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Evaluation of Soybean [*Glycine Max* (L.) Merrill] Germplasm at Multi-Environments of Nepal and Their Stability Assessment using AMMI and GGE Biplot Analysis

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ABSTRACT

A total of 150 soybean germplasms received from various sources were evaluated in a field study at DoAR, Dasharathpur; Surkhet, GLRP, Rampur, Chitwan, and NARC, Khumaltar, Lalitpur during the consecutive years of 2019 and 2020. The study employed an alfa lattice design with three replications to assess diversity, agronomic performance, and the selection of stable, early maturing, and high yielding genotypes from the inner terai to mid hills of Nepal released variety Puja and Tarkari Bhatmas-1 served as standard check. Major quantitative traits like days to flowering, days to maturity, plant height, number of primary branches per plant, number of nodes per plant, number of pods per plants, grain yield, biomass, harvest index and seed weight were recorded. A pooled mean analysis of variance revealed that all recorded traits were found significant difference for genotypic, environmental and genotypic by environmental effect at ($p<0.00$). The results revealed that the following genotypes: 200525(Rampur) (2074.9 kg/ha), NGRC06833 (2074.3 kg/ha), NGRC06835 (2041 kg/ha) and (TGX1987-62F (1988.3 kg/ha) were the highest yielders and ideal genotypes in GGE biplot analysis genotypes 2003KS-KBxTB1-2.1-3 (103 days), NGRC06826 (105 days), 2003KS-TB1xKB-5.34 (105 days) were noted for their early maturity. GGE biplot revealed sufficient diversity among the genotypes. Genotype NGRC06811 lies near the equality line for Surkhet, indicating superior performance in that environment. Conversely 200525 Rampur and NGRC06835 performed better at Rampur, while Seti, Sathiya excelled at Khumaltar. Notably NGRC08243 and Baglung black were poor performers across all three locations concerning the trait grain yield. Among the genotypes Soy Agd-005, NGRC02679, Tarkari Bhatmas 1, Bringi, Pyuthan Bazar-2016, AGS 371 were identified as the most stable whereas NGRC06811, NGRC02716, NGRC06821, Seti, NGRC06832 exhibited significant instability and were the largest contributor to genotype by environment interaction. This study provides valuable insights that can be utilized for future crop improvement efforts in Nepal by leveraging these germplasms.

Keywords: diversity, GGE, soybean, stable, traits

सारांश

बिभिन्न श्रोतबाट प्राप्त भटमासका १५० वटा अनुजातहरूलाई आ.ब. २०७६ र २०७७ मा दसरथपुर सुर्खेत, रामपुर चितवन, र खुमलटार ललितपुरको प्राकृतिक बातावरणमा जातीय भिन्नता तथा जातीय र बाताबरण बिचको अन्तर सम्बन्ध अध्ययन गर्न र बढी उत्पादन दिने, चाँडो पाक्ने तथा अन्य गुणहरु भएका जातहरूको छनौट गर्न अल्फा ल्याटिस डिजाइनमा तथा तिन रेप्लिकेसनमा सिफारिस जातहरू पुजा र तरकारी भटमास-१ लाई मानक जांच मानि यो परिक्षण संचालन गरिएको थियो । तपशिलका मुख्य गुणहरुः फूलफुल्ने दिन, पाक्ने दिन, बोटको उचाई, प्रमुख हाँगाको संख्या, आँख्लाको संख्या, कोसाको संख्या, बिउको तौल, बिउको उत्पादन, हार्भेस्ट इन्डेक्स, जीवित उत्पादन मापन गरियको थियो । सांख्यिकीय विश्लेषण गर्दा प्रयोग गरिएका जातहरुमाः जातीय, वातावरणिय तथा जातीय र वातावरणिय असर सबैमा

तथ्यपरक हुने गरेर भिन्नता देखियो । प्राप्त नतिजा अनुसार अनुजातहरू: २००५२५(Rampur) २०७४.९ केजी/हेकटर, {NGRC०६८३३ (२०७४.३ के जी /हेकटर)}, {NGRC०६८३५ (२०४१ केजी/हेकटर)} र {(TGX १९८७-६२) (१९८८.३ केजी/हेकटर)} उत्पादनको दृष्टिकोणले बढी उत्पादन दिने तथा आदर्श जातहरू पाइयो, अनुजातहरू: २००३ KS–KBxTB१-२.१-३ (१०३ दिन), NGRC०६८२६ (१०५ दिन), २००३ KS–TB1xKB-५.३४ (१०५ दिन) चाँडो पाक्ने पाइयो, यी अनुजातहरूलाई दाता माउको रुपमा तथा सुधारिएको उत्पादन परिक्षणमा स्थिरताको लागि प्रयोग गर्न सकिन्छ । जिजीई बैप्लोटको नतिजा अनुसार अनुजातहरू (NGRC०६८११),{(२००५२५ Rampur) र (NGRC०६८३५)},{सेती र साठिया} ले क्रमशः सुर्खेत, रामपुर र खुमलटारमा राम्रो प्रदर्शन गरेको पाईयो तर (NGRC०८२४३) र (बाग्लुङ्ग कालो) अनुजातहरूले कुनै पनि वातावरणमा राम्रो प्रदर्शन गरेनन् । अनुजातहरु Soy Agd-००५, NGRC०२६७९, Tarkari Bhatmas १, Bringi, Pyuthan Bazar-२०१६, र AGS ३७१ सबैभन्दा स्थिर हुन् भने NGRC०६८११, NGRC०२७१६, NGRC०६८२१, Seti, NGRC०६८३२६८ आदि सबैभन्दा अस्थिर पाइयो । यो अध्ययनको परिणामलाई आधार मानेर अझ गहिरो अध्ययन तथा भटमासबालीको बिकासको कार्यक्रममा सहयोग पुग्ने अपेक्षा गरियको छ ।

INTRODUCTION

Soybean (*Glycine max* [L.] Merrill) is a legume crop that grows in both tropical and temperate climatic regions. It is diploid (2n=2x=40) and is a self-pollinated species with less than 1% cross pollination occurring. Soybean is an important grain and oil seed crop that widely cultivated throughout the world, contributing to more than 50% of the world's oilseed production (Wilson 2008, Soy Stats 2011). World's top six countries are Brazil, USA, Argentina, China, India and Paraguay with production figures of 122 million metric tons, 113 million metric tons, 49 million metric tons, 20 million metric tons, 11 million metric tons and 9 million metric tons respectively (FAOSTAT 2020). Soybean ranks second among legumes in Nepal, and occupying an average of 7.68% (25,758 ha) of the total legume's area and accounting for 8.15% (32,178 Mt) of total legume production (MOAD 2022). It is cultivated from the terai to the high hills 200-2000 meters above mean sea level (msl). It can be successfully grown at an altitude ranging from 500 to 1500 meters above mean sea level either under intercropping with maize in upland condition or on paddy bunds in lowland conditions (Neupane and Bharati 1990). The hill regions contribute about 83% of total soybean area and production, while the mountain and terai regions occupies about 10% and 7%, respectively (MOAD 2020). The major soybean producing districts in Nepal were Kavre, Makawanpur, Kalikot, Salyan, Dadeldhura and Kailali (MOAD 2022). Soybeans are used for various food products, including baby food, dry seed roasted or fried, green pods as vegetable in Nepal. It is often referred to as "poor man's meat" due to its protein content> 40%, and its oil content of around 20%. It is important not only for protein meal and vegetable oil but also for their rich content of lysine and vitamins, making them suitable for both human and animal consumption. Additionally, they are utilized for industrial purposes, such as bio-fuels (Hartman et al. 2011). It contains isoflavones which may protect the human body against cancer, diabetes, osteoporosis, blood pressure, and coronary heart disease.

To date, a total of nine soybean varieties have been released for cultivation till the date. Most of the soybean produced in the country is consumed internally either as a roasted beans or green pods as vegetables. Soybean is a hardy crop grown in marginal land and stress prone environments. The variety Tarkari Bhatmas-1 is suitable for use as green fresh pods or seed soaked overnight and cooked or boiled or fried. Large quantity of soybean grain, flour, crude/refined oil and cake are being imported to meet demand for oil and poultry industries. In 2016/17 imported amount was 212137.325 metric tons, with value of 1698.5356 crore Nepalese rupees (MOAD 2018). The import value was 4628285 thousand Nepalese rupees in 2022 (MOAD 2022). Understanding genetic variability is essential to formulating an effective crop improvement program of the main challenges facing soybean in Nepal are uncertain occurrence of pod blight in the hills, yellow mosaic virus in terai, a low priority for inputs, a lack of flood tolerant varieties, lack of disease resistant varieties, and low utilization of local germplasm in breeding program, so farmers are searching for more new varieties. The objective of this study was to evaluate soybean genotypes at three different climatic conditions of Nepal for phenotypic characterization and to study genotype by environmental effect and to identify potential genotypes for yield attributing and agro-morphological traits which could be utilized for soybean improvement program.

MATERIALS AND METHODS

Plant materials

For this study, a total of 150 soybean accessions including local landraces were critically evaluated to understand the phenotypic and genotypic variations along with their protein and oil content (Table 3). The germplasm studied was collected from several sources, including GLRP Khajura, the National Agronomy Research Center Khumaltar, the National Agriculture Genetic Resource Center (Gen Bank), Khumaltar and the National Plant breeding and Genetic Research Center, Khumaltar. Experimental plant materials include released varieties 7, landraces 98, breeding or crossing lines 18, introduced lines 27. Among them seven released varieties were Lumle Bhatmas -1, LS-77-16-16 (Khajura Bhatmas-1), Seti, Ransom, Tidar, {Puja and Tarkari Bhatmas 1 were check}.

Geographic Location

The entire study was conducted at three different agro-ecological conditions of Nepal. These locations were Directorate of Agricultural Research, Karnali Province, Dasarathpur, Surkhet (28^{0}30" Northern latitude, 81^{0}47" Eastern longitude, and 580-meter above mean sea level); National Agronomy Research Center, Khumaltar, Lalitpur (1360 m asl with coordinates of 85°10′ E and 27°39′ N). and Grain Legumes Research Program, Rampur, Chitwan (N27^{0} 39′ 0.45″ latitude, E84^{0} 21′ 9.1″ longitude and 228 m asl).These locations represent the river basin of the mid-west, central mid hill and inner terai of Nepal respectively, during summer season of consecutive years of 2019 and 2020 providing six testing environments: Surkhet 2019 and 2020, location 1 and year 1 (11) and year 2 (12), Khumaltar 2019 and 2020, location 2 and year 1 (21) and year 2 (22) and Rampur 2019 and 2020, location 3 and year 1 (31) and year 2 (32). All these three sites had coarse textured sandy loam soil. The average monthly weather parameters of the experimental sites are presented in **Table 1** and soil properties in **Table 2**.

Table 1. Weather parameters of experimental sites during crop growing period of 2019 and 2020

Total rainfall (mm) during the month								
	Year	**May**	**June**	**July**	**August**	**September**	**October**	**November**
Dasarathpur Surkhet	2019	10.6	163.5	464.1	179.3	253.1	0.0	10.6
	2020	163.5	290.0	390.2	163.5	58.0	0.0	5.3
Khumaltar	2019	68.6	163.5	511.5	221.5	247.9	10.6	31.6
	2020	131.8	348.1	569.5	142.4	258.4	10.6	0.0
Rampur	2019	105.5	195.1	553.7	247.9	300.6	36.9	15.8
	2020	184.6	411.3	632.8	142.4	269.0	5.3	0.0
Monthly mean relative humidity (%)								
Dasarathpur Surkhet	2019	23.9	41.4	78.8	83.9	84.9	76.8	59.9
	2020	51.8	65.5	84.9	84.9	77.8	51.8	43.2
Khumaltar	2019	37.8	57.7	85.2	87.3	88.1	86.0	74.4
	2020	56.5	79.4	90.8	87.9	88.0	71.9	58.7
Rampur	2019	36.9	54.8	83.9	85.0	86.7	85.5	75.0
	2020	53.1	76.3	89.4	86.7	86.3	70.9	59.1
Monthly mean of minimmum temperature (°C)								
Dasarathpur Surkhet	2019	22.3	26.1	24.6	24.1	21.2	17.4	14.1
	2020	17.4	21.7	23.5	23.6	21.1	17.8	13.0
Khumaltar	2019	20.5	21.4	21.7	22.2	18.5	15.2	12.3
	2020	16.9	19.9	21.9	20.8	20.2	16.9	11.3
Rampur	2019	22.8	22.4	24.6	24.4	20.6	16.9	12.5
	2020	19.4	22.5	23.9	23.1	21.6	17.1	11.0
Monthly mean of maximmum temperature (°C)								
Dasarathpur Surkhet	2019	43.7	44.4	39.1	32.9	32.3	29.5	28.1
	2020	41.6	38.3	33.2	32.3	33.7	33.7	31.4
Khumaltar	2019	38.1	38.0	34.6	31.7	30.1	26.7	25.2
	2020	35.7	32.8	29.8	31.0	29.6	28.8	27.5

Total rainfall (mm) during the month								
	Year	**May**	**June**	**July**	**August**	**September**	**October**	**November**
Rampur	2019	41.8	41.2	37.4	33.9	31.6	29.2	27.8
	2020	39.7	36.1	32.1	33.1	31.9	30.5	29.9
Mean of monthly temperature (°C)								
Dasarathpur Surkhet	2019	33.1	33.9	29.3	28.2	26.7	23.4	20.6
	2020	29.0	29.8	27.8	27.6	27.7	26.4	21.0
Khumaltar	2019	28.8	29.3	26.1	25.8	24.0	20.9	18.3
	2020	26.1	25.7	25.0	25.3	24.3	23.2	18.8
Rampur	2019	31.5	32.2	28.5	28.2	26.3	22.9	19.9
	2020	29.1	28.4	27.3	27.5	26.5	25.3	20.5

Table 2. Soil properties of experimental sites

	Experimental sites		
Parameters	**Khumaltar**	**Rampur**	**Dasarathpur**
pH	4.56	5.88	6.71
Rating	Very acidic	Moderately acidic	Nearly neutral
OM%	1.85	2.60	2.15
Rating	L	M	L
TN%	0.09	0.12	0.14
Rating	L	M	M
Av. P2O5 mg/kg	153.66	18.40	170.00
Rating	H	M	H
Av. K2O mg/kg	40.42	59.35	112.00
Rating	L	M	M
Sand%	11.30	61.00	45.20
Silt%	57.10	30.20	29.70
Clay%	31.60	8.80	25.10
Texture Class	Silty clay loam	Sandy loam	Loam

L=low, M=medium, H=high

Layout and management

An experiment was laid out in an alpha lattice design, incorporating a total 150 entries replicated in three times, with a block size of 5 and block with in replication was maintained 30 entries. The size of each plot was 1 m^2 (single row of 2m length) where the spacing of 50 cm and 10 cm were maintained for row to row and plant to plant respectively. Seeding was done as following; first year planting: Surkhet: 2076-Ashar-22 (6th July, 2019), Rampur: 2076-Ashar-24 (8th July, 2019), Khumaltar: 2076-Jestha-25 (8th June, 2019); Seeding was done as following in second year planting: Surkhet: 2077-Shrawan-02 (17th July, 2020), Rampur: 2077-Shrawan-20 (4th Aug, 2020), Khumaltar: 2077-Jestha-14 (27th May, 2020), The applied dose of the fertilizer was 20:40:20 kg $N:P_2O_5:K_2O$/ha. The calculated amount of fertilizers were urea, DAP (Di-ammonium Phosphate) and MOP (Muriate of Potash) were mixed and incorporated uniformly into the soil as a basal dose at the time of final land preparation. Thinning was done approximately after twenty-five days of sowing and plant population was maintained as 20 plants per plot. Mechanical weeding was done by hand using a hoe, on the 25 and 45 days after sowing to control weeds present. All weeding operation was completed on the same day of weeding. Insecticides chlocyper (chloropyriphos 50%EC+ Cypermethrin5%EC) and Imidachloprid along with sticker was sprayed to control soybean hairy caterpillar, bugs and beetles in the field. Spraying was done at pre flowering and pre pod formation stage. The crop was harvested manually with the help of sickles at the stage when the plants turned into brownish black, leaves dried and drop off. The crop was sundried for required days to reduce moisture level of the grains. Sun drying was continued until the pods were dry enough for threshing. Drying was done in separate plastic sacs for each plot. Manual threshing was used for threshing after sun drying of harvested crop and grains were cleaned by winnowing. After cleaning threshed grains were kept in cotton sacks separately.

Data recording

Average of data recorded from five plants are used for analysis. The following parameters were recorded: days to flowering (DF), days to maturity (DM), plant height cm (Pht), number of primary branches per plant (NPBPP), number of nodes per plant (NNPP), number of pods per plant (NPPP), grain yield kg/ha (GY), hundred seed weight (HSW), total biomass per plot (TBM) and harvest index (HI).

Data analysis

Plot mean values were calculated for all the traits and used for the analysis of variance (ANOVA) using GenStat 18th edition and Additive Main Effects and Multiplicative Interaction (AMMI) (Zobel et al 1988, Guach 1988) and regression models (Eberhart and Russell 1966) for grain yield. The estimation of genetic parameters was analyzed using R-stat version 5.3, ADEL-R, META-R and GEA-R. Phenotypic and genotypic variances for the Alpha lattice design was computed for all traits based on the methods of (Federer 1961).

RESULT AND DISCUSSION

Pooled mean analysis of variance (ANOVA) for agro-morphological traits across the three environments over the two subsequent years of 2019 and 2020 indicated that all the traits: days to flowering, days to maturity, plant height, number of primary branch per plant, number of nodes per plant, number of pods per plant, hundred seed weight, grain yield, harvest index, and total biomass showed highly significant differences in genotypes, environment and G x E interaction effect (**Table 3**) Genotypes 200525(Rampur) (2074.9 kg/ha), NGRC06833 (2074.3 kg/ha), NGRC06835 (2041 kg/ha), TGX1987-62F (1988.3 kg/ha), GC8234GC-13 (1952.2 kg/ha), Kavre (1816.1 kg/ha), NGRC02675 (1754.6 kg/ha), P194159 (1663.4 kg/ha), LS-77-16-16 (Khajura bhatmas-1, 1656.9 kg/ha) and NGRC06809 (1624.3 kg/ha) exhibited high yields across the years and environments than the popular released variety Puja (1604.7 kg/ha). Genotypes 2003KS-KBxTB1-2.1-3 (103 days), NGRC06826 (105 days), 2003KS-TB1xKB-5.34 (105 days), NGRC06820, Sathiya, NGRC06813, Tidar; (106 days) showed early maturity. In terms of the number of pods per plant, the genotypes with higher counts were the genotypes NGRC06833 (110.1), NGRC06835 (108.5), 200525(Rampur) (106.3), TGX1987-62F (102.5), Kavre (94.2), similarly the top five genotypes for higher seed weight were AGS 377 (24.5 g), 2003KS-TB1xKB-5.34 (22.7 g), Dakshinkali-creami bold (22.6 g), 2003KS-KBxTB1-2.1-2 (21.7 g), and 2003KS-TB1xKB-5.14-2 (21.5 g) (Table 3). Breeder can utilize the variability for selection and may use in hybridization for trait improvement, and gene transfer to the other genotypes. Similar results were reported by Baraskar et al (2014). Analysis of variance revealed that mean squares due to genotypes were significant for all the 15 characters indicating varietal differences for all the characters studied. Aditya et al (2011) reported similar findings in soybean where all studied characters were highly significant at (<0.01). Ibrahim et al (2018) also reported similar findings as number of days to 50% flowering, plan height, number of days to 95% maturity, no of pods per plot, no of pods per hectare were significant at (<0.01) level. Hossain et al (2004) reported similar findings as number of days to 50% flowering, plant height, number of pods per plant, hundred seed weight, and yield significant at (<0.01) level. Chandrawat et al (2017) reported variation due to genotypes was significant for all the characters under study. Sulistyo et al (2018) showed similar result as days to flowering, days to maturity, plant height, number of pods per plant, hundred seed weight, and yield all characters were highly significant differences due to genotypic effects.

Table 3. Combined analysis of mean performances of soybean accessions in G x E trial across the locations (Dasarathpur, Khumaltar and Rampur) and over the years (2019-2020)

Genotypes	EN	DF	DM	Pht	NPBPP	NNPP	NPPP	GY	HSW	HI	TBM
2003KS-TB1xKB-5.67	1	51	109	56.0	3.2	8.7	28.2	447.7	19.2	0.26	248
2003KS-TB1xKB-5.14-2	2	52	108	35.5	4.3	9.2	41.0	795.2	21.5	0.37	248
2003KS-TB1xKB-5.64	3	51	107	46.4	3.6	8.6	32.3	486.3	17.6	0.25	287
2003KS-TB1xKB-5.61	4	52	107	43.0	4.0	9.1	35.7	627.8	18.7	0.30	294
2003KS-TB1xKB-5.65	5	53	109	47.6	4.3	9.4	38.3	694.2	18.2	0.32	281
2003KS-TB1xKB-5.66	6	55	110	31.2	3.7	7.6	28.5	534.3	18.8	0.28	278
2003KS-KBxTB1-8	7	52	108	32.3	4.3	9.0	35.0	727.7	17.2	0.33	289
2003KS-TB1xKB-5.32-2	8	53	110	53.9	3.5	9.8	26.4	470.5	19.2	0.24	295
2003KS-TB1xKB-5.62	9	51	112	46.1	3.5	9.5	29.6	445	19.2	0.24	278
2003KS-TB1xKB-5.59	10	57	113	65.4	4.1	8.9	37.1	626.4	20.6	0.30	277
2003KS-TB1xKB-5.45	11	52	107	36.3	4.1	8.8	35.7	701.3	18.3	0.35	251
2003KS-TB1xKB-5.4	12	53	111	34.2	4.3	8.3	33.2	566.3	19.0	0.30	262
2003KS-TB1xKB-5.39	13	51	107	32.8	4.0	9.4	43.9	731.3	18.5	0.33	269
2003KS-KBxTB1-2.1-3	14	50	103	33.0	3.9	8.8	31.7	570.8	18.1	0.31	249
2003KS-TB1xKB-5.69	15	50	107	39.2	3.1	8.6	29.0	425.3	18.7	0.23	282
Solu coll#2-2016	16	58	116	58.2	5.1	10.7	61.9	1318	16.6	0.52	238
2003KS-TB1xKB-5.37	17	53	112	29.9	3.6	8.0	32.4	608.9	19.1	0.31	255
2003KS-TB1xKB-5.34	18	51	105	44.7	4.2	9.2	28.0	522.7	22.7	0.27	278
Bringi,Pyuthan Bazar-2016	19	57	111	57.0	4.9	11.2	59.0	1080.2	16.7	0.47	230
2003KS-KBxTB1-2.1-2	20	55	118	44.9	4.1	10.3	36.6	682.6	21.7	0.35	253
Coll # 166	21	50	116	72.2	4.7	12.1	46.6	855.7	19.3	0.39	272
Brown, Jumla-2016	22	52	109	85.6	4.4	10.7	39.5	753.4	16.6	0.34	289
Soy Agd-011-2	23	58	119	44.2	4.1	9.5	47.9	889.1	14.1	0.41	244
Soy Agd-017	24	54	111	39.9	4.6	9.9	45.3	1024.2	18.0	0.44	256
Soy Agd-010	25	58	115	69.0	4.1	9.5	39.0	760.4	12.6	0.35	258
Soy Agd-013	26	57	113	52.9	4.1	9.0	38.5	794.3	16.8	0.34	292
Soy Agd-001	27	60	119	50.1	4.2	9.1	46.1	850.2	17.9	0.35	287
Soy Agd-014	28	59	119	65.3	4.8	10.8	47.2	868.7	9.1	0.39	265
Coll # 6	29	54	120	63.6	5.3	11.0	46.7	936.2	17.5	0.41	246
Soy Agd-008	30	60	116	62.4	6.3	12.9	77.8	1384.2	12.4	0.52	243
Chainpur Bhatmas 1	31	56	120	72.2	3.9	8.4	44.2	672.1	17.6	0.30	293
Ramechhap collection	32	58	115	45.0	3.9	8.8	44.5	916.3	17.2	0.37	296
Soy Agd-006	33	54	123	86.7	4.7	10.7	44.5	790.6	14.9	0.36	286
Soy Agd-021	34	60	117	61.6	6.3	13.4	80.1	1475.8	9.7	0.56	227
Soy Agd-002	35	60	117	75.6	6.2	13.5	64.6	1220.1	10.0	0.50	240
Soy Agd-005	36	57	114	41.0	4.5	9.5	57.6	999	14.8	0.42	271
Soy Agd-020	37	56	116	46.2	5.6	11.6	54.1	1047.3	13.6	0.43	269
010-10.2	38	52	111	55.0	3.4	9.9	29.5	356.4	17.2	0.18	317
Surkhet#2	39	59	118	82.4	5.0	12.3	54.0	1076.3	18.2	0.43	273
Solu-Small seed	40	54	112	60.8	5.9	13.0	74.9	1357.5	17.2	0.52	244

Genotypes	**EN**	**DF**	**DM**	**Pht**	**NPBPP**	**NNPP**	**NPPP**	**GY**	**HSW**	**HI**	**TBM**
Tanahu-Creami	41	51	111	29.9	3.8	9.7	33.3	604.6	19.2	0.29	291
Dakshinkali-Creami Bold	42	59	118	42.0	4.5	10.4	48.8	888	22.6	0.40	266
Sathiya	43	50	106	44.0	3.6	8.5	25.1	481.8	18.1	0.25	293
TGX1876-4E	44	54	109	63.9	4.8	10.3	53.2	898	9.9	0.38	273
AGS 377	45	53	115	55.3	5.3	11.3	44.6	868.9	23.7	0.41	243
Lumle Bhatmas 1	46	60	120	81.9	6.1	15.1	75.3	1437.6	17.5	0.57	214
AGS 377	47	52	110	46.2	5.0	11.1	72.7	1415.4	24.5	0.51	254
Seti	48	60	118	49.4	4.3	9.2	65.2	1080.5	15.9	0.40	283
NGRC02664	49	54	117	49.7	4.5	10.5	42.4	711	13.5	0.35	253
NGRC02666	50	54	114	43.2	4.5	9.9	57.7	883.2	13.3	0.39	266
NGRC02669	51	56	118	57.6	4.4	10.7	45.2	752.4	11.5	0.33	288
NGRC02671	52	56	118	58.7	4.9	11.7	68.6	936.5	9.2	0.39	274
NGRC02672	53	57	114	61.1	5.6	12.1	55.0	1000.6	9.5	0.45	237
Collection 175	54	52	112	89.2	6.5	14.1	69.9	1226	12.4	0.53	212
NGRC02674	55	53	117	66.0	4.7	10.7	33.7	588.2	6.1	0.30	261
NGRC02675	56	59	121	55.7	5.9	12.5	86.5	1754.6	8.5	0.58	249
NGRC02676	57	54	116	59.5	5.4	12.2	72.4	1299	14.0	0.51	242
Lamjung local	58	53	107	37.1	4.3	8.6	44.1	810.6	14.6	0.35	285
Collection 168	59	55	111	51.1	4.7	9.4	41.3	723.4	16.0	0.35	270
NGRC02679	60	54	115	49.0	4.8	10.5	55.1	945.1	11.7	0.42	250
NGRC02680	61	52	109	35.5	4.5	9.5	42.3	798.3	16.7	0.35	287
NGRC02683	62	56	117	52.5	5.9	12.2	80.9	1565.9	12.7	0.59	215
NGRC02684	63	53	115	58.8	5.0	11.6	53.2	952.3	13.1	0.40	272
NGRC02686	64	53	109	56.5	4.6	11.7	53.1	1022.1	14.4	0.44	260
NGRC02687	65	52	108	71.9	4.9	10.9	43.3	769.2	15.4	0.36	257
Baglung Seto	66	55	121	88.0	6.0	13.5	71.1	1237	13.0	0.50	229
NGRC02690	67	55	119	90.4	6.2	14.6	73.5	1422.3	14.8	0.52	255
NGRC02691	68	55	111	43.7	4.5	9.5	49.6	926.8	15.1	0.40	257
Baglung Khairo	69	53	119	67.8	4.3	8.6	42.2	736.4	13.6	0.33	298
NGRC02693	70	54	110	55.0	4.3	10.3	36.1	608.3	15.5	0.27	307
NGRC02699	71	55	117	67.9	6.2	13.9	74.9	1395.9	16.2	0.53	243
NGRC02703	72	54	116	64.4	4.9	10.6	36.8	657.5	14.8	0.30	304
NGRC02704	73	56	118	46.3	5.2	11.5	60.6	1107.4	14.3	0.48	233
Gulmi Kalo	74	38	110	35.3	5.3	12.8	41.1	786.1	13.1	0.35	272
NGRC02707	75	53	110	48.2	4.8	10.1	41.1	791.8	15.3	0.36	281
Collection #167	76	54	122	75.1	6.5	14.1	55.8	1063.6	12.8	0.46	250
NGRC02710	77	53	116	33.5	5.0	8.6	46.1	866.7	18.5	0.36	290
NGRC02711	78	52	107	50.9	5.3	9.9	51.5	927.4	13.9	0.41	258
NGRC02712	79	53	111	44.8	4.9	9.6	52.3	1005.8	18.4	0.39	288
NGRC02716	80	55	117	57.4	5.5	11.3	50.4	926.2	4.6	0.40	228
NGRC02717	81	58	119	67.2	4.8	11.4	40.3	716.2	5.4	0.35	241
NGRC02719	82	56	119	66.6	5.4	12.3	71.6	1208.2	13.3	0.51	230

Genotypes	EN	DF	DM	Pht	NPBPP	NNPP	NPPP	GY	HSW	HI	TBM
Baglung black	83	54	120	45.0	3.6	8.6	25.8	348	13.8	0.19	286
NGRC05101	84	55	116	54.2	4.1	9.2	31.1	415.3	5.6	0.22	269
NGRC06809	85	51	110	33.9	5.2	10.7	84.8	1624.3	9.2	0.55	253
NGRC06811	86	61	121	61.8	5.0	10.9	58.5	1098.6	9.5	0.41	249
NGRC06812	87	56	117	73.9	5.0	12.1	61.5	1032	17.6	0.42	261
NGRC06813	88	53	106	42.6	5.3	9.8	56.2	1138.1	13.2	0.50	225
Gulmi seto	89	55	127	107.7	4.6	11.4	48.9	739.6	14.9	0.35	244
NGRC06815	90	54	115	49.0	4.7	10.0	41.3	749.1	15.7	0.33	297
NGRC06816	91	57	119	61.5	4.8	11.0	57.0	962.1	15.8	0.41	272
Cololection 161	92	54	121	108.5	3.9	10.2	43.8	731.5	12.5	0.32	261
Collection #178	93	59	125	56.9	4.3	8.5	48.2	378.6	14.7	0.22	277
NGRC06820	94	52	106	35.1	4.7	8.8	46.3	882.4	15.4	0.39	262
NGRC06821	95	53	109	55.1	6.0	11.7	61.6	1162	14.0	0.49	227
NGRC06822	96	56	121	107.9	4.6	9.6	59.9	838.7	10.8	0.35	283
NGRC06823	97	55	117	60.6	5.2	12.6	57.4	973.5	16.6	0.43	251
Collection # 1 mangalpur	98	53	108	51.3	4.8	10.5	48.5	859.9	13.8	0.40	259
VI (Bhojpur)	99	54	122	88.3	5.6	11.6	51.3	880.4	17.6	0.37	275
NGRC06826	100	52	105	38.7	5.0	9.8	52.6	1008.6	17.9	0.41	283
Collection 169	101	53	109	65.7	4.5	10.6	52.1	759.9	15.9	0.36	269
NGRC06828	102	63	120	82.9	4.2	10.0	29.5	470.1	5.6	0.26	238
NGRC06829	103	54	110	57.8	3.6	8.7	25.8	456.4	13.5	0.24	284
NGRC06830	104	55	118	70.1	4.8	11.4	59.4	1090	18.1	0.45	243
Haripur Khairo Bhatmas-1	105	55	123	68.0	3.9	9.3	37.5	616.9	18.5	0.30	277
NGRC06832	106	54	114	49.5	5.2	10.4	55.1	1104.8	14.3	0.44	247
NGRC06833	107	59	120	82.2	5.9	12.9	110.1	2074.3	16.2	0.63	245
NGRC06834	108	52	107	40.0	4.7	10.3	45.2	929.2	16.9	0.37	290
NGRC06835	109	61	118	87.2	5.8	14.3	108.5	2041	8.9	0.62	249
NGRC07367	110	56	111	54.9	4.9	11.4	45.9	922.7	15.7	0.39	287
NGRC07368	111	57	118	48.5	6.1	13.5	75.7	1569.1	15.4	0.57	228
NGRC07369	112	55	111	47.5	4.5	9.6	28.8	521.8	16.0	0.27	281
Tandi coll # 2	113	62	128	72.4	4.3	10.7	41.4	628.3	12.7	0.31	269
NGRC08243	114	54	113	59.3	5.0	11.3	49.4	859.4	14.2	0.36	245
NGRC08244	115	57	120	59.9	4.8	12.2	50.0	994.5	12.6	0.40	292
NGRC08245	116	53	116	73.5	5.0	11.7	44.1	820.6	14.8	0.38	264
G-8586	117	52	108	34.3	4.5	10.9	64.2	1209.4	9.6	0.48	254
TGX1987-62F	118	62	122	54.3	5.7	12.5	102.5	1988.3	9.0	0.62	238
TGX1835-10F	119	63	120	74.0	5.4	13.3	67.1	1309.3	9.2	0.53	218
AGS 371	120	58	117	39.8	5.0	11.6	55.1	1108	18.8	0.50	224
TGX311-23D	121	55	111	87.1	6.0	13.6	78.7	1479.7	13.1	0.56	228
200525(Rampur)	122	55	115	74.3	6.4	14.3	106.3	2074.9	9.8	0.62	252
Chitwan-9	123	55	109	58.6	4.8	11.5	49.9	884.7	12.2	0.35	305
Tidar	124	52	106	46.8	4.0	10.2	33.7	578.3	7.9	0.29	290

Genotypes	**EN**	**DF**	**DM**	**Pht**	**NPBPP**	**NNPP**	**NPPP**	**GY**	**HSW**	**HI**	**TBM**
TGX1989-19F	125	63	122	63.9	5.0	12.4	54.6	1124.9	8.3	0.42	274
Ankur	126	55	117	64.6	6.1	13.5	73.0	1376.9	7.9	0.50	251
TGX1485-ID	127	58	120	72.6	6.0	12.9	70.7	1210.4	11.6	0.48	266
CM9125	128	63	119	70.1	5.9	13.8	80.4	1529	9.0	0.54	255
TGX1987-42F	129	59	116	67.8	5.9	14.4	86.7	1575.5	9.7	0.57	231
272W	130	56	116	65.6	5.9	13.4	82.4	1480.7	8.8	0.53	256
GC8234GC-13	131	61	117	66.9	6.3	14.2	93.7	1952.2	9.0	0.61	246
G8754	132	56	118	77.7	6.0	14.2	81.2	1456.7	18.3	0.54	232
P194159	133	56	116	56.2	6.0	13.4	86.6	1663.4	8.6	0.58	237
LS-77-16-16	134	50	107	42.1	5.2	10.7	73.6	1656.9	10.9	0.57	243
IARS-87-1	135	56	118	56.2	5.1	11.2	58.3	1114.9	12.7	0.44	278
SB0-122	136	56	114	48.2	4.9	11.0	64.1	1304.1	10.3	0.48	274
AGS-376	137	58	119	57.4	5.3	11.0	50.6	935.3	12.6	0.42	258
TGX1987-14F	138	51	110	50.2	5.4	11.5	59.4	1197	13.8	0.48	256
F778817	139	62	118	52.0	5.4	11.2	63.9	1306.7	10.7	0.50	255
TGX1987-62F	140	63	118	55.8	5.3	12.2	65.9	1310.5	9.1	0.49	260
Kavre	141	56	115	73.2	5.4	12.7	94.2	1816.1	8.2	0.58	254
Ransom	142	60	120	59.8	5.4	11.7	65.1	1303.5	14.3	0.51	252
Sindhuli Khairo	143	57	115	62.0	4.6	10.8	40.8	690.6	8.9	0.32	279
Palpa	144	51	113	39.4	4.0	9.9	35.6	585	11.2	0.29	263
Bajura	145	55	124	82.8	4.3	9.2	41.1	629.9	9.7	0.31	287
TGX1987-11E	146	58	120	80.3	5.7	12.8	83.2	1579.2	14.6	0.54	267
TGX1990-8F	147	61	121	59.2	5.0	12.5	69.4	1247.4	14.3	0.49	258
TGX 1925-1F	148	57	116	69.9	5.4	13.3	58.3	1083	15.2	0.45	265
Puja	149	55	118	59.1	6.1	12.5	83.6	1604.7	14.4	0.57	239
Tarkari bhatmas 1	150	51	108	29.0	3.7	8.9	49.5	972	18.4	0.41	284
Grand Mean		**55**	**115**	**58**	**5**	**11**	**54**	**993**	**14.32**	**0.408**	**262**
P value											
Genotypes (G)		<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
Environment (E)		<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
G*E		<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
CV %		3.69	2.08	12.85	11.59	11.24	12.45	14.1	7.51	10.63	9.53
LSD (0.05)		4.00	4.65	13.88	1.1	2.416	13.07	224	2.11	0.069	430

Additive main effects and multiple interactions (AMMI) analysis

The results of the AMMI analysis of variance for soybean grain yield involving one hundred and fifty soybean genotypes across three environments over the two consecutive years showed that 5.8% of the total sum of squares was attributed to environmental effects, 63.8 % to genotypic effects and 30% to genotype × environment interaction effects (**Table 4**). GGE biplot analysis showed that PC1 and PC2 accounted 69% and 36.5% of GGE sum of squares respectively over the years. The two principal components explained a total of 100% variation among the accessions. The polygon view of the GGE-biplot analysis helps the detection of cross-over and non-crossover genotype-by environment interaction, as well as the identification of possible mega environments in multi-location yield trials (Yan et al 2007). The yield performance and stability of the accessions were evaluated by Farshad et al 2011 using average environment coordination (AEC) method.

Table 4. ANOVA for AMMI analysis of variance for grain yield of 150 soybean accessions tested in three environments over the years 2019- 2020

Source	SS	PORCENT	PORCENAC	DF	MS	F	PROBF
ENV	35256982	5.8	5.8	2.0	17628491	176.9	0
GEN	388593490	63.8	69.6	149.0	2608010	26.2	0
ENV*GEN	185092681	30.4	100.0	298.0	621116	6.2	0
PC1	58805977	63.5	63.5	150.0	392039	3.9	0
PC2	33740363	36.5	100.0	148.0	227975	2.3	0
PC3	0.0	0.0	100.0	146.0	0.0	0.0	1
Residuals	224249341	0.0	0.0	2250.0	99666	NA	NA

Based on plot mean and CV%, 37 genotypes including NGRC06809, LS-77-16-16, GC8234GC-13, 200525(Rampur), TGX1987-62F, NGRC06835, NGRC06833, P194159, etc (**Figure 3**) produced higher grain and stability. These entries can be considered as stable and good performer because they had high mean yield and low CV%. All genotypes in the quadrant IV were more stable than the other with red color. **Figure 2** indicated 21 accessions (7) 2003KS-KBxTB1-8, (13) 2003KS-TB1xKB-5.39, (26) Soy Agd-013, (27) Soy Agd-013, (31) Chainpur Bhatmas 1, (32) Ramechhap collection, (42) Dakshinkali-Creami Bold, (44) TGX1876-4E, (48) Seti, (58) Lamjung local, (61) NGRC02680, (63) NGRC02684, (77) NGRC02710, (87) NGRC06811, (96) NGRC06822, (99) VI (Bhojpur), (106) NGRC06832, (108) NGRC06834, (116) NGRC08245, (136) SB0-122 and (139) F778817 were adaptable, 12 accessions {(17) 2003KS-TB1xKB-5.37, (18) 2003KS-TB1xKB-5.34, (24) Soy Agd-017, (25) Soy Agd-010, (26) Soy Agd-013, (59) Collection 168, (73) NGRC02704, (84) NGRC05101, (120) TGX1835-10F, (124) Tidar, (127) TGX1485-ID, (133) P194159 (2) 2003KS-TB1xKB-5.14-2, (5) 2003KS-TB1xKB-5.65 and (47) AGS 377 were stable and the only one that common in these two categories was (26) Soy Agd-013, which was adaptable and stable for trait grain yield. If the coefficient of regression (*bi*) is close to 1 we have adaptable genotypes (all genotypes in red color) and conversely, if the variability (*s*2 *di*) is near zero, we have stable genotypes (genotypes in blue color) and if the genotypes that are both adaptable and stable are represented green color. This indicates that these genotypes are least affected by the interaction effects, and are therefore the most stable. The most ideal accessions should exhibit a combination of high yield and stable performance across a range of production environments.

Which genotype performs where and mega environments with GGE bi-plot

One of the most attractive features of a GGE biplot is its ability to show the which-won-where pattern of a genotype by environment data set (**Figure 3**). Figure 3 indicated that accessions 86, 122, 107, 109, 48, 106, 114 and 83 were the vertex accessions which showed the highest yield in specific environments. Entry 86 (NGRC06811) lies near the equality line of Surkhet so it does better in that environment, entries 122 (200525 Rampur) and 109 (NGRC06835) performed better at Rampur and 48 (Seti), 106 (Sathiya) at Khumaltar. While entries 114 (NGRC08243) and 83 (Baglung black) were poor performers across all three locations for the trait grain yield. Other entries which lie near the equality line Khumaltar (47, 136, 16, 134), Surkhet (119, 117, 88, 95) and Rampur (111,62, 85, 149) which showed better performance in their respective environments (**Table 3 and Figure 3**).

Ranking accessions relative to the ideal genotype

An ideal genotype should have the highest mean performance and be absolutely stable (that is, performs the best in all environments). Such an ideal genotype is defined by having the greatest vector length of the high yielding accessions and with zero GEI, as represented by an arrow pointing to it (**Figure 4**). Thus, using the ideal genotype as the center, concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype. Entry numbers 107 (NGRC06833),109 (NGRC06835),118

(TGX1987-62F) and 122 {200525 (Rampur)} which fell into the center of concentric circles were the ideal genotype in terms of stability, compared with the rest of the accessions. In addition, entries 56 (NGRC02675), 141 (Kavre) and 131 (GC8234GC-13) are located on the next consecutive to concentric circle, may be regarded as desirable accessions in terms of higher yielding ability. While most undesirable, unstable and low grain yield than grand average entries are 83 (Baglung black), 93 (Collection #178), 38 (010-10.2) etc. (**Figure 4 and Table 3**).

AMMI biplot stability analysis

Genotypes or environments on right hand side of the vertical line had higher seed yield than those on the left side. Khumaltar environment on the right-hand side of the midpoint of the main effect axis seemed to be most favorable but Surkhet environment was identified to be relatively unfavorable as this position was farther from the left hand side of the midpoint axis whereas Rampur exhibited the position close to average seed yield and therefore, said to be average environment (**Figure 5).**

We can observe that the genotypes 122, 109, 107, and 118 had the biggest average yield across the environments (**Figure** 5). Entries 83, 38, 3, 103 etc were poor performer for grain yield as shown in opposite direction of environmental vector. The genotypes more stable and near of the origin were 36, 60, 150, 19. 120 (**Figure** 5). For the length of the vectors, the environments that classify the genotypes more effectively.

GGE biplot analysis based on mean vs. stability

The results showed that entries 86, 80, 95, 48, 106 etc are the most unstable and significant contributors to genotype by environment interaction (GEI). Genotype 118 is the most stable with a higher yield across the environments with low or no contribution to the genotype by environment interaction (GEI) but entry 131 has a similar grain yield but is unstable than 118 (**Figure 6**). Additionally, genotypes 38 and 83 are poor yielders but exhibited stable.

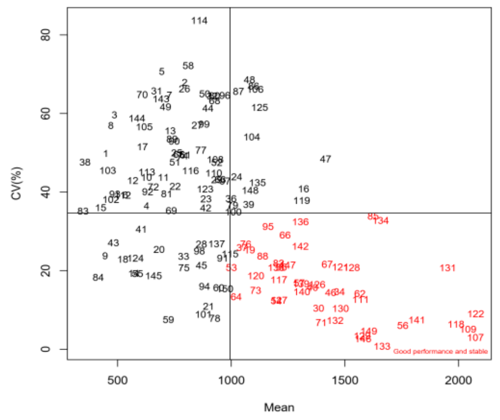

Figure 1 Stability and high yield soybean accessions based on Plot mean and CV over the years 2019-2020

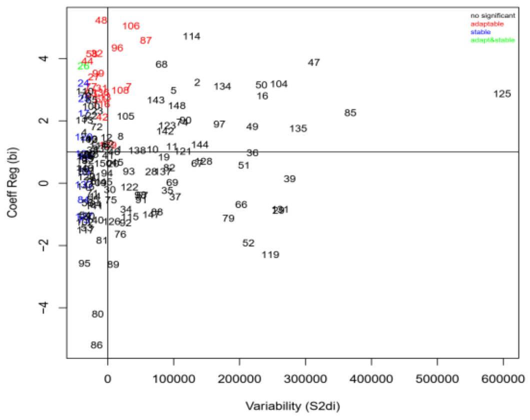

Figure 2. Adaptable, stable and stable-adaptable soybean accessions based on variability and regression coefficient over the years 2019-2020

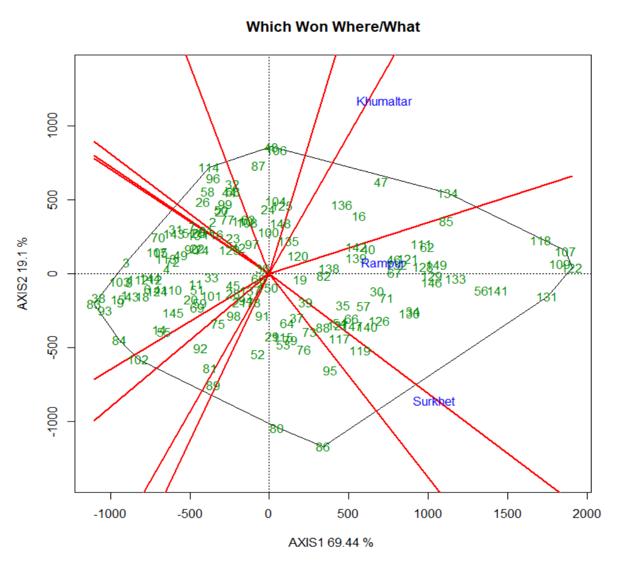

Figure 3. The which-won-where/what view of the GGE biplot for grain yield of 150 soybean genotypes

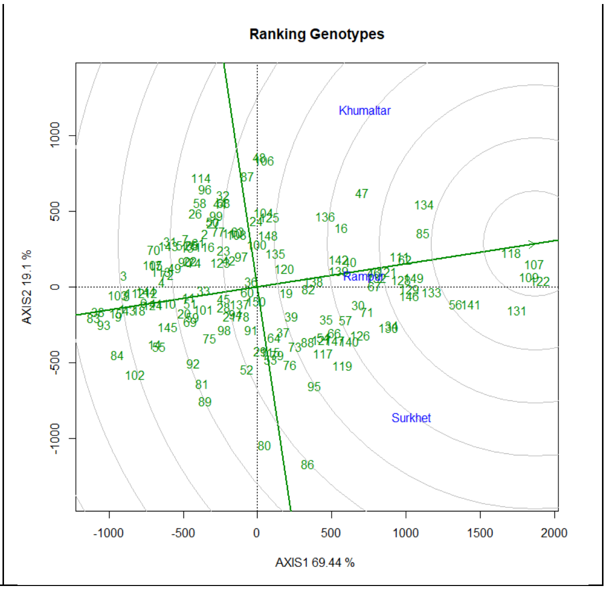

Figure 4. GGE biplot based on genotype-focused scaling for comparison of the genotype with ideal genotype over the years 2019-2020

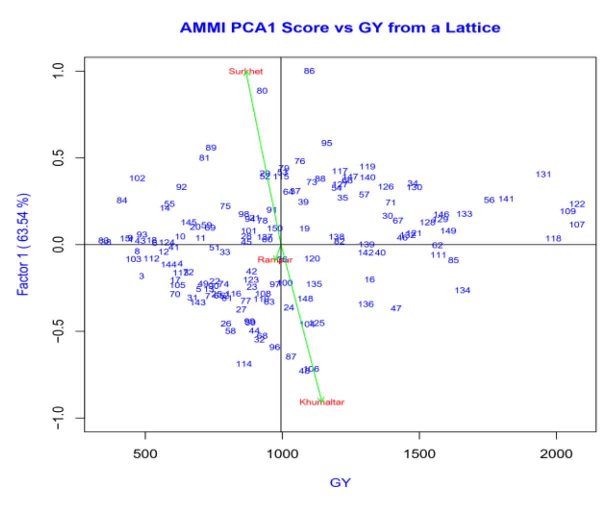

Figure 5. AMMI biplot stability analysis of grain yield across the environment over the year 2019 and 2020.

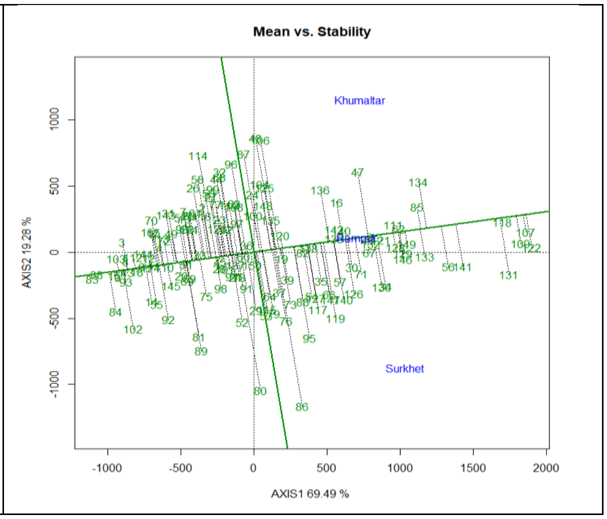

Figure 6. GGE biplot based on mean vs. stability.

DISCUSSIONS

Identifying the best-performing genotypes that were adapted at the particular location or stable genotypes for numerous locations (Yan 2011). Yan (2000) reported that the GGE biplot "Mean versus Stability" is a useful method for assessing genotypes in both dimensions. The measure of each genotype's instability is the length of its projections to the dotted lines on the average environmental axis (AEA), which approximates their contributions to the GxE interaction. Thus, in all test conditions, the genotype's yield stability decreases with increasing vector size as reported by Yan (2011 and 2000). Silva et al 2022 also reported similar findings for significant G*E interaction.

A popular multivariate method for METs (Multi Environmental Trials) of various agricultural crops, the GGE biplot analysis was created by Yan et al. in 2011 and 2020. It groups the genotype effect (G) with the multiplicative effect of the G x E interaction and subjects them to principal component (PC) analysis, which produces a variety of graphic configurations (biplots) that provide information about the genotype's performance and yield as well as identifying the formation of mega-environments, ranking superior and stable genotypes, and particular genotype combinations with environments (Yan, 2011 and Bosi et al., 2022. MET are conducted to assess the yield stability performance of genetic materials under different environmental conditions, (Delacy et al. 1996, Yan et al 2000, Yan and Rajcan, 2002). According to (Allard and Bradshow 1964) yield performances of a genotype cultivated in diverse settings often varied significantly. The term genotype-by-environment (GxE) interaction refers to these alterations that were impacted by the various environmental factors. Ceccarelli 1989 noted, GxE interaction must be either exploited by selecting superior genotype for each specific target environment or avoided by selecting widely adapted and stable genotype across wide range of environments. Many techniques have been used to analyze multi-environment trial data to disclose patterns of GxE interaction, including regression coefficient (Finlay and Wilkinson 1963), sum of squared deviations from regression (Eberhart and Russell 1966), stability variance (Shukla 1972), coefficient of determination (Pinthus 1973), coefficient of variability (Francis and Kanneberg 1978), and additive main effects and multiplicative interaction (AMMI) (Zobel et al. 1988). Another tool, called GGE-biplot, was suggested by Yan et al (2000) and has several advantages for the graphical display of the GxE interaction pattern of multi-environment trial data. Genotype by environment interaction (GxE) is visually represented in a two-way table through the use of GGE biplot analysis, which takes into account both genotype (G) and GxE effects (Yan et al. 2000).

Principal component analysis (PCA)-based GGE biplot is a useful tool for thoroughly examining the data from multi-environment trials. It makes possible to visually examine the connections between genotypes, test environments, and GxE interactions. According to Yan and Kang (2003) and Yan and Tinker (2006), it is a useful tool for the following purposes: (i) mega-environment analysis (e.g., "which-won-where" pattern), in which case particular genotypes can be suggested for particular mega-environments; (ii) genotype evaluation (the mean performance and stability); and (iii) environmental evaluation (the ability to discriminate among genotypes in target environments) and shows a two-way table of GxE interaction (Yan et al. 2000).

According to some research (Laffont et al. 2007, Yan and Kang 2003, Samonte et al. 2005), GGE biplot analysis is a helpful multi-location trial analysis method for the analysis of GE interactions. It has also been used to evaluate varieties of wheat (Yan and Hunt 2001, Yan et al. 2000), and soybean (Yan and Rajcan, 2002). Stability characteristics like regression coefficient (bi), and deviation from regression (S2di) of the accessions were evaluated following basic linear regression approach “LR model” (Finlay and Wilkinson 1963, Eberhart and Russell 1966).

CONCLUSION

In conclusion, we observed sufficient phenotypic diversity among the studied soybean accessions. Ideal and high yielder genotypes for grain yield included 122- 200525(Rampur), 107- (NGRC06833), 109–(NGRC06835) and 118 (TGX1987-62F), along with early genotypes 2003KS-KBxTB1-2.1-3, NGRC06826, 2003KS-TB1xKB-5.34, are suitable across the three environments can be used as donor parent or advanced yield trials. Furthermore, entries 86 (NGRC06811), {122 (200525 Rampur) and 109 (NGRC06835)} and {48 (Seti) and 106 (Sathiya)} lie near the equality line of Surkhet, Rampur and Khumaltar respectively so they do better for grain yield at respective specific environment. While entries 114 (NGRC08243) and 83 (Baglung black) are poor performer in all three locations for the trait grain yield. Among the genotypes Soy Agd-005, NGRC02679, Tarkari Bhatmas 1, Bringi, Pyuthan Bazar-2016, AGS 371 were identified as the most stable, and genotype Soy Agd-013 which was adaptable and stable for grain yield. This study offers insightful information for utilizing these germplasms in future crop improvement in Nepal.

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