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Multi-Environment Evaluation of Soybean Genotypes in Nepal: Application of AMMI and GGE Biplot for Improving Crop Stability and Productivity

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ABSTRACT

Soybeans are a vital legume with significant nutritional and economic importance, contributing to global edible oil and protein supplies. In Nepal, soybean cultivation is expanding, yet its performance varies due to environmental heterogeneity and genotype-environment interaction. In the present study, the performance of 18 soybean genotypes over 5 locations during the rainy season of 2019 and 16 soybean genotypes over locations during the rainy season of 2020 was carried out in an alpha lattice design and investigated using AMMI and GGE biplot analysis to assess adaptability and stability using combined ANOVA, AMMI, and GGE biplot analyses. In 2019, the environment contributed the most to variation in grain yield (27.84%), followed by genotype x environment interaction (55.31%) and genotype (16.83%). Conversely, in 2020, environment explained 65.8% of the variation, with genotype contributing only 5.14% and genotype x environment interaction 29.04%. Overall, the combined analysis revealed that genotype x environment interaction was a significant source of variation, particularly in 2019. The GGE biplot effectively visualized the relationships between locations and genotypes, with the first two principal components explaining 81.22% of the variation. It identified superior genotypes such as G-1873, TGX-1445-ID, and SB0122 in terms of high grain yield. Notably, G-1873 was closest to an ideal genotype, exhibiting both high yield and stability. The "Which-Won-Where" analysis grouped the testing sites into two mega-environments: one with three locations where G-1873 was the top performer, and another with a single location where GC8234GC-13 excelled. Locations like Surkhet, Salyan, and Doti were identified as the most suitable for soybean cultivation, being closest to the ideal in the concentric circle representation. Overall, the findings provide valuable insights for soybean breeding programs aimed at improving yield stability and adaptability across diverse environments in Nepal. The identification of location-specific genotypes will facilitate targeted cultivar development and deployment, ultimately supporting Nepal's soybean industry and reducing reliance on imports.

Keywords: *Soybean, Genotype x Environment Interaction, AMMI, GGE biplot, Stability.*

1. Introduction

Soybean (*Glycine max* (L.) Merrll is a self-pollinating diploid crop with 2n=2x=40 chromosomes and a genome size of 1100 Mbp[2]) that has been known to play an important role in the world of agriculture and nutrition. Locally called Bhattmas or Bhatta in Nepali, it is also called the golden bean, miracle bean, crop of the planet, and gods sent golden bean because of its large scale of usability, and is thus known as the Golden gift of nature to mankind. Soybean, being the major crop in the global agricultural economy, is the most important seed legume. It contributes a quarter of the world's stock of edible oil and about two-thirds of the protein concentrate in the world that is fed to livestock. At the moment, it is the leading oilseed in the country and in the world arena. It is a multifaceted nutritional food crop that is a source of low-cost, high-quality protein (40-50 percent), high-digestibility vegetable oil (20 percent) with zero cholesterol, carbohydrates/ soluble sugars (35 percent), and ash (5 percent). It also contains a lot of vitamins B, C, E, and minerals, and has medicinal properties [9,16,17,11,13,14, 15], soybeans have one of the highest rates of biological fixation of nitrogen and can fix up to 180 kg N/ha symbiotically. This legume is widely grown in Nepal, and it is specifically in the Mid Hills where the legume is grown that it covers nearly 80 percent of the soil and the total production of soybean in the country [6].

It is widely cultivated in the Terai and inner Terai areas as a mono crop because of its great yield capacity and intense need for soy meal and cake meal by the poultry and livestock industry. Soybeans are a great supplement food crop to cereals, particularly in developing countries where malnutrition is a widespread situation. It can be used in the processing of seeds into baby foodstuffs and other products that are available in the market to diabetic patients, which include soy milk, tofu, and soy sauce. The green pods are eaten in fresh form like vegetables, and the dry seeds are usually roasted or fried into healthy snacks. Its green leaves can be used as green manure and fodder. Soybean proteins have many health advantages, such as lowering cholesterol levels, reducing the symptoms of menopause, and lowering the chances of many chronic ailments, including cancer, heart disease, and osteoporosis. Soybeans contain isoflavones (daidzein and genistein), which help in reducing cholesterol, decreasing cancer risk, and alleviating the probability and consequences of osteoporosis.

The soybean crop is also very adaptive to a wide range of agro-ecological environments since it can grow at altitudes as low as 500 to 1500 meters above sea level [6]. It is the third largest acreage and second largest production grain legume in Nepal after lentils and black gram. It is commonly cultivated in rice bunds or intercrops like maize in the mid-hills. The hectares of soybean in the world amount to 137,927,342, which produces 388,097,784.67 tons, with a production of 2.81 tons/ha [25]. In Nepal, soybeans are planted in 24, 921 hectares, yield 35,138 tons, and the average productivity is 1.410 tons/ha [12]. The number of acres of soybean acreage in Nepal increased by a factor of 10 between 2015-16 and 2020-21, the production level rose by 11 percent, and the productivity by 4 percent. The same period saw Nepal import 1,275, 201 tons of soybean oil worth $608.865 million USD and export 331,764.5 tonnes worth $59.65 million USD. Also, imports also consisted of 79730.9 tons of soybean grains valued at 4.9799 USD, 810.7 tons of soybean sauce worth 0.587 USD, and 244337 tons of soybean cake valued at 15.4905 USD. These data show that Nepal is reliant on imports of raw materials, which are essential in their feed and food sectors, which means that they are not self-reliant.

The environmental variability also has a great impact on the growth of soybean and causes large levels of genotype-and-environment-interactions (G×E), which leads to inconsistent genotypic responses. Genotypes may not be able to perform consistently relative to each other in different environments because of the existence of large Gx E interactions on a trait such as seed yield [8]. Multi-environment trials (MET) have therefore been extensively used by plant breeders to compare the relative performance of genotypes across multiple target environments. These experiments play an important role in the determination of the adaptability and the stability of the genotypes and thus help in the selection of the better and more robust types [10]. Ideal stable genotypes are those genotypes that have the genetic ability to perform well in favorable conditions and are also able to give satisfactory yields in unfavorable conditions. Many statistical techniques, such as regression analysis, have been created to test interaction patterns of G×E [7]. These include, most successfully, the Additive Main Effects and Multiplicative Interactions (AMMI) and the Genotype-Genotype by Environment interaction (GGE), which help break down the additive (linear) and multiplicative (bilinear) aspects of G×E interaction, providing useful insights into the interpretation of multi-environment data to breeding programs. Some statistical models have been put forward to use the positive G + E interactions and assist in breeding decisions in terms of cultivar selection and recommendations to particular environments. Thus, the research will evaluate the soybean genotypes with the adaptability and stability of grain yield under various conditions by the AMMI and GGE bi-plot models with a soybean breeding improvement model.

2. Materials and Methods

2.1 Experimental sites

Soybean yield trials were carried out in the field of seven different environments across the country, of which five of them (Surkhet, Rampur, Khajura, Dailekh, Doti) in the 2019/2020 crop seasons and five different environments (Salyan, Doti, Dailekh, Khajura and Nawalpur) in the 2020/21 crop season. Geographical details are depicted in the Table 1.

Table 1: Experimental sites used for evaluation of soybean genotypes in Nepal

Parameters	Dailekh	Salyan	Surkhet	Doti	Khajura	Rampur	Nawalpur
Altitudes(m)	1250-1355	1480	580	610	181	228	144
Longitudes(E)	81°72′	32°24′	81°47′	80°55′	81°37′	84°19′	85°35′
Latitudes(N)	28°85′	28°14′	28°30′	29°15′	28°06′	27°40′	27°3′
Max Temp(°C)	28.95	28.58	37.5	27.67	46	43	39
Min Temp(°C)	15.12	14.12	5	12.16	5.4	2-3	7
Rainfall(mm)	185.07	184.74	1100	170.04	1000-1500	1500	1600-1700

2.2 Experimental details

2.2.1 Experimental layout and research design: This experiment received an array of eighteen soybean genotypes determined in the 2019 season and 16 different soybean genotypes determined in the rainy season of 2020, which were designed using a Simple Alpha Lattice Design. In 2019 and 2020, respectively, the experiment was repeated with 3 x 6 block replications and 4 x 4 block replications.

2.2.2. Sowing: Sowing was carried out from the 1st to the end of July 2019- 2020 in the monsoon season, and the crop geometry was 50cm x 10 cm (row to row x plant to plant) with seed being sown manually. The planting depth was 4-5cm, and the seeding rate was 60 kg/ha, which was the recommended rate. Each plot was 12 m^2, or 4 meters x 3 meters, and in six rows. A total of 36 plots were used in the research. In 2019 and 2020, the size of the blocks was 216 and 192 m^2, respectively. The extra thinning of the plants was done following the initial weeding after sowing of 25 days.

2.2.3 Fertilizers: The chemical fertilizer dosage recommended was to be applied as a basal dose at 20 kg nitrogen (N), 40 kg phosphorus ($P_2 O_5$), and 20 kg potassium ($K_2 O$) per hectare at the final land preparation.

2.2.4. Intercultural operations: Pendimethaline herbicide was applied 3 days after sowing in the field. At 25 days of sowing, the first manual weeding was performed, and at 45-50 days of sowing, the second manual weeding was carried out, and earthing up was then done.

2.2.5 Disease pest: Disease and pest incidences were rated using a protocol that had been developed by the Plant Pathology Research Center. Disease-pest occurrences were controlled by the need to apply fungicides and insecticides when it becomes economically disadvantageous. Spododure-laden pheromone traps were also placed to reduce the infestation of the Spodoptera in the field.

2.2.6 Plant genetic materials: The genetic materials used in this experiment were all acquired in the International Institute of Tropical Agriculture (IITA), Nigeria, and the National Agriculture Genetic Resources Centre (NAGRC- Gene Bank) and variety puja were standard checks with eighteen and sixteen soybean genotypes (Annex i and ii).

Annex: i Soybean genotypes used for multi-environment yield trial at different locations, 2019

SN	Genotypes	Pedigree	Source
1	LS77-16-16	Breeding line	IITA
2	IARS87-1	Breeding line	IARI
3	SBO 122	Woods-yellow	USA
4	TGX1485-ID	Breeding line	IITA
5	F778817	Breeding line	IITA
6	AGS371	Breeding line	AVRDC
7	G1873	Breeding line	IITA
8	TGX1989-41F	Breeding line	IITA
9	TGX1990-94F	Breeding line	IITA
10	TGX1989-21F	Breeding line	IITA
11	TGX1987-62F	NGGM	IITA
12	Kavre local	SB0112	Nepal
13	TGX1990-18F	Breeding line	IITA
14	TGX1805-31F	Breeding line	IITA
15	GC8234GC-13	Breeding line	IITA
16	SB0095	Tayha hum white	Nepal
17	TGX1835-10F	TGx1213-ID x TGx1445-3E	IITA
18	Puja (SC)	UPSM534 x S38	PAU

Annex: ii Soybean genotypes used for multi-environment yield trial at different locations, 2020

SN	Genotypes	Pedigree	Source
1	TGX1989-19F	Breeding line	IITA
2	Ankur	SPS from a composite of 22 crosses	PAU
3	SBO122	Woods-yellow	USA
4	TGX1485-ID	Breeding line	IITA
5	Tampomas	Breeding line	IITA
6	TGX1890-106FN	Breeding line	IITA
7	G1873	Breeding line	IITA
8	CM9125	Breeding line	IITA
9	TGX1987-42F	Breeding line	IITA
10	G758	Breeding line	IITA
11	COLL # sikare	Breeding line	IITA
12	KAVRE	SB0112	Nepal
13	TGX1805-31F	Breeding line	IITA
14	GC8234GC-13	Breeding line	IITA
15	SB0095	Tayha hum white	Nepal
16	Puja (Std. Chk.)	UPSM534 x S38	PAU

Data Collection: The quantitative traits were measured on 10 randomly selected plants, and then IBPGR Descriptors (Anonymous, 1985). The quantitative data were measured in plant basis (plant height cm), pods/plant (P/P), and seeds/ pod (S/P) and quantitative parameters of morphology data were entered as days to 50 percent flowering (DF), days to maturity (DM), 100-seed weight in grams (HSWT), and yield/ gram (GY). The results of these samples were used to estimate the performance of each genotype with regard to the traits of interest.

Statistical analysis

The mean values of the traits were determined and used as the input in the analysis of variance (ANOVA). In order to estimate the genetic parameters, R-stat version and GEA-R software were used to analyze the results with the main emphasis on the main effects of environment (E), genotype (G), and their interplay (GE). Such a major GE interaction variance led to the further division of this component. Further analysis of the GE interaction was performed with the help of the GGE biplot model [19]. The GGE biplot has been drawn on the basis of the first two principal components (PC1 and PC2), which were calculated using the data of environment-oriented yields [20]. The GGE model used was:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij} \quad (1)$$

Where Yij is measured mean of genotype i(=1,2,….,n) in environment j(=1,2…,m), μ is the grand mean, βj is the main effect of environment j, μ + βj being the mean yield across all genotypes in environment j, λ1 and λ2 are the singular values (SV) for the first and second principal component (PC1 and PC2), respectively, ξi1 and ξi2 are eigenvectors of genotype I for PC1 and PC2, respectively, ŋ1j and ŋ2j are eigen vectors of environment j for PC1 and PC2, respectively, εij is the residual associated with genotype i in environment j. PC1 and PC2 eigen vectors cannot be plotted directly to construct a meaningful biplot before the singular values are partitioned in to the genotype and environment eigenvectors. Singular value partitioning was implemented by:

$$g_{i1} = \lambda_1^{f_1} \xi_{i1} \ and \ e_{ij} = \lambda_1^{1-f_1} \eta_{ij} \quad (2)$$

Where f1 is the portion factor for PC1. The f1 can range between 0 and 1. To visualize the relationship among genotypes, the GGE biplot based on genotype metric (that is, f=1; S.V.P=1) is appropriate, and environment metric (f=0; S.V.P=2) GGE biplot is important to visualize the relationship among environments. So, the following formulae from equation (1) were formulated to generate the GGE biplot:

$$Y_{ij} - \mu - \beta_j = g_{i1} e_{1j} + g_{12} e_{2j} + \varepsilon_{ij} \quad (3)$$

If the data were environment-standardized, the common formulae to generate the GGE biplot were as follows:

$$\frac{Y_{ij} - \mu - \beta_j}{s_j} = \sum\nolimits_{i=1}^{k} g_{i1} e_{1j} + \varepsilon_{ij} \quad (4)$$

Where sj is the standard deviation in environment j, i=1, 2…., k, gi1and e1j are PC1 scores for genotype i and environment j, respectively. In the present study, we used an environment-standardized model, Equation (4).

Results and Discussion

Combined analysis of variance for yield and yield attributing traits

The overall ANOVA among the varying environments showed the existence of very significant differences in the soy bean grain yield and the allied characteristics, such as the days to flowering, days to maturity, plant height, and hundred seed weight, the differences of which were mostly as a result of genotypic variation (G). There were also great disparities in agronomic characteristics like grain yield, days to flower, days to maturity, and the quantity of seeds per pod as a result of genotype-by-environment interaction (GEI). The environments were found to have a significant difference in agronomic traits, days to flowering, days to maturity, plant height, and hundred-seed weight (Table 2).

The environment led to the highest increase in the proportions of grain yield parameters (27.84%), and genotype led to the lowest percentage of grain yield parameters (16.83), and interaction between genotype and environment (55.31) in 2019. The environment is the most likely source of the variation in the parameters of grain yield in 2020, with 65.8 percent of the variation attributed to the environment, 5.14 percent of the variation attributed to genotype, and 29.04 percent of the variation attributed to genotype x environment interaction. The combined AMMI analysis of the Gollobs test of the locations over the years showed that the environment explained the highest percentage (37.39) of variation in the parameters of grain yield, whereas genotype only explained 7.027%, and the genotype x environment interaction only explained 55.571% of total variation. The results of analyzing the data revealed a range of yield production of soybean genotypes investigated between 1135 kg ha-1 and 1831 kg ha-1. The overall yield of all the test genotypes was 1485 kg ha^{-1} of grain. Genotypes TGX1485-ID had the highest grain yield of 1831 kg ha^{-1}, genotype G1873 had the highest grain yield of 1668 kgha^{-1} and SB0095 had the highest grain yield of 1543kgha^{-1} respectively (Table 3). A combined analysis of variance was done to explain the main effect and to measure the interactions between and among the sources of variability. Table 2 provides the results of the pooled analysis of variance. Genotypes(G) and GEI showed significant differences ($p \leq 0.01$, $p \leq 0.05$) in the genotype (G) and GEI of the genotype of grain yield, flowering days, and maturity days.

Table 2: Combined analyses of variance for the genetic traits of eight soybean genotypes over seven locations during the rainy season of 2019-2020

Statistic	**GY**	**DF**	**DM**	**PLHT**	**NPPP**	NSPP	HSWT
Residual Variance	219511.2	16.95126	22.25078	240.2897	773.552	0.071563	13.27
Grand Mean	1485.129	58.26809	116.9059	84.45286	87.46027	2.065769	14.34
LSD	318.2944	6.273293	4.344766	14.49183	0	0.380464	3.05
CV	31.54743	7.065945	4.034933	18.35495	31.8005	12.94982	25.41
Replicates	2	2	2	2	2	2	2
Environments	5	4	6	6	5	3	5
Genotype significance	0.034701	5.5E-05	0.012922	1.21E-06	1	0.986717	4.484E-04**
GenxEnv significance	0.054271	0.019279	0.010757	0.676115	0.189187	0.035225	1
Env. significance	0.540101	0.000197	0.000667	0.004566	0.763669	0.677947	0.0023

Table 3: Combined mean analysis of variance for the genetic traits of the eight common soybean genotypes over seven locations during the rainy season of 2019-2020

Environment	Genotypes	GY	DF	DM	PLHT	NPPP	NSSP	HSWT
OVERALL	G1873	1668	53	114	72	82	2.05	18.6
OVERALL	TGX1805-31F	1135	67	124	90	94	1.97	14.4
OVERALL	KAVRE	1418	63	118	106	96	2.04	11.8
OVERALL	SB0095	1543	57	116	92	86	2.06	14.9
OVERALL	GC8234GC-13	1461	61	116	91	101	2.13	11.6
OVERALL	SBO122	1535	55	115	80	82	2.05	14.4
OVERALL	TGX1485-ID	1831	57	116	75	83	2.09	14.6
OVERALL	PUJA	1289	53	116	70	74	2.14	14.4

GGE bi-plot analysis

The two most significant sources of variation to evaluate cultivar in a multi-environment trial are the genotype main effect (G) and the genotype x environment interaction (GE), which are referred to as GGE [22]. A GGE bi-plot is used to visualize the genotypic main effect (G) as well as the genotype by environment interaction (GE) of a genotype- by-environment dataset [20]. This is a bi-plot that works exceptionally well with mega-environment analysis because it is able to visually depict the genetic correlations among environments and the which-won-where patterns. It makes it easy to evaluate the test environments in terms of their discriminating ability and representativeness. Besides, the bi-plot helps to assess the genotype based on its average performance and stability in various mega- environments. The current data set revealed that the GGE bi-plot graphically represented interrelationships between the test locations in addition to the genotypes, and PC 1 and PC 2 accounted 79.9%, with PC 1 = 61.5% and PC 2 = 18.4% of the variation in the yield of grain.

Mega-environment analysis

GGE biplot is used to create the best polygons to see or visualize the pattern of interaction of genotype x environment [21]. The polygon view affirms the format of Which-won-where, a visualization of which would be useful to approximate the potential presence of various mega-environs in the target environment [23,20,24].

Figure 1 is a polygon illustration of eight soybean genotypes using seven environments. With this biplot, a polygon was drawn between the vertex genotypes that were furthest away in various directions, which led to the other genotypes being put in the interior of the polygon. The genotypes of the vertex are GC8234GC-13, TGX1485-ID, SB0122, and TGX1805-31F. The polygon will be broken into four sectors, and one of these sectors will not have any test environments. The analysis of the GGE biplot suggests the presence of location-specific adaptability: GC8234GC-13 is better performed in Nawalpur and Sarlahi; TGX1485-ID is more adapted to Khajura, Salyan, Surkhet, and Rampur; SB0122, G1873, and Kavre are more likely to be productive in Doti and Dailekh; TGX1805-31F does not have a particular environment preference. It is interesting to note that Doti has continuously performed within the same sector, and this may indicate that it has been able to perform at the same location. This trend indicates a recurrent mega-environmental analogous situation of where-won-which, and it substantiates the demarcation of the mega-environment. Notably, the conditions of defining mega-environments focus on the pattern of similar environments (which-where) as opposed to a mere similarity in the environment [23,21]. Therefore, Doti can be regarded as a unique mega-location to conduct soybean variety examination and assessment.

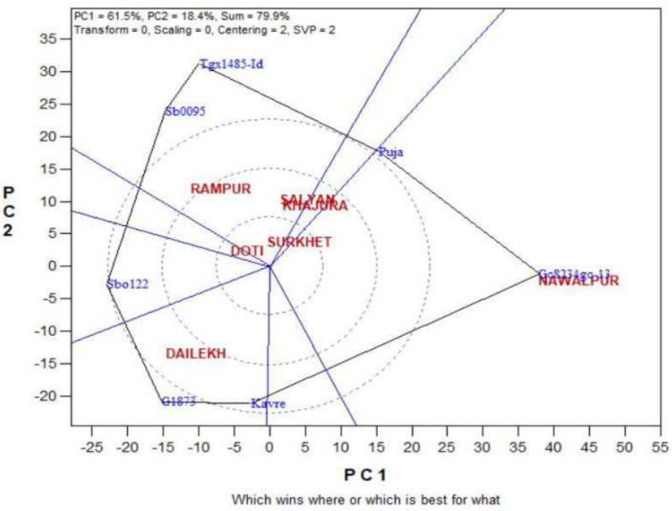

Fig 1. Polygon View of the GGE Biplot for Visualizing the Winning Soybean Genotypes Across Different Environments

Evaluation of Test Environments for Genotype Discrimination and Representation

The main aim of test-environment evaluation is to establish the type of environment that can differentiate superior genotypes in a mega-environment. They ought to have an ideology test environment that has the capability to discriminate between genotypes and also a high level of representativeness to the greater mega-environment [22]. Figure 2 shows the discriminating power versus representativeness of the GGE biplot, through environment-centered scaling [23]. In the present analysis, the single values are completely assigned to the environment scores (SVP = 2). In the case when the data are not scaled (scaling = 0), the length of the line between an environment marker and the biplot origin deals with the discriminating power of the environment. The longer the vectors in the environment, the better they discriminate among the genotypes, whereas the very short vectors give minimal information about the genotype differences [22]. Doti, Surkhet, Khajura, and Salyan became the most discriminating in this research. Nevertheless, the vector of Doti was nearer to the concentric circle, meaning that it provides little information regarding the genotypic variation. The second important feature of test environment analysis is its reflectiveness of the mega-environment. This is plotted using the angle between the environment vector and the average environment axis (the abscissa). Assuming that the SVP = 2, the cosine of this angle is close to the correlation coefficient between the performance of the genotype in that environment and the overall performance. The smaller the angle, the greater the representativeness [24, 22]. Under this criterion, Doti, Surkhet, Khajura, and Salyan were found to be more representative environments where soybean regional trials can be carried out. It is important to note that the vectors of Doti and Surkhet were very close to the average environment axis and therefore they were the most appropriate to use in the selection of better soybean genotypes to use in these growing regions.

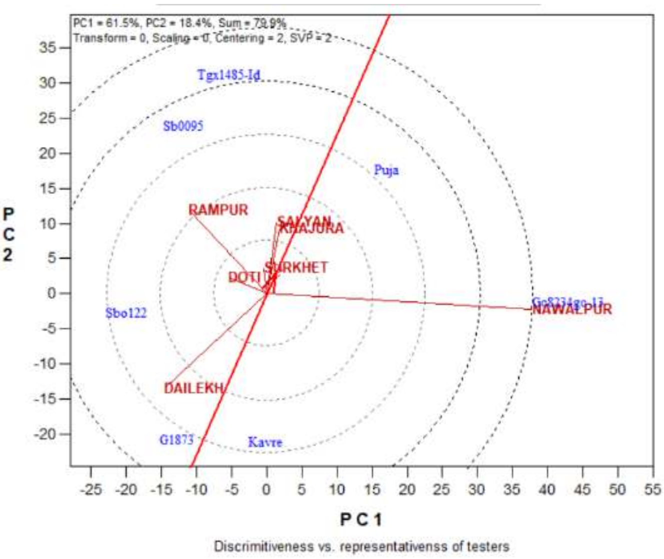

Figure 2 illustrates the relationship between discriminating power and representativeness in the GGE biplot, based on testing 8 soybean genotypes across seven different environments.

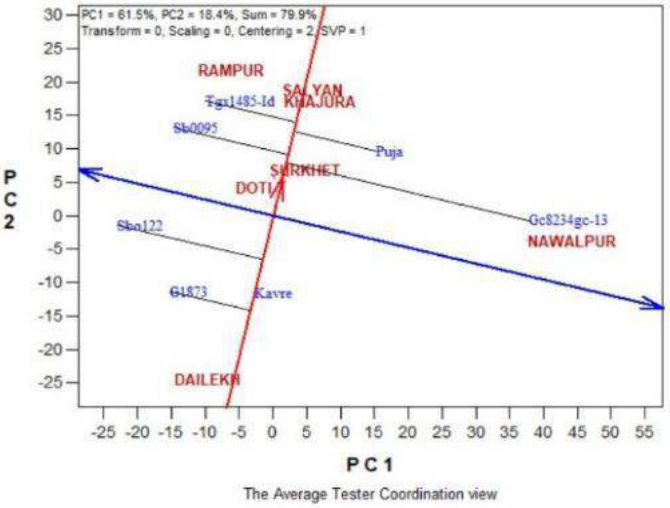

Figure 3. GGE biplot illustrating the ranking of genotypes based on average yield and stability across different environments.

Genotype Evaluation

Average Yield and Stability Performance of Soybean Genotypes in Comparison with an Ideal

To determine the stability and mean yield of eight soybean genotypes, the biplot analysis was done to determine the position of the genotypes and their placement behind an ideal genotype, as shown in Figure 3. The line that goes through the origin and is parallel to the average tester coordinate (ATC) in this biplot is a representation of the overall average performance of the genotypes [21]. The ATC suggests that there is a perpendicular line between the ATC and the origin, which would mean that the genotypes are stable, and the further the genotypes are on the axis of stability, the more stable they are. The genotype possessing the best mean yield and absolute stability will be described as an ideal genotype and will fall at the middle of the concentric circle of the biplot.

This is because this optimum is characterized by the longest vector of all of the genotypes and a minimal projection on the ATC axis, indicating optimum performance and stability. Genotypes G1873, Kavre, and TGX1485-ID were identified to be the most desirable based on these criteria, as they fall in the middle of the concentric circle, which means that they have the highest mean yield but at the same time have the highest stability in the testing environment. On the other hand, other genotypes were prioritized based on the Euclidean distance between them and this ideal point: SB0095, Puja, SB0122, and GC8234GC-13. The most distant genotypes were regarded as less desirable because they perform and are less stable.

Discussion

There was a performance of 18 soybean genotypes in five locations in the 2019 rainy season and 16 soybean genotypes in different locations in the 2020 rainy season in the present study. This, however, was not true because the genotypes differ amongst the years, and as such, only eight genotypes were shared and thus combined to analyze the data on analysis of variance, AMMI, and GGE biplot. The analysis of variance between the environments and years indicated that the environment significantly affected the yield of soybean grains and accounted for about 37.39 percent of the total variation. The model of genotype-by-environment interaction (GE) explained almost twice the environmental contribution and seven times the genotypic effect (7.07) of the total variation. This significant GE effect implies that there are different mega-environments, with each having different genotypes [21]. This has also been observed with Soybean in Nigeria [26], suggesting that the performance of a genotype of soybean in one environmental setting is not stationary in another setting because of strong GE interaction. The observations in Table 3 of the soybean suggest that the GE interaction is of the crossover type. To be more precise, there were five environments out of seven that produced various best-performing genotypes. This difference makes the process of selection more difficult and the development of genotype advice in breeding programs more complicated [5]. Huge and substantial GE interactions are recorded as well in soybean research carried out in Nepal, Ethiopia, and other African locations [3, 4, 8, 18], which are consistent with the results of Asfaw et al. (2009). As far as particular genotypes are concerned, GC8234GC-13, TGX1485-ID, SB0122, and TGX1805-31F were defined as the vertex genotypes, which means that they are more adaptable to specific conditions. GGE biplot analysis has effectively shown that the location-specific genotype GC8234GC-13 was more adaptive to the conditions in Nawalpur; TGX1485-ID was more adaptive to the conditions in Khajura, Salyan, Surkhet, and Rampur; and genotypes SB0122, G1873, and Kavre were more adaptive to the surroundings in Doti and Dailekh. It is worth noting that Doti in both years was concentrated within one sector, and this may indicate the uniformity of performance of the genotype in this place. The "Which-Won-Where" analysis divided the sites of testing into two mega-environments, where one consisted of three sites with G-1873 being the most successful genotype.

Conclusion

Findings of the study showed that genotype x environment (G×E) interaction had a strong influence on the performance of the soybean yield, and then the main effects of the genotype and the environment. Importantly, the magnitude of interaction between G and E was two to four times greater than the magnitude of environmental and genotypic effects, respectively. The pattern of GxE interaction was shown to be of a crossover type with a difference in the ranking of the genotypes in different environments. GGE biplots turned out to be one of the effective means of analyzing and demonstrating the trends of G x E interaction in soybean multi-environment trials, especially regarding test environments and genotype performance. According to the biplot result, genotypes G1873, Kavre, and TGX1485-ID fell at the center of the concentric circle, meaning that the genotypes are characterized by large mean yield and large stability in the environments where the tests were carried out. They can therefore be regarded as the best genotypes to grow soybeans. Also, there were existing mega-environments, Doti and Surkhet, which were close to the center of the biplot and on the average environment axis. This location suggests that such regions are appropriate in the selection and planting of better genotypes of soybean to farm in as they are the best locations to produce soybean.

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