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Genetic variability for yield, related traits and reaction to late blight in potato (*Solanum tuberosum L.*) genotypes at Sinana, South Eastern Ethiopia

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ABSTRACT

This study was conducted to assessing the nature and magnitude of variability for tuber yield, yield related and late blight resistance traits. The experiment was laid out in randomized complete block design with three replications at Sinana Agricultural Research Center. The genotypes showed highly significant ($P<0.01$) differences for all the characters studied. Genotypes exhibited wide ranges of mean values for all characters. The highest total tuber yield (46.1 t ha^{-1}) was obtained from the advanced clone, CIP-392640.524 followed by Belete (41t.ha^{-1}). Late blight appeared early on farmers cultivar Kellacho (48 days after planting) and lately on CIP-399062.102(74 days after planting). Percent severity index (PSI) and area under disease progress curve (AUDPC) ranged between 33-39.7% and 105 to 2370, respectively, for eleven newly introduced clones and the released variety Belete. These genotypes can be categorized as moderately resistances. Other genotypes had higher PSI and AUDPC and fall under late blight susceptible category. High genotypic (GCV) and phenotypic (PCV) coefficient of variations computed which ranged from 22.7 to 51.9% and from 32.8 to 56.7%, respectively, for all the traits except for days to maturity with low values computed for both. Heritability in broad sense (H^2) and genetic advance as percent of the mean (GAM at 5% selection intensity) ranged from 44.5 to 89.5% and 14 to 98.1%, respectively. Both H^2 and GAM high for total tuber yield, marketable tuber yield, average tuber weight, marketable tuber number per hill, percent severity index, days to flowering and area under disease progress curve. This suggested these traits are amenable to selection. 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. But it is necessary to continue the evaluation of genotypes across seasons and locations to identify genotypes that could be released as variety for the study area.

Keywords: Area under disease progress curve, genotype; late blight; percent severity index

Potato has been highly recommended by the Food and Agriculture Organization s a food security crop (FAO, 2014). Potato is known to contain appreciable amounts of proteins, essential vitamins and minerals. Potato is a part of traditional food of Ethiopia and is grown as security crop against crop failures and/or to bridge the food deficit periods (Berga *et al.*, 1994). In general, the contribution of potato to the food security and food self-sufficiency strategy of the country, income generation, soil-based resource conservation, employment opportunity and livelihood improvement is great.

Despite its great contribution, the food potential of this crop has not been fully exploited and utilized in the country. The majority of the Ethiopian population especially in Bale high land depends mainly on cereal crops as food sources that are nutritionally deficient in vitamin and mineral content and low in their yield potential as compared to potato. Integration of these crops in the production and food system of the country is essential since they have great contributions towards food and nutrition security of the country than other crops mainly owing to their nutritional content and high yield per unit area (Gebremedhin *et al*., 2008). Potato is grown by greater than 1.4 million households in Ethiopia. However, the national average tuber yield (11.8 t.ha^{-1}) is very low compared to the world's average yield of 19 t.ha^{-1} (CSA, 2014). The low yields are attributed to many factors, a shortage of good quality seeds of improved potato varieties and the prevalence of various pest and diseases (mainly late bight) have prevented growers from achieving full yield potential (Bekele and Hailu, 2003 and Hirpa *et al*., 2010).

The presence of genetic variability is considered to be the prerequisite in plant breeding program. In most cases, the richer the source materials and germplasms the more and the best varieties can be developed and released. Some countries such as Ethiopia, the potato breeding programmes depend entirely on CIP materials. These introduced potato materials served as base population for developing promising cultivars. 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.

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MATERIALS 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(m.a.s.l.) Average annual maximum and minimum temperatures are 21 and 9^oC, 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 kellecho were planted on 12 August, 2014 during the main cropping season. The experiment was arranged in randomized complete block design (RCBD) with three replications. The spacing between rows and plants was 0.75 m and 0.30 m, respectively. The spacing between plots and adjacent replications was 1 m and 1.5 m, respectively. At both end of each row, tubers of known late blight susceptible (Kellecho) was planted and that were used as inoculums source or "spreader rows". Thus, each genotype or plant in each plot had a chance to receive continuous sources of inoculums under natural distribution.

The middle rows were used for data collection. Data were collected on phenological, growth parameters, tuber yields and yield components, percent severity. Percent severity index and area under disease progress curve was calculated from disease severity collected weekly.

According to Mohan and Thind (1999) depending on calculated percent severity index, the genotypes were classified into highly resistant (up to 5), resistant (5-20) moderately resistant (21-40) and susceptible (>40). Area under disease progress curve was calculated by Campbell and Madden (1990) formula and it was interpreted directly without transformation as the higher the AUDPC, the more susceptible genotype (CIP, 2006).

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance indicated the presence of highly significant ($P<0.01$) differences among genotype for all traits. This suggested the presence of genetic variation among genotypes that could be exploited in selection for desirable traits to improve the productivity of the crop in the study area.

Range and mean Performance

The wide range, not only for tuber yield, but for almost all the other characters and the mean values of the genotypes for the various characters showed differences among the genotypes is an indication that selection is rewarding for improvement of the crop (Table1) . The highest total tuber yield (46.1 t ha^1) was recorded from the newly introduced advanced clone, CIP-392640.524. Other four advanced clones gave total tuber yield higher than the mean tuber yield of the two released varieties (Gudanie and Ararsa). The best performing variety Belete and other eleven advanced clones had relatively lower percent severity index and area under disease progress curve ranged from 33 to 39.7% and 105 to 2370, respectively, at nearly 74 days after planting can categorized as moderately resistances. This suggested the importance of continuous evaluation of these breeding materials because there is the higher chance of obtaining genotypes with high tuber yield and resistance to late blight. Other genotypes including the two released varieties (Gudanie and Ararsa) were susceptible to late blight evident from higher percent severity index and area under disease progress curve. This is in line with the finding of Jaime *et al.*(2014) who reported high susceptible cultivar Shepody had the highest AUDPC value among 10 potato cultivars in Argentina.

Considering both disease parameters (PSI and AUDPC) eleven newly introduced genotype and one released variety Belete were categorized as moderately resistant. Thus, these genotypes are found promising for further improvement as breeding materials. Others may be considered for cultivation using other late blight management option especially in the case of Ararsa and Gudaine. Similar results were reported by Mekonen *et al.*(2009) that moderately resistant cultivar, Gudanie, had a clear AUDPC response to additional fungicide sprays, although apparently for about three sprays.

Estimates of phenotypic and genotypic variation

The estimated phenotypic variation was relatively greater than the genotypic variations in magnitude for all characters considered. The phenotypic and genotypic coefficient of variation values can be categorized as low (<10%), moderate (10-20%), and high (>20%) as indicated by Robinson and Barry,(1966). Genotypic and phenotypic coefficient of variation estimates were >20% considered as high for most of studied traits with low magnitude of differences of the two (phenotypic and genotypic coefficient of variation). Both genotypic and phenotypic coefficient of variation values were moderate(>10) for area under disease progress curve and harvest index, and low(<10) for days to maturity. Baye *et al*. (2005) and Addisu, *et al.* (2013) reported high phenotypic coefficient of variation for tuber weight per hill while moderate phenotypic and genotypic coefficient of variations reported by Shashikamal *et al.*, (2006). The traits which exhibited high estimates of genotypic and phenotypic coefficient of variations had high probability of improvement through selection while traits with low

Table 1: Mean performance of 24 potato genotypes for yield and yield components at Sinana in 2014 bona cropping season

No	Genotypes	DM	PH	SN	LAI	BMY	ATW	HI	MTY	MTNPH	TTY	DDA	PSI	AUDPC
1	CIP-395096.2	111 ^{e}	22 ^{ef}	2 ^{f}	20.7^{b-d}	114^{g-i}	3.7 ^{i}	94^{a}	0.06^{n}	0.7 $^{h-j}$	0.8 ^{j}	63 $^{b-d}$	33.0^{a}	105^{a}
2	CIP-391381.9	98^{a}	49 $^{a-e}$	3.6 $^{b-e}$	6 ^{ef}	102^{hi}	16.6 $^{g-i}$	91 ^{ab}	3 $^{l-n}$	3.2 ^{b}	6 $^{h-j}$	48 ^{e}	80.3^{c-e}	1753 ^{e}
3	CIP-395077.12	105^{cd}	37 $^{b-e}$	2.5^{d-f}	14 $^{c-e}$	253^{d-f}	56 $^{b-f}$	68.7^{d-g}	11.3 $^{h-l}$	0.7 $^{h-j}$	12^{g-i}	63 $^{b-d}$	39.7^{a}	248.6 ^{a}
4	CIP-99062.102	119^{f-h}	71.6 ^{a}	3.6^{b-e}	26^{ab}	273 $^{c-f}$	67 $^{b-d}$	71.2^{c-g}	23.2^{d-f}	1.3 $^{f-i}$	24.5 $^{c-f+}$	74.67 ^{a}	38.67^{a}	105^{a}
5	Belete	114 ^{ef}	71.4^{a}	4.6^{a-d}	26^{ab}	394^{ab}	109 ^{a}	79.8^{b-e}	39.4^{ab}	0.7 h-j	41 ^{ab}	70^{ab}	33^{a}	105 ^{a}
6	CIP396039.103	119^{f-h}	58.7^{a-d}	6.2 ^{a}	22^{a-d}	270^{d-f}	47 $^{c-g}$	88 $^{a-c}$	21 $^{e-g}$	1.3 $^{f-i}$	23.5^{c-f}	48 ^{e}	68^{b-e}	1119.^{d}
7	CIP-399078.11	105^{cd}	51.5^{a-e}	4.7^{a-d}	26^{ab}	258^{d-f}	62 $^{b-d}$	66.5^{e-g}	15.2 $^{f-i}$	0.7 $^{h-j}$	15.9 $^{f-h}$	53 ^{de}	67^{b-e}	575.2^{ab}
8	CIP-395112.19	102^{a-d}	39.8^{b-e}	2.1^{ef}	19^{b-d}	207^{e-h}	114^{a}	84.9^{a-e}	13.2^{g-k}	0.3 ^{j}	13.6 ^{eh}	72.3^{ab}	55.3 $^{a-c}$	332.3 ^{ab}
9	CIP395017.242	105^{cd}	51.9^{a-e}	5.3^{ab}	28 ^{ab}	220^{e-g}	71.8^{bc}	79 $^{b-e}$	21.5^{e-g}	1.4 $^{e-i}$	22.9 $^{c-f}$	72.3^{ab}	38.67 ^{a}	145.8^{a}
10	Kellacho	98^{ab}	33.3^{c-f}	3.4^{b-e}	6.7^{ef}	92^{hi}	12 ^{hi}	68.6^{d-g}	1.4 ^{mn}	1.3^{f-i}	2.7 ^{ij}	48^{e}	82.0^{de}	2014.1^{ef}
11	CIP-395114.5	119^{fh}	61.6^{a-c}	4.5^{a-d}	28^{ab}	418 ^{a}	62 $^{b-d}$	71.7^{c-g}	32.7^{bc}	0.6 $^{h-j}$	33.6 ^{bc}	62.6 $^{b-d}$	33.0a	122.5^{a}
12	CIP-396240.23	119^{f-h}	53^{a-d}	4.6^{a-d}	25.6^{a-c}	293^{b-e}	69.7^{bc}	87 $^{a-d}$	25.5^{c-e}	1.5 $^{e-i}$	26.8 $^{c-e}$	62.6 $^{b-d}$	36.67^{a}	180.8^{a}
13	CIP-397079.26	105^{cd}	30.1^{d-f}	2.1 ^{ef}	12 $^{d-f}$	90.3i	58 $^{b-e}$	84.9^{a-e}	4.1 $^{k-n}$	0.2 ^{j}	4 ^{ij}	48^{e}	91.33^{e}	2370^{g}
14	CIP391058.175	119^{h}	64.8^{ab}	4.8^{a-d}	28.9^{ab}	297^{b-e}	72 ^{bc}	83 $^{a-e}$	29 $^{c-e}$	1.5^{e-h}	31^{bc}	65^{a-c}	33^{a}	105^{a}
15	CIP396029.205	119^{f-h}	65.2^{ab}	3.8^{a-e}	19.9^{b-d}	281^{c-e}	74 ^{bc}	84 $^{a-e}$	26^{c-e}	0.7 $^{h-j}$	27^{cd}	63 $^{b-d}$	37 ^{a}	189.1^{a}
16	Ararsa	112 ^{e}	48.7^{a-e}	2.8^{c-e}	20.5^{b-d}	164^{f-i}	43 $^{c-h}$	76 $^{b-f}$	13 $^{g-j}$	1.1^{g-j}	14^{eh}	63 $^{b-d}$	57^{a-d}	372 ^{ab}
17	CIP-399053.15	98 ^{a}	58.7^{a-d}	4.5^{a-d}	18.5^{b-d}	136^{g-i}	34^{d-i}	81^{a-e}	7.5 $^{i-n}$	2.2 $^{c-f}$	9 $^{g-j}$	48 ^{e}	66 $^{b-d}$	1191^{d}
18	CIP-393382.44	105^{cd}	58.6^{a-d}	3.2 $^{b-e}$	15^{c-e}	127 $^{g-i}$	54 $^{b-f}$	83^{a-e}	10 $^{i-m}$	0.6 $^{h-j}$	11 $^{g-j}$	53 ^{de}	65 $^{b-d}$	1134^{d}
19	CIP396031.201	105^{cd}	19.5^{f}	3.1 $^{b-e}$	17.5 $^{b-d}$	130^{g-i}	27 $^{e-i}$	73 $^{b-g}$	5.5 $^{j-n}$	1 h-j	6.6 $^{h-j}$	53de	33.3^{a}	161 ^{a}
20	CIP395017.229	100^{a-c}	74.6 ^{a}	2.7^{c-e}	25.5^{a-c}	261^{d-f}	44 $^{c-g}$	57 g	14 $^{f-j}$	2.9 $^{b-d}$	16^{d-h}	58 $^{c-e}$	56.6^{ad}	750 ^{c}
21	Guddane	112^{e}	47.9 $^{a-e}$	5.4^{ab}	22 $^{b-d}$	192^{e-i}	58 $^{b-e}$	81 $^{a-e}$	20 $^{e-h}$	2.3 $^{c-e}$	23 $^{c-f}$	63 $^{b-d}$	43^{ab}	581^{bc}
22	CIP-3940.524	114^{e-g}	59.6^{a-d}	4.8^{a-d}	33 ^{a}	383.7^{a-c}	81 ^{b}	87 $^{a-d}$	43.7^{a}	2.4 $^{c-e}$	46.1 ^{a}	58 $^{c-e}$	36.6^{a}	186^{a}
23	CIP-391930.1	98 ^{a}	60.8^{a-d}	4.9^{a-c}	3 ^{f}	140^{g-i}	24 $^{f-i}$	58 fg	3.3 $^{i-n}$	8.7^{a}	11^{g-i}	48^{e}	91.6^{e}	2165^{fg}
24	CIP-396244.12	119^{f-h}	78 ^{a}	4.3^{a-e}	24^{a-c}	366^{a-d}	71^{bc}	81 $^{a-e}$	31^{b-d}	1.4 $^{f-i}$	33 ^{bc}	65^{a-c}	37 ^{a}	264.1^{a}
	Range	**98-119**	**19.5-78**	**2- 6.2**	**6 - 33**	**90-418**	**3.7-114**	**57.5-94**	**0.06-43**	**0.65-8.7**	**0.76-46**	**48-74**	**33-91**	**105-2370**
	Mean	**109**	**58.4**	**3.85**	**20.54**	**228**	**55.8**	**78.8**	**17.5**	**1.721**	**19.41**	**59.31**	**53.7**	**680**
	CV%	**2.4**	**29.8**	**31.7**	**28.2**	**26.3**	**30.4**	**12.1**	**28.2**	**29.2**	**29.3**	**10.3**	**24.9**	**24.6**
	Level of significance	**	**	**	**	**	**	**	**	**	**	**	**	**

Note: *DM= days to maturity, PH=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, MTNPH = marketable tuber number per hill, TTY = total tuber yield t ha$^{-1,}$ DDA = days to late blight appearance, PSI =percent severity index and AUDPC = area under disease progress curve* estimates of genotypic coefficient of variations, improvement through selection is difficult or virtually impractical due to the masking effect of environment on the genotypic effect (Singh, 1990).

Estimate of heritability and genetic advance

The estimated heritability ranged from 44.08 to 89.5% and genetic advance as percent of mean ranged from 14 to 98.1% (Table 2). Both heritability and genetic advance as percent of mean estimates were high for total tuber yield, marketable tuber yield, average tuber weight, marketable tuber number per hill, percent severity index, days to flowering, area under disease progress curve and days to late blight appearance. The high value of genetic advance for these traits showed that these characters are governed by additive genes and selection could be rewarding for the improvement of these traits (Singh, 1990). This indicated a high chance for improving the crop through selection because trait with high heritability and genetic advance is a base for plant breeding to improve the crop through selection (Luthra, 2001). Moderate heritability and genetic advance was computed for tuber dry matter, harvest index and days to maturity.

In conclusion this study revealed the existence of genetic variability in 24 potato genotypes for tuber yield, yield related traits and moderately resistance to late blight. This suggested the higher chance of selecting genotypes to improve the productivity of the crop. However, it is hardly possible to make conclusion with one season experiment, therefore, it is necessary to evaluate genotypes for a number of seasons and locations to recommend the genotypes with high tuber yield and resistance to late blight. In addition, the future potato improvement program in the study area should have to include genotypes highly resistance to late blight other than these because the identified promising genotypes in this study showed only moderate resistance to late blight which can be overpass by the disease very soon. Because the pathogen is known with high mutable characteristics that make resistant varieties susceptible soon after they deployed.

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Table 2: Genotypic and phenotypic coefficient of variances, heritability and genetic advance in 24 potato genotypes for 14 traits at Sinana during 2014 cropping season.

Trait	**ó**^{2}g	**ó**^{2}p	**ó**^2_e	GCV	PCV	H^2	GA (5%)	GAM (%)
DF	321.1	381.7	60.6	30.7	33.5	84.1	33.8	58
DM	61.7	68.7	7	7.2	7.6	89.7	15.3	14
PH	211.4	457	245.6	24.9	36.6	46.3	20.4	34.8
NS	1.3	2.9	1.6	30.1	44.6	45.4	1.6	41.8
LAI	48.5	82.2	33.7	33.9	44.2	59.1	11	53.7
BMY	2699.3	5618.3	2919	22.7	32.8	48	74.2	32.5
MTNPH	10.6	15.2	4.6	44.8	53.3	70.4	5.6	77.4
ATW	654.9	941.9	287	45.8	55.0	69.5	43.9	78.7
HI	73.5	165.2	91.7	10.8	16.3	44.5	11.7	14.9
MTY	139.3	163.9	24.6	47.2	51.2	85.0	22.4	89.7
TTY	130.8	155.9	25.1	51.9	56.7	83.9	21.5	98.1
TDM	8.40	13.3	4.9	11.9	14.9	63.2	4.7	19.5
PSI	442.3	577.8	135.5	39.2	44.7	76.5	37.9	70.5
AUDPC	0.21	0.24	0.03	18.2	19.2	89.5	0.9	35.3

Note: ***ó***^{2}*g =genotypic variance,* ***ó***^{2}*p =phenotypic variance, GCV & PCV=genotypic & phenotypic coefficient of variation,* H^2*=heritability in broad sense, GA (5%)=expected genetic advance, GAM.= genetic advance as percent*

DF=days to flowering, DM= days to maturity, PH=plant height, NS = stem number per hill, LAI = leaf area index, BMY=biomass yield, MTNPH = marketable tuber number per hill, ATW = average tuber weight,

HI = harvest index, MTY marketable tuber yield, TTY = total tuber yield t ha^{-}*, PSI =percent severity index and AUDPC = area under disease progress curve*

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