Agro-morphological and genetic characterization of advanced potato (*Solanum tuberosum L.*) breeding lines in Mahikeng, South Africa

By

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Dissertation submitted in fulfilment of the requirements for the degree Master of Science in Crop Science at the North West University

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STUDENT NUMBER: 24410225

November 2021

ABSTRACT

One of the most important strategies for increasing crop productivity and improvement in potato yield output is the development and introduction of new cultivars. Phenotypic characteristics are the first aspects to consider in crop improvement and breeding as it demonstrates the relationship among genotypes. The study aimed to characterize advanced potato breeding lines (genotypes) using agronomic and morphological traits under Mahikeng growing conditions. Thirty-three potato genotypes obtained from the ARC-VIMP breeding programme were evaluated for agronomic and morphological traits under field conditions using a randomized complete block design with three replications across two seasons. The genotypes were planted during the 2019/2020 and 2020/2021 summer cropping seasons. Data were collected on 15 quantitative traits. The analysis of variance for 12 of the traits revealed a highly significant (P<0.0001) differences among the genotypes and it was not significant for 3 traits. Relatively high genotypic and phenotypic variance values were obtained for emergence percentage, plant height, number of leaves, leaf area, chlorophyll content, individual tuber weight and yield per plant. Plant height, number of leaves, branches and tubers, stem diameter, chlorophyll content, individual tuber weight, tuber length and yield per plant had a heritability of more than 80%. For the morpho-agronomic characters evaluated, cluster analysis revealed that there was variability among the 33 potato genotypes. The genotypes were classified into three primary clusters. Each cluster was subdivided into two sub-clusters: 1 and 2. The grouping helped to identify genotypes that share the same characteristics and that are closely related. Plant height, the number of stems, stem diameter and individual tuber weight had a strong positive correlation with the yield per plant. The first five principal components explained 71.21% of the variation, indicating that there are significant genetic differences between the genotypes which can be utilized for breeding purposes to improve these features.

Characteristics such as tuber shape, size and colour are important for the fresh market and are the key factors considered for the processing industry. The genotypes exhibited high diversity in growth habit, leaf texture, tuber shape, tuber colour, flesh colour, tuber distribution and tuber eye depth. The growth habit was placed into three groups, erect (21.2%), semi-erect (45.5%) and spread (21.2%). There was a wide variation in leaf texture, 3% was coarse- hairy, 3% was smooth/glossy, 12.1% was fine and hairy, 30.3% were fine and 51.5% were coarse. Tuber shape also showed wide variation as 3% was compressed-oblong, 6.1% was oblong, 6.1% long-oblong, 9.1% was round, 12.1% was obovate, 15.2% was compressed and 48.5% was elliptic. Genotypes showed variation in tuber colour, 6.1% was slightly dark cream, 15.2% dark cream, 39.4% was cream and 39.4% was light cream. Flesh colour also showed high variation, 3% was light cream, 6.1% was dark cream, 9.1% was yellow, 24.2% was white, 24.2% was light yellow and 33.3% was cream. There was a slight variation in tuber distribution with 12.1% being evenly distributed and 87.9% predominantly apical. Tuber eye depth showed moderate variation, 3% was deep, 24.2% were medium, 36.4% were protruding and 36.4% were shallow. The genotypes studied showed a great genetic variability which can be considered for crop improvement and breeding.

Keywords: agronomic, breeding, characterization, genotype, morphological, potato.

DECLARATION

I, Zinhle Charlotte Sambo, declare herewith that the dissertation titled: Agro-morphological and genetic characterization of advanced potato (*Solanum tuberosum L*.) breeding lines in Mahikeng, South Africa that I herein submit to the North-West University: is in fulfilment of the requirements for a degree, is my work, has not been submitted to any other university and has been language-edited.

ACKNOWLEDGEMENTS

- Firstly, I would like to thank God for his presence in my life. It is by his faithfulness, mercy and love that I have come thus far.

- I am most grateful to my supervisor, Dr S. Mavengahama for his guidance, support and valuable contribution that led to the success of the research project. I'm also appreciative that he was always available to assist whenever I needed help.

- I would like to thank my co-supervisor, Dr L. Matsaunyane and the ARC-VIMP for providing the necessary planting materials.

- I would also like to thank the Faculty of Natural and Agricultural Science for financial support of this project.

- I would extend many thanks to Mr Russell Mashile for assisting me with all the help I needed at the farm and transportation.

- My heartfelt thanks to my mother, Ms Rebecca Mamba for her continuous support and encouragement.

- My very special thanks to my partner, Mr Z.S Buthelezi for his support and words of encouragement.

- Lastly, special thanks to the Skhumba family for helping me with accommodation and taking me as their own when I had no safe place to stay.

I WILL FOREVER BE GRATEFUL AND GOD BLESS YOU!!!

DEDICATIONS

I dedicate this dissertation to my dearest mother, Ms Rebecca Mamba. She is my number one supporter and she believed in me more than I believed in myself. She is my source of inspiration and the pillar of my strength.

I also dedicate this dissertation to my lovely daughter, Zanokuhle Buthelezi whose presence has pushed me to strive for excellence even more.

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List of Abbreviations

FAO:	Food and Agricultural Organization
GA:	Genetic advnce
PCA:	Principal component analysis

CHAPTER 1

1.1 General Introduction

Potato (*Solanum tuberosum* L.) is one of the major non-grain food crops grown worldwide (FAO, 2019). It is the world's fourth-largest food crop after rice (*Oryza sativa* L.), wheat (*Triticum*) and maize (*Zea mays*). It is a member of the Solanaceae (nightshade) family, which includes tomato, pepper, eggplant, petunia and tobacco. Its cultivation started around 2400 years ago (Weisser, 2010), when it evolved from the poisonous ancestor of the plant nightshade. Potato evolved into its current form when human settlers of Peru managed to domesticate wild potatoes. From Peru with extensive research and the centuries of selective breeding, we now have access to over a thousand different types of potatoes that are grown around the world. In South Africa, potatoes came from Holland to provide food for mariners visiting the cape. The potato industry has since grown to become one of the important food providers in South Africa (DAFF, 2013).

Potatoes are used for both human and animal consumption with an estimated 85% of its dry matter made up of starch and the rest being protein. The crop is a source of low-cost energy for the human diet. Potatoes are a rich source of starch, vitamins C, B1 and minerals. A single potato contains carbohydrates (26g), fiber (2g), protein (3g), vitamin C (27mg), vitamin B6 (0.2mg), iron (1.1mg) and potassium (620mg) (USDA, 2019). It plays a great role in combating malnutrition with its important nutritional value. It is a versatile crop as it can be boiled, fried, baked, mashed and used in stews. It is also used as livestock feed, starch production, production of spirits and industrial alcohol. The total estimated area under potato production in the world is over 20 million hectares with a total production of 359 071 403 tonnes (FAOSTAT, 2020).

The top five countries producing potatoes in the world respectively are China (21.8%), India (14.3%), Ukraine (5.8%), Russian Federation (5.5%) and the United States (5.2%). In Africa, the major producers respectively are Egypt (19.9%), Algeria (17.8%), South Africa (9.7%), Morocco (6.5%) and Tanzania (4.1%). South Africa is ranked the 28th largest potato producer, supplying about 0.8% of the world's total production (FAOSTAT, 2020). South Africa's potato output has grown strongly over the past decades, from 1.2 million tonnes in 1990 to a record 2.5 million tonnes in 2020. In the same period, the potato farming area declined, from 63,000 ha to 52,000 ha but production expanded significantly notwithstanding the decline in hectares as a result of, amongst others, the introduction of new cultivars, an increase in the number of hectares planted under irrigation, better soil practises and chemical control of pest and diseases (PSA, 2016). Important to note is that South Africa is self-sufficient in the production of potatoes, and this is done on less than 1% of the land utilised for agricultural purposes. Most of the 532 farms growing potatoes are relatively large farms, increasingly under irrigation, with yields averaging around 34 tonnes per hectare (Potatoes South Africa, 2016).

According to Potatoes South Africa (PSA), potato production in South Africa takes place in 16 production regions with the 4 major regions, namely Limpopo, Eastern Free State, Western Free State and the Sandveld contributing to between 65%–70% of the total annual production. The main agro-ecological influences are climatic conditions and the availability of irrigation resources. In South African markets, 64% is consumed by informal and formal markets, 20% for processing, 8% for seed potatoes and 8% for exports. South Africa prides itself with a sophisticated seed potato industry which is empowered by the country's rapid rate of urbanization that is the processing sector which utilizes an estimated 400 000 tonnes of potatoes per year, mainly for frozen French fries and crisps.

Increased yield in potato production is ascribed to development and introduction of improved cultivars. The genetic improvement of potatoes, as one of the important cash crops, is essential. The availability of genetic variability makes crop improvement possible. According to Jindal *et al*. (2010), higher chances of improvement through selection are through wider genetic variability in traits. In breeding for genetic improvement, analysis of genotypes is essential which helps understand the genetic relationship of each genotype. Knowledge of genetic variability is of importance to plant breeders because proper management of variation can lead to improved performance of the plant (Welsh, 1990).

According to Cartea *et al*. (2002) as well as Balkaya and Ergun (2008), genetic diversity studies are used in breeding programs when developing varieties with good qualities and also in assessing the taxonomic relationship in different genotypes. Agro-morphological traits are also used to show the genetic relationships of genotypes which is helpful to the success of breeding.

1.2. Problem Statement

Genetic characterization of crops is important and necessary for providing adequate information on the characteristics of given genotypes which contribute to the optimal management of collections and selection. Documented information of appropriate understanding of the variation of new genotypes plays a part in selection and crop improvement strategies. Traits of given genotypes are subjected to environmental factors and their interactions. Advanced breeding lines are genotypes that are yet to be released as cultivars and are still undergoing further breeding and multi-environmental trials. There are no studies done to investigate and document the agronomical and morphological characteristics, similarities and differences on morphological characteristics of these new lines. Therefore, this study was conducted to evaluate and characterize agro-morphological traits of these breeding lines from the Agricultural Research Council potato breeding programme. It was important to note that our site (Molelwane farm) was one of several others in South Africa where these genotypes were tested. For this dissertation, only data from Mahikeng was used for analysis and write-up.

1.3. Justification

As one of the major food crops grown worldwide, the production and crop improvement strategies which include breeding programs become very essential for potatoes. The success of potato breeding programs is highly influenced by the identification of genetic diversity in the gene pool. Identification and characterization help to identify gaps in germplasm collection which is essential for crop conservation and improvement. According to Sudre *et al*. (2010) and Abdellatif *et al*. (2012), genetic improvement programs greatly rely on correct identification and characterization which also help in detecting duplicates in germplasm banks. As mentioned above, this study was intended to test new advanced breeding lines which have not been evaluated before. It was, therefore, necessary for this study to be conducted to identify and characterize these advanced breeding lines to confirm genetic differences using agronomical and morphological traits as well as to generate information on agronomic performance.

1.4. Research questions

- Are the breeding lines being evaluated genetically different according to morphological characteristics?
- Is the yield performance of these new breeding lines significantly different from each other and the check cultivars?

1.5. Aim

- The study aimed to characterize potato advanced breeding lines using agro-morphological traits under Mahikeng growing conditions.

1.6. Objectives

The objectives of the study were:

- To characterize the advanced breeding lines grown in Mahikeng using agro-morphological traits.
- To evaluate the yield and yield-related attributes of the advanced potato breeding lines.

1.7. Hypotheses

- H_0: There is no significant variation in the agro-morphological traits of the advanced breeding lines.

  H_a: There is significant variation in the agro-morphological traits of the advanced breeding lines.
- H_0: There is no significant difference in the yield and yield attributes of the advanced potato breeding lines.

  H_a: There is a significant difference in the yield and yield attributes of the advanced potato breeding lines.

CHAPTER 2

Literature review

2.1. Potato botanical description

Potato is a herbaceous plant from the Solanaceae family and belongs to the genus Solanum. The crop is an annual plant that is grown for its edible underground tubers that are used as a vegetable (Struik & Wiersema, 2001). It has a basic set of 12 chromosomes and is a tetraploid. The potato crop has fibrous roots and the tubers arise separately on stolons from the main underground shoot system. It has an angular stem that is branched and bears compound, alternate leaves up to 30 cm long. The flowers are produced in clusters or cymes and either yellow, white, red, blue, pink or purple with yellow stamens. The fruits are globular berries and contain poisonous alkaloids (Solanine) (Weisser, 2010). Winch (2006) reported that tubers of varieties with white flowers have white skins, while those varieties with coloured flowers tend to have pinkish skins. Potato is a cross-pollinated crop mostly by insects, however, a substantial amount of self-fertilization occurs as well.

2.2. Ecological requirements

2.2.1. Region

As cultivar choice is important, so is the seed quality and region planted in. The region is very important as it includes water and soil quality as well as climatic conditions. These qualities are essential for the successful growth of a cultivar. The success and profitability of potato seed production are greatly influenced by the region as performance differs from region to region. In South Africa, there are two planting times, the summer and winter planting which are different and cultivar performance varies with each planting time. This demonstrates that potato is not only influenced by cultivar but also the region planted in. If a region is not favourable, it comes with risks which include unfavourable temperatures that tend to induce pests and diseases. According to Hochmuth *et al*. (2001) and Pavlista (2002), unfavourable environmental conditions have led to malformations and defects if stress occurs during tuber initiation and early development. One of the defects that result from stress is the translucent ends which affect the market value of potatoes and cause profit loss.

The production region also influences water management such that in dryland systems potatoes are produced with supplementary irrigation during spring and early summer plantings in regions with a temperate climate as there are summer rainfalls. November and December are often avoided because of high temperatures combined with long day lengths which are unfavourable for planting. The potato originated from the South American region, where it is grown under short-day length, cool temperatures, high light intensity and relatively high humidity and most present-day varieties are adapted to the day-length conditions found in Europe (Levy & Veilleux, 2007; Silver, 2013). This means that for potato production a temperate climate is essential for optimal growth (du Plessis & Steyn, 2003).

Tuber initiation is greatly influenced by the day length which is directed by the photoperiod (Silver, 2013). Long days promote higher yield as they allow a longer period for photosynthesis and adequate translocation of assimilates to tubers (Levy & Veilleux, 2007). The adequate translocation of assimilates is important for the assimilation of the dry matter contents needed to produce quality produce for processing (Faulks & Griffiths, 1983). As the direction for storage of photosynthates changes at higher temperatures, a large amount of the dry matter produced is then stored in the leaves (Wolf *et al*., 1990). According to Haverkort (1982), when the potato crop is faced with temperature stress adequate water supply can be a good strategy to avoid such stress as it promotes cooling.

Potatoes are also sensitive to frost and can be damaged if temperatures go as low as 0 °C. According to the FAO (2008), optimum yields are obtained where average temperatures are in a range of 15 to 20 °C. Temperatures between 15 °C and 20 °C are essential in achieving good tuber formation and temperatures above 30 °C or below 10 °C inhibit good tuber formation. Soil temperature also plays a role in tuber initiation and development. According to FAO (2013) and DAFF (2014), the most favourable soil temperatures for planting potatoes are above 7 °C and below 21 °C, provided that the soil is suitably moist.

2.2.2. Soil

Soil is another important factor that affects the growth and quality of potatoes. The soil properties to consider include the soil pH and history of use. The composition affects plant nutrition, water absorption and exposure to diseases and pests (Graves, 2001; Silver, 2013). Potatoes can be grown in different soil types though the most suitable soil types are loamy and sandy loam soils with sufficient organic matter. Well-drained and aerated soils with a depth of at least 600 mm or 400 mm under irrigation, with a pH greater or equal to 5 are mostly suited for higher yields (du Plessis & Steyn, 2003; Black, 2008). It is important to consider soil compaction and aeration as they influence the gaseous exchange and can negatively affect tuber development if there is no sufficient oxygen for the tubers. For soils with poor soil aeration, the soil must be well prepared before planting and avoid disturbance after planting to reduce soil compaction (Lutaladio & Castaldi, 2009).

2.2.3. Water

Another essential factor that influences the growth, yield and quality of potatoes is water availability and supply. The water required for optimum growth differs with cultivars since they have different maturation periods and it also depends on soil type and climatic conditions. According to reports, the crop requires 500-700 mm of water per growing season (FAO, 2013). Soil water contents that are below 65% of field capacity harm tuber yield and quality (Geofrey *et al*., 2014). Most regions of production cannot meet the required soil water content for optimum yield and for that reason most regions require irrigation to avoid water stress. Water stress results in poor marketable yield, as water stress lowers tuber numbers per stem and average tuber weight. This is because with water stress some of the crop processes such as transpiration, carbohydrate translocation and production are compromised (Lynche *et al*., 1995; Pavlista, 2002).

Foti (1999) reported that in an evaluation of different cultivars, the drought-tolerant cultivars yielded good results without irrigation as they were hardly affected by water stress. Under adequate water supply, 85% of potential yield was obtained and the least tolerant cultivars only produced 71%. Potatoes grown for early production were sensitive to water stress, which affected the tuber yield and period of tuber maturation

(Foti, 1999). Theron (2003) reported that water stress also led to the decrease of intrinsic dormancy period of tubers after harvest. Water stress led to disorders such as the sugar-ends, which becomes visible after processing. As water stress affected tuber quality that then led to reduction of specific gravity and starch content despite the period of water stress (Haverkort, 1982; Iwama, 2008).

2.2.4. Fertilization

Fertilizer application influences the growth, plant morphology and yield of crops. According to Hawkins (1954), potato is known to be one of the most receptive crops to fertilisation and it is important to consider the amount of nutrients required for desired yields and quality. It is essential to consider optimum levels of fertiliser application, the correct time of application and the method of application. Both deficient and excessive application showed a negative impact on the growth and development of potatoes. Karenlampi and White (2009) along with Geofrey *et al* (2014) reported that deficiencies and excessive fertilizer application under high temperatures and poor water supply lead to the formation of brown centres and hollow hearts, which cause the tubers to have low specific gravity, have a darker colour and black spot bruising at harvest. According to Hamouz *et al*. (2005), excessive use of fertilizers showed a decrease in the sugar content which affect the quality of produce. Fertilizer application methods include banding, broadcasting and the row fertilizer method.

2.3. South African potato cultivars

For successful potato production, cultivar choice is one essential aspect as it influences the genetic potential for yield and tolerance to biological and environmental conditions. For potatoes, the quality of the propagation material plays a key role in to the realisation of the full potential of cultivars (PSA, 2016). Choice of cultivar is important for increasing potato production and meeting the requirements of the markets and consumers. According to PSA (2016), potato cultivars available in South Africa are divided into three groups according to their growth periods. There is a group of early growing cultivars that grow and reach maturity in less than 100 days and a popular early cultivar is the Vanderplank. The second group is the medium growing cultivar which grows and reaches maturity in 100 to 120 days. This type of cultivar is one of the most grown cultivars in South Africa and some of the popular cultivars on the market are BP1 and Up-to-Date. Together BP1 and Up-to-Date constitute almost 77% of the potatoes grown in the country. The third group of cultivars are the long growing cultivar that grow and reach maturity in longer than 120 days. Examples of long growing cultivars are Sackfiller, Late Harvest, Kimberley's Choice and Cedara. A study conducted by Potato South Africa (PSA) in 2017, reported that the most grown cultivars are Mondial at 38%, Sifra at 19.45% and Valor at 4.46%. Mondial is popular due to its high yield, excellent scab resistance and early maturity during a short day. Potatoes South Africa (2016) reported that BP1, Up-to-Date and VanderPlank are locally bred cultivars that were the most dominant about 15 years ago. The adoption of leading foreign cultivars which are Mondial and Sifra has lowered the production of old local cultivars.

According to Potatoes South Africa (2016), the potato farming sector is increasingly using foreign cultivars for their higher yields and resistance. Development of new improved cultivars is done through research programmes that evaluate and characterize different cultivars in different regions. Reports from PSA showed that there was a change in potato production which resulted in a decline in the number of potato producers. The production of potatoes under dry land conditions declined from almost 50% of the total hectares planted in 1990 to 19% in 2016 (PSA, 2016). Despite the decline in hectares planted yield increased from 21 tons to 43 tons per hectare in 2016. The increase in tons resulted from the availability of improved cultivars, the use of quality seed potatoes and the application of research results.

Since potato is a cool-season crop, it is planted in most regions in South Africa under a climate that is not suited for potato production. South Africa's maximum temperatures are normally higher than the optimal temperatures for potato growth. This results in the importance of cultivar evaluation which helps in selecting the best cultivars with high yields under the different climatic conditions. Most of the foreign cultivars that are currently grown in South Africa were initially evaluated and their growth performances observed and screened. The evaluation of potato cultivars has since then been an ongoing process that aims to increase potential cultivars that have adaptability under the regional climate conditions. The research results of every evaluation trial from around the country make it possible to analyse results and identify widely adapted high-yielding cultivars in different regions.

The main planting period for potatoes in the North West province is from August to September, with some growers extending planting to the middle of October. The second planting period is from mid-January to mid-February. According to an article published by North West Business (2017), North West supplies about 5.4% of South Africa’s potatoes.

2.4. Genetic diversity and variability

Genetic diversity refers to the range of various inherited features of a crop. Genetic diversity analysis is a critical component of potato and other crops’ improvement (Frankham, 2010; Govindaraj *et al*., 2015). A wider genetic diversity increases the likelihood of obtaining suitable genes for desired traits, as well as improved agronomic characteristics. Plant breeders benefit the most from genetic diversity evaluation since it makes it easier to choose excellent parents for crossing and reduces the number of unnecessary crosses (Carpentieri-Pípolo *et al*., 2003; Nkongolo, 2003). Mutations and/or migration are thought to have contributed to the genetic variation found in distinct populations. Morphological and molecular techniques can be used to estimate genetic distances across populations and the number of alleles per locus in populations to measure genetic diversity (Nkongolo, 2003).

Understanding the level of genetic diversity is critical for improving germplasm (Asare *et al*., 2010; Adewale *et al*., 2011; Huynh *et al*., 2013; Egbadzor *et al*., 2014; Ali *et al*., 2015; Gerrano *et al*., 2015). A large genetic foundation helps generate superior genotypes with desirable traits leading to high yield, whereas a small genetic base makes the crop susceptible to a variety of stressors (Singh, 2001; Kuruma *et al*., 2008). Furthermore, maximizing genetic resources could be useful for future introgression initiatives aimed at increasing genetic variety in breeding materials and increasing genetic gain in breeding programs (Huynh *et al*., 2013). Knowledge of genetic diversity is critical in breeding programs to build more efficient germplasm management, usage, fingerprinting and parent selection procedures (Frankel, 1989; Blakeney, 2002; Bucheyeki *et al*., 2009). Characterization of genotypes is essential to explore the genetic diversity among the accessions for desirable parental selections that form the basis for future improvement to support the development of high yielding cultivars.

For successful plant breeding and crop population development, genetic variability in breeding lines is critical. Understanding the degree of crop species diversity is critical since it serves as the foundation for crop selection. Plant breeders can report the impact of the environment on yield by determining variability in yield and yield components of different crop genotypes (Ahmed & Khaliq, 2007; Ullah *et al*., 2012). According to Gatti *et al*. (2005), direct selection only for higher yield cannot be reliable because many factors interact to determine crop yield. Separate yield components are essential because they are less influenced by the environment than yield itself and selection for yield components can be useful to acquire genotypes with better yield abilities (Gatti *et al*., 2005).

2.4.1. Importance of phenotypic and genotypic coefficients of variation

The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) calculations assist in estimating genetic variability in specific traits. When the PCV values for most of the traits are near or equal to the corresponding GCV, they indicate few environmental influences on trait expression. Small variations between PCV and GCV suggest little environmental influence and that additive gene effects play a role, implying that the traits may be improved by selection. The higher the GCV: PCV ratio, the more hereditary rather than environmental factors influenced the trait (Kaushik *et al*., 2007). High PCV shows that environmental influences have a large influence on these qualities, indicating low heredity. PCV and GCV estimations that are relatively similar suggest low environmental effects of the trait and consequently strong heritability. Selection has a good chance of increasing these characteristics.

2.4.2. Heritability and genetic advance

Heritability is helpful in genetic improvement because of its predictive role in indicating the reliability of the phenotypic value as a guide to breeding value (Falconer & Mackay, 1996). It gives proof of genetic control over a trait's expression as well as phenotypic reliability to forecast breeding value (Ullah *et al*., 2012). Heritability estimates are key genetic characteristics that influence how different crop genotypes are selected from a population (Rashwan, 2010). It also estimates which breeding method plant breeders can adopt and genetic advances that can be expected from selection (Ullah *et al*., 2012). According to Sesardic (2005), heritability is the proportion of phenotypic variation that results from genetic differences. Plant breeders use the estimation for selection of desirable characteristics as key for the improvement of these characteristics. In a broad sense, heritability is the total genetic variance that is part of the phenotypic variance that can be altered by genotypic influences (Dudley & Moll, 1969). According to Rashwan (2010) and Manggoel *et al*. (2012), the preponderance of additive gene action in the manifestation of traits is usually shown by high broad-sense heritability scores.

Holland *et al*. (2003) reported that heritability estimates are used to evaluate the expected response to selection for the development of quantitative traits that are regulated by multiple genes, have small additives, are dominant and interact with the environment. As a result, broad-sense heritability is defined as the ratio of total genetic variance to phenotypic variance (Riaz & Chowdhry, 2003). Breeders are focusing more on increasing crop production by estimating the heritability of yield and contributing components as well as variability. The heritability value of a characteristic is useful for determining the efficacy of phenotypic expression-based selection. Depending on the genotypes, broad-sense heritability could be high, medium or low in different crops under different circumstances (Ullah *et al*., 2013). Shahrokhi *et al*. (2013) reported that selection for traits with a heritability of 71-96 per cent or greater could be easier, as they imply a stronger link between genotype and phenotype, with less environmental influence on the phenotype. Due to increasing environmental impacts, it is difficult to make selections for traits with low heritability of less than 45 per cent. Furthermore, when combined with significant genetic progress, higher heritability has cumulative effects and results in a greater response to selection in the next generation (Songsri *et al*., 2008; Ahmed *et al*., 2013).

In a study conducted by Ogunniyan and Olakojo (2014), they reported that for genotypes with a high genetic diversity background, a high heritability was obtained. Characteristics with heritability of more than 80% imply that selection for these characteristics can be effective because there would be a substantial response to direct selection as reported by Shadakshari *et al*. (1995) as well as Singh (2001). Significant heritability combined with high genetic progress, according to Johnson *et al*. (1955) is an important element in determining the subsequent effect of selection. High values show that traits are simply inherited and that the heritability is most likely due to additive gene effects and that selection for these traits may be successful in early generations as reported by Al-Tabbal and Al-Fraihat (2011). Low heritability can also be produced by inbreeding, which reduces genetic variance, or by individuals being raised in a wide variety of contexts, which increases environmental variance.

According to Poehlman and Sleper (1995), plant breeders can use a better understanding of heritability and genetic progress to determine which selection approach is best for improving traits, forecast genetic gain from selection and the relative relevance of genetic impacts on yield plus its components for crop development. Furthermore, the most successful condition for selection for a given character is substantial genetic progress along with high heritability estimates (Malek *et al*., 2014). Estimates of heritability, on their own, do not provide information about projected gains in subsequent generations; they must be combined with estimates of genetic progress, or the change in mean value between successive generations (Shukla *et al*., 2006; Al-Tabbal and Al-Fraihat, 2011).

The genetic advance (GA) estimates are important in determining the type of gene action that controls the expression of a variety of polygenic features. GA values over a certain threshold indicate additive gene action, while GA values below that threshold indicate non-additive gene action (Singh & Narayanan, 1993). As a result, heritability estimates will be beneficial if they are accompanied by a high GA. According to Gashaw *et al* (2010), under one cycle of selection at a specific selection intensity, GA under selection is vital to consider in the improvement of characters in genotypic value for the development of new populations compared to the base population. Low or medium heritability and genetic advance usually indicate that the character is highly influenced by the environment. Although a breeder can increase a character by direct selection, when environmental impacts are substantial, the rate of development will be slow. Furthermore, the combination of heritability and genetic progress would aid breeders in making a speedy direct parental selection for desired characters.

2.5. Agro-morphological characterization

Potato varieties are propagated vegetatively to acquire desired phenotypic characteristics and it is therefore important not to overlook the development of inherent characteristics that include morphology, tuber solids and susceptibility to defects. Each producer should aim to acquire a variety with suitable quality and higher yields. Different methods are commonly used for the characterization of varieties including pedigree, morphology, agronomic performance, biochemical and molecular data

(Mohammadi & Prasanna, 2003). Agronomic and morphological characterization is the first step in the description and classification of plant genotypes (Smith & Smith, 1989). Observation and recording of morphological characters is the typical approach to different variety identification (Nováková *et al*., 2010). Morphological assessment is based on phenotypic characteristics of a plant species that determine diversity and similarity between and within populations. According to Hegde and Mishra (2009), morphological assessment is important in generating information for the identification of duplicates, selection of parents for genetic improvement studies and variety protection. Evaluating crops is mainly based on morphological traits that include quantitative and qualitative traits (Schut *et al*., 1997). Qualitative characterization usually does not require special facilities or procedures, they are easy and inexpensive. Quantitative traits are crucial in a breeding programme for genetic improvement of important traits such as high yield and quality. Liu and Furnier (1993) reported that quantitative traits are influenced by polygenes and have a tendency to vary according to change in environmental conditions due to the effect of genotype by environment interaction.

Morphological descriptors include leaf type, tuber shape and flower colour which can be analysed during different developmental stages of the crop. According to Franco *et al*. (2001), morphological markers are phenotypic characters such as flower colour, seed colour and shape, growth habits, pigmentation, texture, maturity, yield and pest and disease resistance. According to Fongod *et al.* (2012) accessions are best suited to be distinguished by morphological descriptors. The identification of individual varieties is essential at every stage of their production, breeding, registration, seed-production and testing processes to determine the distinctness of plants (Nováková *et al*., 2010). Morphological descriptors for potatoes include sprouting, along with agronomic characters such as plant height, leaf size and various features of the flowers and tubers.

According to Nováková *et al*. (2010), the approach of using morphological descriptors is successful in the process of distinctness, uniformity and stability (DUS) testing and is commonly applied by various researchers and authors. Solis *et al*. (2007) used cluster analysis to separate potato cultivars into different groups using morphological data. According to these researchers, the cultivars clustered into two major groups, for which the first group had semi-early vegetative phase and round tubers, with skins principally purple in colour and secondary white colour, distributed through all tuber or located around the eyes. The second group included potato cultivars with semi late vegetative phases and elongate tubers with dark purple skin. The stem of this group had angular sections that were green in colour and nodes that were reddish and purple.

Multivariate analyses such as bi-plot analysis, cluster analysis and principal component analysis (PCA) are used to analyse agronomic and morphological data to result in a meaningful interpretation and understanding of the variation of traits amongst varieties. The PCA identify plant traits contributing to the most observed variation among genotypes (Afuape *et al*., 2011; Ahmadizadeh & Felenji 2011) which help breeders to select parent lines. According to Lohani *et al*. (2012) along with Sinha *et al*. (2013), the PCA measures the importance and contribution of each component to the total variance. The analysis is important as it analyses groups of correlated variables representing one or more common domains. Cluster analysis forms groups of similar traits based on agronomical, morphological or molecular data. Cluster analysis is a multivariate method aiming at classifying a sample of subjects into different groups/clusters based on a set of measured variables (Cornish, 2007). According to Afuape *et al*. (2011), clustering describes the inherent variation in the population of crop genotypes. This analysis has been used by several researchers for characterization and crop identity study such as potato (Ahmadizadeh & Felenji, 2011; Arslanoglu *et al*., 2011); chilli, (Del *et al*., 2007); sweet potato (Afuape *et al*., 2011); rice (Sinha *et al*., 2013) and green vegetables (Denton & Nwangburuka, 2012).

2.5.1. Correlation analysis

Correlation analysis provides a better understanding of the genetic mechanism of crop production and yield that is highly useful in breeding programs. This is critical for evaluating whether the crop characteristics are heritable and genetically regulated for transmission to the next generation. It is important to understand the correlation of both agronomical traits and morphological traits. Knowledge and understanding of the relationship between yield and its contributing characteristics can help increase the efficiency of plant breeding selection (Lzge *et al*., 2006). According to Vendruscolo *et al*. (2016), when correlation studies are integrated with other analyses such as path analysis, efficiency and reliability of selection improve. In order to achieve an efficient response, the path analysis proposes identifying direct and indirect factors that are highly connected with the basic variable (Wright. 1921).

It allows for the partitioning of correlation coefficients into direct and indirect effects of many qualities on the dependent variable, which aids in the evaluation of cause-effect relationships and effective selection (Dewey & Lu, 1959). Characteristics that are quantitatively and of polygenic inheritance are extremely difficult to change directly in breeding. As a result, to improve these complex qualities, they must be broken down into simpler morphological, physiological and genetic components that may be easily analysed and evaluated. For successful selections in breeding programs, correlations between qualities are important. Positive correlations show that the changes in two variables are in the same direction, whilst negative correlations suggest that they are inversely related. When qualities have a positive correlation, it means that they were selected at the same time.

Several researchers have reported similar findings on the association of characters in potatoes. In a genetic diversity study, Gunel *et al*. (1991) evaluated potato genotypes and reported a highly positive and significant association between tuber yield with big tubers percentage and vegetative period. In another study, Aytac and Esendal (1996) reported that tuber yield showed a positive and significant association with average tuber weight, tubers per plant, big tuber percentage, but a significantly negative correlation with small tuber percentage. Yildirim *et al.* (1997) and Khayatnezhad *et al*. (2011) also evaluated potato genotypes and reported that yield components (tuber number and tuber weight) were associated with tuber yield but they indicated that tuber numbers were more important than average tuber weight. A study conducted by Haydar *et al*. (2009) showed that important characteristics like plant height, number of leaves per plant and tuber weight showed a positive association with tuber yield per plant. Positive association with plant height, number of leaves and tuber weight indicate that vegetative fresh and vigorous plant stature with more tubers produces more yield (Haydar *et al*., 2009).

Khayatnezhad *et al.* (2011) reported a stronger positive association between tuber yield and main stems per plant, plant tuber weight and plant height. These results showed that any positive increase in such characters will suffice and boost the tuber yield. A study conducted by Fekadu *et al.* (2013) suggested a positive correlation in tuber yield with plant height, biological yield and harvest index at both phenotypic and genotypic levels. The study also suggested a negative correlation with small tuber percentage and medium tuber percentage at genotypic and phenotypic levels. A negative correlation between two characters implies selection for improving one character will likely cause a decrease in the other character (Fekadu *et al*., 2013). Anoumaa *et al.* (2016) reported that total tuber yield showed a significant and positive correlation with plant height, total tuber numbers and percentage of marketable tubers.

Hossain *et al*. (1984) conducted an evaluation trial of sixteen exotic germplasm in their generation one at six different locations. The germplasm of the highest yield had 25.97 t/ha but was closely followed by the other six germplasm. The highest proportion of medium grade tubers (38-45 mm) was produced by three germplasm. Kabir *et al*. (1994) conducted evaluation trials at two locations to observe the yield potential of the local germplasm of potato. Results indicated that there was germplasm having reasonably good yield potential as the yields of the germplasm ranged from 8.10 to 22.00 t/ha despite their being infected with various virus diseases.

Luthra (2001) conducted a study of 29 germplasm which showed favourable response to selection for characters that include plant type, dormancy period, number of tubers, average tuber weight and plant vigour based on high heritability estimate and high genetic advance for tuber yield, average tuber weight, plant height and number of leaves suggested scope of improvement for these traits. Their study suggested characteristics like vigour, erect, tall with long and wider leaves, producing more tubers or average tuber weight, having shallow or medium eyes and oval or round regular shape were to be considered for improvement in potato. In a study with 28 hybrid lines, the results showed that there were significant variations among the progenies which indicated that there is a scope of selection for improved germplasm. Tuber yield ranged from 20.67 to 32.44 t/ha. Individual plants were selected from the progenies based on tuber yield and size, shape and colour of the tubers in the hill which would be evaluated in subsequent years for germplasm development (Anonymous, 2003).

An evaluation trial of twenty-six germplasm of potato was conducted by Masoodi (2010) for yield and yield attributing traits. Analysis of variance indicated significant differences among the germplasm, that should enable their use in future improvement programs. Five of the germplasm performed best in respect of yield and most of the yield attributing traits and could be utilized for commercial growing and hybridization programs for future improvement in the available germplasm resources. Nakitandwe *et al*. (2003) conducted a selection of high yielding potato germplasm from Standard International Field Trials (SIFT) at five different locations in Uganda. Phenotypic correlation showed that mean tuber weight and the number of tubers per plant had the highest correlation values and the multiple regressions indicated that these also retained in the regression equation across all locations, indicating that these were the most important components of tuber yield.

Ozkaynak *et al*. (2003) researched the correlation coefficients between tuber yield and 12 yield components, as well as the direct and indirect influences on yield in different potato germplasm. Tuber yield, plant height, node number, leaf length, leaf width, leaflet length, leaflet width, tuber number and average tuber weight all showed significant positive associations. The most critical components for tuber yield in potatoes were tuber number and average tuber weight, according to path coefficient analysis.

Bhagowati and Saikia (2003) conducted a study to investigate the relationship of character connection and path coefficients between yield and its five components in thirty true potato seed germplasm, comprising hybrids and open-pollinated populations. Tuber yield was found to be significantly and positively associated with plant height, primary branch number, leaf number, number of tubers per plant and average tuber weight in a correlation analysis. Because it exhibited a positive significant link with all four remaining yield components, plant height was recognized as an essential yield feature. A negative relationship was observed between tuber number and average tuber weight, indicating the necessity to break this link. The importance of tuber number and individual tuber weight was underlined by the path analysis since they had the highest direct effect on tuber yield. Plant height, primary branch number, and leaf number all had significant indirect effects on average tuber weight, showing that they are important in the selection process.

Tuber number had a negative indirect effect on yield via leaf number and average tuber weight, while tuber number had a negative indirect effect on yield via leaf number and average tuber weight. Roy and Singh (2006) conducted a correlation and path analysis investigation with eighteen potato (*Solanum tuberosum L.*) germplasm in four different conditions. The results showed a substantial positive relationship between quantitative features and overall tuber yield. Plant height, number of branches per tuber, number of tubers per plant and tuber output per plant have all been identified as factors in improving total tuber yield.

2.6. Summary of literature review

In conclusion, potato is a herbaceous plant from the Solanaceae family and belongs to the genus Solanum. For its successful production, cultivar choice is an important aspect as it influences the genetic yield potential. The choice of cultivar is important for increasing potato production and meeting the requirements of the markets and consumers. Varieties are propagated vegetatively to maintain desired phenotypic characteristics and it is therefore important not to overlook the development of inherent characteristics that include agronomy, morphology and tuber solids. Agronomic and morphological characterization is the first step in the description and classification of plant genotypes. Characterization is important as it generates information for the identification of duplicates, selection of parents for genetic improvement studies and variety protection. Genetic diversity analysis is a critical component of potato crop improvement and it reports the impact of the environment on yield by determining variability in yield and yield components of different crop genotypes.

CHAPTER 3

Morpho-agronomic characterization of advanced potato breeding lines

Abstract

As one of the most significant cash crops, potato improvement is important. One of the most important strategies for increasing crop productivity and improvement in potato output is the development and introduction of new cultivars. Agronomical traits demonstrate the genetic relationship of genotypes which is helpful to the success of breeding for improvement in potatoes. The study aimed to characterize advanced potato breeding lines (genotypes) using agronomic traits under Mahikeng growing conditions. Thirty-three potato genotypes obtained from the ARC-VIMP breeding were evaluated in a field for agronomic traits using a randomized complete block design with three replications across two seasons. The genotypes were planted during the 2019/2020 and 2020/2021 summer cropping seasons. Data were collected on 15 quantitative traits. The analysis of variance for 12 traits revealed highly significant ($P<0.0001$) differences among the genotypes and no significance for 3 quantitative traits. Relatively high genotypic and phenotypic variance values were obtained for emergence percentage, plant height, number of leaves, leaf area, chlorophyll content, individual tuber weight and yield per plant. Plant height, number of leaves, branches and tubers, stem diameter, chlorophyll content, individual tuber weight, tuber length and yield per plant had a heritability of more than 80%. For the agronomical characters evaluated, cluster analysis revealed that there was variability among the 33 potato genotypes. The genotypes were classified into three primary clusters using cluster analysis. Each cluster was subdivided into two sub-clusters: 1 and 2. The grouping helped to identify genotypes that share the same characteristics and that are closely related. Plant height, number of stems, stem diameter and individual tuber weight had a strong positive correlation with the yield per plant. The first five principal components explained 71.21% of the variation in the current study, indicating that there is significant genetic variation among genotypes that can be utilized for breeding reasons, according to the principal component analysis. The analyzed traits revealed a great deal of genetic variety, which can be used to improve these features through breeding.

Keywords: agronomic, correlation, genotype, traits, tuber.

3.1. Introduction

Identification of genotypes is through agronomic and morphological characterization as the first step in the description and classification of plant genotypes (Smith & Smith, 1989). Genotypes can easily be differentiated visually by physically observing morphological characteristics. Agronomic parameters and morphological characters have been used successfully for the selection of desirable traits in various other crops. Direct useful information about specific traits of agronomic performance and genetic relationships are provided by agronomic and morphological characterization which promote the efficient utilization of genotype collections (Pagnotta *et al.*, 2009; Khoury *et al.*, 2010; Elameen *et al.*, 2011; Laurie *et al.*, 2013). Action strategies for developing new cultivars are defined by the knowledge of agronomic characteristics, as agronomic characterization of genotypes is one of the first steps of a breeding program. According to Schuch and Bird (1994), agronomic characteristics have been the centre of breeding programs. In potatoes, characteristics such as tuber shape, size (tuber length and diameter) and handling are important for the fresh market industry and are the key factors considered for the processing industry.

The sustainable maintenance and increased use of crop genetic resources are through genotype characterization (Sergio & Gianni, 2005). Characterization results in a successful breeding programme by identifying heritable characteristics and monitoring the enhanced utilisation of genotypes (Upadhyaya *et al*., 2008). Knowledge and understanding of genetic diversity enable plant breeders to use particular accessions for parental selection and widen the genetic base of the crop. According to Nagalakshmi *et al.* (2010), a successful breeding programme is associated with genotypes of high genetic diversity. Genotypes with high genetic diversity and variation are used for crop improvement because of their wide genetic pool. Agronomic characterization is also used to reveal the extent of genetic relatedness and similarities in phenotype characteristics indicate genetic similarity of genotypes (Kisua *et al*., 2015). Agronomic characteristics have been successfully used for the selection of desirable traits and they also contributed to the understanding of the association between yield and its component traits in order to facilitate effective selection for yield improvement (Al-Tabbal & Al-Fraihat, 2012; Manggoel *et al*., 2012).

3.2. Aim, Objectives and Hypotheses

3.2.1. Aim

- The study aimed to characterize advanced potato breeding lines using agronomic traits under Mahikeng growing conditions.

3.2.2. Objectives

The specific objectives were:

- To morphologically characterize the advanced breeding lines grown in Mahikeng using agronomic traits.
- To evaluate the yield and yield-related attributes of the advanced potato breeding lines.

3.2.3. Hypotheses

- H_o: There is no significant variation in the agronomic traits of the advanced breeding lines.

  H_a: There is significant variation in the agronomic traits of the advanced breeding lines.
- H_o: There is no significant difference in the yield and yield attributes of the advanced potato breeding lines.

  H_a: There is a significant difference in the yield and yield attributes of the advanced potato breeding lines.

3.3. Materials and methods

3.3.1. Site description

The potato genotypes were planted at the Molelwane Farm, which is part of the North-West University at Mahikeng campus, in South Africa. The geographic coordinates of Molelwane farm are S25°48’00’’, E25°38’21’’. Planting was done in an open field. Mahikeng's climate is a local steppe climate. The temperature average is 23.7 °C. The average annual rainfall is 450 mm. Precipitation is lowest in July, with an average of 2 mm. Most of the precipitation falls in January, averaging 108 mm. At an average temperature of 23.7 °C, November to January being the hottest months of the year.

June and July are the coldest months, with temperatures averaging 11.3 °C. Summer temperatures range between 22 ºC and 35 ºC and winter brings with it dry, sunny days and chilly nights. The average winter temperature is 16 ºC but can range from 2 to 20 ºC in a single day.

3.3.2. Planting material used

The genotypes used in this study were obtained from the Agricultural Research Council of South Africa Potato Breeding Programme. They were advanced breeding lines that were at the stage of multi-environment testing and North-West University Mahikeng Campus was one of the testing sites. For proprietary reasons the specific information about the identification of the genotypes cannot be listed in this dissertation. We coded GenoA for the first genotype to GenoA to GenoGG for the last one.

Table 3.1. Planting materials used.

Geno	NR	INCLUSIONS	CULTCODE
GenoA	F01	Vanderplank	
GenoB	F03	BP1	
GenoC	F04	Mondial	
GenoD	F05	Hertha	
GenoE	F06	Mnandi	
GenoF	F07	Up-to-date	
GenoG	F08	Lanorma	
GenoH	F09	13-0695-056	2880
GenoI	F10	13-0695-069	2885
GenoJ	F12	13-0695-148	2902
GenoK	F15	13-0696-001	2913
GenoL	F16	13-0696-003	2915
GenoM	F17	13-0696-008	2916
GenoN	F19	13-0696-066	2887
GenoO	F20	14-0479-002	2636
GenoP	F21	14-0479-006	2640
GenoQ	F22	14-0479-008	2642
GenoR	F23	14-0708-001	2669
GenoS	F27	14-0708-009	2623
GenoT	F28	14-0708-010	2624
GenoU	F29	14-0708-015	2629
GenoV	F30	14-0708-016	2630
GenoW	F31	14-0709-003	2633

Geno	NR	INCLUSIONS	CULTCODE
GenoX	F33	15-0720-006	2681
GenoY	F34	15-0720-047	2722
GenoZ	F35	15-0720-068	2743
GenoAA	F36	15-0720-075	2750
GenoBB	F37	15-0721-003	2756
GenoCC	F38	15-0721-045	2798
GenoDD	F39	15-0721-059	2812
GenoEE	F40	15-0722-021	2844
GenoFF	F41	15-0724-003	2871
GenoGG	F42	15-0724-007	2874

3.3.3. Trial establishment and management

Thirty-three (33) genotypes were planted during the 2019/2020 and 2020/2021 summer cropping seasons. Soil analysis was done before planting to determine the type, fertility status and pH of the field. The field was ploughed by disking to prepare a fine seedbed and destroy weeds. Each replication had thirty-four plots, with 1 m spacing between rows and 30 cm between plants in the same row. Each plot had 30 seed tubers planted, which were placed at a depth of 20 cm and ridged to a height of 20-25 cm from the soil surface after 5 weeks of planting. The potatoes were grown under typical conditions of the region with irrigation, using a sprinkler system. NPK (3:2:1) fertilizer was applied before planting at a rate of 220 kg/ha and top-dressing of limestone ammonium nitrate (LAN (28%N) was applied 5 weeks after planting at a rate of 120 kg/ha.

Table 3.2. Chemical properties of the field soil

Chemical property	Value
P (mg/L)	39
K (mg/L)	262
Ca (mg/L)	704
Mg (mg/L)	268
Exch. Acidity (cmol/L)	0.07
Total cations (cmol/L)	6.46
Acid sat. %	1
pH (KCl)	5.96
Zn (mg/L)	4.7
Mn (mg/L)	36
Cu (mg/L)	1.1

3.3.4. Experimental design and layout

The study was laid out in a randomized complete block design with three replications, with thirty-three potato genotypes. A spacing of 1 m was maintained between rows and the potato seeds were placed 30 cm apart within the rows. Thirty potato tubers of each of the 33 genotypes were planted in each replication.

3.3.5. Data collection

PARAMETERS

Data for agronomic and yield atributes were recorded on five randomly selected plants from each plot as per the descriptors reported by Huaman *et al*, 1977 and Mackay *et al*, 1985.

The following quantitative data were recorded:

3.3.5.1. Agronomic data

- Days to emergence.

  The date of emergence was observed and recorded when 50% of the plants germinated.

- Emergence percentage.

  The emergence percentage was calculated by recording the number of plants that emerged from the soil divided by the number of seeds planted and multiplied by 100.

- Plant height (cm).

  Plant height was measured by a measuring tape from the ground level to the tip of the highest leaf. It was measured every two weeks.

- The number of leaves, the number of stems per plant, the number of branches per plant and number of tubers per plant were counted manually. Number of leaves, stems per plant and branches per plant were counted every two weeks and number of tubers per planted were counted after harversting.

- Stem diameter and tuber diameter (mm).

These were measured using a Vernier Calliper. Stem diameter was measured every two week and tuber diameter was measured after harvesting.

- Chlorophyll content.

Chlorophyll content was measured with a CCM-200 plus chlorophyll content meter. It was measure every two weeks.

- Leaf area (cm^2)

The leaf length and leaf width were measured every two weeks, ten leaves were were measured in five plants making a total of fifty leaves. The leaf area was calculated from a formula described by Saxena and Singh (1965):

$$LA= LL*LW*0.75$$

Where:

- LL-leaf length
- LW-leaf width
- 0.75- is a leaf area constant coefficient

3.3.5.2. Yield attributes parameters

- Tuber weight (g).

It was measured using a digitally accurate analytical electronic balance laboratory weighing scale. The data was collected at harvesting.

- Yield per plant (g).

Yield per plant was calculated by the total weight of tubers in five sample plants and divided by 5. The data was collected at harvesting.

- Yield per plot.

  Yield per plot was calculated from the total weight of tubers of all plants in the net plot. The data was collected at harvesting.

- Yield per hectare (t).

  Yield per hectare was calculated from the yield per plot and converted to tonnes. The data was collected at harvesting.

3.3.5. Statistical analysis and data presentation

An analysis of variance (ANOVA) was performed on all variables to determine the significance of differences between means of genotypes using the statistical package (SAS version 9.4, 2021). Where the F-test detected significant treatment differences, the means were separated using the Tukey's Honestly Significant difference test at a 5% significance level. Results are presented in charts, tables and graphs.

3.3.5.1. Estimation of genetic variance components

The mean square error (MSE) and phenotypic variances were estimated as per Johnson *et al*. (1955) as well as Syukur and Rosidah (2014). The mean square error (MSE) was considered as error variance (σ^2_e). Genotypic variances (σ^2_g) were derived by subtracting MSE from the genotypic MS and dividing by the number of replication multiplied by the number of seasons as shown below:

$$\text{Genotypic variance, } \sigma^2_g = \frac{\mathrm{GMS} - \mathrm{MSE}}{\mathrm{rs}}$$

Where,

GMS = Genotypic mean square

MSE = Mean square Error

r = Number of replication

s = Number of seasons

The phenotypic variances (σ^2_p), were derived by adding genotypic variances (σ^2_g) with the error variances (σ^2_e), as given by the following formula:

Phenotypic variance, $\sigma^2_p = \sigma^2_g + \sigma^2_e$

i. Estimation of genotypic and phenotypic co-efficient of variation

Genotypic and phenotypic co-efficient of variation was calculated by the formula suggested by Singh and Chaudhary (1985);

Genotypic co-efficient of variation (GCV) = $\frac{\sqrt{\sigma_g^2}}{\mathrm{x}} * 100$

Where, σ^2_g = Genotypic variance

x =Population mean

Similarly, the phenotypic co-efficient of variation was calculated from the following formula:

Phenotypic co-efficient of variation (PCV) = $\frac{\sqrt{\sigma_p^2}}{\mathrm{x}} * 100$

Where, σ^2_p= Phenotypic variance

x = Population mean

ii. Estimation of heritability

Broad sense heritability was estimated by the following formula, suggested by Johnson *et al*. (1955) as well as Allard (1960)

Heritability in a broad sense, $h^2{}_b = \frac{\sigma_g^2}{\sigma_p^2} * 100$

Where, $h^2{}_b$ = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p= Phenotypic variance

iii. Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated using the formula suggested by Johnson *et al*. (1955).

$$\text{Genetic advance, GA} = \frac{K*\sqrt{\sigma_p^2} * \sigma_g^2}{\sigma_p^2}$$

Where, K = Selection differential, the value which is 2.06 at 5% selection,

$\sigma^2{}_p$ = Phenotypic variance and

$\sigma^2{}_g$ = Genotypic variance.

Genetic advance as percentage of mean was calculated using the formula suggested by Johnson *et al*. (1955) as follows: Genetic advance (% of mean) = $\frac{\text{Genetic advance}}{\text{Population mean}} * 100$

3.3.5.2. Multivariate analysis

Mean data for each character was subjected to multivariate analysis methods, which is cluster analysis, correlation analysis and principal component analysis (PCA), using the statistical package (XLSTAT, 2021).

i. Cluster analysis

Cluster analysis was done to form groups of similar genotypes based on agronomical traits. Genotypes were divided into groups based on a data set into some number of mutually exclusive groups.

ii. Correlation coefficient analysis

Pearson correlation coefficient analysis was performed to identify any associations between traits.

iii. Principal component analysis (PCA)

Principal component analysis is one of the multivariate techniques to determine the interrelationships among several characters and can be done from the sum of squares and product matrix for the characters. Principal components were computed from the correlation matrix and genotypic scores were obtained for the first component and succeeding components with latent roots greater than unity (Jager *et al*. 1983).

3.4. RESULTS

The agronomic performance of 33 genotypes of potato was investigated under Mahikeng growing conditions and the findings are presented in this section.

3.4.1. Agronomic characterization of potato genotypes

i. Days to emergence

Agronomic characteristics of 33 potato genotypes are shown in Table 3.3 and the number of days to emergence was significantly affected by the genotypes of potatoes of $P<0.01$. Among the genotypes studied GenoK and GenoO had the lowest average days to emergence (15.0), these were followed by GenoBB, GenoR, GenoQ and GenoL (15.33). GenoAA (18.00) and GenoH (17.83) had the highest number of days to emergence while the rest of the genotypes ranged from 15.50 to 17.33. The phenotypic coefficient (14.31) was higher than the genotypic coefficient (11.49) of variation and the character of days to emergence showed a moderate estimate of broad-sense heritability (64.45) along with a moderate genetic advance in per cent of the mean (19.02) as shown in Table 3.5.

ii. Emergence percentage

The analysis of variance showed that the differences in the emergence percentage of the potato genotypes were not statistically significant ($P>0.05$) as shown in Table 3.3. Among the genotypes studied GenoB (99.5%) and GenoF (99.5%) had the highest average emergence percentage, followed by GenoW (99.0%) and GenoY (98.83). The lowest emergence percentage was recorded in GenoU (81.17), GenoGG (82.67) and GenoAA (82.83), while the rest of the genotypes ranged from 84.33% to 97.17%. The phenotypic coefficient (18.61) was higher than the genotypic coefficient (12.85) of variation and the character showed a medium estimate of broad-sense heritability (47.70) along with a moderate genetic advance in per cent of the mean (18.31) as shown in Table 3.5.

iii. Plant height

Highly significant ($P<.0001$) differences amongst genotypes height were observed (Table 3.3). Among the genotypes studied GenoF (47cm), GenoE (46.27cm), GenoY

(43.68cm) had the highest average and were the tallest. Genotypes with the lowest plant height were GenoBB (26.93cm), GenoCC (27.17cm) and GenoDD (28.80cm) while the rest of the genotypes ranged from 29.70cm to 42.70cm. GenoBB was the shortest. The phenotypic coefficient (32.99) was higher than the genotypic coefficient (31.45) of variation and the character showed a high estimate of broad-sense heritability (90.84) along with a high genetic advance in per cent of the mean (61.83) as shown in Table 3.5.

iv. Number of leaves

Potato genotypes studied showed a high significant (P<.0001) difference in the number of leaves (Table 3.3). GenoE (272.50), GenoF (242.67), GenoQ (230.83) were the highest. Genotypes with the lowest average number of leaves were GenoAA (112.50), GenoCC (122.00) and GenoS (128.17) while the rest of the genotypes ranged from 132.67 to 222.33. The phenotypic coefficient (52.97) was higher than the genotypic coefficient (48.89) of variation and the character showed a high estimate of broad-sense heritability (85.18) along with a high genetic advance in per cent of the mean (93.08) as shown in Table 3.5.

v. Number of stems

There were high significant (P<.0001) differences amongst genotypes for the number of stems (Table 3.3). Genotypes with the highest average number of stems were GenoF (4.67), GenoC and GenoL (4.50), GenoT (4.33) were the highest. Genotypes with the lowest average number of stems were GenoM (2.67), GenoJ and GenoO (2.83) and GenoBB, GenoS, GenoDD (3.00) while the rest of the genotypes ranged from 3.17 to 4.00. The phenotypic coefficient (41.04) was higher than the genotypic coefficient (33.06) of variation and the character showed a moderate estimate of broad-sense heritability (64.87) along with a high genetic advance in per cent of the mean (54.93) as shown in Table 3.5.

vi. Stem diameter

A highly significant variation (P<.0001) was recorded in stem diameter (Table 3.3). Potato genotypes GenoJ (10.67 mm), GenoO (10.65 mm), GenoY (10.23 mm) had the thickest diameter. Genotypes with the less thickness stem diameter were GenoBB and GenoCC (5.35 mm), GenoDD (5.97 mm) and GenoEE (7.38 mm) while the rest of the genotypes ranged from 7.38 mm to 10.13 mm. The phenotypic coefficient (39.17) was higher than the genotypic coefficient (37.24) of variation and the character showed a high estimate of broad-sense heritability (90.41) along with a high genetic advance in per cent of the mean (73.05) as shown in Table 3.5.

vii. Number of branches

Highly significant differences (P<.0001) were recorded in the average number of branches (Table 3.3). GenoE (7.17), GenoN (6.83), GenoK (6.17) were the highest. Genotypes with the lowest number of branches were GenoAA and GenoD (1.00), GenoW and GenoB (1.33) and GenoU and GenoS (1.67) while the rest of the genotypes ranged from 2.00 to 5.67. The phenotypic coefficient (132.84) was higher than the genotypic coefficient (121.76) of variation and the character showed a high estimate of broad-sense heritability (84.01) along with a high genetic advance in per cent of the mean (230.24) as shown in Table 3.5.

viii. Leaf Area

The analysis of variance showed that the differences in the leaf area of the potato genotypes were statistically significant (P<.0001) as shown in Table 3.3. Among the genotypes studied GenoGG (34.20 cm^2), GenoFF (31.46 cm^2) and GenoJ (30.80 cm^2) recorded the highest leaf area. Genotypes with the lowest leaf area were GenoD (17.71 cm^2), GenoS (18.77 cm^2) and GenoE (20.11 cm^2) while the rest of the genotypes ranged from 20.31 cm^2 to 29.99 cm^2. The phenotypic coefficient (41.76) was higher than the genotypic coefficient (36.80) of variation and the character showed a moderately high estimate of broad-sense heritability (77.64) along with a high genetic advance in per cent of the mean (66.89) as shown in Table 3.5.

ix. Chlorophyll content

High significant variation (P<.0001) was observed in chlorophyll content among the genotypes studied as shown in Table 3.3. Potato genotypes with the highest chlorophyll content were GenoD (28.35), GenoAA (24.19) and GenoP (23.65) and genotypes with the lowest chlorophyll content were GenoH (11.00), GenoB (12.62) and GenoCC (14.33) while the rest of the genotypes ranged from 14.75 to 23.59. The phenotypic coefficient (52.97) was higher than the genotypic coefficient (48.05) of variation and the character showed a high estimate of broad-sense heritability (82.30) along with a high genetic advance in per cent of the mean (89.92) as shown in Table 3.5.

Table 3.3: Agronomical characteristics of 33 potato genotypes

Geno	**D_E**	**E.P**	**Height**	**No. leaves**	**No. stem**	**Stem Dia**	**Branch**	**L Area**	**Chlo con**
GenoA	17.00	95.00	29.70	132.70	3.50	7.38	2.63	22.43	17.57
GenoB	17.00	99.50	36.20	214.70	4.00	8.32	1.33	22.70	12.62
GenoC	16.17	88.30	42.70	180.30	4.50	9.43	2.17	21.60	21.92
GenoD	16.67	94.00	39.50	160.80	4.00	7.80	1.00	17.71	28.35
GenoE	16.50	90.50	46.30	272.50	4.00	7.93	7.17	20.11	22.14
GenoF	16.17	99.50	47.00	242.70	4.67	8.61	3.33	21.55	20.98
GenoG	16.67	96.80	38.70	152.70	3.33	9.63	3.17	23.07	16.18
GenoH	17.83	88.70	33.20	170.00	3.50	9.16	2.33	29.99	11.01
GenoI	15.83	91.20	32.80	154.60	3.17	9.63	3.83	28.01	20.34
GenoJ	17.00	92.20	34.50	185.30	2.83	10.67	3.67	30.80	15.07
GenoK	15.00	91.70	37.10	206.00	3.50	8.63	6.17	25.09	17.76
GenoL	15.33	88.30	41.10	222.30	4.50	7.41	4.67	24.74	17.45
GenoM	15.50	92.80	36.30	197.20	2.67	8.53	4.33	22.54	19.63
GenoN	17.17	97.20	38.40	156.80	3.33	8.06	6.83	23.85	16.47
GenoO	15.00	96.70	40.90	169.70	2.83	10.65	5.50	21.92	22.39
GenoP	16.50	84.30	39.10	167.50	3.83	10.13	2.83	29.12	23.65
GenoQ	15.33	95.70	38.10	230.80	3.33	9.40	3.50	20.31	15.13
GenoR	15.33	90.00	34.40	161.30	3.50	8.61	2.33	27.81	19.34
GenoS	16.17	87.70	34.70	128.20	2.83	8.26	1.67	18.77	23.59
GenoT	16.17	96.70	37.80	166.50	4.33	9.05	2.00	20.53	19.79
GenoU	17.33	81.20	34.00	176.00	3.60	8.87	1.67	23.38	15.93
GenoV	16.33	96.20	35.00	144.20	3.67	8.72	2.17	22.97	21.54
GenoW	16.67	99.00	37.20	190.00	3.67	7.67	1.33	23.99	18.64
GenoX	16.00	91.80	35.90	190.00	3.17	8.84	2.33	25.40	19.88
GenoY	16.83	98.83	43.70	174.80	3.67	10.23	3.50	27.93	16.59
GenoZ	16.83	94.00	34.10	197.00	3.67	8.20	5.67	28.10	16.11
GenoAA	18.00	82.80	39.30	112.50	3.67	9.85	1.00	26.68	24.19
GenoBB	15.33	88.70	26.90	181.80	3.00	5.35	5.67	23.11	16.61
GenoCC	16.67	85.70	27.20	122.00	3.17	5.36	3.17	23.84	14.33
GenoDD	17.17	87.80	28.80	139.50	3.00	5.97	2.83	24.49	22.31
GenoEE	15.50	91.20	33.40	167.30	3.33	7.38	4.67	23.80	14.75
GenoFF	17.33	85.00	36.90	165.00	4.00	8.45	2.67	31.46	21.53
GenoGG	17.17	82.70	37.10	148.70	3.67	9.46	2.33	34.20	23.13
p- value	0.0031	0.3672	<.0001	<.0001	0.0026	<.0001	<.0001	<.0001	<.0001
Tukey's HSD	3.12^{**}	$27.51^{n/s}$	8.16^{***}	79.18^{***}	1.93^{**}	2.31^{***}	3.93^{***}	14.45^{***}	9.45^{***}
CV	8.52	13.46	9.99	20.39	24.25	12.15	53.11	19.74	22.28
MSG	3.88	163.76	134.69	7437.34	1.51	10.27	16.86	152.39	86.24

Geno	D_E	E.P	Height	No. leaves	No. stem	Stem Dia	Branch	L Area	Chlo con
MSE	1.96	151.82	13.36	1257.77	0.75	1.07	3.11	41.87	17.91
Mean	16.41	91.56	36.6	173.9	3.56	8.53	3.32	32.77	18.99

Geno-Genotype, D_E-Days to emergence, E_P -Emergence Percentage (%), Height-Plant height (cm), No. Leaves-Number of leaves, No. stem-number of stem, Stem Dia- Stem diameter (mm), No. branch-Number of branches, L Area-Leaf Area (cm^2), Chlo con-Chlorophyll content, HSD-Honesty Significance Difference, CV-Covariance Variation, MSG-means square of genotype, MSE-means square error.

x. Number of tubers

There were high statistically significant (P<0.0001) differences in the average number of tubers per plant (Table 3.4). Breeding line GenoL (12.33), GenoM and GenoK (11.33) as well as GenoE and GenoCC (11.00) were the highest. Breeding lines with the lowest number of tubers were GenoAA (4.50), GenoA (5.00) and GenoD (5.67) while the rest of the genotypes ranged from 6.17 to 10.83. The phenotypic coefficient (58.41) was higher than the genotypic coefficient (54.20) of variation and this character showed a high estimate of broad-sense heritability (86.10) along with a high genetic advance in per cent of the mean (103.75) as shown in Table 3.5.

xi. Tuber weight

The differences in the tuber weight of the potato genotypes were high statistically significant (P<.0001) as shown in Table 3.4. Potato genotypes GenoC (142.55g), GenoAA (139.76g), GenoQ (131.35g) were the highest. Genotypes with the lowest individual tuber weight were GenoCC (40.83g), GenoBB (62.82g) and GenoH (66.06g) while the rest of the genotypes ranged from 70.79g to 122.70g. The phenotypic coefficient (58.76) was higher than the genotypic coefficient (53.93) of variation and this character showed a high estimate of broad-sense heritability (84.23) along with a high genetic advance in per cent of the mean (102.11) as shown in Table 3.5.

xii. Tuber length

Potato genotypes studied showed highly significant (P<.0001) differences in the tuber length (Table 3.4). Breeding lines with the highest tuber length were GenoV (8.18cm), GenoC (7.97cm) and GenoU (7.77cm). Breeding lines with the lowest tuber length were GenoCC (4.78cm), GenoBB (5.27cm) and GenoDD (6.17cm) while the rest of the genotypes ranged from 6.43cm to 7.65cm. The phenotypic coefficient (25.11) was higher than the genotypic coefficient (23.67) of variation and this character showed a high estimate of broad-sense heritability (88.86) along with a high genetic advance in per cent of the mean (46.03) as shown in table 3.5.

xiii. Tuber diameter

Highly significant (P<.0001) differences were recorded among the studied potato genotypes for tuber diameter (Table 3.4). Potato genotypes studied GenoQ (5.87cm), GenoAA (5.85cm) and GenoG (5.62cm) were the highest. Genotypes with the lowest tuber diameter were GenoCC (4.23cm), GenoH (4.59cm) and GenoZ (4.70cm) while the rest of the genotypes ranged from 4.67cm to 5.62cm. The phenotypic coefficient (20.15) was higher than the genotypic coefficient (17.55) of variation and this character showed a moderately high estimate of broad-sense heritability (75.85) along with a high genetic advance in per cent of the mean (31.53) as shown in table 3.5.

xiv. Number of eyes

The analysis of variance showed that the differences in the number of eyes of the potato genotypes were statistically significant (P<0.05) as shown in Table 3.4. Among the genotypes studied GenoR (8.83), GenoEE (8.67) and GenoI (8.17) were the highest. Genotypes with the lowest number of eyes were GenoN (4.33), GenoL (4.83) and GenoK (5.00) while the rest of the genotypes ranged from 5.33 to 8.00. The phenotypic coefficient (46.69) was higher than the genotypic coefficient (37.15) of variation and this character showed a moderate estimate of broad-sense heritability (63.31) along with a high genetic advance in per cent of the mean (60.99) as shown in Table 3.5.

xv. Yield per plant

The yield per plant showed a high significant variation (P<.0001) among potato genotypes (Table 3.4). Breeding lines GenoC (924.65g), GenoL (835.33 g) and GenoK (792.74 g) were the highest. Breeding lines with the lowest yield per plant were GenoCC (283.74 g), GenoBB (313.05 g) and GenoH (383.34 g) while the rest of the genotypes ranged from 409.66 g to 745.92 g. The phenotypic coefficient (66.63) was higher than the genotypic coefficient (60.19) of variation and this character showed a high estimate of broad-sense heritability (81.61) along with a high genetic advance in per cent of the mean (112.18) as shown in Table 3.5.

xvi. Yield per plot

The differences in yield per plot of potato genotypes were highly significant (P<.0001) as shown in Table 3.4. Potato genotypes with the highest yield per plot were GenoC (4623.3), GenoL (4176.6) and GenoK (3963.7). Genotypes with the lowest yield per plot were GenoCC (1418.7), GenoBB (1565.3) and GenoH (19.16.7) while the rest of the genotypes ranged from 2048.3 to 3729.6g.

xvii. Yield per hectare

There were statistically high significant (P<.0001) differences in the yield per hectare of the potato genotypes (Table 3.4). Potato genotypes GenoC (30.82), GenoL (27.85) and GenoK (26.42) were the highest. Genotypes with the lowest yield per hectare were GenoCC (9.46), GenoBB (10.44) and GenoH (12.78) while the rest of the genotypes ranged from 13.65 to 24.86 t/ha.

Table 3.4. Yield related characteristics of 33 potato genotypes

Geno	Tubers	T_Wt	T_Lt	T_Dia	No. Eyes	Y/Plant	Y/Plot	Y/Ha
GenoA	5.00	84.84	7.20	7.98	6.67	451.74	2258.10	15.06
GenoB	8.33	92.47	6.92	5.22	6.17	590.18	2950.90	19.67
GenoC	8.50	142.55	7.97	5.40	5.33	924.65	4623.30	30.82
GenoD	5.67	112.17	7.18	5.41	7.00	430.56	2152.80	14.35
GenoE	11.00	89.59	7.07	5.12	7.83	628.88	3144.40	20.96
GenoF	9.00	118.82	7.13	5.52	7.50	745.92	3729.60	24.86
GenoG	6.83	122.70	6.88	5.62	6.00	733.41	3667.10	24.45
GenoH	7.17	66.06	6.60	4.59	6.50	383.34	1916.70	12.78
GenoI	7.67	91.25	7.12	4.99	8.17	495.29	2476.40	16.51
GenoJ	6.67	113.82	7.23	5.44	7.33	629.54	3147.70	20.99
GenoK	11.33	95.49	6.67	5.43	5.00	792.74	3963.70	26.43
GenoL	12.33	96.36	6.63	5.42	4.83	835.33	4176.60	27.84
GenoM	11.33	89.13	7.20	5.20	5.67	674.43	3372.10	22.48
GenoN	9.67	97.06	6.58	5.42	4.33	730.13	3650.70	24.34
GenoO	7.67	103.10	6.77	5.37	6.33	652.44	3262.20	21.75
GenoP	10.83	90.67	6.43	5.33	6.67	739.57	3697.90	24.65
GenoQ	7.67	131.35	7.13	5.87	5.67	727.57	3637.80	24.25
GenoR	8.83	99.25	7.58	5.05	8.83	672.10	3360.50	22.4
GenoS	6.33	106.79	7.58	5.03	8.00	524.28	2583.90	17.23
GenoT	8.17	89.13	7.60	4.73	7.17	664.95	3324.80	22.17
GenoU	7.67	99.70	7.77	4.67	6.50	498.97	2494.90	16.63
GenoV	6.17	105.57	8.18	4.75	6.83	493.31	2466.60	16.44
GenoW	8.17	103.78	7.18	5.03	7.50	519.69	2598.50	17.32
GenoX	7.50	91.18	6.87	5.17	7.33	572.9	2864.50	19.11

Geno	Tubers	T_Wt	T_Lt	T_Dia	No. Eyes	Y/Plant	Y/Plot	Y/Ha
GenoY	9.00	86.37	7.52	5.62	7.33	701.82	3509.10	23.39
GenoZ	8.33	72.63	6.75	4.65	7.50	409.66	2048.30	13.66
GenoAA	4.50	139.76	7.65	5.85	8.00	611.67	3058.30	20.39
GenoBB	7.83	62.82	5.27	4.77	6.33	313.05	1565.30	10.44
GenoCC	11.00	40.83	4.78	4.23	6.17	283.74	1417.70	9.46
GenoDD	7.50	85.03	6.17	5.18	8.00	449.02	2245.10	14.97
GenoEE	9.00	75.24	6.87	4.78	8.67	543.19	2716.00	18.11
GenoFF	9.83	70.79	6.63	5.03	6.67	695.58	3477.90	23.19
GenoGG	8.5	97.69	6.70	4.88	7.00	663.31	3316.60	22.11
p- value	<.0001	<.0001	<.0001	<.0001	<0.05	<.0001	<.0001	<.0001
Tukey's HSD	4.05***	49.94***	1.31***	1.14***	4.30*	382.41***	1911.00***	12.74***
CV	21.76	23.33	8.40	9.89	28.26	28.57	28.57.00	28.57
MSG	20.93	2756.99	2.77	0.86	7.02	135105.94	3383214.80	150.34
MSE	3.29	500.45	0.34	0.26	3.71	29341.52	732757.80	32.56
Mean	8.33	95.88	6.96	5.15	6.81	599.48	2996.29	19.97

Geno- Genotype, Tubers- Number of tubers per plant, T_Wt - Individual tuber weight (g), T_Lt - Tuber length (cm), T_Dia - Tuber diameter (cm), No. eyes- Number of eyes, Y/Plant - yield per plant (g), Y/plot - Yield per plot (g), Y/ha- Yield per hectare (t), Sign-Significance, HSD- Honesty Significance Difference, CV- Covariance Variation, MSG- means square of genotype, MSE- means square error.

Table 3.5. Genetic parameters for yield contributing traits

Traits	σ^2_g	σ^2_p	GCV%	PCV%	$H^2{}_b$	GA	GAM
D_E	3, 55	5,51	11,49	14,31	64,45	3,12	19,02
E_P	138, 46	290,28	12,85	18,61	47,70	16,77	18,31
Height	132,46	145,82	31,45	32,99	90,84	22,63	61,83
No. Leaves	7227,71	8485,48	48,89	52,97	85,18	161,87	93,08
No. Stem	1,39	2,14	33,06	41,04	64,87	1,96	54,93
Stem Dia	10,09	11,16	37,24	39,17	90,41	6,23	73,05
No. Branch	16,34	19,45	121,76	132,84	84,01	7,64	230,24
L Area	145,41	187,28	36,80	41,76	77,64	21,92	66,89
Chlo con	83,26	101,17	48,05	52,97	82,30	17,08	89,92
Tubers	20,38	23,67	54,20	58,41	86,10	8,64	103,75
T_Wt	2673,58	3174,03	53,93	58,76	84,23	97,90	102,11
T_Lt	2,71	3,05	23,67	25,11	88,86	3,20	46,03
T_Dia	0,82	1,08	17,55	20,15	75,85	1,62	31,53
No .Eyes	6,40	10,11	37,15	46,69	63,31	4,15	60,99
Y/Plant	130215,69	159557,21	60,19	66,63	81,61	672,52	112,18

σ^2_g –Genotypic variance, σ^2_p –Phenotypic variance, GCV% - Genotypic coefficient of variation, PCV% -Phenotypic coefficient of variation, $H^2{}_b$ - Heritability in broad sense, GA –Genetic advance, GAM - Genetic advance (% of mean), D_E-Days to emergence, E_P-Emergence Percentage (%), Height-Plant height (cm), No. Leaves-Number of leaves, No. stem-number of stem, Stem Dia-Stem diameter (mm), No. branch-Number of branches, L Area-Leaf Area (cm^2), Chlo con-Chlorophyll content, Tubers- Number of tubers per plant, T_Wt - Individual tuber weight (g), T_Lt - Tuber length (cm), T_Dia - Tuber diameter (cm), No. eyes- Number of eyes, Y/Plant - yield per plant (g).

3.4.2. Cluster analysis

In the current study, the cluster analysis dendrogram clustered the 33 potato genotypes into three major clusters based on the 15 agronomic characteristics evaluated (Figure 3.8). Cluster I was subdivided into two sub-clusters 1 and 2. Sub-cluster A contained GenoA, GenoB, GenoD, GenoG, GenoI, GenoJ, GenoR, GenoS, GenoT, GenoU, GenoV, GenoW, GenoX, GenoY and GenoAA. Sub-cluster B contained GenoP, GenoFF and GenoGG. Cluster II was subdivided into two main sub-clusters A and B. Sub-cluster 1 contained GenoK, GenoL, GenoM, GenoN, GenoO and GenoQ. Sub-cluster 2 contained a singleton GenoC, GenoE and GenoF. Cluster III was also divided into two main sub-clusters 1 and 2. Sub cluster 1 consisted of GenoH, GenoZ, GenoDD and GenoEE. Sub-cluster 2 consisted of GenoBB and GenoCC.

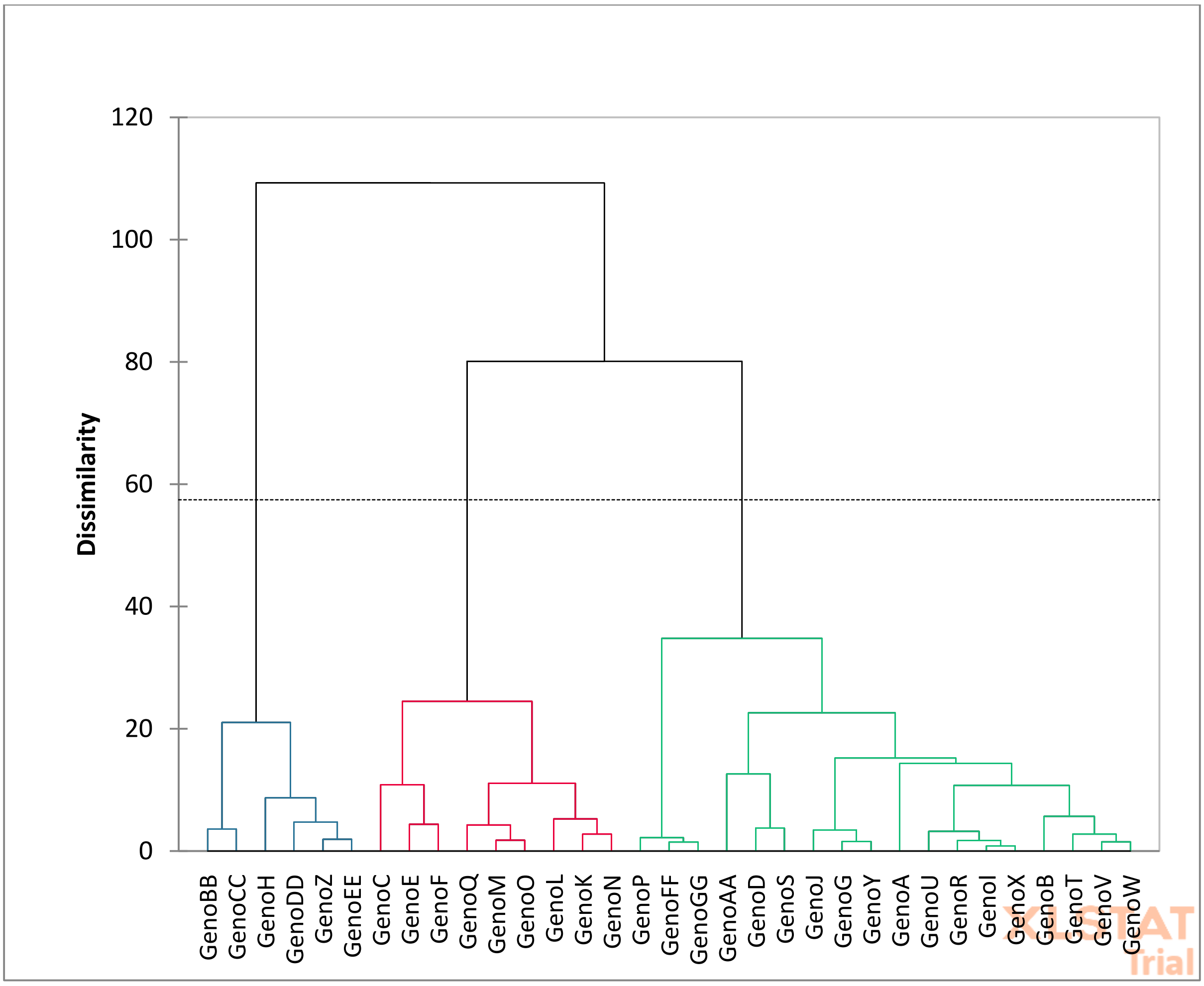


Figure 3.1: Cluster analysis dendrogram displaying relationship among 33 potato genotypes using agronomic quantitative traits

3.4.3. Correlation coefficient analysis

Correlation coefficient analysis was done to determine the inter-relationship among the characteristics studied. The correlation coefficient between the yield per plant and its component characteristic are presented in Table 3.6.

Days to emergence showed a negative correlation with the emergence percentage of $r^{2=}$-0.24. Plant height showed a negative correlation with the days to emergence ($r^{2=}$-0.07) and a positive correlation with the emergence percentage ($r^{2=}$0.29). Days to emergence showed a negative relation with the number of leaves ($r^{2=}$-0.36), while the emergence percentage ($r^{2=}$0.33) and plant height ($r^{2=}$0 .53) showed positive relationships with the number of leaves. The number of stems shows a positive correlation with the days to emergence ($r^{2=}$0.14), emergence percentage ($r^{2=}$0.07), plant height ($r^{2=}$0.58) and the number of leaves ($r^{2=}$0.36). Stem diameter showed a positive correlation with the days to emergence (0.07), emergence percentage (0.11), plant height ($r^{2=}$0.54), number of leaves ($r^{2=}$0.06) and the number of stems ($r^{2=}$0.06). Days to emergence ($r^{2=}$-0.42), number of stems ($r^{2=}$-0.20) and stem diameter ($r^{2=}$-0.15) showed a negative correlation with the number of branches whereas the emergence percentage ($r^{2=}$0.16), plant height ($r^{2=}$0.11) and number of leaves ($r^{2=}$0.44) showed a positive correlation.

Leaf area has shown a positive relation with the days to emergence ($r^{2=}$0.35) and stem diameter ($r^{2=}$0.30) whereas it had a negative relationship with the emergence percentage ($r^{2=}$-0.39), plant height ($r^{2=}$-0.17), number of leaves ($r^{2=}$-0.20), number of stems ($r^{2=}$-0.08) and number of branches ($r^{2=}$-0.02). Chlorophyll content showed a negative correlation with the days to emergence ($r^{2=}$-0.03), emergence percentage ($r^{2=}$-0.22), number of leaves ($r^{2=}$-0.20), number of branches ($r^{2=}$-0.22) and leaf area ($r^{2=}$-0.17) whereas plant height ($r^{2=}$0.34), number of stems ($r^{2=}$0.17) and stem diameter ($r^{2=}$0.14) showed a positive correlation. The number of tubers showed a negative correlation with the days to emergence ($r^{2=}$-0.38), emergence percentage ($r^{2=}$-0.10), stem diameter ($r^{2=}$-0.19) and chlorophyll content ($r^{2=}$-0.17) whereas plant height (0.24), number of leaves ($r^{2=}$0.49), number of stems ($r^{2=}$0.20), number of branches ($r^{2=}$0.53) and leaf area ($r^{2=}$0.12) showed a positive correlation. Tuber weight showed a negative correlation with days to emergence ($r^{2=}$-0.03), number of branches ($r^{2=}$-0.28), leaf area ($r^{2=}$-0.26) and number of tubers ($r^{2=}$-0.37) whereas emergence percentage ($r^{2=}$0.15), plant height ($r^{2=}$0.57), number of leaves ($r^{2=}$0.10), number of stems ($r^{2=}$0.23), stem diameter ($r^{2=}$0.56) and chlorophyll content ($r^{2=}$0.38).

Days to emergence ($r^{2=}$0.06), emergence percentage ($r^{2=}$0.21), plant height ($r^{2=}$0.46), number of leaves ($r^{2=}$0.05), number of stems ($r^{2=}$0.27), stem diameter ($r^{2=}$0.59), chlorophyll content ($r^{2=}$0.28) and tuber weight ($r^{2=}$0.68) have a positive correlation with tuber length, whereas the number of branches ($r^{2=}$-0.38), leaf area ($r^{2=}$-0.17) and number of tubers ($r^{2=}$-0.38) showed a negative correlation. Tuber diameter showed a positive correlation with days to emergence ($r^{2=}$0.05), emergence percentage ($r^{2=}$0.26), plant height ($r^{2=}$0.16), number of stems ($r^{2=}$0.06), stem diameter ($r^{2=}$0.16), chlorophyll content ($r^{2=}$0.10), tuber weight ($r^{2=}$0.38) and tuber length ($r^{2=}$0.24) whereas the number of leaves ($r^{2=}$-0.03), number of branches ($r^{2=}$-0.04), leaf area ($r^{2=}$-0.17) and number of tubers per plant ($r^{2=}$-0.32). Days to emergence ($r^{2=}$0.13), stem diameter ($r^{2=}$0.02), leaf area ($r^{2=}$0.15), chlorophyll content ($r^{2=}$0.27) and tuber length ($r^{2=}$0.22) showed a positive correlation with the number of eyes, while the emergence percentage ($r^{2=}$-0.10), plant height ($r^{2=}$-0.12), number of leaves ($r^{2=}$-0.19), number of stems ($r^{2=}$-0.11), number of branches ($r^{2=}$-0.29), number of tubers per plant ($r^{2=}$-0.37), individual tuber weight ($r^{2=}$-0.06) and tuber diameter ($r^{2=}$-0.15) showed a negative correlation. Yield per plant showed a negative correlation with the days to emergence ($r^{2=}$-0.27) and number of eyes ($r^{2=}$-0.37) and had a positive correlation emergence percentage ($r^{2=}$0.12), plant height ($r^{2=}$0.73), number of leaves ($r^{2=}$0.37), number of stems ($r^{2=}$0.41), stem diameter ($r^{2=}$0.54), number of branches ($r^{2=}$0.14), leaf area ($r^{2=}$0.04), chlorophyll content ($r^{2=}$0.17), number of tubers per plant ($r^{2=}$0.39), tuber weight ($r^{2=}$0.59), tuber length ($r^{2=}$0.39) and tuber diameter ($r^{2=}$0.26)

Table 3.6: The correlation coefficient for 15 agronomic characteristics of potato genotypes characterized

Character	D_E	E_P	Height	No. Leaves	No. Stem	Stem Dia	No. Branch	L Area	Chlo con	Tubers	T_Wt	T_Lt	T_Dia	No. Eyes	Y/Plant
D_E	**1**	-0.24	-0.07	-0.36	0.14	0.07	**-0.42^{*}**	0.35	-0.03	-0.38	-0.03	0.06	0.05	0.13	-0.27
E_P		**1**	0.29	0.33	0.07	0.11	0.16	-0.39	-0.22	-0.10	0.15	0.21	0.26	-0.10	0.12
Height			**1**	0.53^{**}	0.58^{**}	0.54^{**}	0.11	-0.17	0.34	0.24	0.57^{**}	0.46^{*}	0.16	-0.12	0.73^{**}
No. Leaves				**1**	0.36	0.06	0.44^{*}	-0.20	-0.02	0.49^{*}	0.10	0.05	-0.03	-0.19	0.37
No. Stem					**1**	0.06	-0.20	-0.08	0.17	0.20	0.23	0.27	0.06	-0.11	0.41^{*}
Stem Dia						**1**	-0.15	0.30	0.14	-0.19	0.56^{**}	0.59^{**}	0.16	0.02	0.54^{**}
No. Branch							**1**	-0.02	-0.22	0.53^{**}	-0.28	-0.38	-0.04	-0.29	0.14
L Area								**1**	-0.17	0.12	-0.26	-0.17	-0.17	0.15	0.04
Chlo con									**1**	-0.17	0.38	0.28	0.10	0.27	0.17
Tubers										**1**	-0.37	-0.38	-0.32	-0.37	0.39
T_Wt											**1**	0.68^{**}	0.38	-0.06	0.59^{**}
T_Lt												**1**	0.24	0.22	0.39
T_Dia													**1**	-0.15	0.26
No .Eyes														**1**	-0.37
Y/Plant															**1**

D_E-Days to emergence, E_P-Emergence Percentage (%), Height-Plant height (cm), No. Leaves-Number of leaves, No. stem-number of stem, Stem Dia-Stem diameter (mm), No. branch-Number of branches, L Area-Leaf Area (cm^2), Chlo con-Chlorophyll content, Tubers- Number of tubers per plant, T_Wt - Tuber weight (g), T_Lt - Tuber length (cm), T_Dia - Tuber diameter (cm), No. eyes- Number of eyes, Y/Plant - yield per plant (g), *significant at $p<0.05$, **highly significant at $p<0.01$.

3.4.4. Principal component analysis

Principal component analysis grouped 15 quantitative traits into 5 main components, which accounted for the genetic variability among the 33 potato genotypes (Table 3.7) and the first 5 principal components had eigenvalues of more than 1.00. The first two principal components contributed 51.35% of the genetic variability. The first principal component (PC1) had an eigenvalue of 5.57 and accounted for 32.76% of genetic variability. Traits that contributed most to the variability among genotypes were plant height (0.87), number of leaves (0.48), number of stems (0.51), stem diameter (0.61), individual tuber weight (0.71), tuber length (0.55) and yield per plant (0.94). The second principal component (PC 2) had an eigenvalue of 3.16 and accounted for 18.59% of genetic variability. The phenotypic attributes that played the main role in the variability among accessions were number of leaves (0.54), number of branches (0.76), chlorophyll content (-0.43), number of tubers (0.84), individual tuber weight (-0.52), tuber length (-0.62) and number of eyes (-0.48).

Emergence percentage (-0.70) and leaf area (0.83) were the main contributing characters in the third principal component with an eigenvalue of 1.86 and accounted for 10.94% of the total genetic variability among genotypes. Whereas the fourth PC had an eigenvalue of 1.35 and accounted for 7.94% of variability with the number of stems (0.54), chlorophyll content (0.49) and tuber diameter (-0.45) being the main contributing characters. Days to emergence (0.56), number of stems (0.51) and chlorophyll content (-0.54) were the main contributing characters in the fifth principal component with an eigenvalue of 1.19 and accounted for 6.98% of the total variability.

Table 3.7: Principal component analysis for agronomic characters of 33 potato genotypes

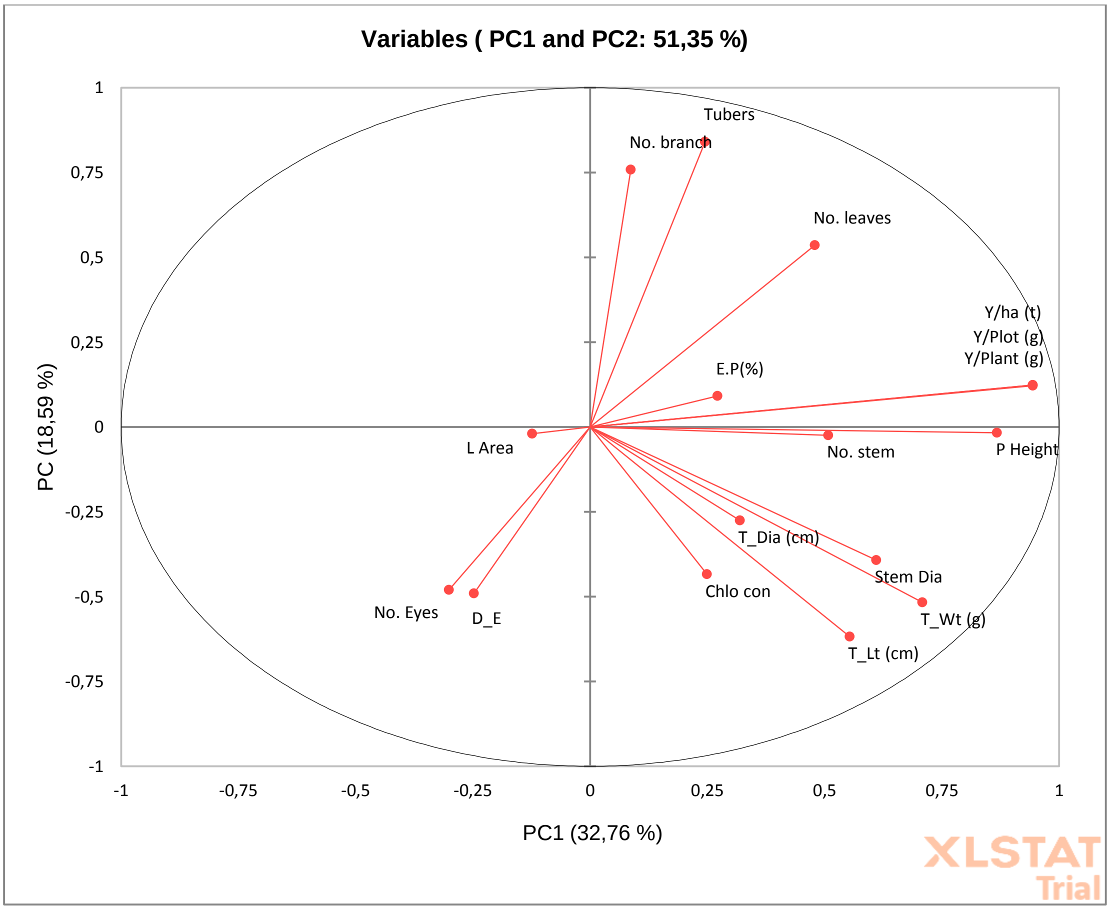
Characters	PC1	PC2	PC3	PC4	PC5
D_E	-0,25	-0,49	0,39	-0,04	**0,56**
E.P	0,27	0,09	**-0,70**	-0,19	0,33
Height	**0,87**	-0,02	-0,02	0,27	0,14
No. leaves	**0,48**	**0,54**	-0,23	0,24	0,29
No. stem	**0,51**	-0,02	0,11	**0,54**	**0,51**
Stem Dia	**0,61**	-0,39	0,26	-0,33	-0,01
No. branch	0,09	**0,76**	-0,12	-0,18	-0,19
L Area	-0,12	-0,02	**0,83**	-0,29	0,12
Chlo con	0,25	**-0,43**	0,03	**0,49**	**-0,54**
Tubers	0,25	**0,84**	0,31	0,21	-0,05
T_Wt	**0,71**	**-0,52**	-0,18	-0,07	-0,13
T_Lt	**0,55**	**-0,62**	-0,15	0,05	0,05
T_Dia	0,32	-0,28	-0,34	**-0,45**	0,04
No. Eyes	-0,30	**-0,48**	0,03	0,36	-0,12
Y/Plant	**0,94**	0,12	0,20	-0,11	-0,10
Eigenvalue	5,57	3,16	1,86	1,35	1,19
Variability (%)	32,76	18,59	10,94	7,94	6,98
Cumulative %	32,7	51,35	62,29	70,23	77,21

PC1-5: Principal component1-5, D_E-Days to emergence, E_P -Emergence Percentage (%), Height-Plant height (cm), No. Leaves- Number of leaves, No. stem- number of stem, Stem Dia- Stem diameter (mm),No. branch-Number of branches, L Area-Leaf Area (cm^2), Chlo con- Chlorophyll content, Tubers- Number of tubers per plant, T_Wt - Individual tuber weight (g), T_Lt - Tuber length (cm), T_Dia- Tuber diameter (cm), No. eyes- Number of eyes, Y/Plant - yield per plant (g).

3.4.5. Principal component bi-plot

The relationships between the different traits and genotypes to principal components are also illustrated in the first two principal component bi-plots (Figure 3.1). A high correlation of the characters in terms of discriminating genotypes was shown by smaller angles between dimension vectors in the same direction. Genotypes that excelled in a specific attribute were displayed closer to the vector line and in the direction of that vector. Whereas genotypes that underperformed in that attribute are displayed far from the vector and in the opposite direction of the vector. Traits that are grouped are positively correlated, whereas those that are far apart are negatively correlated (Figure 3.2). Traits in the first quadrant, which are emergence percentage, number of branches, number of leaves, number of tubers and yield per plant were positively correlated. These traits are negatively correlated with traits in the third quadrant (leaf area, number of eyes and days to emergence).

The principal component genotypes in the observation are scattered in such a way that the distance between them may easily be visualized. Genotypes are divided into quadrants based on how comparable their phenotypic characteristics are (Figure 3.4). The bi-plot indicates the relationship between genotypes (Figure 3.3). Genotypes in the same quadrant are positively correlated. Genotypes in the first quadrant were associated with a high number of branches, leaves and tubers per plant, emergence percentage and yield per hectare. Genotypes in the second quadrant were associated with shortest plants, low stem diameter, tuber diameter, tuber weight and yield per plant. The third quadrant genotypes were associated with a larger leaf area, a high number of eyes and the highest number of days of emergence. Genotypes in the fourth quadrant were associated with taller plants, larger stem diameter, tuber diameter, high tuber weight, tuber length and chlorophyll content.



D_E-Days to emergence, E_P -Emergence Percentage (%), P Height-Plant height (cm), No. Leaves- Number of leaves, No. stem- number of stems, Stem Dia- Stem diameter (mm),No. branch-Number of branches, L Area-Leaf Area (cm^2), Chlo con- Chlorophyll content, Tubers- Number of tubers per plant, T_Wt - Individual tuber weight (g), T_Lt - Tuber length (cm), T_Dia- Tuber diameter (cm), No. eyes- Number of eyes, Y/Plant - yield per plant (g), Y/Plot (g), Y/ha (t).

Figure 3.2: Principal component variable circle showing the correlation among the different agronomic traits of potato genotypes

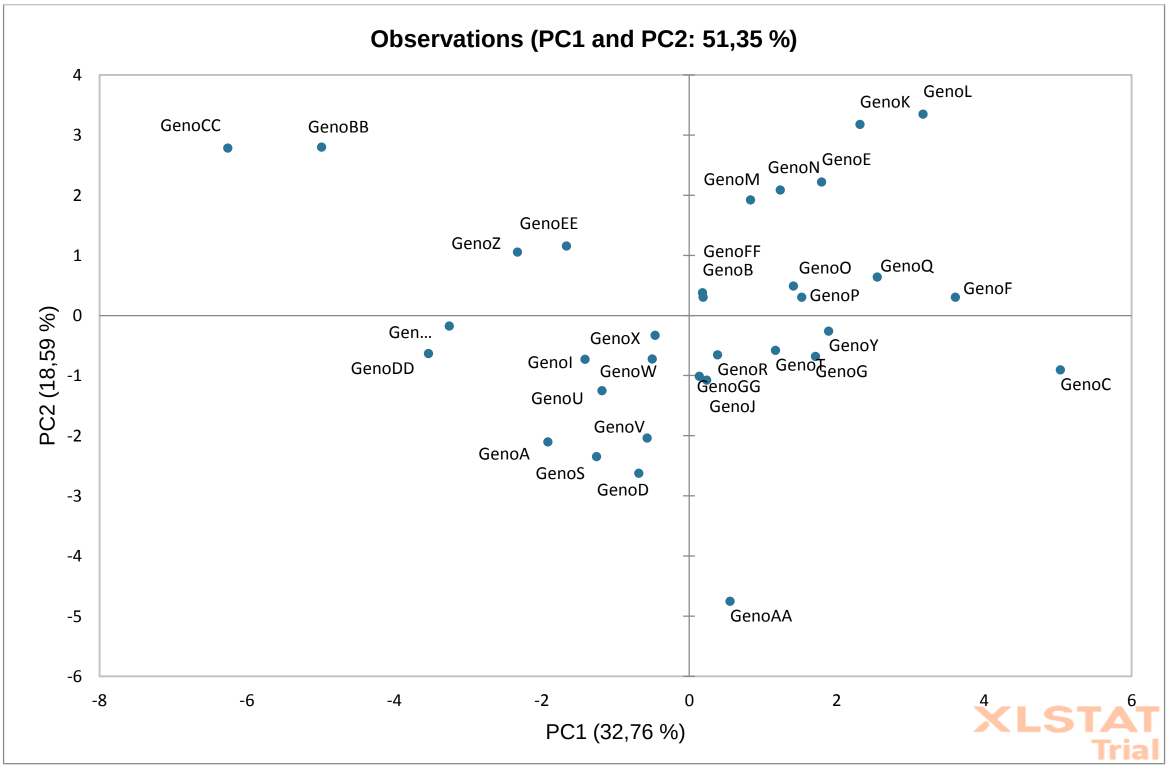


Figure 3.3: The principal component of 33 potato genotypes in the bi-plot

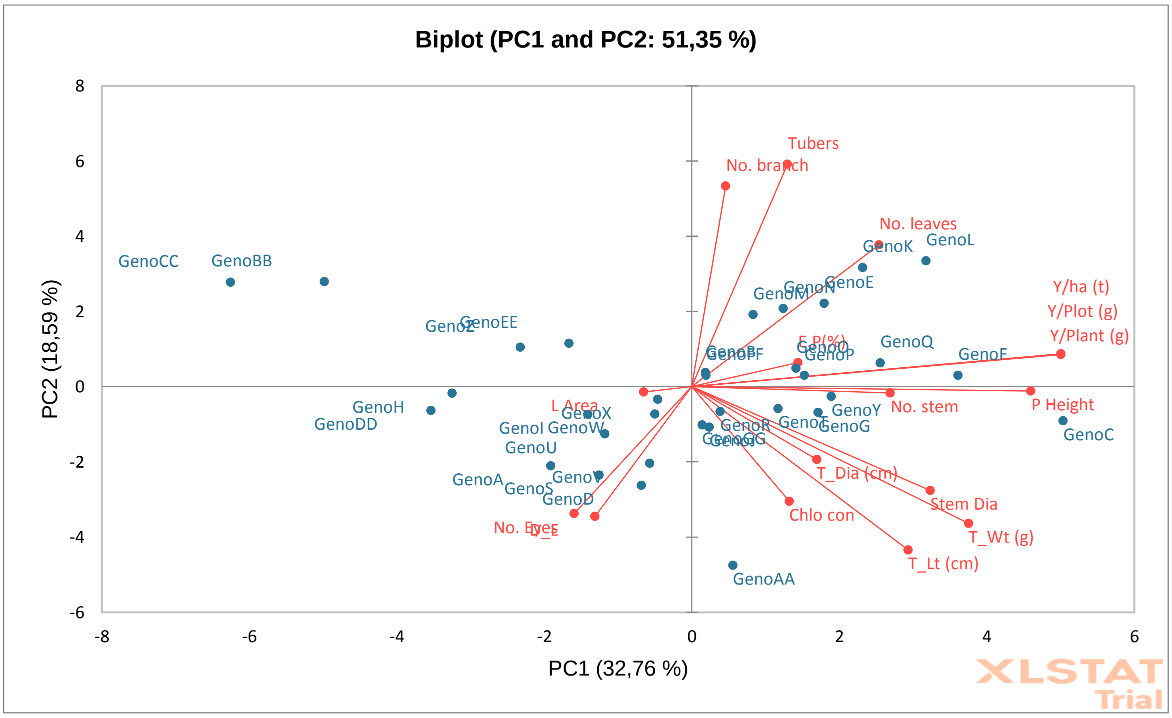


Figure 3.4: Principal component bi-plot showing the variation of potato genotypes by agronomic traits

3.5. Discussion

Genotypes can easily be differentiated by observing morphological characters. Agronomic characterization reveals similarities in phenotypic characteristics of genotypes (Kisua *et al*., 2015). In this study, 33 potato genotypes were evaluated in the field for agronomic traits and showed great variability in the agronomic traits measured and counted. The analysis of variance showed that the differences in the emergence percentage of genotypes were not statistically significant. Plant height, number of leaves, number of stems, stem diameter, number of branches, leaf area, chlorophyll content, number of tubers, individual tuber weight, tuber length, tuber diameter and yield per plant have shown significant variation among potato genotypes. Similar results were reported by Salam (2011); Bilate and Mulualem (2015) along with Anoumaa *et al*. (2016) who reported high significant differences among potato genotypes for quantitative traits. This suggests that the genotypes have a lot of genetic variation and that there is potential to improve genetic diversity for crop improvement (Gerrano *et al*., 2014).

Plant height ranged from 26.93 to 47 cm with a mean of 36.6 cm. Some researchers reported a wider range from the results obtained, Fekadu *et al.* (2013) reported a range from 26.7 to 99 cm and Bilate and Mulualem (2016) reported a range from 36.27 to 99.17 cm. Some researchers reported a narrower range, Khan *et al.* (2013) reported a range from 7.3 to 28.3 cm and Ghebreslassie (2017) reported a range of 11.1 to 35.9 cm. The number of stems ranged from 2.67 to 4.67 with a mean of 3.56. Similar results were reported by Ghebreslassie (2017), who reported a range from 1.2 to 5.6 with a mean of 2.8 and Khan *et al.* (2013) reported a range from 1 to 3 with a mean of 2.09. However, Fekadu *et al.* (2013) reported a greater range of 3.8 to 9.7 with a mean of 5.8. The number of tubers ranged from 4.50 to 12.33 with a mean of 8.33. Similar findings were reported by Ghebreslassie (2017) who reported a range from 4.75 to 19.42 with a mean of 9.03. Tuber yield ranged from 9.46 to 30.82 t/ha with a mean of 19.97 t/ha. These results were in accordance with results reported by Salam (2011), who reported a range from 13 to 30.30 t/ha.

In a breeding program, genetic factors such as genetic variances and heritability are particularly significant in selecting superior parental lines (Alvi *et al*., 2003). The genetic characteristics of the 33 potato genotypes indicated a high variation. Relatively high genotypic and phenotypic variance values were obtained for emergence percentage, plant height, number of leaves, leaf area, chlorophyll content, individual tuber weight and yield per plant. This suggests that the genotype may be reflected by the phenotype and that these traits could be selected and used in breeding (Nyadanu & Direka, 2014). The phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) help in estimating genetic variability in specific traits (Singh, 2000). Deshmukh *et al*. (1986) and Danquah and Ofori (2012) classified phenotypic and genotypic coefficients of variation (PCV and GCV) as high (>20%), medium (10-20%) and low (<10%). In this study, days to emergence, emergence percentage and tuber diameter showed medium/moderate phenotypic and genotypic coefficient of variation whereas the rest of the traits have shown high phenotypic and genotypic coefficient of variation. According to Shukla *et al*. (2006), high PCV and GCV values indicate that there is enough genetic variability to allow for improvement through a selection of the desired characteristics. GCV and PCV had extremely modest differences in all traits, with PCV slightly higher than GCV. Kaushik *et al*. (2007) also reported that the higher the GCV: PCV ratio, the more hereditary rather than environmental factors influenced the trait.

The heritability estimates show which traits are likely to be passed down from one generation to the next (Usman *et al*., 2014; Khan *et al*., 2015). The efficiency of selection is dependent not only on heredity but also on genetic advances. Because of its predictive role in indicating the reliability of phenotypic value as a pointer to the breeding value, heritability is useful for genetic improvement (Falconer & Mackay, 1996). Johnson *et al*. (1955) classified heritability estimates into three categories: low (0–30%), moderate (30–60%), and high (≥60%). In the current study, only the emergence percentage (47.70) had a moderate heritability and the rest of the genotypes had a high heritability (63.31 – 90.84). According to Rashwan (2010) and Manggoel *et al*. (2012), high broad-sense heritability values usually indicate the preponderance of additive gene action in the expression of phenotypes. Selection for traits with a heritability of 71-96% or greater could be easier, as they imply a stronger link between genotype and phenotype, with less environmental influence on the phenotype. In the current study, plant height, number of leaves, stem diameter, number of branches, chlorophyll content, number of tubers, individual tuber weight, tuber length and yield per plant had a heritability of more than 80%. According to

Shadakshari *et al*. (1995) and Singh (2001), selection for traits that have a heritability of more than 80% can be effective because there is a strong response to direct selection. High heritability combined with high genetic advance is a significant element in determining the subsequent effect for selecting the best individuals (Johnson *et al*., 1955). In our study, the number of leaves (161.87) and individual tuber weight (97.90) had the highest genetic advance. Under one cycle of selection at a specific selection intensity, genetic advance (GA) is vital to consider in the improvement of traits in genotypic value for the development of new populations compared to the base population (Gashaw *et al*., 2010). The GA estimates help in determining the sort of gene action that controls the expression of a variety of polygenic traits. GA values over a certain threshold indicate additive gene action, while GA values below that threshold indicate non-additive gene action (Singh & Narayanan, 1993). As a result, heritability estimates will be beneficial if they are accompanied by a high GA.

The cluster analysis demonstrated the existence of diversity among the 33 potato genotypes for agronomical characters studied. The clustering of genotypes represents the relative diversity of genotypes, allowing for the selection of core collection items from each group (Lohani *et al*., 2012). The cluster analysis grouped the genotypes into three major clusters. Each cluster was divided into two sub-clusters 1 and 2. Sub-cluster 1 from cluster I and sub-cluster 2 of cluster II contained singletons (GenoAA and GenoC). Singletons are genotypes that are placed far separated from the rest of the genotypes in a cluster. They are more diversified and, as a result of their superiority over other genotypes, should be given special consideration during selection (Choudhary *et al*. 2013). Genotypes in cluster I were associated with taller plants, low number of leaves and branches, larger leaf area, higher chlorophyll content, low number of tubers, larger tuber length and diameter and higher number of eyes. Genotypes in cluster II had a greater number of leaves, stems, branches and tubers per plant, high individual tuber weight and yield. Genotypes in cluster III had the shortest plants, least number of stems and tubers, small stem diameter, low chlorophyll content, tuber length and tuber diameter, small tuber weight and lower yield.

The correlation coefficients of 15 quantitative characteristics were analyzed. Knowledge of characteristic correlations is useful in developing a successful breeding program for any crop. Plant characters like yield are quantitatively inherited and altered by genetic variables as well as genotype-environment interaction. Selections may be hard and time-consuming to enhance yield directly due to these details. As a result, identifying and using strongly correlated characteristics is preferable and beneficial (Shabanimofrad *et al*., 2013). The number of stems showed a positive correlation with the days to emergence, emergence percentage, plant height and number of leaves. Similar results were reported by Ghebreslassie (2017), who reported that the number of primary stems showed a strong positive correlation with plant height and the number of tubers. Stem diameter showed a positive correlation with the days to emergence, emergence percentage, plant height, number of leaves and the number of stems. The findings were in contrast to the results of Ghebreslassie (2017), who reported a moderately negative correlation between stem thickness (diameter) and the number of primary stems. Ghebreslassie (2017) reported that the more the primary stems per plant the less the thickness and concluded that genotypes with thick stem diameter are associated with bigger tuber size and higher yields than genotypes with many primary stems but thin stem size.

The number of tubers had a negative correlation with the days to emergence, emergence percentage, stem diameter and chlorophyll content whereas plant height, number of leaves number of stems, number of branches and leaf area showed a positive correlation. The current study suggested that an increase in plant height, number of leaves and number of stems led to an increase in the number of tubers. Genotypes that had fewer leaves and the number of stems resulted in fewer tubers and less yield. The results are in agreement with results reported by Ghebreslassie (2017), who reported that the tuber set had a strong positive correlation with the number of primary stems and plant height. The researcher also reported that an accession having more and longer stems are likely to produce more tubers, but usually inversely relate to yield or tuber weight. Felenji *et al*. (2011) along with Ahmadizadeh and Felenji (2011) also reported a positive correlation between the number of stems, plant height and tuber numbers. Similar results were also reported by Anoumaa *et al.,* (2016), who reported that the total number of tubers was significantly and positively correlated with the number of the mean stem. The positive correlation between traits suggests that selecting and improving the major desirable traits in the breeding program will have a positive effect on the secondary traits (Gerrano *et al.*. 2015).

Tuber weight showed a negative correlation with days to emergence, number of branches, leaf area and number of tubers whereas emergence percentage, plant height, number of leaves, number of stems, stem diameter and chlorophyll content. Ghebreslassie (2017) also reported a negative correlation between tuber weight and the number of tubers. According to Felenji *et al*. (2011) and Ghebreslassie (2017), the negative correlation between tuber weight and tuber number can be explained by the fact that the larger the number of tubers produced per plant, the smaller the size of each tuber, which can be linked to resource competition.

The current PCA (Table 3.6) depicts the relative importance and variation of each of the 15 traits. Five components were chosen based on the starting Eigen value of more than 1 in the current study. Each factor loading defines the degree of contribution of each trait with each principal component linked with that trait, while principal component analysis assesses the contribution of each component to the total variance (Nachimuthu *et al*., 2014). These results are in agreement with the results of the bi-plot. Based on agronomical expression, the identified qualities in the components showed significant diversity among genotypes, which can be used for selection. Nsabiyera *et al*. (2012) and Nachimuthu *et al*. (2014) stated that if a trait's total factor loading is less than ≥0.40, regardless of the plus or minus sign, it is considered a substantial contribution to the variability in a component. That the first five components explained 71.21% of the variation in the current study indicates that there is strong genetic variation among genotypes that can be exploited for breeding purposes. The first two components accounted for 51.35% of the total variation. PC1 accounted for 32.76% and PC2 for 18.59% of variation. These results are similar to the findings by Salam (2011) who reported similar findings with the first two PCs accounting for 54.74% variation with PC1 and PC2 accounted for 36.46% and 18.01%, respectively, among 24 potato germplasm. The finding that PC1 and PC2 explained more variation (32.76% and 18.59%, respectively) suggested that selecting materials using these components would be sufficient and recommended. According to Karuri *et al*. (2010), the selection of genotypes from PC1 and PC2 and/or groups with the highest positive deviation from the overall mean can initiate a productive breeding program. This suggests that PCA can be used to determine how each genotype's agronomical trait contributes to the formation of a group or cluster. As a result, it helps in the identification of desired features contained within each genotype/group for future breeding activities. The main component bi-plot (Figure 3.4) among genotypes and traits revealed the level of similarity. Genotypes clustered together in each quadrant based on their traits and are regarded to be closely related. Gerrano *et al*. (2015) reported that genotypes that are close to each other are genetically similar, whereas those that are far from each other are reported to be different. The principal component bi-plot is in agreement with the clustering and correlation analysis using the genotype vs trait relationship.

3.6. Conclusion.

The current study has shown a wide genetic variability among the 33 potato genotypes. The findings of the study support the rejection of the null hypothesis as there was a significant variation in the agronomic traits and yield attributes of different genotypes. The analysis of variance showed that the differences in plant height, number of leaves, stem, branches and tubers, stem diameter, leaf area, chlorophyll content, individual tuber weight, tuber length and diameter and yield per plant of genotypes were statistically significant. Plant height, number of leaves, branches and tubers, stem diameter, chlorophyll content, individual tuber weight, tuber length and yield per plant had a heritability of more than 80%. Cluster analysis grouped the genotypes into three major clusters and each cluster was divided into two sub-clusters. Plant height, the number of stems, stem diameter and individual tuber weight had a strong positive correlation with the yield per plant. The principal component analysis showed that the first five principal components explained 71.21% of the variation in the current study, which indicates that there is strong genetic variation among genotypes that can be exploited for breeding purposes.

CHAPTER 4

Qualitative morphological characterization of advanced potato breeding lines

Abstract

Potato is an annual crop grown for its starchy edible tubers. It is one of the world's main food crops and is important for food security and income generation. Continuous and improved production is important in potato breeding. Cultivar development is important in crop improvement and phenotypic characteristics are the first aspects to consider in crop breeding. Characteristics such as tuber shape, size, colour and handling are important for the fresh market industry and are the key factors considered for the processing industry. In this study, 33 genotypes were studied and characterized based on their qualitative morphological characters. The genotypes exhibited high diversity in growth habit, leaf texture, tuber shape, tuber colour, flesh colour, tuber distribution and tuber eye depth. The growth habit of the genotypes was grouped into three sets, erect (21.2%), semi-erect (45.5%) and spread (21.2%). Leaf shape showed a slight variation, 21.2% were lanceolate and 78.8% were ovate. There was a high variation in leaf texture, 3% were coarse-hairy, 3% were smooth/glossy, 12.1% were fine and hairy, 30.3% were fine and 51.5% were coarse. Tuber shape also showed high variation with 3% being compressed-oblong, 6.1% oblong, 6.1% long-oblong, 9.1% were round, 12.1% were obovate, 15.2% were compressed and 48.5% were elliptic. The genotypes showed variation in tuber colour, 6.1% were slightly dark cream, 15.2% dark cream, 39.4% were cream and 39.4% were light cream. Flesh colour also showed a high variation, 3% were light cream, 6.1% were dark cream, 9.1% were yellow, 24.2% were white, 24.2% were light yellow and 33.3% were cream. There was a slight variation in tuber distribution of genotypes, 12.1% were evenly distributed and 87.9% were predominantly apical. Tuber eye depth showed moderate variation, 3% were deep, 24.2% were medium, 36.4 were protruding and 36.4% were shallow. The genotypes studied showed wide genetic variability which can be exploited for crop improvement and breeding.

Keywords: characterization, leaf, morphological, qualitative, variation.

4.1. Introduction

Assessment of genetic diversity in crop species allows the exploitation of different genotypes so as to develop new and improved varieties for the traits of interest. In any successful breeding programme, parental selection is normally the important factor to consider (Manggoel *et al*., 2012). Agronomic and morphological characterization is the first step in the description and classification of plant genotypes (Smith & Smith, 1989). Agronomic parameters and morphological characters have been used successfully for the selection of desirable traits. Morphological characterization provides an understanding of genetic diversity within a population for high precision diversity analysis and is the pre-requisite for breeding programmes (Adewale *et al.*, 2011). Parental selection is one of the important factors that play an important role in a successful breeding programme (Manggoel *et al*., 2012). Quantitative morphological variation is greatly influenced by environmental factors, however, morphological characteristics can still be powerful and accurately exploited for selection and are essential for breeding programmes. According to Adewale *et al*. (2011), morphological assessment of genotypes to understand the genetic diversity within a population is still applicable for high precision diversity analysis.

Morphological characteristics have been used to study genetic diversity within and among genotypes. Researchers have reported that there are genetic diversity patterns among genotypes of different crops using various techniques. Examples include potato (Khan *et al*., 2013; Teshome *et al*., 2014; Anoumaa *et al*., 2016), tomato (Salim *et al*., 2020; Fernandes *et al*., 2018; Grozeva *et al*., 2020); sweet potato (Maquia *et al*., 2013; Mbithe *et al*., 2016; Ochieng., 2019), rice (Nascimento *et al*., 2011; Onaga *et al*., 2013; Thenmozhi and Rajasekaran, 2013), maize (Beyene *et al*., 2005; Hartings *et al*., 2008; Thakur *et al*., 2017) groundnut (Molosiwa *et al*., 2011; G *et al*., 2015) and Bambara groundnut (Shegro *et al*., 2013; Amara *et al*., 2016). Knowledge and information on genetic diversity are necessary to accelerate crop improvement and breeding programs through the characterization of morphological characteristics. This is also an important step in new cultivar development and essential for the development of a sustainable management strategy for plant genetic resources.

4.2. Aim, objective and hypotheses

4.2.1. Aim

- The study aimed to characterize potato advanced breeding lines using qualitative morphological traits under Mahikeng growing conditions.

4.2.2. Objective

- To characterize the advanced breeding lines grown in Mahikeng using qualitative morphological traits.

4.2.3. Hypotheses

- Ho: There would be no significant variation in the qualitative morphological traits of the advanced breeding lines.

  Ha: There would be significant variation in the qualitative morphological traits of the advanced breeding lines.

4.3. Materials and methods

Site characteristics, planting materials used, crop production, experimental design and layout are described in Chapter 3.

4.3.1. Data collection

The following qualitative data were recorded according to Anoumaa *et al*. (2016).

- Growth habit.
  It was observed and recorded.
- Leaf texture and colour.
  These were observed and recorded.

- Tuber shape, tuber colour and tuber flesh colour.
  These were observed and recorded.

- Eye distribution and tuber eye depth.
  These characteristics were observed and recorded.

4.3.2. Data analysis

The Shannon-Weaver diversity index (H') was used to calculate the phenotypic frequency of alleles controlling each qualitative trait as described by Shannon and Weaver (1949) as follows:

$$H' = 1- \sum_{i=1}^{n} pi \ln pi$$

Where:

H' = Diversity index,

n = Total number of phenotypic classes of traits

Pi: Proportion of genotypes in the i^{th} class of n-class character.

4.4. Results

The morphological performance of 33 genotypes of potato was investigated under Mahikeng growing conditions and the findings are presented and discussed in this section of this chapter.

4.4.1. Growth habit

Growth habit showed moderate variation (Table 4.4.2). The genotypes GenoD, GenoE, GenoJ, GenoT, GenoU, GenoV, GenoAA were erect, 11 genotypes were spread and 15 genotypes were semi-erect.

4.4.2. Leaf shape

Genotypes exhibited a slight variation (Table 4.4.2). Seven potato genotypes were Lanceolate which were GenoD, GenoE, GenoG, GenoJ, GenoT, GenoU and GenoW. The rest of the genotypes were ovate as shown in Figure 4.1.

4.4.3. Leaf texture

Leaf texture showed moderate variation (Table 4.4.2). GenoH was coarse-hairy, GenoEE was smooth/glossy and GenoM, GenoN, GenoFF and GenoGG were fine and hairy while the rest of the genotypes were fine and coarse.

GenoA

GenoB

GenoC

GenoD

GenoE

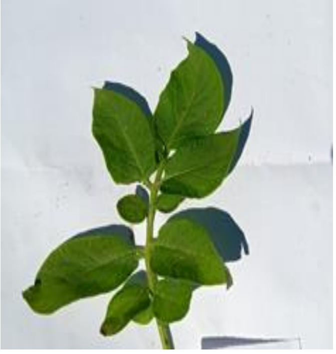
GenoF

GenoG

GenoH

GenoI

GenoJ



GenoK

GenoL

GenoM

GenoN

GenoO

GenoP

GenoQ

GenoR

GenoS

GenoT

GenoU

GenoV

GenoW

GenoX

GenoY GenoZ GenoAA

GenoBB GenoCC GenoDD

GenoEE GenoFF GenoGG

Figure 4.1: Morphological features showing leaf shape. GenoD, GenoE, GenoG, GenoJ, GenoT, GenoU and GenoW are lanceolate. The rest of the genotypes are ovate.

4.4.4. Tuber colour

Potato genotypes showed moderate variation in tuber colour (Table 4.4.2). Breeding lines GenoH and GenoL were slightly dark cream, GenoJ, GenoP, GenoR, GenoU and GenoV were dark cream. Thirteen genotypes were cream while the other 13 were light cream.

4.4.5. Tuber shape

Moderate variation was observed in the tuber shape of different genotypes (Table 4.4.2). The studied genotypes GenoA, GenoB, GenoK and GenoU were obovate, GenoE and GenoO were oblong, GenoQ, GenoX, GenoAA, GenoBB and GenoGG were compressed, GenoL was compressed-oblong, GenoN, GenoCC and GenoDD were round and GenoR and GenoV were long-oblong while the rest of the genotype were elliptic (Figure 4.2).

GenoA

GenoB

GenoC

GenoD

GenoE

GenoF

GenoG

GenoH

GenoI

GenoJ

GenoK

GenoL

GenoM

GenoN

GenoO

GenoP

GenoQ

GenoR

GenoS

GenoT

GenoU

GenoV

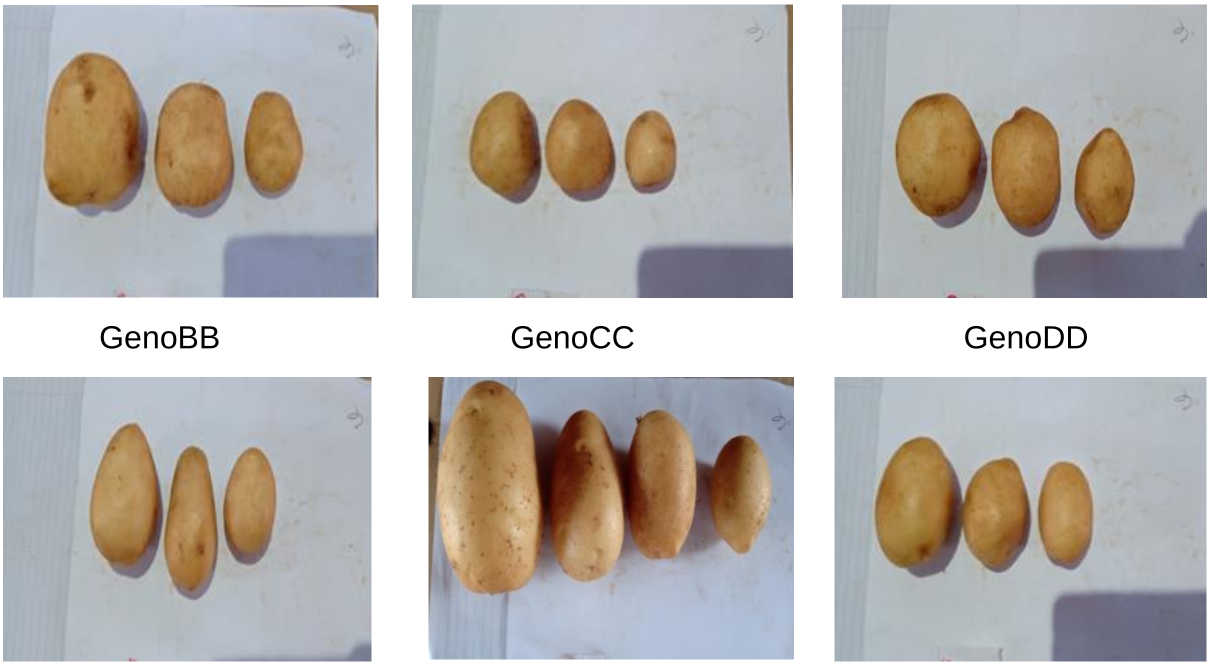
GenoW

GenoX

GenoY

GenoZ

GenoAA


GenoBB GenoCC GenoDD

GenoEE GenoFF GenoGG

Figure 4.2: Morphological features of tuber shape and colour of the genotypes.

4.4.6. Tuber flesh colour

The studied breeding lines showed moderate variation in tuber flesh colour (Table 4.4.2). Among the breeding lines studied GenoGG was light cream, GenoI and GenoL were dark cream while GenoD, GenoX and GenoAA were yellow then the rest of the breeding lines were cream, white and light yellow.

4.4.7. Tuber eye distribution

Potato genotypes showed moderate variation in tuber eye distribution (Table 4.4.2). The studied genotypes GenoA, GenoI, GenoN and GenoQ were evenly distributed and the rest of the genotypes were predominantly apical.

4.4.8. Tuber eye depth

Tuber eye depth of different genotypes showed moderate variation (Table 4.4.2). Among the genotypes studied GenoF was deep and GenoA, GenoG, GenoP, GenoQ, GenoV, GenoX, GenoY and GenoGG were medium and 12 genotypes were protruding while the rest were shallow.

Table 4.1. Morphological characterization of qualitative characteristics.

Geno	**Growth Habit**	**Leaf Shape**	**Leaf Texture**	**Tuber Colour**	**Tuber Shape**	**Flesh Colour**	**Eye Depth**	**Eye D**
GenoA	Semi erect	Ovate	Coarse	Cream	Obovate	Cream	Medium	ED
GenoB	Spread	Ovate	Coarse	Cream	Obovate	White	Protruding	PA
GenoC	Spread	Ovate	Coarse	Light Cream	Elliptic	Light Yellow	Shallow	PA
GenoD	Erect	Lanceolate	Coarse	Cream	Elliptic	Yellow	Protruding	PA
GenoE	Erect	Lanceolate	Fine	Cream	Oblong	Light Yellow	Protruding	PA
GenoF	Spread	Ovate	Fine	Light Cream	Elliptic	Cream	Deep	PA
GenoG	Spread	Lanceolate	Coarse	Light Cream	Elliptic	Light Yellow	Medium	PA
GenoH	Spread	Ovate	Coarse & hairy	Slightly Dark Cream	Elliptic	White	Shallow	PA
GenoI	Semi erect	Ovate	Fine	Cream	Elliptic	Dark Cream	Shallow	ED
GenoJ	Erect	Lanceolate	Coarse	Dark Cream	Elliptic	White	Shallow	PA
GenoK	Semi erect	Ovate	Coarse	Cream	Obovate	Cream	Shallow	PA
GenoL	Semi erect	Ovate	Coarse	Slightly Dark Cream	Compressed Oblong	Dark Cream	Protruding	PA
GenoM	Semi erect	Ovate	Fine & hairy	Light Cream	Elliptic	White	Shallow	PA
GenoN	Spread	Ovate	Fine & hairy	Cream	Round	Cream	Protruding	ED
GenoO	Semi erect	Ovate	Fine	Light Cream	Oblong	Cream	Protruding	PA
GenoP	Semi erect	Ovate	Fine	Dark Cream	Elliptic	Light Yellow	Medium	PA
GenoQ	Semi erect	Ovate	Fine	Cream	Compressed	Light Yellow	Medium	ED
GenoR	Semi erect	Ovate	Coarse	Dark Cream	Long-Oblong	Light Yellow	Shallow	PA

Geno	**Growth Habit**	**Leaf Shape**	**Leaf Texture**	**Tuber Colour**	**Tuber Shape**	**Flesh Colour**	**Eye Depth**	**Eye D**
GenoS	Semi erect	Ovate	Coarse	Light Cream	Elliptic	Cream	Shallow	PA
GenoT	Erect	Lanceolate	Coarse	Light Cream	Elliptic	White	Shallow	PA
GenoU	Erect	Lanceolate	Coarse	Dark Cream	Obovate	Light Yellow	Protruding	PA
GenoV	Erect	Ovate	Coarse	Dark Cream	Long-Oblong	White	Medium	PA
GenoW	Semi erect	Lanceolate	Coarse	Cream	Elliptic	Cream	Shallow	PA
GenoX	Semi erect	Ovate	Coarse	Cream	Compressed	Yellow	Medium	PA
GenoY	Spread	Ovate	Coarse	Light Cream	Elliptic	Light Yellow	Medium	PA
GenoZ	Semi erect	Ovate	Fine	Cream	Elliptic	White	Protruding	PA
GenoAA	Erect	Ovate	Coarse	Light Cream	Compressed	Yellow	Shallow	PA
GenoBB	Spread	Ovate	Fine	Cream	Compressed	Cream	Protruding	PA
GenoCC	Spread	Ovate	Fine	Light Cream	Round	White	Protruding	PA
GenoDD	Semi erect	Ovate	Fine	Light Cream	Round	Cream	Protruding	PA
GenoEE	Spread	Ovate	Smooth/ glossy	Light Cream	Elliptic	Cream	Protruding	PA
GenoFF	Spread	Ovate	Fine & hairy	Cream	Elliptic	Cream	Shallow	PA
GenoGG	Semi erect	Ovate	Fine & hairy	Light Cream	Compressed	Light Cream	Medium	PA

Eye D- Eye distribution; ED- Evenly distributed.

4.5 Diversity index

The Shannon-Weaver diversity index estimate for qualitative traits exhibited diversity in most of the traits (Table 3.7). The diversity index was high for tuber shape (1.55), followed by tuber flesh colour (1.54) and tuber colour (1.18). The lowest diversity was observed in tuber eye distribution (0.36) and leaf shape (0.52). Leaf texture (1.17), tuber colour (1.18), tuber shape (1.55), tuber flesh colour (1.54) and tuber eye depth (1.17) were higher than the average diversity index which was 1.07.

Table 4.2: Shannon-Weaver diversity index of qualitative characteristics for potato genotypes.

Qualitative traits	**Shannon-Weaver (H')**
Growth habit	1.06
Leaf shape	0.52
Leaf texture	1.17
Tuber colour	1.18
Tuber shape	1.55
Tuber flesh colour	1.54
Tuber eye distribution	0.36
Tuber eye depth	1.17
Average diversity index	**1.07**

4.6. Discussion

The results obtained from this study showed a high diversity across the evaluated genotypes concerning leaf texture, tuber shape, tuber colour, tuber flesh colour and tuber eye depth. These results suggest that the genotypes have considerable morphological variation. Characters with low variation among the genotype were growth habit, leaf shape and tuber eye distribution. There was a high variation in leaf texture and tuber shape also showed a high variation with compressed-oblong, oblong, long-oblong, round, obovate, compressed and elliptic. Similar results were reported by Anoumaa *et al*. (2016) except that their results included an ovate shape. Salam (2011) reported two similar shapes, oblong and round. A high variation in tuber shape was also reported by Ghebreslassie (2017) which included round, long –oblong, compressed, oblong, irregular and flattened.

Genotypes showed variation in tuber colour, 6.1% were slightly dark cream, 15.2% dark cream, 39.4% were cream and 39.4% were light cream. The results were in contrast with results reported by Salam (2011) and Anoumaa et al. (2016) who reported genotypes with tuber colours that were red/reddish, brown and dark brown. Flesh colour also showed a high variation, 3% were light cream, 6.1% were dark cream, 9.1% were yellow, 24.2% were white, 24.2% were light yellow and 33.3% were cream. The results are similar to results reported by Arslanolu *et al*. (2011), where the flesh colour was white and creamy; Anoumaa et al. (2016) who reported a flesh colour that was cream and Ghebreslassie (2017) reported a flesh colour that was yellow and white. Tuber eye depth showed a moderate variation, 3% were deep, 24.2% were medium, 36.4 were protruding and 36.4% were shallow. Similar results were reported by Anoumaa *et al*. (2016) and Ghebreslassie (2017) reported tuber eye depths that were shallow and deep. The study resulted into three categories of growth habit, erect (21.2%), semi-erect (45.5%) and spread (21.2%). The results were similar to results reported by Arslanolu et al. (2011) and Anoumaa et al. (2016). However, Arslanolu *et al*. (2011) also report growth habits that were prostrate and extremely erect and Anoumaa *et al*. (2016) reported extremely erect, sub-erect and decumbent. Leaf shape showed a slight variation, 21.2% lanceolate and 78.8% ovate. There was a slight variation in tuber distribution of genotypes, 12.1% were evenly distributed and 87.9% were predominantly apical and these results were similar to the result reported by Anoumaa et al. (2016).

4.7. Conclusion

In conclusion, the study presented qualitative morphological characters of advanced breeding lines which have not previously been characterized. The evaluated genotypes from this study showed that some genotypes possess various valuable characteristics including growth habit, leaf texture, tuber colour, tuber shape, tuber flesh colour, tuber eye distribution and tuber eye depth. The morphological characterization revealed high genetic variation among potato genotypes. These characterizations could help breeders choose and identify genotypes with desired traits for inclusion in variety breeding programs. The genotypes contain useful breeding material that might be employed as parental genotypes or breeding material in future variety development for tuber shapes and colours that are desirable for producers and consumers.

CHAPTER 5

Research overview and conclusion

5.1. General discussion

Potato is an annual crop grown for its starchy edible tubers and one of the major food crops grown worldwide. It is important for food security and income generation. Continuous and improved production is important in potato breeding. Production and crop improvement strategies that include breeding programs remain very essential for the crop. The success of potato breeding programs is highly influenced by the identification of genetic diversity in the gene pool. Crop genetic characterisation is crucial and necessary for giving adequate information on the features of certain genotypes, which helps in collection and selection management. The initial step in describing and classifying plant genotypes is morphological characterisation. Documented information of appropriate understanding of the variation of new genotypes plays a part in crop improvement strategies and selection. Advanced breeding lines are types that have not yet been released and are still being tested in a variety of environments. There has been no research conducted to study and document the agro-morphological similarities and differences of these breeding lines. The study intended to test new advanced breeding lines which have not been characterized before. This study needed to be conducted to identify and characterize these advanced breeding lines to confirm genetic differences using agronomical and morphological traits. The aim and objectives of the study were to characterize potato advanced breeding lines using agro-morphological traits and evaluate the yield and yield-related attributes under Mahikeng growing conditions.

5.2. Summary of research findings

The performance of advanced breeding lines showed a high variation. A high number of tubers per plant was recorded in GenoL (12.33), GenoM and GenoK (11.33) and GenoBB (11). The least number of tubers per plant was recorded in GenoAA (4.50), GenoJ (6.67) and GenoS (6.33). Higher individual tuber weight was recorded in GenoAA (139.76g), GenoQ (131.35g) and GenoJ (113.82g) and lower individual tuber weight was recorded in GenoCC (40.83g), GenoBB (62.82g) and GenoH (66.06g). High yield per plant was recorded in GenoL (835.33g; 27.85t/ha), GenoK (792.74g;

26.42t/ha) and GenoP (739.57g; 24.65t/ha) and low yield per plant was recorded in GenoCC (283.74g; 9.46t/ha), GenoBB (313.05g; 10.44t/ha) and GenoH (383.49g; 12.78t/ha). GenoAA and GenoJ had the highest individual tuber weight but did not attain high yield, because genotypes that had high tuber weight had a low number of tubers. This study revealed that GenoL (27.85t/ha), GenoK (26.42t/ha) and GenoP (24.65t/ha) produced the highest yield.

There was a comparison between the check cultivars and the advanced breeding lines. The highest yield recorded in check cultivars was in GenoC (30.82t/ha), GenoF (24.86t/ha) and GenoG (24.45t/ha) and low yield was recorded in GenoD (14.35t/ha), GenoA (15.06t/ha) and GenoB (19.67t/ha.). The highest yield recorded in this study was 30.82t/ha which is from the check cultivar GenoC (Mondial) and followed by GenoL which is an advanced breeding line. The advanced breeding lines are the ones that resulted in the lowest yield. The lowest yield recorded from check cultivar was GenoD (14.35t/ha) and the lowest from the advanced breeding lines was GenoCC (9.46t/ha). Overall, there were breeding lines that performed better than check cultivars and others resulted in the same yield.

The analysis of variance showed that the differences in plant height, the number of leaves, stems, branches and tubers, stem diameter, leaf area, chlorophyll content, individual tuber weight, tuber length and diameter as well as yield per plant of genotypes were statistically significant. The differences in days to emergence, emergence percentage and number of eyes of genotypes were not statistically significant. Plant height, number of leaves, branches and tubers, stem diameter, chlorophyll content, individual tuber weight, tuber length and yield per plant had a heritability of more than 80%, which means that the selection of these traits can be effective. Cluster analysis grouped the genotypes into three major clusters and each cluster was divided into two sub-clusters. The cluster analysis results were supported by the principal component bi-plot which grouped the genotypes that are positively correlated, whereas those that are far apart are negatively correlated. Correlation coefficient analysis showed that plant height, the number of stems, stem diameter and individual tuber weight had a strong positive correlation with the yield per plant. The principal component analysis showed that the first five principal components explained 71.21% of the variation in the current study, which indicates that there is strong genetic variation among genotypes that can be exploited for breeding purposes.

The study presented quantitative and qualitative morphological characteristics of advanced breeding lines which have not been characterized. The evaluated breeding lines showed that some genotypes had valuable characteristics such as growth habit, leaf texture, tuber colour, tuber shape, tuber flesh colour, tuber eye distribution and tuber eye depth. In qualitative traits, the crop growth habits were divided into three groups: erect, semi-erect and spread. The most observed growth habit was semi-erect (45.5%). The highest yielding advanced breeding lines (GenoL, GenoK and GenoP) were all semi-erect and the lowest yielding advanced breeding lines (GenoH, GenoBB and GenoCC) were all spread and had the least stem diameter. Ovate leaf shape was the most dominating at 78.8% and coarse leaf texture was the most dominating one at 51.5%. Some 48.5% of the genotypes had elliptic tubers. Cream (39.4%) and light cream (39.4%) tuber colours were the most observed colours and cream (33.3%) for flesh colour. The most recorded tuber eye depth was protruding (36.4%) and shallow (36.4%) and 87.9% of genotypes tuber eye distribution were predominantly apical.

5.3. Conclusions

The overall objective of the study was to characterize potato advanced breeding lines based on agronomical and morphological traits. The study was successful to characterize the genetic diversity among potato genotypes. The study showed a wide genetic variability among the 33 potato genotypes. The morphological characterization also revealed high genetic variation among potato genotypes. These characterizations could help breeders choose and identify genotypes with desired traits for inclusion in the plant variety breeding programs. The genotypes contain useful traits that will be employed as parental genotypes or breeding material in future variety development.

5.4. Recommendations

This evaluation should be performed under different environmental conditions and different seasons for further confirmation of the presented results from the current study. Molecular characterization of the potato advanced breeding lines is also recommended to support these present findings by categorizing differences that are not caused by environmental factors. The continued selection of new breeding lines until lines that outperform the check cultivars is also recommended.

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