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RESEARCH ARTICLE

Stability analysis of finger millet genotypes under the hilly regions of Nepal

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Abstract

The aim of this study was to identify stable and high yielding genotypes under various environments and years in different hilly regions of Nepal. Five finger millet genotypes along with farmer's variety (Local check) were tested under command areas of five different stations namely, Hill Crops Research Program (HCRP), Dolakha, National Ginger Research Program (NGRP), Salyan, Agricultural Research Station (ARS), Dailekh, ARS, Surkhet and Regional Agricultural Research Station (RARS), Kaski during 2016 and 2017 winter season under rainfed condition. The experiment was conducted using Randomized Complete Block Design with two replications under farmer's field condition. The genotype x environment (GxE) interaction for grain yield was significant. The genotypes KLE-236 (2.37 t/ha), KLE-158 (2.32 t/ha) and DR-2 (2.02 t/ha) were found higher sensitive to environment and produced the higher mean grain yield across the locations. Joint regression analysis showed that genotypes KLE-236, KLE-158 and DR-2 with regression coefficient of 1.15, 1.17 and 1.12 respectively. The coefficient of determination (R^2) for genotypes, KLE-236, KLE-158 and DR-2 were high as 0.6, confirming their high predictability for the stability across the different locations. Further confirmation from GGE biplot analysis showed that stable genotype KLE-236, KLE-158 and DR-2 were more stable and adaptive genotypes across the tested environments of Dailekh, Surkhet, Salyan and Dolakha respectively. Thus these genotypes could be recommended to farmers for general cultivation across the tested environments.

Key words: Finger millet, G × E interaction, GGE biplot, yield stability

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn) (2n=4x=36) is one of the most important small grain cereals in traditional low input cereal-based farming system (Wolie and Dessalegn, 2011). It ranks 4th in the world among mostly grown cereals after the sorghum, pearl millet and foxtail millet. Finger millet (kodo) is the 4th most important crop of Nepal after rice, maize and wheat in terms of area and production. It occupies an average of 7.9% (26,6799 ha) of the total area covered by cereal crops and accounts for 3.3% (30,2397 t) of total cereal production (MoAD 2015/016).

It is an annual hardy cereal crop grown in the tropical, subtropical areas of world. Nepal is rich in finger millet genotypes, grown upto 3150 m (Upreti, 1999). About 790 accessions have been collected from various parts of Nepal (Gupta *et al.*, 2000) and large diversity within *Eleusine coracana*, two wild species-E. indica and *E. aegyptica* was found (Upadhyay and Joshi, 2003). Finger millet is highly nutritious as its grain contains 65-75% carbohydrate, 5-8% protein, 15-20% dietary fibre and 2.5-3.5% minerals (Chetan and Malleshi, 2007). It helps in alleviating the problems associated with malnutrition and anemia in countries where it is widely consumed as a staple food (Babu *et al.*, 2006). Even though, the continuous breeding program of finger millet is lacking (Dida *et al.*, 2008). But now days because of its health benefits, the crop is now receiving more attention from agronomists and plant breeders. 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. 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).

Evaluation of genotypes for their stability for yield under different environments is an important task in plant breeding programs. The presence of a high genotype x environment (GE) interaction represents a significant problem of related to phenotypic expression of genetic base and makes difficult for decision making in selection. High yield stability usually refers to a genotype ability to perform consistently, whether at high or low yield levels across a wide range of environments. 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. The information on stability of finger millet genotypes across location in Nepal is lacking so the present study was carried out to identify high yielding with widely stable finger millet genotypes across the environments of Nepal.

Material and methods

The experiments were conducted at five different location namely Hill Crop Research Program Dolakha, Regional Agricultural Research Station, Kaski, National Ginger Research Program, Salyan, Agricultural Research Station, Surkhet and Agricultural Research Station, Dailekh during winter season of 2016 and 2017. It was consisted up five genotypes name as KLE-158, KLE-236, GE-0116, DR-2 and local variety. The experiments were designed by researchers and managed by farmers. All the experiments were laid out in RCBD design with two replications. 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 and 10 cm respectively. Seeding was done continuously manually and seed rate was 10 kg/ha. Fertilizers was applied at the rate of 30:30:0 kg/ha N: P_2O_5: K_2O respectively (MoAD 2016/17). 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. Data on grain yield was recorded from net harvested area. 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 ton/ha by using formula (HCRP, 2015/16). To determine stability and identify superior genotypes across environments, genotype, and genotype × Environment (GGE) bi-plot analysis was done using R-analysis. Regression analysis was performed to determine stability and to identify superior genotypes across environments on the basis of regression coefficient.

Grain yield (t/ha) =Yield of plot (kg)×10× (100-Grain moisture %) / Net harvested area (m^2) × (100-12). The experimental data were processed by using Excel 2010 and analyzed by using Gen Stat 17. The treatment means were compared by the Least Significant Difference (LSD) test at 5% level (Gomez and Gomez, 1984; Baral *et al.*, 2016).

Results and discussion

The mean grain yield of finger millet genotypes differed across environments which could be due to different environmental conditions over years and locations. The locations themselves differ greatly in altitude, temperature and rainfall variation that affects performance. The findings of the study showed that on basis of average across locations and years, the genotype KLE-236 (2.35 t/ha) and KLE-158 (2.22 t/ha) produced the highest grain yield followed by DR-2 (1.91 t/ha) and GE-0116 (1.72 t/ha) (Table 1). Similar result was obtained by Dagnachew *et al.,* (2014) and Jawale *et al.,* (2017), who reported differences among finger millet varieties for grain yield. The pooled analysis of variance for grain yield (Table 2) showed that genotypic variation was highly significant for environments, however the genotype and environment interaction was found non-significant.

The environmental factors contributing differences in mean grain yield across five environments and two years may include soil types, sowing dates, sunshine hours and amount of rainfall, humidity during the crop cycle. Regression values above 1.0 describe genotypes with higher sensitivity to environmental change (below average stability) and greatly specify adaptability to high yielding environments. A regression coefficient below 1.0 provides a measurement of greater resistance to environmental change (above average stability), which increases the specificity to adaptability to low yielding environments (Wachira *et al.*, 2002). Thus genotypes KLE-236, KLE-158, DR-2 and GE-0116 were found better specific adapted to low yielding environment and local check were greater resistance to environmental change (Table3). The genotypes namely; KLE-236 (b=1.15, CV=31.1%), KLE-158 (b=1.17, CV=28.7%) followed by DR-2 (b=1.12, CV=33.33%), and their grain yield was above the grand mean yield and theses genotypes were found stable to specific location (Table 3). An ideal genotype should have the highest mean performance and be absolutely stable (Yan and Kang, 2003). AMMI analysis (Zobel *et al.*, 1988) gives estimate of total G×E interaction effect of each genotype and also further partitions it into interaction effects due to individual environments. Low G×E interaction of a genotype indicates stability of the genotype over the range of environments. In GGE biplot analysis genotype, KLE-236 for Dailekh, Surkhet, KLE-158 for Salyan, DR-2 and GE-0116 for Dolakha were most stable and high yielding (Fig1).

In conclusion we have identified the most stable region specific high yielding genotypes which may prove worthy in the finger millet breeding programme of hilly regions of Nepal. Also the identified promising regions specific high yielding genotypes could be released to farmers for general cultivation.

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Table 1: Mean grain yield (t/ha) of finger millet genotypes evaluated at five environments during 2016 and 2017

S.No.	Genotypes	Dolakha		Lumle		Dailekh		Surkhet		Salyan		Grand mean
		2016/17	2017/18	2016/17	2017/18	2016/17	2017/18	2016/17	2017/18	2016/17	2017/18	
1	**KLE-236**	2.36	1.37	3.85	2.91	3.52	2.32	1.12	2.18	1.86	1.99	2.35
2	**KLE-158**	2.94	1.19	3.46	2.47	1.47	2.67	1.00	1.57	3.48	1.99	2.22
3	**GE-0116**	3.25	1.28	1.87	1.67	1.46	2.03	1.00	1.15	2.28	1.21	1.72
4	**DR-2**	3.12	1.36	2.21	2.34	2.29	2.25	1.16	1.86	1.05	1.49	1.91
5	**Check ©**	1.29	1.04	1.72	1.49	1.36	1.06	0.99	1.00	1.05	1.14	1.21
	GM	2.59	1.25	2.62	2.18	2.02	2.07	1.06	1.56	1.94	1.57	
	LSD 0.05	1.39	0.18	0.28	0.56	0.17	0.06	0.1	0.11	0.17	0.05	
	CV (%)	19.31	5.27	3.81	9.29	3.07	1.02	3.26	2.62	3.06	1.19	
	P-value	0.07	0.032	0	0	0	0	0.02	0	0	0	

Table 2: Combined analysis at five environments during 2016 and 2017

Source	Df	SS	MSS	F-value	Pr(>F)
Environment	4	15.989	3.9973	7.2866	5.7E05***
Genotypes	4	15.897	3.9743	7.2446	6.1E05***
Replication	5	0.671	0.1342	0.2446	0.9412
G×E	16	12.974	0.8109	1.4781	0.1331^{ns}
Residuals	70	38.401	0.5486		

****Significant at p<0.001, ns= non significant*

Table 3: Combined mean grain yield (t/ha) in farmer's field trials at five locations during 2016 and 2017

S.No.	Genotypes	Grain yield	Range	Std	CV(%)	R^2	bi
1	**KLE-236**	2.37^{a}	1.12-3.95	0.85	31.1	0.67	1.15
2	**KLE-158**	2.32^{a}	1-4.44	1.03	28.7	0.62	1.17
3	**DR-2**	2.02^{ab}	1-4.75	0.91	30.8	0.65	1.12
4	**GE-0116**	1.82^{b}	0.99-4.75	0.93	33.6	0.56	1.01
5	**Check ©**	1.27^{c}	0.989-1.79	0.25	20	0.87	0.54
	GM	1.96					
	LSD$_{0.05}$	0.46					
	CV(%)	37.68					
	P-value	0.00***					

Means showing different letters in a column differed significantly by DMRT at 5% level of significance.
***Significant at p<0.001

Fig 1: Mean versus stability pattern and ranking of tested genotypes at five locations (each location had two different environments)

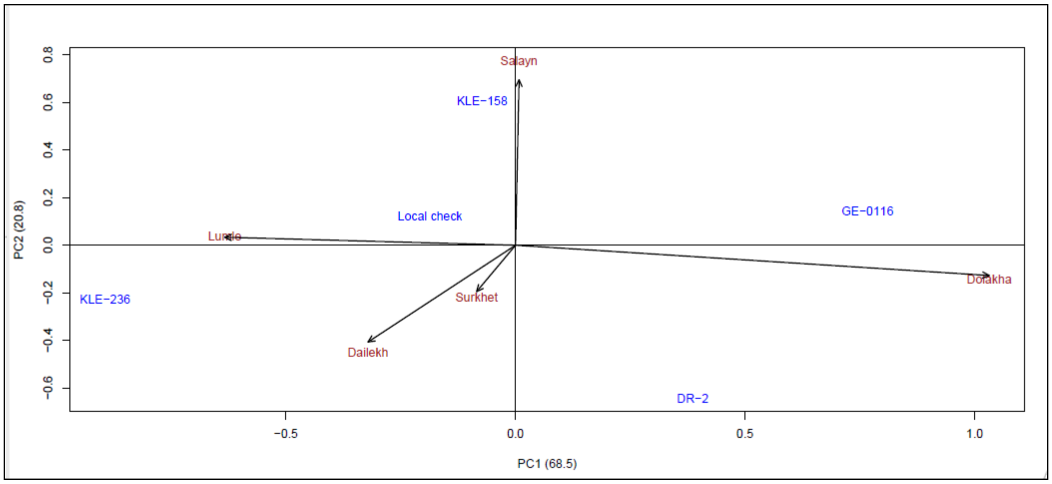

Fig 2: Mean versus coefficient of variation pattern and ranking of genotypes for grain yield at five locations (each location had two different environments)