AUP06-10	2114	18	13	0.80	189655.64	0.79	0.79
CRH257401/11	1789	24	21	0.80	372194.34	0.66	0.78
CRH30440/11	1798	10	3	0.87	21046.72	0.98	0.85
IBGE/AUP/ARBQQ004	2130	15	14	1.00	156302.16	0.88	0.97
PUNJAB SARSON C	2190	22	19	0.92	283939.69	0.77	0.89

4. CONCLUSIONS

Combined *ANOVA* reflected highly significant *GEI* effect and so maximum genetic yield potential of oilseed cultivars is dependent on diverse nature of environments. After rejection of hypothesis of equality of genotypes and environment mean responses, *Duncan LSD test was applied* on both genotypes and environments means which revealed that Helianthus genotypes within groups: (*LG_55_25, NK_Singi, FSS60, NK_S_278, SMH_0917, T_40318*), (*Hysun33, FSS_58, SMH_1027, SMH_1007, Golden_1*), (*Ausigold_4, NK_Tekni*) are similar in performance. But on the other hand, *Napus* genotypes within each group: (*SPS-N7/28, 04K12/13-10-1, NH97-5/2-4, AUP04-10, RM-H/06-1, HYOLA401C, CRH40/10*), (*AUO-03-11, FBHSR45, FBHSR-36*), *(AUP05-11, CRH30440/11, CRH257401/11*) suggested similar response pattern. In context of similarity of environments, it was observed that environment under Helianthus within groups: (*AliAkbar-Multan, ICI-Hyderabad, Dera-Ismail-Khan*), (*RARI-Bahawalpur, ORI-Faisalabad, Four-Brothers*), and (*University of Peshawar, NARC*) were observed to be similar. While *LSD* showed that environments (under *Brassica*) within each groups: (*NARC, KANZO-Sheikhupura*), (*Khanpur, NIFA*) and (*Tandojam, Bahawalpur*) can be declared as similar but *Pioneer-Sahiwal* and *Faisalabad* were observed to be individually different. Also based on JRSA, genotypes: (*SMH1026, Ausigold4, NKS278*) and (*RBN04722, IBGE/AUP/ARBQQ003, FBHSR-18 CRH40/10, KN120-33, IBGE/AUP/ ARBQQ001, IBGE/AUP/ ARBQQ004, PUNJAB-SARSON-C*) can be suggested as most stable in yield performance at tested environments for *Helianthus* and Brassica genotypes respectively. In AMMI analysis using D_i and ASV, Helianthus genotypes such as: LG-55-25, NK-Singi, FSS-60, NK-S-278, SMH0917 were found high yielding, while genotypes: Aditya, SMH-1026, AusiGold4, SMH1007, Hysun33 were observed to be more stable in performance over tested locations. Similarly genotypes: RBN04722, Gold-Star, KN-120-34, FBHSR-18, KN120-33 can be suggested as high yielding Napus cultivars while genotypes within group: CRH30440/11,IBGE/AUP/ARBQQ001, KN120-33, KN-120-34, CRH18140/11 can be declared as stable in performance over tested sites using ASV for Napus. In comparison between JRSA and AMMI analysis it was observed that both methods agreed with, that genotypes: (SMH-1026, AusiGold4) and (RBN04722, FBHSR-18, KN120-33, IBGE/AUP/ARBQQ001) were found most stable and high yielding for Helianthus A. and Brassica Napus respectively.

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