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Assessment of G×E interaction for fibre quality traits in recombinant inbred lines of cotton

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Abstract

The quality of textile processing depends on the several cotton (*Gossypium hirsutum* L.) fibre quality traits, such as micronaire value, fibre length, and fibre strength. The objective of this investigation was to identify stable genotype(s) and suitable season for expression of five fibre quality traits among 220 recombinant inbred lines of cotton. This evaluation was done at Department of Cotton, TNAU, Coimbatore during three seasons (*kharif* 2017-18, Summer 2018 and *kharif* 2018-19) in randomized complete block design with two replications. Genotype×environment interaction (GEI) was studied using the Additive main effect and multiplicative interaction analysis. Pooled analysis of variance revealed highly significant differences among genotypes, environments and interaction effect for Upper half mean length of fibre, uniformity index, bundle strength and fibre fineness. Principal component 1 for upper half mean length of fibre, uniformity index, bundle strength, elongation percentage and fibre fineness accounted for 67.58, 75.40, 80.30, 81.20 and 74.90 per cent respectively of the total variation. Based on genotype stability index, RIL 120 emerged as stable performer for four quality traits *viz.*, UHML, bundle strength, elongation percentage and fibre fineness. Also, six other genotypes *viz.*, RIL 145, 151, 74, 82, 96 and 152 were stable for atleast two quality traits. Based on PC1, AMMI stability value and Genotype stability index, 52 entries were shortlisted for GGE biplot analysis. RIL 134 exhibited the best fibre qualities *viz.*, bundle strength and elongation percentage in E1 season and uniformity index in E3. The genotype RIL 93 expressed its best fibre qualities *viz.*, bundle strength and upper half mean length in E2. So also, the potential of RIL 82 for elongation percentage could be witnessed in both seasons E2 and E3 and for fibre fineness during E1. These genotypes are ideal for multiple traits in same or different seasons. E 1 season (Kharif 2017-18) emerged as representative and discriminating environment for three out of five traits *viz.*, bundle strength, elongation percentage and fibre fineness. Thus the present investigation has led to identification of ideal RI lines for different fibre traits and ideal season for selection and development of improved cotton varieties with good fibre quality.

Keywords: G×E interaction for fibre quality, recombinant inbred lines

Introduction

Cotton is the most important agriculturally produced raw material in the world. For the many developing countries which cultivate it, cotton is a vital basis for employment, rural and industrial development. Ongoing changes in textile processing, particularly the new, improved spinning technologies, have led to increased emphasis on breeding for both improved yield and fiber quality (Patil and Singh, 1995). It is the quality of fibre from ginned seed that determines the economic value and end use.

The indeterminate growth habit of the crop makes the initiation and formation of bolls continuously over a long period of time during the season, and fibre properties of bolls on the same plants can differ because of different environmental conditions during boll growth and development (Bauer *et al.*, 2009). Temperature fluctuations before anthesis and during fibre development have implications in fibre quality changes (Davidonis *et al.*, 2004) [6]. Under inadequate moisture conditions and increasing temperatures, fibre length decreases and fibre micronaire values increase (Reddy *et al.*, 1999) [24]. The effect of G×E varies among fiber traits, which means that certain fiber traits are more sensitive to environmental changes than others, which necessitates the identification of traits with less environmental influence and suitable genotypes with ideal quality in the given set of a population.

The stable performance of a cultivar is based on its genetic makeup (G), environment/season during its growth (S) and as well as the interaction between genotypes and various seasons (G × S). In case of different environmental variables, de Oliveira *et al.* (2005) [7] illustrated about planting season as one of the variables that alters the performance of genotypes. Malambane *et al.*, (2014) [17] insisted on the study of correlation among the variables and genotype × Environment interaction, which gives an exact figure for the performance of genotypes in a range of weather conditions.

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The biplot graphical display of the data is a useful technique that graphically displays the two-way (genotype-environment) data and allows visualisation of the interrelationship among environments and genotypes, and interactions (Yan and Kang 2002) [21]. Two types of biplot models have been extensively used for this purpose viz., AMMI analysis (Gauch, 1992) [31] and GGE biplot analysis (Yan and Kang 2003) [19].

The Additive Main Effects and Multiplicative Interaction (AMMI) model proposed by Williams (1952) [16], Pike and Silverberg (1952) calculates genotypes and environment additive effects using analysis of variance and then analyzes the residual using principal component analysis. The result is least square analysis, with which further graphical representation of the numerical results, often allows a straight forward interpretation of underlying cause of $G \times E$ interaction. However, (Ding *et al.*, 2007) [18] opined that AMMI analysis does not depict the genotypic effects and hence used GGE [genotype main effect (G) and genotype by environment interaction (GE)] biplot for identifying the difference among genotypes as well as for validating the test environment.

According to Farias *et al* (2016) [11], both AMMI and GGE biplot methods provided concordant results for phenotypic stability in discrimination of environment and genotype. Thus, the objective of the present study was to identify stable genotype(s) in cotton for different fibre properties in a large population using AMMI stability value and genotype selection index. The screened lines were further assessed using GGE biplot method.

Materials and Methods

The field testing was conducted at Department of Cotton, Tamil Nadu Agricultural University, Coimbatore during three cropping seasons (Table 1) *kharif* 2017-2018 (E1), summer 2018 (E2) and *kharif* 2018-2019 (E3). 11½N latitude and 77½N longitude. Experimental material consisted of 220 recombinant inbred lines (RILs) derived from the parents MCU 5 with good fibre quality and TCH1218 with good combining ability. These lines were raised with parents as irrigated crop in randomized complete block design with two replications. Distance between plants was 45 cm and row to row distance was 90 cm. In each row, up to 13 plants were maintained. All the suggested agronomic practices including plant protection measures were accomplished throughout the crop growing period in each season.

Table 1: Mean weather data during crop growth in cotton

| Season | Maximum temperature °C | Minimum temperature °C | Average rainfall (mm) |
|------------------|------------------------|------------------------|-----------------------|
| Kharif 2017-2018 | 31.01 | 22.84 | 502.3 |
| Summer 2018 | 33.05 | 22.80 | 378.0 |
| Kharif 2018-2019 | 30.50 | 22.27 | 459.6 |

In each genotype, three plants were randomly selected from each replication to observe five fibre quality traits. The fibre quality traits were as follows: Upper half mean length of fibre (mm), uniformity index, elongation percentage, fibre strength (g/tex) and fibre fineness (µg/inch). Fibre quality traits were measured using STATEX compact high-volume instrument. For assessing fibre properties HVI mode was used.

Stability analysis was carried out using AMMI model in 220 RI lines. The genotypes were ranked based on stability for traits using ASV (AMMI stability value) and GSI (Genotype selection index). Stability analysis using GGE biplot was

computed in 52 RI lines which were selected based on ASV and GSI.

Stability Analysis

The recorded fibre quality traits were subjected to analysis of variance using SPAR version 2.0. Environments were considered as random effects and genotype as fixed effects. The source of variation was partitioned into replication, genotypes and error, while genotype effect was further decomposed into three components as G, E and GEI effects.

AMMI analysis was carried out using PB Tools software version 1.4 (PB Tools, 2014) with the model equation

$$Y_{ij} = \mu + g_i + e_j + \sum \lambda_k \alpha_{ik} \delta_{jk} + R_{ij} + \varepsilon$$

Where, Y_{ij} represents the value of the i^{th} genotype in the j^{th} environment; μ is the grand mean; g_i indicates the mean of the i^{th} genotype; e_j exhibits the mean of the j^{th} environment; λ_k denotes the singular value for principal component (PC) axis k ; α_{ik} and δ_{jk} portrays the PC scores for axis k of the i^{th} genotype and j^{th} environment, respectively; R_{ij} stands for the residual effect and ε is the error term (Gauch 1992). The AMMI stability value (ASV) was computed by the method reported by Purchase *et al.* (2000) [23].

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA_1) \right]^2 + (IPCA_2)^2}$$

Where, SS is the sum of squares, IPCA1 and IPCA2 are the first and second interaction principal component axes, respectively; and IPCA1 and IPCA2 are the genotypic scores in the AMMI model. Genotype selection index (GSI) was calculated following the method devised by Farshadfar and Sutka (2003) [11].

$$GSI_i = RY_i + RASV_i$$

Where, GSI_i is the Genotype Stability Index for i^{th} genotype, RY_i is rank of mean different fibre trait for i^{th} genotype, $RASV_i$ represents rank for the AMMI stability value for the i^{th} genotype for a particular fibre quality trait.

GGE analysis was accomplished using PB Tools software version 1.4 (PB Tools, 2014) with the model equation

$$Y_{ij} = \mu + G_i + E_j + \sum \lambda_k \alpha_{ik} \gamma_{jk} + e_{ij}$$

Where, Y_{ij} indicates the yield of i^{th} genotype in j^{th} environment; G_i and E_j denote the genotype and environment deviations from the grand mean respectively; μ is the grand mean λ_k represents the eigen value of the PCA axis k ; α_{ik} and γ_{jk} specifies the genotype and environment PC scores for the axis k ; n denotes the number of PCs retained in the model and e_{ij} displays the error term.

Results and Discussion

Fibre quality of any cotton genotype is a composite property determined by complex interactions among (1) the genetic potential of the genotype, (2) the environmental fluctuations experienced by the maternal plant from planting through harvest, and (3) the genetically controlled responses of the genotype to those environmental fluctuations. Environmental variations within the plant canopy, among plants, and within and among fields assure that every bale of cotton contains a

highly variable fibre population that encompasses broad ranges in fibre-quality properties. Thus, natural genetic and physiological variations in fibre cell shape, size, and maturity are modulated by fluctuations in the growth environment. A cotton fibre cell responds individually to fluctuations in the macro- and micro-environments so that the fibres on a single seed constitute a continuum of fibre lengths, shapes, cell-wall thicknesses, and maturities (Bradov and Davidonis, 2010).

In the current study, fibre traits recorded from 220 RI lines and the respective parents evaluated across three different seasons at Department of Cotton, Coimbatore were subjected to pooled analysis of variance to check the presence of any significant difference among genotypes, environments and interaction effect for five different fibre quality traits. The results indicated that the effect of genotypes, environments and $G \times E$ interactions were highly significant for Upper half mean length of fibre (UHML), uniformity index, bundle strength and fibre fineness (Table 2) which confirmed that analysis can be continued further to estimate phenotypic stability (Farshadfar and Sutka, 2006) [12]. However, effect of genotypes was not significant for elongation percentage but significant differences for environment and $G \times E$ interactions were noticed.

Combined analysis of variance in RI lines explained that major percentage of sum of square was contributed by $G \times E$ interaction for most of the fibre traits except uniformity index (Tables 2a to 2e). Percentage of contribution by the genotypes for different fibre traits ranged from 13.61% (uniformity index) to 31.31% (Fibre fineness), while for environment it ranged from 2.69% (Fibre fineness) to 53.98% (uniformity index). For $G \times E$ interaction, the contribution among different traits varied from 32.41% (uniformity index) to 66% (Fibre fineness) which is quite high. Interaction percentage of variation for fibre quality traits was 1.8 to 2.6 times larger than that for genotype, which is an indicative of differential responses of genotypes across environments. Campbell and Jones (2005) [5] assessed $G \times E$ interaction for yield and fibre quality in cotton. In their study, environment accounted for high percentage of sum of squares for lint yield and fibre fineness, while genotype accounted higher for fibre elongation. The percentage contribution by $G \times E$ interaction was relatively small. However, $G \times E$ interaction was four times larger than the genotype for lint yield, uniformity index and fibre fineness. Mahmodi *et al* (2011) [16] reported that high significant difference was observed for GE interaction through combined analysis of variance indicating the possibility of selection for stable entries. The GE interaction was five times higher than that of genotype effects.

The interaction of environment based on environment index for fibre quality traits exhibited wide variation in that, while E3 had low interaction, E1 and E2 were highly interactive. E1 was favourable environment for upper half mean length, bundle strength and elongation percentage, on the other hand, E2 was favourable environment for uniformity index and fibre fineness.

For all fibre traits, PC1 and PC2 accounted for 100% of the total variation in the RIL population and contribution of PC1 was higher. Accordingly, Principal component 1 for upper half mean length of fibre, uniformity index, bundle strength, elongation percentage and fibre fineness accounted for 67.58, 75.40, 80.30, 81.20 and 74.90 per cent respectively.

In AMMI, stability is interpreted from the ordinate axis with scores close to zero considered as stable genotypes and

environment. Among RI lines the entries which recorded PC1 scores around zero for fibre traits have been mentioned in Table 3. These lines were stable for different fibre traits across three seasons. AMMI model does not compute accurately for quantitative stability. Essential measure is required to quantify and rank genotypes according to their yield stability. Purchase *et al.* (2000) [23] proposed ASV (AMMI stability value) to cope up with this problem. In ASV the values close to zero are highly stable. The stable lines for fibre traits based on ASV have also been included in the Table.

Stability *per se* should however not be the only parameter for selection, because the most stable genotypes would not necessarily give the best yield performance (Mohammadi *et al.*, 2007) [6], hence there is a need for approaches that incorporate both mean yield and stability in a single index, that is why various authors introduced different selection criteria for simultaneous selection of yield and stability (Atta *et al.*, 2009) [9]. Genotype stability index (GSI) integrates both yield and stability across environments. Genotypes with lower GSI were desirable since they combine high mean yield performance with stability. Accordingly, the lines identified as stable based on low GSI value for five fibre quality traits are presented (Table 3).

Table 2a: Analysis of variance for Upper half mean length of fibre in 220 RI lines across three different seasons in cotton

| | Degrees of freedom | Sum of squares | Mean sum of square | Total variation explained |
|------------------------|--------------------|----------------|--------------------|---------------------------|
| Genotype | 221 | 2224.06 | 10.15** | 28.88 |
| Environment | 2 | 1263.43 | 631.71** | 16.40 |
| Genotype x Environment | 442 | 4213.53 | 9.61** | 54.71 |
| PC1 | 222 | 1423.77 | 6.47** | 67.58 |
| PC2 | 220 | 682.99 | 3.13** | 32.41 |
| PC3 | 218 | 0.00 | 0.00 | |
| Residual | 663 | 1114.36 | 1.68 | |

Table 2b: Analysis of variance for Uniformity index of fibre in 220 RI lines across three different seasons in cotton

| | Degrees of freedom | Sum of squares | Mean sum of square | Total variation explained |
|------------------------|--------------------|----------------|--------------------|---------------------------|
| Genotype | 221 | 5084.39 | 23.22** | 13.61 |
| Environment | 2 | 20168.05 | 10084.03** | 53.98 |
| Genotype x Environment | 442 | 12111.18 | 27.65** | 32.41 |
| PC1 | 222 | 4563.23 | 20.74** | 75.40 |
| PC2 | 220 | 1492.35 | 6.84** | 24.60 |
| PC3 | 218 | 0.00 | 0.00 | |
| Residual | 663 | 1210.83 | 1.83 | |

Table 2c: Analysis of variance for bundle strength of fibre in 220 RI lines across three different seasons in cotton

| | Degrees of freedom | Sum of squares | Mean sum of square | Total variation explained |
|------------------------|--------------------|----------------|--------------------|---------------------------|
| Genotype | 221 | 3444.19 | 15.73** | 22.74 |
| Environment | 2 | 3468.65 | 1734.33** | 22.91 |
| Genotype x Environment | 442 | 8230.11 | 18.79** | 54.35 |
| PC1 | 222 | 3304.93 | 15.02** | 80.30 |
| PC2 | 220 | 810.11 | 3.71** | 19.70 |
| PC3 | 218 | 0.00 | 0.00 | |
| Residual | 663 | 947.37 | 1.44 | |

Table 2d: Analysis of variance for elongation percentage of fibre in 220 RI lines across three different seasons in cotton

| | Degrees of freedom | Sum of squares | Mean sum of square | Total variation explained |
|------------------------|--------------------|----------------|--------------------|---------------------------|
| Genotype | 221 | 6.50 | 0.03 | 24.73 |
| Environment | 2 | 2.69 | 1.35** | 10.24 |
| Genotype x Environment | 442 | 17.09 | 0.04** | 65.04 |
| PC1 | 222 | 6.93 | 0.03** | 81.20 |
| PC2 | 220 | 1.60 | 0.01** | 18.80 |
| PC3 | 218 | 0.00 | 0.00 | |
| Residual | 663 | 21.54 | 0.0326 | |

Table 2e: Analysis of variance for fibre fineness of fibre in 220 RI lines across three different seasons

| | Degrees of freedom | Sum of squares | Mean sum of square | Total variation explained |
|------------------------|--------------------|----------------|--------------------|---------------------------|
| Genotype | 221 | 223.78 | 1.02** | 31.31 |
| Environment | 2 | 19.20 | 9.60** | 2.69 |
| Genotype x Environment | 442 | 471.71 | 1.08** | 66.00 |
| PC1 | 222 | 176.62 | 0.80** | 74.90 |
| PC2 | 220 | 59.23 | 0.27** | 25.10 |
| PC3 | 218 | 0.00 | 0.00 | |
| Residual | 663 | 244.76 | 0.37 | |

** Represent highly significant difference

Table 3: Stable genotypes identified based on PC1 score, ASV and GSI in cotton

| | PC score near to zero | | ASV | | GSI | |
|--------------------------------------|-----------------------|-------------|-------------------------------------|-------------|-------------------------------------|-------------|
| | Genotype (RIL No.) | Pooled mean | Genotype (RIL No.) based on ranking | Pooled mean | Genotype (RIL No.) based on ranking | Pooled mean |
| Upper half mean length of fibre (mm) | 126 | 30.53 | 88 | 28.97 | 78 | 31.86 |
| | 86 | 29.82 | 74 | 29.20 | 5 | 31.86 |
| | 107 | 30.50 | 192 | 31.09 | 192 | 31.09 |
| | 32 | 27.31 | 174 | 28.69 | 145 | 31.63 |
| | 35 | 31.21 | 155 | 28.83 | 120 | 31.35 |
| | 216 | 29.80 | 150 | 29.90 | 35 | 31.21 |
| | 88 | 28.97 | 130 | 29.13 | 81 | 31.05 |
| | 100 | 30.00 | 212 | 27.96 | 82 | 30.67 |
| | 139 | 28.98 | 86 | 29.82 | 84 | 31.41 |
| | 37 | 31.09 | 100 | 30.00 | 39 | 30.31 |
| Uniformity index | 98 | 90.37 | 37 | 86.63 | 17 | 88.49 |
| | 48 | 82.57 | 126 | 86.75 | 98 | 90.37 |
| | 78 | 84.33 | 203 | 84.55 | 64 | 90.91 |
| | 37 | 86.63 | 18 | 87.81 | 15 | 88.35 |
| | 220 | 85.42 | 220 | 85.42 | 11 | 88.85 |
| | 126 | 86.75 | 14 | 82.87 | 156 | 88.07 |
| | 57 | 87.85 | 17 | 88.49 | 18 | 87.81 |
| | 127 | 84.16 | 58 | 85.64 | 176 | 89.65 |
| | 69 | 87.88 | 184 | 85.65 | 82 | 90.69 |
| | 203 | 84.55 | 218 | 84.33 | 51 | 89.38 |
| Bundle strength (g/tex) | 96 | 29.71 | 29 | 26.52 | 120 | 30.41 |
| | 101 | 27.91 | 101 | 27.91 | 82 | 31.30 |
| | 31 | 27.57 | 102 | 28.30 | 96 | 29.71 |
| | 40 | 26.21 | 120 | 30.41 | 145 | 29.09 |
| | 120 | 30.41 | 28 | 27.30 | 152 | 29.63 |
| | 102 | 28.30 | 141 | 27.92 | 97 | 28.65 |
| | 29 | 26.52 | 97 | 28.65 | 93 | 31.06 |
| | 33 | 25.68 | 31 | 27.57 | 186 | 29.79 |
| | 32 | 26.27 | 40 | 26.21 | 89 | 30.11 |
| | 54 | 25.49 | 192 | 27.42 | 133 | 29.09 |
| Elongation percentage | 53 | 5.81 | 154 | 5.87 | 190 | 6.01 |
| | 32 | 5.80 | 141 | 5.87 | 115 | 5.93 |
| | 91 | 5.80 | 100 | 5.87 | 151 | 5.93 |
| | 36 | 5.79 | 120 | 5.88 | 74 | 5.99 |
| | 48 | 5.79 | 159 | 5.88 | 96 | 5.99 |
| | 174 | 5.79 | 192 | 5.86 | 22 | 5.92 |
| | 162 | 5.73 | 16 | 5.86 | 93 | 5.98 |
| | 54 | 5.73 | 219 | 5.86 | 185 | 5.94 |
| | 120 | 5.88 | 42 | 5.86 | 120 | 5.88 |
| | 159 | 5.88 | 207 | 5.76 | 41 | 5.91 |
| Fibre fineness (µg/inch) | 199 | 3.80 | 24 | 3.59 | 152 | 3.07 |
| | 186 | 3.58 | 12 | 4.09 | 120 | 2.89 |
| | 24 | 3.59 | 199 | 3.80 | 123 | 3.01 |
| | 40 | 3.68 | 158 | 3.62 | 119 | 3.05 |
| | 22 | 3.51 | 152 | 3.07 | 112 | 3.00 |
| | 31 | 3.66 | 50 | 3.55 | 131 | 3.21 |
| | 109 | 3.68 | 31 | 3.66 | 94 | 2.97 |
| | 128 | 3.58 | 48 | 3.94 | 129 | 3.23 |
| | 7 | 4.51 | 22 | 3.51 | 220 | 3.20 |
| | 48 | 3.94 | 186 | 3.58 | 195 | 2.92 |

ASV - AMMI stability value
GSI - Genotype stability index

RIL 35 was identified as stable genotype based on PC1 score as well as GSI for upper half mean length. RIL 88 was stable based on PC1 score in addition to ASV. Stable genotype as per ASV and GSI for this trait was RIL 192. For uniformity index, RIL 98 was identified as stable genotype based on PC1 score as well as from GSI. RIL 37, 220 and 126 were stable based on PC1 score in addition to ASV. For bundle strength alone, one RIL, 120 was confirmed as stable across different indices *viz.*, PC1 score, ASV and GSI. Apart from this, RIL 101, RIL 102 and RIL 29 were identified as stable genotypes based on PC1 score as well as from ASV. Two genotypes *viz.*, RIL 199 and RIL 24 were identified as stable based on PC1 score as well as ASV for fibre fineness. RIL 152 was stable based on ASV in addition to GSI.

Based on genotype stability index, six genotypes could be shortlisted as stable for atleast two quality traits *viz.*, RIL 145 for UHML and bundle strength; RIL 151 for UHML and elongation percentage; RIL 74 for uniformity index and elongation percentage; RIL 82 for uniformity index and bundle strength; RIL 96 for bundle strength and elongation percentage and RIL 152 for bundle strength and fibre fineness. One genotype RIL 120 excelled as stable performer for four quality traits *viz.*, UHML, bundle strength, elongation percentage and fibre fineness.

Pretorius *et al* (2015) [13] utilized AMMI model to analyse G × E interaction in cotton and reported NuOPAL as the best performing cultivar in 15 out of 18 observations in fibre yields. According to Riaz *et al* (2013) [17], the genotype with high AMMI stability value are highly unstable across environments. They confirmed two cotton genotypes as stable based on ASV and yield performance. Mahmodi, *et al* (2011)

[16] discriminated 10 and 6 as stable genotypes through AMMI stability value in wheat. Based on genotype stability index, the most stable genotypes were identified as genotype 13 and 10 with high grain yield. Bose *et al.* (2014) [25] conducted field experiment with 12 genotypes for three consecutive years in rice. AMMI stability value and genotype stability index discriminated G11 and G12 as stable genotype.

GGE Biplot analysis

A GGE biplot is a biplot that displays the GGE of a genotype by environment two-way data. The GGE biplot methodology originates from graphical analysis of multi-environment variety trials (MET) data, but is equally applicable to all other types of two-way data. Entry and tester are the two factors in a two-way data.

Mean performance and stability of genotypes

Among 220 RI lines, 32 stable and 20 unstable genotypes numbering 52 were shortlisted based on genotype stability index for five fibre quality traits. The ranking of 52 genotypes based on their mean and stability of performance and relative to an ideal genotype across three environments is presented in Figure 1. Genotypes with high mean performance (except fibre fineness) and stability are the desirable ones in stability analysis. The single-angled line is the AEC abscissa (or AEA) which points to higher mean yield across environments. The double-angled line is the AEC ordinate and it points to greater variability (poorer stability) in either direction (Yan and Tinker, 2006) [30]. Accordingly, in our study, the following genotypes (Table 4) were identified as stable for each trait.

Table 4: Stable RI lines for different fibre quality traits in cotton by GGE biplot analysis

| Trait | Stable genotypes (RIL No.) | Mean performance |
|--------------------------------------|----------------------------|------------------|
| Upper half mean length of fibre (mm) | 93 | 32.76 |
| | 81 | 31.05 |
| | 82 | 30.67 |
| | 123 | 30.23 |
| Uniformity index | 64 | 90.90 |
| | 82 | 90.68 |
| | 98 | 90.36 |
| | 74 | 89.76 |
| Bundle strength | 93 | 31.05 |
| | 89 | 30.11 |
| | 124 | 29.97 |
| Elongation percentage | 82 | 6.02 |
| | 190 | 6.01 |
| | 98 | 6.0 |
| Fibre fineness | 120 | 2.88 |
| | 195 | 2.92 |
| | 123 | 3.01 |
| | 145 | 3.41 |

GGE biplot polygon view

Visualization of 'which won where' pattern of multi environmental analysis is vital to know the possible existence of mega environments in the target environments (Gauch and Zobel, 1997). Polygon view is the best way to visualize the interaction patterns between genotypes and environments (Yan and Kang, 2002). The genotypes which are located on vertices of the polygon is considered as best genotype in one or more environments (Yan *et al.*, 2001).

The polygon view for fibre quality traits are indicated in Fig 2. The ideal genotypes for each environment for each trait extracted from the biplot polygon view are provided in Table 5. For none of the traits, mega environment was noticed. Five

rays divided the polygon into five sectors for the trait upper half mean length of fibre. The three environments were occupied in three different sectors. The vertex genotypes for upper half mean length were RIL 151 and 89 in E1, RIL 93 in E2 and RIL 80 in E3 and are most appropriate for growing in the respective environments. For uniformity index, the polygon was divided into four sectors and RIL 22 in E1, RIL 185 and RIL 4 in E2 and RIL 134 in E3 were the vertex genotypes. The polygon was divided into eight sectors for bundle strength. The vertex genotype was RIL 134, RIL 93 and RIL 24 in E1, E2 and E3 respectively. For elongation percentage, the polygon was divided into seven sectors. For

uniformity index, RIL 134 in E1, RIL 98 and RIL 82 in both E2 and E3 were the vertex genotypes.

Table 5: Ideal RI lines for different traits in different environments in cotton

| Trait | Environment | Vertex genotypes (RIL No.) |
|------------------------|-------------|----------------------------|
| Upper half mean length | E1 | 89 and 151 |
| | E2 | 93 |
| | E3 | 80 |
| Uniformity index | E1 | 22 |
| | E2 | 4 and 185 |
| | E3 | 134 |
| Bundle strength | E1 | 134 |
| | E2 | 93 |
| | E3 | 24 |
| Elongation percentage | E1 | 134 |
| | E2 and E3 | 82 and 98 |
| Fibre fineness | E1 | 82 |
| | E2 | 76 |
| | E3 | 97 |

Thus, it could be concluded that RIL 134 exhibited the best fibre qualities *viz.*, bundle strength and elongation percentage in E1 season (Kharif 2017-18) and uniformity index in E3 (Kharif 2018-19). The genotype RIL 93 expressed its best fibre qualities *viz.*, bundle strength and upper half mean length in E2 (Summer 2018). So also, the potential of RIL 82 for elongation percentage could be witnessed in both seasons E2 and E3 (Summer 2018 and Kharif 2018-19) and for fibre fineness during E1 (Kharif 2017-18). These genotypes are ideal for multiple traits in same or different seasons.

Ali *et al* (2017) [19] conducted multi environment test to identify relatively stable genotype in cotton. A total of 28 genotypes were tested during two seasons and at three locations. Based on GEI and GG-biplot analysis, genotypes NIBGE-4 and IR-NIBGE-2620 were identified as vertex and ideal cultivars with more stability and seed cotton yield. Sadabadi *et al* (2018) [31] studied the effect of G × E interaction on 38 cotton genotypes at three locations. Through GGE biplot analysis, six superior or the winning genotypes on the vertex of the polygon were identified. Also, Hashemabad was found as appropriate location for ER26 genotype while TJ82 was identified as the best and most stable genotype.

Farias *et al* (2016) [11] reported the effect of G × E interaction across eight environments in 16 cotton genotypes. GGE biplot analysis resulted in two stable genotypes for yield across all environments. Here, six environments were clustered in single sector indicating a single mega environment, while other two environments were in different sectors.

Evaluation of environments based on GGE biplot

The cosine of angle between environment vector and the Average Environment Axis (AEA) helps to identify the correlation between the genotype performance in that environment and across the environment (Yan *et al.*, 2007). The length of the vector of the test environment measures the ability to discriminate genotypes in the test environment. Test environments making small angle with the AEA was considered as the most representative environment (Oyekunle *et al.*, 2017) [14]. Fig. 3 depicts the representative and discriminative ability of the locations studied.

In our study, E 1 season (Kharif 2017-18) emerged as representative and discriminating environment for three out of five traits *viz.*, bundle strength, elongation percentage and fibre fineness. The season Summer 2018 (E2) also fell in the

same category for uniformity index. So, in these two seasons, genotypes/RILs can be selected for their general adaptation of above mentioned traits. Regarding upper half mean length of fibre, selection for specifically adapted RILs can be done based on the values obtained during Kharif 2017-18 season (E1). The data recorded during summer 2018 season (E2) is less discriminating among the lines studied.

The correlation between the environments represented by the vectors of all three environments facilitates the determination of the relationship between the environments. Cosine of angle between the locations shows the correlation among them (Yan, 2001) [16]. Acute angle represents positive, obtuse angle depicts negative and large G×E and right angle represents no correlation between environments (Yan and Tinker, 2006). GGE biplot for relationship among the tested locations for fibre traits are shown in Fig. 4. The environment E3 fell at the vertex for the traits *viz.*, uniformity index, and bundle strength. In case of upper half mean length and elongation percentage acute angle was observed in all three environments which indicate positive correlations between them. For bundle strength, positive correlations were observed between E1 and E2; fibre fineness showed positive correlations between E2 and E1 and E2 and E3. Negative correlation among environments E1 and E3 for fibre fineness and among E1 and E2 for uniformity index was realized.

Stable genotypes based on AMMI and GGE analysis

The recombinant inbred lines which were stable based on both GGE biplot and GSI for different traits are given in Table 6. It could be observed that 11 different RILs were found to be stable for one of the five quality traits. One genotype RIL 82 was stable performer with high mean performance for upper half mean length and uniformity index.

Table 6: Stable genotypes from both GSI and GGE biplot in cotton

| Trait | Stable genotype RIL No. | Pooled Mean |
|------------------------|-------------------------|-------------|
| Upper half mean length | 81 | 31.05 |
| | 82 | 30.67 |
| Uniformity index | 64 | 90.90 |
| | 82 | 90.68 |
| | 98 | 90.36 |
| | 74 | 89.76 |
| Bundle strength | 93 | 31.05 |
| | 89 | 30.11 |
| Elongation percentage | 190 | 6.01 |
| Fibre fineness | 120 | 2.88 |
| | 123 | 3.01 |
| | 145 | 3.41 |

Greveniotis and Sioki (2017) [17] stated that through GGE biplot, fluctuations of fibre traits were confirmed. G2 was ideal genotype for fibre length with E4 as better environment to discriminate. G1 reached ideal for fibre strength with E2 for better promotion. ELSA (G1) with CELIA (G2) seemed to be more suitable cultivars for Greek mega-environment. Xu *et al.* (2013) [4] evaluated cotton lines based on GGE biplot to identify best location for fibre length. They reported that 15 trial locations were suitable for fibre length selection, 10 locations were moderately suitable and other two were unsuitable for selection.

Conclusion

Based on PC1/ASV and GSI RIL 120 emerged as stable performer for four quality traits *viz.*, UHML, bundle strength, elongation percentage and fibre fineness. Based on GGE biplot RIL 134 exhibited the best fibre qualities *viz.*, bundle strength and elongation percentage in E1 season and uniformity index in E3. The genotype RIL 93 expressed its best fibre qualities *viz.*, bundle strength and upper half mean length in E2. So also, the potential of RIL 82 for elongation

percentage could be witnessed in both seasons E2 and E3 and for fibre fineness during E1. These genotypes are ideal for multiple traits in same or different seasons. E 1 season (Kharif 2017-18) emerged as representative and discriminating environment for three out of five traits *viz.*, bundle strength, elongation percentage and fibre fineness. Thus the present investigation has led to identification of ideal RI lines for different fibre traits in cotton and ideal environment for development of improved varieties with good fibre quality.

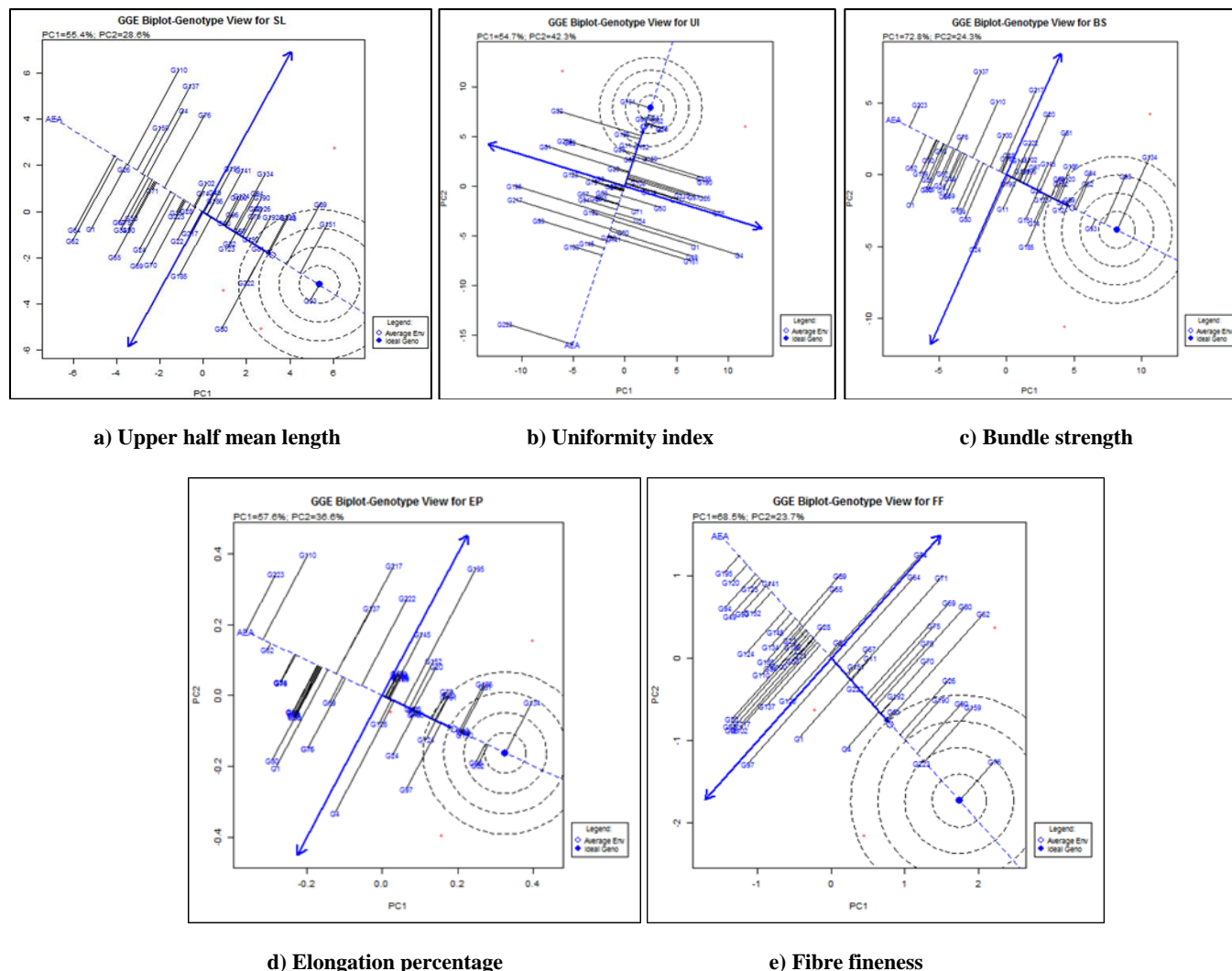
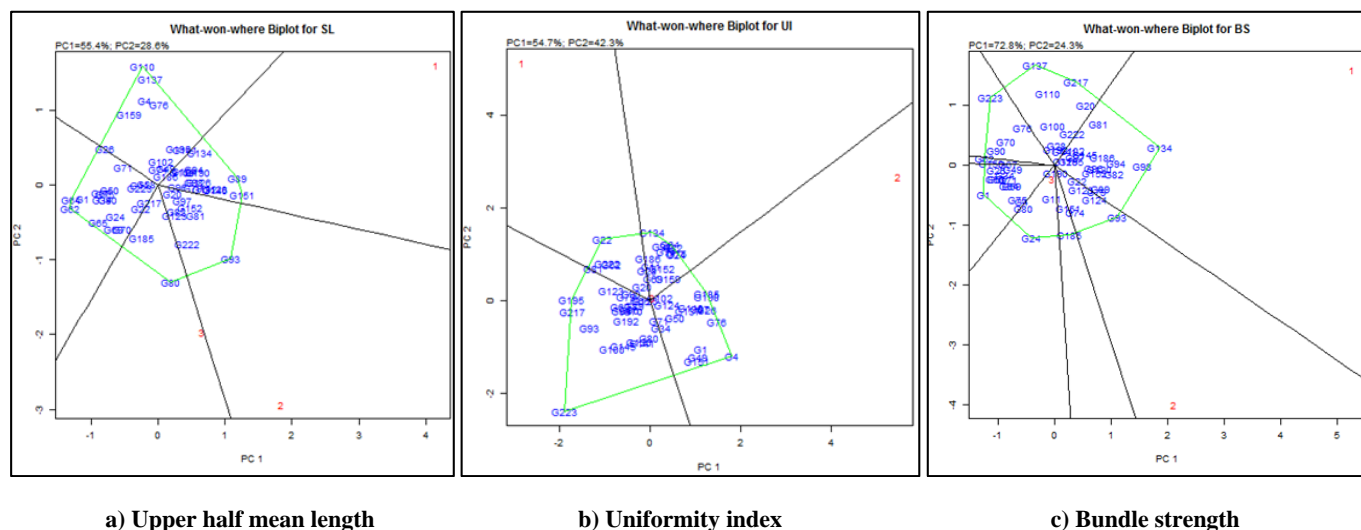
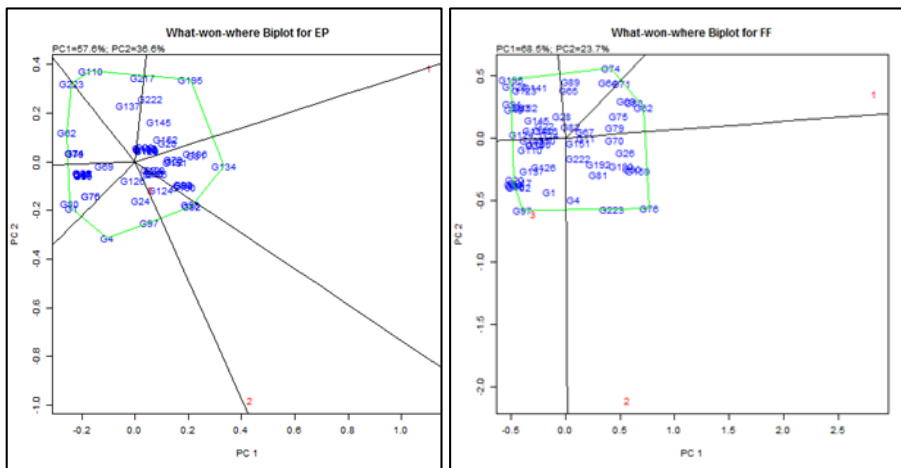


Fig 1: Average Environment Axis (AEA) view of GGE biplot showing the mean performance and stability of genotypes in cotton

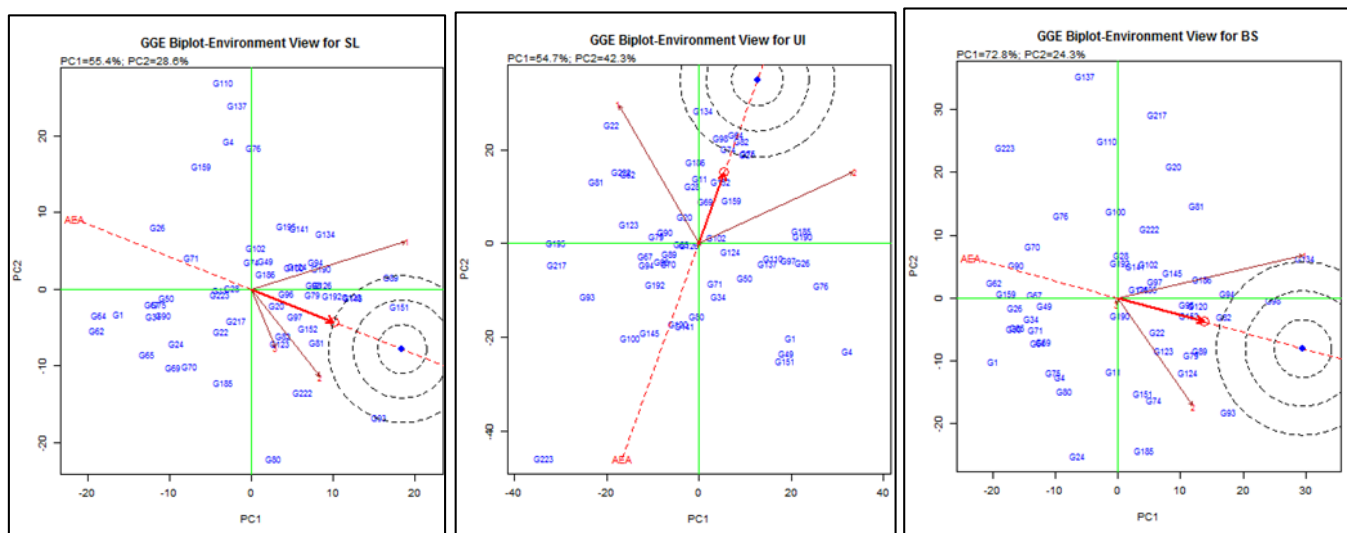




d) Elongation percentage

e) Fibre fineness

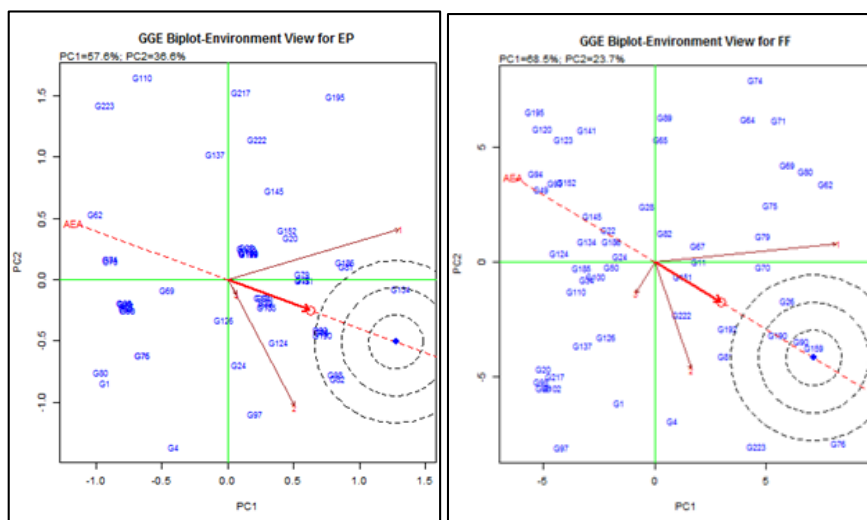
Fig 2: Polygon view of GGE biplot for different traits in RI lines of cotton



a) Upper half mean length

b) Uniformity index

c) Bundle strength



d) Elongation percentage

e) Fibre fineness

Fig 3: Comparison of environments with ideal environment

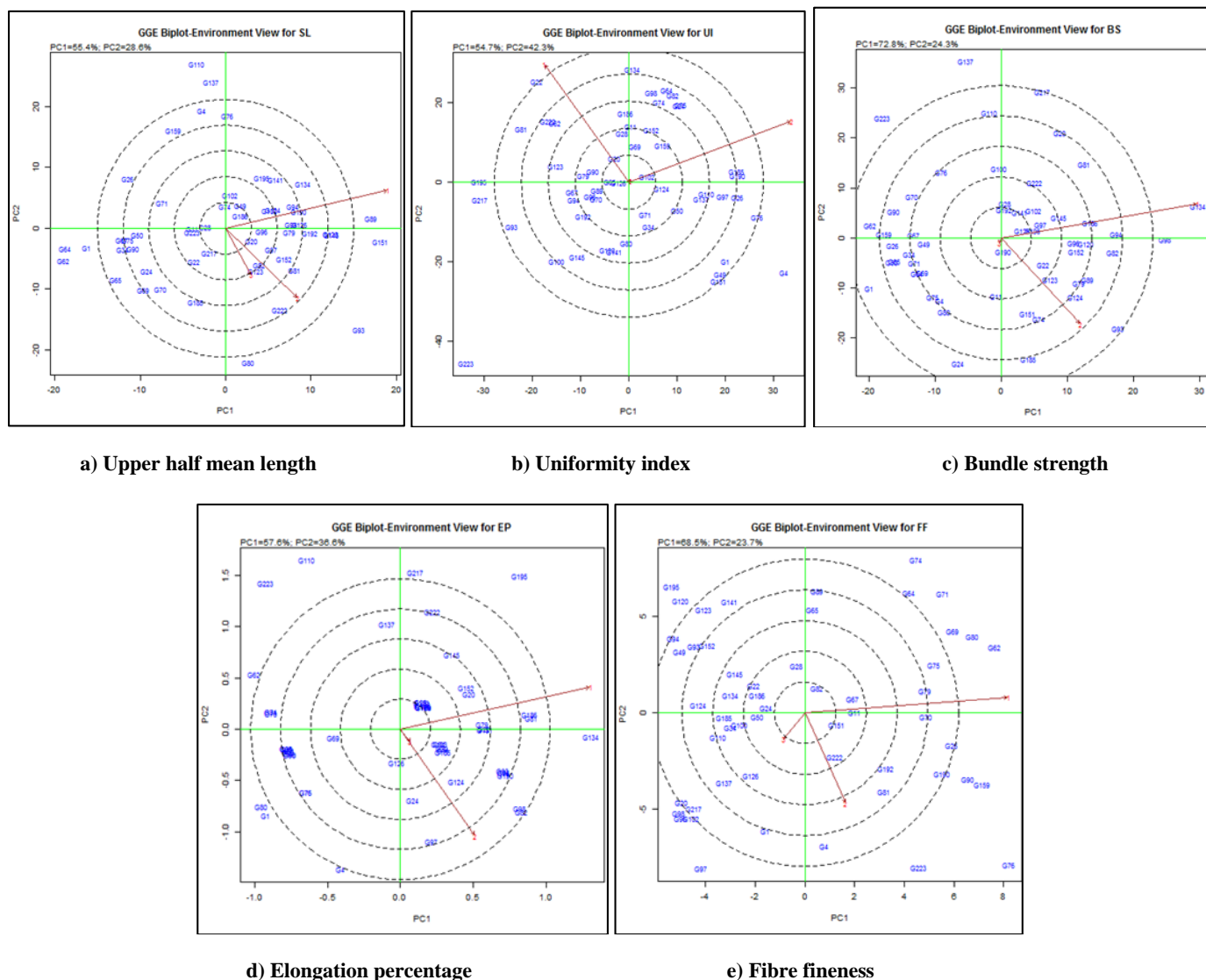


Fig 4: GGE biplot showing relationship among the test environments

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