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Genotypes × environment interaction for grain yield of finger millet under hilly region of Nepal

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ABSTRACT

Grain yield stability on new finger millet genotypes through G × E interaction analysis is an important task for finger millet breeding programs. Sixteen promising finger millet (*Eleusine coracana* (L.) Gaertn.) genotypes were evaluated in randomized complete block design replicated over two locations *viz*. Kabre, Dolakha; and Vijaynagar, Jumla, Nepal over three years (2017, 2018 and 2019). The stability parameters were computed for grain yield after Eberhart and Russell. The pooled analysis of variance revealed that the genotypes and genotype × environment (G × E) interaction were significant for grain yield. The genotypes KLE-559 produced the highest grain yield (3.32 t ha^{-1}). The genotypes namely KLE-559 (b = 1.15) and ACC#2843 (b = 1.12) had more than unity regression indicating the genotype's suitability towards favorable environments. GGE biplot showed genotype KLE-559 was stable genotype under tested environments. Thus, this genotype was recommended for release as variety to improve finger millet production in hilly environments of Nepal.

Keywords: Finger millet, *Eleusine coracana* (L.) Gaertn, G × E interaction, GGE biplot, yield parameters

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1 Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn. subsp. coracana) is fourth staple food crop after rice, maize and wheat in Nepal. It is nutritionally superior in comparison with rice, wheat and maize (Adhikari et al., 2018). It occupies an average of 7.9% (2,63,497 ha) of the total area covered by cereal crops and accounts for 3.3% (3,13,987 t) of total cereal production (MoLAD, 2019). The status of finger millet is now changing from neglected and underutilized crop to an emerging high potential crop for health food and functional food product with high value (Kandel and Shrestha, 2019). Identification and release of promising variety of finger millet is the most promising and deliverable technology for increasing productivity (Kandel et al., 2019; Dhami et al., 2018). Artificial hybridization and recombination breeding for varietal improvement in finger millet could not be taken up in a big way because of small floret size. Under this situation, agronomic as well as field selection is one of the alternative breeding methods which can be applied to enhance the genetic variation (Dhami et al., 2018). The information on genetic variation in the landraces, accession and genotypes is a must for breeding programs for crop improvement (Adeniji et al., 2008; Basafa and Taherian, 2009). Under the same management conditions, variation in grain yield is principally explained by the effects of genotype and environment (Dingkuhn et al., 2006). So information of genotype × environment interaction leads to successful evaluation of stable genotype, which could be used for general cultivation. The level of performance of any character is a result of the genotype (G) of the cultivar, the environment in which it is grown (E), and the interaction between G and E (GEI). Interaction between these two explanatory variables gives insight for identifying genotype suitable for specific environment. The environmental effect is typically a large contributor to total variation (Blanche et al., 2009). Moreover, G × E interactions greatly affect the phenotype of a variety, so the stability analysis is required to characterize the performance of varieties in different environments, to help plant breeders in selecting desirable varieties. The characters which recorded significant G × E were used for stability analysis of Eberhart and Russell (1966). A genotype with unit regression coefficient ($b_i = 1$) and deviation not significantly different from zero ($S^2d_i = 0$) was taken to be a stable genotype with unit response. GGE biplot analysis provides a framework for identifying target testing locations and discriminates genotypes that are high yielding and stable. The GGE biplot is constructed by plotting the first two principal components (PC1 and PC2) derived from singular value decomposition of the environment centered data (Shrestha, 2013). The objective of this research was to examine the GGE stability models in selection for grain yield and stability among finger millet genotypes for hilly region of Nepal.

2 Materials and Methods

2.1 Experimental Site and materials

The experiments were conducted at two different location namely kabre, Dolakha and Vijayanagar, Jumla during 2017, 2018 and 2019. The geographic coordinates for these sites are Kabre, Dolakha (27°39′59.99″N, 86°1′60″E, 1700 masl) and Bijayanagar, Jumla (29°16′28″N, 82°11′1″E, 2580 masl) (HCRP, 2018). Sixteen finger millet genotypes *viz.* KLE-178, ACC#2843, GE-0383, Farmer's variety (Local check variety), ACC#6022, GE-0382, NE-94, GE-0356, GE-0150, KLE-236, GE-0480, KLE-559, KLE-216, ACC#2827-1, Sailung kodo-1 (Standard check) and ACC#2211 were received from Hill Crops Research Program, Dolakha, Nepal for these experiments. The source of these finger millet genotypes was Nepal Agricultural Research Council, Hill Crops Research Program, Dolakha, Nepal. The origin of these genotypes was Nepal

2.2 Experimental procedures

The experiments were designed and managed by researchers. All the experiments were laid out in RCBD design with three replications with mono condition. Each set consisted of farmer's variety to compare the performance of tested genotypes. The plot size was 6 m^2. The space between row to row and plant to plant was 10 cm and 10 cm, respectively. Fertilizers was applied at the rate of 30:30:0 kg ha^{-1} N: P_2O_5: K_2O respectively (HCRP, 2018). Ten tons of farmyard manure per hectare was applied as before 20-30 days of sowing. Half dose of N and full doses of P and K were applied as basal dose and remaining half of N was applied as side dressing at the time of tillering growth stage. The plots were kept free of weeds manually.

2.3 Data collection and analysis

Data on growth traits, grain yield and yield attributing traits were recorded according to protocol adapted by HCRP (2018). Each plot was harvested excluding border rows and grain moisture content for each plot was recorded and grain yield was adjusted to 12% moisture basis. The grain yield per plot was converted into t ha^{-1} by using formula (HCRP, 2018).

$$Y_G = \frac{Y_p \times 10 \times (100 - HMP)}{(100 - HMP) \times NPA} \tag{1}$$

where, Y_G = Grain yield (t ha^{-1}), Y_p = Yield of plot (kg), HMP = Grain moisture percentage at harvest, DMP = Desired moisture percentage, i.e. 12%, NPA = Net harvest plot area (m^2). The significant G × E were used for stability analysis of Eberhart and Russell (1966). A genotype with unit regression coefficient ($bi = 1$) and deviation not significantly different from zero ($Sd^2i = 0$) was taken to be a stable genotype with unit response. As described by Eberhart and Russell (1966), the behavior of the cultivars was assessed by the model $Y_{ij} = m + b_i I_j + d_{ij} + \bar{e}_{ij}$, where Y_{ij} = observation of the i-th ($i = 1, 2, \ldots, g$) cultivar in the j-th ($j = 1, 2, \ldots, n$) environment, m = general mean, b_i = regression coefficient, I_j = environmental index obtained by the difference among the mean of each environment and the general mean the regression deviation of the i-th cultivar in the j-th environment and $\bar{e}_{ij}$ = residual error, d_{ij} = j - interaction of i-th genotype in the j-th environment.

Analysis of variance (ANOVA) was carried out on the data to assess the genotypic effects and mean comparisons among treatment means were estimated by the least significant difference (LSD) test at 5% levels of significance (Gomez and Gomez, 1984; Shrestha, 2019). The analysis of variance was performed using RCBD design to derive variance components derived using the software packages META-R developed by CIMMYT, Mexico. The stability analysis was done using GEAR software Version 4.1 (Pacheco et al., 2015).

3 Results and Discussion

3.1 Genotype × environment effects

The genotypes were highly significant for grain yield and number of plants per square meter. They were

Table 1. Combined Mean performance of finger millet genotypes in Dolakha and Jumla in 2017, 2018 and 2019

Genotypes	50% DTH	75% DTM	PH (cm)	NPS m^{-2}	FN H^{-1}	TGW (g)	GY (t ha^{-1})
KLE-178	118	156	88	56	7	4	2.95
ACC#2843	119	154	86	61	8	3	2.86
GE-0383	118	155	83	56	7	3	1.54
Farmer's variety	125	159	94	56	7	4	2.67
ACC#6022	116	155	91	64	8	3	2.44
GE-0382	121	155	89	62	7	3	2.58
NE-94	117	152	83	67	7	3	2.73
GE-0356	122	161	86	63	7	2	2.45
GE-0150	120	157	94	70	8	3	3.31
KLE-236	120	159	90	70	7	3	3.25
GE-0480	120	159	85	69	8	3	1.9
KLE-559	123	161	96	63	6	4	3.32
KLE216	113	156	83	74	7	4	2.31
ACC#2827-1	119	158	87	70	7	3	2.65
Sailung kodo-1†	125	161	89	68	8	3	2.52
ACC#2211	128	164	95	70	7	3	2.88
Grand Mean	120	158	89	65	7	3	2.65
CV(%)	2.19	2.02	7.55	7.65	12.86	10.96	14.26
LSD(0.05)	10.67	6.56	14.91	6.44	2.47	1.17	0.52
F-test (G)	ns	*	ns	**	ns	ns	**
G x E	**	**	ns	ns	**	**	**

† Standard check; **, * = Significant at 0.01 and 0.05 probability levels, respectively; ns= Non-significant, DTH = days to heading, DTM = Days to maturity, PH = Plant height, NPS = No. of plant stand, FN H^{-1} = Finger no. per head, TGW = Thousand grain weight, GY = Grain yield

Table 2. Grain yield performance of the finger millet genotypes in Dolakha and Jumla in 2017, 2018 and 2019

Genotypes	2017		2018		2019	
	Dolakha	Jumla	Dolakha	Jumla	Dolakha	Jumla
KLE-178	4.25	5.08	2.02	1.96	4.31	1.62
ACC#2843	3.25	5.443	2.1	1.91	3.1	1.75
GE-0383	2.46	1.767	1.26	1.22	2.81	0.89
Farmer's variety	2.67	5.903	1.89	1.34	3.25	1.61
ACC#6022	2.9	5.737	1.18	1.49	3.2	2.06
GE-0382	2.37	4.313	1.74	1.53	3.46	2.5
NE-94	2.08	5.02	1.5	1.83	3.97	1.63
GE-0356	3.23	6.807	1.86	2.03	4.4	2.23
GE-0150	3.15	5.35	0.87	1.3	4.24	1.1
KLE-236	2.09	6.293	1.88	2.59	4.51	2.81
GE-0480	1.98	3.917	0.87	1.03	3.26	1.08
KLE-559	2.11	5.473	2.59	2.52	4.2	2.17
KLE-216	1.99	4.373	1.1	1.3	3.34	1.87
ACC#2827-1	3	5.053	1.35	1.6	3.16	1.69
Sailung Kodo-1†	5.69	4.987	1.77	0.91	3.7	1.88
ACC#2211	4.82	6.383	2.26	0.9	3.8	1.72
Grand Mean	1.47	5.11	1.64	1.59	3.67	1.8
CV (LSD(0.05)	0.47	0.57	0.5	0.54	0.64	0.4
F test	*	*	*	*	*	*

† Standard check; * = Significant at 0.05 probability level; LSD = Least significant difference at 0.05 level; CV= Coefficient of variation

Table 3. Grain yield performance and stability parameters of finger millet genotypes in Jumla and Dolakha using Eberhart and Russell model in 2017, 2018 and 2019

Genotypes	Grand Mean (t ha^{-1})	Stability parameters				
		Sd	CV(%)	b_i	S^2d_i	R^2
KLE-178	2.95	0.6793	25.43	0.6081	0.3011**	0.7741
ACC#2843	2.86	0.0896	22.04	1.12	0.0902	0.9979
GE-0383	1.54	0.4916	26.77	0.0887	0.3598**	0.0315
Farmer's variety	2.67	0.6008	22.73	0.5842	-0.1356	0.9132
ACC#6022	2.44	1.4546	57.97	1.4798*	-0.107	0.9997
GE-0382	2.58	1.3453	38.93	1.3006	0.1935*	0.9028
NE-94	2.73	1.1145	56.19	1.0644	-0.1704	0.881
GE-0356	3.31	1.4897	51.1	1.448*	0.2184*	0.9637
GE-0150	2.45	1.6665	35.11	0.4327	-0.0673	0.4071
KLE-236	3.25	0.3852	29.1	1.3894*	1.7249**	0.8598
GE-0480	1.9	0.6217	35.51	0.4881	0.1224	0.5955
KLE-559	3.32	0.271	25.42	1.1522	0.0676	0.9275
KLE-216	2.31	1.2511	53.9	1.2673	0.0873	0.9911
ACC#2827-1	2.65	1.1318	53.36	1.1516	0.1081	0.9999
Sailung kodo-1†	2.52	1.1503	44.19	1.1408	0.162	0.9501
ACC#2211	2.88	1.319	64.38	1.3407*	0.2072*	0.9992
Grand Mean	2.65					

† Standard check; Sd = Standard deviation, CV= Coefficient of variation, b_i = regression coefficient R^2 = coefficient of determination (Eberhart and Russell, 1966), * = Significant at 0.05 probability level, ** = Significant at 0.01 probability level

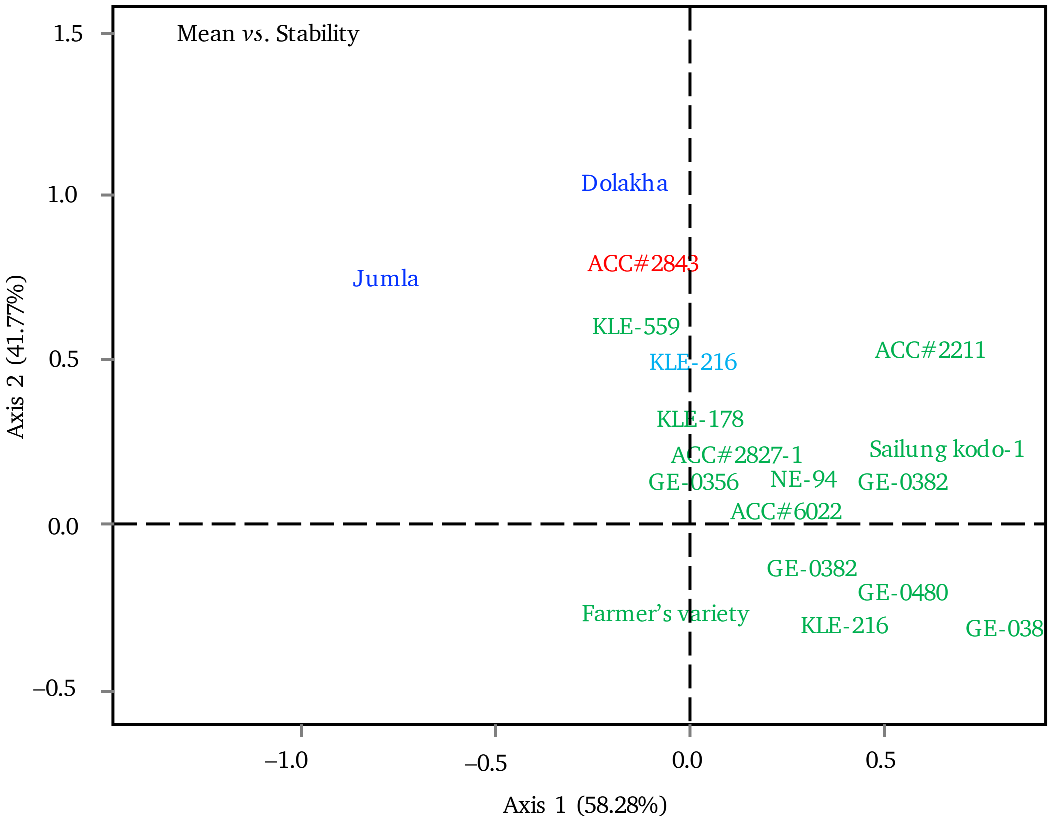

Figure 1. GGE biplot showing ranking of Finger millet genotypes for mean yield and stability

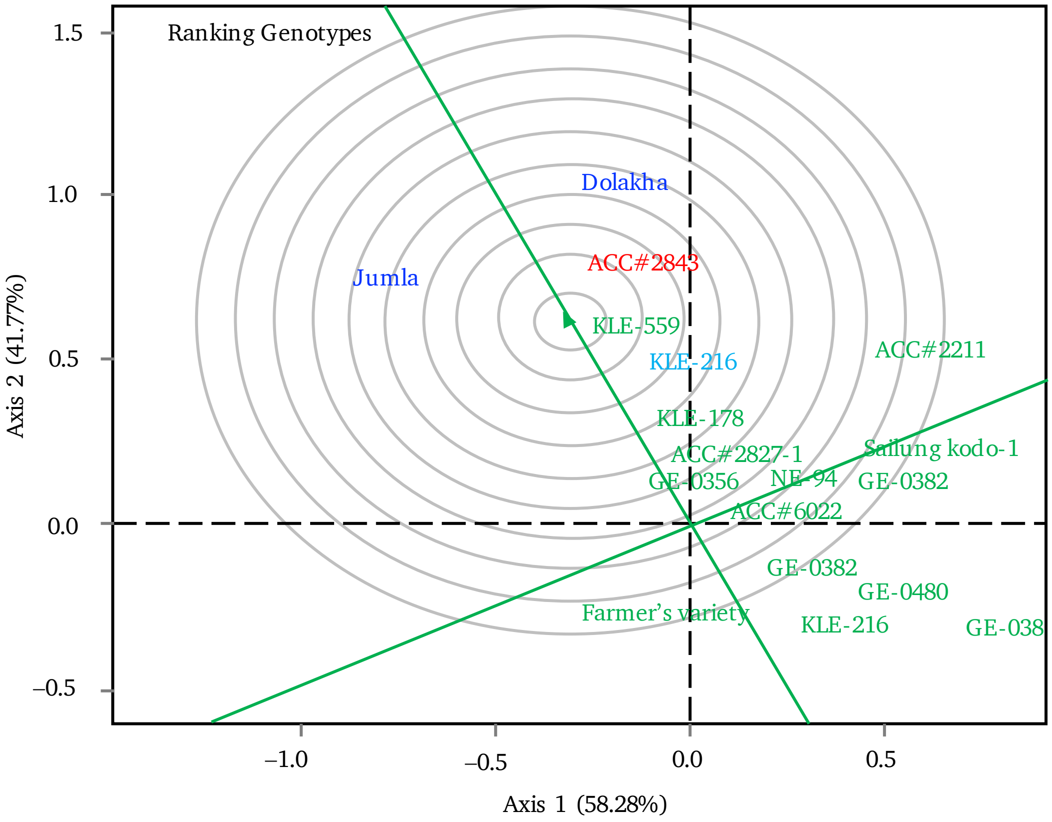

Figure 2. Comparison of finger millet genotypes with the ideal genotype

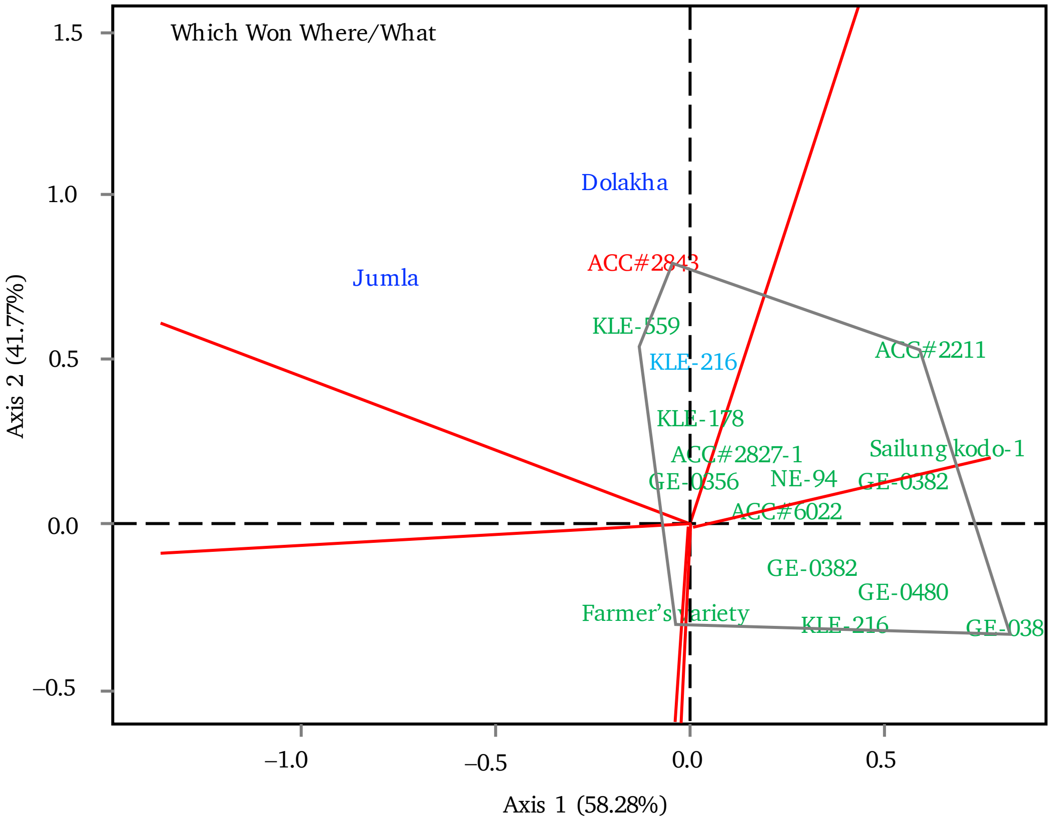

Figure 3. Polygon view of the GGE biplot based on grain yield for the environments

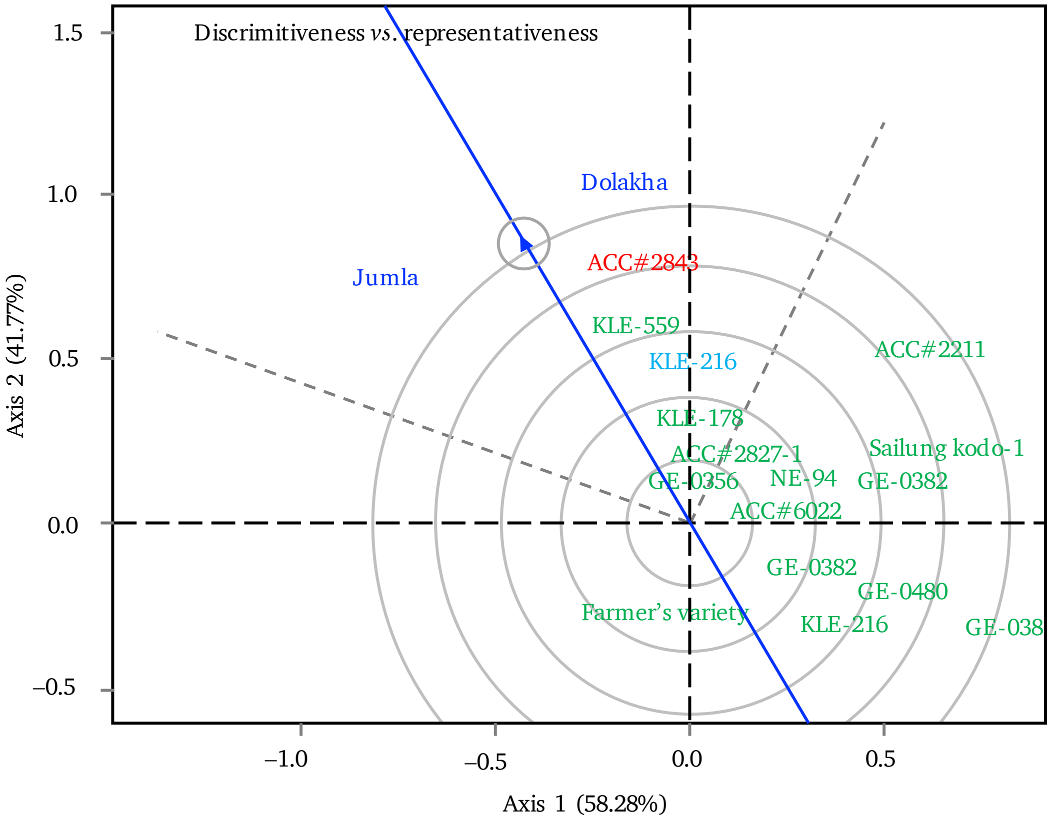

Figure 4. Biplot showing finger millet genotypes with respect to their environments

significant for days to maturity (75%) whereas genotypes were non significant for days to heading (50%). The genotype × environment interaction were highly significant for grain yield, thousand grain weight, finger number per head, days to heading (50%) and days to maturity (75%). G × E was non significant for plant height and no. of plant stands per square meter (Table 1). The mean grain yield of finger millet genotypes varied across the locations which could be due to different environmental conditions over years and locations. The environmental factors contributing differences in mean grain yield across two environment and three years may include soil types, sowing dates, sunshine hours and amount of rainfall, humidity during the crop cycle. The genotypes KLE-559 (3.32 t ha^{-1}), KLE-236 (3.25 t ha^{-1}), KLE-178 (2.95 t ha^{-1}), ACC#2311 (2.88 t ha^{-1}) and ACC#2843 (2.86 t ha^{-1}) produced the higher grain yield (Table 2). Dagnachew et al. (2014) and Jawale et al. (2017) who reported differences among finger millet varieties for grain yield. Thus significant variation in performance of finger millet genotypes in mid hill region of Nepal was observed across location and year (Dhami et al., 2018). Similarly the results were reported by Tsehaye and Kebebew (2002) who found the presence of genetic variability in yield and yield related traits of finger millet germplasm. In general, the regression coefficient values above 1.0 describes the genotypes with higher sensitivity to environmental change (below average stability) and greatly specify adaptability to high yielding environment (Wachira et al., 2002). In our study the genotypes ACC#2843, KLE-559 and KLE-236 were found stable and better adapted to Dolakha and Jumla environment of Nepal (Table 3). Similar results was also reported by Dhami et al. (2018).

3.2 Stability analysis

Stability in the yield performance is the major concern to the breeder and influenced mostly by genotype × environment interaction. An ideal genotype gives the highest yield across tested environment and is suitable in its performance. For broad selection, the ideal genotypes are those that have both high mean yield and high stability. An 'ideal' view was drawn (Fig. 1) that showed genotypes ACC#2843.KLE-559 and KLE-236 was the closest to the ideal genotype more desirable line. Fig. 2 showed that the genotype ACC#2843, KLE-559 and KLE-216 were most suitable than other genotypes because they are near to ideal genotype. This genotype consists of the smallest concentric ring indicating more stability. The GGE biplot (Fig. 3) represented a polygon indicating that the vertex genotypes were ACC#2843, ACC#2211, GE-0382 and Farmer's variety. The genotypes positioned on the vertexes had the longest distance from the biplot origin, they were supposed to be the most responsive either best or the poorest at one or every environment. The allocation of potential mega-environment was shown by 'which won where' graph. The lines perpendicular to the polygon separated the mega-environment. The genotypes ACC#2843, KLE-559 and KLE-216 were suitable for hilly region of Nepal.

Genotypes with high mean, b_i>1 with non-significant $\delta^2 d_i$ are considered as below average in stability. Such genotypes tend to respond favourably to better environments but give poor yield in unfavourable environments. Hence, they are suitable for favourable environments (Eberhart and Russell, 1966). The genotypes namely KLE-559 (b = 1.15), ACC#2843 (b = 1.12) and ACC#2827-1 (b = 1.1516) had more than unity regression indicating the genotype's suitability towards favorable environments (Table 2). In GGE biplot analysis the genotype closer to the performance line is considered more stable than the one placed farther from performance line. The genotypes more close to concentric circle indicates higher mean yield. An ideal genotype should have the highest mean performance and be absolutely stable (Yan and Kang, 2002). An ideal genotype, which is located at the center of the concentric circle is the one that has both high mean yield and high stability (Yan and Kang, 2002). Therefore the results showed that genotype KLE-559 was stable (Fig. 2). Similar findings were reported in buckwheat by Kandel et al. (2019).

4 Conclusions

The performance and yield stability across different environments varied among finger millet genotypes. Based on results, finger millet genotypes namely KLE-559 and ACC#2843 gave higher grain yield and showed adaptability under favorable environments. The genotype KLE-559 was found stable genotype. Thus, this genotype was recommended for possible release for wider adaptability across Jumla and Dolakha and other areas with similar agro-ecology in the country.

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Conflict of Interest

The authors declare that there is no conflict of interests regarding the publication of this paper.

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