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Evaluation of Groundnut Genotypes for Yield and Yield Attributing Traits through Genotype by Trait Biplot Analysis

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***Abstract*: The evaluation of genotypes based on multiple traits is very important to select stable varieties for breeding programs. Therefore, this study was conducted to understand the genotype x trait interaction on nine promising groundnut genotypes in a randomized complete block with three replications at the research block of Agricultural Research Station, Belachapi, Dhanusha, Nepal during the two successive seasons of 2019 and 2020 using genotype by trait biplot method. Combined analysis of variance showed that the genotypes and genotype x interaction were significantly ($P \leq 0.01$) different for most of the studied traits. The first two principal components (PC1 and PC2) accounted for 72.51% of the total variation in genotypes. GT biplot analysis showed that the number of pods per plant, 100 seeds weight, and harvest index were the most influencing traits to select genotypes for high yield. Moreover, genotype ranking indicated ICGV 07214 and ICGV 05155 genotypes were superior and stable genotypes based on yield and other traits. So, this study suggests that these genotypes could be used as parental lines or as pure lines for the development of new varieties.**

***Keywords*: Biplot, genotype, groundnut, trait, yield.**

1. Introduction

Groundnut (*Arachis hypogaea* L.), commonly known as peanut, is an herbaceous annual plant of the Fabaceae family. It is one of the important oilseed crops grown in more than 100 countries around the world as a source of edible oil [1], [2]. Groundnut is increasingly being accepted as a functional food and protein extender in developing countries and the seed contains 36%-54% oil, 16-36% protein, and 10-20% carbohydrates [3]. Globally, it is grown on a total area of approximately 33 million ha with total annual production (excluding shell) of 54 million tons in 2021 [2]. About 60% of the global production comes from Asia, with China (33.9%) and India (18.9%) as the lead producers in the world followed by Nigeria (8.5%) and the United States of America (5.4%) [2]. In Nepal, groundnut is the 6th important oilseed crop both in terms of area coverage and production and covers an area of 5,328 ha with a total annual production (including shell) of 7,397 t [4]. In Nepal, the cultivation of groundnut was confined to kitchen gardens only during the 1970s and its commercial cultivation began around the early 1980s [5]. In Nepal, the productivity of groundnut is relatively low (1.38 t/ha, including shell) compared to China (3.8 t/ha, excluding shell) India (1.7 t/ha, excluding shell), and Bangladesh (1.9 t/ha, excluding shell) [2], [4]. The lack of high-yielding variety with desirable traits is one of the major causes of low productivity in Nepal [6]. The crop has high potential due to its high oil content and suitability to grow even under rainfed conditions.

The main goal of breeders is to develop superior varieties based on the evaluation of different traits under multi-environment tests. The evaluation of several traits in different environments creates problems especially when there is a negative correlation among the traits [7]. The GGE biplot is a versatile and flexible analysis method for the selection of genotypes by means of graphical representations. Though, the method has been introduced for the analysis of multi-environmental tests can be used for genotype by trait also [8]. The genotype by trait (GT) interaction method, one of the GGE biplot methods, is an excellent tool for the identification of genotype by trait interactions (Yan and Rajcan, 2002). In the GT biplot, genotypes are considered as lines and traits as testers [9]. The GT biplot analysis helps in studying genotype by trait relationships [8, 10, 11]. Moreover, it also aids in the evaluation of genotypes on the basis of multiple traits [12]. The GT biplot approach has been applied in durum wheat [13], rice [14], wheat [15], spinach [16], and cowpea [17] to identify the relationships between traits and to evaluate the genotypes on the basis of multiple traits. The objective of this study was to evaluate the groundnut genotypes based on multiple traits and to study the interrelationships between different yield-attributing traits using the GT biplot method.

2. Materials and Methods

A. *Plant Material*

A total of nine genotypes including two released varieties provided by the Oilseed Research Program, Nawalpur, Sarlahi, Nepal were evaluated (Table 1).

B. *Experimental Site*

The field experiment was carried out during the rainy season

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(July to November) for two consecutive years (2019 and 2020) at the research block of the Agricultural Research Station, Dhanusha, Nepal. The experimental site is located at 26°52' 20' N latitude, 85° 56' 56' E longitude, and at an altitude of 107 m above mean sea level. The soil of the experimental field was sandy loam in texture, medium fertility, and neutral pH. The experimental location is characterized by a sub-tropical and humid climate. The climatic data during the experimental periods of 2019 and 2020 are given in Fig. 1.

Table 1
Details of genotypes used in the experiment

Genotype	Code	Source
ICGV 95358	G1	ORP*, Nawalpur, Sarlahi
ICGV 07213	G2	
ICGV 07214	G3	
ICGV 00350	G4	
ICGV 05155	G5	
ICGV 06319	G6	
ICGV 99089	G7	
Baidehi	G8	
Jayanti	G9	

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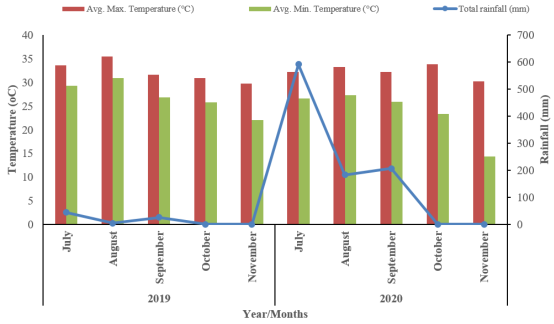

Fig. 1. Meteorological data of the experimental location in 2019 and 2020

C. *Experimental Design and Cultural Practices*

The experiment was laid out in a randomized complete block design with three replications. Seeds of each genotype were sown in plots of 4 m × 2.1 m with inter and intra-row spacing of 30 and 20 cm, respectively. Sowing was done in the 1st week of July in both years. Fertilizers were applied at the rate of 20:40:20 $N:P_2O_5:K_2O$ kg/ha. The crop was managed following the standard recommended practices for groundnut in Nepal as recommended by Oilseed Research Program, Nawalpur, Sarlahi, Nepal.

D. *Data Collection and Analysis*

To record the yield attributing traits, sampling was performed from the middle three rows in order to eliminate the border effect. At harvest, 10 plants from the middle three rows were taken randomly for the observations of growth and yield attributing traits. Plant height (PHT) was measured from the base to the top of the plant using a graduated measuring tape. The final plant stand (FSTD) per plot was recorded before the harvest of the crop. Days to 75% flowering (DF), number of pods/plant (PDP), number of seeds per 100 seeds (NSHP), and 100 seeds weight (HSW) were recorded. The net plot (excluding two border rows) was harvested and the pods were sun-dried, cleaned, and recorded the pod yield/plot. The pod yield/plot was converted into pod yield/ha (YLD) at 12% moisture by using the following formula [18].

$$\text{Grain yield}=\frac{(100\text{-MC}) \text{ X Plot yield (kg) X } 10000 \text{ m}^2}{(100\text{-}12) \text{ X Plot area}}$$

The harvest index (HI) was calculated as the ratio of biomass yield to pod yield multiplied by 100.

The pooled experimental data were subjected to a one-way analysis of variance (ANOVA) and the least significant difference (LSD) test was used to detect the significant

Table 2
Combined analysis of variance (mean square values) for yield and yield traits of groundnut genotypes over years

SV	df	FSTD	PHT	DF	PDP	NSHP	HSW	HI	YLD
Year	1	1360.02	2780.67**	112.67	684.09**	17102.24**	339.00**	2.94^{ns}	12230498.40**
Replication/Year	4	2.04	4.85	3.59	4.46	96.35	0.2	0.84	40446
Genotype	8	1178.83	456.73**	14.35	253.70**	509.25**	118.35**	50.49**	878639.00**
Genotype x Year	8	736.27	316.03**	9.08	341.59**	1272.03**	249.85**	0.27ns	1065341,00**
Pooled error	32	10.18	2.72	1.55	1.92	63.52	3.88	0.43	49154

SV: source of variation: df: degree of freedom, **significant at $P \leq 0.01$; ns: non-significant, FSTD: final stand count/plot; PHT: plant height (cm); DF: days to flowering; PDP: number of pods/plant; NSHP: number of seeds/100 pods; HSW: 100-seeds weight (g); HI: harvest index; YLD: pod yield (kg/ha)

Table 3
Mean values of yield and its related traits of ground genotypes over years

Genotype	FSTD	PHT	DF	PDP	NSHP	HSW	HI	YLD
G1	78	48.0	32	46	163	43.0	36.5	2624.77
G2	75	73.4	32	37	167	41.5	35.3	1989.52
G3	106	70.8	33	59	172	48.5	40.7	2772.54
G4	97	59.8	32	42	173	41.7	39.1	2554.61
G5	112	59.4	34	50	169	43.0	41.8	2742.2
G6	114	61.9	30	40	147	40.7	38.7	2287.42
G7	92	50.9	32	48	169	47.2	41.4	2742.67
G8	88	64.4	30	38	158	38.0	34.8	1950.59
G9	104	70.0	32	36	178	35.5	34.7	1903.16
Mean	78	48.0	32	46	163	43.0	36.5	2624.77
LSD (0.05)	3.75	1.94	1.46	1.63	9.37	2.31	38.6	260.7
CV (%)	3.3	2.7	3.9	3	4.8	4.8	1.7	9.7

FSTD: final stand count/plot; PHT: plant height (cm); DF: days to flowering; PDP: number of pods/plant; NSHP: number of seeds/100 pods; HSW: 100-seeds weight (g); HI: harvest index; YLD: pod yield (kg/ha) differences among the genotypes with regard to various traits at a 5% level of significance. The GT biplot analysis was performed considering genotypes are entries and traits are testers [8], [9]. The GenStat discovery 15th edition software was used for ANOVA and biplot generation [19].

3. Results and Discussion

A. Combined Analysis of Variance and Mean Performance

The results of combined ANOVA (Table 2) revealed that the effects of genotype, year, and genotype x year were significant ($P \leq 0.01$) for all traits except the genotype x year interaction effect for HI. The significant effect of genotype x year indicates the performance of genotypes varied over years. The mean values of FSTD, PHT, DF, PDP, NSHP, HSW, HI, and YLD for each genotype over years are shown in Table 3. The mean values of FSTD/plot, PHT, DF, PDP, NSHP, HSW, HI, and YLD across the two years varied between 75-14, 48.0-73.4 cm, 30-34 days, 36-59, 147-178, 35.5-48.5 g, 34.7-41.8%, and 1903.16-2772.54 kg/ha, respectively. Mean values over two years showed that genotypes G2, G3, and G9 had significantly taller plants than the other genotypes with values of 73.4, 70.8, and 70.0 cm, respectively. While significantly shorter plants were recorded in G1 (48.0 cm) and G7 (51.0 cm). For FSTD/plot, G6, G5, G3, and G9 were the top four genotypes with values of 114, 112, 106, and 104, respectively. The maximum number of days taken to flowering (34 days) was observed in G5 followed by G3 (33 days) and G4 (32 days) while the earliest flowering (30 days) was recorded in G6 and G8. Similarly, the maximum number of pods/plant (59) was recorded in G3 followed by G5 (50), and G7 (48). The highest NSHP (178) was recorded in G9. However, it was statistically at par with G4 (173), G3 (171), G5 (169), and G7 (169). For HSW, G3 and G7 were the top two genotypes with values of 49 and 47 g, respectively. The genotypes G5, G7, and G3 were the top performers for HI with values of 41.8, 41.8, 41.4, and 40.7%, respectively. The genotypes, G3, G7, G5, G1, and G4 produced significantly higher pod yields (>2554 kg/ ha) compared to other genotypes. The variations in the performance of genotypes over years might be due to variations in meteorological parameters, especially in rainfall and temperatures. The performance of genotypes varies over environments significantly and the environment has more influence due to GxY interaction [20]. The differences in yield and yield traits might be due to the fact that the yield traits are regulated by the genetic makeup of varieties. Our results are in accordance with the findings of [21], [22], who also reported significant differences in yield and yield traits among groundnut varieties.

B. GT Biplot Analysis

1) Polygon view of GT biplot

The GT biplot of the mean performance of groundnut genotypes explained 72.51% of the total variation of the standardized data (Fig. 2). The first two principal components (PC1 and PC2) explained 52.74 and 19.78%, respectively. The polygon view (which-won-where/what) of the GT biplot based on data across years is shown in Fig. 2. The polygon view of the GT biplot divides the biplot into sectors via perpendicular lines (thick axes) passing from the polygon sides and the graph is used for the identification of the most appropriate genotype for every trait. If the genotypes and traits are located in the same sector when starting from the lower right part of the graph, they are closely related [24], [25]. The winning genotype for a trait or set of traits in a sector is the vertex genotype. However, sectors without traits indicate genotypes falling in these sectors including the vertex one are considered to be poor performers for all traits [25]. Genotypes within the polygon and close to the origin are less responsive to trait changes [26], [27]. Fig. 2 is divided into five sectors and the genotype-trait combinations fall into two sectors only. It is apparent that G3 and G9 genotypes were at the vertex and G5 was near the vertex. These genotypes were identified as superior genotypes. Genotype G9 in terms of PHT; G3 and G5 for most of the traits except plant height. G1, G6, G7 and G8 genotypes were poor performers as they are located in the sector without traits and the G4 genotype did not react to any of the observed traits due to its proximity to the origin (Fig. 2.)

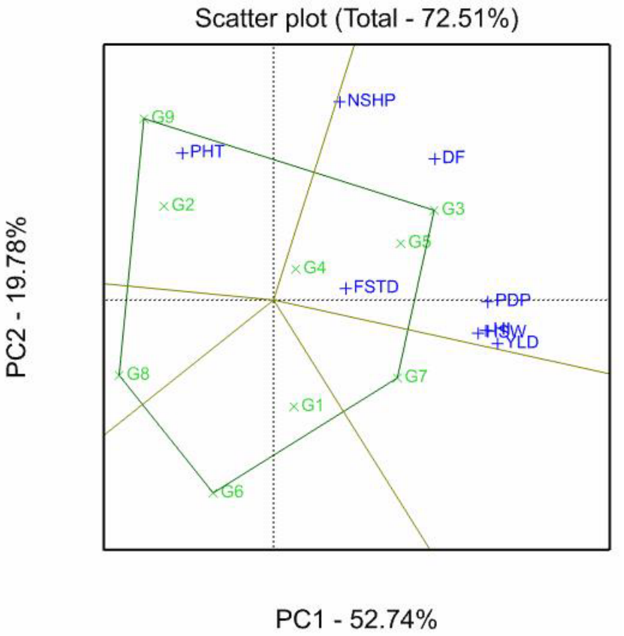

Fig. 2. The polygon (which-won-where/what) view of genotype main effect plus genotype x trait interaction effect (FSTD: final stand count/plot; PHT: plant height (cm); DF: days to flowering; PDP: number of pods/plant; NSHP: number of seeds/100 pods; HSW: 100-seeds weight (g); HI: harvest index; YLD: pod yield (kg/ha))

2) Relationship among traits

The relationship among traits by genotype profiles is shown in Fig. 3. A biplot illustrated as a graph can be bi-directionally interpreted in different ways [9], [24], [28]. The cosine of the angle between the vectors of the two properties approaches the Pearson correlation between them. Therefore, an angle smaller than 90° indicates a positive correlation, an angle greater than 90° indicates a negative correlation, and an angle of 90° indicates that there is zero correlation. Considering this principle of the GT biplot, Fig. 3. indicates that yield was positively correlated with HSW, HI, PDP, FSTD, DF, and

NSHP. However, it was negatively correlated with PHT. These results are consistent with earlier correlation studies on yield and yield attributes of groundnut [29], [30].

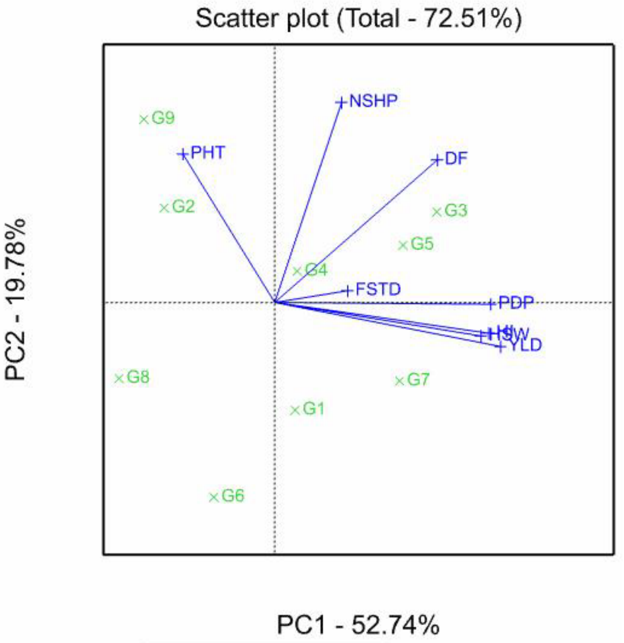

Fig. 3. Correlation among traits by genotype profile (FSTD: final stand count/plot; PHT: plant height (cm); DF: days to flowering; PDP: number of pods/plant; NSHP: number of seeds/100 pods; HSW: 100-seeds weight (g); HI: harvest index; YLD: pod yield (kg/ha)

3) *Genotype ranking based on mean and stability*

The genotypes are evaluated based on a vertical mean axis and a horizontal axis in the mean vs. stability view the of GT biplot. If the genotypes are located below the vertical axis, they are undesirable whereas, if they are located above the vertical axis, they are desirable. On the other hand, genotypes located near or at the center of the horizontal line are stable and unstable if they move away from the horizontal line [31], [32]. Therefore, genotypes located closer to the stable line (horizontal axis) and have high mean values of trait means that they are more favorable than others [24], [33]. The G5 genotype was quite stable because it is located at the center of the horizontal axis, but; G3 was the most favorable as they are located near the center of the horizontal axis and performed superior to other genotypes on all traits. The genotypes, G1, G6, G8, and G7 were undesirable genotypes because they are located below the vertical axis. Other genotypes that are located above the vertical axis were desirable based on trait profiles (Fig. 4).

4) *Comparison of genotypes based on ideal genotype*

The comparison of genotypes based on the ideal genotype is shown in Fig. 5. In this diagram, the representative “ideal center” over the property mean values marked with an arrow, and the genotypes are evaluated based on this point according to their nearness or distance to this center [24], [31]. The most ideal genotypes are located in the center, whereas genotypes located on the mean vertical axis, but far from the center, are ideal; genotypes located below the vertical axis are undesirable [8], [34]. Accordingly, G3 and G5 were identified as more ideal than G4 and G7 because they are located at the nearest to the “ideal center”, while G1, G2, G6, G8 and G9 are located below the vertical axis and far from the “ideal center” and were considered as undesirable genotypes.

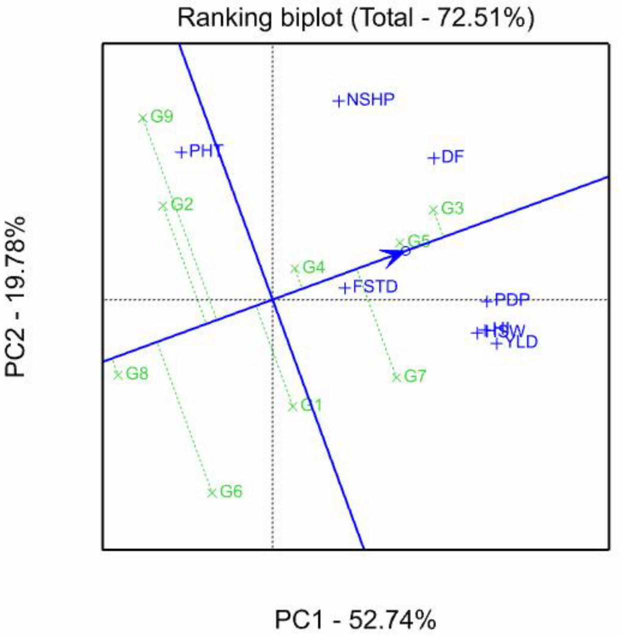

Fig. 4. Ranking view of genotypes based on traits (FSTD: final stand count/plot; PHT: plant height (cm); DF: days to flowering; PDP: number of pods/plant; NSHP: number of seeds/100 pods; HSW: 100-seeds weight (g); HI: harvest index; YLD: pod yield (kg/ha))

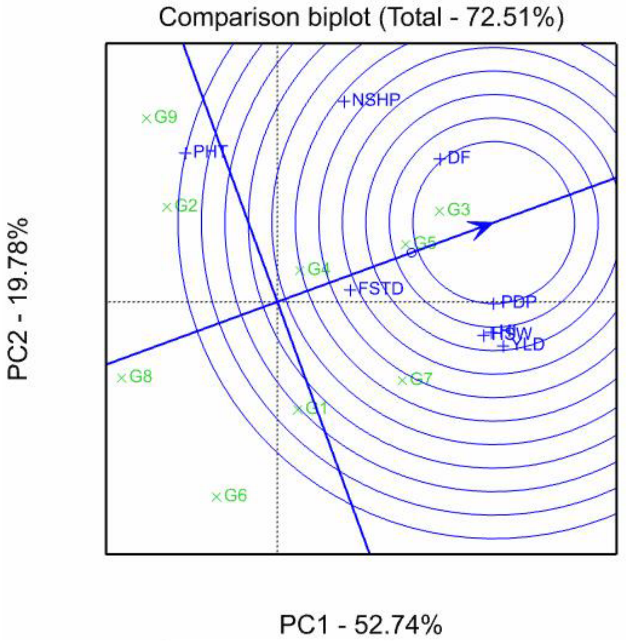

Fig. 5. Comparison view of genotypes based on traits (FSTD: final stand count/plot; PHT: plant height (cm); DF: days to flowering; PDP: number of pods/plant; NSHP: number of seeds/100 pods; HSW: 100-seeds weight (g); HI: harvest index; YLD: pod yield (kg/ha))

4. Conclusion

The results of the study indicated the number of pods per plant, 100 seeds weight, and harvest index were the most influencing traits to select improved grain yield. Thus, they could be used for future groundnut breeding programs. Genotypes, ICGV 07214 and ICGV 05155G3 were found as superior genotypes based on yield and other traits. These genotypes could be used as parental lines or as pure lines for the development of new varieties.

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