



Association of Characters for Higher Tuber Yield of Potato (*Solanum tuberosum* L.) Genotypes Grown in Eastern Plains of Nepal

Tika Ram Chapagain^{1*}, Amit Prasad Timilsina¹, Manish Kumar Thakur¹,
Kumar Mani Dahal¹ and Giridhari Subedi¹

¹Nepal Agricultural Research Council, Nepal.

Authors' contributions

This work was carried out in collaboration among all authors. Author GS designed the study and arranged the test materials, author TRC implemented the experiment, performed the statistical analysis, and prepared the first draft of the manuscript, author MKS collected the data, authors APT and KMD managed the literature searches and prepared the final draft of the manuscript. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/AJAHR/2021/v8i430124

Editor(s):

(1) Dr. Paola A. Deligios, University of Sassari, Italy.

Reviewers:

(1) Naveen Kumar K. J, Davangere University, India.

(2) Simon Chibi, Zimbabwe Open University (ZOU), Zimbabwe.

Complete Peer review History: <http://www.sdiarticle4.com/review-history/76366>

Original Research Article

Received 25 August 2021
Accepted 02 November 2021
Published 09 November 2021

ABSTRACT

An experiment was conducted to study characters associated with higher yield potential of potato genotypes at the Directorate of Agricultural Research, Tarahara, Nepal during two consecutive winter seasons of 2018 and 2019. A total of eleven potato genotypes (CIP 394600.52, CIP 396012.266, CIP 393371.159, PRP 266265.15, CIP 395443.103, CIP 393371.164, PRP 336769.1, PRP 136368.9, PRP 25861.11, CIP 377957.5 and PRP 225861.5) were evaluated in a Randomized Complete Block Design with four replications. Each treatment received a 7.2 m² plot area with 60 cm row to row and 25 cm plant to plant spacing, accommodating 48 plants per plot. Cultural practices were done as per the recommendations and fungicide was not applied for late blight of potato (*Phytophthora infestans*) control. The observed data were subjected to variance, correlation and cluster analysis. Analysis of variance showed significant differences for some plant and tuber characteristics. From the pooled analysis of two years' data, the genotype 'PRP 266265.15' was found to be a suitable genotype in plains due to its higher yield (21.91 t/ha) and

*Corresponding author: Email: chapagaintika@gmail.com;

other yield characteristics. The higher quantity of over seed-size and under seed-size tuber contributed to the highest tuber yield of PRP 266265.15. The weight ($r = 0.928^{**}$) and number ($r = 0.483^{**}$) of the over seed-size tuber had a positive significant correlation with tuber yield per hectare. Further research is needed to study yield stability of the genotype 'PRP 266265.15' in various locations with similar production environments.

Keywords: biplot; cluster; correlation; genotypes; potato.

1. INTRODUCTION

Potato (*Solanum tuberosum* L.) is one of the major food crops of the world. It is also one of the most important and dominant tuber crops in Nepal, which ranks 24th as a potato producer, accounting for 0.84% of total global potato production [1], and ranks fifth in area coverage, second in total production, and first in productivity among Nepal's food crops [2]. Its area, production and productivity were 193,997 ha, 3,112,947 tons and 16.05 tons per ha respectively in Nepal in the fiscal year 2018/19 [3]. Its imports into the country were about 355,913 mt while 536 mt were exported in the year 2017/18 [4]. Compared to countries like Bangladesh (20.4), China (18.8), India (22.6), The Netherlands (36.6) and the USA (49.8), the potato productivity in Nepal was less (15.8 t/ha) based on 2018 data [1]. The low productivity in Nepal as compared to other countries is due to a lack of quality planting materials, the prevalence of insect pests and diseases, inadequate research on varieties for different locations and adoption of new varieties of potato being relatively low in many parts of Nepal [5]. The majority of potato growing areas in Nepal are still occupied by low yielding and late-blight susceptible local potato varieties. Improved varieties have high yield potential and the choice of improved varieties is the most critical factor determining productivity [6]. Moreover, the demand for high yielding varieties with resistance to major diseases and pests has remained very high in Nepal [7].

In the plains of Nepal, potato is cultivated in a rice-based farming system. Population growth and urbanization are creating opportunities for smallholders to improve their incomes and diversify rice-based farming systems in Asia [8]. However, due to lack of irrigation, fertilizer, improved varieties, diseases, insect pests and management practices, yield has not been achieved at its potential [9]. Therefore, this experiment was carried out with the objective of identifying high yielding potato genotypes suitable for the eastern plains

of Nepal to address the problem of low potato yield.

2. MATERIALS AND METHODS

2.1 Site Description

The experiment was conducted at the Directorate of Agricultural Research, Tarahara, which is situated in the eastern part of Nepal. It is located at 26°42'16.85" North latitude and 87°16'38.43" East longitude at an elevation of 136 meters above sea level. It is climatically sub-tropical. The soil is clay loam and slightly acidic with a pH of 6.5.

2.2 Experimental Design and Data Analysis

Experiments were laid out in a Randomized Complete Block Design (RCBD) with 11 genotypes as treatments and were replicated four times. The genotypes used were: CIP 394600.52, CIP 396012.266, CIP 393371.159, PRP 266265.15, CIP 395443.103, CIP 393371.164, PRP 336769.1, PRP 136368.9, PRP 25861.11, CIP 377957.5 and PRP 225861.5. National Potato Research Program, Khumaltar, Nepal provided the genotypes for this experiment. The well-sprouted potato tubers of seed size 25-50 g were planted in the field at a spacing of 60 cm by 25 cm with a plot size of 7.2 m². The chemical fertilizers and farmyard manure were applied @ 100:100:60 kg NPK ha⁻¹ and 20 t ha⁻¹, respectively. Other cultural practices including irrigation, weeding and earthing-up were done according to the recommendations. The parameters including emergence (at 15 and 30 DAS), uniformity using the scale from 1 to 5 (1=very poor, 2=poor, 3=fair, 4=good, 5=excellent), ground cover (% of ground cover by foliage), number of main stem per plant, plant vigor using a scale from 1 to 5 (1=very weak, 2=weak, 3=intermediate, 4=vigorous, 5=very vigorous), plant height, late blight tolerance (1 to 9 scale with lower value more tolerant) and weight of undersized tuber (<25 g), seed tuber (25-50 g) and oversized tubers (>50 g) and yield

were recorded accordingly. Data analysis was done by using RStudio software (packages used viz. agricolae, variability, hclust, GGEBiplots) and treatment means were compared by Duncan's Multiple Range Test (DMRT) at a 5% level of significance.

3. RESULTS

3.1 Plant Characters

The analysis of variance for the pooled mean of the tested genotypes differed significantly for emergence at 15 and 30 days after sowing (DAS), main stem per plant, plant height and tolerance to late blight. However, they did not differ for uniformity, ground cover and plant vigour (Table 1). The maximum emergence was recorded in CIP 396012.266 at both 15 DAS (32.88) and 30 DAS (43.50). However, at 30 DAS, this genotype only differed with CIP395443.103 which had the least emergence at both the stage of counting. Plant uniformity, which was recorded on a 1-5 scale, was found higher in CIP 393371.159. Plant vigor, which was also recorded on a 1-5 scale, was found higher in genotype CIP 394600.52 (4.19) followed in CIP394600.52 (4.19). Ground coverage was found higher in CIP 393371.159. The highest number of main stem/plant was found in CIP 396012.266 (4.93) which differed from PRP 225861.5, CIP 377957.5 and CIP 395443.103. On the 1-9 scale, the highest level of tolerance to late blight was observed in PRP 225861.5 (1.69) which only differed with CIP 377975.5 (3.94) and PRP 336769.1 (3.31).

3.2 Tuber Characteristics

The analysis of variance for the pooled mean of the tested genotypes differed significantly for the number of under sized tubers and weight per plot. The highest and lowest number of under sized tubers were recorded in PRP 225861.5 and CIP 393371.159, respectively (Table 2). The highest and lowest tuber weight of undersized tubers per plot recorded in PRP 136368.9 and CIP 393371.159, respectively. The number of seed size tuber and their weight did not differ statistically among the tested genotypes, however, highest number of seed size tuber and their weight were recorded in PRP 136368.9 (110.38) and PRP 25861.11 (4347.19 g plot⁻¹).

The number of over seed-size tuber did not vary. However, the weight of the tubers varied among genotypes. The pooled mean for over seed-size tuber was found higher in CIP 393371.164 and PRP 136368.9 recorded the minimum number of over seed size-tuber. The highest and lowest weight of over seed-size tuber was recorded in CIP 393371.159 and PRP 136368.9, respectively. The total number of potatoes per plot was found non-significantly different with highest of genotypes PRP 225861.5 (301.25) and lowest of CIP 393371.159 (213.25).

3.3 Marketable Yield (t ha⁻¹)

The pooled mean for marketable yield (t ha⁻¹) differed statistically among tested genotypes. The highest tuber yield (21.91 t ha⁻¹) was obtained from PRP 266265.15 which was at par with CIP 394600.52, CIP 396012.266, CIP 393371.159, CIP 395443.103 and CIP 393371.164. The lowest yield (14.04) was obtained from PRP 336769.1. The average yield of the tested genotype was 17.79 t ha⁻¹.

3.4 Correlation between Traits

The total number of tubers, number and weight of under-sized and seed-sized tuber had negative non-significant correlation with tuber yield. All the remaining variables were found to have positive correlation with tuber yield. Ground coverage showed significant positive correlation with tuber yield (Table 3). The weight ($r = 0.928^{**}$) and number ($r = 0.483^{**}$) of the over seed-size tuber had positive significant correlation with tuber yield per hectare. These categories of tubers had positive significant correlation with total tuber per plot.

3.5 Clustering of Genotypes

The cluster analysis grouped 11 genotypes into four clusters (Fig. 1). The clusters (left to right in Fig. 1) comprised of one, two, three and five genotypes in the first, second, third and fourth clusters, respectively. Highly promising genotypes viz. PRP 266265.15, CIP 394600.52 and CIP396012.266 were grouped in the third cluster. These genotypes had higher tuber yield, emergence (>40), main stem per plant (>4.00), plant height about 50 cm, total tuber per plant (>250 per plot) and tolerant to late blight.

Table 1. Plant characteristics and late blight scoring of potato genotypes tested at DoAR, Tarahara in 2018 and 2019

| Genotypes | E15 | E30 | Uni | GC | Stp | PV | PH | LB |
|------------------|----------------------|----------------------|------------|-----------|---------------------|-----------|--------------------|--------------------|
| CIP 394600.52 | 25.00 ^b | 40.38 ^{ab} | 3.75 | 88.75 | 4.01 ^{a-d} | 4.19 | 50.23 ^b | 2.75 ^{bc} |
| CIP 396012.266 | 32.88 ^a | 43.50 ^a | 3.75 | 78.75 | 4.93 ^a | 4.03 | 49.68 ^b | 2.31 ^{bc} |
| CIP 393371.159 | 11.75 ^{def} | 40.50 ^{ab} | 4.25 | 90.00 | 3.83 ^{a-d} | 3.94 | 50.50 ^b | 2.06 ^c |
| PRP 266265.15 | 23.88 ^b | 42.25 ^a | 4.13 | 83.75 | 4.35 ^{abc} | 4.13 | 53.53 ^b | 2.44 ^{bc} |
| CIP 395443.103 | 5.13 ^f | 34.88 ^c | 3.71 | 80.63 | 2.84 ^d | 3.63 | 60.83 ^a | 2.40 ^{bc} |
| CIP 393371.164 | 16.00 ^{cde} | 40.75 ^{ab} | 4.13 | 87.50 | 3.66 ^{a-d} | 3.94 | 52.43 ^b | 2.13 ^c |
| PRP 336769.1 | 20.50 ^{bc} | 39.63 ^{abc} | 3.88 | 81.88 | 4.33 ^{abc} | 3.75 | 62.08 ^a | 3.31 ^{ab} |
| PRP 136368.9 | 12.50 ^{def} | 38.25 ^{abc} | 3.88 | 85.63 | 4.23 ^{a-d} | 3.88 | 53.43 ^b | 2.41 ^{bc} |
| PRP 25861.11 | 19.13 ^{bcd} | 36.38 ^{bc} | 4.00 | 82.50 | 4.67 ^{ab} | 3.78 | 38.08 ^c | 2.19 ^c |
| CIP 377957.5 | 20.25 ^{bc} | 38.38 ^{abc} | 4.00 | 83.75 | 3.21 ^{cd} | 4.03 | 51.53 ^b | 3.94 ^a |
| PRP 225861.5 | 10.38 ^{ef} | 38.63 ^{abc} | 3.88 | 83.75 | 3.26 ^{bcd} | 3.94 | 42.23 ^c | 1.69 ^c |
| Mean | 17.94 | 39.40 | 3.93 | 84.26 | 3.93 | 3.92 | 51.31 | 2.51 |
| F-test | *** | * | NS | NS | * | NS | *** | ** |
| LSD (<0.05) | 6.87 | 4.72 | - | - | 1.21 | - | 5.28 | 0.97 |

Values in a column with different letter(s) are significantly different at 0.05 level of significance by DMRT. Significance level for ANOVA: * $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$ and NS = non-significant, E15 = emergence at 15 DAS, E30 = emergence at 30 DAS, Uni= uniformity, GC=ground coverage, Stp = main step per plant, PV = plant vigour, PH = plant height, LB=late blight tolerance

Table 2. Tuber characteristics and yield of potato genotypes tested at DoAR, Tarahara in 2018 and 2019

| Genotypes | UN | UW | MN | MW | LN | LW | TPL | YH |
|------------------|----------------------|-----------------------|-----------|-----------|-----------|-----------------------|------------|----------------------|
| CIP 394600.52 | 56.13 ^{cd} | 499.49 ^d | 100.25 | 4061.20 | 100.63 | 9355.14 ^{ab} | 257.00 | 19.33 ^{a-d} |
| CIP 396012.266 | 81.75 ^{abc} | 869.95 ^{a-d} | 101.13 | 3942.91 | 91.88 | 8149.30 ^{bc} | 274.75 | 18.00 ^{a-e} |
| CIP 393371.159 | 40.63 ^d | 468.58 ^d | 68.63 | 3139.70 | 104.00 | 11696.60 ^a | 213.25 | 21.26 ^{ab} |
| PRP 266265.15 | 97.00 ^{ab} | 972.11 ^{abc} | 89.88 | 3264.48 | 111.75 | 11539.56 ^a | 298.63 | 21.91 ^a |
| CIP 395443.103 | 62.58 ^{bcd} | 580.88 ^{cd} | 89.92 | 3200.98 | 86.96 | 9804.18 ^{ab} | 239.46 | 18.87 ^{a-d} |
| CIP 393371.164 | 49.75 ^{cd} | 469.91 ^d | 68.88 | 2782.15 | 119.13 | 10991.80 ^a | 237.75 | 19.78 ^{abc} |
| PRP 336769.1 | 61.00 ^{cd} | 684.31 ^{bcd} | 98.75 | 3601.66 | 82.88 | 5826.13 ^c | 242.63 | 14.04 ^e |
| PRP 136368.9 | 103.25 ^a | 1177.95 ^a | 110.38 | 4248.76 | 77.13 | 5749.66 ^c | 290.75 | 15.52 ^{cde} |
| PRP 25861.11 | 111.25 ^a | 1128.00 ^a | 97.88 | 4347.19 | 83.50 | 6670.43 ^c | 292.63 | 16.87 ^{b-e} |
| CIP 377957.5 | 82.00 ^{abc} | 946.09 ^{abc} | 78.63 | 3259.24 | 88.25 | 6636.49 ^c | 248.88 | 15.06 ^{de} |
| PRP 225861.5 | 112.75 ^a | 1056.24 ^{ab} | 102.75 | 3735.69 | 85.75 | 6082.48 ^c | 301.25 | 15.10 ^{de} |
| Mean | 78.00 | 804.86 | 91.94 | 3598.54 | 93.80 | 8409.25 | 263.35 | 17.79 |
| F-test | *** | *** | NS | NS | NS | *** | NS | ** |
| LSD (<0.05) | 31.69 | 390.21 | - | - | - | 2281.42 | - | 4.03 |

Values in a column with different letter(s) are significantly different at 0.05 level of significance by DMRT. Significance level for ANOVA: ** $P \leq 0.01$, *** $P \leq 0.001$ and NS = non-significant UN = number of under seed-size tuber (<25 g), UW = weight of under seed-size tuber, MN= number of seed-size tuber (25-50 g), MW = weight of seed-size tuber, LN = number of over seed size tuber (>50 g), LW = weight of over seed-size tuber, TPL= total tuber per plot, YH = tuber yield ton per hectare

Table 3. Correlation between different traits of potato genotypes

| | GC | Stp | PV | PH | UN | UW | MN | MW | LN | LW | TPL | YH |
|-----|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|------------|-----------|
| E30 | -0.140 NS | 0.317 * | 0.192NS | -0.033 NS | -0.04 NS | 0.001 NS | -0.0083 NS | -0.017 NS | 0.169 NS | 0.137 NS | 0.092 NS | 0.148 NS |
| GC | | 0.035NS | 0.293 NS | 0.119 NS | -0.311 * | -0.251 NS | 0.0664 NS | 0.279 NS | 0.265 NS | 0.374 * | -0.078 NS | 0.472 ** |
| Stp | | | 0.268 NS | -0.051 NS | 0.168 NS | 0.197 NS | 0.4775 ** | 0.498 ** | -0.199 NS | -0.081 NS | 0.3055* | 0.107 NS |
| PV | | | | -0.153 NS | 0.116 NS | 0.126 NS | 0.2447 NS | 0.267 NS | -0.063 NS | 0.141 NS | 0.205 NS | 0.268 NS |
| PH | | | | | -0.384 * | -0.270 NS | 0.0215 NS | -0.132 NS | 0.056 NS | 0.226 NS | -0.289 NS | 0.166 NS |
| UN | | | | | | 0.945 ** | 0.2699 NS | 0.353 * | -0.444 ** | -0.441 ** | 0.767 ** | -0.224 NS |
| UW | | | | | | | 0.1983 NS | 0.367 * | -0.501 ** | -0.444 ** | 0.645 ** | -0.214 NS |
| MN | | | | | | | | 0.767 ** | -0.366 * | -0.403 ** | 0.598 ** | -0.164 NS |
| MW | | | | | | | | | -0.484 ** | -0.364 * | 0.468 ** | -0.016 NS |
| LN | | | | | | | | | | 0.647 ** | -0.018 NS | 0.483 ** |
| LW | | | | | | | | | | | -0.241 NS | 0.928 ** |
| TPL | | | | | | | | | | | | -0.009 NS |

Significance level for correlations: * $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$

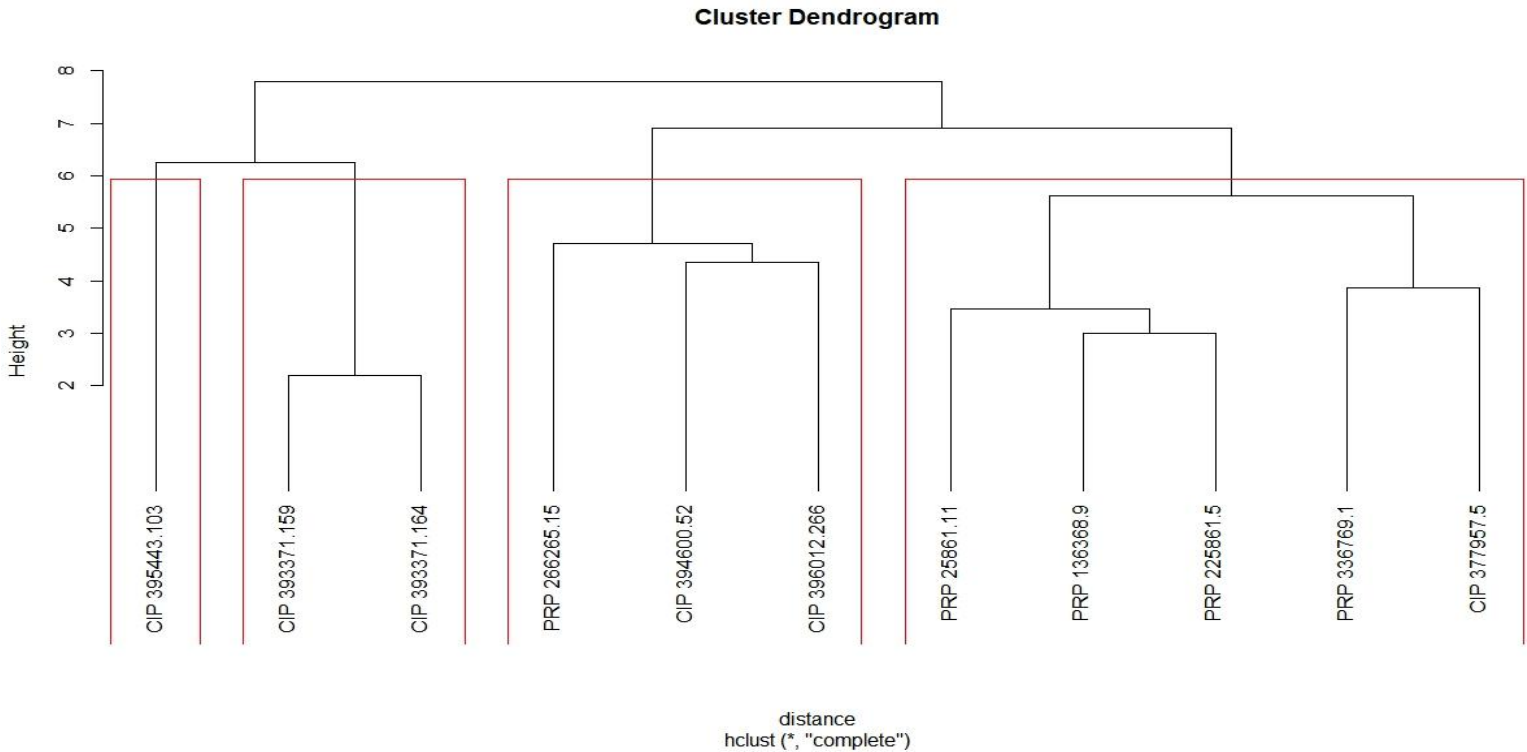
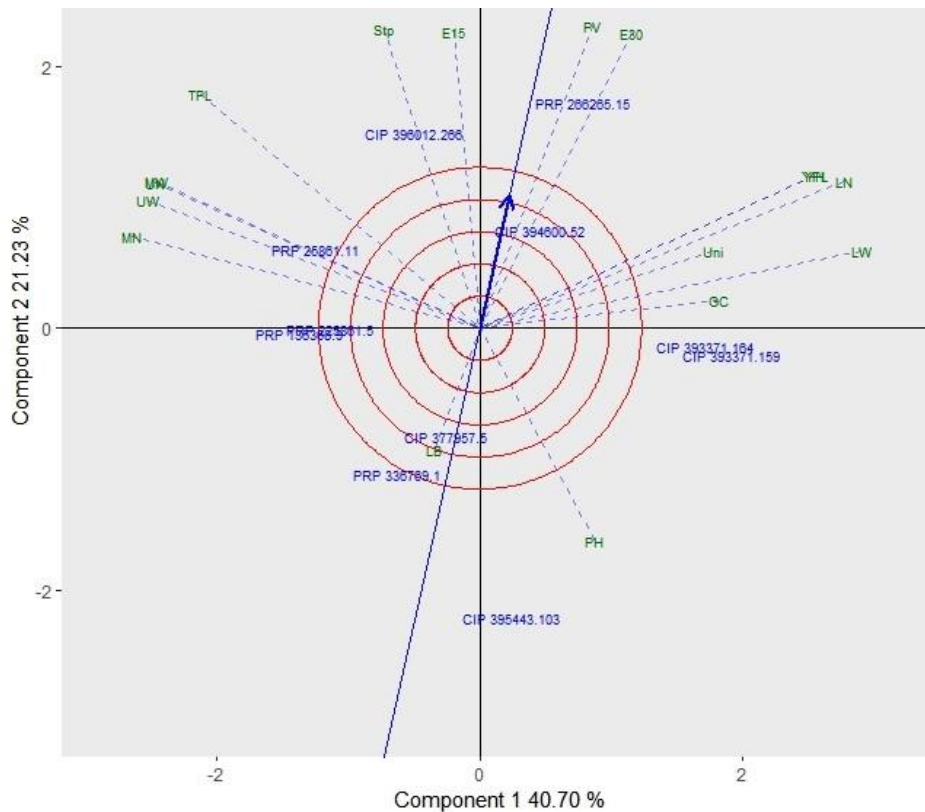


Fig. 1. Clustering of potato genotypes based on plant and tuber characteristics



GGE Biplot showing components 1 and 2 explaining 61.93% of the total variation using Column Metric Preserving SVP and Tester-Centered G+GE with scaling by standard deviation

Fig. 2. The discrimination and representation view of the GGE biplot to show the discriminating ability and representativeness of the traits with potato genotypes

3.6 GGE Biplot for Genotype-by-Trait Relationship

GGE biplot analysis for the discriminating and representativeness of traits (Fig. 2) was carried out to find out more informative traits for the selection of genotypes. The analysis explained 61.93% of the total variation of the standardized data. It reflects the moderate complexity of the relationships among the measured traits. The first two principal components (PC1 and PC2) explained 40.70% and 21.23% of total variations, respectively. The polygon view of the GGE biplot (Fig. 3) helps to identify genotypes with the highest values for one or more traits. Among the genotypes, PRP 266265.15, CIP 396012.266, PRP 25861.11, PRP 25861.11, PRP 136368.9, PRP 336769.1, CIP 395443.103 and CIP 393371.159 are at the vertex of the polygon. Among the vertex genotypes, PRP 266265.15 and CIP 396012.266 are also grouped in the second group in cluster analysis (Fig. 1). Here, major yield traits plant vigour, emergence at 30

DAS, over-seed size tuber, uniformity, ground cover are located in the sector of the polygon where PRP 266265.15 (vertex genotype).

4. DISCUSSION

The difference in potato genotypes on their morphological, tuber and yield characteristics is attributed to the genetic makeup of the test materials. They did not show any statistical difference for uniformity, ground cover and plant vigour. The emerging capability, which was positively correlated with yield, differed among the genotypes at 15 and 30 DAS. Higher number of plants at 30 DAS had higher tuber yield. They were more vigorous as compared to late emerging genotypes. Plant height showed a weak positive but non-significant correlation with tuber yield. 12. Fukuda et al. [10] also found positive correlation of tuber yield with plant height. In general, plants with medium height (≤ 50 cm) had higher tuber yield as compared to tall (60 cm) and short (> 50 cm).

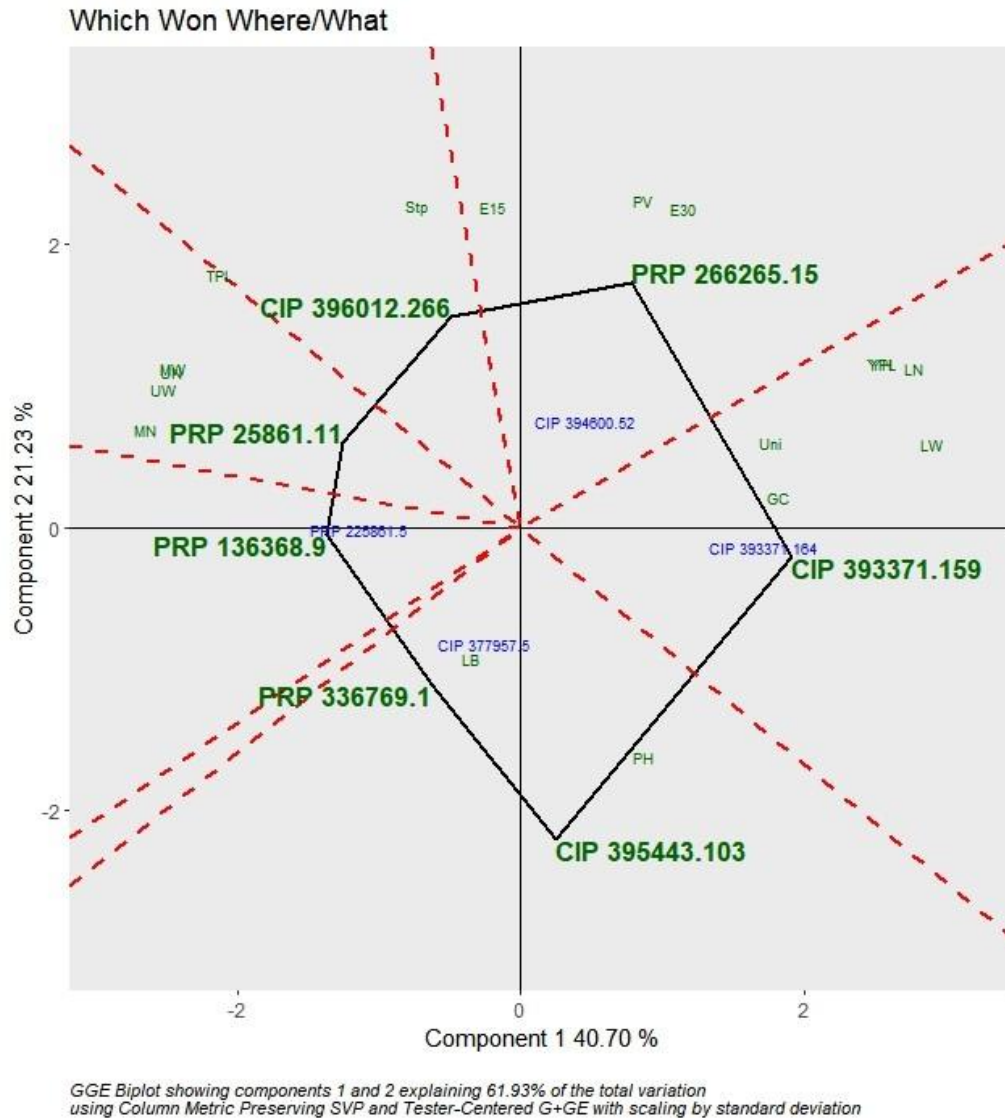


Fig. 3. The which-won-where view of the GGE biplot to show which traits most contributed to which genotypes

The highest tuber yield obtained in genotypes PRP 266265.15 followed by CIP 393371.159 and CIP 393371.164 was mainly contributed by the number of over-seed size tubers and this finding is in agreement with NPRP [11]. All these genotypes had more than 100 over seed-sized tubers per plot. Yuan et al. [12] also reported positive correlation of tuber size with tuber yield. PRP 266265.15 performed better in the plains of Nepal. In our experiment, genotype PRP266265.15 produced 21.91 t ha⁻¹ tuber yield which was in agreement with the performance of this genotype in the mid (altitude 115 m at Parwanipur) and western (altitude 181 m at

Khajura) plains of Nepal with a yield of 26.12 and 24.08 t ha⁻¹, respectively [11]. Likewise, it was found to produce yield of 34.75 and 26.01 t ha⁻¹ at farmers' field at 1000 m and 550 m altitude of mid hills agro-ecology of Nepal, respectively [9]. These findings suggest that genotype PRP 266265.15 is suitable across the plains and lower mid-hills condition of Nepal.

Potato tuber yield was found positively correlated with morphological characters, which is in agreement with Tiwari et al. [13]. In this experiment, the number of over seed-size tubers and weight had strong positive association with

the productivity of potato. This result is in agreement with Fukuda et al. [14] as they also found positive correlation between large tuber percentage and tuber yield. However, a weak negative non-significant association ($r = -0.009$) was found between the number of tubers per plot with the productivity. It could be due to many genotypes having fewer over-seed size tubers as compared to under seed-size tubers. The result of this study suggests that the productivity of potato mainly depends on the number and weight of over seed-size tubers.

Productivity is the key parameter for the selection of a genotype in many breeding programs. From GGE Biplot analysis, traits like plant vigour (PV), emergence at 30 DAS (E30), tuber yield (YH), the number (LN) and weight of the over seed-size tuber (LW), uniformity (Uni), ground coverage (GC) were found in the sector where the genotype PRP 266265.15 lies. It suggests that these traits are more representative for genotype selection because this genotype was identified as the highest yielder from analysis of variance for tuber yield. Moreover, traits that have a smaller angle with the "Average environment axis" (an arrow) is more representative [14]. Fitting of genotypes in the vertex of the polygon (Fig. 3) showed that PRP 222265.15 is the best genotype because it is in the vertex where most of the yield contributing and positively correlated traits lie. Treatments in the vertex are the best or the unsuitable treatments in some or all of the traits since they had the longest distance from the origin of biplot [15].

5. CONCLUSION

Genotype 'PRP 266265.15' was identified as a suitable genotype in the eastern plains because of its better performance in terms of yield and other yield attributing characteristics. It is also at par with CIP 394600.52, CIP 396012.266, CIP 393371.159, CIP 395443.103 and CIP 393371.164 genotypes in terms of tuber yield which are more than the average national productivity of potato (16.5 t ha^{-1}). It is suggested that further evaluation of these genotypes across diverse agro-climatic conditions is needed to determine yield stability.

ACKNOWLEDGEMENTS

The authors would like to thank Mr. Ramesh Bhujel, Mr. Ganga Prasad Ghimire, Ms. Sabita Sharma, Mr. Dilli Bhattarai of Directorate of

Agricultural Research, Tarahara for their support during the experiment. We would also like to thank Nepal Agricultural Research Council for funding this research and National Potato Research Programme for providing potato genotypes under coordinated varietal evaluation program.

DISCLAIMER

Authors are responsible for any issues raised regarding this experiment.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. FAOSTAT. Crop statistics. Food and Agriculture Organization of the United Nation; 2019. Available:<http://www.fao.org/faostat/en/#data/QC>.
2. NPRP. Annual report. National Potato Research Programme. Nepal Agricultural Research Council, Khumaltar, Lalitpur, Nepal; 2018.
3. MoALD. Statistical information on Nepalese agriculture. Ministry of Agriculture and Livestock Development, Nepal; 2020.
4. DoC. Export and import situation of Nepalese agricultural products. Department of Custom, Ministry of Supply and Commerce, Nepal; 2019.
5. Giri RK, Chalise B, Paneru PB, Subedi GD, Khadka K, Dhakal R, Gautam S. Evaluation of nutrient-dense potato genotypes at Jumla District of Nepal. 2017. In: Proceedings of Ninth National Horticulture Workshop.
6. Gairhe S, Gauchan D, Timsina K. Adoption of improved potato varieties in Nepal. J. Nepal Agricultural Research Council. 2017;3:38-44.
7. Khatri BB, Sharma BP, Chaudhary D, Luitel BP, Ahamad S, Chapagain TR. On-farm performance of three advanced potato clones in different agro-ecological zones of Nepal; 2010. In: Proceedings of Ninth Outreach Research Group Workshop, Khumaltar, Kathmandu, Nepal.
8. CIP. Annual Report. Build, Innovate, Transform: Collaborative solutions for global challenges. Lima, Peru. International Potato Center; 2020.

9. NPRP. Annual report. National Potato Research Programme, Nepal Agricultural Research Council, Khumaltar, Lalitpur, Nepal; 2020.
10. Fekadu A, Petros Y, Zelleke H. Genetic variability and association between agronomic characters in some potato (*Solanum tuberosum* L.) genotypes in SNNPRS, Ethiopia. International Journal of Biodiversity and Conservation. 2013;5(8):523-528.
11. NPRP. Annual report. National Potato Research Programme, Nepal Agricultural Research Council, Khumaltar, Lalitpur, Nepal; 2019.
12. Yuan J, Murphy A, Koeyer DD, Lague M, Bizimungu B. Effectiveness of the field selection parameters on potato yield in Atlantic Canada. Canadian Journal of Plant Science. 2016;96:701-710.
13. Tiwari A, Mishra A, Saxena V, Saxena S, Raghuvanshi AP. Association of characters and selection parameters for high tuber yield in Potato (*Solanum tuberosum* L.). The Journal of the Society for Tropical Plant Research. 2020; 7(1):205–208.
DOI: 10.22271/tpr.2020.v7.i1.026
14. Yan W, Tinker NA. Biplot analysis of multi-environment trial data: Principle and applications, Canadian Journal of Plant Science. 2006;86(3):623-645.
Available:https://doi.org/10.4141/P05-169
15. Sabaghnia N, Janmohammadi M. Biplot Analysis of silicon dioxide on early growth of sunflower. Plant Breeding and Seed Science. 2016;73:87-98.
Available:http://ojs.ihar.edu.pl/index.php/pbss/article/view/235

© 2021 Chapagain et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:
The peer review history for this paper can be accessed here:
<http://www.sdiarticle4.com/review-history/76366>