PHENOTYPIC STABILITY STUDIES FOR SEED YIELD IN *Brassica napus* L.

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ABSTRACT:

Rapeseed and mustard is most important oilseed crop in Pakistan. Lack of genotypes with wide stability across environments has been one of the most important constraints of rapeseed and mustard production in the country. Field experiments were conducted at eight different locations in 2018-19 and 2019-2020, in order to estimate seed yield stability. Eight advanced rapeseed genotypes were grown under randomized complete block design with 3 replications. Mean seed yield during 2018-19 range from 1891 to 2219 kg/ha. While mean seed yield during 2019-20 range from 1591 to 2016 kg/ha. Pooled analysis of variance showed highly significant differences among genotypes (G), locations (L), years (Y) and significant G x L, L x Y and G x L x Y interaction. However, G x L x Y interaction was greater than G x L and G x Y interaction so each location in each year was treated as separate environment. From this study it is concluded that the stable genotypes changes by changing the stability parameters used in computing stability analysis. For example during 2018-19, biplot drawn between CV (%) and seed yield (kg/ha) marked the RR-8-1 and RBN-13016 as stable genotypes while the biplot between b_i and S^2di showed CHS-9 and RBN-13017 as the adaptable genotype in this period. In the same cropping season 2018-19 according to Eberhart and Russel (1966) method the genotype RBN-13016 was marked as the stable genotype over the location under study because it showed above average yield response and regression coefficient near to unity and has low value of S^2d_i with high R^2_i value. Similarly during 2019-20, biplot drawn between CV (%) and seed yield (kg/ha) marked the RR-8-1 and CHS-9 as stable and good performing genotypes while the biplot between b_i and S^2di showed none of the genotypes as stable or adaptable genotype in this period. During the cropping season 2019-20 according to Eberhart and Russel (1966) genotypes RR-8-1 was found to be stable genotype over the location under study due to its above average yield response and regression coefficient near to unit with low value of S^2d_i and high value of $R^2_{i.}$ Current study indicated that there is great genetic diversity among brassica genotypes under variable climatic conditions and this variation can be exploited in the future breeding programs in developing climate resilient high yielding varieties

Key words: Biplot, *Brassica napus,* Genetic Diversity, Phenotypic Stability, Pooled Analysis of Variance, Regression Coefficient, Seed Yield,

Introduction:

Rapeseed and mustard are two important oilseed crops. These crops belong to the Brassicaceae family and are renowned for their high oil content and versatile uses. Rapeseed, also known as canola, is primarily grown for its oil, which is widely used in cooking, industrial applications, and biofuel production. Rapeseed genotypes come in first place among Pakistan's oilseed crops (Economic survey of Pakistan,2023) and can be profitably grown in a number of regions, but production is much lower than it could be because of improper genotype selection, abiotic and biotic stresses and poor management practices [20],[24].Moreover, rapeseed and mustard sector in Pakistan has faced challenges related to stability, including fluctuations in production and variable yields. To improve stability, various strategies have been implemented, such as the introduction of high-yielding and disease-resistant varieties, adoption of improved agronomic practices, dissemination of knowledge through farmer training programs, and the provision of financial incentives and subsidies. Rapeseed genotypes with high yields and oil percentages have the ability to narrow the gap between local production and consumption.

Rapeseed crops can thrive in environments with little or no water and can be successfully grown in rainfed areas [22]. Ali et al. [3], Mahto and Haider [18] and Sutariya et al. [27] reported that the stability of genotype among environments can be utilized effectively to produce stable lines with better tolerance to environment. Dillon et al. [8] and Brar et al. [6] recommended that genotypes stable at various locations can be efficiently utilized in upcoming breeding efforts to produce stable strains that have more tolerance. Thus only breeding for improved cultivars suitable for different agro-climatic regions of Pakistan would allow for a more stable rapeseed and mustard production system, reducing the vulnerability of the crops to the pest disease and adverse weather conditions. Environmental changes have a significant impact on crop yield, which has a knock-on effect on food supply and the agricultural economy. Phenotypic stability studies is an important tool in identification of such genotypes which have better performance in terms of high yield

promoting sustainable production. A crop variety's success is dependent not only on how well it performs but also on how consistently it performs over a range of environments. This is because the phenotypic performance of a genotype is frequently represented by a variety of agro-ecological variables. Multi-environment trials (METs) are commonly conducted in rapeseed research to assess the stability of genotypes across different environments or growing conditions. Genotypes that have less contribution to G-E interaction have stable yield over different environments [5]. In this study trials are conducted to evaluate the performance of rapeseed varieties or breeding lines at multiple locations over multiple years to capture the genotype by environment interaction. G-E interactions have a significant impact on genotype stability across environments, which is important for plant breeding. This study is conducted by using parametric methods of G-E interaction to identify stable genotypes in terms of seed yield over two years. Stability Analysis involves use of regression coefficient and computing Sd and CV as suggested by Francis and Kannenberg [12]. The aim of this study is to analyze response of different genotypes in different seasons and locations to identify stable ones in terms of seed yield.

Material and Method

Plant material and field conditions:
Experiment consisted of eight genotypes of rapeseed (*B. napus*) grown at eight different agro-ecological zones of Pakistan during two cropping seasons of Rabi 2018-19 and 2019-20. The genotypes were sown under irrigated conditions and the trial was laid down in a randomized complete block design with 3 replications. Plot size of 4 rows of 5 meter length with 30 cm row spacing. Experiments were sown at each site with recommended seed rate in the month of October (Table 1). Fertilizer @ 90N: 60 P_2 O_5 Kg/ha was applied and incorporated at the time of seed bed preparation. Irrigation, weed and pest control measures were applied whenever required. Seed yield per plot was estimated by harvesting and threshing the 4 rows from each plot and converted into kg/ha.

Statistical analysis:
A pooled analysis of variance over location was computed assuming replications and location effects as random and genotypes were considered as fixed variable [26]. In present studies two major concepts of stability parameters were utilized to access the stability of the genotypes under study. In one stability is accessed through computing Sd and CV as suggested by Francis and Kannenberg [12] which measure the variation within a genotype across environment. The other concept utilized is to determine the stability through regression slop as suggested by Eberhart and Russel [10].In this method, slop of regression provide an indication of regions of adaptability and stability

Table 1: Location description and sowing dates of trial

Code	Growing season	Locations	Abbreviation	Sowing date
L_1	2018-19	Oilseeds Research Program, NARC, Islamabad	NARC	20-10-2018
	2019-20	Oilseeds Research Program, NARC, Islamabad	NARC	12-10-2019
L_2	2018-19	Barani Agricultural Research Institute , Chakwal	BARI	05-10-2018
	2019-20	Barani Agricultural Research Institute , Chakwal	BARI	09-10-2019
L_3	2018-19	Oilseed Research Institute, AARI, Faisalabad	ORI	18-10-2018
	2019-20	Oilseed Research Institute, AARI, Faisalabad	ORI	11-10-2019
L_4	2018-19	Regional Agriculture Research Institute, Bahawalpur	RARI	16-10-2018
	2019-20	Regional Agriculture Research Institute, Bahawalpur	RARI	17-10-2019
L_5	2018-19	Arid Zone Research Institute, Bhakkar	AZRI	05-11-2018
	2019-20	Arid Zone Research Institute, Bhakkar	AZRI	11-10-2019
L_6	2018-19	Arid Zone Research Center, Dera Ismail Khan	AZRC	26-10-2018
	2019-20	Arid Zone Research Center, Dera Ismail Khan	AZRC	17-10-2019
L_7	2018-19	Nuclear Inst. for Food & Agriculture, Peshawar	NIFA	13-10-2018
	2019-20	Nuclear Inst. for Food & Agriculture, Peshawar	NIFA	10-10-2019
L_8	2018-19	Agriculture Research Institute, Tandojam	ARI	29-10-2018
	2019-20	Agriculture Research Institute, Tandojam	ARI	22-10-2019

RESULTS AND DISCUSSION:

This study comprised of eight rapeseed canola lines. Data recorded regarding seed yield kg/ha for the two years from eight different locations is presented in the Tables 2 and 3.

Table 2: Mean seed yield (kg/ha) of 8 rapeseed genotypes at 8 locations during 2018-19

Genotypes	NARC	BARI	ORI	RARI	AZRI	AZRC	NIFA	ARI	Mean	Rank
RR-8-1	2845	1665	3204	1556	1191	2689	2914	1692	2219	2
KN-309	2817	1631	2715	1472	934	2616	2764	862	1976	6
RBN-13016	2698	2155	3141	1694	1476	1883	3275	1797	2265	1
CHS-9	2760	1808	3185	1056	1059	2247	3746	1336	2150	3
RBN-13017	2579	1993	3026	1472	969	2047	3319	683	2011	4
CHS-2	2889	1881	2585	1139	910	1698	3541	1363	2001	5
Super Canola	2741	2052	2667	1222	1045	1802	2781	1117	1928	7
14CBN009	2135	2035	2259	1056	1087	2063	3108	1389	1891	8
Location Mean	**2683**	**1903**	**2848**	**1333**	**1084**	**2131**	**3181**	**1280**	**2055**	
Minimum	2135	1631	2259	1056	910	1698	2764	683	1891	
Maximum	2889	2155	3204	1694	1476	2689	3746	1797	2219	
CV %	4.6	10.3	5.82	10.84	22.5	3.07	27.5	15.5		
LSD (5%)	217	345	290	253	NS	114.7	NS	346.4		
Location LSD (5%)										

The mean seed yield performance of eight rapeseed genotypes at eight locations revealed large fluctuations within environment as well as between environment for both years as given in Table 2 and 3. During 2018-19 highest average seed yield of 3181 kg/ha was recorded at NIFA, Peshawar followed by ORI, Faisalabad and NARC, Islamabad with average seed yield 2848 and 2683 kg/ha respectively. On the average of eight locations six genotypes out yielded the check Super Canola (1928 kg/ha) and these include RBN-31016 (2265 kg/ha), RR-8-1(2219 kg/ha), CHS-9 (2150 kg/ha), RBN-13017 (2011 kg/ha), CHS-2 (2001 kg/ha) and KN-309 (1976 kg/ha).Three genotypes produced more yield as compared to experimental mean (2055 kg/ha) **.**

Table3: Mean seed yield (kg/ha) of 8 rapeseed genotypes at 8 locations during 2019-20

Genotypes	NARC	BARI	ORI	RARI	AZRI	AZRC	NIFA	ARI	Mean	Rank
RR-8-1	2162	2517	2274	1581	531	2350	2628	2087	2016	1
KN-309	1743	2041	2155	1120	725	1837	2324	1377	1665	7
RBN-13016	1306	2231	1680	1476	550	2031	2545	2014	1729	4
CHS-9	2242	2133	2097	1117	594	2137	2462	1608	1799	3
RBN-13017	1405	2561	2585	1269	350	1994	2711	1650	1816	2
CHS-2	1624	2378	2201	1357	481	2139	2241	1356	1722	5
Super Canola	1032	2189	1655	1128	606	3047	2573	1339	1696	6
14CBN009	1299	2189	1734	1024	211	1789	2739	1746	1591	8
Location Mean	**1602**	**2280**	**2048**	**1259**	**506**	**2166**	**2528**	**1647**	**1754**	
Minimum	1032	2041	1655	1024	211	1789	2241	1339	1591	
Maximum	2242	2517	2585	1581	725	3047	2739	2087	2016	
CV %	6.95	-	5.51	1.50	53.3	6.66	21.6	16.6		
LSD (5%)	195.0	-	197.6	31.9	NS	253.2	NS	478.9		
Location LSD (5%)										

During 2019-20, across locations, NIFA, Peshawar was found to be best location with mean seed yield 2528 kg/ha and followed by BARI Chakwal (2280 kg/ha), AZRC (2166 kg/ha) and ORI Faisalabad (2048 kg/ha). On the basis of average of eight locations five genotypes out yielded the check Super Canola (1696 kg/ha) i.e. RR-8-1(2016 kg/ha), RBN-13017 (1816 kg/ha), CHS-9 (1799 kg/ha), RBN-31016 (1729 kg/ha), and CHS-2 (1722 kg/ha). Three genotypes produced more yield as compared to experimental mean (1754 kg/ha).

The present research elucidated the Genotypes x Environment Interaction (GEI) of elite brassica genotypes for seed yield. Overall, genotypes showed significant variation in different environment. The rapeseed crop growth was

significantly affected by environment variation, which further had an impact on seed yield [14]. According to Hussain et al. [15], environmental variance can have negative effect on a plant's physiological activity that ultimately reduce rapeseed growth and seed yield. It was observed that using improved and climate resilient genotypes rapeseed yield can be enhanced by approximately 18–38% [9]. Current study reported, all the genotypes showed significant variation in all environment which indicates that environment directly affected the seed yield. These findings agree with the results of other scientists [16], [1], [2] who noticed variations in the genotype into environment interaction thus resulting change in performance of rapeseed cultivars for yield associated traits.

Pooled analysis of variance showed highly significant differences among genotypes (G), locations (L), years (Y). Highly significant differences among the genotypes for seed yield indicated the presence of sufficient genetic variation among the genotypes. Significant G x L, L x Y and G x L x Y interaction suggested different response of the genotypes due to the presence of heritable variations among the genotypes at different locations in different years. However, G x L x Y interaction was greater than G x L and G x Y interaction suggesting that each location in each year would be treated as separate environment. The same results were reported by Gazal etal. [13] and Mubashir *et al* [19]. The identical outcomes have been also recorded in other crops and published by Ali et al., [4] in groundnut, Khan et al., [17] in chickpea and Ali et al [3] in Brassica. In Current studied pooled analysis of variance showed highly significant differences among the entire factor except G x Y.

Table 4 : Pooled ANOVA for seed yield among 8 rapeseed genotypes at 8 locations during 2018-19 & 2019-20

Source	DF	SS	MS	F	P
Replication	2	304498	152249		
Genotype (G)	7	4773467	681924	6.63	0.000
Location (L)	7	168800000	24110000	234.61	0.000
Year (Y)	1	8005627	8005627	77.89	0.000
G x L	49	1.1810000	241104	2.35	0.000
G x Y	7	427428	61061.1	0.59	0.760
L x Y	7	2.7240000	3892103	37.87	0.000
G x L x Y	49	1.0230000	208881	2.03	0.000
Error	302	31040000	102778		
Total	431				
CV%	16.88				

The Stability parameters studied for two years are discussed separately as below

Stability parameters for the year 2018-19

A biplot was drawn between Coefficient of variation (%) and average seed yield (kg/ha) taking mean seed yield along x-axis and CV on Y-axis (Fig). The two central lines of the biplot represent the overall mean of SY and CV. The genotypes viz; RR-8-1 and RBN-13016 marked as stable genotypes because their seed yield was higher than the overall mean and their CV% was less than overall CV%. Here in this plot we considered only 2 parameters i.e. good performance and CV% for determining the stability of the genotypes tested under varied environmental conditions.

Stability of the genotypes was also determined by drawing another biplot between Eberhart(b_i) and Russel coefficient of variability (S^2di) .This biplot showed CHS-9 and RBN-13017 as the adaptable genotypes and no genotype was categorized as stable or adaptable stable according to this plot (Fig 2).

The stability parameters presented in table 5 revealed that the regression coefficient (bi) of eight genotypes ranged from 0.82 to 1.26 for 14CBN009 and CHS-9. The genotypes CHS-9, RBN-13017 and CHS-2 having regression coefficient 1.26, 1.16 and 1.12 respectively greater than unity ($b_i>1.0$) indicated that these genotypes are suitable for favorable environments only. In contrast the genotype 14CBN009 ($b_i = 0.82$) had regression coefficient less than unity ($b_i<1.0$) indicating that this genotype is suitable for poor environments. Out of eight genotypes RBN-13016 is marked as the stable genotype over the location under study because it showed above average yield response (2264.9 kg/ha) and regression coefficient near to unit ($b_i = 0.83$) and has low value of S^2d_i (7889). Its R^2_i value was also high (0.91) confirming its stability.

Table 5 : The stability parameters studied during the year 2018-19

	*	*	Francis	Eberhart & Russell	*	*
Genotype	Mean	Sd	CV%	B_i	S^2di	R^2
14CBN009	1891.5	689.2	36	0.82	26289	0.88
CHS-2	2000.7	921.8	46	1.12	28345	0.93
CHS-9	2149.5	1012	47	1.26	-12812	0.98
KN-309	1976.4	843.6	43	0.99	73530	0.86
RBN-13017	2011	941.4	47	1.16	16545	0.94
RBN-13016	2264.9	686.6	30	0.83	7889	0.91
RR-8-1	2219.3	769.7	35	0.9	54039	0.86
Super Canola (C)	1928.3	746.4	39	0.92	-5773	0.95

A biplot was drawn between Coefficient of variation (%) and average seed yield (kg/ha) taking mean seed yield along x-axis and CV on Y-axis. According to this plot during 2019-20, RR-8-1 and CHS-9 were marked as stable and good performing genotypes because their seed yield was higher than the overall mean and their CV% was less than overall CV% (Fig 3). The biplot between Eberhart (b_i) and Russel coefficient of variability (S^2di) showed none of the genotype as stable or adaptable during the year 2019-20 (Fig 4).

Stability parameters for the year 2019-20

The stability parameters presented in table 6 revealed that the regression coefficient (bi) of eight genotypes ranged from 0.820to 1.20 for KN-309 and RBN-13017. The genotypes CHS-9, 14CBN009 and Super Canola having regression coefficient 1.20, 1.13 and 1.10 respectively significantly greater than unity ($b_i>1.0$) indicated that these genotypes are suitable for favorable environments only. In contrast the genotypes KN-309 ($b_i = 0.80$) and RBN-13016 ($b_{i=}0.89$) and CHS-9 ($b_{i=}0.91$) had regression coefficient significantly less than unity ($b_i<1.0$) indicating that these genotypes are suitable for poor environments. Out of eight genotypes RR-8-1 was marked as the stable genotype over the location under study because it has above average yield response and regression coefficient near to unit and has low value of S^2d_i. .Its high R^2_i value (0.933) also confirmed its stability.

Table 6 : The stability parameters studied during the year 2019-20

	*	*	Francis	Eberhart & Russell	*	*
Genotype	Mean	Sd	CV%	B_i	S^2di	R^2
14CBN009	1591	762.55	47.9	1.13	25008	0.933
CHS-2	1722	646.03	37.5	0.96	12642	0.932
CHS-9	1799	644.04	35.8	0.91	51200	0.852
KN-309	1665	549.67	33.0	0.80	12868	0.906
RBN-13017	1816	812.78	44.8	1.20	36907	0.926
RBN-13016	1729	624.02	36.1	0.89	43698	0.859
RR-8-1	2016	678.86	33.7	1.01	15343	0.933
Super Canola (C)	1696	838.40	49.4	1.10	201403	0.730

According to Chattopadhyay et al. [7] and Sah et al. [25] a single method may not be reliable in estimating the stability of genotype across environments for yield related traits. Several methods have been set for assessing the stability of genotype x environment interactions like Finlay and Wilkinson [11], Eberhart and Russell [10] and Perkins and Jinks [21]. Eberhart and Russell [10] suggested that stable genotypes can be referred on the basis of high mean value, regression coefficient of the genotypes on location (b_i) squared deviations from regression (S^2d). A genotype with high regression coefficient (b>1) and low squared deviations ($S^2d=0$) is more stable to environment while low regression coefficient (b<1) is said to be low responsive to environments and genotype which has unit regression coefficient (b=1) is said to be average responsive to environments. Current studies revealed that the genotypes CHS-9, RBN-13017 and CHS-2 during year 2018-19 while the genotypes CHS-9, 14CBN009 and Super Canola during 2019-20 had higher regression coefficient

than unity (b_i>1.0) indicated these genotypes are stable for seed yield. The genotypes 14CBN009, KN-309 and RBN-13016 and CHS-9 had regression coefficient less than unity (b_i<1.0) indicating that these genotypes are suitable for poor environments. Rashid et al. [2002] reported similar results during study of stability of yield and yield related attributes in mustard.

Conclusion:

From this study it is concluded that the stable genotypes changes by changing the stability parameters used in computing stability analysis. For example during 2018-19, biplot drawn between CV (%) and seed yield (kg/ha) marked the RR-8-1 and RBN-13016 as stable genotypes while the biplot between b_i and S^2di showed CHS-9 and RBN-13017 as the adaptable genotype in this period. In the same cropping season 2018-19 according to Eberhart and Russel [10] method the genotype RBN-13016 was marked as the stable genotype over the location under study because it showed above average yield response and regression coefficient near to unity and has low value of S^2d_i with high R^2_i value. Similarly during 2019-20, biplot drawn between CV (%) and seed yield (kg/ha) marked the RR-8-1 and CHS-9 as stable and good performing genotypes while the biplot between b_i and S^2di showed none of the genotypes as stable or adaptable genotype in this period. During the cropping season 2019-20 according to Eberhart and Russel [10] genotypes RR-8-1 was found to be stable genotype over the location under study due to its above average yield response and regression coefficient near to unit with low value of S^2d_i and high value of R^2_i. Current study indicated that there is great genetic diversity among brassica genotypes under variable climatic conditions and this variation can be exploited in the future breeding programs in developing climate resilient high yielding varieties

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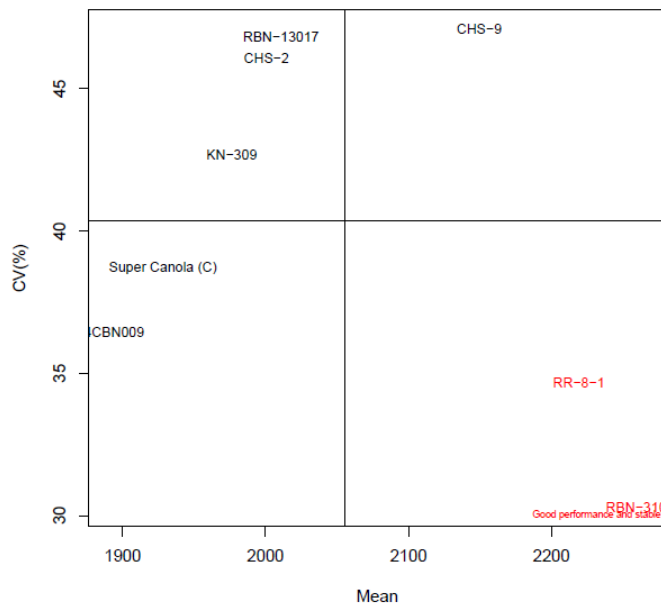
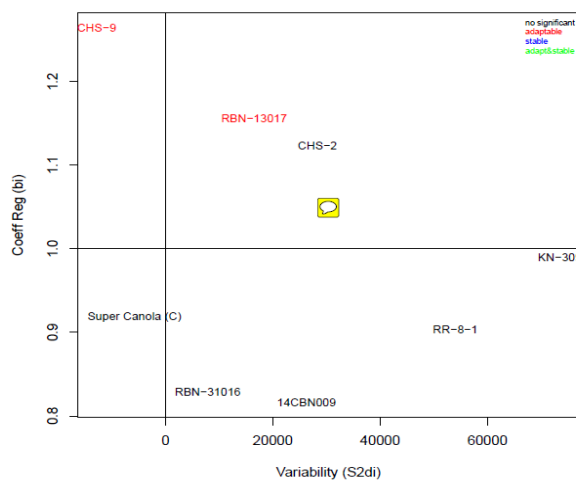Fig 1: A biplot between CV (%) and Seed yield (kg/ha) for 2018-19

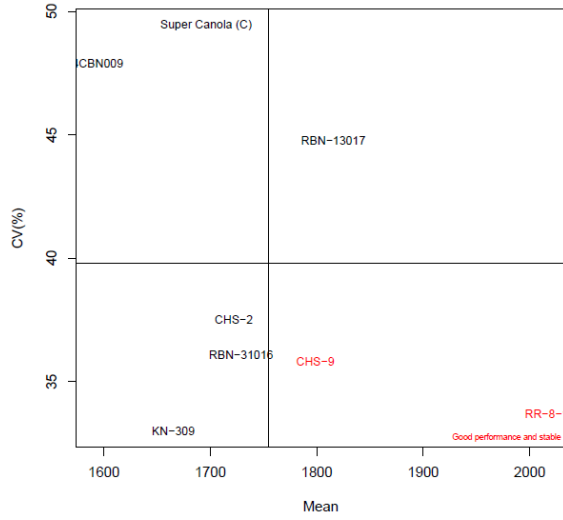Fig.2: A biplot between b_i and S^2di for 2018-19

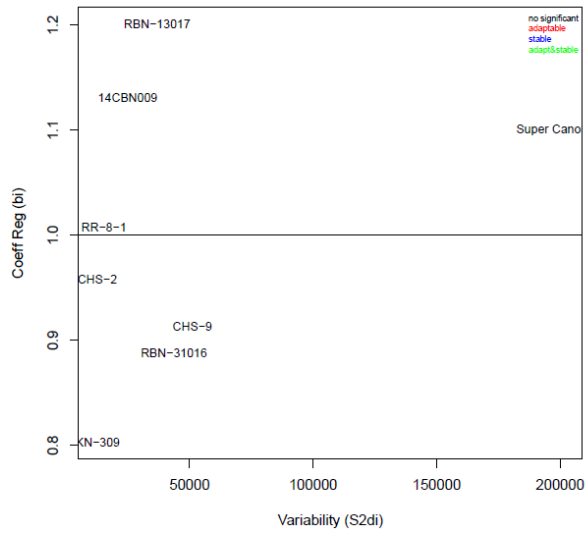Fig 3: A biplot between CV (%) and Seed yield (kg/ha) for 2019-20

Fig.4: A biplot between b_i and S^2di for 2019-20