GENETIC VARIABILITY STUDIES OF TWENTY POTATO GENOTYPES

BY

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DEPARTMENT OF PLANT SCIENCE
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DECLARATION

I hereby declare that this thesis was written by me and is a record of my research work. It has not been presented in any previous thesis for a higher degree. References made to published and unpublished literature have been duly acknowledged.

_________________________ _________________________

Danbaba Anthony Kude Date

The above declaration is confirmed:

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Chairman Supervisory Committee

DEDICATION

To the memory of my late father Danbaba Kude Agau who ensured that I must be an educated man

CERTIFICATION

This thesis entitled “PRINCIPAL COMPONENT ANALYIS OF TWENTY (20) POTATO GENOTYPES” by DANBABA ANTHONY Kude meets the Regulations Governing the Award of the Degree of Masters of Science (M.Sc.) of Ahmadu Bello University, Zaria, and is approved for its contribution to scientific knowledge and literary presentation.

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ABSTRACT

Twenty potato genotypes were evaluated in Randomized Complete Block Design Replicated three times for their yield potentials and agronomic characteristics. The experiment was conducted at the Research Farm of the potato programme of National Root Crops Research Institute, Kuru, Plateau State, during the 2005, 2006 and 2010 cropping seasons. Results showed that the genotypes differed significantly for all the traits. Five genotypes 375400.00, Desiree, WC732-1, 392278.4, and 676008 were most promising based on tuber yield and other agronomic traits. Famosa an elite genotype did not perform better than these promising genotypes. Year effect was significant for all the traits except plant height while genotype x year interaction was significant except emergence counts, internodes length, plant height and number of leaves/plant suggesting the need to evaluate these genotypes for more number of years. The genotypes were grouped into 5 clusters based on Mahalanobis D^2, high inter-cluster differences were observed between cluster III and V, and IV and V implies that genotypes in these different cluster groups can be used as parents in hybridization and expected to give a wide array of segregants. The correlation and path coefficient analysis indicated higher magnitude genotypic correlation coefficients than the corresponding phenotypic estimates, thereby indicating that there is strong inherent association between these characters. Tuber number/plant, showed the highest positive direct effect on tuber yield. This indicates that tuber number could be used as indirect selection index for improving tuber yield. Principal component extracted from the correlation matrix showed that average tuber weight, number of eyes/tuber and plant height had significant loadings on the first axis. The second axis shows number of stems had negative significant loading.

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CHAPTER ONE

INTRODUCTION

Potato (S*olanum tuberosum.* L). Belong to the solanaceous family consisting of 90 genera and 2,800 species. Many wild species occur more specifically in the Andes of Peru and Bolivia of which the cultivated potato must have been derived (Brown; 1973). Wild species also occur in Mexico and Central America.

Potato spread to Europe first to Spain in 1573 (Salaman., 1937 and Hawks., 1990). And to Italy and later England in 1596. From this Spanish source, potato spread through Europe and Asia and from England it spread to British overseas colonies including U.S.A, India and China. It was grown in Japan, Africa and West Indies in the 17th century.

Potato is world's fourth most important food crop, after wheat (*Triticum aestivum L.),* maize (*zea mays* L.) and rice (*oryza sativa*. L.) (F.A.O., 2001). Nearly 3.5 billion people (3/4 of the world's population inhabit the more than one hundred potato producing countries of the world (CIP., 1988). Potato production world wide stands at 293 millions tons and covers more than 18 million hectares, one third of this figure is produced in the developing world (Horton., 1988). Annual production is growing fast and the rate of potato production is among the highest in the world. Average world production is 16 t/ha, in the Netherlands and U.S.A it exceeds 100 t/ha and in Africa the average is 7t/ha,. This depends on climate and topography (F.A.O., 2002).

China is now the world's largest potato producer since the break-up of U.S.S.R. Area planted to potatoes is growing faster in developing countries than any other major food crop over the last 30yr period studied (F.A.O., 1998). Production and consumption is now shifting from Europe to Asia and Africa. The European

Union produces 40 million tons while in Africa, Egypt, South Africa, Algeria and morocco produce more than 80% of potatoes in Africa. Growth rates in each of these countries has been strong, Egypt for example has 5%growth rate per annum between 1998-2006. Expanding access to irrigation has been a major factor facilitating this growth in output and high average yields (14-28 t/ha). Rising incomes, tourism and for North Africa Producers, a lucrative winter export market has been added advantage. In Nigeria, potatoes were introduced during the 1920,s, probably by the European tin miners on the Jos plateau. Production was limited to small garden plots until the Second World War when the British colonial government encouraged potato cultivation to help feed service men in West Africa. Government records showed an increase in annual production from a mere 180 tons in 1940, to 1,732 tons in 1944. Formal potato research in Nigeria date back to 1940 with the establishment of the government farm at Riyom near Jos (Okonkwo., 1995). In 1961 a seed potato multiplication project was established by the ministry of Agriculture (Okonkwo, 1995). Potato breeding programme was established in 1964 with experimental sites at Ganawuri, Tarhoss and Vom on the Jos Plateau. The Institute for Agricultural Research (IAR) Samaru assumed responsibility for the potato breeding programme in 1972. Total land area under production in 1940 was 30 hectares and total production in tons per ha was 180 increased to about 80,000 Hectares of land under production in 2001, resulting in total production in tones of about 800,000 tones (Amadi and Ene-bong, 2005).

The potato production zones in Nigeria include: Jos plateau, mambilla plateau, Obudu Hills, Biu Plateaus, Zaria province, and other Northern states such as Kaduna, Kano, Sokoto, Borno and Jigawa .

The potato crop is one of the world's most valuable basic food crops, it is mostly consumed by humans all over the world. It is superior to other tuber crops in protein production per unit area and to most others in terms of energy production (Vander Zaag., 1976). Its protein is particularly valuable because it contains high amounts of essential amino acids than most crops. Based on its use mainly as a food crop, it can reduce poverty and achieve food security Ortiz *et al*., 1993).

Consumption of fresh potato per person is higher as in Europe than nowhere else in the world. Ireland has the highest rate of consumption (140kg) per person and is closely followed by Portugal (130kg) per person Britain consumes a lot of processed potatoes. The lysine content of potato complements cereal-based diets, which are deficient in this amino acid. Potato is an important food staple in the developing world, and plays an important role in Agricultural development in Africa, Asia, and Latin America. The food value of potato tuber contains 75-78% moisture, 17-20% carbohydrates, 1.8-2.0 protein, fiber 1.2% fats >1% and 1.2% Ash. The tuber can be boiled either peeled or unpeeled, roasted, deep fried or cooked by microwave. When tubers are peeled, they are trimmed before boiling and condiments are added. Deep frying can convert potato into two main forms known as French fries and crisp.

Potatoes are also used in feeding livestock. In Europe, potatoes are a major livestock feed. The use of potato as livestock feed has declined because they have become more expensive relative to alternative feed stuffs and energy sources and also human consumption is rising (Barton., 1989).

Small quantities of potato are used by commercial industries in the production of starch, flour, alcohol and potato dextrin's which is use in bookbinding, corrugated cardboards, stamps and gummed labels (Amadi., 2006.). Other uses besides food includes its use as a source of vitamin, raw slices are use to cure Rheumatism and ulcer.

There are good prospect for the expansion of potato market, if potato yields can be increased fast enough to catch up with yields of competing tuber crops such as cassava and yam. Meeting the growing demand for food and industry will depend largely on the success of research in the development of new varieties, introduction and screening of exotic varieties and ascensions to local conditions and multiplication and distribution to farmers of basic seed of existing varieties. Development of new varieties that will yield better than the existing varieties is crucial. Consequently, household consumption and industrial needs can be met, and the excess share of production may be sold. Thus, higher production and utilization would lead to income growth and better living conditions.

Some improved varieties and ascensions have been screened and are with the farmers, the yields have been insignificant at the farmer level and low compared with the world's average of 16 t/ha. The average yields in Nigeria are as low as 4-5 t/ha or even less.

The aim of a plant breeder is to select superior genotypes for constituting an improved or agronomically useful population, which can be further used in the breeding programme. For selection to be effective, broad-based random-mating populations with wide range of variability have to be used.

One of the major problems of potato production is low multiplication ratio which ultimately affects the final yield of the crop. The potential utilization of potato for industrial purpose may not be realized in view of the acute shortage of potato crop because of low productivity. There is therefore an urgent need to increase productivity. One remedial option among others is to increase research and development efforts towards solving these problems. Therefore, this study was undertaken to achieve the following objectives:

1. To determine the genetic variability for agronomic traits in twenty (20) potato genotypes obtained/generated from different countries.
2. To form a broad-base strategy for clonal selection aimed at improving tuber yield.
3. To estimate phenotypic and genotypic correlations of yield and yield components of tuber
4. To estimate direct and indirect contributions of different traits to yield and their implication for selection.
5. To determined genetic diversity of potato genotypes
6. To determined principal component analysis in potato

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Genetic variability in potato Genotypes

Any successful hybridization programme for varietal improvement depends mainly on the chosen parents or breeding stock having wide genetic diversity and variability (Rashid and Sarkar,1987, (Teshome *et al,* 2001). Knowledge of the nature and magnitude of genetic variability expressed from generation to generation enables the breeder to discriminate effectively and helps the breeder to know the source of germplasm (Tommooka., 1991) (Kang *et al., 1983)* As a vegetatively propagated crop it is expected that the tubers are reasonably stable, this stability is not absolute (Howard, 1970). Mutation occur in potato (Heiken., 1958). Such mutations and segregation of chance seedlings are responsible for genetic variability. Moreover, potato fruit or berry contains on average about 260 seeds (Accatino 1980). Each seed, if it germinates and becomes established may because of this heterozygosity, give rise to a new variety of which many of the traits show continuous variation (Jones *et al*., 1985) which is the basis for crop improvement.

Burton (1966a) studied plant height at flowering stage and classified them to be short, medium or tall, he quantified them as <45cm, 45-60cm and >60 cm respectively. He found variability among genotypes. Gopal (1999) observed a higher co efficient of variation for plant height than tuber yield in a random population of potato.

Khadga *et al* (1999) in their study on evaluation and genetic variability in some clones of potato identified five clones with high genetic variability in agronomic characters such as number of leaves per plant, tuber yield per plant, number of stem per plant and average tuber yield compared to commercial varieties. Chaudhary and

Sharma (1984) studied 58 diverse potato genotypes and indicated a significant genotypic and phenotypic variations and greatly identified ten varieties that were early maturing (<70 days). Birhman and Kaul (1989) also recorded significant genotypic and phenotypic variations in potato genotypes with respect to other traits such as number of nodes and stem number. Anderson and Howard (1981) observed that tuber yield and number of leaves, number of stem and internode length showed significant differences among genotypes with phenotypic coefficient of variability ranging from 15.8 to 26.18%.

Mcintosh (1927) working on the criterion of classifying stem number per plant, grouped primary stems as few (2-3); medium (4-9) or many (10 or above) though he cautioned that the storage of the seed tubers can influence profoundly the number of stems.

2.2 Variability in Tuber yield.

Yield is a complex quantitative trait, which results from several biochemical and metabolic processes, each of which is under genetic control. For effective improvement, simultaneous selection of the most important yield components is necessary since the use of yield as an index alone is inefficient. Breeders' work must be based mainly on traits that in some way are related to yield it and, as a result, germplasm evaluation should be carried out to find genetic variability of these traits (Monti, 1987). Ceaser *et al,* (1981) reported significant variations in tuber yield. CIP (1977) in trials of nearly 2000 clones at ten locations in Peru, observed that 2.3% of the population gave average yields of over 20 t/ha, 34.6% gave 10-20 t/ha and 63% gave less than 10t/ha. Average percentages of dry matter in the tubers ranged from 25 to 36percent. Quite a number of factors contribute to the differences in yield between cultivars which have been bred and selected. These factors include planting early in the season, the amount of photosynthate that is diverted to tuber growth rather than to foliage growth and replacement and the longevity of the foliage. Ceaser *et al* (1981) in their study of growth of four cultivars in six locations tested for three years, classified hybrids into three groups (I) Early varieties that bulk very rapidly with a 24-hour photoperiod, matured 8-9 weeks are recommended for production in areas with a short cropping season Are low in yield than varieties that matured in 10 weeks are recommended for extensive soil and climatic conditions are intermediate in tuber yield and (II) The medium or inter mediate tuber yielding (III) Late maturing, with high yield are recommended for areas with most favourable soil and climatic conditions.

2.3 Heritability

Differences occur between individuals of a species in the expression of a particular trait. Such differences, whether they arise mainly from the genetic make up of the individual or due to environmental effect can be described in terms of heritability concepts (Obilana and Fakorede., 1981). Sneep (1977) applying the concepts of unreplicated three –row plots for the evaluation of early generation barley lines, observed that larger number of replications, small environmental variance give more precise estimates of heritability. The heritability concept and its estimates are also useful in the selection of superior individuals to generate superior varieties or strains (Obilana and Fakorede, 1981). When reliable estimates of genetic and environmental components of variance are available, heritability under recurrent selection programme Can be estimated. (Marfo and Hall, 1992) also reported that it is important to evaluate heritability of traits, since it will determine the progress that can be made in transferring this trait into different genetic backgrounds. Heritability estimates for quantitative traits of potato have been reported in many literatures. However, such studies in potato (*Solanum_ tuberosum.*_) have not led to any consensus. (Dayal *et al* 1972).For instance

Thompson and Mendoza (1984) and Gopal and Minocha (1998) found higher heritability for average tuber weight in potato than for tuber number but Maris (1969) found little difference in the heritability values of these characters. Khadga and Rastogi (1999) recorded high broad sence heritability for all agromomic characters in potato except plant height. Knapp *et al* (2001) reported higher broad sence heritability for most of the characters studied except percent emergence at 30 days after planting. Gopal (1999) observed that heritability values for plant height, number of stems, number of leaves and number of tubers varied between seasons as well as between years He noted that the values ranged between moderate (≈ 0.50-0.75) to high (>0.75)heritability in the broad sense. Plant height, number of eyes, plant vigour and maturity had high broad sense heritability (0.75, 0.80, 0.88 and 0.92) respectively in both seasons. He also reported moderate heritabilities for number of nodes, number of stems, tuber yield, tuber number, average tuber weight and plant posture (0.45, 0.47, 0.49, 0.54, 0.58 and 0.62 respectively Brown *et al* (1987) also observed a moderate to high broad sense heritability estimates for potato, tuber yield (33%), number of tubers per plant (56.55%,) number of stems per plant (63.8%) and days to maturity, (77.82%). They asserted that the low values of heritability estimate for tuber yield could be due to large environmental variation, while moderate to high estimates in the other traits were due to the reduction of environmental variance

2.4 Correlation and path co-efficient analysis

The correlation coefficient measures the relationships among traits. Correlations provide only limited information because they disregard complex interrelationships among traits. Accordingly, they must be used with caution in making decision regarding indirect selection criteria (Board *et al,* (1997). A path coefficient analysis is a standard partial regression coefficient that measures the direct influence on one trait on another trait and permits the separation of correlation coefficient into components of direct and indirect effects for a set of priori cause and effect interrelationship. Kang *et al* (1983) demonstrated that partitioning correlation coefficient into direct and indirect effects provide more useful information. Yield, being a complex quantitative trait, is influenced by various component traits. For effective improvement, simultaneous selection of the most important yield components is necessary. For this reason, knowledge of the magnitude and nature of the association between yield and the related characters is important.

Ali *et al* (1986) reported that when phenotypic and genotypic correlation coefficients are very close in magnitude, then the environmental variance and covariance had been reduced to zero. Bos and Qi (1997) also reported that within clones, purelines and single cross hybrid the phenotypic correlation between two traits is equal to the environ mental correlation. Variation between plants, which is due to variation with regard to the quality of experienced growing conditions, cause plants environmental deviation for a trait and its environmental deviation for another trait to be correlated. Wright (1921) in another study observed that when two traits are positively correlated, then selection for increased in one trait is expected to improve the other trait. Khadga and Rastogi (1999) reported a positive and significant phenotypic correlation between tuber yield per plant and plant height, and between tuber number per plant and average tuber weight. He also observed a negative phenotypic correlation between first flower open with plant height, and between number of stems per plant and number of leaves per plant. Singh and Singh (1987) and Maris (1969) reported a significant association between plant height and tuber yield. Patel *et al* (1973) and Desai and Jaimini (1998) reported that plant height has no association with tuber yield. Ogunbodede (1988) noted that there have been reports of positive associations between seedling vigour and yield in several crops, he concluded that specialize seedling vigour traits might be useful selection criteria for yield in most crops. Maris (1969) and Gopal *et al* (1994) reported that among tuber yield components, average tuber weight has a positive and significant correlation with tuber yield. In a similar study Maris (1996) reported a positive and significant association between average tuber weight and tuber number. Tarn and Tai (1984) in their study on Heterosis and variation of yield component in F1 hybrid between group tuberosum and group andigena potatoes reported a significant positive correlation between tuber number and tuber yield and between average tuber weight and tuber yield in Tuberosum families. In another study, Gopal (1999) revealed that phenotypic and genotypic correlation coefficients between plant height and internodes length were positive and significant.

(rp=0.87; rg=0.90-0.93).The same author also reported a positive correlation coefficient between plant height and maturity (rp=0.45,-0.49, rg=0.51-0.54), Tai (1976) recorded a negative association between number of nodes and plant vigour (rp=-0.43 to –0.49; rg =-0.44 to-0.75) while a positive correlation coefficient was recorded between plant height and plant posture (rp=0.54-0.62; rg =0.70-0.82). Garg and Bhutani (1978) reported tuber yield of 22 potato varieties to be positively correlated with maturity.

Path coefficient analysis is particularly useful in explaining the interpretation of the interrelationship (Ado *et al.,* 1988). Ali *et al.,* 1992 reported that path-coefficient analysis were performed in accordance with the causal relationships using either genetic or phenotypic correlation coefficients in separate models. Use of path analysis requires the determination of causal relationships among variables, based on either a priori evidence or a postulated hypothesis (li; 1956). (Williams *et al.,* 1990). Observed that more than one interpretation of the causal relationships among variables may be possible. Khadga and Rastogi (1999) reported that tuber number per plant and average tuber weight had high direct effect on tuber yield per plant and concluded that these two traits were strongest forces influencing tuber yield in potato. In another study (Sidhu *et al.,* 1978) indicated that selection to improve tuber yield per plant should be based on plant vigour combined with stem number per plant. The direct effect revealed by path analysis reduced the apparent importance of some correlations and indicated that for breeding purposes in potato breeding program, average tuber yield and number of tubers per plant are the traits which must deserve attention with regard to their influence on tuber yield.

2.5 Genetic Advance

One method of achieving greater success on the improvement of a particular trait is to estimate it's genetic advance. (Gopal., 1999). It is expressed as a percentage of the mean at 5% intensity so that comparison could be made among various characters, which had different units of measurement. Dayal and Upadhya (2001) in their studies on correlation on 1000-true seed weight, tuber yield and other morphological traits in potato reported higher genetic advance for most characters except non-reducing sugar and percentage emergence at 30 days after planting. Dayal *et al* (1972), Gaur *et al* (1978), Sidhu and Pandita (1979) and Garg and Bhutani (1991) reported high genetic advance for tuber yield while tuber number and average tuber weight had a low genetic advance.

Claudhary and Sharm (1989) and Birhman and Kaul (1989) reported higher genetic advance for plant height, plant vigour and tuber number, whereas average tuber weight had a low genetic advance. (patel *et al.,* 1973) reported genetic advance that ranged form 18% for plant vigour to 76% for tuber yield and concluded that improvement of tuber yield may be attained by 76%. Gopal (1999) observed that genetic advance varied with character, season and year, he observed that genetic advance for tuber number ranged between 24.57% in autumn and 104.405 in spring, he also recorded a narrow range of moderate values of 39.52-58.69, 34.89-44.91 and 52.82-65.63% for average tuber weight, plant vigour and internodes length, respectively and concluded that characters with high genetic advance will not be difficult to improved.

2.6 Classification of potato genotypes

One method of identifying accessions and assessing genetic and phenotypic relatedness is to perform classification on a large collection of individuals using a statistical procedure such as cluster analysis (An derberg; 1973). Multiple characters for each individual are used to group accessions into cluster classes. Individuals within a given cluster class are similar, while individuals from different from classes are not. Similarly measurements among clusters are also determined so that relationships between groups can be established. Use of classification data can offer the breeder an objective judgment determining which widely differentiated individuals to use as parents. Cluster analysis can also be used to classify newly introduced accessions into known populations groups and determine similarity or novelty with existing collection (Henning *et al*., 2002.

The D^2 statistic is another useful multivariate statistical tool for effective discrimination among various genotypes on the basis of genetic diversity to realize substantial production and improvement in this crop, studies on genetic divergence deserves special attention. The knowledge of genetic diversity is important for successful selection of parents for hybridization work. (Bhat., 1970). Teshome *et al.* (2002) grouped 15 genotypes of potato into five clusters using Mahalanobis D^2 statistic. The study revealed that the clustering pattern indicated that the geographical diversity need not to be necessarily related to the genetic diversity, parallelism was noticed between geographical origin and genetic diversity. Genotypes from different geographical origins were group together under the same cluster. He concluded that geographical distribution was not related to genetic diversity. In a related study Naskar and Ravindran., (1996) reported that the intra and inter cluster D^2 value among 20 potato genotypes between clusters 1 and V(D^2= 27364.611,D= 165.423) was found to be the highest. The least inter-cluster distance was noticed between cluster II and IV (D^2 = 1081.318, D = 32.883). They concluded that these highly divergent clusters on hybridization would produce would produce heterotic hybrids and a greater spectrum of variability in the segregating generations. They also observed that the intra-cluster distance of cluster III, and V was highest and concluded that genotypes in these clusters may be considered as parents in hybridization programme in potato breeding. Similar conclusions were reported by Mondal *et al* .In D^2 analysis involving 14 agronomic characters. Sheflay (2000) grouped 16 potato genotypes into 5 clusters and concluded that cluster V recorded the highest mean values for all the characters under study except plant height, number of tubers and stem number per plant. They also observed that highest tuber yield per plant exhibited by the cluster V 28.4t/ha and number of leaves/plant made the greatest contribution `to genetic divergence. In a resent study Mondal (2003) observed a lower intra-cluster distance than inter cluster distance and suggested that both heterogenous and homogeneous nature exist between and within groups, respectively. Haydar *et al* (2007) in their study, involving 30 genotypes of potato observed that the maximum diversity was contributed by tuber weight/plant. They also found out that the highest intra-cluster distance was observed in cluster VI and lowest in cluster II. Similar reports have been observed in chick pea (Ahmed *et al* 2002) and in mung bean (Rahman *et al* (2002).

2.7 Principal Component Analysis (PCA)

The multivariate principal component analysis (PCA) is usually referred to as a data reduction technique. It is used to identify a small set of variables that account for a large proportion of the total variance in the original variables (Bolch and Huang, 1984). It can also be used to illustrate the relationships among environments and genotypes on each trait. (David et al,2005),(Yan and Kang ,2003) used the biplot technique of pc1 vs pc2 for each trait while genotypes and environments are presented by makers on the plot .(Haydar et al ,2007) working on 30 potato genotypes use principal component analysis to ascertain the contribution of characters towards diversity of the genotypes, their result showed that characters such as tuber weight/plant, contributed more to genetic diversity than the remaining characters (0.134) and was followed by plant height (0.0365) on the first axis while, average tuber weight (0.1240) contributed more on the second axis and was followed by plant height (0.0156). (Vijayan, 2005) in his study of principal component, plant height (0.999) was contributing more to variation and was followed by number of tubers

(0.3540). In the second principal component number of tubers/plant (0,997) was accounted for maximum variation and was followed by number of stems per plant.

CHAPTER THREE

3.1 Experimental Site

The experiment was conducted at the research farm of Natural Root Crops Research Institute. Kuru. Kuru is geographically located between (lat 08 44N and long 09(1 44E). The soil is sandy loam the mean annual rainfall of the area ranges between 1105-1273.04mm starring from April to September reaching its peak between July/August each year. The mean annual maximum and minimum temperature is about 24.50C and 19.4°C respectively. The area has a mean monthly relative humility of 62.9%. The high altitude of the area allows for its low temperature for most part of the year.

3.2 Genetic Background and Description of Materials

Twenty genotypes were used. The genotypes were obtained form the germplasm collection of potato programme. National Root Crops Research Institute Vom. The genotypes comprises four (4) from USA (Br63-18, WC723-2, WC732-1 and B9450-9) one from Mexico (Bertita). Two from Holland, (Famosa and Desiree), two from Nigeria (RC767-2 and 20037-4) and eleven (11) from CIP Kenya (Ruslin Ruaka, 3870025, 392254.016, 392278.4, 676008, 392287.45, 396430.010, 392287.024, 390340.043, 375400.00 and 387300.8).

Table 1: Origin Pedigree and description of the genotypes

Place of origin	Lines/variety	Origin/Pedigree	Brief Description
1. USA	Br63-18	Developed by USDA (1970) Atzimba XA-1 University of Wisconsin as a single cross)	Numerous stems. Medium oval leaves. Produce flowers purple in colour. Plant is erect. Medium maturity (70-85 days) tuber is oval, shallow eyes. Skin colour is light. Yellow flesh colour is yellow with short dormancy.
2. USA	WC732-2	Developed by USDA (1972) Greta X P-1) university Wisconsin as a single cross	Medium stems, oval leaves. Purple flowers. Abundant fruits. Spreading stem medium to late maturity (70-90 days) long slender tubers with medium, deep colour and fresh colour yellow. Medium dormancy.
3. USA	WC732-1	Development by USDA (1972). Greta XP-1. University of Wisconsin as a single cross	Few stems. Over leaves purple flowers. Crect stem medium maturity long tubers, deep eyes purples skin and fresh colour, medium dormancy
4. USA	B9450-9	Developed by USDA (1977) X P.1.37745) Single cross	Few greenish stems, medium oval leaves, purples flowrs, no fruits, spreading stem medium maturity, large
5. Mexico	Bertita	Developed in Mexico as collection from local germplasm (1970)	Tall and erect, green stem, small pointed leaves few fruits, medium to late maturity, tubers round and oval in size. Skin colour red or pink and white fresh medium dormancy
6. University Wargenigen Holland	Desiree	Developed in Holland as a cross line derived from single cross (Urgenta X Despecche) (1976)	Numerous stems. Thick and brownish eyes. Pink skin colour. Fresh colour pale yellow, medium dormancy
7. University Wargenigen Holland	FAMOSA	Developed as a single cross between Trium F X Kerfer B/53 (1976)	Few stems, purples at base has large leaves. White flowers, few fruits, erect growth. Habit. Late maturity, tuber shape is oval. Large shallow eyes, light shallow eyes, light yellow skin colour fresh colour is light yellow, medium dormancy
8 NRCRL. Nigeria	RC767-2	Developed in Nigeria as a double cross 311.5 X Atzimba X local	Has few stems. Medium to large leaves, white flowers, many fruits, tall, erect and laterm
9. NRCRL. Nigeria	2007-4	Developed in Nigeria as a single cross from Berfita X Br63-18 and developed a line20037-4 in kuru (2004)	Few stems, medium broad oval leaves, produce furits has spreading plant habit is medium to late maturity. Tubers are round tootlong small in size, while skin colour, medium eyes and short dormancy
10 CIP. Kenya	387300.25	Developed in CIP Kenya as local germ plasm collection	Have few stems, with small short leaves, purple flowers. With erect growth habit, late maturity, long tuber shape and small in size with deep eyes, pink skin colour and yellow flesh colour with long dormancy.
11	3922554.016	"	"
12	392278.4	"	"
13	676008	"	"
14	393387.45	"	"
15	39430.010	"	"
16	392287.024	"	"
17	390430.043	"	"
18	375400.00	"	"
19	387300.8	"	"
20	Ruslin Ruaka	"	"

3.3 Experimental Design and layout

Twenty genotypes of potato were planted in Kuru for threes years in a Randomized complete Block design (RCBD) with three replications.

Individual plots were made up of three rows of 3m long; the intra and inter row spacing were 30cm and 100cm respectively; giving a plant population of 33, 333 plants/ha. Gross plot size was 3x3 and a net plot size of 2x3m were used in the experiment each of the gross plots contained three rows and the boarder rows formed the discards. Fertilizer (NPK 15:15:15) application was done immediately after planting at the rate of 600kg/ha by band placement. All other cultural practices were carried out according to the National Root crops research Institute (NRCRI) potato programme recommendations.

3.4 Data collection

Data were collected from five competitive plants (i.e two from one row and three from the other row of each plot of twenty plants per plat on per plant basis). The mean of five plants was used for statistical analysis. The characters included:

1. Vigour score 1-5; 1 = very high vigour, 5 = very poor
2. Plant emergence at 4WAP
3. Plant growth habit score 1-3, 1 = erect, 3 = prostrate.
4. Number of stems: The number of main stems were counted and recorded for each plant
5. Plant height: The height of the plant was measured from the ground level to the tip of the leaves to the nearest 0.01 centimetre using a ruler.
6. Number of leaves per plant: The number of leaves of each plant were counted and recorded

7. Number of Nodes: The number of nodes of each plant were counted and recorded on the longest stem only
8. Internode length: The internode length was measured with a ruler on each plant and recorded.
9. Days to maturity: The number of days from planting to the date when about 50% of the leaves senescence.
10. Tuber number: The tubers were dug and the number of tubers for each plant was counted and recorded.
11. Number of eyes: The number of eyes of each tuber were counted and recorded.
12. Tuber yield: Each of the tuber from the harvested plot was weight to the nearest 0.01kg
13. Average tuber weight:: $\frac{\text{Total tuber yield}}{\text{number of tubers}}$

Statistical Analysis

The ANOVA was based on plot means. The statistical model used for the analysis of variance (ANOVA) and expected mean square (EMS) was based on the following linear model according to Snedecor and Cochran (1980).

$Y_{ijk} = \mu + E_i + G_k + (GE)\ ij + e_{ijk}$

Where :

Y_{ijk} = the K^{th} observation on I^{th} entry in J^{th} replication;

μ = the general mean;

Ei = the effect of I^{th} year; 1 = 1,2,3

Gk = the effect of K^{th} genotype; K= 1…..20

$(GE)_{ij}$ = the interaction effect between k^{the} genotype in the I^{the} year.

E_{ijk} = the error associated with each observation.

The form of analysis of variance is as presented in Tables 2-4.

For each year, the components of variance were estimated from expected mean square for each trait by using observed mean squares, thus;

$$\delta_e^2 = M_e \text{ and}$$

$$\delta_g^2 = \frac{m_g \quad Me}{r}$$

The form of the combined analysis of variance for threes years is presented in Table 3.

The component of variance and their standard errors were estimated from expectation of mean squares by equating the observed mean squares to their expectation as follows:

For individual year:

$$\delta_e^2 = \text{Me with S.E.} = \sqrt{{}^{2}\ \frac{Me}{df \quad 2}\ {}^{2}}$$

$$\delta_{gy}^{2} = \frac{Mgy \quad Me}{r} \text{ with S.E} \sqrt{\frac{1}{r}^{2}\ \ {}^{2}\frac{Mgy^{2}}{df \quad 2}\ {}^{2}\frac{me^{2}}{df \quad 2}}$$

$$\delta_g^2 = \frac{m_g \quad Mgy}{ry} \text{ with S.E.} \sqrt{\frac{1}{ry}^{2}\ \ {}^{2}\frac{Mgy^{2}}{df \quad 2}\ {}^{2}\frac{mg^{2}}{df \quad 2}}$$

Table 2. Form of Analysis of variance with Expected mean square for one year..

Source of variation	d.f	M_S	EMS
Replication	(r-1)	M_r	
Genotypes	(g-1	Mg	$\delta_e^2 + r\delta_g^2$
Error	(r-1) (g-1)	M_e	δ_e^2
Total	rg-1	M_t	

Where;

r = number of replications

g = number of genotypes

δ_e^2 = Error variance

δ_g^2 = Total genetic variance among entries.

MS = The observed mean square

M_r = Replication mean square

M_g = Genotype mean square

M_e = Error mean square

M_t = Total mean square.

Table 3. Form of combined Analysis of variance with expected mean square.

Source of variation	d.f	MS	EMS
Years	y-1		
Replication/year	y(r-1)		
Genotypes	(g-1)	M_g	δ_e^2 + r δ_{gy}^2 + ry δ_g^2
Genotypes x year	(g-1) (y-1)	M_{gy}	δ_e^2 + r δ_{gy}^2
Pooled error	y(g-1) (r-1)	M_e	δ_e^2
Total	ygr-1	M_t	

Where;

y = Number of years

r = Number of replication

g = Genotypes

MS = Mean squares

M_g = Genotype mean square

M_e = Error mean square

M_{gy} = Genotype x year interaction mean square

M_t = Total mean square

δ^2_{gy} = Genotype x year interaction variance.

δ^2_e = Error variance.

The phenotypic variance among the lines were estimated as follows

$$\text{For individual year: } \delta^2_{ph} = \delta^2_g + \frac{\delta^2{}_e}{\mathrm{r}} \text{ with S.E} = \sqrt{\frac{1}{r}^{2}}\ ^{2}\ \frac{Mg}{df \quad 2}^{2}$$

$$\text{For combined year: } \delta^2_{ph} = \frac{\delta^2{}_e}{ry} + \frac{\delta^2{}_g}{r} + \delta^2_g \text{ with SE} = \sqrt{\frac{1}{r}^{2}}\ ^{2}\ \frac{Mg}{df \quad 2}^{2}$$

To determine whether the variation among entries and their interaction with year were significantly different from zero, f-test was used for both single and combined analysis of variance as follows:

Individual year: $F = \frac{mg}{me}$ with df = (g-1) (r-1)(g-1)

Combine years: $F = \frac{mg}{me}$ with df – (g-1(r-1)(g-1)

And $F = \frac{mgy}{me}$ with df = (g-1) (y-1), y(r-1)(g-1)

Duncan multiple Range test (DMRT) was used to test significant difference between means.

According to mode and Robinson (1959) the expectation of mean products, in the analysis of covariance has the same form as the expected mean squares of analysis of variance and therefore the procedure for the analysis of covariance are analogous to those used for the analysis of covariance and covariance for a pair of character (x and y) with the expected mean cross-products. The form of analysis of variance and covariance are presented in table 4.

Table 4. Form of analysis of covariance with expected mean product for a single year for two characters x and y

Source of variation	df	Mp xy	EMCP
Replication	(r-1)	MP_r	
Genotypes	(g-1)	MP_g	$\delta_e^2 \quad r\delta_g^2$
Error	(r-1) (g-1)	MP_e	δ_e^2
Total	rg-1	M_t	

Table 5: Form of combined analysis of covariance with expected mean product for two characters x and y.

Source of variation	df	Mp Xy	EMCP
Replication /year	y(r-1)		
Genotypes	(g-1)	MP_g	
Years	(y-1)	MP_y	$\delta_{xy}^2 \quad r\delta_{gygx}^2 \quad ry\delta_{gxgy}^2$
Genotypex year	(g-1) (y-1)	MP_{gy}	$\delta_{xy}^2 \quad r_{gygx}^2$
Pooled Error	y(g-1) (r-1)	MP_e	δ_{xg}^2
Total	rgy-1	M_t	

Coefficient of variation

The genotypic coefficients of variations were estimated using the formula:

GCV = $100 X \sqrt{\frac{\delta_g^2}{\bar{x}}}$ as described by

Lothroup *et al* 1984.

Where:

GCV = genotypic coefficient of variation

δ_g^2 = The estimate of genetic variance.

$\bar{x}$ = grand mean of the respective character.

Genetic Divergence

The genetic divergence of the 20 genotypes was estimated using mahalanobis D2 Statistic (Mahalanobis, 1936). The d^2 values for "k' traits between ith and jth genotypes was computed as:

D^2 = (Yit –Yjt)

Tocher's method described by Rao (1952) was used in grouping the 20 genotypes into clusters with the aid of D^2 being treated as the square of the generalized distance.

Genetic advance

The expected genetic advance (%) was estimated from the formula by Johnson *et al* (1955) as

$$GS = K \frac{(100\delta g)}{(\bar{x})} \times h^2$$

Where K= 2.06 (for 5% selection in large samples from a normally distributed population), is the selection differential measured in terms of phenotypic standard deviations.

δ_g^2 genetic variance

$\bar{x}$ The population mean

h^2 heritability

Correlation

The genotype, phenotypic and error correlations were estimated from the component of variance using the formula suggested by singh and chadharry (1979).

Genotypic correlation $r_{gxy} = \dfrac{\delta_{gxgy}}{\sqrt{\delta_{gx}^{2}.\delta_{gy}^{2}}}$

Where: The phenotypic correlation coefficient were computed using mean squares and mean cross product as follows:

$$rph \quad \frac{mgxgy}{\sqrt{M_{gx}.M_{gy}}}$$

r_{gxy} = correlation coefficient of character x and y

δ_{gxgy}^{1} Genotypic covariance of character x and y

δ_{gx}^{2} Genotypic variance of character x

δ_{gy}^{2} Genotypic variance of character y.

Where;

r_{ph} = Phenotypic correlation coefficient x and y

M_{gx} = entry mean square of the character x

M_{gy} = entry mean square of the character y.

M_{gxgy} = entry mean cross product of the character x and y

The error correlation was computed for a pair of character using the error mean square as described by (Singh and Chandhary, 1979; Obilana and Fakorede, 1981).

$$r_{exy} = \frac{\delta_{xy}^{2}}{\sqrt{\delta_{x}^{2}.\delta_{y}^{2}}}$$

Where:

r_{exy}= error correlation coefficient for character x and y

δ_x^2 = error variance for character x

δ_y^2 = error variance for character y

δ_{xy}^2 = error covariance for character x and y

Heritability (broad sense)

Heritability was computed as ratio of genetic variance (δ_{ph}^2) to phenotypic variance (δ_{ph}^2)

Heritability (h^2) and their standard error SE's were estimated thus:

Heritability on entry mean basis

$$h^2 = \frac{\delta_g^2}{\frac{\delta_e^2}{ry} \quad \frac{\delta_{gy}^2}{y} \quad \delta_g^2} \text{ and SE } = \frac{S.E.\delta_g^2}{\frac{\delta_e^2}{ry} \quad \frac{\delta_{gy}^2}{y} \delta_g^2}$$

On a plot basis

$$h^2 = \frac{\delta_g^2}{\delta_e^2 \quad \delta_{gy}^2 \quad \delta_g^2} \text{ and S.E } = \frac{S.E\delta_g^2}{\frac{\delta_e^2}{ry} \quad \delta_{gy}^2 \quad \delta_g^2}$$

Where:

δ_e^2 = estimation of the error variance

δ_{gy}^2 = Genotypic x year interaction variance

δ_g^2 = genetic variance

r = number of replications

y = number of years

3.5 Path Analysis

The correlation coefficients were used to develop the following simultaneous equations in order to work out the path coefficients (P_1-P_5) suggested by Wright (1921) and illustrated by Devey and L_u (1957).

$r_{15} = P_1 + r_{12} P_2 + r_{13} P_3 + r_{14} P_4$……………………………………………(1)

$r_{25} = r_{12} P_1 + P_2 + r_{23} P_3 + r_{24} P_4$……………………………………………(2)

$r_{35} = r_{13} P_1 + r_{23} P_2 + P_3 + r_{34} P_4$……………………………………………..(3)

$r_{45} = r_{14} P_1 + r_{24} P_2 + r_{34} P_3 + P_4$………………………………………………(4)

where P_1-P_4 are path coefficients while r_{12}-r_{45} and the coefficients of correlation. Between the dependent variables and independent the direct and indirect effects of individual and combined (two factors) contributions of yield components to tuber yield per plant were determined using path-coefficient analysis. The combined contribution was estimated using the formula:

$c_y\ 2P_iP_jr_y$

where,

c = combined effect of i and j, r_{iij} = coefficient of correlation between I and j, I and j are the direct and indirect effects of individual and combined (two factors) contributions of yield components to tuber yield per plant. The contribution of the remaining unknown factor is measured as the residual factor, which is calculated using the formula.

Residual factor 9R) = $\sqrt{[1 \quad (p_1^2 r_{15} \quad P_2 r_{15} \quad P_2 r_{25} \quad P_3 r_{35} \quad P_3 r_{35} \quad P_4 r_{45}}$

3.6 Principal Component Analysis

The treatment means were included in a principal component Analysis (PCA) performed with STAT ITCF (Philippeau, 1992). The principal component is a multivariate procedure which rotates the data such that maximum variabilities are projected on to the axes. The first principal component is the combination of variables that explains the testing the statistical significance of factor loadings. An introductory treatment of principal component analysis, loading is considered to be ‘large’ if its absolute value exceeds. 40

CHAPTER FOUR

RESULTS

4.1 Mean Performance

The mean performance for agronomic traits for 2005, 2006 and 2010 are presented in Tables 6, 7 and 8, respectively, mean performance for the three years were similar for some traits and in others different. For most of the agronomic traits, the mean values were higher in 2010 than 2005 and 2006. Based on the mean performance for days to maturity (50% senesce), Table 6 the genotypes can be grouped into 3 maturity groups; early maturing genotypes senescing 60-70 days, (three genotypes namely: B9450-9, 676008 and 3922780.4) medium maturing types which senescence in 71 -80 days (nine genotypes namely, RC7716, Bertita, WC732-1, desiree, 375400.00, 396430.00, Br63-18, 392287.024, 387300.8 and 396430.010) and late maturity from 81 and above days. (Eight genotypes namely; Ruslin Ruaka, 392254.016, WC321-2, RC 762-6, 392287.45, 390430-043, 20037.4 and Famosa) two class groups were recorded based on plant height as, medium 45 to 60 and tall 60 to 75. 396430 had the highest tuber yield of 0.93kg/plan followed by 375400.001, which also had a tuber yield of 0.89kg/plan and 392287.45 had the lowest yield (0.45/plan)

Results of the mean performance in 2006 for the agronomic traits are presented in Table 7. The table shows a similar trend based on number of nodes/plant and days to maturity (50% senescence). In terms of mean tuber yield performance however, 396430.010, and 37,5400.00 recorded the highest mean yields that were not significantly different from one another (1.09kg/plant and 0.94/plan) respectively. The lowest tuber yield was observed in 392287.45 with a yield of only 0.43kg/plan.

The mean performance for 2010 for agronomic traits are presented in Table 8. The table shows a similar trend based on days to maturity (50% senescence), number of leaves and plant height. In terms of mean tuber yield performance however, clone 396430.010, recorded the highest tuber yield per plant, but was not significantly different from Ruslin Ruaka, WC732-1 and 392278.4. The lowest tuber yield was observed in clone 375400.00 (0.33kg/plan) and RC762.6 (0.36kg/plan)

The mean performance for the combined analysis is presented in Table 9. The trend of performance of various genotypes across the three years separated the genotypes into three 3 distinct groups; early genotypes which senescence in 60 -69 days (three genotypes namely; B9450.9, 676008, and 392278.4), the medium maturity groups flowered in 70-80 days (sixteen genotypes namely, Br63-18, Rashin Ruaka, 392254.106 RC7716, Bertita, WC312-2, WC732-1, RC762.6, 396430.010, Desiree, 392287.024, 390430.043, 375400.00, 387300.8, famosa and 20037.4) and late maturing which were those that senesced in 80 days and above. (one genotype, only; 396430.010) Similarly the mean performances for plant height indicate that some genotypes were short to medium 42-55cm and tall 60-71cm. 375400.00 was the highest yielding genotypes, but the yield of one genotype Desiree was statistically comparable. Also number of stems in this study were classified as few (2-3) and medium (4-9).

The mean, range, phenotypic, genotypic coefficient of variation and genetic advance for 2005 is presented in Table 10. For all the agronomic traits the widest range was recorded for plant height, followed by days to maturity and emergence counts in that order. An appreciable amount of range was recorded for each trait. For the agronomic traits, phenotypic coefficient of variation 9PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all characters. The highest PCV and GCV were recorded for average tuber weight and tuber number per plant (43.28 and 33.20, 34.31 and 33.62) respectively. The least estimate for both the PCV and GCV was in days to maturity.

On genetic advance, the highest was recorded in Tuber number per plant (67.83) the lowest was recorded in number of nodes per plant.

Table 11, shows the mean, range, phenotypic, genotypic coefficient of variation and genetic advance for 2006. The widest range was observed in plant height, followed by day to maturity and number of leaves per plant in the order. Phenotypic coefficients of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters. The highest PCV and GVC were recorded for number of main stems per plant and average tuber weight (44.52 and 42.04, 38.60 and 27.71) respectively. The least estimate for both the PCV and GCV was in Days to maturity.

Expected genetic advance values varied with character. Tuber weight per plant recorded the highest, while vigour score recorded the lowest. Low to moderate values were recorded in the remaining characters.

Mean, range, phenotypic, genotypic co-efficient of variation and genetic advance for 2010 are presented in Table 12. The widest range was observed in plant height followed by number of leaves per plant and days to maturity in that order .Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation except in Growth habit, plant height, number of stems/plant and days to maturity. The highest PCV and GCV were recorded in tuber number per plant and tuber weight per plant (56.94 and 55.15, 37.29 and 34.61) respectively. The least estimate for both the PCV and GCV was in plant in plant height.

Expected genetic advance values varied with character number of stems per plant recorded the highest while internode length recorded the lowest. Low to moderate estimates were recorded in the remaining characters.

The mean, range, phenotypic, genotypic coefficient of variation and genetic advance across the three years are presented in Table 13. For all the agronomic traits the widest range was recorded for plant height, followed by days to maturity and emergence counts in that order. On a whole, an appreciable amount of range was recorded for each trait. For the agronomic traits, phenotypic coefficients of variation (PCV) were higher than the corresponding genotypic coefficients of variation (GCV) for all characters. The highest PCV and GCV were recorded for emergence counts and Average tuber weight (37.56 and 37.28, 28.74 and 24.12) respectively. The least estimate for both the PCV and GCV was in days to maturity.

Expected genetic advance values varied with character. The highest genetic advance was recorded in emergence counts, while internode length / plant had the lowest. Plant vigour, number of leaves/plant, days to maturity, plant height, plant posture, number of eyes, number of nodes/plants, tuber number, average tuber weight and tuber yield had low to moderate values.

TABLE6: Mean performance of potato genotypes for thirteen agronomic traits for 2005

Genotypes	Growth Habit	No. of Nodes plant.	Internodes length(cm)	Plant height(cm)	No. of main stems /plant	Days to maturity	Emergence counts	No. of Eyes /Plant	No of leaves/plant	Vigor score	Tuber number/ plant	Tuber weigh(kg)	Average tuber number
R. Ruaka	2.53a	13.33ab	2.88ab	69.57a	2.53abc	80.07abcde	15.35cde	6.73de	17.93abcd	2.37ab	5.27e	0.65bcd	0.125
Br63-18	2.07ab	13.80abc	2.75ab	54.73bcdef	2.20abcd	76.77bcde	18.83abc	8.40cd	19.23ab	1.93abc	9.07cd	0.54cde	0.060
392254.016	1.87ab	11.53abc	2.16ab	41.87ef	1.93bcd	82.6abc	9.67gh	8.0bcde	14.87de	2.13abc	11.60abc.	0.52cde	0.045
Rc7716	2.20abc	11.00bc	2.97ab	57.73abcd	3.4a	74.07e	19.0ab	8.53bcd	17.27bcde	2.20abc	13.20ab	0.61cde	0.046
Bertita	2.40ab	16.00a	2.01b	51.80cdef	2.13bcd	74.13e	19.00ab	8.53bcd	17.20bcde	2.67ab	10.73bcd	0.53cde	0.049
Wc321-2	2.13ab	10.53bc	3.57ab	58.10abcd	2.47abc	83.67ab	19.67a	7.53bcde	17.20bcde	1.40c	7.00de	0.63bcd	0.090
Wc732-1	2.20abc	13.87abc	2.33ab	66.87ab	1.53cd	74.13e	13.67ef	19.00a	17.27bcde	2.27abc	7.27cd	0.76abc	0.105
392278.4	2.27abc	9.73c	2.27ab	52.23cdef	3.13ab	66.60f	19.00ab	9.87b	14.73de	2.07abc	11.20bc	0.72abcd	0.064
676008	1.67bcd	11.73abc	5.73a	50.27cdef	2.80ab	64.07f	14.33def	8.4bcd	14.67de	2.13cde	10.00bcd	0.64cde	0.064
Rc762-6	1.880ab	13.60ab	2.73ab	54.77bcdef	2.13bcd	82.53abc	8.00hi	8.13bcde	20.73a	2.87a	8.53cde	0.62cde	0.073
392287.45	1.73bcd	12.73abc	1.49b	41.33f	1.53cd	84.4a	6.00i	5.73c	14.73de	2.27abc	10.47bcd	0.40e	0.038
396430.010	1.8ab	11.40abc	2.29ab	46.10def	2.60abc	76.27cde	11.33fg	9.47bc	15.13cde	1.87bc	13.33ab	0.93a	0.070
Desiree	1.53cd	14.13abc	4.05ab	58.67abcd	2.33abc	75.33de	19.67a	6.93de	16.00cde	2.33cd	9.47bcd	0.63cde	0.067
392287.024	2.20abc	14.80ab	2.41ab	64.63abc	2.40abc	76.77bcde	15.67bcde	8.40bcd	17.40bcde	2.80ab	9.33cd	0.49de	0.070
390430-0432	2.13ab	12.73abc	2.03b	57.73abcd	2.93ab	82.6abc	19.00b	7.73bcde	17.67abcsde	2.07abc	10.53bcd	0.89ab	0.047
375400.00	1.60cd	13.40abc	1.53b	46.93def	2.73abc	75.20de	2.00j	7.27cde	15.47cde	2.27abc	14.93a	0.57cde	0.060
B9450-9	2.23abc	11.40abc	2.10ab	47.93def	2.33abc	63.73f	17.00abcd	8.13bcde	14.40e	2.1abc	9.27cd	0.65bcd	0.061
387300.8	1.40d	13.80abc	3.31ab	68.67ab	1.07d	77.67abcde	19.67a	8.07bcde	17.87abcd	2.27abc	7.20de	0.73abcd	0.090
FAMOSA	1.60cd	15.27ab	2.19ab	67.43ab	2.33abc	80.40abcde	18.67ab	7.93bcde	18.20abc	2.53ab	8.13cde	0.68bcd	0.090
200037-4	2.13ab	12.53abc	2.60ab	56.13abcde	2.13abcd	81.93abcd	19.00ab	8.80bcd	15.67cde	2.33ab	8.87cde	0.68bcd	0.077
GRAND Mean	1.975	12.867	2.668	56.675	2.333	76.107	16.682	8.60	15.200	2.230	9.77	0.643	0.070

Means with the same letter(s) in a column are not significantly different according to DMRT

Table 7: mean performance of potato genotypes for thirteen agronomic traits for 2006.

Genotypes	Growth Habit	No of nodes plant	Internode length(cm)	Plant height(cm)	No. of mainstems/ plant	Days to maturity	Emergence counts	No. of Eyes/plant	No. of leaves/plant	Vigour score	Tuber No/plant	Tuber weigh /plan
R. Ruaka	2.2abc	13.37bc	3.76.abc	57.60ab	1.80abcde	74.47bcdefg	14.33bcd	9.67b	45.07abc	2.87ab	8.13bcdef	0.71
Br63-18	2.07abcd	13.57bc	3.6133abc	61.33ab	2.67bcd	65.60h	18.33abc	9.13b	41.20abc	2.73ab	9.13bcde	0.54ef
392254.016	1.73de	11.70bc	3.91abc	56.37ab	2.13bcdf	75.00bcdef	9.00ef	11.13b	40.63abc	2.47ab	8.77bcde	0.54ef
Rc7716	2.33a	10.73bc	4.31abc	65.80a	2.53bcde	70.87efgh	19.33a	10.30b	44.60abc	2.67ab	10.60abcde	0.64de
Bertita	2.07abcd	18.23a	3.91abc	57.40ab	2.27bcdef	72.33cdefgh	19.33a	10.20b	43.00abc	2.47ab	7.93cdef	0.69cde
Wc312-2	2.07abcd	11.00bc	3.95abc	57.33ab	1.53ef	72.13defgh	19.33a	17.8a	48.33ab	2.33ab	8.00cdef	0.68cde
Wc732-1	1.87bcd	14.4abc	4.63ab	55.33ab	2.20bcdef	79.47b	12.00de	8.73b	47.73abc	2.73ab	11.27abcd	0.59cde
392278.4	2.27ab	9.63c	2.93c	57.87ab	4.07a	71.93defgh	18.67ab	10.87b	47.60abc	2.07b	12.87a	0.79bc
676008	1.80cd	12.00bc	3.74abc	52.40ab	1.60def	70.90efgh	14.00cd	9.73b	43.13abc	2.67ab	7.47ef	0.72bcd
Rc762.6	1.73de	11.80bc	3.53abc	37.63b	2.00bcdef	78.80bcd	7.33f	7.33bc	43.87abc	2.53ab	4.87fgh	0.63cde
392287.45	1.73de	12.47bc	3.97abc	60.00ab	1.47ef	81.33ab	3.00g	8.67b	33.93bc	3.13ab	4.03gh	0.43f
396430.010	1.67de	11.27bc	3.47abc	48.73ab	2.3bcdef	80.27b	8.33ef	8.20b	43.33abc	2.93ab	9.60abcde	1.09a
Desire	2.00abcd	12.80bc	4.19abc	63.00ab	2.73bc	72.07defgh	19.67a	8.13b	34.73bc	2.40ab	11.47abc	0.73cde
392287.024	2.07abcd	15.00ab	3.57abc	63.13ab	2.17bcdef	69.53fgh	14.00cd	8.00b	42.33abc	2.53ab	7.80def	0.62def
390430.043	2.07abcd	13.50bc	3.61abc	59.53ab	2.83b	72.40cdfgh	17.67abc	10.00b	52.73a	2.40ab	11.67ab	0.56ef
375400.00	1.4e	13.13bc	3.29bc	49.53ab	1.40f	86.73a	0.00g	3.80c	32.33c	2.27ab	3.20h	0.94ab
B9450.9	2.8cd	13.13bc	3.88abc	63.43a	1.80bcdef	67.50gh	14.00cd	10.87b	40.93abc	2.67ab	10.27abcde	0.74bcde
387300.8	2.700abcd	13.70abc	4.11abc	58.37ab	1.667cdef	77.2bc	18.00abc	7.60bc	45.20abc	2.53ab	8.13bcdef	0.67de
Famasa	2.2abc	15.40ab	4.79a	72.07a	2.4bcdef	79.2bc	16.67abc	9.27b	52.60a	2.93ab	7.13efg	0.83acd
200037.4	1.87bcd	12.83bc	3.73abc	58.67ab	1.87bcdef	68.33fgh	18.67ab	10.93b	43.20abc	2.27ab	10.67abcde	0.78cd
Grand mean	1.945	12.98	3.84	57.986	2.172	74.349	13.933	9.522	43.325	2.58	8.65	0.71

Means with the same letter(s) in a column are not significantly different according to DMRT

Table 8. Mean performance of Potato genotypes for thirteen Agronomic traits for 2010.

Genotypes	Growth habit	No. of Nodes/ plant	Emergence Count	Internode Length	Plant Height	Number of Main stems	Days to Maturity	No. of Leaves/pl	Vigour Score	Tuber eyes/Plant	No. of Tubers/Plant	Tuber Weight/pl	Average Tuber Weight
R. Ruaka	3.3a	12.98abc	14.00bcd	3.77abc	56.07ab	1.87cde	74.20bcdefg	43.47abc	3.20a	10.33b	9.13bede	0.94a	0.102a
Br63-18	1.8abcd	13.70abc	19.00bcd	3.64abc	59.00ab	2.67bcd	68.67h	39.00abcd	2.47abc	10.20b	10.20bcde	0.65fg	0.063de
392254.106	2.07abcd	11.60bc	10.67ef	3.89abc	54.67ab	2.13bcdef	73.07bcdefg	35.00abcd	2.53abc	13.13b	10.07bcde	0.73de	0.072cd
RC7716	2.33abcd	10.73bc	19.33a	4.37ab	65.20a	2.26bcde	69.60gh	42.53abc	3.33a	12.13b	11.67abc	067ef	0.06de
Bertita	2.07abcd	17.88a	19.67a	3.94abc	60.33ab	2.07bcdef	72.33cdegh	52.60a	3.27a	12033b	8.87bcdefg	063fg	0.070cd
WC312-2	2.0abcd	10.23bc	16.67ab	3.85ab	57.07ab	1.53ef	76.40defg	45.83abc	2.47abc	21.43a	8.53bcdefg	0.91b	0.110a
WC732-1	1.87abcd	14.8abc	13.33ef	4.10ab	55.57ab	2.27bcde	81.13ab	45.27abc	2.67abc	10.27b	12.07abcd	0.94a	0.080c
392278.4	2.77abc	9.50c	18.67a	3.21ab	57.53ab	4.07a	70.93efgh	45.00abc	3.13ab	12.13b	13.87a	0.94a	0.070cd
67008	1.93abcd	12.60bd	14.00bcd	3.69ab	50.07ab	1.60ef	70.47bcdefg	41.80abc	2.73bc	10.93b	8.64bcdefg	0.67efg	0.080c
RC762.6	1.93abcd	13.4bc	8.67e	3.39ab	35.80b	2.07bcdef	74.47bcdefg	42.73abc	3.53a	8.67bc	6.0fgh	0.36g	0.060de
392287.45	1.87abcd	12.5abc	3.67f	3.82ab	59.67ab	1.60ef	81.67ab	33.73cd	3.13b	10.67b	8.00bcdefg	0.45fg	0.056ef
396430.010	1.67abcd	11.30abc	8.33e	3.50abc	47.67ab	2.00bcdf	77.07bcde	41.27abc	2.400bc	8.86bc	11.80bc	0.95a	0.081c
Desiree	2.00abcd	14.28abc	19.33a	4.29ab	62.33ab	2.93bc	71.40defgh	49.87b	2.53ab	9.33b	12.47abc	0.74de	0.059de
392287.024	2.0abcd	14.30abc	15.00cd	3.65ab	68.87a	2.60bcd	75.07de	33.00cd	2.67abc	8.60bc	8.00bcdefg	0.74de	0.903b
390430.043	2.13abcd	15.00ab	18.33a	3.55ab	59.80ab	2.93bc	70.17efgh	36.93abcd	2.60abc	11.00b	11.80abc	0.54efg	0.046fg
375400.00	1.40cd	13.50abc	2.33g	3.19b	56.93ab	1.93cde	84.13a	42.73abc	3.13ab	6.60bc	8.33bcdefg	0.33g	0.040g
B9450.9	1.80cd	11.60abcc	17.00ab	4.11ab	63.80a	1.53ef	65.13h	52.60a	2.07ab	11.20b	11.87bc	0.74de	0.062de
387300.8	2.07abcd	13.7abc	18.67a	4.21ab	60.00ab	1.73cdef	76.67defg	43.873abc	2.20bc	8.6bc	9.13bcdef	0.82bcd	0.090b
Famosa	1.8abcd	15.40ab	20.00a	4.81a	71.87a	2.40bcdef	77.80bcde	52.60a	3.20a	10.00b	7.93bcdefg	0.89bc	0.113a
020037.4	1.73bcd	12.7abc	17.33ab	3.80abc	58.00ab	1.900bcdef	68.33fgh	43.87abc	2.73abc	12.60b	11.13abc	0.83bcd	0.075c
Grand Mean	2.03	13.09	14.70	3.84	58.01	2.21	70.18	42.06	2.67	10.95	10.00	0.72	0.074

Means with the same letter(s) in a column are not significantly different according to DMRT

Table 9: Mean Performance of Potato genotypes for thirteen Agronomic traits combined across years

Genotype	Growth Habit	No. of Nodes/Plant	Emergence Counts	Internode Length(CM)	Plant Height(CM)	Number of Main stems	Days to Maturity	Number of Leaves/Plant	Vigour Score	Tuber eyes/Plant	Number of Tubers/Plant	Tuber Weight	Average Tuber Weight
Ruslin ruaka	2.68a	13.23a	14.22cd	3.45ab	61.10abc	2.04cdef	76.22bcdef	40.01abc	2.81ab	9.40bc	7.51g	0.77cdef	0.105c
Br63-18	1.98abcd	13.69abc	18.56ab	3.33ab	59.45abcde	2.5abc	70.68ghi	36.81bc	2.38abc	9.37bc	9.47cdefg	0.58ef	0.061h
392254.106	1.91abcd	11.61cde	9.78e	3.32ab	50.97cde	2.06bcdef	76.89bcdef	34.46bc	2.58abc	11.28b	10.15abcde	0.60ef	0.060i
RC7716	2.29ab	10.82de	19.22a	3.88ab	62.91abcd	2.72ab	71.51ghi	39.35abc	2.37ab	10.32bc	11.82ab	0.64de	0.055j
Bertita	2.18abcd	17.97a	19.33a	3.28ab	56.51abcde	2.18def	72.92ghi	41.90abc	2.80ab	10.35bc	9.18bcdefg	0.62de	0.070g
WC312-2	2.07abcd	12.73bc	18.56ab	3.79ab	57.57abcde	1.87ef	77.40bcdef	42.31ab	2.08c	15.59a	7.84fg	0.75cde	0.095d
WC732-1	1.98abcd	13.87abc	13.00d	3.69ab	60.60abc	1.75ef	77.91bcdef	41.83abc	2.56abc	12.67b	10.20abcde	0.86bc	0.079ef
392278.4	2.57a	12.68bc	17.22ab	2.38b	55.88abcde	3.76a	69.82hij	41.26abc	2.42abc	10.95bc	12.65a	0.82bc	0.065h
676008	1.80abcd	12.58bc	14.11cd	4.39a	50.91bcde	2.00def	68.59hij	37.94bc	2.49abc	9.69bc	10.45abcde	0.82bc	0.065h
RC762.6	1.82abcd	11.36cde	8.00e	3.22ab	42.73e	2.07cdef	78.60bcde	39.63abc	2.73ab	8.04bcd	6.47g	0.68cd	0.080ef
396430.010	1.75de	12.57bc	4.22f	3.09b	53.68bcde	2.17def	82.46a	30.67cd	3.04a	8.36bcd	7.50fg	0.55ef	0.088de
396430.010	1.74de	11.32cde	9.33e	3.09b	47.50de	2.30bcd	77.87bcder	37.94bc	2.67ab	8.84bc	11.58abc	0.43f	0.068gh
Desiree	1.84abcd	13.74abc	19.55a	4.17a	61.33abc	2.66bc	72.93ghi	31.28cd	2.27abc	8.13bcd	11.13abcd	0.89ab	0.083de
392287.024	2.09abcd	14.70abc	14.89cd	3.21ab	65.54ab	2.39bcd	72.76ghi	37.49bc	2.51abc	8.33bcd	8.38defg	0.70cde	0.064h
390430.043	2.11abcd	13.74abc	18.33ab	3.07b	58.89abcd	2.90b	72.46ghi	45.93a	2.60ab	9.58bc	11.82defg	0.67cde	0.152a
375400.00	1.47e	13.34abc	2.78g	2.67b	51.13bcde	2.02cdef	74.02defgh	29.74d	2.49abc	5.91d	8.82defg	0.94f	0.048j
B9450.9	1.94abc	12.04bcd	16.00bc	3.36ab	58.39abcd	1.89ef	65.45j	35.18bc	2.33ab	10.29bc	10.47abe	0.68cde	0.065h
387300.8	1.84abcd	13.73abc	18.78ab	3.84ab	62.35abcd	1.48f	77.15bcdef	39.82abc	2.28abc	8.11bcd	5.11g	0.71cde	0.140b
Famosa	1.87abcd	15.36ab	18.44ab	3.93a	70.46a	2.38bcdef	79.13abc	46.87a	2.80ab	9.07bc	7.73fg	0.80bcd	0.103c
20037.4	1.91abcd	12.69bc	18.33ab	3.38ab	57.60abcde	1.96bcdef	72.86ghi	38.83abc	2.15abc	10.22abcde	0.78bcd	0.78bcd	0.076fg
Grand Mean	**1.99**	**13.19**	**14.63**	**3.43**	**57.28**	**2.26**	**74.38**	**38.46**	**2.54**	**9.75**	**9.43**	**0.67**	**0.071**

Means with the same letter(s) in a column are not significantly different according to DMRT

Table 10: Mean range, phenotypic, genetypic coefficient of variation and genetic advance of potato genotypic in 2005.

Plant character	Mean	Range	Phenotypic coef var %	Genotypic coef var %	genetic advance(as % mean)
Growth habit	1.98	1.53 – 2.53	16.48	10.98	21.35
No. of nodes/ plant	12.87	9.73–16.00	12.73	6.82	7.41
Internodes length	2.67	1.48–5.73	35.56	16.76	16.24
Plant height	56.68	41.33–69.56	15.20	13.16	23.41
No. of main stems	2.33	1.06–3.40	23.75	17.98	28.33
Days to maturity	76.11	63.73–84.40	7.92	7.41	14.22
Emergence counts	9.77	5.26–14.93	24.11	21.25	38.49
No. of Eyes	8.60	5.73–19.33	30.45	29.27	57.88
No. of leaves/ plant	16.68	144–20.73	15.95	14.89	28.58
Vigor score	2.23	1.40–2.80	14.80	8.15	9.42
Tuber number	15.20	2.00–19.66	34.31	33.62	67.83
Tuber weight	0.64	0.39–0.92	19.04	15.55	26.44
Average tuber weight	0.07	0.04–0.12	43.28	33.20	49.00

Table11: Mean, range, phenotypic, genotypic coefficient of variation and genetic advance of potato genotypes in 2006.

Plant character	Mean	Range	Phenotypic coef. Var. %	Genotypic coef. Var. %	Genetic advance (% mean)
Growth habit	19.45	1.4– 2.33	12.01	10.28	18.10
No. of nodes	12.98	9.63–18.23	14.78	9.87	13.65
Internodes length	3.84	2.93–4.78	13.07	7.72	9.37
Plant Height	57.98	37.63–72.07	12.30	10.05	16.88
No. of main stems	2.17	1.4–40.67	44.52	42.04	81.64
Days of maturity	74.34	66.6- 86.73	7.18	6.59	12.51
Emergence counts	13.93	0.00- 19.67	18.37	16.72	31.38
No. of Eyes	9.52	3.86- 17.80	27.05	23.47	41.87
No. of leaves/ plant	43.32	32.33- 52.73	12.39	6.63	7.32
Vigor score	2.58	1.86- 3.00	10.23	6.50	0.09
Tuber number	8.65	0.00- 19.33	6.40	6.24	5.34
Tuber weight	0.71	0.43- 1.09	32.61	31.34	62.16
Average tuber weight	0.09	0.048- 0.29	38.60	27.71	39.85

Table12: Mean, range, phenotypic, genotypic coefficient of variation and genetic advance of potato genotypes in 2010.

Plant character	Mean	Range	Phenotypic coef. of var.%	Genotypic coef. Var.%	Genetic advance(% mean)
Growth habit	2.03	1.67 – 3.60	10.45	11.02	17.10
No. of nodes/plant	13.09	9.01 – 17.88	14.23	7.64	14.32
Internodes length	3.84	3.19–4.81	14.12	8.15	10.81
Plant height	58.01	35.80–71.87	9.19	11.43	17.82
No. of main stems	2.21	1.53–4.07	41.60	43.42	85.64
Days to maturity	70.18	65.13–84.13	7.71	35.62	22.58
Emergence counters	14.70	2.33–19.67	18.69	16.95	32.53
No. of Eyes	10.95	6.60–21.43	24.73	23.18	49.83
No. of leaves/plant	42.06	33.00–52.60	12.22	2.21	27.31
Vigor score	2.67	2.07–3.53	10.20	2.05	28.09
Tuber number/plt	10.00	6.00-13.87	56.94	55.15	10.19
Tuber weight/plt	0.72	0.33-0.94	37.29	34.61	69.80
Average tuber weight	0.074	0.04-0.11	22.61	21.93	43.83

Table 13: Mean, Range, Phenotypic, Genotypic coefficients of variation and Genetic advance in Agronomic trait in the 3 years combined

Plant character	Mean	Range	Phenotypic coef. var .(%)	Genotypic coef Var .(%)	Genetic advance (%of mean)
Growth habit	1.99	1.47 – 2.68	11.73	9.12	14.63
Number of Nodes/plant	13.99	10.82 – 17.97	14.10	13.14	35.84
Internode length/ plant (cm)	3.34	2.38 – 4.39	16.64	6.67	5.54
Plant height (cm)	57.28	42.73 – 70.46	11.37	8.29	12.35
Number of main stems/ plant	2.26	1.48 – 3.76	21.53	17.20	28.42
Days of maturity	74.38	65.45 – 82.46	5.80	14.48	6.78
Emergence counts	14.63	2.78 – 19.33	37.56	37.28	76.34
No. of Eyes/ tuber	9.75	5.91 – 15.59	12.85	11.95	20.64
No. of leaves /plant	38.40	29.74 – 46.87	10.30	6.32	8.13
Plant vigour	2.54	2.08 – 3.04	10.44	6.96	5.88
Tuber number/ plant	9.43	5.11 – 12.65	14.73	3.00	38.65
Tuber yield(kg)	0.67	0.43 – 0.94	20.30	19.96	45.66
Average tuber weight/plant.	0.07	0.048 – 0.15	28.74	24.12	41.67

4.2 Mean squares

In the 2005 evaluation, genotypes mean squares were significant for plant height and number of nodes/ plant and highly significant for the rest of the agronomic traits except internode length Table 14. In the year 2006 Table 15, mean square estimates attributed to the genotype were highly significant (P = 0.01) for number of main stems, days to maturity, emergence counts number of eyes, tuber number, tuber weight, average tuber weight and posture and were significant (P = 0.05) for number of nodes, plant height and number of leaves. There was no significant difference on internode length.

In 2010 Table 16 mean squares for genotypes were significant (p=0.05) for growth habit, number of nodes per plant, number of leaves per plant and average tuber weight and were highly significant (p=0.01) for number of mainstems per plant, Days to maturity, Emergence counts, number of eyes per plant, number of tubers per plant and tuber weight per plant. There was no significant difference on inter node length, plant height and vigour score.

The mean square from the combined analysis of variance are presented in Table 17: Differences between years were highly significant (P = 0.01) for internode length, days to maturity, number of eyes/tuber, number of leaves, plant vigour, tuber number and average tuber weight and were not significant for plant posture, number of nodes per plant and plant height. Genotypic mean square was significant for plant posture, number of nodes, plant height, number of leaves and tuber number and highly significant for the rest of the agronomist traits except internode length and plant vigour. The year x genotype interaction effect was highly significant for days to maturity and significant for tuber number and not significant for the remaining traits.

Table 14: Mean squares estimates for agronomic traits in 2005

Source of Variation	DF	GH	NNP	IL	PH	NMS	DM	EC	NET	NLP	VS	TN	TW	ATW
Replication	2	0.37	4.05	5.30	62.40	0.18	52.58	12.05	10.40	1.86	0.38	7.40	0.01	0.03
Genotypes	19	0.30*	8.04*	2.75ns	222.70*	22.41*	108.97**	81.59**	20.58**	16.64**	0.33ns	8.91**	0.04*	0.12**
Error	38	0.16	5.73	3.35	55.69	34.51	13.66	3.24	1.57	3.71	0.22	2.74	0.02	0.014

*= Significant at 5% , **= Significant at 1% Ns = not significant, GH = Growth habit, NNP= Number of nodes per plant, IL = Internode length, NMS = Number of main stems, DM= Days to maturity, EC= Emergence counts, NET = Number of eyes per tuber, NLP = Number of leaves per plant, VS= Vigour score, TN= Tuber number, TW = Tuber number, TW= Tuber weight, ATW = Average tuber weight.

Table 15: Mean square estimates for agronomic trait in 2006.

Source of variation	DF	DF	GH	NNP	IL	PH	NMS	DM	EC	NET	NLP	VS	TN	TW
Replication	2	0.104	6.394	0.340	59.641	0.687	86.946	16.017	94.525	201.867	2.166	14.161	0.003	0.002
Genotypes	19	0.164**	11.036	0.580Ns	164.534*	1.149**	85.537	100.873	19.914**	86.415*	0.209Ns	19.661	0.068**	0.1431**
Error	38	0.044	6.127	0.492	152.611	0.315	13.467	5.315	4.929	61.640	0.210	3.361	0.012	0.0149

*= Significant at 5% , **= Significant at 1% Ns = not significant, GH = Growth habit, NNP= Number of nodes per plant, IL = Internode length, NMS = Number of main stems, DM= Days to maturity, EC= Emergence counts, NET = Number of eyes per tuber, NLP = Number of leaves per plant, VS= Vigour score, TN= Tuber number, TW = Tuber number, TW= Tuber weight, ATW = Average tuber weight.

Table 16: Mean square estimates for agronomic traits in 2010

Source of variation	DF	DF	GH	NNP	IL	PH	NMS	DM	EC	NET	NLP	VS	TN	TW
Replication	2	0.07	5.39	0.44	37.94	0.24	53.91	5.55	46.28	408.44	2.31	16.71	0.03	0.03
Genotypes	19	0.14*	11.03*	0.47ns	178.14ns	1.12**	70.74**	89.38**	26.42**	99.92*	0.54ns	13.34**	0.10**	0. 03ns
Error	38	0.06	5.13	5.13	0.52	148.80	0.24	28.36	5.32	46.07	0.33	4.59	0.02	0.01

*= Significant at 5% , **= Significant at 1% Ns = not significant, GH = Growth habit, NNP= Number of nodes per plant, IL = Internode length, NMS = Number of main stems, DM= Days to maturity, EC= Emergence counts, NET = Number of eyes per tuber, NLP = Number of leaves per plant, VS= Vigour score, TN= Tuber number, TW = Tuber number, TW= Tuber weight, ATW = Average tuber weight.

Table 17: Means square estimates from the combined analysis for agronomic traits

Sources of variation	DF	DF	GH	NNP	IL	PH	NMS	DM	EC	NET	NLP	VS	TN	TW
Replication	2	0.08	8.06	3.96	19.56	0.15	121.95	27.46	82.93	130.56	0.46	2.94	0.03	0.04
Year	2	0.02ns	0.02ns	40.94**	161.70ns	0.78ns	92.58*	37.41*	26.62*	219.48**	3.67**	37.63**	0.15	0.17*
Genotypes	19	0.33	18.16	1.81ns	254.22*	1.48*	130.32*	180.64*	19.16*	58.65*	0.35ns	6.40*	0.11*	0.14*
Genotype/year	38	0.14ns	0.92ns	1.53ns	121.10ns	0.59ns	62.19*	1.79	20.83*	36.67ns	0.18ns	11.91*	0.05ns	0.01ns
Error	114	0.11	5.84	1.92	109.92	0.36	13.67	4.17	3.73	33.38	0.27	3.78	0.14	0.01

*= Significant at 5% , **= Significant at 1% Ns = not significant, GH = Growth habit, NNP= Number of nodes per plant, IL = Internode length, NMS = Number of main stems, DM= Days to maturity, EC= Emergence counts, NET = Number of eyes per tuber, NLP = Number of leaves per plant, VS= Vigour score, TN= Tuber number, TW = Tuber number, TW= Tuber weight, ATW = Average tuber weight.

4.3 Estimates of variance components

The estimates of genotypic, phenotypic and environmental variance for the agronomic traits for 2005, 2006 and 2010 are presented in Table 18, 19 and 20. Generally, as a trend the phenotypic variance were slightly higher than the corresponding genotypic variances for both years and for all traits. In the first year the highest variance estimates were recorded for plant height, days to maturity, and tuber number/ plant in that order. The least estimates was for average tuber weight. In 2006, highest estimates of variance were recorded for plant height, tuber number, number of leaves and days to maturity respectively. The least estimate in agronomic traits was average tuber weight. Also in 2010, heighest estimates for variance components were recorded in Days to maturity, plant height, tuber number and number of leaves per plant.

The variance component estimates combined across the three years is presented in Table 21. The phenotypic variance components were generally higher in magnitude than that of genotypic components for agronomic traits.

The highest genotypic variance was recorded for emergence counts (29.81), plant height (22.19) and days to maturity (11.36). Low estimates were recorded for tuber yield, (0.018) average tuber weight (0.021) and plant posture (0.032). Genotype x year interaction component was high for days to maturity (11.36) followed by number of eyes (5.70) and plant height (3.73) Negative genotype x year interaction variance component was obtained for number of nodes per plant (-1.63), emergence counts (-0.79), vigour score (- 0.03) and average tuber weight (-0.0029). The error variance component estimates was highest for plant height and least for tuber weight. The genotypic variance exceeded plot error variance estimate only on emergence counts. The genotypic variance was higher than the genotype x year component in all traits except number of eyes per tuber.

Table 18: Estimates of variance components for agronomic traits for 2005.

Type of var.	Growth Habit	N0. of nodes/plant	Internodes length	Plant height	No. of main stems	Days to maturity	Emergence counts	No. of Eyes	No. of leaves/plant	Vigor score	Tuber number	Tuber weight	Average tuber weight
$\delta^2 g$	0.05	0.77	-0.20	55.67	0.18	31.77	4.31	6.33	6.17	0.03	26.12	0.01	0.31
SE$\pm$	0.04	1.01	0.44	23.50	0.10	11.24	0.95	2.11	1.75	0.04	8.36	0..01	0.01
$\delta^2 ph$	0.10	2.68	0.90	74.23	0.31	36.32	5.55	6.86	7.08	0.10	27.20	0.02	0.01
SE$\pm$	0.03	0.28	0.09	7.60	0.03	3.72	0.57	0.70	0.72	0.01	2.78	0.01	0.02
$\delta^2 e$	0.16	5.74	3.34	55.70	0.19	13.67	3.71	1.77	2.74	0.23	3.24	0.02	0.02
SE$\pm$	0.05	1.70	1.04	17.19	0.12	4.22	1.15	0.48	0.85	0.07	1.00	0.01	0.02

Table 19: Estimates of variance component for agronomic traits in 2006

Type of var.	Growth Habit	No. of nodes/ plant	Internode length	Plant height	No. of mainstems	Days to maturity	Emergence counts	No. of eyes	No. of leaves	Vigor score	Tuber number	Tuber weight	Average tuber weight
σ^2_g	0.04	1.64	0.09	33.97	0.83	24.02	22.80	4.99	8.26	0.03	29.16	0.05	0.04
SE$\pm$	0.02	3.90	0.08	0.97	0.37	0.86	5.43	0.09	0.86	0.03	0.34	0.21	0.01
σ^2_{ph}	0.05	3.68	0.25	30.87	0.94	28.51	2.04	6.63	28.81	0.07	30.93	0.05	0.03
SE$\pm$	0.06	0.37	0.03	5.21	0.10	2.92	0.67	0.68	2.95	0.01	3.17	0.01	0.01
σ^2_e	0.04	6.13	0.49	164.53	0.32	13.43	31.36	4.93	61.64	0.21	5.32	0.03	0.01
SE$\pm$	0.01	1.89	0.15	50.78	0.01	2.94	1.04	1.52	19.02	0.07	1.64	0.03	0.01

Table 20: Estimates of variance components for agronomic traits in 2010

Type of variance	Growth habit	No. of Nodes/pl.	Intern ode length	Plant height	No. of main stems	Days to maturity	Emerge nce count	No. of eyes/pl	No. of leaves/pl	Vigor score	Tuber number/ pl	Tuber weight	Ave. tuber weight
σ_g^2	0.05	1.48	0.10	43.97	0.92	27.02	6.21	6.44	10.86	0.03	30.41	0.06	0.04
SE$\pm$	40.02	0.90	0.07	12.97	039	0.86	3.02	2.10	72.14	0.30	10.81	0.02	0.18
σ_{ph}^2	0.05	3.47	0.29	28.43	0.85	29.26	7.55	7.33	26.40	0.07	32.42	0.07	0.03
SE$\pm$	0.01	0.28	0.03	6.21	0.08	3.35	0.89	0.78	2.92	0.01	4.22	0.01	0.01
δ^2e	0.07	5.32	0.52	148.81	0.24	28.37	5.32	159.44	61.64	0.30	4.60	0.03	0.01
SE$\pm$	0.01	1.58	0.04	10.02	0.02	2.23	0.42	0.33	19.10	0.02	0.31	0.02	0.04

Table 21: Estimates of variance components for agronomic traits combined across 3 years

Type of var.	Growth habit	No. of Nodes/p lant	Internod es length	Plant height	No. of stems	Days to maturity	Emergenc e score	No. of eyes	No. of leaves /plant	Vigour score	Tuber number / plant	Tuber weight / plant	Average tuber weight
σ_g^2	0.02	1.4.0	-0.01	16.10	0.12	12.90	19.61	1.72	2.81	009	0.29	0.01	0.01
SE$\pm$	0.08	0.86	0.01	14.54	0.01	7.46	9.33	1.48	0.57	0.01	0.07	0.01	0.01
σ_{gy}^2	0.01	1.61	0.48	3.73	0.08	16.10	0.79	5.70	1.10	-0.03	2.70	0.01	-0.01
SE$\pm$	0.01	0.61	0.21	1.67	0.07	7.60	0.47	2.17	0.51	0.02	0.84	0.01	0.01
δ_{ph}^I	0.04	2.54	0.08	33.60	0.20	18.72	26.61	2.70	7.40	0.04	0.80	0.02	0.02
SE$\pm$	0.01	0.94	0.09	13.10	0.08	6.73	9.33	1.02	6.17	0.02	0.02	0.01	0.01
δ_e^2	0.11	5.80	1.39	109.92	0.36	13.67	4.10	3.73	33.38	0.27	3.70	0.01	0.02
SE$\pm$	0.03	1.31	1.30	12.61	0.08	3.14	0.96	0.99	7.30	0.62	0.87	0.01	0.01

Table 22: Grouping Of 20 Potato Genotypes Into Different Clusters

Cluster	Number	Grouping	(Genotypes)				
I	6	392254.016	Bertita	390430.043	B9450-9	FAMOSA	200037-4
II	4	Rc7716	396430.010	Rc762-6	392287.024		
III	4	Rustling Ruaka	Br63-18	676008	392287.45		
IV	3	392278.4	Desiree	387300.8			
V	3	We 312-2	Wc732-1	375400.00			

Table 23: Average Intra and Inter Cluster D^2 – Value

Cluster	I	II	III	IV	V
I	1.8834	10.4406	4.3301	4.1281	11.8028
II		2.3611	4.1140	2.9802	13.8101
II			10.7311	8.6377	25.306
IV				2.8386	17.0946
V					6.0970

4.3 Mahalanobis D^2 analysis.

Multivariate analysis based on Mahalanobis D^2 statistics or relative magnitude of D^2 values grouped all the twenty genotypes into five clusters. Cluster 1 was the largest and consisted of seven genotypes. Clusters II and III each accommodated maximum number of four genotypes. Cluster IV and V had 3 genotypes each. The average inter cluster distance were higher than the average intra cluster distances. Inter-cluster distance between III and V (25.306) and followed by cluster IV and V (17.0946) and the lowest is between cluster II and IV (2.9802). The maximum intra cluster distance was observed in cluster III (D^2 = 10.7311) followed by cluster V (D^2 = 1.8834).

4.5 Correlation Coefficients

Genotypic correlations between the various traits, computed from the combined data for three years are presented in table 24. In most cases the genotypic correlations coefficient were higher than the phenotypic correlation coefficients. Highly significant positive genotypic correlations coefficients were observed between growth habit and plant height (rg = 0.8426), days to maturity (rg=0.6029), emergence counts (rg=0.9670), tuber weight (rg=0.9942) and growth habit and Average tuber weight (rg=0.8531). number of nodes per plant also had a significant positive genotypic correlation with number of stems (rg=06661) and tuber number per plant (rg=0.4080). internode length per plant had a slightly significant positive association with plant height (rg=0.97792), days to maturity (rg=7307), emergence counts (rg=0.8454) and number of leaves (rg=4148) was also a significant positive genotypic correlation coefficient between plant height and number of stems (rg=0.5479) and tuber weight (rg=6321). The result of the present study also indicated that number of stems per plant had a significant + positive genotypic correlation with days to maturity (rg=0.7661), emergence counts (rg=0.4729), number of eyes (rg=4189) and number of leaves (rg=0.7419). days to maturity had significant positive genotypic correlation with tuber weight per plant (rg0.4522). Emergence counts has a high significant positive genotypic correlation with vigour score (rg0.9136), tuber weight per plant (rg=0.7225) and with average tuber weight (rg=0.4344) number of eyes per plant had a significant positive genotypic correlation with number of leaves per plant (rg=0.4832) and tuber had a significant positive genotypic correlation with tuber number/plant (rg=6863).

Vigour score also had a significant positive genotypic correlation with average tuber weight (rg=0.5182). tuber number per plant also show highly significant positive genotypi9c correlation with tuber weight per plant (rg=0.6224) and with average tuber weight (rg=0.8434).

There was also a significant positive phenotypic correlation between growth habit with tuber weight per plant. (rg=0.5747) and between number of nodes per plant and number of stems per plant (rg=0.6661). in ternode length also had a significant positive phenotypic correlation with plant height. (rg=0.4774). Number of nodes also had a significant positive phenotypic correlation with tuber number per plant (rg0.4080). Days to maturity shows a significant positive phenotypic correlation with vigour score and tuber number (rg=0.9740 and 0.4420) respectively. Average tuber weight had a significant phenotypic correlation with tuber number (rg=0.576).

Table 24: Genotypic (above diagonal) and phenotypic below diagonal) correlation coefficients of thirteen (13) Characters of potato genotypes

character	GH	NN	IL	PLHT	NS	DM	EMC	NE	NL	VS	TN	TW	AVTW
GH		0.3030	0.0306	0.8426**	0.0693	0.6029*	0.9670**	-0.1936	0.3423	0.0299	-0.1363	0.9942**	0.8531*
NN	0.0237		0.3670	0.1227	0.6661*	0.1762	0.1081	-0.5454*	0.3228	0.2835	0.4080*	0.2273	-0.0431
IL	0.0165	0.3470		0.9792**	0.0844	0.7307**	0.8454**	0.2344	0.4148*	-0.0363	0.1651	0.0291	-0.0431
PLHT	0.2840	0.1277	0.4774*		0.5479*	0.3629	0.0388	-0.1963	0.1109	-0.7883**	0.2787	0.6321*	-0.3451
NS	0.2843	0.6661*	0.0221	0.0483		0.7661**	0.4729*	0.4189*	0.7419**	0.0648	0.2950	0.0520	0.3416
DM	0.2677	0.1762	0.0398	-0.3552	-0.2100		-0.1693	-0.0937	0.2745	0.1551	0.3895	0.4522*	0.2413
EMC	0.2550	0.1081	0.0396	-0.0225	-0.0623	-0.1141		-0.1773	0.2958	0.913**	0.2404	0.7325*	0.444*
NE	-0.1416	-0.5454*	0.1001	0.1644	-0.0616	-0.0170	-0.1063		0..4832*	0.1813	0.8231**	0.1454	-0.4344*
NL	0.1262	0.3228	0.2208	-0.8245**	0.1146	0.1710	0.2372	0.0401		0.3201	0.6863*	0.1454	-0.8148**
VS	0.2790	0.2835	-0.0144	-0.2408	0.0475	0.9740**	0.3434	0.0707	0.0637		0.1275	0.2567	0.5182*
TN	-0.1109	0.4080*	0.1831	0.2306	0.0407	0.2926	0.0451	0.2604	0.1360	0.1165		0.6224**	08434**
TW	0.5747*	0.2773	0.0112	0.0361	0.0252	0.4429*	0.2029	0.2020	0.2029	0.0461	0.1100		0.8345**
AVTW	0.2431	-0.0431	-0.0248	-0.4121*	0.2416	0.1314	-0.1431	-0.2186	-0.3177	0.2817	0.5976*	0.5897	

*,** Significant at 5 and 1% probability level, respectively, GH=Growth habit, NN= number of Nodes, IL=Internode length (cm)

PLHT = plant height (cm), NS=Number of stems plant^{-1}, DM= days to maturity (50% senescence) EMC=Emergence count, NE=number of eyes plant^{-1}, NL=number of leaves plant^{-1}, VS=vigour score, TN= Tuber number plant^{-1} TW= tuber weight plant^{-1} (kg)

AVTW= Average tuber weight.

4.4 Path Coefficient Analysis

The result of path coefficient analysis and the direct and indirect contributions of plant height, number of stems per plant, number of tubers per plant, number of leaves per plant, average tuber weight and number of eyes per plant and presented in fig. 1 and table 25. At the genotypic level, number of leaves per plant (0.21636) exerted the highest direct effect on tuber yield per plant. This was followed by number of tubers per plant (0.13337) number of eyes per plant (0.12619) and plant height (0.06628).

The yield was negatively affected by average tuber weight (-0.11692) followed by number of stems per plant (-0.01457) even though, the correlations, (0.8345, 0.2273 respectively were positive and higher in magnitude.

Plant height had a low positive indirect effect on the yield which was mainly through number of stems per plant (0.02633) followed by number of leaves per plant (0.02469) average tuber weight (0.0416) and number of stems per plant (0.0013) while it was negative through number of eyes per plant (-0.00598). The total indirect elect 0.0493 was positive at genotypic level.

Number of stems per plant exerted low positive indirect effected on number of eyes per plant and average tuber weight (0.05994, 0.01340 respectively). The indirect effect was negative and much less through other characters on yield. The total indirect effect (0.04594) was positive.

Number of leaves perplant exerted positive indirect effect only through number of stems per plant (0-.00091), number of tubers per plant (0.03163). and plant height (0.00756). the indirect effect via other characters were negative and low. The total indirect effect (-0.01340) was negative.

Number of tubers per plant had a positive indirect effect on the yield via number of leaves per plant (0.05132) followed by plant height (0.01308), number of eyes per plant

(0.00872) and number of stems per plant (0.00090), while it was negative via average tuber weight (-0.00469). the total indirect effect (0.06953) was positive.

The indirect effect of average tuber weight was negative through plant heigh (-0.00236) and number of eyes per plant (-0.00804) while it was positive via number of stems per plant (0.00167), number of leaves per plant (0.07430) and number of tubers per plant (0.00535). the total indirect effect was (0.07092).

Also the indirect effect of number of eyes per plant was positive and low through number of tuber per plant (0.00943) and average tuber weight (0.00745). It was negative through plant height (-0.00314), number of stems per plant (-.0.00692) and number of leaves per plant. The total indirect effect (-0.01618) was negative.

Number of leaves per plant through average tuber weight was negative. This negative indirect effect via average tuber weight counter balanced the high positive direct effect of number of leaves per plant on tuber yield resulting in lower correlation coefficient between number of leaves per plant and tuber weight per plant. The direct positive effect of tuber number per plant on tuber yield per plant was low compared to its high association with tuber yield per plant. Thus, its high correlation is mainly due to its positive indirect effect via number of leaves per plan. Plant height had a low direct positive effect on tuber yield. However, its high correlation with tuber yield was due to its high positive indirect effect via number of tubers per plant. It also exerted a negative indirect effect via number of eyes per plants.

The residual effect determines how best the causal factors account for the variability of the dependent factors. In the present study its estimates, 0.26 genotypic path analysis means that 74% of the total variation in tuber yield per plant were explained at genotypic leaves. Thus some others 26% at genotypic levels that were not considered in this study need to be included in the analysis to account more appropriate for the total variation of the tuber yield.

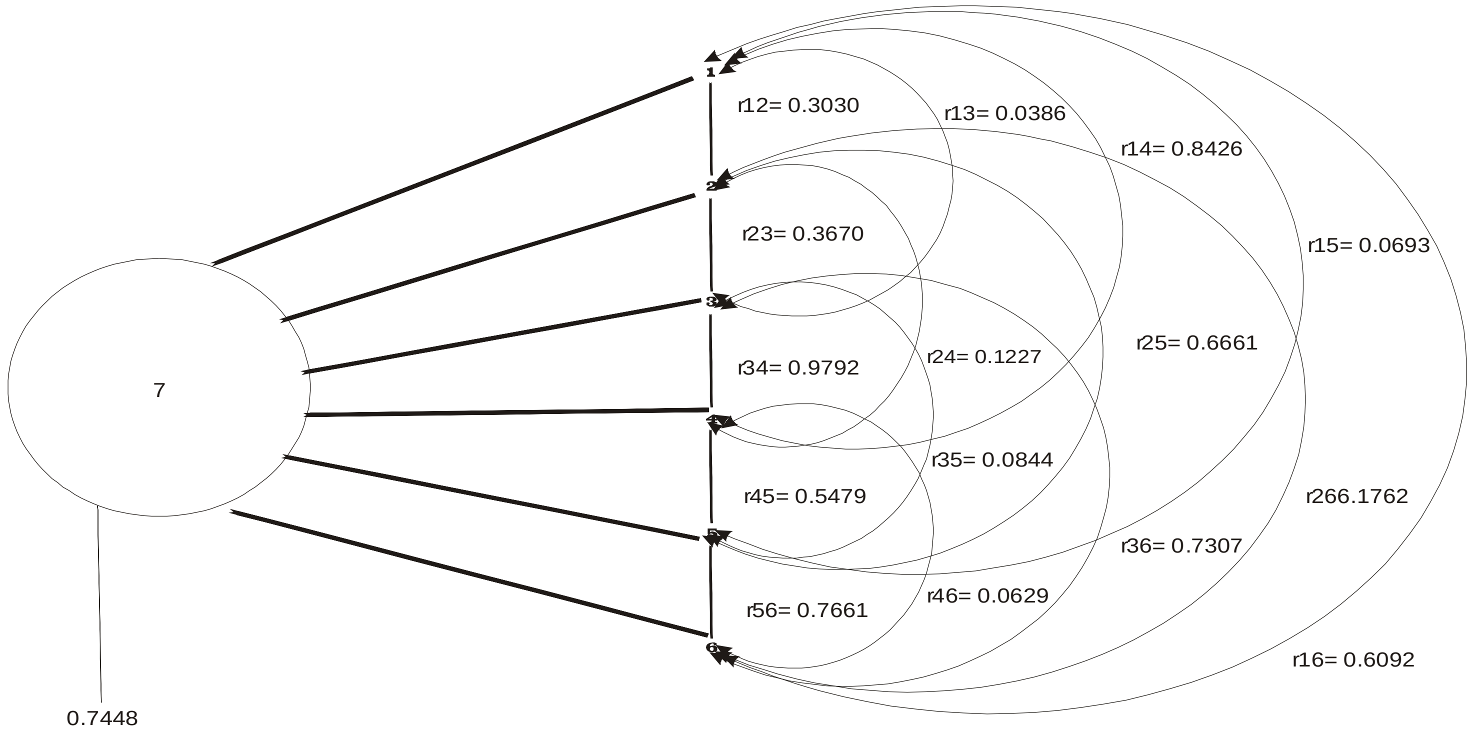

Fig. Path diagram for agronomic traits

Key: 1 = Plant height

2 = Number of main stems

3 = Number of tubers

4 = Tuber weight

5 = Number of eyes/tuber

6 = Average tuber weight

Table 25: Genotypic direct (bold) and indirect effects of some characters on potato tuber yield Per plant.

Character	Plant height	Number of stems plant^{-1}	Number of leaves plant $^{-1}$	Number of tubers plant^{-1}	Average tuber weight	Number of eyes plant^{-1}	Genotypic correlation with tuber yield
Plant height	**0.06628**	0.0013	0.02469	0.02633	0.00416	-0.00598	0.11560
Number of stems plant-1	-0.0057	**-0.01457**	-0.01348	-0.00822	0.01340	0.05994	0.03650
Number of leaves plant-1	0.00756	0.00091	**0.21636**	0.03163	-0.04015	-0.01341	0.20290
Number of tubers plant-1	0.01308	0.00090	0.05132	**0.13337**	-0.00469	0.00892	0.20290
Average tuber weight	-0.00236	0.00167	0.07430	0.00535	**-0.11692**	-0.00894	-0.04600
Number of eyes plant-1	-0.00314	-0.00692	-0.02300	0.00943	0.00745	**0.12619**	0.12619

4.5 Heritability estimates

Heritability estimates on family and plot basis are presented for 2005, 2006, 2010 and combined in Table 26. Most estimates for 2005, 2006, 2010 (except average tuber weight) and the combined on family basis, were higher than estimates based on plot basis. These estimates were generally high for all agronomic traits. Apart from estimates for number of leaves/plant which was negative (-0.707) in the 2010, other estimated values ranged from 0.118 for number of nodes/plant to 0.960 for tuber number/plant in 2005. The same estimates in 2006 ranged from 0.126 for vigour score to 0.943 for tuber number/plant. Similarly the estimate were similar in 2010 and range for 0.215 for internodes length to 0.948 for tuber weight. The combined analysis ranged from 0.032 for internode length to 0.938 for emergence counts. All heritability estimates were positive except for number of leaves which was negative but moderate. Estimates based on family basis were generally high with values ranging from 0.160 for internode length to 0.960 for tuber number/plant. Estimates on plot basis ranged from 0.032 for internode length to 0.897 for emergence counts. The family basis were more reliable.

Table 26: Broad sense heritability estimates for potato genotypes grown over three years.

	2005		2006		2010		Combined	
	Family	**Plot basis**	**Family**	**Plot basis**	**Family**	**Plot basis**	**Family**	**Plot basis**
Growth habit	0.47±0.343	0.226±0.166	0.733±0.349	0.476±0.207	0.534±0.374	0.356±0.245	0.581±0.248	0.319±0.219
Number of nodes	0.29±0.034	0.118±0.055	0.445±0.094	0.302±0.211	0.421±0.241	0.372±0.198	0.52±0.281	0.167±0.058
Inter nodes length (cm)	0.22±0.084	0.14±0.064	0.349±0.309	0.152±0.134	0.215±0.021	0.192±0.056	0.16±0080	0.032±0.016
Plant height (CM)	0.75.0317	0.50±0.084	0.668±0.255	0.171±0.065	0.713±0.312	0.543±0.0113	0.413±0.191	0.401±0.198
Days of maturity	0.875±0.305	0.699±0.25	0.343±0.311	0.641±0.236	0.682±0.275	0.418±0.213	0.612±0.301	0.312±0.210
Emergence counts	0.77±0.272	0.537±0.119	0.843±0.312	0.152±0.057	0.972±0.413	0.518±0.184	0.502±0.290	0.491±0.220
Number of eyes/tuber/plant	0.871±0.247	0.691±0.186	0.150±0.287	0.150±0.0114	0.541±0.231	0.343±0.118	0.431±0.192	0.431±0.190
Number of leaves/plant	0.871±0.24	0.731±0.261	0.753±0.316	0.560±0.225	0.707±0.483	0.412±0.198	0.612±0.321	0.321±0.210
Vigour score	0.303±0.367	0.889±0.186	0.435±0.004	0.126±0.001	0.671±0.293	0.370±0.112	0.170±0.061	0.063±0.023
Tuber number	0.960±0.307	0.889±03245	0.943±0.334	0.804±0.342	0.948±0.512	0.832±0.430	0.356±0.122	0.256±0.086
Tuber weight	0.667±0.33	0.385±0.392	0.804±0.392	0.804±0.342	0.948±0.512	0.832±0.430	0.356±0.122	0.25±0.086
Average tuber Weight	0.490±231	0.280±0.030	0.532±0.282	0.74±0.48	0.832±0.512	0.678±0.468	0.471±0.021	0.581±0.039

4.6 Principal component of analysis estimates

Principal component, eigen values, percentage or proportion and cumulative effects estimates are shown in Table 27. The table indicated that three principal components were identified which explained 97.64 per cent per total variation. The first principal components accounted for 66.93 per cent of variation, while the second and third accounted for 19.68 and 11.04 per cent, respectively.

The eigen vectors and principal components are given in table 28 table indicated that in the first principal component, the characters that contributed more to diversity are plant height (0.490960), number of tubers per plant (0.462558). The rest of characters were showing negative variation.

As in the second principal component, number of eyes per plant accounted for (0.407717) and was followed by number of tubers per plant (0.38302), plant height was next (0.250156) and tuber weight per plant (0.207641) in the positive direction. However, number of stemsper plant (0.280654) and average tuber weight (00.380687) were contributing to the variation in negative direction.

In the third principal component number of stems per plant (0.226974) contributed more to maximum diversity, average tuber weight (0.226061), number of tubers per plant contributed (0.041696). Plant height (-0.3558557) and number of eyes per plant (-0.07948) contributed to variation in the negative direction.

Table 27: Eigen Values Proportion and Commutative Effects

Principal Component	Eigen Value	Proportion	Cumulative Effects
PRIN 1	5.67693	0.6693	06693
PRIN 2	2.35440	0.1968	0.8660
PRIN 3	0.889966	0.1104	0.9764

Table 28: Eigen values principal component analysis of potato

S/N	Characters	Prin 1	Prin 2	Prin 3
1	Plant height	0.490960	0.250156	-0.355857
2	Number of stems per plant	0.261684	-0.280654	0.226974
3	Number of tubers per plant	0.462558	0.383802	0.041696
4.	Tuber weight per plant	0.331466	0.207641	0.100182
5.	Number of Eyes per plant	-0.113305	0.407717	-0.079148
6.	Average tuber weight	-0.057169	-0.380687	0.226061

CHAPTER FIVE

DISCUSSION

5.1 Mean Performance

Mean performance in the three years of study for most characters have similar trend. However, the mean performance for the third year of study was higher than the first and second year. Environmental factors were most likely to be responsible for these variations. Unfortunately, these are variables over which the breeder has very little control.

The choice of genotypes and breeding procedure to be adopted in an improvement programme will depend upon the mean performance and on the magnitude and quality of genetic variability present (Eckebili *et al,*. 1977). For most of the characters considered, the ranges of values were wide and the mean differences observed were significant. This agrees with the findings of various workers (Sidhu and Pandita, 1979; Birhman and Kaul, 1989) who reported that variations exist amongst potato genotypes for different attributes. This highly significant variation in plant attributes within a population suggests that selection is possible for each character. But for an improved population, a wide range in the expression of character may not be desirable. For instance uniform emergence may be desirable where cultural activities such as fertilizer application are to be done at the early stage of plant growth. Besides, it is conventional to breed for plants that have uniform growth, early maturing and high yielding. Date to maturity had a wide range of 63 – 85 days. This means that genotypes selection for different maturity regimes that will be suitable to the different ecological zones is practicable.

The overall picture suggests that high amount of genetic variability or diversity exits among the genotypes studied. In other words, they are diverse in their genetic base. This may not be surprising because the genotypes were derived from local collections and crosses from different countries and climate, which could warrant adaptive variability. Since variability in a population suggests a possibility of improvement through selection, it means theoretically that the greatest amount of improvement can be obtained in emergence counts and plant height which have the highest genetic variations, presence of genetic variability in genotypes is an essential requirement for achieving success in selection programme (Singh and Singh, 1979) and play a vital role in a successful breeding programme (Babaji et al,. 2006).

Coefficient of variation describes the amount of variation in genotypes. High phenotypic and genotypic coefficient of variation suggests high degree of phenotypic and genotypic variability in those characters exhibiting them. Thus, with reference to this study, the highest potential for selection lies in the traits emergence counts, average tuber weight, number of main stems / plant and tuber yield since these traits indicated high genetic coefficient of variation. Also, in this study, it was observed that higher values for phenotypic coefficient of variation than genotypic coefficients of variation indicate the presence of environmental variation which also resulted in lower phenotypic correlation coefficients compared to genotypic correlation coefficients. These findings are in agreement with Gopal, (1999). However, genetic variation alone cannot determine the amount of variation that is heritable. Heritability estimates most accompany the genetic coefficient of variation to make it meaningful.

Genetic advance for characters such as emergence counts, tuber yield, average tuber weight, number of nodes/plant and number of main stems were high, this suggest that improvement in these characters should not be difficult. This agrees with an earlier recommendation by Gopal, 1992. So a combine selection for tuber yield and average tuber weight should be a better strategy for improving tuber yield.

Variances are pertinent to any improvement programme since they directly relate to the amount of variability contained in a population. Accurate estimates of variance components provides basis for critically evaluating breeding and testing procedure. The indication of significant genotypic variances for certain traits is an indication of possible improvement for the traits, since traits that indicated significant phenotypic variances also had significant genotypic variances by implication, it means that selection for these agronomic traits based on the phenotype is likely to result in an appreciable genetic advancement. Emergence counts with the highest genotypic variance are of little use to a breeder who intends to breed for uniform growth and high yielding potatoes. All other characters associated with yield have appreciable genotypic variances. It then means that further improvement of most of the agronomic characters is feasible via simple selection with appropriate selection intensity. Simple selection can be done with recurrent selection programme where greater emphasis is on quantitative traits. Sharma (1980) noted that owing to negative correlation between yield and some traits, a reduction in the traits occurred mainly due to selection favouring yield alone.

The variances attributable to genotype x year interaction were relatively lower than the genetic variance but significant. Interaction containing year terms are particularly interesting to applied breeders, this is because they reflex it fluctuations in environment, which in most part cannot be predicted in advance (Allard and Bradshaw, 1964).

In this study, genotypes x year effect for most of the traits studied were significant. The significance of genotype x year interaction for the genotypes indicates that the relative performance among genotypes for each of the two years of testing was not the same; they require that testing over several years be done. For traits like vigour score/plant, average tuber weight, number of nodes/plant and plant posture, genotype x year effects were small, negative and non-significant. This implies the consistency of the traits over the years and suggests that the traits are stable, as they are minimally influenced by environment.

5.2 Clustering Pattern

The clustering pattern in the present study indicates that the geographical diversity needs not to be necessarily related to genetic diversity. Parallelism was noticed between geographic origin and diversity. Genotypes originating from different geographical regions were grouped together under same cluster. Cultivars from same geographical origin were accommodated in different clusters. This demonstrated that geographical distribution was not related to genetic diversity. This finding was in agreement with the findings of Mondal, 2003. And disagrees with an earlier report by (Naskar and Ravindran, 1996). This may perhaps be due to the free exchange of breeding materials from one location to another (Verma and Mehta, 1976). Besides it may be due to the fact that the nature of selection pressure operating under respective domestic conditions might be similar across geographic barriers. Thus, it is evident that geographical diversity though important may not be the sole factor determining genetic divergence. The present study has show that factors other than geographic diversity might have been responsible for the grouping of the clones. Moreover, the highly heterozygous nature, mutation and segregation of chance seeds, might have contributed to the diversity. Clones like RC7716 from Nigeria which have been grouped under different clusters would be possible due to factors like genetic architecture of the population, past history of selection and degree of general combining ability. (Murthy and Arunachalam, 1989).

High D^2 values along with maximum inter-cluster distance among genotypes should be considered while choosing genotypes as parents for hybridization (Showemimo, 2004). In this study, high inter-cluster distance was noticed between cluster III and V and IV and V imply that these clones included under these highly divergent clusters can be used as parents in hybridization and would produce heterotic hybrids and a greater or wide spectrum of variability in the segregating generations. As stated by Bhat (1973), highly divergent genotypes may produce a wide range of variability enabling further selection. So the genotypes of these clusters may be considered for selection of parents in hybridization programme in potato. Similarly maximum intra-cluster distance was observed for cluster III and minimum for cluster I. The genotypes belonging to cluster III and V may be considered as parents for hybridization programme, because genotypes within these cluster having high degree of divergence would produce more desirable breeding materials for achieving maximum genetic advance. The minimum intra-cluster value was exhibited by cluster I which indicated the limited genetic diversity existing among the constituent genotypes, and when crossed, are not likely to produce any appreciable heterosis.

Therefore, crosses involving any two or more members of cluster I is not likely to lead to any heterosis in yield. The intra-cluster distance was much lower than the inter cluster one, this suggest heterogeneous and homogenous nature between and within groups respectively (Ahmed et al,. 2002).

5.3 Correlations Coefficient

Knowledge of correlations between traits of economic importance are not only of interest from theoretical consideration of quantitative inheritance of characters, but of practical value since selection is usually concerned with changing two or more traits simultaneously. Therefore a breeder needs to know how his population will respond when selection pressure is applied for a single trait. Improvement in one trait as a result of selection of another depends not only upon the genotypic and phenotypic correlation between them, but also upon the genotypic and phenotypic variances associated to them. (Shivaji and Gritton, 1975).

Genotypic correlation provides a measure of genetic association between traits and thus helps to identify the more important as well as less important traits to be considered in breeding programme. For most of the association in this study, the genotypic correlation coefficient was higher than the phenotypic correlation coefficient. Alhassan (2005) reported higher genotypic correlations of character than phenotypic correlations in sorghum genotypes. (Abdalla *et al*, 1994) also reported higher genotypic correlations of character than phenotypic correlations in sorghum genotypes under different water regimes. Diz and Shank (1995) obtained genotypic and phenotypic correlation coefficients, which in some cases differed in magnitude but in other cases did not. Where genotypic correlation coefficients are higher than phenotypic correlation coefficient, Johnson *et al* (1955) explained that there are strong inherent relationships between these characters. When the opposite is the case, Sidwel (1975) asserted that environmental effects or non-additive effects are acting on the traits in the same direction.

Tuber yield was positively and significantly correlated with Tuber number/plant and average tuber weight. Theoretically, it means that tuber number/plant and average tuber weight could be used as a selection index to improve tuber yield. The negative and significant genotypic correlation observed between number of nodes and number of eyes/tuber, and average tuber number suggests that number of nodes will have less activity in these characters; it suggests that selection for lower number of nodes will result in improvement on tuber number and average tuber weight. Days to maturity, had a significant positive genotypic correlation with tuber yield indicating that high yielding genotypes may be late in maturity. This agrees with Morris, (1988).

Among the foliage characters, positive and significant correlation coefficients were found between plant height and plant posture and number of nodes and number of main stems. The positive high correlations between these pairs indicate that a change in one is accompanied by a corresponding change in its components i.e. number of nodes and internode length. There was no association between number of nodes and internode length indicating that plant height and its components could be improved simultaneously. Tuber yield had a strong association with number of leaves and plant height. When numbers of leaves are many, there will be a greater surface area for photosynthesis; greater photosynthesis can translate into more photosynthates, ultimately resulting in increase in tuber yield. This is exhibited by significant and positive correlation of the photo synthetically active part of the plant with tuber yield at both genotypic and phenotypic levels. Mohammed *et al* (2003) and Amadi (2007) in maize and potato respectively have also indicated a positive association between photo synthetically active leave number and grain yield and active leave number and tuber yield, respectively.

Tuber number was negatively associated with average tuber weight. Thus, to avoid the risk of selecting clones with fewer over sized tubers, it is suggested that a standard may be fixed for the minimum number of tubers required in the selected types before employing selection for tuber yield and average tuber weight. These findings agree with the recommendation of an earlier study by Killick (1977). Plant vigour had a positive and significant association with tuber yield, this indicate that vigorous plants are expected to have a high tuber yield.

5.4 Path analysis

Genotypic correlations were found between yield and its components traits. However, as correlation between more variables are considered, the indirect association become more complex, less obvious and somewhat confusing. At this point, path coefficient analysis provide an effective means of untangling direct and indirect causes of association and permit a critical examination of the specific forces to produce a given correlation and measure the relative importance of each causal factor. The positive and significant genotype correlations as well as high direct effect of number of tubers on tuber yield is an indication that number of tubers/plant was the most reliable component for selecting high yielding potato genotypes. The large residuals observed in this study imply that there are probably other traits other than those indicated in the pathways that contributed to the dependent variable. This is to say that path coefficient analysis in this study did not account for all variations in agronomic traits as indicated by the magnitude of the residual effect. There may be possible traits in addition to the six traits that are not indicated in the path analysis that contributed to the tuber yield for agronomic traits.

5.2 Heritability and genetic advance

Heritability estimates in the broad sense were quite high due to high genetic variance estimates. Most of the characters studied were highly heritable. Obilana and Fakorede (1978), in a critical review of heritability stated that if a trait were strongly influenced by some environmental variations, its heritability would be low in a population. On the other hand, if the environmental influence is low or controlled, the same traits would tend to have high heritability. Higher heritability associated with high genetic advance of the mean [GAM] observed for characters like, emergence counts, number of tubers per plant and tube wait per plant indurations predominance of addition gene action this there is much scope for improving these characters based on direct selection similar of nodes per plant and number of stems per plant Desaiand Jaimini [1998] moderate heritability associated with moderate GAM was observed for number of leaves per plant which indicates that the trait is governed by both addition and non additive gene effects.

5.5 Principal component analysis

The use of principal component analysis gave us the possibility to have an idea of genetic divergence among the genotypes. In order to visualize patterns of character association involved in the correlation matrix, the principal component analysis was adopted (Kendal, 1965), so as to extract axes responsible for the genetic diversity among the genotypes. The axes extracted from a correlation matrix are independent of one another (Morishima et al, 1967).

The principal component indicated that plant height, number of tubers/plant, tuber weight and number of eyes/tuber were positive. This suggests that these four characters contributed maximum towards diversity. The greater diversity in the present materials is due to these five characters which will offer a good scope for improvement of yield through proper selection of parents genotypes for potato production.

CHAPTER SIX

6.1 Summary and Conclusion

Twenty genotypes of potato (*solanum tuberosum .L.*). Obtained from National Root crops research Institute, Potato Programme (NRCRI), Kuru, International centre for potato research, (CIP) United States Department of Agriculture, Netherlands and Kenya were evaluated for two seasons; 2005 and 2006 at Kuru- Jos Plateau in a complete randomized block design with three replications. Data were taken on agronomic traits and subjected to analysis of variance.

Mean performance differed significantly in the three years of evaluation for some traits, while for some others mean performances were not significantly different in the three years. Each trait exhibited a considerable range for its expression.

The coefficient of variation observed were generally moderate, the highest phenotypic coefficient of variance was observed for emergence counts 37.56% followed by average tuber weight 28.74%. The phenotypic variance components were consistently higher than the genotypic variances for virtually all traits. The magnitude of genotypic variances and coefficient of variation is suggestive that improvement is feasible via selection in these traits.

Emergence counts recorded the highest genotypic variance. This is particularly useful for a breeder who intends to breed for uniform growth in potato, and machine harvesting.

The genotypic mean square estimates for combined analysis were highly significant for agronomic traits. The genotype x year mean squares was not significant for all agronomic traits except maturity and tuber number indicating stability over the years. Mean square estimates for year was significant for all traits except plant posture and number of nodes/plant.

Based on Mahalanobis D^2 statistics, the genotypes were grouped into five clusters with cluster I having the maximum number of genotypes (5). Cluster III and V shows the highest inter-cluster difference 25.306 which implies that high heterotic offspring and wide spectrum of variability is expected in segregating generations of crosses involving the members of these groups.

Genetic correlations of tuber yield with the primary components of yield were highest for plant posture, signifying that genetic factors controlled the expression of these traits. Phenotypic and genotypic correlations were positive and significant for yield with plant height (0.6321), days to maturity (0.4420) and tuber number per plant (0.8434), indicating that selections based on phenotypes can be effective in improving these traits.

Path coefficient analysis indicated that most of the traits have negative indirect effects on tuber yield via average tuber weight. However a large positive indirect effect on tuber yield via plant height and number of main stems per plant was recorded.

Heritability estimates for the traits ranged from low to very high. The highest estimate of 96% was observed for tuber number/plant.

Principal component analysis also revealed that plant height, tuber number/plant, number of main stems and tuber weight were positive indicating that these characters contribute to maximum genetic diversity in the population.

The study showed that these genotypes: 396430.010, 375400.00 and Famosa were high yielding and can be successful in producing diverse and potentially useful sources of breeding materials. Characters such as plant height, maturity, emergence counts, number of eyes/tuber and tuber number/plant combine high heritability, high phenotypic coefficient variance, high genetic advance can be considered as good estimates of genetic gain to be expected from selection on phenotypic basis.

The presence of genetic variability for agronomic traits suggests that further improvement of these genotypes for agronomic traits can be achieved by hybridization and selection. However, traits that were negatively correlated, improving them simultaneously, will require a multi-trait index selection which will be the most efficient way to improve them.

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