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# Analysis of genotype x environment interactions for yield and quality traits in vegetable soybean (*Glycine max* (L.) Merill)

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## Abstract
Soybean [*Glycine max* (L.) Merrill] is the world's leading source of oil and protein. It has the highest protein content of all food crops and is second in terms of oil content among food legumes. Study on genotype x environment interaction (GE) and stability of twenty-one newly developed lines derived from the cross between five gain and three vegetable soybean varieties. Analysis was conducted for yield contributing traits with oil and protein at the green stage over three environments in Maharashtra during Kharif 2019. Analysis indicated that the AMMI (AMMI1-AMMI5) were highly significant (*P*< 0.01) for all the traits. The partitioning of TSS (total sum of squares) exhibited that the genotypic and environment effect was a predominant source of variation followed by GE interaction. For green pod yield per plant four lines and green seed yield per plant five lines were identified as stable lines among which line VS-5-276-17 had the best performance. Among the stable performing lines for 100 green seed weight per plant line, VS-2-128-17 had the highest reading. For oil and protein content at the green stage line, VS-4-266-17 was identified as better-performing as well as stable for three locations, The objectives of the experiment were to determine the magnitude of GEI and stability of newly developed lines and thereby identify widely and/or specifically adapted genotypes under Maharashtra conditions. Such an outcome of the present study could be recurrently employed in the upcoming research to define predictive, more rigorous recommendation strategies as well as to explain stability concepts for recommendations for vegetable soybean.

**Keywords:** Vegetable soybean, AMMI analysis, G*E interaction, Biplot analysis

## Introduction
Soybean is a "Miracle bean" having a great nutritional and industrial value (Hossain *et al*. 2003) [16]. Soybean is the highest protein (40%) containing food crops and is second only to groundnut in terms of oil content (20%). Among food legumes, excellent balance of amino acids was found in Soybean protein (Wolf and Cowan, 1975) [42] particularly vegetable soybean called Edamame had potential on another level as it is sweet in taste and less in trypsin inhibitor content than grain soybean. No other vegetable legume can beat the nutrition value of Edamame. Maharashtra was the leading state in soybean cultivation but there is lakh of awareness among the people for vegetable soybean maybe because of adaptive germplasm in this region was very less. In India, few reports on this aspect were found therefore there is a great need to develop improved vegetable soybean varieties. Yield, protein, and oil contents are three major attributes that are specially measured by soybean breeders, farmers, and marketers. Genotype and environment interaction acting a key role in the expression of phenotype, and must be assessed when specifying cultivars for the breeding program (Prado *et al*. 2001) [27]. The presence of significant G*E for quantitative traits such as yield can seriously limit the feasibility of selecting superior genotypes (Flores *et al*. 1998) [11]. However, the G*E can be properly utilize through various approaches revealed by Gauch and Zobel (1996) [12], Kang (1998) [18]. Hence in the present study 21 improved lines were developed by conscious selection as vegetable type soybean and constituted a preliminary adaptation and stability analysis of best soybean lines for production in Maharashtra. The specific objectives were to (i) identify and recommend lines that have the potential for specific and wide adaptation (ii) assess the presence and magnitude of genotype x environment interaction, (iii) identify environments with strong or weak interactive forces.

Analysis of multi-environment trail enables breeders to detect and understand the effect of genotype x environment interaction (GEI) on the eventual performance and performance ranking of a genotype (Sharifi *et al.* 2017) [33]. A mixed linear model was used for estimation of variance components and AMMI analysis was applied for stability of genotypes and environments for those traits. Comparing with other model of stability analysis AMMI model is considered to be better at explaining the effects of G×E interactions, thereby defining clarification of multi-environmental data set (Bhartiya *et al.* 2017) [3] and the Precision in the this model is achieved by separation of structural variation from uproar (Nassir and Ariyo 2011) [24] therefore, it has been widely used in the evaluation of the stability of yield-related traits as shown by Adie *et al.* (2014) [2], Kahram *et al.* (2013) [17], Samonte *et al.* (2005) [31], Sousa *et al.* (2015) [34], Wang *et al.* (2016) [39] in earlier investigation and quality-related traits similar results wear given by Guo *et al.* (2004) [14] and Su *et al.* (2010) [35].

## Materials and Methods
**Genotypes and Field experiments:** Twenty-one advanced lines of vegetable soybean were obtained from a cross between three vegetable and five-grain type soybean varieties. The pedigree information is presented in Table No 1. The genotypes have undergone repeated selfing from F1 to F8 generation to sidestep any probable contamination. The experiment was conducted at three locations representing three regions of Maharashtra state *viz.*, Field of Agharkar research institute at Baramati (18.15°N, 74.58° E), Field of Agril. Botany, Dr. PDKV, Akola (20.7 N 77.07E) and Experimental field of Golegaun college of Agriculture, VNMKV, Parbhani (19.15°N, 76.46°W), Planting was done with a spacing of 50 cm from row to row and 15 cm from plant to plant for all three locations. Randomized block design with three replications was employed and standard crop management practices were adopted across all the locations. Data on five randomly selected plants from each replicate were recorded for yield contributing traits.

**Table 1:** Pedigree of advanced line

| | Name of the genotype | Cross from which genotype derived |
|---|---|---|
| 1. | VS-1-17-17 | Himso-1563 × NRC-55 |
| 2. | VS-1-28-17 | Himso-1563 × NRC-55 |
| 3. | VS-1-67-17 | Himso-1563 × NRC-55 |
| 4. | VS-1-75-17 | Himso-1563 × NRC-55 |
| 5. | VS-1-80-17 | Himso-1563 × NRC-55 |
| 6. | VS-2-128-17 | JS-SH-93-37 × Swarna Vasundhara |
| 7. | VS-2-130-17 | JS-SH-93-37 × Swarna Vasundhara |
| 8. | VS-2-141-17 | JS-SH-93-37 × Swarna Vasundhara |
| 9. | VS-3-99-17 | MACS-1037 × Swarna Vasundhara |
| 10. | VS-3-108-17 | MACS-1037 × Swarna Vasundhara |
| 11. | VS-4-198-17 | MACS-1188 × AGS-459 |
| 12. | VS-4-219-17 | MACS-1188 × AGS-459 |
| 13. | VS-4-223-17 | MACS-1188 × AGS-459 |
| 14. | VS-4-227-17 | MACS-1188 × AGS-459 |
| 15. | VS-4-238-17 | MACS-1188 × AGS-459 |
| 16. | VS-4-244-17 | MACS-1188 × AGS-459 |
| 17. | VS-4-245-17 | MACS-1188 × AGS-459 |
| 18. | VS-5-265-17 | JS-SH-93-05 × Swarna Vasundhara |
| 19. | VS-5-173-17 | JS-SH-93-05 × Swarna Vasundhara |
| 20. | VS-5-276-17 | JS-SH-93-05 × Swarna Vasundhara |
| 21. | VS-5-266-17 | JS-SH-93-05 × Swarna Vasundhara |

## Estimation of protein content (%)
Protein content of seeds harvested at R6 (Green) stage was assessed by Bradford method and expressed on per cent basis for each genotype. The estimation method is based on the protein dye binding method. The binding of Commassie Brilliant Blue (CBB) G-250 to protein in acidic condition shift the λmax of dye from 465 nm to 595 nm. Absorption of the blue colored protein dye complex at 595 nm is straightly related to concentration of protein present in sample (Sengar and Chaudhary, 2014 [32], Khanande *et al* 2016 [19]).

## Estimation of oil content (%)
Nuclear Magnetic Resonance (NMR spectrometry) at the Instrumental cell, Oilseed Research Unit, Dr. PDKV, Akola was used to define the oil composition of soybean seeds. For this purpose, 25-30 gm of (drayed seed of R6 stage) each soybean genotype was measured with three replications. The oil content of soybean seeds was determined by calibrating the NMR signal in contradiction of a suitable reference using MQC Benchtop NMR Analyzer, Oxford instrument.

## Gollobs test and additive main effect and multiplicative interaction (AMMI) model for stability analysis
Gollob's test provides the significance of the F-test in the form of pooled ANOVA for genotypes, environment, and genotype × environment. This test uses the ratio between the mean square for axis n against an estimate of the error term in the ANOVA table which is used to determine the appropriate number of the principal component axis to be retained in a multiplicative model (Gollob 1968) [13]. Additive main effect and multiplicative interaction (AMMI) were used to determine the stability of the genotypes across locations. The Statistical model for AMMI analysis is as follows.

$$Yij = \mu + gi + ej + \sum_{k=1}^{n} \lambda k \alpha ik \gamma jk + eij$$

where $Yij$ = yield of the $i$th genotype in the $j$th environment, $gi$ = mean of the $i$th genotype minus the grand mean, $\lambda k$ = square root of the eigenvalue of the PCA axis $k$, $\alpha ik$ and $\gamma jk$

are the principal component scores for PCA axis *k* of the *i*th genotype and the *j*th environment, respectively, and *eij* is the residual. The environment and genotypic PCA scores are expressed as unit vector times the square root of $\lambda k$; i.e. environment PCA score = $\lambda k\ 0.5 Yik$; genotype PCA score = $\lambda k\ 0.5\alpha ik$ (Farshadfar *et al.* 2001) [10].

AMMI uses both additive and multiplicative components of a two-way data structure hence is a hybrid model. The model splits the variance into additive and multiplicative variance there after uses PCA (principal component analysis) to the interaction variation to a new set of coordinate axes which explains the interaction pattern in more detail. GEA-R software was used to perform the additive main effect and multiplicative interaction (AMMI) test and to derive AMMI1 and AMMI2 biplot plots (Pacheco *et al.* 2015) [26]. In the AMMI1 biplot, the mean of individual trait is presented in X-axis, while Y-axis represents the IPCA1 score concerning that trait. In AMMI2 biplot, PC1 and PC2 scores of different genotypes and environments are plotted in the X- and Y-axis,

respectively, and the polygon is extracted by connecting the furthest genotypes in the biplot to identify "which-wins-where" patterns.

## Result and Discussions
### Phenotypic means by locations and genotypes
The mean performance of all lines across the three environments showed wide range variability *viz.*,166.58 to 260.44 g) for green pod yield line VS-3-108-17 had the highest mean Green Pod Yield (260.44 g) while, genotype VS-4-245-17 having the less mean GPY across all environments. For green seed yield per plant it ranged from 73.60g (VS-1-80-17) to 154.99g (VS-5-244-17) however, 100 seed weight was varied from 28.39g to 42.80g noted in line VS-1-75-17 and VS-4-244-17 respectively. The mean reading for total sugar content was varied from 14.05% (VS-2-141-17) to 22.36% (VS-4-223-17). Considering oil content observed range was 18.51% (VS-1-75-17) to 20.84% (VS-5-266-17) as shown in table no 2.

**Table 2:** Mean performance of lines across the locations

| Sr. No | Name of genotype | Green pod yield per plant | | | | Green seed yield per plant | | | | 100 green seed weight per plant | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | Akola | Parbhani | Baramati | Mean | Akola | Parbhani | Baramati | Mean | Akola | Parbhani | Baramati | Mean |
| 1 | VS-1-17-17 | 162.28 | 155.47 | 195.47 | 171.07 | 69.34 | 70.19 | 91.19 | 76.91 | 32.53 | 28.05 | 34.8 | 31.79 |
| 2 | VS-1-28-17 | 145.83 | 182.83 | 233.50 | 187.39 | 121.12 | 69.42 | 86.17 | 92.24 | 22.66 | 28.05 | 39.17 | 29.96 |
| 3 | VS-1-67-17 | 184.27 | 148.56 | 211.02 | 181.28 | 74.11 | 82.24 | 102.18 | 86.18 | 34.21 | 32.34 | 43.88 | 36.81 |
| 4 | VS-1-75-17 | 190.33 | 152.55 | 192.55 | 178.48 | 71.77 | 68.69 | 91.58 | 77.35 | 29.32 | 21.32 | 34.52 | 28.39 |
| 5 | VS-1-80-17 | 179.41 | 140.16 | 180.16 | 166.58 | 60.04 | 70.28 | 90.49 | 73.60 | 27.02 | 33.53 | 38.25 | 32.93 |
| 6 | VS-2-128-17 | 200.42 | 186.00 | 330.98 | 239.13 | 210.98 | 96.80 | 115.84 | 141.21 | 32.32 | 39.5 | 43.41 | 38.41 |
| 7 | VS-2-130-17 | 177.54 | 186.73 | 226.73 | 197.00 | 120.35 | 95.57 | 115.45 | 110.46 | 29.48 | 26.27 | 41.6 | 32.45 |
| 8 | VS-2-141-17 | 192.40 | 172.00 | 241.00 | 201.80 | 146.20 | 106.91 | 127.50 | 126.87 | 32.77 | 26.99 | 42.97 | 34.24 |
| 9 | VS-3-99-17 | 223.10 | 207.98 | 247.98 | 226.35 | 133.33 | 85.21 | 122.38 | 113.64 | 31.31 | 29.34 | 41.05 | 33.90 |
| 10 | VS-3-108-17 | 243.36 | 139.15 | 186.67 | 189.73 | 76.72 | 85.53 | 107.49 | 89.91 | 33.54 | 28.97 | 42.27 | 34.93 |
| 11 | VS-4-198-17 | 253.24 | 205.00 | 245.00 | 234.41 | 125.67 | 73.78 | 99.62 | 99.69 | 30.31 | 36.47 | 37.23 | 34.67 |
| 12 | VS-4-219-17 | 157.92 | 204.65 | 244.65 | 202.41 | 130.52 | 86.52 | 109.52 | 108.85 | 30.35 | 28.85 | 34.07 | 31.09 |
| 13 | VS-4-223-17 | 277.15 | 177.40 | 217.40 | 223.98 | 95.82 | 81.13 | 104.13 | 93.69 | 27.18 | 34.73 | 43.93 | 35.28 |
| 14 | VS-4-227-17 | 234.99 | 141.79 | 189.20 | 188.66 | 71.68 | 78.58 | 100.96 | 83.74 | 30.5 | 31.36 | 45.1 | 35.65 |
| 15 | VS-4-238-17 | 273.35 | 213.65 | 253.65 | 246.88 | 130.15 | 100.36 | 123.36 | 117.96 | 32.83 | 28.18 | 36.57 | 32.53 |
| 16 | VS-4-244-17 | 192.35 | 213.03 | 253.03 | 219.47 | 131.53 | 72.71 | 95.71 | 99.98 | 41.26 | 43.17 | 43.97 | 42.80 |
| 17 | VS-4-245-17 | 162.95 | 184.33 | 224.33 | 190.54 | 154.55 | 82.67 | 105.67 | 114.30 | 32.28 | 40.67 | 40.57 | 37.84 |
| 18 | VS-5-265-17 | 248.52 | 218.57 | 314.23 | 260.44 | 208.57 | 84.13 | 107.47 | 133.39 | 32.35 | 43.65 | 41.23 | 39.08 |
| 19 | VS-5-173-17 | 204.53 | 206.00 | 351.91 | 254.15 | 209.45 | 92.95 | 115.95 | 139.45 | 33.00 | 36.2 | 40.93 | 36.71 |
| 20 | VS-5-276-17 | 251.00 | 204.33 | 279.02 | 244.78 | 144.90 | 98.53 | 221.53 | 154.99 | 32.33 | 29.1 | 40.37 | 33.93 |
| 21 | VS-5-266-17 | 203.23 | 196.00 | 306.99 | 235.41 | 180.99 | 92.42 | 113.12 | 128.84 | 38.25 | 24.83 | 44.07 | 35.72 |

| S. No. | Name of genotype | Oil content in green stage | | | | Protein content in green stage | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Mean | Akola | Parbhani | Baramati | Mean | Akola | Parbhani | Baramati | Mean |
| 1 | VS-1-17-17 | 14.11 | 20.61 | 18.69 | 19.60 | 19.63 | 25.74 | 23.58 | 25.94 | 24.17 |
| 2 | VS-1-28-17 | 19.12 | 19.47 | 18.35 | 18.68 | 18.83 | 24.24 | 22.14 | 26.14 | 24.76 |
| 3 | VS-1-67-17 | 16.11 | 20.66 | 18.50 | 18.21 | 19.12 | 23.91 | 23.29 | 27.08 | 26.14 |
| 4 | VS-1-75-17 | 15.92 | 18.96 | 18.96 | 17.61 | 18.51 | 25.99 | 25.23 | 27.21 | 27.81 |
| 5 | VS-1-80-17 | 18.20 | 20.00 | 18.55 | 19.07 | 19.21 | 28.10 | 26.31 | 29.01 | 27.47 |
| 6 | VS-2-128-17 | 16.42 | 20.18 | 18.69 | 18.97 | 19.28 | 28.11 | 26.16 | 28.15 | 26.28 |
| 7 | VS-2-130-17 | 21.66 | 20.90 | 19.17 | 18.79 | 19.62 | 27.03 | 25.03 | 26.78 | 21.82 |
| 8 | VS-2-141-17 | 14.05 | 20.63 | 19.55 | 19.26 | 19.81 | 22.27 | 20.27 | 22.91 | 21.51 |
| 9 | VS-3-99-17 | 18.02 | 20.72 | 18.94 | 18.98 | 19.55 | 21.06 | 19.06 | 24.41 | 26.89 |
| 10 | VS-3-108-17 | 15.33 | 20.77 | 19.05 | 18.95 | 19.59 | 27.23 | 25.23 | 28.22 | 27.42 |
| 11 | VS-4-198-17 | 18.77 | 19.84 | 19.37 | 18.11 | 19.11 | 28.27 | 28.05 | 25.93 | 28.26 |
| 12 | VS-4-219-17 | 15.53 | 19.80 | 19.04 | 19.80 | 19.55 | 27.18 | 28.26 | 29.34 | 27.73 |
| 13 | VS-4-223-17 | 22.36 | 20.93 | 18.61 | 19.89 | 19.81 | 28.11 | 26.15 | 28.94 | 28.01 |
| 14 | VS-4-227-17 | 13.99 | 20.18 | 18.55 | 19.58 | 19.44 | 30.20 | 25.11 | 28.72 | 27.74 |
| 15 | VS-4-238-17 | 16.99 | 20.18 | 18.05 | 19.38 | 19.20 | 28.15 | 26.11 | 28.97 | 28.02 |
| 16 | VS-4-244-17 | 18.58 | 20.01 | 18.83 | 20.09 | 19.64 | 28.97 | 26.01 | 29.08 | 26.96 |
| 17 | VS-4-245-17 | 20.46 | 19.80 | 19.80 | 17.89 | 19.16 | 27.03 | 25.23 | 28.62 | 27.27 |
| 18 | VS-5-265-17 | 16.46 | 20.63 | 20.63 | 18.55 | 19.94 | 28.15 | 26.11 | 27.55 | 25.70 |
| 19 | VS-5-173-17 | 14.22 | 20.73 | 19.73 | 20.84 | 20.43 | 25.24 | 22.01 | 29.86 | 27.39 |
| 20 | VS-5-276-17 | 18.79 | 20.18 | 19.51 | 20.18 | 19.96 | 27.30 | 26.10 | 28.76 | 27.80 |
| 21 | VS-5-266-17 | 16.88 | 20.77 | 20.77 | 20.97 | 20.84 | 28.11 | 26..00 | 27.49 | 25.09 |

## Analysis of variance

Genotypes used for yield test trials are commonly treated as static effects. Since mixed linear model approaches can estimate variance components and predict random effects as well (Zhu, 1989) [48]. Results presented genotypic, environmental and G*E interaction effects are highly significant (P< 0.001) for all the traits except total sugar content where G and E showed significance for this trait (Table 3) but the non-significant effect of GE interaction was observed.

Environmental component contributed 30.25% to the total variation for Green pod yield per plant, 26.47% for Green seed yield per plant, 44.63% for 100 green seed weight, 38.22% for protein content (%) at the green stage and 19.49% for oil content (%) at the green stage. Similarly, genotype component contributed 39%, 38.20%, 23.36, 30.34% and 69% of total variation while, G*E comprised of 31.37%, 35.32%, 31.99%, 31.42%, and 12% for Green pod yield per plant, Green seed yield per plant,100 green seed weight, protein content at the green stage, and oil content at green stage respectively (Table 3). The G*E interaction of yield and its components and other quality characters of soybean has been studied by several investigators in the past *viz.*, Chandrakar *et al*. (1998) [7], Rajanna *et al*. (1998) [29], Radi *et al*. (2003) [28], Yothasiri *et al*. (2000) [45] and Gurmu *et al*. (2009) [15].

**Table 3:** AMMI analysis of variance for 21 genotypes evaluated at three locations

| Source | DF | GPY | GSY | 100GSW | OC-R6 | PGS |
|---|---|---|---|---|---|---|
| Environment (E) | 2 | 60091.30** | 27144.36** | 1544.93** | 27.86** | 98.07** |
| Genotype (G) | 20 | 7620.36** | 3916.41** | 80.89** | 2.21** | 34.66** |
| Genotype X Environment (G × E) | 40 | 3115.00** | 1810.74** | 55.38** | 1.15** | 2.92* |
| PC1 | 21 | 4767.98** | 3425.14** | 71.76** | 1.53** | 3.85** |
| PC2 | 19 | 1288.02** | 26.41 | 22.37** | 0.72 | 1.89 |
| Residuals | 126 | 258.53 | 101.62 | 7.40 | 0.62 | 1.71 |
| % SS due to E | | 30.25 | 26.47 | 44.63 | 38.22 | 19.49 |
| % SS due to G | | 39.00 | 38.20 | 23.36 | 30.34 | 69.00 |
| % SS due to G × E | | 31.37 | 35.32 | 31.99 | 31.42 | 12.00 |
| % SS due to PC1 | | 80.35 | 99.30 | 76.49 | 69.97 | 69.24 |
| % SS due to PC1 | | 19.64 | 0.69 | 21.57 | 30.02 | 30.75 |

*Significance at 5% level, **Significance at 1% level
GPY green pod yield per plant; GSY Green seed yield per plant; GSW green seed weight; PG protein content

## Stability Analysis

In this investigation, the main emphasis is on the identification of stable lines which were mostly adapted for important yield and quality contributing traits to three regions of Maharashtra or lines adapted to specific environments. The AMMI model is frequently used to assess the stability of a single trait, however, the stability of each trait is known to fluctuate differentially among cultivars this findings wear in accordance with, Guo *et al*. (2004) [14], Liu *et al*. (2011) [21], Liu *et al*. (2013) [20] and Zhang *et al*. (2014) [46] therefore Stable yield is an essential characteristic, second only to high yield, for an elite cultivar (Zhangxiong *et al*. 2017) [47]. AMMI method, which is centered on principal component analysis, was used to scrutinize the stability of these newly developed lines regarding important yield and quality traits. Two biplots (AMMI 1 and AMMI 2) were used to validate stability. Two biplots (AMMI 1 and AMMI 2) were used to define the stability of this advanced line for each of the six traits. AMMI 1 biplot of main effects are revealed along the abscissa and the ordinate characterizes the first principal component (PC1) score. The elementary idea of the AMMI 1 biplot is to provide means for the trait under consideration and the main purpose of the AMMI 2 biplot is to recognize the lines with specific environmental adaptation AMMI 2 biplot explain the degree of interaction of each line and environment. The lines and environment are outer most from the origin being least desirable.

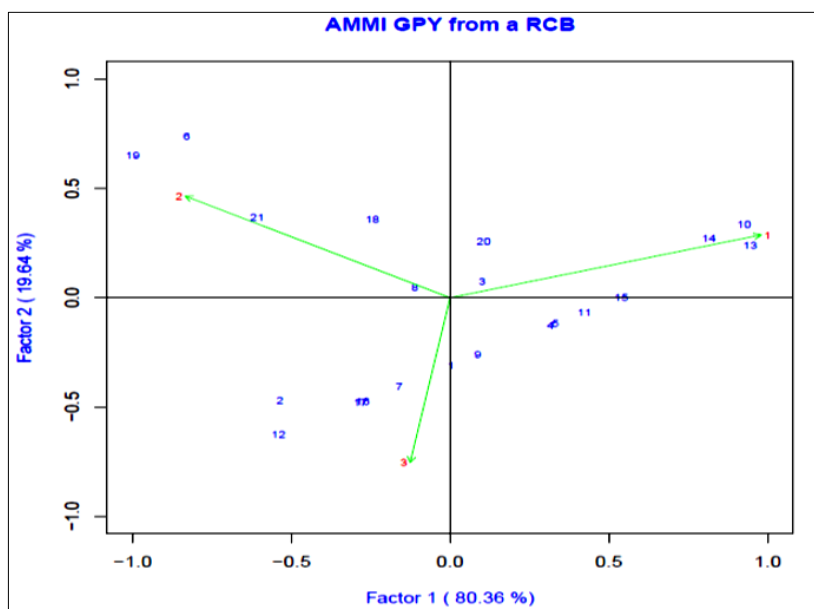## Additive main effect and multiplicative interaction for green pod yield per plant

AMMI1 biplot abscissa and ordinate show the trait main effect and first principal component (PC1) term, Thus, genotypes VS-2-130-17, VS-2-141-17, VS-3-99-17 and VS-5-276-17 were found to be stable across environments for Green Plant Yield. However, plant breeders are interested in genotypes having high mean along with stability for a particular trait, hence VS-5-276-17 had the highest mean green pod yield across the three environments (Fig.1).
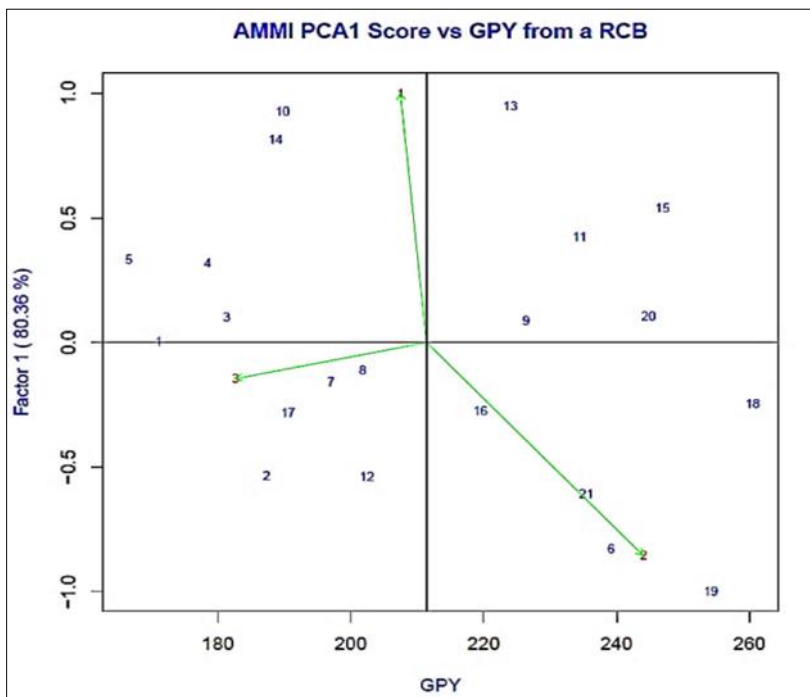
**Fig 1:** Biplot for genotype by environment interaction of green pod yield across the environments showing the effects of primary and secondary components

In AMMI2, the biplot abscissa and ordinate use the first and second principal component terms (PC1 and PC2), respectively. If the first two PC explain more than 60% of the (G×GE) variability in the data, and the combined (G×GE) effect account for more than 10% of the total variability, then the biplot adequately approximates the variability in G×E data (Yan *et al*. 2010) [43]. In the case of GPY, the AMMI2 biplot explained 100% of the genotype and genotype × environment variation. The distance of the environment and genotype vectors is quite prominent from the biplot origin (Fig 2). Thus, the AMMI2 biplot validated the existence of interaction of 21 vegetable soybean genotypes with three environments for Green Pod Yield.



**Fig 2:** Biplot for the primary component of interaction (PC1) and average green pod yield (g). Vertical line at the center of biplot indicates general grand mean

**Additive main effect and multiplicative interaction (AMMI) analysis of variance for green seed yield per plant:** Considering AMMI biplot, VS-2-141-17, VS-3-99-17, VS-4-219-17, VS-4-238-17, VS-5-276-17 were found to be stable across locations. Out of which VS-2-141-17, followed by VS-4-238-17 and VS-5-276-17 found to be the best line with high stability across the locations and high green seed yield per plant. Line VS-1-67-17 and VS-4-227-17 were found to be stable lines for Akola location while genotype VS-4-245-17 was found to be suitable for the Parbhani location, (Fig 3). Similarly, Radi *et al*. (2003) [28] also evaluated five soybean genotypes under diverse locations and years. Their result has shown that seed yield is noticeably exaggerated by varying locations and years.
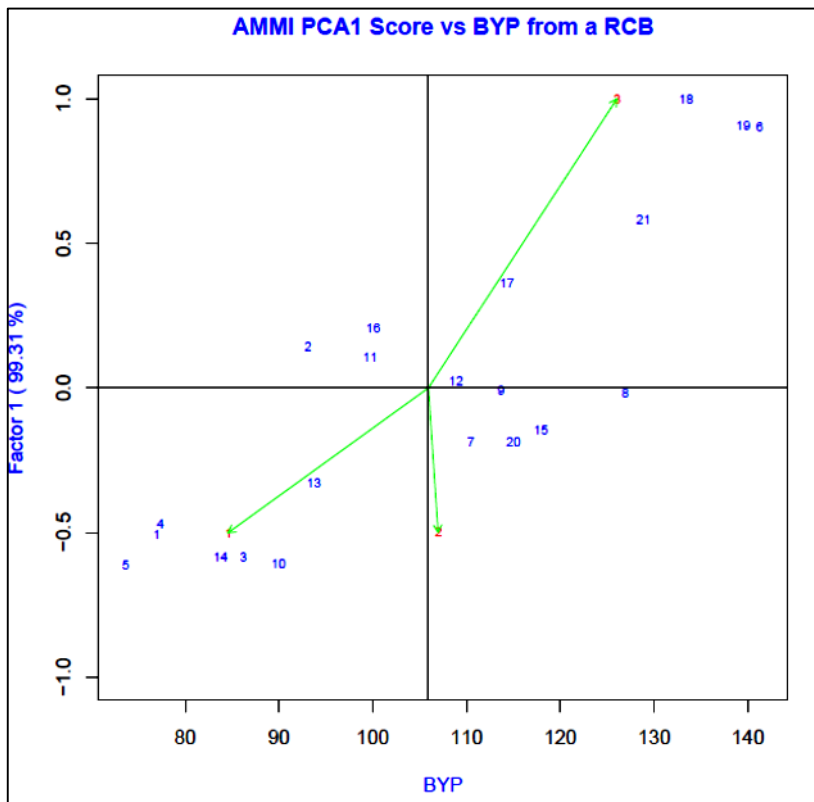
**Fig 3:** Biplot for genotype by environment interaction of green seed yield per plant across the environments showing the effects of primary and secondary components

The first principal component accounted for 99.30% while the second PC accounts for only 0.69% (Table 4.7), interaction sum of squares indicating the two interacting environments only. The biplot (PC1 vs PC2) presents the spatial pattern of the first two PC axes of the interaction effect corresponding to the genotypes and helps in the visual interpretation of the G*E pattern and identify genotypes or environments that exhibit low, medium, or high level of interaction effects. Most of the lines were close to the origin, hence they are most stable (Fig 4). Environments with a short length of arrow lines do not exert strong interactive forces. Those with long spokes (length of arrow lines) exert strong interaction. Environment 3 (Parbhani) having shorter spokes produce weak interaction result wear in accordance with Abou Sen (2020) [1].
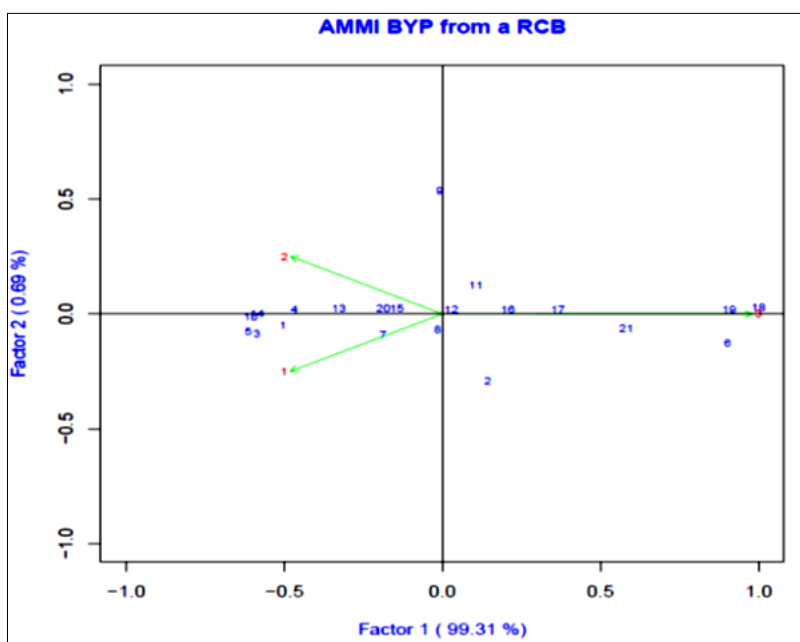


**Fig 4:** Biplot for the primary component of interaction (PC1) and average green seed yield (g). Vertical line at the center of biplot indicates general grand mean

**Additive main effect and multiplicative interaction (AMMI) analysis of variance for 100-green seed weight per plant:** Considering AMMI1 for 100 Green seed weight, genotype VS-1-17-17, VS-1-28-17, VS-2-128-17, VS-3-99-17, VS-4-219-17 and VS-5-266-17 were found to be stable lines for all three locations out of which VS-5-266-17

followed by VS-2-128-17 was found to be stable with a high mean. Line VS-1-80-17 was found to be stable for this trait in location 3 while line VS-4-227-17 performed best over location 2 (Baramati) (Fig 5).
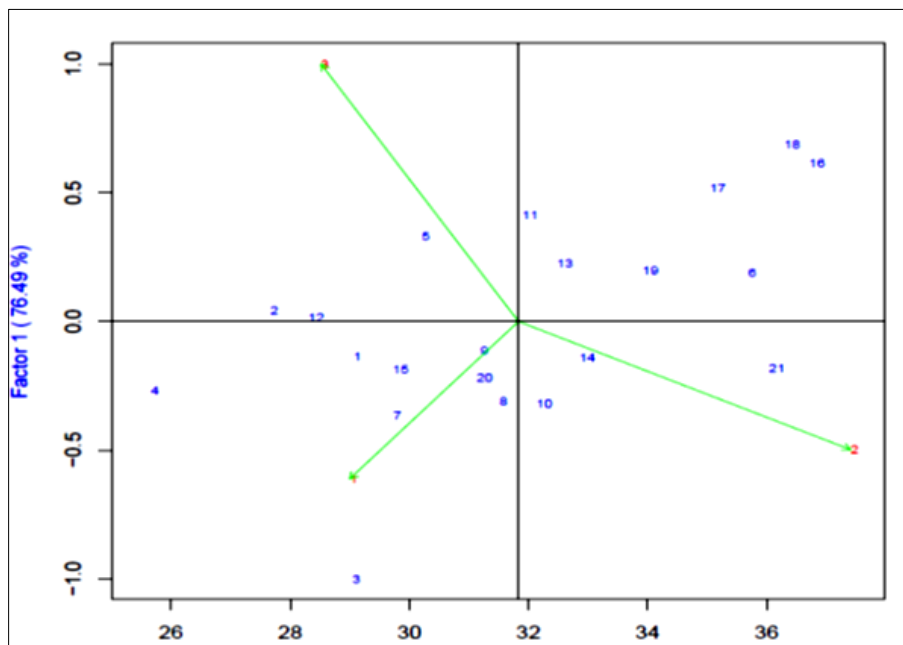


**Fig 5:** Biplot for genotype by environment interaction of 100-green seed weight across the environments showing the effects of primary and secondary components

PC1 and PC2 of 100-green seed weight per plant accounted for 76.49% and 21.57% of interaction, respectively which indicates all three environments are interacting for this trait.

For yield subsidizing traits there were altered winning lines for each environment indicates the presence of crossover type of GEI. The presence of crossover GEI validates the need for stability analysis (Yan and Tinker, 2006) [44]. In other studies, Bhartiya *et al*. (2017) [6] also testified a higher contribution of GEI to total variation with values of 60% and 41%, respectively. Other studies *viz*., Gurmu *et al*. (2009) [15]; Rakshit *et al*. (2012) [30] and Vaezi *et al*. (2017) [38] found the environment to be the highest contributor to the total variation. Tukamuhabwa *et al*. (2012) [37] and Mushoriwa (2013) [22] and Mwiinga *et al* (2020) [23] also found the presence of crossover GEI in their studies as they found different winning genotypes in the different test environments as well as Tang *et al*. (2013) [36] suggested that stability is largely diverse among different traits.
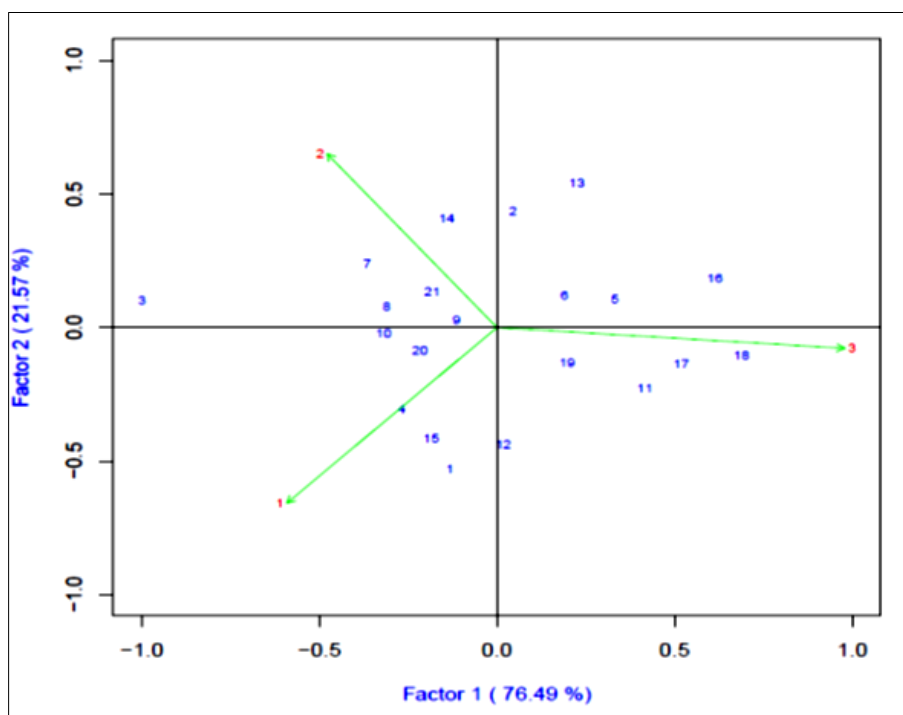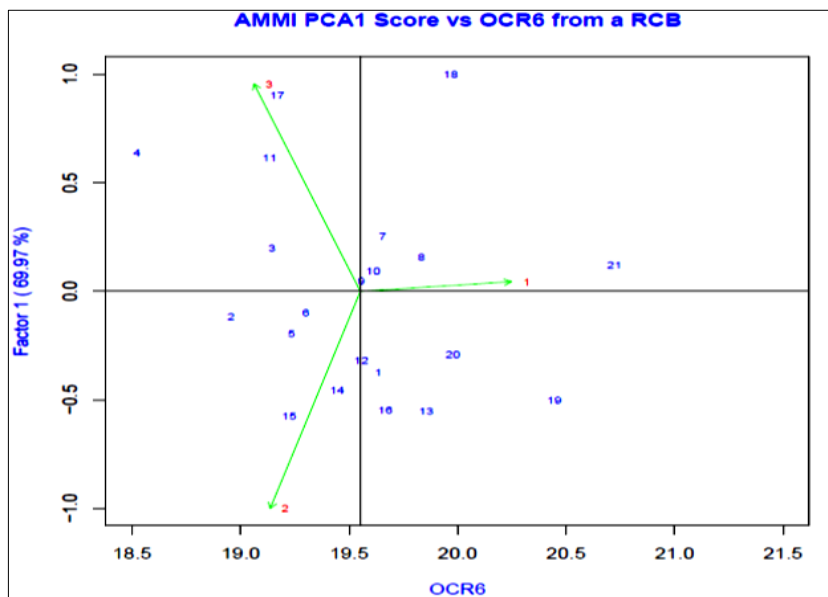


**Fig 6:** Biplot for the primary component of interaction (PC1) and average 100-green seed weight (g). Vertical line at the center of biplot indicates general grand mean

**Additive main effect and multiplicative interaction (AMMI) analysis of variance for oil content in the green stage (OC-R6)**

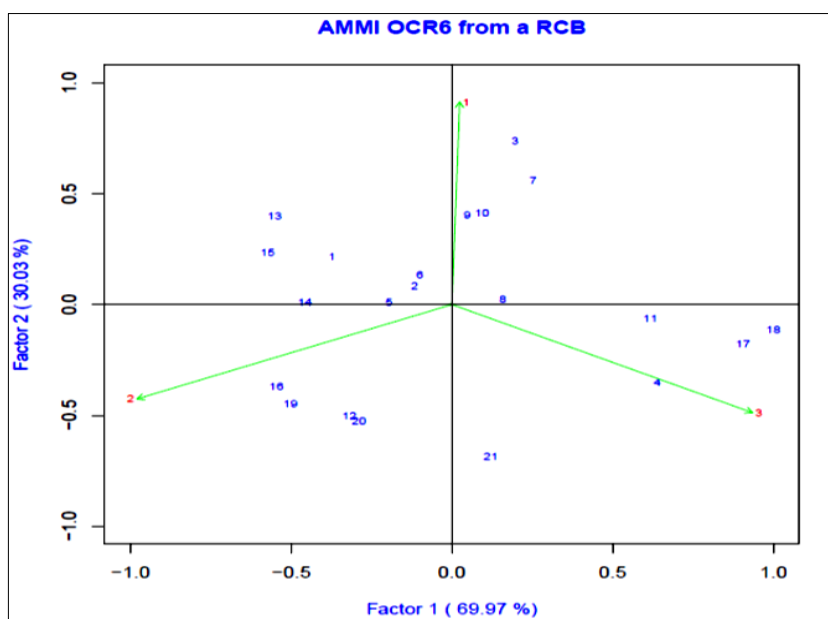In the AMMI1 biplot, genotypes for this trait line VS-1-28-17, VS-1-80-17, VS-2-128-17, VS-3-99-17, VS-3-108-17, and VS-5-266-17 found to be stable across the location out of which VS-5-266-17 could be a promising genotype for oil content across environments. Since its mean oil content is greater than the other lines Fig 7



**Fig 7:** Biplot for genotype by environment interaction of OC-R6 across the environments showing the effects of primary and secondary components

PC1 and PC2 of oil content in the green stage accounted for 69.97% and 30.02% of interaction, respectively. In the AMMI2 biplot, Location Akola was comparatively nearer to zero than the rest of the locations, it was more stable and this might be the finest location concerning oil content in the green stage. The remaining two locations had high interactive force as they are farthest from the origin towards negative PC1 score similarly Arslanglou *et al.* (2011) [3] and Chaudhary and Wu (2012) [8] also found that protein content % and oil content % differed significantly for genotype, environment, and their interactions soybean genotypes conducted at different sites. Many researchers study the oil content at the R8 stage as High temperature during the growing season was correlated with high oil content (Wolf *et al.* 1982) [41]. Environment plays a critical role in the oil content of soybean seed (Bellalouil *et al.* 2015) [5]. Some other researchers reported that high air temperature mainly in the pod filling period increased the oil percentage of soybean seed (Dornbos and Mullen, 1992 [9]; Bellalouil *et al.*, 2011 [4] and Bellalouil *et al.* 2015) [5]. We observed that oil content at the R6 stage was less than the R8 stage similarly Wilcox and Cavin (1995) [40] reported that structural components of seed are controlled by genotype, maturity, growing season, geographic location, and agronomic practices.



**Fig 8:** Biplot for the primary component of interaction (PC1) and average OC-R6 content. Vertical line at the center of biplot indicates general grand mean

**Additive main effect and multiplicative interaction analysis of variance Protein content in the green stage**
In the AMMI1 biplot, lines VS-1-28-17, VS-1-80-17, VS-2-128-17, VS-4-227-17, VS-4-238-17, VS-5-276-17, and VS-5- 266-17 were found to be stable across the location. Out of which VS-5-266-17 was found to be the best stable line with the highest mean (Fig 9). Similar result wear found by Njoroge and Oyoo (2020) [25].
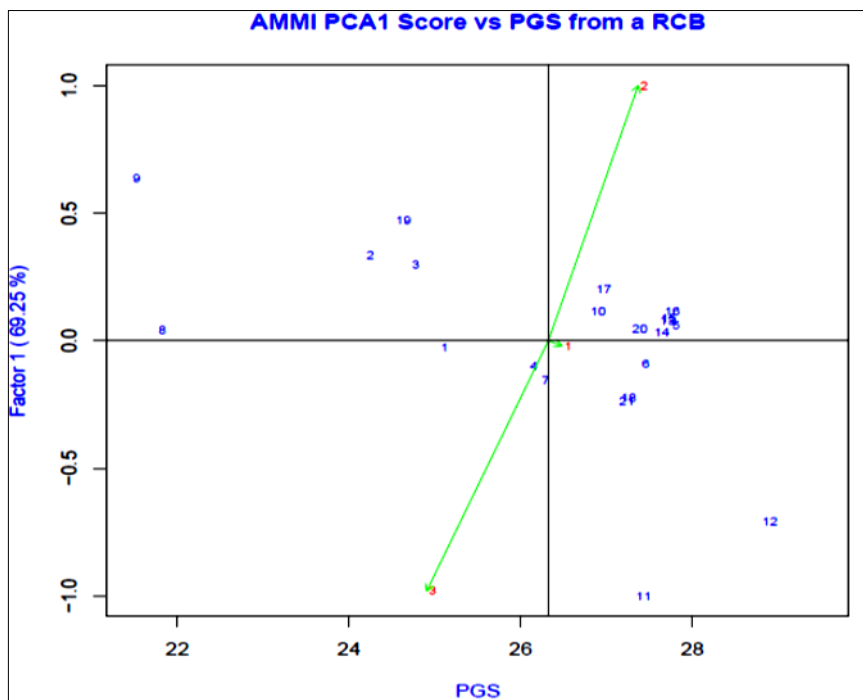


**Fig 9:** Biplot for genotype by environment interaction of protein content in green stage across the environments showing the effects of primary and secondary components

PC1 and PC2 of protein content in the green stage accounted for 69.24% and 30.75% of interaction, respectively. All locations have high interactive forces as they are far away from the origin and Genotype VS-1-28-17, VS-1-80-17, VS- 3-108-17, VS-4-223-17, and VS-4-245-17 are most stable because of their closeness to the origin. From the projection line, VS-3-99-17 was specifically adapted to environment 2 (Baramati) as presented in Figure 10.
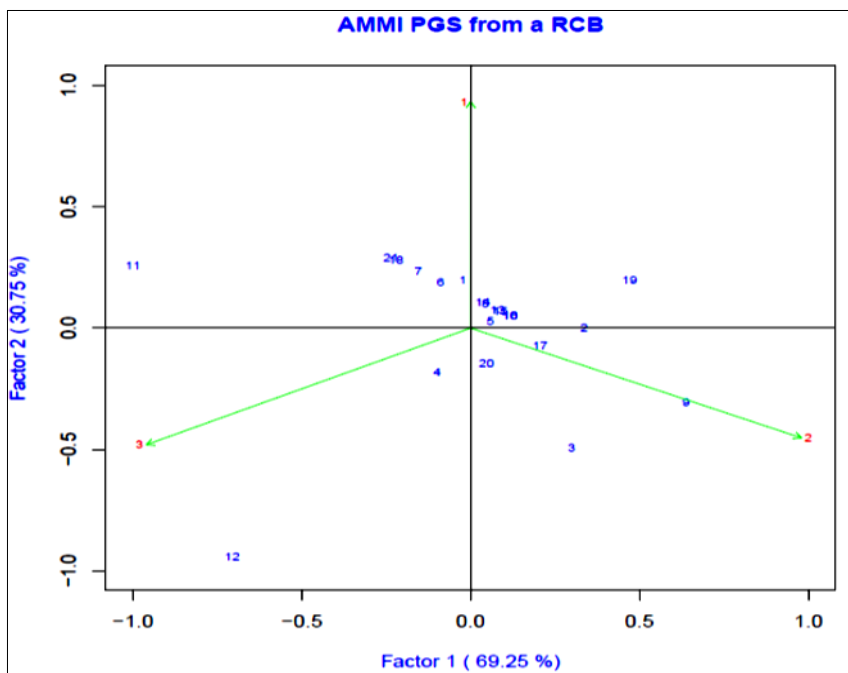


**Fig 10:** Biplot for the primary component of interaction (PC1) and average protein content in green stage. Vertical line at the center of biplot indicates general grand mean

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