Genetic Variability Studies in Potato (Solanum tuberosum L.) Genotypes in Bale Highlands, South Eastern Ethiopia

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Abstract

Twenty four potato genotypes were planted in randomized complete block design with three replications at Sinana Agricultural Research Center to investigate the nature and magnitude of variability for tuber yield and yield related traits. The mean squares due to genotypes were highly significant ($P \le 0.01$) for all the characters studied. High genotypic (51.9, 47.2 and 45.8) and phenotypic (56.7, 55 and 51.2) coefficient of variation were observed for total tuber yield, marketable tuber yield and average tuber weight in order of magnitude. High heritability (85 and 83.9%) coupled with high genetic advance as percent of mean (98.1 and 89.7) recorded for total tuber yield and marketable tuber yield respectively. The study revealed that the presence of genotypic variability in tested genotypes indicating higher chance of selecting genotypes with high yield and resistant to late blight.

Keywords: Variability; Heritability; Genetic advance; potato.

1. Introduction

Potato (Solanum tuberosum L.) is an important world crop that belongs to the family of Solanaceae (Haward, 1969) is an important food source in the world. Like many other countries in the world, potato is a very important food and cash crop especially on the highland and mid altitude areas of Ethiopia(Gebremedhin *et al.*, 2008) Potato cropping systems help to improve resilience especially among smallholder farmers by providing direct access to nutritious food, increasing household incomes and reducing their vulnerability to food price volatility (André *et al.*, 2014). Potato is a highly heterozygous out crossing species which is asexually propagated, via tubers, for food production and germplasm maintenance. Sexual propagation and the production of 'true' seed allow breeders to generate genetic variation, and as a clonal crop, there are opportunities to exploit both additive and non-additive variation (Mackay, 2007). Potato breeding scheme begins with the evaluation and selection of parental material, the crossing of the selected parents and the selection of elite clones from these progeny of crosses for further testing and potential release as cultivars. A cycle is complete when elite lines are introduced as parents for the next cycle.

Potato cultivar development uses a phenotypic-based selection strategy. Parents are chosen on the basis of their own performance or from intuition and experience of their worth from previous successes as parents (Gopal *et al.*, 1992). This knowledge is gained gradually by the breeder as progeny flow through breeding steps. Knowledge of the genetic parameters of traits, such as heritability and genetic advance, are also required to help guide an effective breeding strategy. In practice, the true variance components are unknown but are estimated from the data (Mackay, 2007)

2. Material and Methods

This experiment was conducted in Southeastern Ethiopia, Bale Zone, at Sinana Agricultural Research Center. Sinana is located at 07^0 N and 40^0 10' E at an altitude of 2400 masl. Average annual maximum and minimum temperatures are 21 and 9°C, respectively. The dominant soil type is pellic vertisol and slightly acidic (Nefo *et al.*, 2008). A total of 24 potato genotypes which consisted of 20 advanced clones, three released varieties as standard checks and one farmers cultivar were used(Table 1). All genotypes were planted during main cropping season of 2014. The experiment was arranged in randomized complete block design with three replications. The spacing between rows and plants was 0.75m and 0.30m, respectively. The spacing between plots and adjacent replications was 1 m and 1.5 m, respectively. Recommended management practices were carried out as per the requirement of the crop. The data were analyzed using SAS

| Tuble Te: Elst of pound genotypes used in the study. | | | | | | | | | |
|--|----------------|----|----------------|-----|----------------|----|----------------|--|--|
| No. | Accession code | No | Accession code | No. | Accession code | No | Accession code | | |
| 1 | CIP-395096.2 | 7 | CIP-396244.12 | 13 | CIP-391930.1 | 19 | CIP-395077.12 | | |
| 2 | CIP-392640.524 | 8 | CIP-395114.5 | 14 | CIP-391381.9 | 20 | CIP-399053.15 | | |
| 3 | CIP-396031.201 | 9 | CIP-396029.205 | 15 | CIP-395112.19 | 21 | Ararsa | | |
| 4 | CIP-397079.26 | 10 | CIP-399062.102 | 16 | CIP-393382.44 | 22 | Belete | | |
| 5 | CIP-395017.242 | 11 | CIP-395017.229 | 17 | CIP-391058.175 | 23 | Guddane | | |
| 6 | CIP-399078.11 | 12 | CIP-396240.23 | 18 | CIP-396039.103 | 24 | Kellacho | | |
| | | | | | | | | | |

Table 15. List of potato genotypes used in the study.

The source of all genotypes except the local cultivar "Kellacho" was CIP

3. Results and Discussion

Analysis of variance indicated the presence of highly significant ($P \le 0.01$) differences among genotype for all traits (Table 2). This suggested the presence of genetic variation among genotypes that could be exploited in selection for desirable traits.

Table 2. Mean squares from analysis of variance for tuber yield and its components.

| 1 5 | 5 | | 1 | | |
|---|-------|----------|-------|------|--------|
| | Rep | Genotype | Error | LSD | CV (%) |
| Trait | (2) | (23) | (46) | (5%) | |
| Plant height(PH) | 508 | 869.4** | 243.6 | 25.5 | 29.8 |
| Stem number per hill(SN) | 2.7 | 5.4** | 1.5 | 2.1 | 31.7 |
| Leaf area index(LAI) | 15.3 | 179.4.** | 33.6 | 9.5 | 28.2 |
| Biomass yield (BMY) | 2070 | 30489.** | 3609 | 98.7 | 26.3 |
| Average tuber weight(ATW) (g) | 108.9 | 2251.6** | 287 | 27.8 | 30.4 |
| Harvest index(HI) (%) | 195.1 | 312.2** | 91.6 | 15.7 | 3.6 |
| Marketable tuber yield (MTY) t ha ⁻¹ | 65.9 | 439.7** | 24.5 | 8.1 | 28.2 |
| Unmarketable tuber yield(unMTY) | 1.6 | 9.3** | 0.3 | 0.8 | 29.2 |
| Total tuber yield (TTY) t ha ⁻¹ | 80.1 | 443.1** | 32.4 | 9.4 | 29.3 |
| | | | | | |

** , highly significant at P \leq 0.01. Numbers in parenthesis stands for the degree of freedom, Rep = replication, LSD (5%) = least significant different at 5% probability level and CV (%) =coefficient of variation in percent.

Table 3. Genetic variability of tuber yield and its components

| | Range | Mean | | | σ^2_e | | | | GA | GAM (%) |
|-------|------------|------|--------------|--------------|--------------|------|------|-------|------|---------|
| Trait | | | $\sigma^2 g$ | $\sigma^2 p$ | | GCV | PCV | H^2 | (5%) | |
| PH | 19.5-78 | 58.4 | 211.4 | 457 | 245.6 | 24.9 | 36.6 | 46.3 | 20.4 | 34.8 |
| NS | 2-6.2 | 3.85 | 1.3 | 2.9 | 1.6 | 30.1 | 44.6 | 45.4 | 1.6 | 41.8 |
| LAI | 6-33 | 20.5 | 48.5 | 82.2 | 33.7 | 33.9 | 44.2 | 59.1 | 11 | 53.7 |
| BMY | 90.3-418.6 | 228 | 2699.3 | 5618.3 | 2919 | 22.7 | 32.8 | 48 | 74.2 | 32.5 |
| ATW | 3.8-114.5 | 55.8 | 654.9 | 941.9 | 287 | 45.8 | 55.0 | 69.5 | 43.9 | 78.7 |
| HI | 57.5-94 | 78.8 | 73.5 | 165.2 | 91.7 | 10.8 | 16.3 | 44.5 | 11.7 | 14.9 |
| MTY | 0.06-43.7 | 17.5 | 139.3 | 163.9 | 24.6 | 47.2 | 51.2 | 85.0 | 22.4 | 89.7 |
| TTY | 0.8-46.1 | 19.4 | 130.8 | 155.9 | 25.1 | 51.9 | 56.7 | 83.9 | 21.5 | 98.1 |

 σ^2 g =genotypic variance, σ^2 p =phenotypic variance, GCV=genotypic coefficient of variation in percent, PCV=phenotypic coefficient of variation in percent, H²=heritability in broad sense, GAM.= genetic advance as percent mean, plant height, SN = stem number per hill, LAI = leaf area index, BMY=biomass yield, ATW = average tuber weight, HI = harvest index, MTY = marketable tuber yield, TTY = total tuber yield t ha⁻¹

In the present study, the phenotypic variance was in general higher than the genotypic variance for all the characters (Table 3). Thus it suggests the substantial influence of environment besides the genetic variation for expression of these traits. Genotypic and phenotypic coefficient of variation estimates were high(>20%) for total tuber yield, average tuber weight, marketable tuber yield, number of stem per plant, leaf area index, plant height and biomass yield with low magnitude of differences of the two.

Both Genotypic and phenotypic coefficient of variation values were moderate for harvest index. This is in agreement with results reported by (Baye *et al.*, 2005 and Addisu, *et al.*, 2013) that high GCV and PCV for tuber weight per hill while moderate GCV and PCV were reported by (Shashikamal *et al.*, 2006). The traits which exhibited high estimates of GCV and PCV has high probability of improvement through selection while the improvement of traits is difficult or virtually impractical through selection which exhibited low estimates for both variability components due to the masking effect of environment on the genotypic effect (Sing, 1990).

High heritability (>60%) was exhibited for marketable tuber yield, total tuber yield, average tuber weight and tuber dry mater content while moderate heritability exhibited for the remaining characters. This is in accordance with the findings of (Choudhary and Sharma, 1984; Roy and Singh, 2006) who reported high

estimates of heritability for average tuber weight, number of tubers per plant and total tuber yield. Hence, these characters are amendable for selection to improve the crop. High(>20%) genetic advance as percent of mean also recorded for total tuber yield, marketable tuber yield, average tuber weight, leaf area index, number of stem per plant, plant height and biomass yield while moderate for harvest index. High heritability coupled with high genetic advance as percent of mean recorded for the traits viz. total tuber yield, marketable tuber yield and average tuber weight. Hence, these characters were predominantly governed by additive gene action and can be improved through simple selection (Sing, 1990).

In conclusion the study revealed that the presence of considerable variability in tested genotypes for economic importance traits and the higher chance of selecting genotypes with high yield and moderately resistant to late blight which indicated evaluation of breeding materials at early generation can be a base for plant breeding to improve the crop through selection. In the absence of creating variation through crossing in the country, it is necessary to introduce potato genotypes every time from the source. The introduced genotypes need to be evaluated for target area or for wide adaptability across regions in the country.

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