Evaluation of Turmeric (*Curcuma longa* L.) Genotypes for Growth and Yield Attributes in Plains of Eastern Nepal

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ABSTRACT

An experiment was conducted in order to identify the productive genotype of turmeric for the plains of Nepal. In 2017 and 2018, seven promising turmeric genotypes (CI 0207, CI 0205, CI 9102, CI 1312, CI 0503, CI 0507, and CI 0201) were compared with KKH-1 in a Randomized Complete Block Design with four replications at the Directorate of Agricultural Research, Tarahara, Nepal. The plants were 30 cm x 30 cm apart, with 40 plants per 3.6 m^2 plot area. Cultural practices were followed in accordance with the recommendations. Analysis of variance, correlation, cluster, and GGEbiplot analysis were performed on the observed data. From the pooled analysis of two years of data, the results showed significant differences in plant height and fresh rhizome yield among genotypes. The rhizome yield of KKH-1 was found significantly higher (19.36 t ha^{-1}) than CI 0205 and CI 9102 and at par with other genotypes. Weight of mother rhizome had significant positive correlation (r = 0.602**) with yield of fresh rhizome. Though KKH-1 yielded the highest fresh rhizome, the cluster and GGEbiplot analysis identified CI0207 as one of the potential turmeric clones next to KKH-1.

Keywords: Biplot, cluster, correlation, genotypes, turmeric

1. INTRODUCTION

Turmeric (*Curcuma longa* L.) is one of the important spice crops among the five major spice crops (ginger, garlic, dry chili, and turmeric) of Nepal [1]. It has covered a wide range of ecological regions of Nepal from east to west and inner terai, foot hills to mid-hills up to an altitude of 1600 masl. It requires less care and management and is generally grown both as sole crop and inter-cropping in fruit orchards or in agro-forestry plantations on marginal land. In

Nepal, it is grown on 10,160 hectares in the country and yield was reported 98,904 tonnes with a productivity of 9.73 t ha^{-1} [2]. Turmeric thrives well in those areas, where ginger grows successfully but its cultivation area is less than ginger. Therefore, turmeric is annually imported in contrast to the export of ginger. In 2020, 537.10 tonnes of fresh turmeric with a value of NRs. 68,912,239 were imported [3]. It signifies the importance of this crop in Nepal which has got less priority in research.

Selection of highly productive genotypes is the major thrust of turmeric research in Nepal. The National Ginger Research Program also conducts research on turmeric, especially focuses on varietal improvement, soil and crop management, disease and pest management, post-harvest handling, storage, value chain addition and processing aspects [4]. The development of new varieties with superior characteristics, i.e., high yielding, increased disease and insect pest resistance, and high curcumin content, is the need of the hour [5]. This effort made it possible to release a variety Kapurkot Haledo-1 (KKH-1) in Nepal which has a curcumin content of 4.89 percent and aromatic oils of 6.65 percent [6]. However, the information on varieties suitable for the eastern plains is scanty and very little systematic efforts have been made to evaluate the improved turmeric cultivars for their suitability to this region. The work should be concentrated on the introduction of new high yielding genotypes of turmeric in this region [7; 8]. Hence, the current research was carried out to find a suitable genotype(s) as an alternative to released or local turmeric cultivar.

2. MATERIALS and METHODS

2.1 Site description

This research was conducted at Directorate of Agricultural Research, Tarahara which lies in the eastern part of Nepal. It is situated at 26º42'16.85" N latitude and 87º16'38.43" E longitude at an elevation of 136 amsl. The climate is sub-tropical with clay loam soil which is slightly acidic (pH of 6.5).

2.2 Experimental design and data analysis

This experiment was set to compare seven promising turmeric genotypes (CI 0207, CI 0205, CI 9102, CI 1312, CI 0503, CI 0507 and CI 0201) with the released variety (KKH-1) for two consecutive years in 2017 and 2018. The experiment was laid out in a randomized complete block design (RCBD) with the plant spacing of 30 x 30 cm between and within the row. Individual plot size was 3.6 m^2 (3 m × 1.2 m). Crop was planted in mid-April both the years. Manure and fertilizers were applied @ 30 t ha^{-1} and NPK 30:30:60 kg ha^{-1}, respectively. Total amount of farm yard manure and, half dose of N, full dose of P_2O_5 and half of K_2O were applied as basal dose. The remaining half dose of N was applied in two split doses at 30 and 60 days after emergence and remaining half dose of K_2O was applied at 60 days after emergence [5]. Mulching was done with dry forest leaves immediately after planting. Weeding was done two times during crop season. During crop period, data on crop stand, tillers per clump, plant height, finger length of mother and fresh rhizome, number of mother and fresh rhizome per plot were recorded. In both the years, crop was harvested in November and the rhizome yield was recorded. RStatudio software was used for data analysis (packages used viz. hclust, GGEBiplots, agricolae, variability) and treatment means were compared by Duncan's Multiple Range Test (DMRT) at a 5% level of significance.

3. RESULTS

3.1 Morphological characters

Most of the morphological parameters did not vary among the tested genotypes, however, plant height differed significantly (Table 1). The highest number of leaves per shoot was recorded in CI 0205 (8.90) and the lowest in CI0503 (7.07). KKH-1 was the tallest (64.93 cm) genotype followed by CI 1312 (60.03 cm) and the shortest was CI 0210 (48.80 cm). Likewise, the highest number of tillers per clump (2.43) was observed in CI 0205 and CI 0207, though they were non-significant with the others.

Table 1. Morphological characters of turmeric genotypes at DoAR, Tarahara in 2018 and 2019

Genotypes	Plant Population	Number of leaves/shoot	Plant height (cm)	Number of tillers/clump
CI 0207	34.33	7.97	57.57a-d	2.43
KKH-1	36.50	7.83	64.93a	2.40
CI 0205	33.83	8.90	59.20abc	2.43
CI 9102	31.67	7.10	50.10cd	2.27
CI 1312	35.33	7.77	60.03ab	2.13
CI 0503	34.33	7.07	57.03a-d	2.27
CI 0507	32.00	7.47	52.30bcd	2.17
CI 0210	34.17	7.43	48.80d	2.17
Mean	34.02	7.69	56.24	2.28
F-test	NS	NS	**	NS
LSD (<0.05)	-	-	8.61	-

*Values in a column with different letter(s) are significantly different at 0.05 level of significance by DMRT. Significance level for ANOVA: **P ≤ 0.01, and NS = non-significant.*

3.2 Rhizome and yield attributing characters

The major rhizome yield attributing characters were observed non-significant, however, fresh rhizome yield differed among the tested genotypes (Table 2). Out of 40 rhizome planted, higher number of mother rhizome recovered from CI 0207 and CI 0503 (14.83) followed by CI 0210 (13.00) and the lowest number of mother rhizome (10.00) obtained from CI 0507 and CI 9102. The highest number of fresh rhizome per plot (50.33) was obtained from KKH-1 followed by CI 0207 (49.83). The average finger length of fresh rhizome (8.03 cm) was higher than average of finger length of mother rhizome (6.31 cm). Though not significant, fresh rhizome of CI 0205 had longest finger (8.64 cm) followed by KKH-1 (8.38 cm). The CI 0507 genotype had highest mother rhizome yield per plant (11.59 g) and fresh rhizome yield per plant (197.63 g). On hectare basis, CI 0507 yielded highest mother rhizome (1.00 t ha^{-1}) followed by KKH-1 (0.98 t ha^{-1}). Similarly, KKH-1 yielded significantly higher fresh rhizome yield (19.36 t ha^{-1}) than CI 0205 and CI 9102 genotypes and at par with remaining genotypes.

Table 2. Rhizome and yield characteristics of turmeric genotypes at DoAR, Tarahara in 2018 and 2019

Genotypes	**Finger length of MR**	**Finger length of FR**	**Number of MRP**	**Number of FRP**	**MRYP (g)**	**FRYP (g)**	**MYRRH (t ha^{-1})**	**FRYH (t ha^{-1})**
CI 0207	6.48	8.28	14.83	49.83	10.22	175.72	0.93	16.79ab
KKH-1	6.50	8.38	11.83	50.33	9.59	189.84	0.98	19.36a
CI 0205	6.00	8.64	11.00	48.83	6.29	148.43	0.59	13.85b
CI 9102	6.18	7.90	10.00	45.17	7.11	155.94	0.63	14.07b
CI 1312	6.11	7.78	10.50	46.33	6.13	165.73	0.60	16.27ab
CI 0503	6.52	7.73	14.83	45.50	8.72	167.25	0.84	16.18ab
CI 0507	6.61	7.27	10.00	42.83	11.59	197.63	1.00	17.43ab
CI 0210	6.12	8.28	13.00	48.83	10.29	180.01	0.97	17.24ab
Mean	6.31	8.03	12.00	47.42	9.3	172.91	0.81	16.39
F-test	NS	NS	NS	NS	NS	NS	NS	*
LSD (<0.05)	-	-	-	-	-	-	-	4.59

*Values in a column with different letter(s) are significantly different at 0.05 level of significance by DMRT. Significance level for ANOVA: *P ≤ 0.05and NS = non-significant, MRP = Mother rhizome per plot, FRP = Fresh Rhizome per plot, MRYP = Mother rhizome yield per plant, FRYP = Fresh rhizome yield per plant, MRYH = Mother rhizome yield per hectare, FRYH = Fresh rhizome yield per hectare.*

3.3 Correlation between traits

All the observed traits have positive correlation with fresh rhizome yield (t ha^{-1}) (Table 3). Both the mother and fresh rhizome yield per plant had positive significant correlation with fresh rhizome yield on hectare basis. The morphological and rhizome characters had positive but non-significant relationship with the fresh rhizome yield. Tiller per plant had positive significant correlation with finger length of fresh rhizome, however, length of the mother rhizome had negative correlation with the finger length of fresh rhizome.

Table 3: Correlation between morphological and rhizome yield characters of turmeric at DoAR, Tarahara, Nepal in 2017 and 2018

	PH	TL	MRP	FRP	LMR	LFR	MRYH	FRYH	MRYP	FRYP

NL	0.584 **	0.210 NS	-0.220 NS	0.177 NS	-0.162 NS	0.23 NS	-0.158 NS	0.0281 NS	-0.1951 NS	-0.067 NS
PH		0.171 NS	-0.108 NS	0.220 NS	0.135 NS	0.163 NS	-0.026 NS	0.2048 NS	-0.1104 NS	0.014 NS
TL			0.148 NS	0.312 NS	-0.531 **	0.614 **	-0.100 NS	0.0356 NS	-0.0934 NS	-0.031 NS
MRP				0.367 NS	0.238 NS	0.371 NS	0.629 **	0.2062 NS	0.5937 **	0.206 NS
FRP					-0.018 NS	0.541 **	0.229 NS	0.3335 NS	0.0842 NS	0.069 NS
LMR						-0.305 NS	0.422 *	0.196 NS	0.4335 *	0.2823NS
LFR							0.081 NS	0.1234 NS	0.0342 NS	0.022 NS
MRYH								0.5285 **	0.9901 **	0.592 **
FRYH									0.4535 *	0.915 **
MRYP										0.602 **

*Significance level for correlations: * $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$, NL = number of leaves per shoot, PH = plant height, TL = number of tillers per plant, MRP = mother rhizome per plant, FRP = Fresh Rhizome per plant, LMR = finger length of mother rhizome, LFR = finger length of fresh rhizome, MRYH = Mother rhizome yield per hectare, FRYH = Fresh rhizome yield per hectare, MRYP = Mother rhizome yield per plant, FRYP = Fresh rhizome yield per plant.*

3.4 Clustering of genotypes

Based on the results of the cluster analysis, the eight different turmeric genotypes were divided into two groups (Figure 1). The first cluster (left to right in Figure 1) comprised of genotypes viz. CI 0507, CI 0503, CI 0210, CI 9102, CI 1312 and the genotypes CI 0205, CI 0207 and KKH-1 grouped in the second cluster. Morphological characters (number of leaves, plant height, and number of tillers) and rhizome character (finger length of fresh rhizome) were similar among the genotypes of the second cluster. Among the genotypes, similarity between CI 0207 and KKH-1 and differences between CI 0205 and CI 0507 was high.

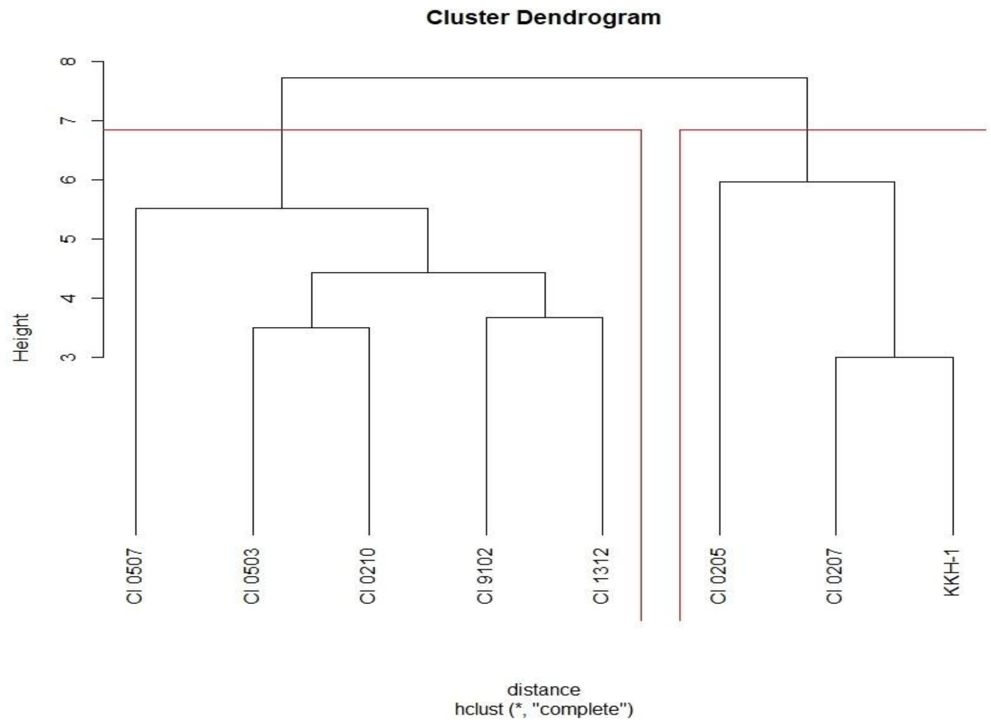
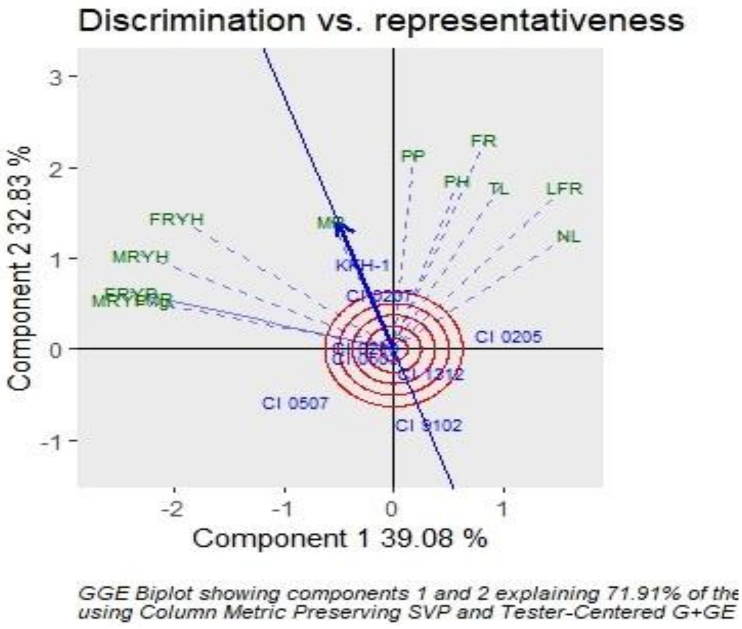


Figure 1. Turmeric genotypes clustering based on plant and rhizome characteristics

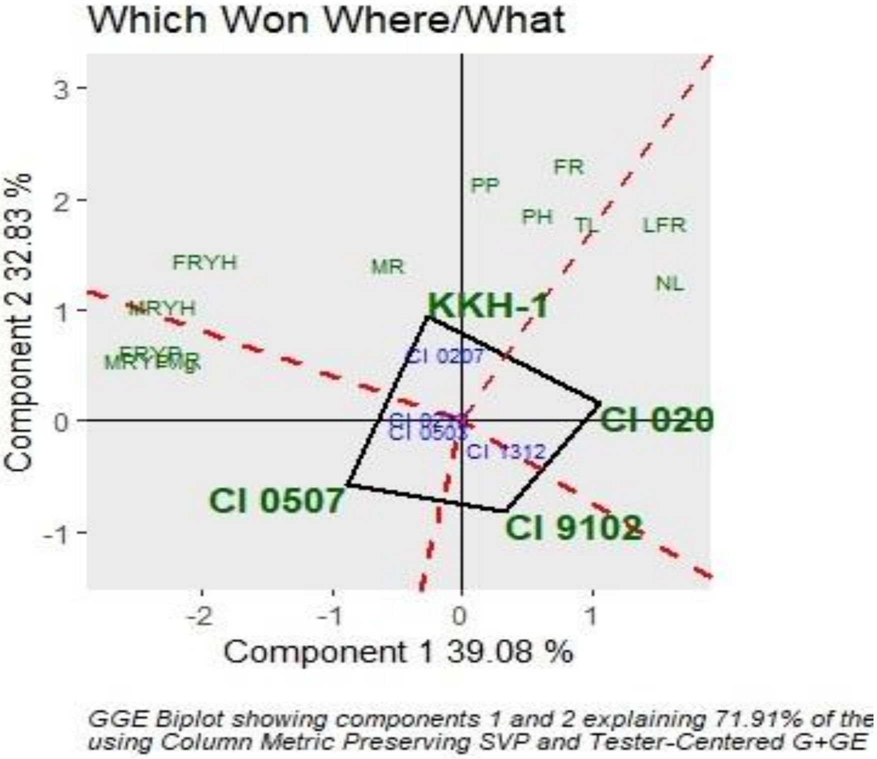
3.5 GGE Biplot for genotype-by-trait relationship

GGE biplot analysis was done with aim to find out informative traits to help in selecting turmeric genotypes. The two principal components (PC1 and PC2) explained 71.91% of total variation with share of 39.08% and 32.83% of total variations by PC1 and PC2. This figure represents the moderate degree of complexity of the relationship among the attributes that are being measured. Average Environment Axis (AEA, an arrow in Figure 2) passes through the observed traits and genotypes KKH-1 and CI 0207 lie on the AEA. All the observed traits appeared in the first and second quadrant. Yield of fresh rhizome (FRYH) was observed more close to KKH-1 and CI 0207 and other genotypes were observed too far from this trait. GGE biplot polygon view as depicted in Figure 3 aids in the identification of genotypes with the highest values for one or more characteristics. Among the genotypes, KKH-1, CI 0507, CI9102, CI 0205 are in the vertex of polygon. Genotypes CI0207, CI1312, CI0503 and CI0210 were located inside the polygon. Out of these genotypes, CI0503 and CI1213 were even below the origin of polygon. Moreover, traits like number of mother and fresh rhizome per plot, plant population, plant height, number of tiller per plant and fresh rhizome yield per hectare were located around the vertex genotype KKH-1. Among the vertex genotypes, KKH-1, CI 0507, CI9102, CI 0205 are also grouped in the second group in cluster analysis (Figure 1). Here, all the observed traits are located in the sector of the polygon where KKH-1 (vertex genotype) is present.



GGE Biplot showing components 1 and 2 explaining 71.91% of the
using Column Metric Preserving SVP and Tester-Centered G+GE

Figure 2. The GGE biplot to show the discriminating ability and representativeness of the traits with turmeric genotypes.



GGE Biplot showing components 1 and 2 explaining 71.91% of the
using Column Metric Preserving SVP and Tester-Centered G+GE

Figure 3. The “which-won-where” view of the GGE biplot based on the interactions of genotypes and observed characteristics showing the which turmeric genotype won the contribution of which characteristic

4. DISCUSSION

Turmeric genotypes did not differ significantly for most of the morphological and rhizome characters, however, significant difference were recorded for plant height and fresh rhizome productivity. The analysis of the observed traits showed that tested genotypes (clonal propagation) had minimum phenotypic variation. They might have genetic diversity which was not carried out under this study. However, the recorded differences in some traits could be attributed to genetic make-up of the genotypes and the effect of growing environment. However, Ahamad et al [9] observed significant differences among eight turmeric genotypes for tiller per plant (2.30-3.00), plant height (25.70- 44.9 cm), number of leaves per clump (4.5-5.7) and fresh rhizome yield (14.20-20.70 t ha^{-1}). The difference between these two studies could be attributed to different genotypes and growing environment. We recorded the fresh rhizome productivity of turmeric genotypes ranging from 13.85 to 19.36 t ha^{-1}. However, higher fresh rhizome yield of 19.28 to 33.64 t ha^{-1} and 28.92 to 38.49 t ha^{-1} were obtained in the western plains (Banke) and hill of Nepal (Kapurkot), respectively, with the same genotypes [5]. The highest yield CI 0507 (38.49 t ha^{-1}) and CI 0205 (33.64 t ha^{-1}) was obtained in Banke and Kapurkot, respectively, followed by KKH-1[5]. The higher yield could be due to the effect of growing environment. Though, CI 0507 and CI 0205 did not record higher yield than KKH-1 in our study, their grouping in the same cluster indicated that these are potential genotypes and might be location specific. Additionally, in Banke, genotypes had higher plant height (86-108 cm) than that of our experiment (48.80-64.93 cm). Moreover, positive but non-significant association (r = 0.205 NS) of plant height with fresh rhizome yield in our experiment indicated that the lower yield might be due to less growth of the plant. In this study, we found significant positive correlation of weight of mother rhizome with yield of fresh rhizome which is in agreement with result obtained by Verma et al [10]. It indicates that increased recovery of mother rhizome also contributes to increase fresh rhizome yield.

The tested genotypes grouped only in two clusters. It indicates for less diversity for observed traits among genotypes. Within the cluster, KKH-1 and CI 0207 were more similar as compared to CI 0205 which was also appeared in the first quadrant of GGEbiplot. In GGE biplot, Average Environment Axis (AEA) is the line passing through the average environment and the biplot origin. A test environment showing a smaller angle with the AEA is more representative than other test environments [11]. In this study, KKH-1 and CI 0207 are more close to AEA, it clearly indicated that these two genotypes are more representative to the observed traits. Furthermore, fresh rhizome yield per hectare is also close to AEA and KKH-1, therefore, if yield of fresh rhizome is considered the main trait of genotype selection, KKH-1 is superior to the others.

Major traits like number of mother and fresh rhizome per plot, plant population, plant height, number of tiller per plant and fresh rhizome yield per hectare were clustered around vertex genotype KKH-1 indicates that this genotype was more responsive to those observed traits. In relation to the productive performance, the genotypes located on the vertex of the polygon which are farther from the origin than the other genotypes within the sector bounded by major traits are classified as the most responsive. In addition, the genotypes located within the polygon are the least responsive to the stimuli of the environments (traits) [12]. Therefore, genotypes CI0207, CI1312, CI0503 and CI0210 were identified as less responsive to observed traits under this experiment.

5. CONCLUSION

Seven promising turmeric genotypes (CI 0207, CI 0205, CI 9102, CI 1312, CI 0503, CI 0507, and CI 0201) compared with KKH-1 at the Directorate of Agricultural Research, Tarahara, Nepal. The tested genotypes had less diversity for observed traits. Kapurkot Haledo-1 (KKH-1), one of the two resealed clones of turmeric in Nepal, performed better over other clones. Though, all the genotypes produced higher yield as compared to the national average yield of turmeric (9.73 t ha^{-1}) in Nepal, it is recommended to plant KKH-1 in the eastern plains of Nepal. In addition, the cluster and GGEbiplot analysis identified CI0207 as one of the potential turmeric clones next to KKH-1.

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COMPETING INTERESTS

Authors have declared that no competing interests exist

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