GENETIC VARIABILITY FOR YIELD, YIELD RELATED TRAITS AND REACTION TO LATE BLIGHT IN POTATO (*Solanum tuberosum* L.*)* GENOTYPES AT SINANA, SOUTH EASTERN ETHIOPIA

MSc THESIS

GETACHEW ASEFA

MAY 2015

HARAMAYA UNIVERSITY, HARAMAYA

Genetic Variability for Yield, Yield Related Traits and Reaction to Late Blight in Potato (*Solanum tuberosum* L.*)* Genotypes at Sinana, South Eastern Ethiopia

A Thesis Submitted to the School of Plant Sciences

School of Graduate Studies

HARAMAYA UNIVERSITY

In Partial Fulfillment of the Requirements for the Degree of

MASTER OF SCIENCE IN AGRICULTURE (PLANT BREEDING)

Getachew Asefa

May 2015

Haramaya University, Haramaya

HARAMAYA UNIVERSITY

SCHOOL OF GRADUATE STUDIES

I hereby certify that I have read and evaluated this thesis entitled **"Genetic Variability for Yield, Yield Related Traits and Reaction to Late Blight in Potato (*Solanum tuberosum* L.) Genotypes at Sinana, South Eastern Ethiopia"** prepared, under my guidance, by Getachew Asefa. We recommend that it be submitted as fulfilling the thesis requirement.

Wassu Mohammed (PhD)	_____	_____
Major Advisor	Signature	Date
Tesfaye Abebe (PhD)	_____	_____
Co-advisor	Signature	Date

As member of the Board of Examiners of the MSc Thesis Open Defense Examination, We certify that we have read, evaluated the Thesis prepared by Getachew Asefa, and examined the candidate. We recommended that the Thesis be accepted as fulfilling the Thesis requirement for the Degree of Master of Science in Plant Breeding.

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DEDICATION

To my lovely daughter; Fenet Getachew

STATEMENT OF AUTHOR

By my signature below, I declare and affirm that this thesis is my own work. I have followed all ethical and technical principle of scholarship in the preparation, data collection, data analysis and completion of this thesis. Any scholarly matter that is included in this thesis has been given recognition through citation.

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Name: Getachew Asefa Signature:_____

Date: _____

School/ Department: Plant Science

Haramaya University, Haramaya

BIOGRAPHICAL SKETCH

The author was born on 21 December 1984 G.C at Ali, Agarfa Woreda, Bale Zone South Eastern Ethiopia. He went to the same zone, Golocha Woreda, Abonga Elementary School in 1992 where he had completed his elementary education in 1997. He joined Yebsana Kakula Junior Secondary School in 1998 and studied 7^{th} and 8^{th} grades until 1999. He then joined Agarfa Senior Secondary School in 2000 where he had completed his high school in 2003. The author joined Haramaya University College of Agriculture in 2004/5 for his higher education and graduated in 2007 with Degree in Plant Production and protection (CPP).

Soon after graduation, he was employed by the then Bale Agricultural Development Enterprise, the present Oromia Seed Enterprise in 2008 as Agronomist. After serving one year the author left the enterprise and employed by Oromia Agricultural Research Institute as junior Researcher I, in Horticulture and Seed Spice technology generating case team. He served as a junior entomologist until he joined the School of Graduate Studies in 2013/2014 to pursue his MSc. Degree in Plant Breeding.

ACKNOWLEDGEMENTS

First of all, the author is highly indebted to his advisors Dr Wassu Mohammed and Dr. Tesfaye Abebe for their inexorable instruction, guidance and encouragement throughout the implementation of the research and preparation of this thesis.

The author is very grateful to Oromia Agricultural Research Institute for giving him an opportunity, and for paying him his monthly salary while he was on study leave and covering research budget. The author is also indebted to Sinana Agricultural Research Center for their constant assistance in provision of materials and facilities.

The author's deepest gratitude is due to Horticulture and seed spice technology generating case team staffs for their unreserved assistance during both field and laboratory research and he would like to extend his thanks to all SARC staff colleagues for their encouragements and friendly criticisms, which directly or indirectly contributed for my success.

Special thanks also due to Mr. Shure Soboka of SARC, Department of Soil Science, for his invaluable comments, assisting in laboratory for quality parameters and for sharing his accumulated experiences, and also my word of thanks due to Mr. Alemu Worku former national potato research coordinator and Wubet Awoke of Adet Agricultural Research Centre, Department of Horticulture, for their invaluable support in providing potato seed tuber from Adet Agricultural research Center to Addis Abeba.

The author would like to thank his wife, Tejitu Ketema for shouldering responsibilities of our home during his whole study period.

At last, but not least, he would like to express his deepest thankfulness to his mother, W/o Desi Dadi, and his brothers Diriba Asefa for their encouragement during the study. It is also a privilege to extend my spatial thanks to Ato Ketema Gemeda, Toleshi Mengistu, Tsehay Ketema, Sintayehu Ketema and Getahun Ketema for their patience and understanding when I was totally devoted to this work at the expense of their conveniences.

ABBREVIATIONS AND ACRONYMS

ANOVA	Analysis of Variance
ARARI	Amhara Regional Agricultural Research Institute
AUDPC	Area Under Disease Progress Curve
CIP	International Potato Center
DDA	Days to Disease Appearance
EIAR	Ethiopian Institute of Agricultural Research
FAO	Food and Agricultural Organization
HARC	Holleta Agricultural Research Center
PSI	Percent Severity Index
RCBD	Randomize Complete Block Design
SARC	Sinana Agricultural Research Center

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ABSTRACT

The highlands of Bale is known with potato production, but the productivity of the crop is low due to the growing of low yielding genotypes susceptible to late blight. This needs to develop varieties with high yield and resistant to late blight. Therefore, this study was conducted to evaluate 24 potato genotypes with the objective of assessing the nature and magnitude of variability for tuber yield, yield related and late blight resistance traits, and association of tuber yield with other traits. The experiment was laid out in randomized complete block design with three replications at Sinana Agricultural Research Center. The genotypes showed highly significant ($P \leq 0.01$) differences for all the characters studied, except for starch and specific gravity. 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 curve (AUDPC) ranged between 33-39.7% and 105 to 2370, respectively, for 11 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, area under disease progress curve and days to late blight appearance. This suggested these traits are amenable to selection. Marketable tuber yield, average tuber weight, marketable tuber number per hill and stem number per plant had high and positive direct effect on total tuber yield, while unmarketable tuber yield, unmarketable tuber number per hill, percent severity index and area under disease progress curve on total tuber yield had negative direct effects. Various other characters also influenced the total tuber yield favorably or unfavorably via other characters. This suggested the importance of selecting of genotypes with high and low mean values for the traits that showed positive and negative direct and indirect effects on yield, respectively. 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 approved as variety for the study area.

Keywords: Area under disease curve; Genotype; Late blight; Percent severity index; Variability;

1. INTRODUCTION

Potato (*Solanum tuberosum* L.) is an important world crop that belongs to the family of Solanaceae, genus *Solanum,* sub-genus pachstemonum and section tuberarium (Haward, 1969). The basic chromosome number of the genus *Solanum* is 12 (Hawkes, 1990). Cultivated potato include diploid (2n=2x=24), triploid (2n=3x=36), tetraploids (2n=4x=48), pentaploid (2n=5x=60) as well as hexaploid (2n=6x=72). Out of these, tetraploids have been the most productive and wide spread genotype (Dodds, 1962). With the exception of few hybrids, all cultivated potatoes are included in a single species, *Solanum tuberosum* L. (Hawakes, 1956). Potato has its origin in the Andes of South America and was first cultivated in the Andes in the vicinity of Lake Titicaca near the present border of Peru and Bolivia (Horton, 1987).

More than a billion people eat potatoes, and the total global potato production exceeds 374 million metric tons per year. Potato has been highly recommended by the Food and Agriculture Organization (FAO) as a food security crop. Potato is the third most important food crop in the world after rice and wheat in terms of human consumption (FAO, 2009; FAO, 2014). 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 was introduced to Ethiopia in the 19th century by a German Botanist Schimper (Pankhrust, 1964). Since then, potato has become an important garden crop in many part of Ethiopia. Potato is grown by greater than 1.4 million households. It also created a direct employment opportunity to at least 1.4 million household growers excluding those involved at wholesaler, retailer, transportation and processing areas. 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 acreage and yield are attributed to many factors, a shortage of good quality seeds of improved potato varieties, low input use, unfavorable weather and soil physico-chemical properties and the prevalence of various pest and diseases (mainly late bight) have prevented growers from achieving full yield potential (Kassa and Beyene, 2003; Gildemacher *et al*., 2009 and Hirpa *et al*., 2010)

Potato is a crop which has high potential and significant contributions towards household food and nutritional security, income generation and provision of energy, local industries and natural resources base conservation (Gebremedhin *et al*., 2008). In addition, it 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, as ready for harvest during "hunger months (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 specially 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 contribution 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).

The main hurdle to the crop productivity is growing of potato genotypes introduced at different time with different levels of late blight resistance/susceptibility. Although potato cultivars resistant to late blight are being developed, better resistance to late blight is needed, as are optimal strategies for deploying resistance. Late blight is especially important in the traditional potato growing areas. If not controlled, losses may reach 100 percent (Rubio-Covarrubias *et al*., 2005). In highland areas of Ethiopia, late blight and bacteria wilt (*Ralstonia solanacearum*) are the most important economic diseases that cause an estimated yield loss of up to 70% (Mekonen *et al*., 2011). The presence of genetic variability is considered to be the prerequisite in any 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 (Haile Michael, 1979). The variety development, which involves evaluation, selection, release and registration procedures pass

through several stages (George and Otim, 2007). 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.

Bale Zone known by its different agro ecologies, with suitable environmental condition for potato production. But, the production of this crop is not as much as the potential of the Zone. The most bottlenecks for potato production are lack of improved varieties and late blight (*Phytophthora infestans*). Different observers indicated different resistant varieties with chemical (Mancozeb 80% WP) shown different reaction towards this disease. According to Abreham (2009) varieties are differing in their reaction to late blight infection. The evaluation of different potato clones for their resistance to late blight disease showed considerable difference among the clones in their area under disease progress curve (AUDPC). Assessing and generation of data on the extent and pattern of genetic variability for yield and reaction to late blight in the available population and advanced clones is essential for further improvement of the crop. Similarly, information on extent and nature of interrelationships among different traits of potato genotypes and traits contributing to tuber yield are also required in formulating efficient scheme of multiple trait selection.

The productivity of potato in Bale zone is less than the national average 11.8 $t.ha^{-1}$ (CSA, 2014). Among the factors contributing to this low production and productivity is the use of local cultivars that are low in yield and susceptible to disease. Although improved potato varieties resistant to late blight are being developed, the availability of the varieties to the farmers in the region is very low. On the other hand, varieties with major gene resistance are quickly overcome by *P. infestans*(Wastie, 1991). Therefore, varieties with better resistance to late blight are needed every time. Hence, it is necessary to evaluate and identify genotypes that are high yielding and resistant to late blight. Accordingly, this stud was undertake with following objectives.

Objectives:

- To study the nature and magnitude of variability for tuber yield, yield related and late blight resistance traits in potato genotypes
- To determine association between tuber yield and other traits.

2. LITERATURE REVIEW

2.1 Origin, Distribution and Importance of Potato

It has just been shown that great genetic diversity of the cultivated potato species and related wild species exists in the Andean region of South America. Moreover, the concentration of specific diversity is greater between the central areas of Peru and Bolivia. In this region, numerous native cultivars also show great variation in leaf type, flower color and tuber characters such as shape and color. This evidence, according to Pavilov's method for determining the center of origin of a crop plant, indicates that this region is within the domain area where potatoes are originated (Bukasov, 1939).

The largest numbers of species, about 54% of the South American species, are found in Peru (Ochoa, 1975). Within the cultivated species, the sub-species *tuberosum* is the only one grown worldwide. However, native cultivars of this species have been cultivated for many centuries in Southern Chile. The sub-species *andigena* is still widely distributed in the Andean zones of Venezuela, Colombia, Ecuador, Peru, Bolivia and Northern Argentina. It is also cultivated in some areas of Guatemala and Mexico. However, the area with the greatest variation of this species has been located between central Peru and central Bolivia (Huaman, 1980).

Today potato is grown in about 140 countries, more than 100 of which are located in the tropical and sub tropical region (Beukema and Van der Zaag, 1990). Potato was introduced to Ethiopia in the 19th century by a German Botanist Schimper (Pankhrust, 1964). Since then, potato has become an important garden crop in many part of Ethiopia for long period of times. Currently, it is produced throughout the country and has significant contributions towards household food and nutritional security, income generation and provision of energy, raw material for local industries and natural resources base conservation (Gebremedhin *et al*., 2008).

Potato produces more calories and protein per unit area with minimum time and water than most of the major food crops (Upadhya, 1995). It is cultivated worldwide under various environmental conditions. It can be found in both temperate and tropical regions from the sea level to 4000 m

above sea level (André *et al*., 2014). The amount of variability that exists in the germplasm collection of any crop is of the utmost importance for breeding better varieties. Particularly, genetic variability for a given character is a basic prerequisite for its improvement by systematic breeding (Engida *et al*., 2007). Potato is the most important food crop, after cereals, in human diet. It surpasses wheat (*Triticum aestivum* L), rice (*Oriza sativa* L.) and maize (*Zea mays* L.) in the production of dry matter and protein per unit of area (Mohammad *et al.,* 2013). It is a very important food and cash crop in Ethiopia, especially in the high and mid altitude areas. It has a promising prospect in improving the quality of the basic diet in both rural and urban areas of the country.

As a food crop, it has a great potential to supply high quality food within a relatively short period and is one of the cheapest sources of energy. Moreover, the protein from potato is of good composition essential amino acids. Potato also has substantial amounts of vitamins, minerals and trace elements. Such a crop is very important for countries like Ethiopia, where inadequate protein and supplies of calories are the apparent nutritional problems (Berga *et al.*, 1994). If carefully grown, it gives the highest yield of nourishment per hectare of all basic foodstuffs in Ethiopia. Furthermore, the production period is also only 90 to 120 days.

2.2 Genetic Variability

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. Population improvement by recurrent selection is therefore combined with varietal development of elite clones. The new germplasm may possibly undergo several cycles of recurrent selection and then be introduced as parents in the main breeding population undergoing multiple-trait recurrent selection and deployment of advanced lines. (Beukema and Zaag, 1990).

Progeny testing is used to identify the best families and the most promising parental material for use in crossing i.e. those parents that have high general combining ability or breeding values. The best clones from within the best families are identified from further replicated field trials. These selections can be taken forward as potential cultivars for commercial deployment and/or used as parents in the next cycle. This reduces cycle time and is expected to increase the rate of genetic gain in the breeding population. Selection of superior parents can be based on their general combining ability from progeny tests, or mid-parent values or other cross prediction methods for untested clones (Brown *et al*., 1988).

Genotypic variation is an essential component of any conventional crop breeding programme. Conventionally, plant breeders recombine the desired genes from crop varieties and related species by sexual hybridization, and develop new cultivars with the desirable traits such as high yield and resistance to disease, insect and pests, and drought (Kromann *et al.,* 2014). Rasui *et al*. (1995) reported genotypic variation values for plant height and tuber yield per plant to be 19.4 and 16.9% respectively. Genetic variability was low for dry matter and harvest index Sharma, (1999) where as it was reported to be high for shoot number, shoot height, leaf area index and tuber yield (Sandhu and Kang 1998). There is a wide variation for characters and genotypes differed significantly in metric character but minimum variability was noted in respect to days to flowering, 51 and 88 days being the extreme value.

2.2.1 Genotypic and Phenotypic Variability

Potato cultivar development traditionally 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. Multiple crosses are made between selected parents and seedlings are grown as individual spaced plants in the field or individual pots in the glasshouse, which is common practice in many breeding steps for the seedling generation (Gopal *et al*., 1994). This is followed by one or two stages of visual mass selection of clonal, un replicated plots. At these initial stages, individual plants and clonal plots are selected based on their appearance or ‘general worth’ by the breeder. The selections are then carried forward through several clonal stages of replicated trials, with further selections made at each stage from

measurement and formal statistical analysis for numerous traits **(**Caligari *et al.*,1986). Phenotypic coefficient of variation was higher than the genotypic coefficient of variation for plant vigor, tuber number, tuber yield, and average tuber weight but not for plant height. Likewise, genotypic coefficient of variation was much higher for tuber yield and its component than for the foliage character (Sharma, 1999). However, the lowest and highest variation was observed with regards to tuber number. Naike *et al*. (1998) reported that among the micro tuber yield components, average micro tuber weight had the highest genotypic and phenotypic coefficient of variation.

The amount of genotypic and phenotypic variability existing in species is the most important determinant factors toward initiating breeding program for developing better varieties in a crop. Welsh (1981) reported that genetic variability is of immense importance to breeders because it could be transferred to the progeny and the proper management of this diversity can promote stability in the performance of the plant. Variability is the occurrence of differences among individuals due to differences in their genetic composition and/or the environment in which they are raised (Falconer and Mackay, 1996). If the character expression of two individuals could be measured in identical environment, differences in the expression would result from genetic control and hence such variation is called genetic variation. Information on the nature and magnitude of genetic variability present in a crop species is thus important for developing effective crop improvement program (Singh *et al*., 1993).

2.2.2 Heritability in Broad Sense

Potato breeders should continually strive to improve the efficiency of their selection methods and seek to improve the effectiveness of their breeding strategies. Knowledge of the genetic parameters of traits, such as heritability and genetic correlations, 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).

Heritability can be defined, in broad sense, as the proportion of the genotypic variability to the total variance (Allard, 1960). It refers to the portion of phenotypically expressed variation, within a given environment and it measures the degree to which a trait can be modified by selection.

According to (Falconer and Mackay, 1996) heritability in narrow sense is defined as “the ratio of additive genetic variance to phenotypic variance”. Since broad sense heritability does not give a clear picture of transmissibility of variation from generation to generation (because the genetic variation includes the fixable and non-fixable dominance and epistatic variation), its utilization is limited in plant improvement program. In contrast, estimate of heritability in a narrow sense can give clear picture than that of broad sense (Falconer and Mackay, 1996).

Estimation of heritability as a ratio of genotypic to phenotypic variance may vary greatly depending upon the unit for which variance is considered (Johnson *et al.,* 1955). The greater the proportion of the total variability (i.e., due to environment), the more difficult will it be to select for inherited differences. Conversely, if environmental variability is small in relation to genotypic differences, selection will be efficient because the selected character will be transmitted to its progeny. Generally, heritability indicates the effectiveness with which selection of genotypes can be based on phenotypic performance. Heritability value by itself cannot provide the amount of genetic progress that would result from selection of the best individuals (Johnson *et al.,* 1955). However, genetic progress expected from selection increases with an increase in genotypic variance. In potato high heritability coupled with high genetic advance is an important factor for predicting the resultant effect for selecting the best individuals. High GCV along with high heritability and high genetic advance will provide better information than single parameters alone (Iqbal *et al*., 2003).

Heritability is very important to plant breeders as it gives an indication of the effectiveness with which selection of genotypes could be executed based on phenotypic performance of quantitative characters. Quantitatively inherited characters are different in heritability. A character such as yield that is greatly influenced by environment has low heritability (Poehlman and Sleper, 1995). Characters are not influenced by environment usually which have high heritability.

2.2.3 Genetic Advance

Although modern genomics offers great promise for accelerating genetic gain and the rate of cultivar development, the investigation of field-based approaches to improve the efficiency of conventional selection methods should not be neglected. In more recent years, attention has been

concentrated on advancing molecular-based selection methods; there has been inertia in the research and development of conventional, field-based breeding (Gopal *et al*., 1992). The investigation of methods and approaches for the evaluation of potato in a breeding strategy may provide opportunities to improve selection efficiency and therefore the genetic response to selection.

Genetic gains are also more likely to be significant if the diversity and level of genetic variability of desirable traits is sufficient (Biswas *et al*., 2008). Therefore, knowledge of the genetic diversity present within existing germplasm is crucial for effective utilization of genetic resources by plant breeders (Martins *et al*., 2006). Improvement in the mean genetic value of the selected plants over the base population is usually termed as genetic advance under selection. It measures the difference between genotypic values of generation obtained from the selected population over the mean value of the base population. Genetic advance under selection is a genotypic value which depends on three things (Allard, 1960). These are genetic variability, heritability or masking effect of non genetic variability on the genetic variability and the selection intensity applied.

Genetic progress would increase with increase in the variance. Therefore, the utility of estimates of heritability is increased when they are used in conjunction with the selection differential, the amount that the mean of the selected lines exceeds the mean of the entire group (Johnson *et al.*, 1955). According to Burton and De Vane (1953) genetic advance tell us the estimate of the expected gain for a particular character through selection.

2.3 Association of Characters

2.3.1 Correlation

The various characteristics of crop plants are generally interrelated or correlated. Such correlations can be either negative or positive. In plant breeding and genetic studies, correlated characters are of prime importance because genetic causes of correlations through pleiotropic action or developmental interactions of genes and changes brought about by a natural or artificial selection (Sharma, 1999). In order to facilitate selection in breeding for high yield therefore, it is

logical to examine various components and give more attention to those having great influence on yield.

Character association studies provide reliable information on the nature, extent and directions of selection (Kumar and Chauhan, 1979). The knowledge of genetic correlations between different yield attributes is vital when the breeder is confronted with problem of introducing a quantitatively inherited character into some agronomically superior cultivars from wild or uneconomic genotypes. Seed yield is a polygenically controlled complex character and is dependent on a number of component traits that are also quantitatively inherited. Selection on seed yield *per se* is often less effective, making it imperative to go for indirect selection through component traits (Singh, 1983). Sharma (1998) discussed the presence of three types of correlations in quantitative genetics and these are phenotypic, genotypic and environmental correlations. The association between two characters that can be directly observed is the correlation of phenotypic values or phenotypic correlations. Phenotypic correlations measure the extent to which the two observed characters are linearly related. It is determined from measurements of the two characters in a number of individuals of the populations. Genetic correlation is the associations of breeding values (i.e., additive genetic variance) of the two characters.

Genetic correlation measures the extent to which degree, the same genes or closely linked genes cause co-variation (simultaneous variations) in two different characters. The correlation of environmental deviations together with non-additive genetic deviations (i.e., dominance and epistatic genetic deviations) is referred to as environmental correlation (Falconer and Mackay, 1996; Sharma, 1998). Studies on genotypic and phenotypic correlations among characters of crop plants are useful in planning, evaluating and setting selection criteria for the desired characters in breeding program (Johanson *et al*., 1955). Correlations between different characters of crop plants may arise either from genotypic or environmental factors. Environmental correlations arise from the effect of overall environmental factors that vary at different environments. Correlations due to genetic causes are mainly pleiotropic effects of genes and linkage (a phenomenon of genes inherited together) between genes affecting different characters. Pleiotropy is the property of a gene, which affects two or more characters; as a result it causes

simultaneous variations in the two characters when the genes are segregating (Falconer and Mackay, 1996).

Correlation coefficient analysis helps to determine the nature and degree of relationship between any two measurable characters (Burhan, 2007). Characters that are not easily measured or which are largely influenced by the environment has low heritability ratio hence, there is a need to examine the relationships among various characters. Knowledge of the correlations that exists between important characters may facilitate the interpretations of the results already obtained, and provide the basis for planning more efficient breeding program in the future. However, as the number of independent variables influencing a particular dependent variable increases, certain amount of interdependence is expected. Thus, correlations may be insufficient to explain the associations in a manner that will enable one to decide on either a direct or an indirect selection strategy (Dewey and Lu, 1995).

Correlation coefficients may range in value from -1 to +1. Phenotypic correlations can normally be estimated with a high degree of accuracy. Estimates of genetic correlations however, usually have high standard errors because of difficulties to avoid the directional effects of confounding factors (i.e., dominance and epistatic genetic effects) on additive genetic correlation estimates. In addition, genetic correlations are strongly influenced by gene frequencies, and therefore, may differ markedly in different populations (Falconer and Mackay, 1996).

According to Grafuis (1959) increasing total yield would be made easier by selecting for components because the components are more simply inherited than the total yield itself. There are a number of reports indicating correlations of characters among themselves and with yield in potato. Gopal (2001) reported no significant association between plant height and tuber yield. On other hand Meris (1969) reported that the correlation between plant height and tuber yield was positive and strong. Significant association between plant height and tuber yield has been reported by Jaime *et al.* (2014) found plant height to be of little importance for tuber yield. Tesfaye *et al.* (2012) indicated presence of a strong, positive association between tuber dry matter content, starch content and starch yield ($r = 0.81$; $P < 0.01$), DMC and SY ($r = 0.67$; $P < 0.01$) and SC and SY ($r = 0.82$; $P < 0.01$) and suggested the possibility of simultaneous

improvement of these quality governing factors as they are controlled by the same genetic factors. On the other hand, tuber weight was negatively correlated with tuber dry matter content although the correlation was non-significant. Rasui *et al*. (1995) reported that tuber yield per hectare was significantly and positively correlated with plant vigor(r=0.86), foliage cover (r=0.38), starch content(r=0.42), yield per hill(r=0.95), and specific gravity(r=0.42). Sandu and Kang (1998) also reported significant and positive correlation of tuber yield with shoot height, shoot number and leaf let index. Maturity has positive correlation with plant height, mean tuber weight, tuber number and tuber yield. The correlation between maturity and plant height however, was weak where as correlation between maturity and mean tuber weight, tuber number per plant and tuber yield per plant strong and highly significant(Meris, 1969). Thus, studies on correlation enable the breeder to know the mutual relationship between various characters and determine the component characters on which selection can be used for genetic improvement.

2.3.2 Path Coefficient Analysis

Tuber yield is a complex character associated with many interrelated components. Generally, a path coefficient analysis is needed to clarify relationships between characteristics, because correlation coefficients describe relationships in a simple manner. Path coefficient analysis shows the extent of direct and indirect effects of the causal components on the response component. In most studies involving path coefficient analysis, researchers considered the predictor characters as first-order variables to analyze their effects over a dependent or response variable such as yield. This approach might result in multiple for variables, particularly when correlations among some of the characters are high. There may also be difficulties in interpretation of the actual contribution of each variable, as the effects are mixed or confounded because of colinearity. Samonte *et al*. (1998) adopted a sequential path analysis for determining the relationships between yield and related characters in rice (*Oryza sativa* L.) by organizing and analyzing various predictor variables in first, second and third order paths, Agrama (1996) and Mohammad *et al*. (2013) used this model for determining interrelationships among grain yield and related characters in maize. Yildirim *et al.* (1997) suggested that mass selection with few cycle of recurrent selection could be practiced for its improvement. Selection for tuber yield, which is a polygenic trait, often leads to changes in other characters.

Majid *et al*. (2011) indicated path analysis of tuber yield and its traits demonstrated that plant height, medium tuber weight and big tuber weight evolved the highest direct influence, 2.19, 0.8 and 0.6, respectively. Conversely, main stems per plant had a positive and low direct effect 0.18 with an indirect negative effect via tuber weight per plant (-1.3) and positive effect with average tuber weight (0.23) and tubers per plant (0.31) on tuber yield. In addition to the indirect effects of plant height, tubers per plant was stronger than its direct effects. Abraham *et al*, (2014) also reported path coefficient analysis based on tuber yield as a dependent variable obtained positive direct effect for harvest index, stems per plant, days to emergence, tuber per plant, plant height and biological yield. Days to emergence, stems per plant, biological yield and harvest index exerted positive highest phenotypic direct influence on tuber yield. However, days to flowering, days to maturity, small, medium and big tuber percentage exerted high negative direct influence on tuber yield. Conversely tuber per plant and plant height had positive and low direct effect on tuber yield. The stems per plant had the maximum direct effect on tuber yield followed by days to emergence.

Therefore, knowledge of the relationship that exists between tuber yield and other characters and also interrelationships among various characters is necessary to be able to design appropriate selection criteria in potato breeding program. According to Grafuis (1959) increasing total yield would be made easier by selecting for components because the components are more simply inherited than be total yield itself. Thus, studies on correlation enable the breeder to know the mutual relationship between various characters and determine the component characters on which selection can be used for genetic improvement. In study carried by Hossain *et al*. (2000) average tuber weight and number of tuber per plant had maximum positive direct effect on potato tuber yield.

3. MATERIALS AND METHODS

3.1 Experimental Site

This experiment was conducted in Southeastern Ethiopia, Bale Zone, at Sinana Agricultural Research Center which is nearly 463 km away from Addis Abeba, 33 and 55 km away from the zonal capital Robe and nearby town Goba, respectively. Sinana is located at 07^0 N and 40^0 $10^{'}$ E at an altitude of 2400 (m.a.s.l. The area possesses a bimodal rainfall type. This bimodal rainfall system has created favorable condition to produce crops twice annually or double crop production season. 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).

3.2 Experimental Materials and Design

A total of 24 potato genotypes which consisted of 20 advanced clones, three released varieties as standard checks and one farmers cultivar in Bale were used (Table 1). Ararsa potato variety was released by Sinana Agricultural Research Center in 2006 for the highlands of Bale (2400-3350 m.a.s.l.) while Belete and Guddane were released by Hollota Agricultural Research Center in 2010 and 2006, respectively, for mid to highlands of Ethiopia (1600-2800 m.a.s.l.). The farmers cultivar Kellacho is used as local check and it is susceptible to late blight. Belete is known as resistant variety to late blight while Ararsa and Guddane are moderately resistant varieties.

All the 24 genotypes were planted at Sinana Agricultural Research Center on station during main cropping season of 2014. The experiment was arranged in randomized complete block design (RCBD) with three replications and each plot was 3.6 m x 3 m = 10.8 m^2 wide consisting of four rows, which accommodated 12 plants per row and thus 48 plants per plot. 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 two middle rows were used for data collection.

Table 1. List of potato genotypes used in the study.

No.	Accession code	No.	Accession code
1	CIP-395096.2	13	CIP-391930.1
2	CIP-392640.524	14	CIP-391381.9
3	CIP-396031.201	15	CIP-395112.19
4	CIP-397079.26	16	CIP-393382.44
5	CIP-395017.242	17	CIP-391058.175
6	CIP-399078.11	18	CIP-396039.103
7	CIP-396244.12	19	CIP-395077.12
8	CIP-395114.5	20	CIP-399053.15
9	CIP-396029.205	21	Ararsa (CIP-90138.12)
10	CIP-399062.102	22	Belete (CIP-393371.58)
11	CIP-395017.229	23	Guddane (CIP-386423.13)
12	CIP-396240.23	24	Kellacho

Note: The source of all genotypes except the local cultivar "Kellacho" was CIP. The genotypes listed from 1-20 were recently introduced and are under evaluation at Adet Research Center (National Potato Research Center).

3.3 Experimental Procedures

Land preparation: The experimental field was cultivated to a depth of 25-30 cm by a tractor and ridges were made manually after levelling.

Planting: Medium sized and well sprouted seed tubers were planted at the side of ridges at the spacing of 0.75 m between ridges and 0.30 m between tubers on 12 August, 2014 during the main cropping season after the rain commenced and the soil was moist enough to support emergence. The planting depth was maintained at 5 cm (Mohammad *et al*., 2013).

Fertilizer application: fertilizer application was made as per the national recommendation made for the crop which is 92 kg P_2O_5 ha^{-1} in the form of Diammonium Phosphate (200 kg ha^{-1}) and the whole rate was applied at planting. Nitrogen fertilizer was applied at the rate of 75 kg ha^{-1} in the form of Urea in two splits, half rate after full emergence (two weeks after planting) and half rate at the initiation of tubers (at the start of flowering).

Harvesting: For yield estimation, tubers were harvested from the two middle rows, leaving the plants growing at both end of each row which was planted for inoculum source and left also the two border rows to avoid edge effects.

3.4. Data Collection

Data were collected on phenological, growth parameters, tuber yields and yield components, tuber quality attributes and disease as described below.

3.4.1 Phenological Data

Days to 50% flowering (DF):- was recorded as actual number of days taken from emergence to the days at which 50% of the plants in each plot produced flowers.

Days to maturity (DM):- recorded by counting days from emergence to days on which more than 90% of the plant in each plot attained physiological maturity.

3.4.2 Growth Parameters

Plant height(PH): The height of 10 plants in each plot were measured in centimetre from the ground surface to the tip of the main stem and averaged to get the mean plant height.

Stem number (SN): Data on this parameter was recorded as the average stem count of five hills per plot at 50% flowering. Only stems that were emerged independently above the soil as single stems were considered as main stems.

Leaf area index (LAI): To determine leaf area index, five plants (hills) was used from each plot. Individual leaf area of the potato plants was estimated from individual leaf length from formula developed by Firman and Allen (1989) and leaf area index was determined by dividing the total leaf area of a plant by the ground area covered by a plant.

$\text{Log}_{10}(\text{leaf area in cm}^2) = 2.06 \times \log_{10}(\text{leaf length in cm}) - 0.458$

Biomass yield (BMY): five plants were randomly selected and weighed from each plot at 90% physiological maturity i.e., both above ground plant parts (stem, branch, and leaves) and underground plant parts (root, stolon and parts of the stem remaining underground) was recorded after air-drying the samples for one week and was further oven-dried at 75^{o}C for 72 hours to constant mass.

3.4.3 Yield Components

Marketable tuber number per hill (MTNPH): Number of tubers harvested from five plants (hills) which were counted as marketable after sorting tubers which had greater or equal to 20 g weight, free from disease and insect attack. The average number of marketable tubers was counted and registered.

Unmarketable tuber number per hill (unMTNPH): The tubers that are sorted as diseased, insect attacked and small-sized (< 20 g) from five plants as indicated in the above was recorded as unmarketable tuber number. The average number of unmarketable tubers was counted and registered.

Average tuber weight (ATW) (g/tuber): It was determined by dividing the total fresh tuber weight to the respective total tubers number which harvested from five plants (hills) as indicated above.

Harvest index (HI) (%): was calculated as the ratio of dry mass of tubers to the dry mass of total biomass with the following formula.

$$\text{Harvest index} = \frac{\text{Dry mass of tubers}}{\text{Dry mass of total biomass}} \text{x}100$$

3.4.4 Tuber Yield

Total tuber yield (TTY) (t/ha): This was determined as the sum of the weights of marketable and unmarketable tubers from the net plot area and converted to tons per hectare

Marketable tuber yield (MTY) (t/ha): The total tubers weight which were free from diseases, insect pests, and greater than or equal to 20 g in weight determined from the net plot area and was converted to tons per hectare

Unmarketable tuber yield (unMTY) (t/ha): was determined by weighting tubers that were sorted out as diseased, insect attack and small-sized (< 20 g) from the net plot area and converted to tons per hectare

4.5 Tuber Quality Attributes

Tuber dry matter content (MC) (%): Five fresh tubers were randomly taken from each plot, washed, weighed and sliced at harvest, dried for seven days under sun and finally in oven at 75^{o}C for 72 hours until a constant weight attained and dry matter percent calculated according to (William and Woodbury, 1968).

$$\text{Dry matter} = \frac{\text{weight of sample after drying(g)}}{\text{initial fresh weight of sample(g)}} \text{x100}$$

Specific gravity of tubers (Sg): was determined by the weight in air and in water method. Five kg tuber of all shapes and sizes were randomly taken from each plot. The tubers were washed with water. Then after the sample was first weighed in air and then re-weighed suspended in water. Specific gravity was calculated according to (Kleinkopf *et al.,* 1987) formula.

$$\text{Specific gravity} = \frac{\text{Weight in air}}{\text{Weight in air} - \text{Weight in Water}}$$

Starch (%): The percentage of starch was calculated from the specific gravity as follows:

Starch (%) =**17.546 + 199.07 × (sp-1.0988)** (Talburt and Smith, 1959). Specific gravity was determined as indicated above by the weight in air and weight in water method.

Moisture content (MC) (%): Moisture content of tubers was determined by oven drying method. Five gram of each sample was accurately weighed in Petri dish (W1). The partially covered dish was placed in oven at 105°C for 12 hours**.** Then the Petri dish was placed in desiccators at room temperature for 30 minutes to cool. The sample was reweighed after cooling (W2). The percent moisture content was calculated as:

$$\text{Moisture (\%)} = \frac{\text{(W1-W2)}}{\text{Wt. of sample}} \times 100$$

3.4.6 Disease Data

Days to onset of the disease (DDA): - was recorded by counting days from planting to the first appearance of late blight symptom in each plot (genotype).

Disease severity

Disease severity was taken on the basis of the percentage of leaf area affected by late blight. The first reading was taken at 48 days after planting. The reading was started on the onset of late blight (1-5% infection). After onset of the disease scoring was continued at an interval of seven days until nearly 74 days after planting. The 1-9 disease scale described by (Heinfnings, 1987) was used as listed in Appendix Table 3.

3.4.2.1 Percent severity index (PSI)

Percent severity index was calculated from disease severity on the basis of the percentage of leaf area affected by late blight and calculated for each disease assessment as follows.

$$\textbf{Percent Severity index \%} = \frac{\text{Summation of numerical rating}}{\text{No. plants examined} \times \text{Maximum disease score}} \times 100$$

The percent severity index of foliar blight that was expressed in percent of the infected leaf area used for disease rating scale given by Mohan and Thind (1999) and depending on the final record of percent severity index, the genotypes were classified into highly resistant, resistant, moderately resistant and susceptible as per the scale indicated in Table 2.

Table 2. Percent Severity index and resistance category

Percent Severity index	**Category**
Up to 5	Highly Resistant
5-20	Resistant
21-40	Moderately Resistant
Above 40	Susceptible

3.4.2.2 Area under disease progress curve

It 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).

$$\text{AUDPC} = \sum_{i=1}^{n-1}\left(\frac{yi + yi+1}{2}\right)(t_{i+1} - t_i)$$

Where "t" is the time of each reading, "y" is the percent of affected foliage at each reading and "n" is the number of readings. The variable "t" can represent Julian days, days after planting.

3.5. Data Analysis

3.5.1 Analysis of Variance

Collected data was subjected to analysis of variance (ANOVA) for RCBD following the procedure outlined by Gomez and Gomez (1984) using SAS ver. 9.1.3 computer software. Means that are significantly different were compared using Duncan Multiple Range Test (DMRT) of probability at 5% probability of significance.

Table 3. Analysis of variance table for randomized complete block design and expected mean square

Source of variations	df	MS	Expected Mean Squares
Replications (r)	(r - 1)	MSr	$\sigma^2e + g\sigma^2r$
Genotypes (g)	(g - 1)	MSg	$\sigma^2e + r\sigma^2g$
Error	(r - 1) (g - 1)	MSe	σ^2e

df = degree of freedom, MS = Mean squares, r = replication, g = genotypes, MSr =mean squares due to replications, MSg = Mean squares due to genotypes, MSe = Mean squares due to error.

3.5.2 Phenotypic and Genotypic Variances

The phenotypic and genotypic variances of each trait were estimated from the RCBD analysis of variance. The expected mean squares under the assumption of random effects model was computed from linear combinations of the mean squares and the phenotypic and genotypic

coefficient of variations were computed as per the methods suggested by (Singh and Chaudery, 1985).

Genotypic variance (σ^2_g) = (MSg – MSe)/r where:- σ^2_{g-} = genotypic variance, MSg = mean square due to genotype, MSe = environmental variance (error mean square) and r = number of replication.

Phenotypic variance (σ^2_p) = σ^2_g + σ^2_e where:- σ^2_p = phenotypic variance, $\sigma^2_{g=}$ genotypic variance, $\sigma^2_{e=}$ environmental variance.

Genotypic Coefficient of Variation. $GCV = \frac{\sqrt{\sigma 2g}}{\text{grand mean}}$ x100 where, σ^2_g=genotypic variance.

Phenotypic Coefficient of Variation. $PCV = \frac{\sqrt{\sigma 2p}}{\text{grand mean}}$ where, σ^2_p=phenotypic variance.

3.5.3 Broad Sense Heritability (H^2)

Broad sense heritability was estimated based on the formula given by (Allard, 1960) as follows:

Heritability in broad sense H^2_b = σ^2_g/σ^2_p where:- $h^2_{b=}$ heritability in broad sense, $\sigma^2_{p=}$ phenotypic variance, $\sigma^2_{g=}$ genotypic variance

3.5.4 Estimation of Genetic Advance

Genetic advance and genetic advance as percent of means were estimated as described by (Allard, 1960) as:

Genetic Advance (GA) = k σ_p H^2 Where:- K= the standardized selection differential at 5 % (2.063), σ_p = phenotypic standard deviation and $H^{2=}$heritability in broad sense

Genetic advance as percent of mean (GAM)= (GA/*X*) × 100 , where GA= genetic advance, and ***X*** **=** mean of population.

3.5.5 Phenotypic and Genotypic Correlations

Phenotypic correlation is observable correlation between two variables which include both genotypic and environmental effects, while genotypic correlation is the inherited association between two variables. This is computed by calculating variance and then covariance at phenotypic and genotypic level.

Phenotypic correlation coefficient (rp_{xy}) = $covp_{xy}$/ $\sqrt{\sigma^2 p_x \ \sigma^2 p_y}$ where:- $covp_{xy=}$ phenotypic covariance between character x and y, $\sigma^2 p_{x=}$ phenotypic variance of character x and $\sigma^2 p_{y=}$ phenotypic variance of character y.

Genetic correlation coefficient (rg_{xy})= $covg_{xy}$/ $\sqrt{\sigma^2 g_x \ \sigma^2 g_y}$ where:- $covg_{xy=}$ genetic covariance for character x and y, $\sigma^2 g_x$ = genotypic variance for character x and $\sigma^2 g_y$ = genotypic variance for character y.

3.5.6 Path Coefficient Analysis

In the path coefficient analysis tuber yield was taken as resultant variable while the rest of characters were considered as causal (independent). The direct and indirect effects of the independent character on tuber yield per plant was estimated by the formulae of (Dewey and Lu 1959). $\mathbf{r_{ij} = P_{ij} + \Sigma r_{ik} P_{kj}}$

Where, $\mathbf{r_{ij}}$ is association between the independent variable (i) and dependent variable (j) as measured by correlation coefficient; P_{ij} is component of direct effect of the independent variable (i) on the dependent variable (j) as measured by path coefficient; and $\Sigma r_{ik} P_{kj}$ is summation of components of indirect effects of a given independent variable (i) on a given dependent variable (j) via all other independent character (K). To determine P_{ij} values square matrices of the correlation coefficients between independent characters in all possible pairs were inverted and then multiplied by the correlation coefficient between independent and dependant characters.

The residual effect was estimated as described in Dewey and Lu (1995):-

$\mathbf{\sqrt{1-R^2}}$ **where,** $\mathbf{R^2 = \Sigma P_{ij} r_i}$

4 RESULTS AND DISCUSSIONS

4.1. Analysis of Variance

Analysis of variance indicated the presence of highly significant ($P \leq 0.01$) differences among genotype for all traits except for starch content and specific gravity (Table 4). 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. Various researchers reported the existence of significant variation among genotypes for different traits. Smita *et al.* (2009) reported significant differences among genotypes for plant height, number of tuber per plant, marketable tuber yield per plot and total tuber yield per plot. Misgana *et al*. (2014) also reported plant height, average tuber weight, large size tuber, average tuber weight and tuber yield showed significant difference among the tested varieties. However, crop reaction to blight disease, showed non-significant variation among the tested varieties. This may be due to less factors affecting for late blight development. Mean squares for genotypes were highly significant for tuber yield and dry matter content signifying the existence of considerable variation among the genotypes. On the contrary, mean square for specific gravity found to be non-significant indicating that the absence of significant differences among the genotypes for the specific trait. The non-significant difference among genotypes was also reported (Tekalign, 2011)

Moreover, the genotypes tested for late blight resistance showed significant differences for all disease evaluation parameters. This may allow breeders to select resistant genotypes to enhance the productivity of the crop. Late blight [*Phytophthora infestans* (Mont.) de Bary] can destroy a potato field within a few days (Razukas *et al*., 2008). If not controlled, losses may reach 100 percent (Rubio-Covarrubias *et al*., 2005) and even lower infection levels may make the crop unfit for storage (Heinfnings 1987). In the highlands of Ethiopia, late blight and bacteria wilt (*Ralstoniasolanacearum*) are the most important economic diseases that cause an estimated yield loss of up to 70% (Mekonen *et al*., 2011).

Table 4. Mean squares from analysis of variance for 20 characters of potato genotypes at Sinana in 2014, bona cropping season

Trait	Rep (2)	Genotype (23)	Error (46)	LSD (5%)	CV (%)
Days to flowering(DF)	31.4	995.4**	58.9	12.6	14.4
Days to maturity(DM)	3.2	192.3**	7.0	4.4	2.4
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
Marketable tuber number per hill (MTNPH)	12.3	36.1**	4.4	3.4	28.7
Unmarketable tuber number per hill (unMTNPH)	1.12	1.57**	0.4	0.1	22.6
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
Tuber dry matter content (TDM) (%)	7.9	30.2**	4.8	3.6	9.1
Specific gravity of tubers(Sg)	0.02	0.01ns	0.06	0.04	2.3
Moisture content of tuber (MC) (%)	25.1	28.63**	7.4	4.5	3.7
Starch content of tuber (g/100g)	6.1	9.2ns	8.9	4.9	7.1
Days to late blight on set (DDA)	201.3	794.8**	83.7	15	15.1
Percent severity index (PSI) (%)	442.7	1090.7**	178.4	21.9	24.9
Area under disease progress curve(AUDPC)	0.01	0.68**	0.03	0.3	6.2

** & ns, highly significant at $P \leq 0.01$ and non-significant, respectively. 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.

4.2. Mean Performances of Genotypes

Potato genotypes had a wide range variation for total tuber yield ranged from 0.8 to 46.1 t ha^{-1} with the mean performance of 19.4 t ha^{-1} (Appendix Table 1). The mean total tuber yield of released varieties (Belete, Gudanie and Ararsa) was in the range between 15.9 to 41 t ha^{-1}. The four advanced clones (CIP-392640.524, CIP-395114.5, CIP-396244.12 and CIP391058.175) gave total tuber yield higher than the mean tuber yield of the two released varieties (Gudanie and Ararsa) while one clone (CIP-392640.524) had statistically the same mean total tuber yield with the best performing released variety Belete. Moreover, six advanced clones had higher marketable tuber yield than Gudenie and Ararsa of which CIP-392640.524 had the same mean value with best performing variety Belete. CIP-391930.1 and CIP-391381.9 advanced clones had higher unmarketable tuber yield than the mean of three released varieties. Addisu *et al.* (2013) and Baye *et al*. (2002) also reported some of the newly introduced potato genotypes had higher tuber yield than the existing commercial potato varieties. This indicated the presence of variation in genotypes under study for total tuber yield that can be exploited in improving the crop. However, the newly introduced advanced clones and released varieties performed statistically the same for starch content and specific gravity.

The mean value of biomass yield per plant ranged from 90.3 to 418.6g with the overall mean of 228g per plant. Eleven out of twenty advanced clones had biomass yield per plant higher than the two released varieties Gudanie and Ararsa, while CIP-395114.5 had statistically similar biomass yield with released and best performed variety Belete. The farmers cultivar (Kellacho) and two advanced clones (CIP-397079.26 and CIP-391381.9) had the lowest biomass yield per plant less than the genotypes overall mean biomass yield. The average plant height of the genotypes was 58.4cm. Among the tested genotypes 52% had plant height above the overall mean value including released and best performed variety Bellete, and 48% had below the mean value including released variety Ararsa and Gudanie. With respect to stem number per plant the mean value ranged from 2.0 to 6.2 with means performance of 3.85. The mean performance of released varieties; Belete, Gudanie and Ararsa had 4.6, 4.5 and 2.8 number of stems, respectively, while five advanced clones (CIP396039.103, CIP395017.242, CIP-391930.1, CIP391058.175 and CIP-392640.524) had mean number of stems in the range between 4.8 to 6.2 which was higher than

the released varieties. The more number of stems the higher possibility of producing more number tuber. Therefore, the observed wide ranges of variation for growth parameters can be considered in improvement of the crop through selection. This result is in agreement with the report with Berga and Caesar (1990) that observed wide ranges of stem number per plant and total tuber yield of potato. Morena *et al*. (1994) showed that the number of stem per plant (hill) is influenced by inherent ability of varieties.

Days to maturity ranged from 98 to 119 days with the overall mean of nearly 109 days. According to Beukema and Vander Zaag (1990) 50% of the tested genotypes were grouped as early, 12.5% as medium and 37.5% as late maturing groups with >114 days to maturity. Days to flowering showed narrow ranges from 55 to 69 days from planting. Similar results were reported by Asmamaw (2007) that early flowering and physiological maturity at Adet than Chilga and Dabat that may be attributed to the higher growing temperature of Adet than the other locations. Addisu *et al*.(2013) also reported wide ranges of variations for most of studied traits.

The disease parameters viz. Percent Severity Index (PSI), Area Under Disease Progress Curve (AUDPC) and days to first late blight appearance (DDA) results are given in Appendix table 3. Late blight appeared early at 48 days after planting on farmers cultivar Kellacho and other five advanced clones (CIP-399053.15, CIP-397079.26, CIP-396039.103, CIP-391930.1 and CIP-391381.9) followed by three advanced clones (CIP-399078.11, CIP-396031.201 and CIP-393382.44) which appeared at 53 days after planting. Late blight appeared very late on CIP-399062.102 at 74 days after planting. The disease appeared at 70 days on Belete and at 63 days on Ararsa and Guddanie. There was wide range difference of 26 days between the first disease symptom appearance on susceptible and relatively resistant genotypes. Jaime *et al.* (2014) suggested that potato genotypes which developed late blight symptom early are susceptible and genotypes that developed late blight in the crop cycle are resistant.

Percent severity index was calculated starting from 48 days after planting at onset of the disease on susceptible genotypes to 74 days from planting at which disease severity leveled off or when the susceptible check had 100% infection. The percent severity index ranged from 48 to 74 days after planting, the percent severity index calculated was used to categorize the genotype in to

different resistance and susceptible group. The calculated percent severity index ranged from 33 (CIP-391058.175, CIP-395096.2, CIP-395114.5, CIP-396031.201 and Bellete) to 91.67% (for advanced clone (CIP-391930.1). From all 24 genotypes, there was no genotype with percent severity index of < 20 at nearly 74 days after planting. Hence, there were no both highly-resistant and resistant genotypes from the newly introduced materials and released varieties. However, eleven advanced clones and Belete had percent severity index that ranged from 33 to 39.7 and can be categorized as moderately resistance while others including released varieties Guddine and Ararsa recorded above 40% and categorized as susceptible (Table 2).

The calculated AUDPC was ranged as low as 105 (CIP-391058.175, CIP-399062.102, CIP-395096.2, Bellete) and as high as 2370 for (CIP-397079.26). Most of the genotypes including the released variety Ararsa and gudenie had high AUDPC. According to Campbell and Madden (1990), from 24 potato genotypes (CIP-395096.2, CIP-395077.12, CIP-99062.102, Belete, CIP-395114.5, CIP395017.242 CIP-396240.23, CIP391058.175, CIP396029.205, CIP396031.201, CIP-3920524 and CIP-396244.12) categorized as tolerance. However, other genotypes including released varieties Ararsa and Gudaine which were considered as susceptible. The AUDPC is very convenient summary of plant disease epidemics that incorporates initial intensity, the rate parameter and duration of epidemic which determine final disease intensity (Andre *et al*., 2014). Hence, the effect of disease resistance on crop can be evaluated by using area under disease progress curve (Boiteux, 1995). This is in agreement 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.

In 2014 main cropping season there was high severity of late blight on potato in Bale high lands (personal observation). At 48 days after planting, late blight appeared on some genotypes. This indicated that in the process of improving potato variety through selection attention should have to be given to assess the disease onset as early as possible. Similar results was reported by Buddhi *et al.* (2013) which indicated late blight severity observations in the field should be started at 30 days after planting and continued up to 76 days until the susceptible check had 100% infection.

Considering both disease parameters (PSI and AUDPC) 11 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 Mekonin *et al*.(2009) that moderately resistant cultivar, Gudanie, had a clear AUDPC response to additional fungicide sprays, although apparently for about three sprays. Several research on potato late blight have demonstrated that highly resistant (immune or nearly immune) phenotypes can frequently indicate an active major R gene, for which compatibility in the pathogen population is absent or extremely rare. If an incompatible potato genotype is released for use by farmers in most cases there will be selection of compatible pathogen population and a corresponding "loss" of resistance (Forbes, 2012). For this reason, some researchers have recommended selection of those phenotypes which demonstrate resistance, but are still infected (Forbes and Landeo, 2006).

4.3 Variability Components

The variability components (genotypic and phenotypic variances and coefficient of variations, heritability in broad sense and genetic advance as percent of mean) were estimated for traits and results are presented in Table 5. However, the results excluded the two quality related traits (specific gravity and starch content).

4.3.1 Estimates of Phenotypic and Genotypic Variation

The estimated phenotypic variation was relatively greater than the genotypic variations in magnitude for all characters considered. Phenotypic coefficient of variation ranged from 7.5 for days to maturity to 56.7% for total tuber yield (Table 5). 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). Most of the traits had phenotypic coefficient of variation >20% that can be considered as high. However, days to maturity had phenotypic coefficient of variation < 10% that can be considered as low. Moderate phenotypic coefficient of variation was observed for days to late blight appearance; harvest index and tuber dry matter. The results suggested that the high scope for selection among the genotypes for most of the

characters that exhibited high phenotypic coefficient of variation and likely to practice selection for traits with moderate values, but practically selection is impossible in traits with low phenotypic coefficient of variation. Similar findings were reported by Baye *et al*. (2002**)** that high phenotypic coefficients of variation for days to 50% flowering, tuber weight per hill, marketable tuber yield and total tuber yield.

Table 5. Genotypic and phenotypic coefficient of variances, heritability and genetic advance in 24 potato genotypes for 18 traits at Sinana during 2014 cropping season.

Trait	□ σ^2g	σ^2p	σ^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
DDA	63.3	100.6	937.3	13.4	16.9	62.9	13.0	21.9
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

σ^2g =genotypic variance, σ^2p =phenotypic variance, GCV=genotypic coefficient of variation in percent, PCV=phenotypic coefficient of variation in percent, H^2=heritability in broad sense, GA (5%)=expected genetic advance at 5% selection intensity, GAM.= genetic advance as percent mean, DF=days to flowering, DM= days to maturity, plant height, SNPH = 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^{-1} TDM=Tuber dry matter content, DDA = days to late blight appearance, PSI =percent severity index and AUDPC = area under disease progress curve.

Genotypic coefficient of variation ranged from 7.2 for days to maturity to 51.9% for total tuber yield. Most of the studied trait had > 20% genotypic coefficient of variation which considered as high while area under disease progress curve, tuber dry matter and harvest index had moderate genotypic coefficient of variation. These indicated that the traits are controlled by genetic factor and the higher chance of improvement of the crop through selection. However, days to maturity had < 10% which considered as low. Kumar *et al*. (2005) reported high genotypic variance for average tuber weight, tuber number per plant; plant height and average tuber yield whereas Shashikamal (2006) reported high genotypic variation for tuber weight and tuber number.

Both genotypic and phenotypic coefficient of variation estimates were high for unmarketable tuber yield, total tuber yield, average tuber weight, marketable tuber number per hill, marketable tuber yield, percent severity index, number of stem per plant, leaf area index, plant height, days to flowering, biomass yield and unmarketable tuber number per hill with low magnitude of differences of the two (phenotypic and genotypic coefficient of variation). Both genotypic and phenotypic coefficient of variation values were moderate for area under disease progress curve, days to first late blight appearance, harvest index and tuber dry matter and low 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 estimates the improvement through selection is difficult or virtually impractical due to the masking effect of environment on the genotypic effect (Sing, 1990).

4.3.2 Estimate of Heritability and Genetic Advance

The estimated heritability ranged from 44.08 to 89.5% for biomass yield and area under disease progress curve, respectively (Table 5). The heritability was categorized as low (0 - 30%), moderate (30 – 60%) and high (> 60%) as suggested by Robinson *et al*. (1955). Accordingly, high heritability was exhibited for days to maturity, area under disease progress curve, marketable tuber yield, days to flowering, total tuber yield, percent severity index, marketable tuber number per hill, average tuber weight, tuber dry mater content and days to late blight

appearance. Moderate heritability was recorded for leaf area index, biomass yield, plant height, stem number per plant and harvest index. These finding is in accordance with the findings of Choudhary and Sharma (1984) and Roy and Singh (2006) who reported high estimates of heritability for dry weight of tuber, average tuber weight, number of tubers per plant, total tuber yield, dry matter percentage. Hence, these characters are amendable for selection to improve crops.

Genetic advance as percent of mean ranged from 14 for days to maturity to 98.1% for total tuber yield (Table 5). The genetic advance as percent mean was categorized as low (0 - 10%), moderate (10 – 20%) and high (>20%) as suggested by Johnson *et al*. (1955). Accordingly, high genetic advance as percent of mean recorded for total tuber yield, marketable tuber yield, average tuber weight, marketable tuber number per hill, percent severity index, days to flowering, leaf area index, number of stem per plant, area under disease progress curve, plant height, biomass yield and days to late blight appearance. Whereas moderate genetic advance as percent of mean was observed for tuber dry matter, harvest index and days to maturity. Chaudhary and Sharma (1984) reported moderate genetic advance as percent of mean for harvest index, plant height and fresh weight of tuber per plant. This is in line with Baye *et al*. (2005) and Adisu *et al*, (2013) indicated moderate genetic advance as percent of mean for pant height, biomass yield and average tuber weight. The moderate genetic advance suggested both the additive and non-additive variances are operating in expression of these traits (Luthra, 2001).

Burton and Devane (1953) suggested that genotypic coefficient of variation along with heritability estimates would provide a reliable estimate of the amount of genetic advance to be expected through phenotypic selection. The estimates of heritability and genetic advance as percent of mean should always be considered simultaneously as high heritability is not always associated with high genetic gain (Johnson *et al.*, 1955). 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; Tuncturk and ÇiftÇi 2005). Moderate heritability and genetic advance was computed for tuber dry matter, harvest index and days to maturity.

4.5 Association of Characters

4.5 1 Phenotypic and Genotypic Correlations

The estimates of genotypic and phenotypic correlation coefficients between total tuber yield, marketable and unmarketable tuber yield and all possible pairs of yield components, phenological and growth parameters of potato genotypes are presented in Table 6.

4.5. 1.1 Genotypic and phenotypic correlations of tuber yield to other characters

Genotypic correlation coefficient values ranged as low as r_g=-0.09 between total tuber yield and unmarketable tuber number per hill and as high as r_g=0.99 between total tuber yield and marketable tuber yield. Positive and significant genotypic correlations in the range between r_g =0.43 and r_g = 0.99 was observed between total tuber yield per hectare and marketable tuber yield, leaf area index, plant height, stem number per plant, tuber dry matter content, average tuber weight, biomass yield, marketable tuber number per hill, days to maturity, days to late blight appearance and moisture content of tubers. Girma (2001) observed positive and significant correlation between plant height and total tuber yield (r = 0.89**) and marketable tuber number per pant with tuber yield(r = 0.79**). This is in agreement with Jaime *et al.* (2014) who reported significant association between tuber yield and stem number per plant, tuber dry matter content, average tuber weight and biomass yield. Therefore, improvement of total tuber yield in potato is possible through selection of genotypes that performing best than others for those strongly correlated traits. This showed that total tuber yield per hectare is the end product of components of several yield contributing characters.

Negative and significant genotypic correlations was recorded between total tuber yield and percent severity index (r_g=-0.8) and area under disease progress curve (r_g=-0.6). This result indicated that selection of genotypes with low disease severity increased the total tuber yield and selection should be against the high disease infection as a breeding strategy. Hamed *et al.* (2011) reported the presence of negative genotypic correlations between total tuber yield and small size tuber per plant. Similar results were reported by Fekede (2011) who indicated negative association of tuber yield with percent severity index and area under disease progress curve.

Positive and significant genotypic correlations that ranged from r_g =0.46 to r_g = 0.99 was observed between marketable tuber yield and days to maturity, plant height, stem number per plant, leaf area index, biomass yield, marketable tuber number per hill, average tuber weight, moisture content, days to first late blight appearance, tuber dry matter and total tuber yield. Hence, improvement of marketable tuber yield per hectare in potato is possible through selection of those traits which had strong correlation to the trait. This indicated that those positively and significantly correlated traits are responsible for tuber yield improvement. This is in agreement with the results obtained in earlier studies (Berga and Caesar, 1990; Yibekal, 1998). Tekalign and Hammes (2005) observed a considerable positive and significant association between marketable tuber yield and biomass yield, average tuber weight, moisture content and tuber dry mater indicating the possibility to improve tuber yield by considering those correlated positively and significantly. However, negative and significant genotypic correlation was observed between marketable tuber yield and percent severity index (rg=-0.84) and area under disease progress curve (0.61) indicating both diseases parameters are influenced marketable tuber yield.

Strong positive and significant association at genotypic level was recorded between unmarketable tuber yield and unmarketable tuber number per hill (r_g = 0.83). However, negative and significant genotypic correlation which ranged from $r_{g=}$-0.41 to $r_{g=}$ -0.51 was recorded between unmarketable tuber yield and days to maturity, leaf area index, average tuber weight, days to first late blight disease appearance and harvest index. Yildirim *et al.* (1997) reported the presence of negative significant association between unmarketable tuber yield and moisture content, average tuber weight and small tuber number per plant. This is in line with previous reports by Khayatnezhad *et al*. (2011) and Hamed (2011) who reported the presence of negative

significant association between small tuber per plant and average tuber weight. Hence selection of the low mean value for these traits is important to improve marketable tuber yield per hectare. The association of most of the traits with total tuber yield at phenotypic level exhibited similar trend with genotypic association except the correlation coefficient values differences which ranged from r_p=-0.07 (between total tuber yield and unmarketable tuber number per hill) to r_p=0.98 (between total tuber yield and marketable tuber yield). Positive and significant phenotypic correlations that ranged from r_p=0.40 to r_p=0.98 was observed between total tuber yield and moisture content, days to maturity, plant height, leaf area index, biomass yield, marketable tuber yield, days to first disease appearance and tuber dry matter. However, negative and significant phenotypic association was recorded between total tuber yield and percent severity index and area under disease progress curve. Amadi and Ene-Obong (2007) reported the significant correlation of tuber yield with tuber number and tuber weight as well a plant height, main stem per plant, average tuber weight, tuber weight per plant. Similar results were reported by Girma (2001) that positive and significant association of total tuber yield to plant height, biomass yield, average tuber weight and tuber dry matter content. Therefore, improvement of tuber yield in potato is possible through selection for those positively correlated traits.

Phenotypic correlation between marketable tuber yield per hectare and marketable tuber number per hill, days to maturity, plant height, leaf area index, biomass yield, average tuber weight, tuber dry matter, moisture content, days to first late blight appearance and total tuber yield was significant and positive. On other hand, unmarketable tuber number per hill and unmarketable tuber yield was negatively correlated to marketable tuber yield in phenotypic correlation. This is in agreement with the finding of Abraham, *et al*. (2014) that reported positive significant correlation between tuber yield and biological yield, plant height, tuber per plant, stems per plant and tuber number per plant. Among the 17 characters studied, unmarketable tuber number per hill had positive and significant phenotypic association with unmarketable tuber yield per hectare (r=0.76) while it exhibited negative but non-significant with all other traits. Marketable tuber yield associated positively and significantly with most of growth parameter and yield components. This result indicated that both tuber number and size increment are responsible for yield improvement. This is in agreement with the results obtained in earlier studies (Berga and Caesar, 1990)

4.5 1.2 Genotypic and phenotypic correlations among characters other than tuber yield

Phenology of the crop and growth traits viz. days to maturity, plant height, number of stems per plant, leaf area index and biomass yield showed positive and significant associations both at genotypic and phenotypic levels with majority of yield components and the two quality attributes such as marketable tuber number per hill, average tuber weight, tuber dry matter and moisture content of tubers while negatively correlated with unmarketable tuber number per hill, percent severity index and area under disease progress curves. Except unmarketable tuber number per hill all growth traits and yield components showed negative and significant associations with disease parameters viz. percent severity index and area under disease progress curve both at genotypic and phenotypic levels (Table 6). In addition, this group of trait showed positive and significant associations among them except moisture content of tuber and tuber dry matter had negative and significant associations. Berga and Caesar (1990) reported positive correlations of stem number per pant and leaf area index with average tuber weight, large tuber size per plant, tuber dry matter and harvest index. Similar results reported by Girma (2001) observed positive and significant correlation between plant height and marketable tuber number per hii(r = 0.89**). This indicated selection of high mean value of such traits encourage improvement of tuber yield.

The yield components viz. marketable tuber number per hill, average tuber weight and tuber dry matter had positive and significant associations among them both at genotypic and phenotypic levels except unmarketable tuber number per hill which showed negative association. Assefa (2005) reported positive and highly significant correlation between tuber dry matter and average tuber weight and marketable tuber number per plant. This result indicated that traits which are correlated positively and significantly are responsible for yield improvement, hence, selection of high mean value will be encourage improvement of tuber yield. This is in agreement with the results obtained in earlier studies (Yibekal, 1998). Most of the traits had negative and significant associations with disease parameters except unmarketable tuber number per hill which had positive association. The disease parameters, percent severity index and area under disease progress curve had positive and significant associations in both genotypic and phenotypic correlation to each other. This implies disease parameters negatively affected growth and yield components which contributed directly or indirectly to tuber yield improvements.

Table 6. Genotypic (above diagonal) and phenotypic (blow diagonal) correlations of 17 characters in 24 potato genotypes studied at Sinana, in 2014 cropping season

Variables	DM	PH	SN	LAI	BMY	MTN	unMTN	ATW	HI	MTY	unMTY	TDM	MC	DDA	PSI	AUDPC	TTY
DM	1	0.34	0.31	0.61*	0.58*	0.72**	-0.22	0.43*	0.37	0.74**	-0.41*	0.51*	-0.62*	0.51*	-0.78**	-0.62*	0.7**
PH	0.32*	1	0.31	0.5*	0.51*	0.51*	0.04	0.5*	-0.07	0.54*	0.02	0.54*	-0.29	0.31	-0.35	-0.18	0.56*
SN	0.24	0.18	1	0.4*	0.26	0.59*	-0.4*	0.22	-0.06	0.54*	0.31	0.33	-0.16	-0.1	-0.29	-0.06	0.56*
LAI	0.54**	0.49**	0.31	1	0.68*	0.73**	-0.29	0.63*	0.11	0.85**	-0.41*	0.71**	-0.53*	0.61*	-0.8**	-0.73**	0.82**
BMY	0.47**	0.36*	0.15	0.41*	1	0.69*	-0.12	0.48*	-0.16	0.72**	-0.31	0.57**	-0.42*	0.42*	-0.61*	-0.59*	0.69*
MTN	0.64**	0.44**	0.55**	0.67**	0.44**	1	-0.06	0.58*	0.19	0.90**	-0.3	0.56*	-0.45*	0.33	-0.68**	-0.48**	0.88**
unMTN	-0.20	0.03	0.38*	-0.24	-0.10	0.00	1	-0.47**	-0.29	-0.15	0.83**	-0.3	0.28	-0.4*	0.25	0.48*	-0.1
ATW	0.41*	0.44**	0.16	0.58**	0.25	0.54**	-0.42*	1	0.11	0.72**	-0.41*	0.53*	-0.31	0.64*	-0.64*	-0.51*	0.74**
HI	0.28	-0.02	0.00	0.17	-0.16	0.23	-0.19	0.18	1	0.11	-0.51*	0.21	-0.24	0.11	-0.18	-0.15	0.11
MTY	0.70**	0.48**	0.41*	0.68**	0.52**	0.80**	-0.13	0.65**	0.07	1	-0.31	0.62*	-0.46*	0.53*	-0.84**	-0.61*	0.99**
unMTY	-0.40*	0.01	0.26	-0.37*	-0.24	-0.24	0.76**	-0.39	-0.31	-0.23	1	-0.31	0.31	-0.41*	0.35	0.56*	-0.21
TDM	0.44**	0.46**	0.22	0.59**	0.35	0.45**	-0.29	0.48**	0.14	0.53**	-0.26	1	-0.75**	0.42*	-0.57*	-0.52*	0.59*
MC	-0.54**	-0.25	-0.14	-0.38*	-0.27	-0.39	0.21	-0.25	-0.19	-0.44**	0.24	-0.57**	1	-0.5	0.64*	0.52*	-0.4*
DDA	0.43*	0.23	-0.02	0.44**	0.27	0.27	-0.35*	0.55**	0.07	0.46**	-0.38	0.30	-0.42**	1	-0.79**	-0.79**	0.53*
PSI	-0.7**	-0.28	-0.26	-0.7**	-0.37*	-0.6**	0.18	-0.6**	-0.15	-0.73**	0.33*	-0.46**	0.48	-0.68**	1	0.81**	-0.8**
AUDPC	-0.60**	-0.16	-0.02	-0.65**	-0.44**	-0.43**	0.43**	-0.46**	-0.13	-0.57**	0.55**	-0.45**	0.41**	-0.69**	0.76**	1	-0.6*
TTY	0.65**	0.49**	0.42*	0.63**	0.49**	0.77**	-0.07	0.63**	0.05	0.98**	-0.16	0.49**	-0.40*	0.43*	-0.67**	-0.52**	1

*,and **, significant at P≤ 0.05 and P≤ 0.01 respectively. DM= days to maturity, plant height, SN= stem number per hill, LAI = leaf area index, BMY=biomass yield, MTNPH = marketable tuber number per hill, unMTNPH = unmarketable tuber number per hill, ATW = average tuber weight, HI = harvest index, MTY = marketable tuber yield, unMTY = unmarketable tuber yield t ha^{-1}, TTY = total tuber yield t ha^{-1} TDM=Tuber dry matter content, MC= moisture content of tuber,DDA=days to late blight appearance, PSI=percent severity index and AUDPC= area under disease progress curve.

4.5.2 Path Coefficient Analysis

The direct and indirect effects of traits at genotypic and phenotypic levels are presented in Table 7 and 8, respectively. Marketable tuber yield (0.97) followed by average tuber weight (0.17), stem number per plant (0.05), tuber dry matter (0.04), harvest index (0.04), days to first late blight appearance (0.03), moisture content(0.03) and biomass yield (0.03) had maximum positive direct effect at genotypic level on total tuber yield. Other traits such as leaf area index and marketable tuber number per hill also exerted positive direct effect on total tuber yield. This suggested that these characters are good contributors to increase tuber yield and selection of genotypes with highest values for these traits leads to the increment of tuber yield. Hossain *et al*. (2000) reported positive direct genotypic effects of tuber yield per plant, average tuber weight and harvest index on total tuber yield. On other hand, days to maturity, plant height, unmarketable tuber yield, unmarketable tuber number per hill, percent severity index and area under disease progress curve exerted negative direct genotypic effect on tuber yield (Table 7). Majid *et al*. (2011) reported the direct genotypic but negative effect of small tuber per plant and plant height on tuber yield. This suggested that selection is better to be directed genotypes with low mean values for these traits since selection in favor of genotypes with high mean values will lead to the reduction of tuber yield.

The path coefficient analysis indicated that the various characters influenced the tuber yield favorably or unfavorably via other characters. Days to maturity and growth parameters viz. plant height, stem number per plant, leaf area index and biomass yield exerted positive indirect genotypic effect via average tuber weight marketable tuber yield and days to first late blight appearance. Similarly yield components namely marketable tuber number per hectare, average tuber weight and harvest index besides exerting positive direct effect on total tuber yield also showed favorable indirect influence on total tuber yield through leaf area index, marketable tuber yield, tuber dry matter, days to first late blight appearance and moisture content of tubers. Sattar *et al*. (2007) suggested that plant height, biomass yield and stem number per plant had high positive indirect effect on tuber yield. Hence, these characters are more important than other traits for the genetic improvement of potato. Majid *et al*. (2011) also reported number of stem per plant had a positive indirect effect via tuber weight per plant and average tuber weight.

In other case, most of growth parameters and yield components are exerted negative genotypic indirect effect via, unmarketable tuber number per hill, unmarketable tuber yield and both disease parameters viz. percent severity index and area under diseases progress curves.

The residual of the analysis at genotypic level was 0.047 (Table 7). This implies the parameters considered in this study explained 95.3% for total tuber yield and the remaining 4.7% is expressed by other parameters not considered in this study. This further explained the parameters chosen for this study were good.

Phenotypic path coefficient analysis results revealed that marketable tuber yield (1.10) followed by marketable tuber number per hill (0.05), average tuber weight(0.04), tuber dry matter(0.03) and plant height(0.03) had maximum positive direct effect on tuber yield (Table 8). Other traits such as stem number per plant, leaf area index, harvest index and days to first late blight appearance also exerted positive direct effect on total tuber yield. Pandey *et al*. (2005) indicated that number of tubers per plant showed a positive direct effect on tuber yield in potato. This is in line with Abraham *et al*. (2014) indicated stems number per plant, plant height and average tuber weight had positive direct phenotypic effect on tuber yield. Hence, these traits will be given due consideration during selection. On the other hand, unmarketable tuber number per hill, unmarketable tuber yield, percent severity index and area under disease progress curve exerted negative direct effect on tuber yield.

The path coefficient analysis indicated that the various characters influenced total tuber yield favorably or unfavorably via other characters phenotypically (Table 8). Particularly, marketable tuber yield, marketable tuber number per hill, average tuber weight, leaf area index, biomass yield, and plant height influenced total tuber yield positively through other traits while percent severity index and area under disease progress curve affected total tuber yield negatively via other traits. Residual at phenotypic level was 0.150, that implies the parameters considered in this study explained 85% of tuber yield and the remaining 15% is expressed by other parameters not considered in this study. This further explained the parameters chosen for the studies were good in explaining the observed tuber yield variations.

Table 7. Genotypic direct (underlined) and indirect effect of 16 characters on potato tuber yield at Sinana, 2014 cropping season

Variable	DM	PH	SN	LAI	BMY	MTN	unMTNPH	ATW	HI	MTY	unMTY	TDM	MC	DDA	PSI	AUDPC	rg
DM	**-0.02**	0.00	-0.01	0.04	-0.02	0.01	-0.02	0.08	0.01	0.72	-0.04	-0.02	0.02	-0.02	-0.05	-0.03	0.70**
PH	-0.01	**-0.01**	-0.01	0.01	-0.02	0.00	0.00	0.09	0.00	0.53	0.00	-0.02	0.01	-0.01	-0.02	0.02	0.56*
SN	-0.01	0.00	**0.05**	0.00	-0.01	0.00	0.04	0.04	0.00	0.53	0.03	-0.01	0.00	0.00	-0.02	0.01	0.56*
LAI	-0.01	-0.01	-0.02	**0.01**	-0.02	0.01	-0.03	0.11	0.00	0.82	-0.04	-0.03	0.02	-0.02	-0.05	0.07	0.83**
BMY	-0.01	-0.01	0.01	0.01	**0.03**	0.00	-0.01	0.08	-0.01	0.70	-0.03	-0.02	0.01	0.03	-0.04	-0.01	0.70**
MTN	-0.01	-0.01	-0.03	0.01	-0.02	**0.01**	-0.01	0.10	0.01	0.88	-0.03	-0.02	0.01	-0.01	-0.04	0.05	0.89**
unMTN	0.00	0.00	-0.02	0.00	0.00	0.00	**-0.09**	-0.08	-0.01	-0.15	0.08	0.01	-0.01	0.01	0.02	-0.05	-0.10
ATW	-0.01	-0.01	-0.01	0.01	-0.01	0.00	-0.05	**0.17**	0.00	0.71	-0.04	-0.02	0.01	-0.02	-0.04	0.05	0.75**
HI	-0.01	0.00	0.00	0.00	0.01	0.00	-0.03	0.02	**0.04**	0.11	-0.05	-0.01	0.01	0.00	-0.01	0.02	0.10
MTY	-0.01	-0.01	0.02	0.01	0.02	0.01	-0.01	0.13	0.00	**0.97**	-0.03	-0.02	0.01	0.06	-0.05	-0.02	0.99**
unMTY	0.01	0.00	-0.01	0.00	0.01	0.00	0.08	-0.08	-0.02	-0.26	**-0.10**	0.01	-0.01	0.01	0.02	-0.06	-0.20
TDM	-0.01	-0.01	-0.02	0.01	-0.02	0.00	-0.03	0.09	0.01	0.60	-0.03	**0.04**	0.02	-0.01	-0.04	0.05	0.60*
MC	0.01	0.00	0.01	-0.01	0.01	0.00	0.03	-0.05	-0.01	-0.45	0.03	0.03	**0.03**	0.02	0.04	-0.05	-0.43*
DDA	-0.01	0.00	0.00	0.01	-0.01	0.00	-0.04	0.11	0.00	0.52	-0.04	-0.02	0.02	**0.03**	-0.05	0.08	0.53*
PSI	0.01	0.00	0.01	-0.01	0.02	0.00	0.02	-0.11	-0.01	-0.82	0.04	0.02	-0.02	0.02	**-0.06**	-0.08	-0.83**
AUDPC	0.01	0.00	0.00	-0.01	0.02	0.00	0.05	-0.09	-0.01	-0.60	0.06	0.02	-0.02	0.02	0.05	**-0.10**	-0.59*

Residual =0.047

DF=days to flowering, DM= days to maturity, plant height, SNPH = stem number per hill, LAI = leaf area index, BMY=biomass yield, MTNPH = marketable tuber number per hill, unMTNPH = unmarketable tuber number per hill, ATW = average tuber weight, HI = harvest index, MTY = marketable tuber yield, unMTY = unmarketable tuber yield t ha^{-1}, TDM=Tuber dry matter content, MC= moisture content of tuber, PSI=percent severity index, AUDPC=area under disease progress curve.

Table 8. Phenotypic direct (underlined) and indirect effect of 16 characters on potato tuber yield at Sinana, 2014 cropping season

Variable	DM	PH	SN	LAI	BMY	MTN	unMTN	ATW	HI	MTY	unMTY	TDM	MC	DDA	PSI	AUDPC	r_p
DM	**-0.03**	0.01	0.00	-0.02	0.00	-0.04	-0.01	0.02	0.01	0.77	-0.01	-0.01	0.00	0.01	-0.09	0.04	0.65**
PH	-0.01	**0.03**	0.00	-0.02	0.00	-0.03	0.00	0.02	0.00	0.53	0.00	-0.01	0.00	0.00	-0.03	0.01	0.49**
SN	-0.01	0.01	**0.02**	-0.01	0.00	-0.04	0.02	0.01	0.00	0.45	0.01	-0.01	0.00	0.00	-0.03	0.00	0.42*
LAI	-0.01	0.01	0.01	**0.03**	0.00	-0.04	-0.01	-0.02	0.00	0.75	-0.01	-0.02	0.00	0.01	-0.09	0.05	0.63**
BMY	-0.01	-0.01	0.00	-0.01	**0.01**	-0.03	-0.01	0.01	0.00	0.57	-0.01	-0.01	0.00	0.00	-0.04	0.03	0.49**
MTN	-0.02	0.01	0.01	-0.02	0.00	**0.05**	0.00	0.02	0.01	0.89	-0.01	-0.01	0.00	0.00	-0.08	-0.03	0.77**
unMTN	0.01	0.00	0.01	0.01	0.00	0.00	**-0.05**	-0.02	0.00	0.14	0.03	0.01	0.00	0.00	0.02	-0.03	-0.07
ATW	-0.01	0.01	0.00	-0.02	0.00	-0.04	-0.02	**0.04**	0.00	0.72	-0.01	-0.01	0.00	0.01	-0.07	0.03	0.63**
HI	-0.01	0.00	0.00	-0.01	0.00	-0.02	-0.01	0.01	**0.02**	0.08	-0.01	0.00	0.00	0.00	-0.02	0.01	0.05
MTY	-0.02	0.01	0.01	-0.02	0.00	-0.05	-0.01	0.03	0.00	**1.10**	-0.01	-0.02	0.00	0.01	-0.09	0.04	0.98**
unMTY	0.01	0.00	0.00	0.01	0.00	0.02	0.04	-0.02	0.01	-0.26	**-0.03**	0.01	0.00	0.00	0.04	-0.04	-0.16
TDM	-0.01	0.01	0.00	-0.02	0.00	-0.03	-0.01	0.02	0.00	0.59	-0.01	**0.03**	0.00	0.00	-0.06	0.03	0.49**
MC	0.01	-0.01	0.00	0.01	0.00	0.03	0.01	-0.01	0.00	-0.48	0.01	0.02	**0.00**	-0.01	0.06	-0.03	-0.40*
DDA	-0.01	0.01	0.00	-0.02	0.00	-0.02	-0.02	0.02	0.00	0.50	-0.01	-0.01	0.00	**0.01**	-0.08	0.05	0.43*
PSI	0.02	-0.01	0.00	0.03	0.00	0.04	0.01	-0.02	0.00	-0.80	0.01	0.01	0.00	0.02	**-0.12**	-0.05	-0.67*
AUDPC	0.02	0.00	0.00	0.02	0.00	0.03	0.02	-0.02	0.00	-0.63	0.02	0.01	0.00	-0.01	0.09	**-0.07**	-0.52*

Residual=0.150

DF=days to flowering, DM= days to maturity, plant height, SNPH = stem number per hill, LAI = leaf area index, BMY=biomass yield, MTNPH = marketable tuber number per hill, unMTNPH = unmarketable tuber number per hill, ATW = average tuber weight, HI = harvest index, MTY = marketable tuber yield, unMTY = unmarketable tuber yield t ha^{-1} TDM=Tuber dry matter content, MC= moisture content of tuber, PSI=percent severity index, AUDPC=area under disease progress curve

5. SUMMARY AND CONCLUSION

Potato is produced at highlands of Bale, but the productivity of the crop is low due to unavailability of improved varieties with high tuber yield and resistant or tolerant to late blight. Therefore, this study was conducted at Sinana Agricultural Research Center in 2014 during the main cropping season to study the nature and magnitude of variability for tuber yield, yield related traits and late blight resistance in 24 potato genotypes and to determine the association of tuber yield with other traits. The experiment was laid out in randomized complete block design with three replications.

The presence of highly significant variation among genotypes was observed for all traits except for starch and specific gravity indicating the higher chance of selecting genotypes for tuber yield, yield components and late blight resistance. Wide ranges of mean values were recorded for all characters except for starch and specific gravity. 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 (CIP-392640.524, CIP-395114.5, CIP-396244.12 and CIP391058.175) 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 11 advanced clones (CIP-391058.175, CIP-395096.2, CIP-395114.5, CIP-396031.201, CIP-392640.524, CIP-396240.23, CIP-396244.12, CIP-399062.102, CIP-395017.242, CIP-396029.205 and CIP-395077.12) 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. These genotypes might not be considered for future improvement unless the breeding objective is set to develop varieties for late blight free cropping season (eg. irrigation production).

High magnitudes of genotypic and phenotypic coefficient of variations were observed from 22.7 to 51.9% and from 32.8 to 56.7%, respectively for most of crop phenology, growth and disease

parameters. Such traits have high probability of improvement through selection. Low magnitude of genotypic and phenotypic coefficient of variation was recorded for days to maturity. 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. This indicated these characters are governed by additive genes and selection could be rewarding. Moderate heritability and genetic advance was computed for tuber dry matter, harvest index and days to maturity.

Total and marketable tuber yield showed positive and significant with most of phenological, growth parameters, and yield components except negative and significant with percent severity index and area under disease progress curve. Most of phenological, growth parameters and yield components also showed positive and significant among themselves. Biomass yield, leaf area index, average tuber weight, moisture content of tubers and tuber dry matter were correlated positively with most of the characters. Both at genotypic and phenotypic level, marketable tuber yield, average tuber weight, harvest index and moisture content had positive direct effect on total tuber yield. Other traits such as leaf area index, biomass yield, marketable tuber number per hill, average tuber weight and marketable tuber yield had positive indirect effect on total tuber yield via other traits, However, days to maturity, unmarketable tuber yield and tuber number per hill, percent severity index and area under disease progress curve exerted negative direct and indirect effect through other trait on total tuber yield. This result suggested the importance of considering marketable tuber yield, average tuber weight, marketable tuber number per hill, biomass yield and leaf area index in selection of genotypes for high tuber yield because of their strong correlation to yield and had positive direct or indirect effect on tuber yield. However, selection of genotypes for the lower mean values for unmarketable tuber yield and tuber number per hill, percent severity index and area under disease progress curve is necessary since these traits had highly negative and significant correlation to yield as well as they exerted strong negative direct or indirect effect on tuber yield.

The present study revealed the existence of high genetic variability in 24 potato genotypes for tuber yield, yield related traits and 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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APPENDIX

Appendix Table 1. Mean performance of 24 potato genotypes for yield and yield components and quality attributes at Sinana in 2014 bona cropping season.

No.	Genotypes	MTNPH	unMTNP	ATW	HI	MTY	unMTY	TTY	TDM	Sg	MC	starch
1	CIP-395096.2	2.0 ^{j}	(4.6) 3.4 $^{a-e}$	3.7 ^{i}	94^{a}	0.06^{n}	0.7 $^{h-j}$	0.8 ^{j}	24.8^{c-h}	1.07^{ab}	72^{e-i}	12^{bd}
2	CIP-391381.9	4.9 $^{f-j}$	(16.1)4.4 ^{ab}	16.6 $^{g-i}$	91 ^{ab}	3 $^{l-n}$	3.2 ^{b}	6 $^{h-j}$	21^{g-j}	1.09^{ab}	77.5^{a-d}	13.8 $^{a-d}$
3	CIP-395077.12	4.5 $^{g-j}$	(1.8) 1.8^{a}	56 $^{b-f}$	68.7^{d-g}	11.3 $^{h-l}$	0.7 $^{h-j}$	12^{g-i}	20.6 $^{h-j}$	1.07^{ab}	78 ^{ab}	12 ^{bd}
4	CIP-99062.102	8.2 $^{b-g}$	(8.7) 3.4^{a-e}	67 $^{b-d}$	71.2^{c-g}	23.2 $^{d-f}$	1.3 $^{f-i}$	24.5 $^{c-f}$	25 $^{b-f}$	1.07^{ab}	72.8^{c-i}	12.9^{b-d}
5	Belete	9.8 ^{bc}	(4.6) 2.6 $^{d-g}$	109 ^{a}	79.8^{b-e}	39.4^{ab}	0.7 h-j	41 ^{ab}	29 ^{ab}	1.09^{ab}	72d^{e-i}	19 $^{a-d}$
6	CIP396039.103	11.7^{ab}	(12) 3.9 a-c	47 $^{c-g}$	88 $^{a-c}$	21 $^{e-g}$	1.3 $^{f-i}$	23.5^{c-f}	24.9^{c-g}	1.09^{ab}	74.5^{a-i}	12.9^{b-d}
7	CIP-399078.11	6.8 $^{c-h}$	(3.4) 2 ^{fg}	62 $^{b-d}$	66.5^{e-g}	15.2 $^{f-i}$	0.7 $^{h-j}$	15.9 $^{f-h}$	28 $^{a-c}$	1.09^{ab}	75.5^{a-g}	14.9^{a-d}
8	CIP-395112.19	5.6 $^{e-j}$	(2.5) 2.$^{1\ e-g}$	114^{a}	84.9^{a-e}	13.2 $^{g-k}$	0.3 ^{j}	13.6 ^{eh}	24.7^{c-h}	1.08^{ab}	75 $^{a-h}$	13.9 $^{a-d}$
9	CIP395017.242	8.7 $^{b-f}$	(5.7) 2.8 $^{c-g}$	71.8^{bc}	79 $^{b-e}$	21.5 $^{e-g}$	1.4 $^{e-i}$	22.9 $^{c-f}$	25 $^{c-g}$	1.09^{ab}	71.4^{f-j}	18^{a-d}
10	Kellacho	3.5 $^{h-j}$	(9.3) 3.2 $^{b-f}$	12 ^{hi}	68.6^{d-g}	1.4 ^{mn}	1.3^{f-i}	2.7 ^{ij}	21.5^{f-j}	1.08^{ab}	73.5^{b-i}	16 $^{a-d}$
11	CIP-395114.5	14.1^{a}	(12.3)3.9 $^{a-c}$	62 $^{b-d}$	71.7^{c-g}	32.7^{bc}	0.6 $^{h-j}$	33.6 ^{bc}	23.9^{d-i}	1.09^{ab}	73 $^{b-i}$	12.9^{b-d}
12	CIP-396240.23	10.1^{bc}	(4.6) 2.6 $^{d-g}$	69.7^{bc}	87 $^{a-d}$	25.5 $^{c-e}$	1.5 $^{e-i}$	26.8 $^{c-e}$	30.5^{a}	1.08^{ab}	66.6^{j}	20^{a}
13	CIP-397079.26	3.6 $^{h-j}$	(3.1) 2.3 $^{d-g}$	58 $^{b-e}$	84.9^{a-e}	4.1 $^{k-n}$	0.2 ^{j}	4 ^{ij}	20.5^{h-j}	1.09^{ab}	77.5^{a-e}	12.9^{b-d}

Appendix Table 1. *Continued*…

14	CIP391058.175	9.7^{b-d}	(5.6) 2.8 $^{c-g}$	72 ^{bc}	83 $^{a-e}$	29.2 $^{c-e}$	1.5^{e-h}	31^{bc}	27 $^{a-e}$	1.07^{ab}	70 $^{h-j}$	19.8^{abc}
15	CIP396029.205	9.5 $^{b-e}$	(3.7) 2.4^{d-g}	74.8 ^{bc}	84 $^{a-e}$	26.4 $^{c-e}$	0.7 $^{h-j}$	27 ^{cd}	24.9^{c-g}	1.13^{a}	71 $^{g-j}$	14.9^{a-d}
16	Ararsa	5.7 $^{d-j}$	(6.5) 3.5 $^{a-d}$	43 $^{c-h}$	76 $^{b-f}$	13.5 $^{g-j}$	1.1^{g-j}	14.6^{eh}	17.6 ^{j}	1.08^{ab}	76^{a-g}	19.9^{abc}
17	CIP-399053.15	4.7 $^{f-j}$	(9) 3 $^{c-g}$	34.9 $^{d-i}$	81 $^{a-e}$	7.5 $^{i-n}$	2.2 $^{c-f}$	9 $^{g-j}$	21.6^{f-j}	1.08^{ab}	77.9^{a-c}	12.9^{b-d}
18	CIP-393382.44	8.2 $^{b-g}$	(3) 2.2^{d-g}	54 $^{b-f}$	83.4^{a-e}	10.7 $^{i-m}$	0.6 $^{h-j}$	11 $^{g-j}$	24^{d-i}	1.07^{ab}	74.9 $^{a-h}$	18.9^{a-d}
19	CIP396031.201	3.4 $^{h-j}$	(6.3) 3 $^{c-g}$	27.5 $^{e-i}$	73 $^{b-g}$	5.5 $^{j-n}$	1 h-j	6.6 $^{h-j}$	22.9 $^{e-i}$	1.09^{ab}	75 $^{a-h}$	13.9^{a-d}
20	CIP395017.229	6.2 $^{c-i}$	(7.8) 2.9 $^{c-g}$	44 $^{c-g}$	57.5 g	14 $^{f-j}$	2.9 $^{b-d}$	16.9^{d-h}	26.7^{a-e}	1.08^{ab}	72.7^{c-i}	15.8^{a-d}
21	Guddane	6.7 $^{c-h}$	(8.2) 3.3 $^{a-f}$	58 $^{b-e}$	81.6 $^{a-e}$	20.7 $^{e-h}$	2.3 $^{c-e}$	23 $^{c-f}$	23.8^{d-i}	1.09^{ab}	74.9^{a-h}	18.9 $^{a-d}$
22	CIP-3940.524	14.2 ^{a}	(5.8) 2.9 $^{c-g}$	81 ^{b}	87 $^{a-d}$	43.7^{a}	2.4 $^{c-e}$	46.1 ^{a}	25.8 $^{b-f}$	1.07^{ab}	76.6^{a-f}	12.9^{b-d}
23	CIP-391930.1	2.5 ^{ij}	(21.0) 4.6^{a}	24.4 $^{f-i}$	58 fg	3.3 $^{i-n}$	8.7^{a}	11.5^{g-i}	20 ^{ij}	1.07^{ab}	78.9 ^{a}	12.9 $^{b-d}$
24	CIP-396244.12	11.1^{ab}	(6.46) 3 $^{c-g}$	71.8^{bc}	81.2 $^{a-e}$	31.7 $^{b-d}$	1.4 $^{f-i}$	33 ^{bc}	27.9 $^{a-d}$	1.09^{ab}	69.4 ^{ij}	19^{a-d}
Range		2-14.2	1.8-4.6	3.78-114.5	57.5-94	0.06-43.7	0.65-8.7	0.76-46.1	17.6-30.5	1.07-1.13	66-78.9	12 -20
mean		7.3	3.02	55.8	78.8	17.5	1.721	19.41	24.33	1.1	74.1	15.5
CV%		28.7	22.6	30.4	12.1	28.2	29.2	29.3	9.1	2.3	3.7	34.6
Level of significance		**	**	**	**	**	**	**	**	ns	**	ns

Means followed by the same letter within a column are not significantly different at the prescribed level of probability. ** = significant at 1% and ns = non significant. at 1% and 5%. MTNPH= marketable tuber number per hill, unMTNP=unmarketable tuber number per hill, ATW= average tuber weight, MTY= marketable tuber yield, unMTY= unmarketable tuber yield, TTY= total tuber yield, TDM=tuber dry matter, Sg=specific gravity, MC=moisture content and starch.

Appendix Table 2. Mean performance of 24 potato genotypes for phenology and growth parameters at Sinana in 2014 cropping season.

No.	Genotypes	DF	DM	PH	SN	LAI	BMY
1	CIP-395096.2	59.6^{ab}	111.3 ^{e}	22 ^{ef}	2 ^{f}	20.7^{b-d}	114^{g-i}
2	CIP-391381.9	55 ^{a}	98^{a}	49.6 $^{a-e}$	3.6 $^{b-e}$	6 ^{ef}	102.7^{hi}
3	CIP-395077.12	57.3^{ab}	105^{cd}	37 $^{b-e}$	2.5^{d-f}	14 $^{c-e}$	253.2^{d-f}
4	CIP-99062.102	62 ^{b}	119^{f-h}	71.6 ^{a}	3.6^{b-e}	26.5^{ab}	273.7 $^{c-f}$
5	Belete	57.3 ^{ab}	114.3 ^{ef}	71.4^{a}	4.6^{a-d}	26.8^{ab}	394.9^{ab}
6	CIP396039.103	62 ^{b}	119^{f-h}	58.7^{a-d}	6.2 ^{a}	22^{a-d}	270.2^{d-f}
7	CIP-399078.11	62 ^{b}	105^{cd}	51.5^{a-e}	4.7^{a-d}	26.8^{ab}	258.5^{d-f}
8	CIP-395112.19	62 ^{b}	102.7^{a-d}	39.8^{b-e}	2.1^{ef}	19^{b-d}	207.5^{e-h}
9	CIP395017.242	62 ^{b}	105^{cd}	51.9^{a-e}	5.3^{ab}	28.5 ^{ab}	220.6^{e-g}
10	Kellacho	69 ^{c}	98^{ab}	33.3^{c-f}	3.4^{b-e}	6.7^{ef}	92.5^{hi}
11	CIP-395114.5	62^{b}	119^{fh}	61.6^{a-c}	4.5^{a-d}	28^{ab}	418.6 ^{a}
12	CIP-396240.23	59.6^{ab}	119^{f-h}	53^{a-d}	4.6^{a-d}	25.6^{a-c}	293.4^{b-e}
13	CIP-397079.26	57.3 ^{ab}	105^{cd}	30.1^{d-f}	2.1 ^{ef}	12.7 $^{d-f}$	90.3i
14	CIP391058.175	59.6 ^{ab}	119^{h}	64.8^{ab}	4.8^{a-d}	28.9^{ab}	297.4^{b-e}
15	CIP396029.205	57.3 ^{ab}	119^{f-h}	65.2^{ab}	3.8^{a-e}	19.9^{b-d}	281.6^{c-e}
16	Ararsa	55 ^{a}	112 ^{e}	48.7^{a-e}	2.8^{c-e}	20.5^{b-d}	164.2^{f-i}
17	CIP-399053.15	59.6^{ab}	98 ^{a}	58.7^{a-d}	4.5^{a-d}	18.5^{b-d}	136.9^{g-i}
18	CIP-393382.44	62 ^{b}	105^{cd}	58.6^{a-d}	3.2 $^{b-e}$	15^{c-e}	127 $^{g-i}$
19	CIP396031.201	59.6 ^{ab}	105^{cd}	19.5^{f}	3.1 $^{b-e}$	17.5 $^{b-d}$	130^{g-i}
20	CIP395017.229	57.3^{ab}	100^{a-c}	74.6 ^{a}	2.7^{c-e}	25.5^{a-c}	261.6^{d-f}
21	Guddane	59.6 ^{ab}	112^{e}	47.9 $^{a-e}$	5.4^{ab}	22 $^{b-d}$	192.9^{e-i}
22	CIP-392640.524	62 ^{b}	114.3^{e-g}	59.6^{a-d}	4.8^{a-d}	33 ^{a}	383.7^{a-c}
23	CIP-391930.1	55 ^{a}	98 ^{a}	60.8^{a-d}	4.9^{a-c}	3 ^{f}	140^{g-i}
24	CIP-396244.12	57.3^{ab}	119^{f-h}	78 ^{a}	4.3^{a-e}	24^{a-c}	366.9^{a-d}
Range		55-69	98-119	19.5-78	2 - 6.2	6 - 33	90.3-418.6
mean		59.6	109	58.4	3.85	20.54	228
CV%		4.7	2.4	29.8	31.7	28.2	26.3
Level of significance		**	**	**	**	**	**

Means followed by the same letter within a column are not significantly different at the prescribed level of probability. ** = significant at 1% and ns = non significant. at 1% and 5%. DF=days to flowering, DM=days to maturity, PH=plant height, SN=stem number per plant, LAI=leaf area index, BMY=biomass yield.

Appendix Table 3. Mean performance of 24 potato genotypes for late blight disease parameters at Sinana in 2014 bona cropping season

Genotypes	DDA	PSI 74-DAP	AUDPC
CIP-395096.2	63 b-d	33.0a	105a
CIP-391381.9	48 e	80.3c-e	1753 e
CIP-395077.12	63 b-d	39.7a	248.6 a
CIP-399062.102	74.67 a	38.67a	105a
Belete	70ab	33a	105 a
CIP-396039.103	48 e	68b-e	1119.d
CIP-399078.11	53 de	67b-e	575.2ab
CIP-395112.19	72.3ab	55.3 a-c	332.3 ab
CIP395017.242	72.3ab	38.67 a	145.8a
Kellacho	48e	82.0de	2014.1ef
CIP-395114.5	62.6 b-d	33.0a	122.5a
CIP-396240.23	62.6 b-d	36.67a	180.8a
CIP-397079.26	48.e	91.33e	2370g
CIP391058.175	65.3a-c	33a	105a
CIP396029.205	63 b-d	37.0 a	189.1a
Ararsa	63 b-d	57.a-d	372.1 ab
CIP-399053.15	48 e	66 b-d	1191.6d
CIP-393382.44	53 de	65.6 b-d	1134.5d
CIP396031.201	53de	33.33a	161.2 a
CIP395017.229	58 c-e	56.67ad	750.5 c
Guddane	63 b-d	43.3ab	581.0bc
CIP-3920 -524	58 c-e	36.67a	186.7a
CIP-391930.1	48e	91.67e	2165.6fg
CIP-396244.12	65.3 a-c	37.00 a	264.1a
mean	59.31	53.7	680
CV%	10.3	24.9	24.6
Level of significance	**	**	**

Means followed by the same letter within a column are not significantly different at the prescribed level of probability. ** = significant at 1% and ns = non significant. at 1% and 5%. DDA= days to late blight appearance, PSI = percent severity index 74 days after planting date, AUDPC= area under disease progress curve, CV= coefficient of variation, LSD= least significance difference

Appendix Table 4. Key for assessing severity of late blight under field conditions (Henfing, 1987)

Score	***Phytophthora infestans* (%)**		**Symptoms**
	Severity average (%)	**Severity range(%)**	
1	0	0	*P. infestans* not observed
2	2.5	Trace - 5	*P. infestans* present. Maximum 10 injuries per plant
3	10	5 -15	Plants seem to be healthy, but injuries can be easily observed. There are no more than 20 affected leaves
4	25	15-35	*P. infestans* is easily observed on the plants. About 25% of the leaf area is affected by injuries.
5	50	35- 65	Plants look green, but each one is affected by the pathogen, lower leaves are necrotic. About 50% of the leaf area is destroyed
6	75	65- 85	Plants look green with brown spots. About 75% of the leaf area is affected. Leaves in the middle of the plant are destroyed
7	90	85-95	Only upper leaves are green. Most of leaves are affected and many stems have external injuries
8	97.5	95-100	Plants look brown, few upper leaves are green and most of the stems are hardly affected or dead
9	100		Leaves and stems are destroyed