MASTER THESIS

T.R.
NİĞDE ÖMER HALİSDEMİR UNIVERSITY
GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCES
DEPARTMENT OF AGRICULTURAL GENETIC ENGINEERING

GENOTYPE X ENVIRONMENT INTERACTION AND STABILITY ANALYSIS OF POTATO BREEDING LINES

ERIC KUOPUOBE NAAWE

September 2020

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Supervisor
Prof. Dr. Mehmet Emin ÇALIŞKAN

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The study titled “Genotype by Environment Interaction and Stability Analysis of Potato Breeding Lines” and presented by Eric Kuopuobe NAAWE under the supervision of Prof. Dr. Mehmet Emin ÇALIŞKAN has been accepted as Master of Science thesis by the jury at the Department of Agricultural Genetic Engineering of Niğde Ömer Halisdemir University, Graduate School of Natural and Applied Sciences.

Head : Prof. Dr. Mehmet Emin ÇALIŞKAN, Niğde Ömer Halisdemir University, Ayhan Şahenk Faculty of Agricultural Sciences and Technologies, Department of Agricultural Genetic Engineering

Member : Assoc. Prof. Dr. Ufuk DEMİREL, Niğde Ömer Halisdemir University, Ayhan Şahenk Faculty of Agricultural Sciences and Technologies, Department of Agricultural Genetic Engineering

Member : Assist. Prof. Dr. Necmi BEŞER, Trakya University, Faculty of Agriculture, Department of Genetics and Bioengineering

CONFIRMATION:

This thesis has been found appropriate at the date of 21/09/2020 by the jury mentioned above who have been designated by Board of Directors of Graduate School of Natural and Applied Sciences and has been confirmed with the resolution of Board of Directors dated …./…./2020 and numbered ……

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Prof. Dr. Murat BARUT

DIRECTOR

DECLARATION OF THESIS

I declare that this thesis was written by myself, and I further confirm that all information included in this Thesis is scientific and is in accordance with the University's rules and regulations. Any information and materials used from external sources as well as help received and all sources used in preparing and finalizing this thesis research work, have been duly acknowledged in the thesis.

Eric Kuopuobe NAAWE

SUMMARY

GENOTYPE BY ENVIRONMENT INTERACTION AND STABILITY ANALYSIS OF POTATO BREEDING LINES

NAAWE, Eric Kuopuobe
Nigde Omer Halisdemir University
Graduate School of Natural and Applied Sciences
Department of Agricultural Genetic Engineering

Supervisor :Prof. Dr. Mehmet Emin ÇALIŞKAN

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This study was conducted in 2019 to evaluate genotype by environment interaction (GEI) and stability analysis of twelve potato breeding lines and three standard cultivars in three different environments in respect to yield and quality traits. Finlay and Wilkinson's regression model, and Additive Main Effects and Multiplicative Interactions (AMMI) analysis were used to evaluate GEI and stability of potato genotypes. There were highly significant ($p \leq 0.01$) effects of genotype (G), environment (E) and GEI on yield and quality traits of potato genotypes tested. The breeding line MEÇ1407.17 gave the maximum yields of 967.0 g/plant, 41.77 t/ha and 41.60 t/ha while Russet Burbank produced the lowest yields of 400.8 g/plant, 17.04 t/ha and 16.66 t/ha for total plant yield, total tuber yield and marketable tuber yield, respectively. The breeding lines gave higher dry matter content and specific gravity than standard cultivars. The highest dry matter content (25.6%) and specific gravity (1.106) were obtained from the breeding line of MACAR1402.10 while Agria gave the lowest values of 19.15% and 1.076. Sivas location was the best environment in terms of tuber yield. The breeding lines MEÇ1407.17, MEÇ1407.05, MEÇ1407.08 and MEÇ1411.06 were identified as candidate cultivars due to their high tuber yield and stable performances across different environments.

Keywords: Potato, cultivar breeding, adaptation, AMMI, Finlay and Wilkinson

ÖZET

PATATES ISLAH HATLARININ GENOTİP X ÇEVRE İNTERAKSİYONU VE STABİLİTE ANALİZİ

NAAWE, Eric Kuopuobe
Niğde Ömer Halisdemir Üniversitesi
Fen Bilimleri Enstitüsü
Tarımsal Genetik Mühendisliği Anabilim Dalı

Danışman : :Prof. Dr. Mehmet Emin ÇALIŞKAN

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Bu çalışma, oniki patates ıslah hattı ve üç standart çeşidin verim ve kalite özellikleri açısından üç farklı çevredeki genotip-çevre interaksiyonu (GEI) ve stabilite analizlerini yapmak amacıyla 2019 yılında yürütülmüştür. Patates genotiplerinin GEI ve stabilitelerini belirlemek için Finlay ve Wilkinson'un regresyon modeli ile Eklemeli Ana Etkiler ve Çarpımsal İnteraksiyonlar (AMMI) analizi kullanılmıştır. Denemeye alınan patates genotiplerinin verim ve kalite özellikleri üzerine genotip, çevre ve GEI'nun çok önemli ($p \leq 0.01$) etkilerinin olduğu belirlenmiştir. MEÇ1407.17 ile sırasıyla bitki verimi, toplam yumru verimi ve pazarlanabilir yumru verimi açısından en yüksek değerleri verirken, aynı özellikler açısından en düşük değerler sırasıyla ile standart Russet Burbankçeşidinden elde edilmiştir. Denemeye alınan tüm ıslah hatları standart çeşitlere göre daha yüksek kuru madde oranı ve özgül ağırlık değerlerine sahip olmuşlardır. Ortalama en yüksek kuru madde oranı (%25.6) ve özgül ağırlık (1.106) elde edilirken, her iki özellik açısından en düşük değerler sırasıyla %19.5 ve 1.076 ile standart Agria çeşidinden elde edilmiştir. Yumru verimi açısından Sivas lokasyonu en iyi çevre olarak belirlenmiştir. Islah hatları MEÇ1407.17, MEÇ1407.05, MEÇ1407.08 ve MEÇ1411.06 tüm çevrelerdeki yumru verimi ve stabil performansları nedeniyle ümitvar çeşit

***Anahtar Sözcükler*:** Patates, çeşit ıslahı, adaptasyon, AMMI, Finlay ve Wilkinson

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SYMBOLS AND ABBREVIATIONS

Symbols	**Description**
AMMI	Additive main effect and multiplicative interaction
BTN	Big tuber number
CV	Coefficient of variation
DF	Degree of freedom
DMC	Dry matter concentration
E	Environment
FAO	Food and agricultural organization
G	Genotype
GEI	Genotype by environment interaction
GLM	Generalized linear model
IPC	Interaction principal component
LSD	Least significant difference
MTW	Marketable tuber weight
MTY	Marketable tuber yield
MTN	Medium tuber number
NSP	Number of stem per plant
NTP	Number of tuber per plant
PH	Plant height
pH	power of hydrogen proton
SE	Stand establishment
SG	Specific gravity
STN	Small tuber number
TPY	Total plant yield
TTY	Total tuber yield
USDA	United State Department of Agriculture
%	Percentage
°C	Degree centigrade

CHAPTER I

INTRODUCTION

The current global population growth and the glaring effects of climate change behoves on plant breeders and agronomists to work assiduously to identify high yielding, and stable crop varieties to meet the food security and nutritional needs of human life. Population growth and its counterparts; industrialization and urbanization are drastically reducing arable lands, degrading the fertile agricultural fields, diversification of agro-zones, establishment of intra-climate modification, and make it difficult for cultivated crops to adopt and give high and stable yield (Islam and Karim, 2020). Plant breeders and agronomists need to keep pace with this trend of rising in population and climate change at all costs to sustain life through the breeding of high yielding and stable crop genotype.

Potato (*Solanum tuberosum* L) is a vital annual tuber crop of the *Solanaceae* family which is ranked the 1st and 3rd most important tuber and food crop respectively on a global scale per human consumption (Devaux et al. 2014), and is cultivated in over 100 countries for its nutritional value. The global production increased from 267 million metric tonnes to about 374.5 million metric tonnes since 1983, with approximately 19.25 million hectares of cultivated land area. The *Solanum* genus is one of the 98 genera of the *Solanaceae* family of which potato is the most important non-grain crop with approximately 5000 cultivated species. Potato is rich in carotenoids, flavonoids, caffeic acid, Vitamin A, B6, and C, carbohydrates (Ezekiel et al., 2013) and antioxidant properties which help in digestion, heart health, blood pressure maintenance, lower risks of stroke, brain function, and nervous system coordination. It is used in various ways such as French fries, chips, dehydrated potatoes, freshly used products, and alcohol production.

Food security is a global issue and no country has escaped the zone of food insecurity despite its level of development. It is defined as the access to sufficient, safe, and nutritious food always physically, socially, and economically to meet the dietary needs and food preferences for active and healthy living (Gibson, 2012). The diverse golden benefits of potato, its high yield per unit area than cereals and other major crops (Miheretu et al., 2014) including its diverse agronomic and climatic features led to its diversified

distribution in the temperate, subtropical and the Mediterranean zones from Peru (centre of origin) in the South American continent. This triggered global interest and the recommendation of the International Potato Center (CIP), the Food and Agriculture Organization of the United Nations (FAO), and food processing industries have taken a keen interest and acting as the major driving force behind the growth of the potato cultivation and market (Floros et al., 2010), as food security, poverty alleviation, and global health improvement crop (FAO, 2017). This has projected the crop average production growth rate (CAPGR) at 1.06% during the 2019-2024 forecast period (FAO 2017) with competing production efforts among nations including Turkey in recent times which increase potato demand and consumption.

The rise in population along with climate change has diversified agro-ecological zones in the world which affect the biological and physiological yield performance of crops (Raza et al., 2019) making adaptation very difficult for crops (Onyango, 2019) due to differences in traits, resistance and /or susceptibility (Dube et al., 2016; Di Vittorio et al., 2016; Singh and Singh, 2017). Upon climate change, previously cultivated fields behave and present themselves as different agro-zones (FAO, 2017) and so affecting crop adaptation to the different agro-ecological environments (Nyahunda and Tirivangasi, 2019). Anthropogenic activities including other biotic and abiotic stresses induce soil nutrient depletion hinder the progress of potato breeders, as the energy and efforts of potato breeders do not reflect the yield output and so mitigating against the full realization of potato yield and production to meet market demand (Kang et al., 2004; Voss-Fels et al., 2019).

It is worthwhile for plant breeders to keep pace with these effects through the sustainability of agriculture (Lammerts van Bueren et al., 2018) to identify strategies to breach the production gap and realization of the potentials of potato to feed the ever-rising global population. Agronomist and potato breeders in their role to feed the world has employed genotype by environment interaction and stability analysis in their breeding programs as a mechanism to produce new potato cultivars suitable for the diverse agro-ecological conditions, adaptation, and yield stability levels created by climate change and to meet global consumer demand and preference (Kivuva et al., 2014; Aliche et al., 2018).

Genotype by environment interaction (GEI) is a multifactorial phenomenon that leads to the differential phenotypic expression of genotypes qualitatively and quantitatively because of different environmental parameters and nutrient accessibilities (Kivuva et al., 2014). The extent of response of a genotype to environmental fluctuation defines the genotype as wide or specific adaptation, and the resilience of the genotype against environmental fluctuation defines its stability. This phenomenon is a fundamental principle in all fields of agriculture in the identification of desired, suitable, and stable genotypes by reducing the association between phenotypic and genotypic values and cause a natural selection of living organisms from one environment to another. GEI has been employed in several crop breeding studies to facilitate selection and cultivar certification which brings about suitable crop production, adaptation (Raymundo et al., 2018; Ngailo et al., 2019), release and provision of the right cultivar and thus the study of GEI and stability are never out of breeding programs. Though this delay certification processes (Dwivedi et al., 2019; Rono et al., 2016), breeders can identify superior cultivars, and the best environments for the crop cultivation This has necessitated this research on potato in Turkey over diverse environmental locations to identify potato breeding lines with broad (general) and specific adaptability before registration as a new cultivar.

The analysis of GEI and stability parameters have been made feasible by the development of several statistical tools and models. These statistical models and tools have been employed in several crops including potato globally either singly, jointly or in comparison with other models and tools. These evaluate and estimate the interaction and relationship of crop genotype and environment (Hongyu et al., 2014) through regression coefficient bi (Finlay and Wilkinson, 1963), the sum of squared deviations from regression S2di (Eberhart and Russell, 1966), stability variance σ2 (Shukla, 1972), coefficient of determination and coefficient of variability (Francis and Kannenberg, 1978) and stability parameters of α′ and λ (Tai, 1971). These models include; general linear model (GLM) procedure of SAS software, bilinear models (AMMI and GGE), GENSTAT software among others to perform principal component analysis, ANOVA, regression on the mean, and factorial regression models for the establishment of adaptability and stability analysis of GEI.

Having said this, the aim of this research was to investigate the adaptability and stability levels of different potato breeding lines through the yield performance analysis of the genotype in different environments.

CHAPTER II

REVIEW OF LITERATURE

2.1 Biology of Potato

Potato (Solanum tuberosum L.) belonging to the Solanaceae family (nightshade) consists of solitary or cymose inflorescence which have bisexual flowers, hermaphroditic syncarpous, hypogynous, and diverse floral colours. The floral whorls consist of the pentavalent calyx, corolla, and stamens with each united and valvate aestivated, and its gynoecium is bi-pistillate with superior ovary. Potato is a self-pollination plant and can also exhibit cross-pollination with mostly green berry or capsulate fruits, mostly green with the axile type of placentation containing endospermous seeds of about 150 on average. Its leaves are simple to pinnately compound, having net venations and of an alternate breaching pattern.

Potato cultivation takes four to nine months from sowing to harvest, due to different genotypic makeup and origin (Maresma et al. 2019) requiring temperatures of 15 to 20˚C, pH of 4.8 to 8.5 for optimum yield and in diverse soil types leading to differences in maturation period. Potato is mostly cultivated on ridges to prevent tubers exposure to light which makes the tubers green; an indication of increased glycoalkaloids and solanine levels, which are hazardous to human health (Chowański et al., 2016). The tubers are underground swollen stems (rhizome or stolon), with auxiliary buds (eyes) which develop into a new shoot and scaly leaves. The crop is propagated vegetatively by planting pieces of tubers (botanical seeds) and from the sexually formed seeds. Its tubers are morphologically oval to round, of about 20% dry matter and 80% water composition, with varied flesh and skin colours, and sizes due to cultivar genetic makeup, agronomic practices, soil type, location, temperature, maturity, postharvest storage types and conditions.

2.2 Taxonomic and Genetic Diversity of Potato

Potato (Solanum tuberosum) is a genetically diverse plant in the Solanum with both domesticated and wild types of about 1500 to 2000 species (Burton, 1989) with two

groups; tuber-bearing species (Petota section) and the non-tuber bearing species (Etuberosa). Hawkes (1990) has also sub-grouped the tuber-bearing as Potatoe and Estolonifera whiles the non-tuber-bearing as Etuberosa and Juglandifolia 228 species, whiles Spooner and Hijmans (2001) outlined 196 species, and Spooner (2009) reported 110 species. Spooner et al. (2007) stated that 141 infra-specific taxa of potato exist within the cultivated potato germplasm. In 2016, Spooner et al., added the S. tuberosum as a member of the tuber-bearing potatoes and reported that, 232 wild species. The wide variation in the wild species in the gene pool and distribution is an indication of high tolerance to biotic and abiotic stresses (Machida-Hirano, 2015). Wang et al. (2017) collected and identified 288 different species of potato using SSR and AFLP techniques which indicated a high genetic diversity with different levels of biotic and abiotic stresses resistance and adaptabilities.

Several taxonomic classifications of potato had been given which is blamed on interspecific hybridization, sexual and asexual reproduction, species divergence, auto- or allopolyploidy, phenotypic plasticity, high morphological similarity among species among others (Spooner, 2009; Machida-Hirano, 2015). Machida-Hirano (2015), stated that cultivated potato varieties are either landraces, native varieties, or improved varieties with variety of tuber shapes, skin, and flesh colours (CIP, 2014) and grow within elevations of 3000–4000m above sea level.

Potato is cytologically diploid (2n = 2x = 24), triploid (2n = 3x = 36), tetraploid (2n = 4x = 48), pentaploid (2n = 5x = 60) or hexaploid (2n=6x=72) with a basic chromosome number of 12 (Gavrilenko, 2007). While the diploid, tetraploid, and allohexaploids are sexually fertile, the triploid and pentaploids are sexually sterile reproduced by vegetative propagation. About 75% of the Solanum tuberosum species are the diploids which and self-incompatible, the tetraploid 15% and the remaining are self-compatible, express inbreeding depression and male sterility. (Watanabe, 2015). Spooner et al. (2007) reclassified the cultivated potatoes as S. tuberosum (the Andigenum group consisting of diploids, triploids, and tetraploids and the Chilotanum group consisting of lowland tetraploid Chilean landraces); S. ajanhuiri (diploid); S. juzepczukii (triploid); and S. curtilobum (pentaploid). The S. ajanhuiri (Hawkes, 1990, Spooner et al., 2007) is believed to have originated through natural hybridization between diploid cultivars of S. tuberosum (Andigenum group) and S. megistacrolobum. The S. juzepczukii traces its

origin the diploid cultivar of S. tuberosum L. Andigenum group, and S. acaule Bitter (Rodríguez et al. 2010) whiles the S. curtilobum is from the tetraploid forms of S. tuberosum L. Andigenum group (S. tuberosum subsp. andigenum) and S. juzepczukii Bukasov (Hawkes, 1990; Rodríguez et al., 2010) are tolerance and cultivated in frost affected areas within 4000m (Spooner et al., 2010) and content high glycoalkaloids with a bitter taste and detoxified by freeze-drying for human consumption. The triploid S. chaucha is naturally hybridized between S. tuberosum subsp. andigena and S. stenotomum and the S. phureja (2n = 2x = 24) are identified as the short-day plant with low tuber dormancy whereas S. stenotomum (2n = 2x = 24) the most primitive and first domesticated potato from the diploid wild forms which is involved in the establishment of other cultivated species Huamán and Spooner (2002) presented a revised classification of S. tuberosum on morphological basis to possess eight cultivar groups as Ajanhuiri, Andigenum, Chaucha, Chilotanum, Curtilobum, Juzepczukii, Phureja, and Stenotomum and in 2007 Spooner et al., grouped it into four.

2.3 Origin and History of Potato

Potato origin is traced to the South-American continent in Peru and Bolivia, and its domestication started between 800 and 500 BC by the Inca indigents (Spooner et al., 2005) and its archaeological history date back to 2500BC (Harris et al., 2014). Their distribution started in 1532 to Spain and later to major parts of the European continent in the 1600s. Between 1600 and 1800s, the significance of potato rose and distributed globally to its current regions with intensified cultivation and production. Potato initially faced acceptance challenges in Europe with great suspicion as treat to human when it was introduced, because they contain toxic substances such as the glycoalkaloids. It was associated with leprosy or have narcotic agents (Kim and Lee, 2019) until it was discovered as a food crop in Ireland in Europe and the North Americas around the end of the 17th century. This discovery and climatic, soil suitability, the high yielding and energy content of the crop per hectare more than other food crops speedily increase the popularity of the potato for several societal and economic reasons. Its special great influence on the rise in the Irish population has been associated to be the turning point and today it is a global crop cultivated in over 100 countries and within latitudes 70° N to 50° S at an altitude of 4,000 m from sea elevation (Çalışkan et al., 2010).

2.4 Potato in Turkey- Past and Present

The commercialized cultivation of potato (patates as in Turkish) in Turkey started around 1872, about 72 years since its introduction into the Anatolia region of the country from the Russian Caucasus. From its introduction with some local varieties called ruskartoe, potato cultivation and consumption has progressively grown till date, making the country to become the second biggest producer of potato after Iran in the whole of the Middle East's as of 2007. Nationwide, potato (patates) is second to tomatoes (domates) as a horticultural crop grown in about 158 000 ha of land. The Anatolian region in Turkey being the most important cultivation zone of the country, account for almost half of the production area with intensive cultivation being conducted in the Aegean and Mediterranean coasts. For a decade now, Nigde; located in the central parts of Turkey, has become the best cultivation city of potato.

Turkey is currently ranked the 14th producer of potato globally with a cultivated area of 144,706 hectors as of 2016. Potato is roughly about 170 years in Turkey as it is stated to have existed in the country during the 1850s. There exist records of the crop production in the Erzurum province in the Anatolia region since the 1870s (Şenol, 1971; Çalışkan et al., 2010). Reports had it that, the potato was introduced into Turkey through the Anatolia region from Russia and Caucasia by several immigrants during the time. This is supported by the fact that in the Eastern Anatolia region, potato still has a Russian name “kartol”. During this time, the production of potato realized slow growth until after the establishment of the Turkish Republic that saw production increasing massively in the country (Çalışkan et al., 2010). The production increase from 73 thousand tonnes in 1925 to 4.5 million tonnes in 2010; about 61 times increase after 85 years. Çaliskan et al. (2010) attributed this rise to the 1970 national potato project and the 1980s subsidization of the private sector potato production by the government. It is stated that, coming down from 1999 to 2009, the area and production of potato cultivation declined by 35% and 28% respectively.

In 2014, the area cultivation of potato in Turkey was 128 thousand ha accounting for a yield of 4.1 million tonnes (Anonymous, 2014), of which a greater percentage of the planting seeds are imported from about 16 different countries. Over the years, the Turkish potato industry had relied on potato cultivation seeds from outside the country to supply

growing materials to potato farmers, this cost the country a lot of money. In 2016, through a research project called "Turkey's First National Potato Seed Production" by Turkey's Food, Agriculture and Livestock Ministry's Potato Research Institute, led to the registration of two varieties of the first domestically grown potato seeds; Fatih and Onaran2015. Ozkaynak et al. (2018) research to develop virus tolerant potato varieties in Turkey from 2008 to 2016, release 4 early and 3 main potato varieties with high adaptation ability, high yield, and good quality characteristics to be used in commercial and large-scale production in the country, including other sister countries. Similarly, the Nigde Potato Research Institute has trademarked 'Nahita' a national potato variety and 7 other varieties in 2018 which were to be grown in 15 different countries and domestic breeding companies in 2019. The goal of these along with several other researches ongoing in the country is aimed to produce domestic planting seeds potato for the country and cut down the dependence on imported seeds and varieties into the country.

2.5 Production Trend of Potato

The high calorie properties of potato per acre than other food crops as identified by the Americans and Europeans when introduced from the West Andes have greatly improved food security. This, coming to the knowledge of other continents is stated to be the leading force for the population increase in the American and European territories since the 17th century (Nunn and Qian, 2011; Lisiecka et al., 2019). The potato has thus become the most important root crop globally and the 4th most grown crop overall making it the third important food crop after wheat and rice. These reasons have led to a remarkable change in global potato production, especially in Asia some decades ago, and uprising Africa. America and Europe were the historical potato production and consumption zones where per capita earnings, and consumption approaches hundreds of pounds such as in Poland, Germany and Russia with relatively lower production and consumption in Asia and Africa (Lisiecka et al., 2019). Potato growth and production had hence increased rapidly than any food crop in Africa and Asia since the 1960s. In 2005, for the first time, the combined potato production of Africa, Asia, and South America exceeded that of Europe and the United States (de Haan and Rodriguez, 2016). And today, China, India, and Russia are by far the largest producers in the world, with a national production output of 88, 45, and 30 million tons, respectively, registered in 2013, compared with 52, 19, and 9 million tons for the 28 member countries of the European Union, the United States, and

the centre of crop origin, respectively. Over 3 decades (1981–2011), the total potato cropping area in the Americas and Oceania has remained stable. However, during that period, Africa and Asia have seen staggering growth, with 300% and 237% increases in total area. In contract, the cropping area in Europe halved during that period.

Now, high competition exists between America, Europe, the Asian countries, and other developing nations with China dominating global production and consumption since 2010 (FAOSTAT, 2019; Lisiecka et al., 2019). In 2019, China lead the global potato production with 93M tonnes followed India with 51M tonnes and Ukraine with 23M tonnes, constituting about 45% of global production, while Turkey is placed 20th with 4.55M tonnes. These surpassed the then leading potato producing countries such as Germany, the United States, Russia, and Poland, which is expected to continue in the coming years (FAOSTAT, 2019). Other developing countries has joint hands with China in the potato production and now at a minimum of 70% global production of potato with a 1% annual growth rate in the developing countries and a 1% decrease in production in the developed countries since 2010. This trend is due to governmental actions in the developing countries aimed at boosting food security by promoting the cultivation and consumption of potato especially by the Chinese Academy of Agricultural Sciences in 2015 whiles there is a progressive decline in potato production by acres area and farms in the United States of about 2.9 million from the 1950s to 2015 in acres and about 36 million in farms from 1980s to 2012 (Lisiecka et al. 2019) but an increased in yield over the years due to improving breeding technologies (FAO, 2017).

2.6 Quality Traits of Potato

Potato quality traits are essential in breeding programs for agronomic and industrial purposes. The quality of a potato cultivar is dependent on yield resilience and stability, and the consumer acceptability of the tuber seeds by other breeders, and consumer acceptability and preference (Halterman et al., 2016; Hameed et al., 2018). The agronomic quality of potato is linked with consumer acceptability such as yield, dry matter content, specific gravity, beta carotene content, reducing sugars, drought-tolerant, pest and disease resistance, tuber shape, and eyes set in the determination of good potatoes for breeding and the consumption market (Halterman et al., 2016).

Potato tuber quality is an important aspects of potato production, which biologically; consider the proteins, carbohydrates, minerals concentrations, flavour, and texture and industrially as tuber shape, cold sweetening, starch quality, and colour of the processed product (Carputo et al., 2005). Potato quality is also categorised as external and internal quality traits whose preference change with market specificities of which skin colour, tuber size and shape, and eye depth forms the external traits, whiles nutrient, culinary, after-cooking and or processing quality, dry matter content, flavour, sugar and protein content, starch quality, type and amount of glycoalkaloids form the internal traits. Koch (2018) reported that consumers on a general note, prefer tubers with a firm and smooth skin without a hollow heart, no cracks or injuries, no protuberances, no recessed eyes or stolon attachment and tuber sizes of 150-200g either for fresh or other industrial uses.

High phytochemical absorbance frequency is a very important quality trait (Koch, 2018), which is a good source for several minerals in the diet (Andre et al., 2007; Subramanian et al., 2011). Dry matter content (DMC) is very important in potato in chips and French fry processing. Tubers with high DMC have fewer reducing sugars, good greasy texture chips, low bitter pit diseases, and give high quality French fries and chips (Koch, 2018) with low oil absorbance, and low acrylamides production in the production process. Breeders prefer medium tuber seed with good growth vigour devoid of diseases and pests, produce more stems.

Cultivar, time storage method, and agronomic practices affect potato quality. Accordingly, different potato cultivars have different quality features such as tuber yield, DMC, stem number per plant, and respond differently to mechanical stresses during harvesting transportation, and tuber grading. This mechanical impact leads to physiological weakness, cracks development, and reducing the sprouting potential of the sowed tubers. The length of storage of the tubers also affects the germination of the tubers as longer storage time reduces the germination potential of the tubers. It is recorded that, field practices such as irrigation, weed control, mineral especially potassium, phosphorus and nitrogen application have a great agronomic effect on the quality traits of potato. Lack or delayed irrigation retard growth and time to tuber initiation of potato.

Potato cultivars have diverse agronomic features physically and chemically and so bred for specific functional and nutritional traits valuable for breeders and the consumer

market, thus the agronomic and breeding classification of potato varieties are based on features of the plant and tuber characteristics (Furrer et al., 2017). It has been reported that vegetative features of potato are based on the number of stems per the plant, plant height, leaf shape and number, branching-pattern and types, leaf and stem texture, and the flower colour. The potato yield or tuber features for their characterization are dependent on tuber shape, number of buds or eyes, skin texture, skin and flesh colour. Physiologically, breeders focus on the maturation type, distribution of pigmentation, disease resistance (Burton, 1989; Furrer et al., 2018), and the leaf senesces period.

Several parameters have been reported to affect potato tuber quality. Koch, 2018, in a study of the effect of potassium and magnesium nutrition on potato tuber quality and plant development, reported that; cultivar, agronomic practices, and type and time of storage affect tuber quality. It is also stated that tuber handling during and after harvest might cause mechanical injuries leading to tuber cracks and change in moisture content. Agronomic practices are a key determinant of potato tuber quality as it encompasses mineral nutrients such as potassium (K), nitrogen (N), phosphorus (P), water supply and biotic interactions. Potato is sensitive to drought and water stress and closes its stomata at low soil moisture deficits which leads to decrease photosynthesis and transpiration rates compared to other agronomic crops. Due to the shallow root zones of potato, it requires frequent water irrigation especially in areas of low soil water holding capacities and high evapotranspiration. Water deficiencies in potato fields cause reduced leaf area and foliage weight, dark cast and a wilted appearance which affect the photosynthetic frequency and the distribution of photosynthetic assimilate to the tubers leading to heat stress, tuber malformations, physiological disorders (brown centre, hollow heart, translucent end), and bruise susceptibility.

Nitrogen is a principal component of protein and chlorophyll and thus plays a major role in the growth, development as well as plant yield. Sandhu et al. (2014) reported that N and P fertilizers are the most important nutrient for potato plants which maintain higher haulm growth, tuber bulking, and high tuber number and dry matter production. Israel et al. (2012) show that the highest marketable yield (35 t ha^{-1}) was recorded with the application of 165 kg ha^{-1} of nitrogen and 60 kg ha^{-1} of phosphorus. Thus, N and P interaction influence marketable tuber of potato with an increase by 88% (Burtukan, 2016). Firew et al. (2016) in a research to determine the effect of nitrogen and phosphorus

on yield and yield components of potato under irrigation condition, stated that an application of nitrogen and phosphorus influences the yield of potato. They observed the highest yield at a rate of 56 kg ha^{-1} of nitrogen and 138 kg ha−1 of phosphorus application but beyond these yields reduces.

Similarly, Wubengeda et al. (2016) in an experiment in to determine optimal irrigation regime and NP fertilizer rate for potato found that yield of potato increase with increasing application of nitrogen and phosphorus up to a maximum tuber yield of 31.80 tha−1 at 244 kg ha^{-1} and 206 kg ha^{-1} of nitrogen and phosphorus application rate respectively. Desalegn et al. (2016) studied the effects of nitrogen and phosphorus fertilizer levels on yield and yield components of potato and recorded the highest yield by 361% over the control treatment from the combined rate of nitrogen and phosphorus 50/135 kg ha^{-1}.

2.7 Genotype by Environment Interactions in Potato

GEI as the differential phenotypic output due to corresponding effects of genotypic and environmental interactions which produce an array of phenotypes that fluctuate with varying environments. Agronomist and plant scientists are conscious of the significant flux in yield performance among cultivated crops in their research, due to interactions of genes with the environment over years. This made crops cultivar to fluctuate in their performance due to GEI and so impose a challenge in identifying superior cultivars (Badu-Apraku et al., 2012; van Eeuwijk et al. 2016; Raza et al., 2019 Kwabena et al. 2019). It is stated that understanding the interaction of genotype and environment (G×E) is important in achieving breeding objectives, identifying ideal test conditions, recommend the best environment for optimal cultivar adaptation, and reduce. Kang et al. (2004) stated that GEI is an ancient, universal principle that exist in all living organisms and categorised GEI into two broad segments as crossover and non-crossover interactions. It is stated that the significance of GEI is lost when the ranks of genotype over several environments do not change and thus crossover and non-crossover GEI do not exist.

Crossover interaction is the differential phenotypic output of cultivars to diverse environments with a change in rank order between environments which is interpreted by intersecting lines in the graphical display (Jalata, 2011; Adu, 2012; de Leon et al., 2016).

Crossover interaction is very vital for crop breeders as compared with non-crossover interaction as it gives breeders information of specific adaptation and aids to assess the interaction degree and frequency. It is non-additive and non-separable in nature, helps in the development of locally adapted crop cultivars with known phenotypic sensitivity to environments (Ortiz et al. 2007; Wolfe et al. 2015; Bustos-Korts, 2017). It established that no genotype has a superior phenotypic output in all instances in a series of selection over environments. Crossover interaction is the major hindrance in GEI due to uncertainties in the traits of a cultivar and so needs series of investigations in different environments (Cooper and Delacy 1994; Crossa et al. 2015; Muthoni et al. 2015). Yan et al. (2007) state that cultivars with high and stable yields showing little GEI interactions are the sole desire of breeders or agronomists which will lessen and save breeders time and resources. Non-crossover interaction is observed when the phenotypic rank of one genotype from one environment to another never cross as interpreted graphically by parallel lines. There may be a change in the individual yield magnitude of the genotype but not their superiority as the rank order of genotype across environments remains unchanged. The genotypes are genetically heterogeneous whiles test environments maybe homogeneous or genotype being genetically homogeneous while environments are heterogeneous (Ortiz et al. 2007; Morley et al., 2016).

Eberhart and Russell (1966) outlined stratification of heterogeneous agro-zones into small identical sub-zones with breeding programs aimed at specific sub-regions, and the selection of genotype with broad environmental stability as methods of developing genotypes with low G×E interaction. Crossa et al. (2015) classified these interactions into qualitative and quantitative forms of GEI as essential in breeding potato genotypes with specific adaptations. These are vital steps necessary for certification of breeding line with their agro-zones specificities (Alberts, 2004) and have being implored in the study of G×E interaction of potato and other crops (Biru, 2017), and is vital for heritability purposes (Caliskan et al., 2007; Kaya and Akcura, 2014; Demirel et al., 2017). High GEI leads to low heritability and so GEI emphasizes the need to breed exceptional genotype in different environments (Carvalho et al., 2109). Genotype by environment has been revealed to influence all stages of crop breeding (25 – 45% positively or negatively) as this affect the partitioning of resources and the heritability of traits (Kaya and Akcura, 2014; Tiwari et al., 2019; Li et al., 2020). Thus, multi-environment testing of potato crop reveals hidden traits of genotypes and help in the identification of specific and broad

adaptation of genotypes. Affleck et al. (2007) evaluated potato genotype in different environment and stated that, the yield performance, stability and quality traits of genotype vary with environment. They identified Russet Burbank and Umatilla Russet as low yielding genotypes and good for both French fry colour and total sugars quality whiles Cal White as stable and high yielding with average stability for French fry colour.

In 2017, Gurmu et al. found highly significant differences between evaluated traits in a study to estimate the magnitude of G x E interactions on yield stability and quality traits of sweet potato, whiles Ngailo et al. (2019) stated that GEI analysis is key for cultivar selection, release, and the identification of suitable production and test environments. In a study in Northwest China, to find the genetic variations of 26 potato genotype, Bai et al. (2014) found genotype G4 (L02277) high yielding and stable genotypes, G1 (T200882), G8 (L022718), and G2 (CK0708) as medium yielding and generally stable, and one mega-environment with several discriminating abilities among the environments. Changing environments affect the genotypic expression of crops resulting in inconsistencies in the phenotypic performance as genes are suppressed or expressed phenotypically with different environmental features because of GEI. This leads to cultivar segregation as manifested in changes in rank order of the genotype (crossover GEI), or alterations in genotype performance without affecting the rank order (Muthoni et al. 2015).

Day length is an agronomic factor that has a role in plant cultivation. Plants mostly inherit the climatic and diurnal conditions of their place of origin, giving off their best in the optimal conditions of their agro-zone of origin. Potato originating from the temperate climate of short-day length and cool temperature, perform best under these conditions (Porter and Semenov, 2005). Potato tuberization is induced by short days and prevented by long days and tuber initiation is early at low temperatures but delayed at high temperatures. Warm nights and long days' yield few to no tuber yield. Potato tuber formation can therefore be controlled in a greenhouse setup where photoperiod and temperature conditions can be altered but somewhat a challenge in field conditions (Pourazari et al., 2018; Kim et al., 2019). Temperature affect radiation use efficiency, photosynthesis, tuber initiation, and development of potato. High temperature affects photosynthesis of potatoes as optimal yield occurs at approximately 24°C and decreases drastically at 30°C, reducing stomatal conductance, facilitate leaf senescence, and divert

source-sink rate due to interrupted photosynthesis (Lehretz et al.,2019). This it is reported that metabolic and vegetative growth rates of potato slowed down while tuber development increase cooler temperatures but experience cold shock at extremely low temperatures. Optimum vegetative and reproductive growth of potato occur within 15 and 21°C where stolon initiation, tuber growth, dry matter content, and specific gravity are at their best deposition, and photorespiration, light interception, radiation use efficiency also at optimum rates. Unusual growth, multiple stolon formation, and abnormal tuber shape and development occur outside these temperatures. Potato yield is lost at high night temperatures due to reduced harvest index and delayed tuber induction, initiation of rapid tuber growth which leads to reduce apportioning of photosynthetic materials (Struik, 2007; Kim and Lee, 2019).

Plants are sensitive to water at all growth periods which might vary with species and cultivar. Too much water in a potato field is inhibitory to iron uptake resulting in unhealthy growth and yellowing of the leaves of the plants and tuber rotting occurs, leaching of nutrients, and spread of infections. This has been reported to cause potato yield loss to 25%. Soil moisture is important for the tuber development of potato plants during the growth cycles. It mitigates soil temperatures and results in uniform tuber sizes, shapes, high yield, high specific gravity, and starch content and reduce the levels of reducing sugars. Adequate moisture is needed for stolon initiation and tuberization which ensures the maximum number of potential tuber initiation and increases yield potential. Sprouting, flowering, tuber initiation and maturation, and early leaf senesces occur with an inadequate water supply, and the longer the periods of drought or low soil moisture, the higher the reduction in potato yield. Potato growth, adaptability, yield, and quality are particularly determined by soil and climatic parameters, agronomic practices, and genetic makeup (Hameed et al., 2018). Soil conditions contribute to agronomic traits and harvest traits. Aside from temperature, pH and nutrient levels of the soil affect potato growth and yield as they maintain good and healthy plants, and thus good quality tuber yield. Potato germination is adversely affected at soil temperature < 4°C, thus affecting the stand establishment of the crop due to low sprouting (Placide et al., 2019). High SG and DMC are related characters that are also temperature-dependent mostly occurring at 15 - 24°C during the tuber growth phase (Tessema et al., 2020; Wasilewska-Nascimento et al., 2020).

Potato yield and marketable tuber sizes are affected by soil pH lower soil pH yield fewer but larger tubers because of the insufficiency of potassium (K) in the soil. K helps in initiating many stolon's, and it is made available at higher soil pH above 4.5. Edaphic factors such as soil pH, Soil Organic Matter (SOM), Soil electrical conductivity (EC), Cation exchange capacity (CEC), and sodium adsorption rate (SAR) have been enlisted as soil quality parameters that influence GEI and crop yield (Puntel et al., 2016) as they determine the quantity and quality of mineral nutrients available for the crop usage (El-Ramady et al., 2018). Soil electrical conductivity (EC), an indicator of soil health, measures the amount of salts in soil (salinity of soil) that affects crop yields, crop suitability, plant nutrient availability, and activity of soil microorganisms which influence key soil processes. Cation exchange capacity (CEC) influences and provide a buffer against soil acidification. The ions associated with CEC include calcium (Ca^{2+}), magnesium ($Mg^{2+),}$ sodium (Na^{+}), and potassium (K^{+}) heavily affect soil nutrient availability, soil pH, and the soil's reaction to fertilizers and other ameliorants (Walker et al., 2008).

Nitrogen is an integral part of chlorophyll and influences photosynthesis. Proper N in the soil optimizes potato yield and quality (Muleta and Aga, 2019), whiles N insufficiency reduces growth and light interception, early crop senescence, and yield (Schisler et al., 2000; Slininger et al., 2007). Excess nitrogen results in a delay of tuber set, reduced yields, and reduced tuber dry matter content (Muleta and Mosisa, 2019), and cause nitrate leaching or runoff (Bach et al., 2013; Muleta and Mosisa, 2019) Generally, potato is processed for consumption through boiling, mashing, frying, etc., before consumption. These processes go through different mechanisms that influence the chemical and nutrient composition to maintain or decrease the quality of the processed products (Burgos et al., 2020). The texture and colour of potato chips and French fries is dependent on the starch and reducing sugar content of the raw potato tubers. The pattern and nature of the arrangement of the polysaccharides cell wall and parenchymatous cell determine the processed food quality and contribute to the tuber fibre content (Furrer et al., 2018). Generally, potato tubers with a small and closely packed polysaccharides cell walls and parenchymatous cells a hard and cohesive nature which is contrarily to tubers with large and loosely packed cells. These are important in the release of nutrients and starch digestion in the body (Singh et al., 2013).

The nutritional and processing quality of potatoes and potato products are affected to a larger extent by the starch structural characteristics and amylose-to-amylopectin ratio among cultivars (Burgos et al., 2020; Furrer et al., 2018). Temperature, storage facilities, and environmental conditions affect the processing and nutrient quality. A variety of cooking methods are used in cooking potatoes including roasting, baking, and microwaving. These techniques are reported to affect differently the endogenous nutrients in potatoes through leaching of water-soluble nutrients, degrading of heat-volatile nutrients, and draining of water which concentrates nutrients (Decker and Ferruzzi 2013). The water content of boiled potato is 77%, baked potato 75%, microwaved potatoes 72%, French fries 61%, and potato chips 2% (Decker and Ferruzzi, 2013; Robertson et al., 2018). These differences in water content also occur in serving sizes. It is reported that boiled and microwaved potatoes have a serving size of; 90 g, baked potato 138 g, French fries 85 g, whiles potato chips have a serving size of 28 g (Beals, 2019).

Potassium decrease from 421 mg/100 g to 328 mg/100 g in boiled potato and other minerals as they leach into the water whiles vitamin C degrade and decrease in thermal fluxes from 19.7 mg/100 g in raw potatoes to 7.4 mg/100 g in boiled potatoes (Furrer, 2018; Siddique et al., 2015). Less use of water in cooking has little impact on potassium and vitamin C concentrations, thus baking, microwave and frying has less effect on potassium but large effects on heat-sensitive nutrients. A research on the effect of cooking on potato phytonutrients reported that folate, CGA, and vitamin C increase, decrease, and stay unchanged after cooking (Lisiecka et al., 2019; Furrer et al., 2018; Féart et al., 2019). Phenolics content decreases by 50% in all cooking forms with slight differences between boiling and microwaving whereas anthocyanins extractability rises by 15-fold in potato (Perla et al., 2012; Lachman et al., 2013; Lisiecka et al., 2016). The quality of potatoes is used to characterize potato on composition, cooking characteristics, and use. Based on these, potato has been categorised into four; close (do not burst, readily break, don't crumble), soaty (same as waxy, but also watery and translucent), floury (often burst spontaneously, crumble easily), and waxy (firm flesh, only breaks down by kneading). These variations in the texture of potato are attributed to differences in dry matter content starch type and nutritional impact (Furrer et al. 2018) due to photosynthetic distribution. Floury potatoes have drier and mealier texture because of high amylose and starch content (20% to 22%) whiles the waxy type has amylopectin of ranging from 16–18%.

2.8 Yield Stability

Crop stability is important in any crop breeding program (Cobb et al., 2019; Voss-Fels et al., 2019) which is the consistency in yield of a crop in different environments, which must be conducted in the development of successful new genotype (Bach et al., 2013; Van Eeuwijk et al., 2016). Seed companies gained much interest in spatially stable crops while plant growers are interested in temporally stable. Miheretu et al. (2014) revealed Genotype 394640-539 as high yielding and stable across all environment. Potato genotype stability is stated to be understood accurately, as Yan and Kang (2003) established that, crop performance is a function of multi-factor effects determining stability. Stability has been considered as biological stability and agronomic stability.

Biological stability refers to genotype constant yield performance across environments. Biological stability is undesirable as agricultural sciences seek to improve and increase crop yield with improving agronomic practices. Agronomic stability is preferred by agricultural sciences as genotype performance is in relation to environmental inputs. Agronomic stability has been grouped into general adaptation, and specific adaptation. General adaptable genotypes yield well in a wide range of environments whiles in specific adaptation agronomic stability is manifested over a limited range of environments.

2.9 Model use in GEI Analysis

Several statistical models have been developed to identify high yielding and stable genotype of crops. Additive Main Effect and Multiplicative Interaction (AMMI) (Gauch, 1992) was developed to estimate the effect and relation between environment and agricultural crop performance. GGE biplot analysis has also been implored to identify mega-environments and the optimized environments for different genotype stating that GGE combined with other statistical tools is important for testing the stability and quality of new potato genotype (Affleck et al. 2007). GGE biplot model has been used widely in different crops to identify high yielding and stable crops varieties in different locations in GEI analysis (Yan and Kang, 2003; Yan and Tinker, 2006; Laurie et al., 2015). Bai et al. (2014) stated that the use of GGE techniques is a vital tool for summarizing, examining, and analysing potato trials for the investigation of interactions between genotype and multi-environments. The use of GGE biplot is important which has the ability to

graphically display a genotype and an environment into a pattern of "which– won – where", identify high yielding and stable genotypes and the best environment (Yan and Tinker, 2006; Yan et al., 2007) and provides the needed information about the genotype degree of stability and yield output. Muthoni et al. 2015 used additive main effects and multiplicative interaction (AMMI) analysis and genotype main effect and genotype x environment interaction (GGE) biplot analysis to estimate the magnitude of GEI on potato tuber yield and bacterial wilt resistance and best representative and discriminating environments for potato testing.

The additive main effects and multiplicative interaction (AMMI) analysis (Gauch and Zobel, 1997) that is based on the genotype main effect which is retained as additive effects, and the multiplicative component as the GEI treatment (Gauch and Zobel, 1988) has been adopted by researchers in several breeding studies. The genotypic main effects approach uses analysis of variance (ANOVA) for the effects caused by genotype and environments whereas the GEI component uses principal component analysis (PCA) for the GEI. AMMI has been employed in several GEI analyses including potato (Ngailo et al., 2019), sweet potato (Caliskan et al., 2007) and it successfully analysed GEI and stability. Wassu (2017) use AMMI to study genotype x environment interaction, stability and coheritability of tuber internal quality traits in potato cultivars which help in the selection of Bulle, Araarsaa, Guasa, Bete, Bubu, and Belete as stable potato cultivars for specific gravity, and Mara Charre, Chala, Bubu, Bedasa and Gera for starch content, and as stable genotype. Hongyu et al. (2014) stated that the use of AMMI in genotype × environment interaction studies brings accuracy, understanding and the structuring of interactions between genotypes, and the delineation of mega-environments and genotypes stability.

CHAPTER III

MATERIALS & METHODS

3.1 Plants materials

Fifteen (15) potato genotypes, which were consisted of twelve (12) breeding lines developed at the Agricultural Genetic Engineering Department, Niğde Ömer Halisdemir University, and three (3) commercial cultivars, were used in the study. The list of genotypes used in the study was given in Table 1. They were tested for yield and quality performances in three different locations, Niğde, Konya, and Sivas in 2019.

Table 3. 1. List of genotypes and genotypes codes, and environment names and codes, Genotypes

SN	Code	GENOTYPE	Pedigrees (♀ x ♂)
1	MCR1	MACAR1402.10	White Lady x W870
2	MCR2	MACAR1402.11	White Lady x W870
3	MCR3	MACAR1406.04	01.509 x Latona
4	MCR4	MACAR1406.07	01.509 x Latona
5	MCR5	MACAR1409.09	99.463 x Kolibri
6	MEÇ1	MEÇ1402.07	Alegria x Lindita
7	MEC2	MEÇ1402.09	Alegria x Lindita
8	MEC3	MEÇ1405.06	(Alegria x Challenger) x Borwina
9	MEC4	MEÇ1407.05	(GalaxChallenger) x (Allegria)
10	MEC5	MEÇ1407.08	(GalaxChallenger) x (Allegria)
11	MEC6	MEÇ1407.17	(GalaxChallenger) x (Allegria)
12	MEC7	MEÇ1411.06	Ke-11 x Jelly
13	AGRA	AGRIA	Quarta x Semlo
14	MADA	MADELEINE	Leyla x KO 85-1002
15	RUBB	RUSSET BURBANK	Mutated Burbank (no specific parent)

Environment								
SN	Code	Environment	SN	Code	Environment	SN	Code	Environment
1	NGDE	Nigde	2	SVAS	Sivas	3	KNYA	Konya

3.2 Experimental method

3.2.1 Site selection and location

The study was conducted in three different locations: Niğde, Konya and Sivas provinces in 2019. These were selected based on their similar crop growing seasons from April to October. Konya lies within 37.8746° N, 32.4932° E and it is 1029m above sea level with

yearly average temperature, rainfall, and relative humidity of 11.3 °C and 337 mm, and 52.2, respectively. Nigde lies within 37.9698° N, 34.6766° E and is 1244m altitude with yearly average temperature and precipitation of 10.3°C, and 338mm respectively whiles Sivas lies between 39°45′N 37°01′E at an elevation of 1,278 m. Sivas has an annual maximum, average and minimum temperatures of around 15.1°C, 8.9°C and 3.1°C, and an average yearly and monthly precipitation of 427.4mm and 35.6mm respectively. The monthly temperature and rainfall of the study site during the research period are presented in Table 3.2

Table 3.2 Monthly mean temperature and rainfall for Konya, Nigde, and Sivas in 2019

	Locations	May	June	July	August	September	October
Mean Temperature (^{o}C) (1981-2010)	Konya	15.7	20.4	23.6	23.4	18.9	12.7
	Niğde	15.3	19.7	22.9	22.7	18.2	12.4
	Sivas	13.6	17.4	20.4	20.5	16.5	11.0
Mean Temperature (^{o}C) (2019)	Konya	19.7	23.0	24.3	24.8	21.0	17.3
	Niğde	17.6	21.3	22.2	22.6	18.2	15.1
	Sivas	16.0	20.6	19.8	20.8	?	?
Rainfall (mm) (1981-2010)	Konya	38.6	20.5	7.8	5.6	11.3	29.7
	Niğde	46.4	24.5	5.7	5.3	7.6	30.4
	Sivas	58.8	34.8	10.3	5.9	16.7	41.0
Rainfall (mm) (2019)	Konya	5.4	31.8	8.2	2.0	10.2	6.4
	Niğde	26.2	43.4	8.3	6.0	6.0	13.7
	Sivas	18.8	48.4	18.6	6.0	?	?

Source: Turkish State Meteorological Service

3.2.2 Experimental design and setup

The field experiment was layout in a Randomized Complete Block Design with four replications in all three locations. Each plot was consisted of two rows of 8.1 m in length and 0.75 m apart. The crop was planted in Konya on 05/05/2019, Niğde on 16/05/2019, and Sivas on 20/05/2019. The seed tubers were planted using a two-row planter with 0.3 m in-row spacing and planting distance at a planting density of 54 tuber seeds per plot (27 tubers per row). Plots were fertilized with 150 kg/ha N-P-K before planting using a compound fertilizer (N–P–K) in the form of 15–15–15, and an additional 250 kg/ha N (as urea) was side-dressed as three split applications during tuber initiation and bulking stages in Sivas and Konya locations while the amount of basal and side-dressed fertilizers were 100 kg/ha N-P-K and 200 kg/ha urea in Niğde, respectively. The seed potato was treated with a fungicide (active ingredient: 100 g/l *Penflufen*+18 g/l *Prothioconazole*) at 20

ml/100 kg seed rate and an insecticide (active ingredient: 350g *Thiamethoxam*) at 20 ml/100 kg seed rate before planting. The experimental plots were irrigated with overhead sprinklers when needed in all locations. The pre-sowing herbicide (active ingredient: 70% *Metribuzin*) was applied to soil at the rate of 750 g/ha, and the plots were maintained as weed-free by hand weeding during growing period.

The harvesting was done on 09/10/2019 at Nigde location, on 11/10/2019 at Konya location and on 15/10/2019 at Sivas location using a two-row harvest machine. The harvested potato tubers were collected in bags per plot and labelled with the block and plot number. The tubers were transported to the Laboratory of Faculty of Agricultural Sciences and Technologies for grading, weighing, dry matter and specific gravity analysis.

3.3. Evaluated Traits

Stand establishment (%): The number of plants in each plot was counted at the flowering stage and the emergence rate was calculated as by dividing the plants germinated over the number of seed tuber sowed multiplied by hundred.

Plant height (cm): The heights of ten randomly selected plants for each plot were measured at the flowering stage using measuring tape at ±1 cm accuracy and their mean calculated.

Number of stems per plant: The number of main stems per plant was counted on ten randomly selected plants in each plot at the flowering stage and their mean number computed.

Tuber size grading (%): The total number of tubers of each genotype per plot was sorted into three grades: cull (<30 mm or damaged), the second class (30-50 mm in diameter), and the first-class (>50 mm), and the proportion of each grade in total weight was calculated.

Total tuber yield (t/ha): Total yield of each genotype was calculated by counting and weighing of all tubers in each plot.

Marketable tuber yield (t/ha): The marketable sizes of the tubers (>30 mm) was calculated using total yield and percentage of marketable tubers.

Number of tubers per plant: All tubers in each plot were counted and the number of tubers per plant was calculated by dividing the total tuber number with the number of plants per plot (stand establishment)

Mean tuber weight (g): Mean tuber weight was calculated by dividing the total tuber weight of each plot by the number of tubers of each plot.

Dry matter content (%) and specific gravity analysis

The dry matter content and the specific gravity of the potato tubers was measured by digital hydrometer PW2050 (Martin Lishman). Two kilograms of potato tubers were weighed in air and then in water to obtained displaced dry weight and the specific gravity of the tubers using Martin Lishman protocols.

Figure 3.1. Martin Lishmans's digital potato hydrometer (PW2050) used to measure specific gravity and dry matter content of potato crop

Chips and French Fry Quality

Two to four healthy potato tubers (plate a) were selected from each breeding line, replication, and location, and put into a plate and labelled with the genotype name, location, and replication code. The tubers were dry-cleaned with a wet towel and peeled with a handheld potato peeler (plate b). One to two peeled tubers were cut into 10 mm by 10 mm by 10 cm strips using a manual French fry chipper. The strips were rinsed in tap water, blanched for 1min at 100℃, and the water drained by transferring strips into a

stainless-steel sieve. The blanched strips were drained and air-cooled. The other one to two peeled tubers were also sliced using a potato chips slicer, rinsed with tap water, and drained off the water using stainless steel sieve. The blanched French fry strips and the sliced chips were deep-fried at 180℃ for 3minutes using sunflower oil.

Immediately after frying, French fries and chips were drained from the oil and placed in a plastic tray lined with a paper towel, to drain excess oil and cooled to ambient temperature. Ten French fries and chips each for each breeding line and location were randomly selected and a Chroma meter CR-400 (Konica Minolta, Japan) used to measure the colour parameters to obtain the mean Hunter L*, a*, and b* colour coordinates. Where; L* is a measure of lightness (0 = black to 100 = white), a* is a measure of redness and (+a* = redness; −a* = greenness), and b* is a measure of yellowness (+b* = yellowness; −b* = blueness). The experiment was done between 23 – 26/10/2019 for Nigde location, and between 4 -7/ 11/2019 for Sivas and Konya location. The USDA colour chart was scaled from 000 to 4.

3.4 Statistical analysis

The data for all the traits were analysed using the General Linear Model (GLM) procedure of SAS software (SAS Institute, Cary, N.C., United States) to examine genotype, environment, and G x E interaction effects by analysis of variance. Statistix statistical software (version 8.1) was used to perform the mean comparison test of Duncan's Multiple Range Tests at a 5% level of significance where the genotype effect was considered as fixed and the environmental effects as random. Stability parameters were analysed using additive main effect and multiplicative interactions AMMI, and Stability-soft online software by a joint regression analysis according to Finlay and Wilkinson (1963). Correlation analysis was also performed to assess the interrelationships among the various traits.

3.5 Finlay and Wilkinson model

The Finlay and Wilkinson (1963) model is given below where the environmental main effect Ej is used as a regresor.

$Yij = \mu + Gi + Ej + GEij + eij$

$Yij = \mu + Gi + Ej + biEj + \epsilon ij$

$Yij = \mu + Gi + (1 - bi)\, j + \epsilon ij$

$Yij = \mu + Gi + bi * Ej + \epsilon i$j

$Yij = \mu + Gi + bi * Ej + \epsilon ij$

Where

Yij is the ith genotype mean in the jth environment, i=1, 2,..., v; j=1,2,...,b

μ is the overall mean of the ith genotype, *bi* is the regression coefficient that measures the response of the genotype of varying environments, eij is the deviation from the regression of the ith genotype at the jth environment. Regression coefficient *bi* (i Yij I j) / j. Ij is the environmental index Ij Yij i v yij ij vb I 2 j. Slope (*bi**) is a measure for adaptability, *bi* =1; average adaptability, *bi*> 1, genotypes with higher than average adaptability, *bi* < 1, genotypes with lower than average adaptability.

3.6 AMMI analysis

The genotype and environment interaction was accessed using AMMISOFT statistical software following the protocol of Gauch and Moran, 2019. This model operates on two analytical principles: the variance and singular value decomposition principles on one component (principal component analysis), and the additive component for the genotype effects (gi), environmental effects (ej), and multiplicative for the interaction effect (ge)ij as elaborated by Gauch et al. (2011), and Gauch (2013) based on (Gauch, 1992) model:

Yijr = μ + gi + ej + br(ej) + Xn k=1 λkαikγjk + ρij + εij (1)

Where; Yijr is the phenotypic trait of genotype i in environment j for replicate r, μ is the grand mean, gi is the genotype main effects as deviations from μ, ej is the environment main effects as deviations from μ, λk is the singular value for the Interaction Principal Component (IPC) axis k, αik, and γjk are the genotypes and environment IPC scores (i.e. the left and right singular vectors) for axis k, bi(ej) is the effect of the replication r within the environment j, r is the number of replications, ρij is the residual containing all multiplicative terms not included in the model (1); n is the number of axes or principal components (PC) retained by the model, and εijr is the experimental error.

CHAPTER IV

RESULTS AND DISCUSSION

4.1 Stand Establishment (SE)

The result for the general ANOVA and combined AMMI ANOVA for SE showed highly significant differences ($P \leq 0.01$) among the genotypes, and the GEI ($P < 0.05$) whiles there was no-significant ($P > 0.05$) differences among the environments (Table 4.1 and Table 4.2). Table 4.2 showed that the genotypes accounted for 38.84% of the treatment sum of squares whiles GEI accounted for 56.79% of the treatment sum of squares. There was also significant effect of the IPC1 which accounted for 76.39% of the GEI sum of squares whilst there was no significant effect of the residual (Table 4.2). This shows the genotypic vigour of the genotypes against environmental fluctuations and thus environment has no influence on the stand establishment of the genotypes. The differences in the stand establishment are attributed to genotypic effect due to differences in origin and parental combination which led to the significant GEI with the different environmental factors. This is reflected in the mean stand establishment among the genotypes (Table 4.3) where there was a significant difference between the genotype with the highest SE and the genotype with the lowest SE and the rest of the genotypes. The significant ($P < 0.001$) genotypic (G) and GEI on the SE is an indication that the potato genotypes have varied germination and survival rates in the test environments. The non-significant difference ($P > 0.05$) (Table 4.1, 4.2) in SE among the locations, indicate the outstanding biological vigour of the breeding lines against environmental impediments.

Table 4.1. Analysis of variance of stand establishment (SE) for 15 potato genotypes grown in three different environments

Source	DF	SS	MS	F	P-value
Genotype (G)	14	1287.56	91.9683	2.42	0.005**
Environment (E)	2	145.6	72.7984	1.91	0.151ns
G x E	28	1880.54	67.1623	1.77	0.017*
Error	135	5132.19	38.0162		
Total	179	8445.89			
Grand mean	93.7				
CV	6.6				

Table 4.2. AMMI analysis of variance of stand establishment (SE) for 15 potato genotypes grown in three different environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	179	8449	47.20			
Treatment	44	3314	75.33**	43.43		
Genotype (G)	14	1287	91.95**		38.84	
Environment (E)	2	145	72.41 ns		4.37	
G x E	28	1882	67.22*		56.79	
IPC1	15	1438	95.86*		(43.38)	76.39
Residual	13	444	34.18ns		(13.41)	23.61
Error	135	5134	38.03	56.57		
Blocks/Env	9	355	39.41ns			
Pure Error	126	4780	37.93			

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *p≤0.05, ** p≤0.01, ^{ns} p≥0.05

The significant genotypic (G), and GEI on the SE is an indication that the potato genotypes have varied emergence and survival rates in the test environments. The large contribution (56.79%) of the GEI to the total variation and the different genotype winners across the environment depicted crossover type of GEI. In Table 4.3, the genotype means across the environments, shows that MADELEINE recorded the highest SE of 97.1%, whiles MACAR1402.11 recorded the lowest SE of 85.1% among genotypes while among the environments, Nigde recorded the highest SE of 94.5% followed by Sivas with 93.2% and the Konya with 93.1%. The occurrence of the crossover GEI led to the fact that MEÇ1407.17 recorded the highest SE of 99.1% in Nigde but in Sivas, MACAR1402.10 and MACAR1406.04 recorded the highest SE of 97.3% whiles in Konya MADELEINE recorded the highest SE of 97.7%. Also, the lowest SE in Nigde was found in MACAR1402.10 (86.6%) whiles in Sivas and Konya the lowest SE was found in MACAR1402.11 (72.5) and MEÇ1407.05 (87.5) respectively.

In this research, the stability of the genotypes was estimated using; Finlay and Wilkinson (1963) regression coefficient (bi), Eberhart and Russel (1966) deviation from regression S^2di, Shukla (1972) stability variance (σ_i^2), Francis and Kannenberg (1978) environmental coefficient of variance (CV), Kang (1988) Rank Sum and AMMI Model. Finlay and Wilkinson (1963) proposed the regression coefficient as the stability model to evaluate the adaptation response of genotypes under changing environments by plotting stability parameters such as regression coefficient (bi) with the mean variables. The regression coefficient measures the departure of actual slope ($1 + B = b_i$) from one (1) (as a measure of adaptability), which interpret that, genotype is said to have; average adaptability or sensitivity to environmental influences when bi = 1, higher than average sensitivity when bi > 1, and lower than average or less sensitive to environmental fluctuations when bi < 1, thus measures the genotypic responsiveness to environmental changes. The genotype could be placed among 4 quadrats depending upon its behaviour for the measured variable in fluctuating environments (i.e., poorly adapted to a favourable environment, well adapted to a favourable environment, poorly adapted to the unfavourable environment, and well adapted to the unfavourable environment).

Table 4.3. Two-way table of stand establishment (SE) for 15 potato genotypes grown in 3 different environments*

GENOTYPES	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	86.6 *d*	97.3 *ab*	90.3 *bcd*	91.4
MACAR1402.11	91.2 *abcd*	72.5 *e*	91.6 *abcd*	85.1
MACAR1406.04	93.1 *abcd*	97.3 *ab*	96.8 *ab*	95.7
MACAR1406.07	95.4 *abc*	95.3 *abc*	93.0 *abcd*	94.5
MACAR1409.09	95.4 *abc*	95.3 *abc*	92.6 *abcd*	94.4
MEÇ1402.07	92.1 *abcd*	95.5 *abc*	91.2 *abcd*	92.9
MEÇ1402.09	95.0 *abcd*	89.8 *bcd*	97.2 *ab*	94.0
MEÇ1405.06	95.4 *abc*	92.0 *abcd*	92.6 *abcd*	93.3
MEÇ1407.05	94.4 *abcd*	97.0 *ab*	87.5 *cd*	93.0
MEÇ1407.08	94.4 *abcd*	95.5 *abc*	95.4 *abc*	95.1
MEÇ1407.17	99.1 *a*	96.5 *ab*	89.3 *bcd*	95.0
MEÇ1411.06	97.2 *ab*	90.0 *bcd*	91.2 *abcd*	92.8
AGRIA	97.2 *ab*	94.9 *abcd*	95.4 *abc*	95.8
MADELEINE	96.3 *ab*	97.2 *ab*	97.7 *ab*	97.1
RUSSET BURBANK	97.2 *ab*	92.6 *abcd*	94.9 *abcd*	94.9
Mean	94.5	93.2	93.1	93.7

*: Different letters within a row and column indicate significance at $p \leq 0.05$ in Duncan test

The variance deviation from the regression (S^2di) by Eberhart and Russel (1966) was proposed of which genotypes with an $S^2di = 0$ are stable, while genotypes with an $S^2di > 0$ indicate un-stability across environments. The stability variance (σ_i^2) of genotype across environments was also suggested by Shukla (1972) which states that genotypes with small values are more stable. More so, the coefficient of variation (CVi) in 1978 was proposed by Francis and Kannenberg as a stability statistics combining the CV, mean yield, and environmental variance of genotypes with high mean yield, low CVi, low environmental variance (EV), are considered desirable. Furthermore, Kang's rank-sum which employs the yield and σi^2 by adding the yield and stability variance to each genotype, and the genotypes with the lowest rank-sum depict the most desirable (Kang, 1988).

For the IPC1 mode of stability analysis by the AMMI model, the degree of adaptation of genotype to the environment is determined by the distance of the genotype to the IPC1.The lesser the distance away from the IPC1 axis, the lesser the G*E interaction, which confers on the genotype a general adaptation to diverse environments. Thus, the genotype will have a similar yield outcome over several different environments. On the other hand, the further away of a genotype to the IPC1 axis, the high the interaction of G*E, making the genotype to be specifically adaptive to a specific environment, thus unstable. High yielding genotype with less G*E interaction is desired as the best genotype to meet the breeder's aim.

The SE stability estimates showed different ranking patterns among bi, S^2d, and σ^2 for the genotypes. Genotypes MACAR1402.11, MACAR1406.07, MEÇ1405.06, AGRIA, and MADELEINE were stable for bi (Table 4.4, Figure 4.1); MACAR1406.07, MACAR1409.09, MEÇ1407.08, AGRIA, and MADELEINE were stable for S^2d; whilst MACAR1406.07, MACAR1409.09, MEÇ1405.06. and AGRIA were stable for σi^2. For the Francis & Kannenberg CV, MACAR1406.07, MACAR1409.09, MEÇ1405.06, MEÇ1407.08, AGRIA, and MADALEINE have high SE and low CV and so are desirable (Table 4.4). Whilst the AMMI model IPC1 score shows MACAR1406.07, MACAR1409.09, MEÇ1407.08, AGRIA, and MADALEINE to be the stable genotypes.

Table 4.4. Stability estimation of stand establishment of potato breeding lines grown in three different environments

Genotype	Mean SE	Finlay & Wilkinsin	Eberhart & Russel		Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ^2	CV	KR	IPC1
MACAR1402.10	91.37	-2.02	6.99	39.62	5.93	28	1.65
MACAR1402.11	85.12	0.51	34.07	136.65	12.85	30	-3.54
MACAR1406.04	95.69	-1.77	0.42	11.09	2.4	14	0.43
MACAR1406.07	94.56	1.01	0.13	-0.76	1.38	8	0.22
MACAR1409.09	94.4	1.21	0.2	-0.43	1.66	11	0.27
MEÇ1402.07	92.94	0.27	1.43	5.23	2.43	20	0.74
MEÇ1402.09	94.01	3.31	0.36	7.56	4.04	18	0.33
MEÇ1405.06	93.32	1.34	0.31	0.11	1.93	14	-0.34
MEÇ1407.05	92.98	2.92	3.96	19.84	5.29	24	1.18
MEÇ1407.08	95.1	-0.44	0.03	1.72	0.61	9	0.12
MEÇ1407.17	94.98	4.33	0.8	17.33	5.3	17	0.49
MEÇ1411.06	92.81	2.89	1.39	9.32	4.17	23	-0.74
AGRIA	95.83	0.89	0.15	-0.66	1.28	4	-0.24
MADALEINE	97.07	-0.64	0.00	2.46	0.73	7	0.05
R. BURBANK	94.91	1.18	1.05	2.99	2.44	13	-0.62

CV, coefficient of variation; IPC A, interaction principal component analysis axis; ASV, Additive Main Effects and Multiplicative Interaction (AMMI) stability value

In Figure 4.1, the relationship of genotypes adaptation (regression coefficient “bi”) and the mean stand establishment (SE) was generated which showed that, MEÇ1402.07 has average adaptability (stability), whilst the rest of the genotypes have specific adaptability. MEÇ1407.17, MEÇ1405.06, MEÇ1402.09, MACAR1409.09, RUSSET BURBANK, AGRIA, and MACAR1406.07 are well adapted to favourable environments whiles MACAR1402.11, MEÇ1411.06, and MEÇ1407.05 are poorly adopted to favourable environment. On the other hand, MACAR1406.04, MEÇ1407.08, and MADELEINE are well adopted to unfavourable environment whiles MACAR1402.10 is poorly adopted to unfavourable environment. This shows that genotypes that are well adapted to unfavourable environment are tolerant genotypes whiles MACAR1402.10 is very sensitive to unfavourable environmental conditions.

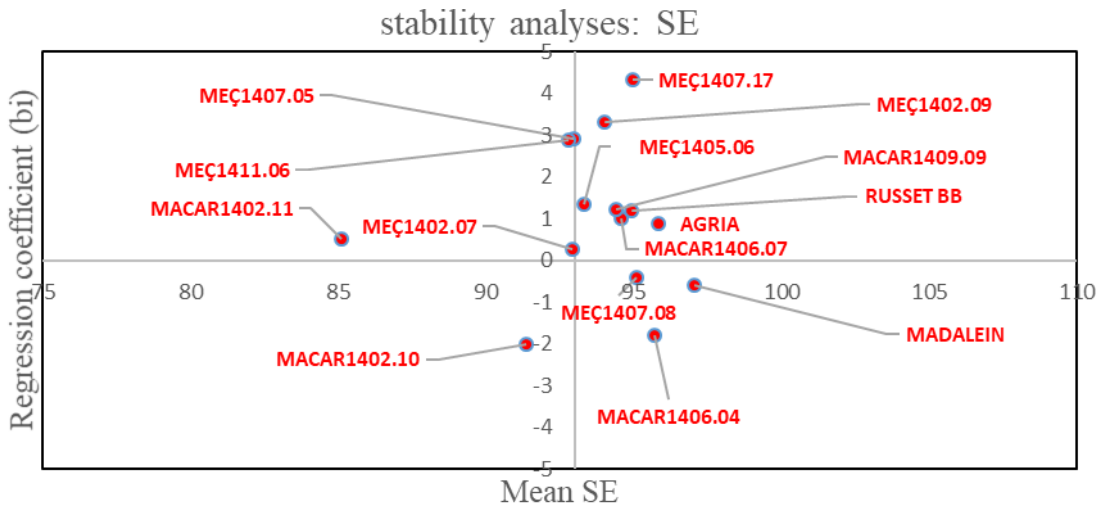

Figure 4.1. Relationship of genotype adaptation (regression coefficient 'bi') and mean stand establishment (SE) of 15 potato genotypes grown in three diverse environments

Also, the IPC1 scores against the mean SE biplot for the AMMI stability analysis tells the degree of adaptability of the genotype to the environment based on the distance of the genotype to the IPC1 axis. The lesser the distance away from the IPC1 axis, the lesser the G*E interaction, which confers on the genotype a general adaptation to diverse environments. Thus, the genotype will have a similar yield outcome over several different environments. On the other hand, the further away of a genotype to the IPC1 axis, the high the interactive G*E, making the genotype to be specifically adaptive to a specific environment, thus unstable. High yielding genotype with less G*E interaction is desired as the best genotype to meet the breeder's aim. Genotype and environment close to the IPC1 origin have less response to environmental changes, thus, have general (broad) adaptability to a wide range of environments.

In this study, the environments were widespread for stand establishment than the genotype with Nigde (NGDE) and Konya (KNYA) being generally less interactive while Sivas (SVAS) was highly interactive and unstable (Figure 4.2). Except for MACAR1402.11, which is highly interactive and unstable with the environments, almost all the other genotypes were generally adapted and stable with generally less interaction IPC1 scores for the SE. This reflects that there is less variation between stand establishments of the genotypes across environments.

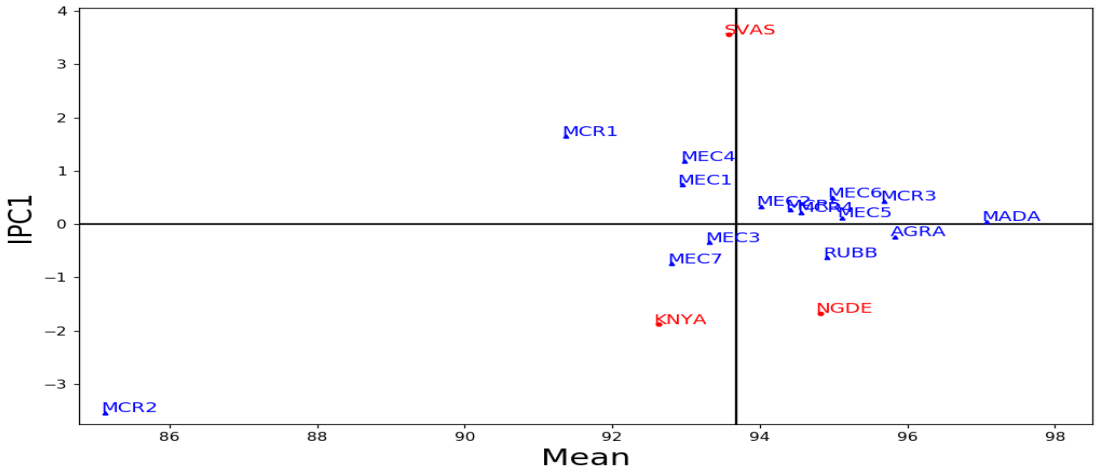

Figure 4.2. AMMI biplot analysis of interaction principal component analysis (IPCA-1) with mean of stand establishment of potato genotype evaluated across three different environments. (Note: MCR1 =MACAR1402.10, MCR2 = MACAR1402.11, MCR3 = MACAR1406.04, MCR4 = MACAR1406.07, MCR5 = MACAR1409.09, MEÇ1 = MEÇ1402.07, MEC2 = MEÇ1402.09, MEC3 = MEÇ1405.06, MEC4 = MEÇ1407.05, MEC5 = MEÇ1407.08, MEC6 = MEÇ1407.17, MEC7 = MEÇ1411.06, AGRA = AGRIA, MADA = MADELEINE, RUBB = RUSSET BURBANK; KYNA = Konya, NGDE = Nigde, SVAS = Sivas*)*

4.2 Number of Stems per Plant (NSP)

There were very high significant (P≤0.001) effects of genotype, environment, and genotype by environment interaction on the number of stems (NSP) of the potato for both the general ANOVA and the AMMI ANOVA with a grand mean of 4.79 and CV of 9.42 (Table 4.5 and Table 4.6). The GEI accounted for 44.73% of the treatment sum of squares more than the genotype and environment (Table 4.5). There was also a significant difference for the IPC1 and the residual (P<0.001) and the block/environment (P<0.05). The treatments explained 94.52% of which the genotype, environment, and genotype by environment interaction respectively accounted for 37.9%, 17.55%, and 44.73% of the treatment sum of squares. This shows that the potato stem number is affected by cultivar and environmental factors due to the genotypic variability and environmental fluctuations.

Table 4.5. Analysis of variance for the number of stems per plant (NSP) of 15 potato genotypes grown in 3 different environments

Source	DF	SS	MS	F	P-value
Genotype	14	80.746	5.7676	28.24	0.000***
Environment	2	37.595	18.7977	92.03	0.000***
Genotype x Environment	28	95.583	3.4137	16.71	0.000***
Error	135	27.575	0.2043		
Total	179	241.5			
CV	9.4				

DF = degree of freedom, SS = sum of square, MS = mean square, CV = coefficient of variation, *p≤0.05, ** p≤0.01

Table 4.6. AMMI analysis of variance for the number of stems per plant (NSP) of 15 potato genotypes grown in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	179	240.8	1.345			
Treatment	44	213.4	4.85***	94.52		
Genotype	14	80.5	5.75***		37.9	
Environment	2	37.45	18.73***		17.55	
G x E	28	95.46	3.41***		44.73	
IPC1	15	69.73	4.65***		(32.68)	73.05
Residual	13	25.72	1.98***		(12.05)	26.95
Error	135	27.36	0.2	5.48		
Blocks/Env	9	3.844	0.43*			
Pure Error	126	23.52	0.19			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sun of squares *p≤0.05, *** p≤0.001

In Table 4.7, the highest and lowest mean NSP for genotypes occurred in MEÇ1407.08 (6.1) and MACAR1406.04 (3.9) respectively, with significant effects between the highest and lowest stem numbers within and across environments. Across the environments, MEÇ1402.09, MEÇ1407.08, and MACAR1409 had the highest stem number respectively for Nigde, Sivas, and Konya whilst MACAR1406.04, and MACAR1406.07 respectively recorded the lowest stem number for Nigde and Sivas, and Konya. For the environment mean NSP, Nigde recorded the highest mean of 5.7stems, followed by Sivas with 4.2stems and Konya with 3.9stems. The differences in NSP ranking across the environment were attributed to the presence of crossover type of GEI whilst within the environment, the difference might be due to the genotypic differences among the genotypes.

Table 4.7. Two-way tables of the number of stems per plant (NSP) for 15 potato genotypes grown in three different environments

GEN	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	3.8 *mnop*	3.5 *opq*	4.7 *hijk*	4.0
MACAR1402.11	3.6 *opq*	3.4 *opq*	5.8 *cd*	4.3
MACAR1406.04	3.4 *pq*	2.5 *r*	5.8 *cd*	3.9
MACAR1406.07	5.6 *def*	6.7 *b*	3.6 *opq*	5.3
MACAR1409.09	5.7 *cde*	4.5 *hijkl*	6.7 *b*	5.6
MEÇ1402.07	4.3 *klmn*	3.7 *nopq*	4.3 *jklm*	4.1
MEÇ1402.09	5.9 *cd*	3.1 *qr*	5.4 *defg*	4.8
MEÇ1405.06	4.9 *fghij*	4.4 *ijklm*	6.3 *bc*	5.2
MEÇ1407.05	4.7 *hijk*	2.6 *r*	4.8 *ghijk*	4.0
MEÇ1407.08	5.0 *fghi*	7.3 ***a***	5.9 *cd*	6.1
MEÇ1407.17	5.8 *cd*	4.7 *hijk*	5.7 *cd*	5.4
MEÇ1411.06	5.9 *cd*	4.5 *hijkl*	6.3 *bc*	5.6
AGRIA	4.7 *hijk*	3.9 *lmnop*	4.7 *hijk*	4.4
MADELEINE	5.5 *def*	4.3 *klmn*	5.1 efgh	5.0
RUSSET BURBANK	4.6 *hijkl*	4.0 *lmno*	4.7 *hijk*	4.4
Mean	5.7	4.2	3.9	

*: Different letters within a row and column indicate significance at p≤0.05 in Duncan test

The estimates of the NSP stability in Table 4.8 showed that except MACAR1402.11, MACAR1406.04, MEÇ1402.09, and MEÇ1407.08 which have larger values of S^2d and thus not stable, the rest of the genotypes are stable with smaller S^2d values. For the bi estimates, MACAR1402.10, MEÇ1407.17, and MADALEINE were revealed to be stable. The Shukla stability variance also identified MACAR1402.10, MEÇ1402.07, MEÇ1407.17, AGRIA, and RUSSET BURBANK as stable genotypes, whilst Francis and Kannenberg coefficient variation, and Kang's rank sum did not identify any genotypes as desirable and stable. The AMMI IPC1 score for the NSP in Table 4.8 shows that, MEÇ1402.07, MEÇ1407.17, MEÇ1411.06, AGRIA, MADALEINE, RUSSET BURBANK are stable genotypes.

In Figure 4.3, the coefficient regression (bi) biplot against the mean stem number (NSP) showed that MEÇ1407.17 and MADELEINE are very well adapted to all environments whiles MACAR1402.10 was poorly adapted to all environments. On the other hand, MACAR1406.07 and MEÇ1407.08 are tolerant and well adapted to unfavourable environments while MEÇ1405.06, MACAR140909, and MEÇ1411.06 adapted well to favourable environment. On the contrarily, MEÇ1402.07, RUSSET BURBANK, and AGRIA are very sensitive to environmental influences and poorly adapted to

unfavourable environments whereas MACAR1402.11, MACAR1406.04, MEÇ1402.09, and MEÇ1407.05 are poorly adapted to favourable environments.

Table 4.8. Stability estimation of number of stem per plant of potato breeding lines grown in three different environments.

Genotype	Mean NSP	Finlay & Wilkinsin Regression	Eberhart & Russel (1966)	Shukla (1972)	Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ^2	CV	KR	IPC1
MACAR1402.10	4	1.02	0.02	0.02	15.77	19	-0.01
MACAR1402.11	4.26	1.97	0.15	0.88	30.86	22	-0.39
MACAR1406.04	3.89	2.8	0.12	1.58	43.49	28	-0.71
MACAR1406.07	5.29	-2.64	0.05	4.89	28.96	20	1.41
MACAR1409.09	5.61	1.93	0.00	0.25	19.19	11	-0.36
MEÇ1402.07	4.11	0.62	0.00	0.00	9.01	15	0.15
MEÇ1402.09	4.77	2.20	0.19	1.22	30.84	20	-0.45
MEÇ1405.06	5.20	1.64	0.03	0.20	18.64	14	-0.26
MEÇ1407.05	4.04	2.10	0.05	0.58	30.88	23	-0.41
MEÇ1407.08	6.06	-1.44	0.21	2.91	19.37	15	0.92
MEÇ1407.17	5.40	1.00	0.02	0.02	11.56	8	0.00
MEÇ1411.06	5.55	1.61	0.01	0.10	16.42	9	-0.23
AGRIA	4.43	0.74	0.01	-0.02	9.82	28	0.1
MADALEINE	4.95	0.79	0.06	0.18	12.56	20	0.09
RUSSET BURBANK	4.42	0.65	0.00	-0.01	8.38	27	0.14

CV, coefficient of variation; IPC A, interaction principal component analysis axis; ASV, Additive Main Effects and Multiplicative Interaction (AMMI) stability value

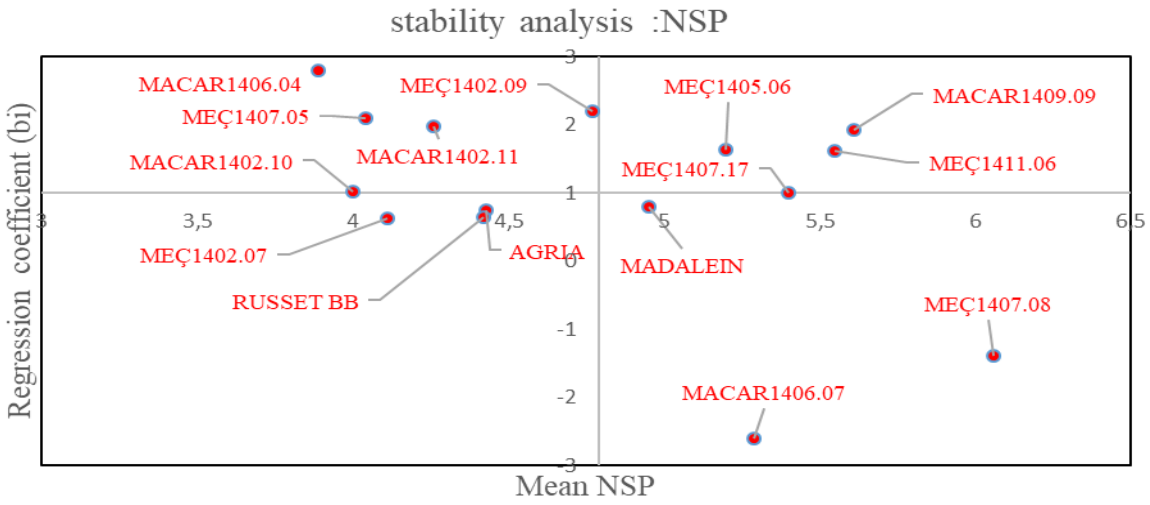

Figure 4.3. Relationship of genotype adaptation (regression coefficient 'bi') and the mean number of stems per plant (NSP) of 15 potato genotypes grown in three diverse environments

For the AMMI biplot analysis, MACAR1402.10, MEÇ1402.07, RUSSET BURBANK, AGRIA, MADELEINE, MEÇ1405.06, MEÇ1407.17, MEÇ1411.06, MACAR1409.09, MEÇ1407.05, MACAR1402.11 have general adaptability (Figure 4.4). MACAR1406.07 and MEÇ1407.08 are highly interactive with the environment and specifically adapted to a kind of environment. An approximately equal number of genotypes have stems number below the mean value as they are above the mean stem. Also, an approximately equal number of genotypes are located above and below the IPC1 origin. For the environment, Nigde (NGDE) environment is less responsive to changes and is stable for the number of stems per plant whiles Sivas (SVAS) and Konya (KNYA) are sensitive to environmental influences.

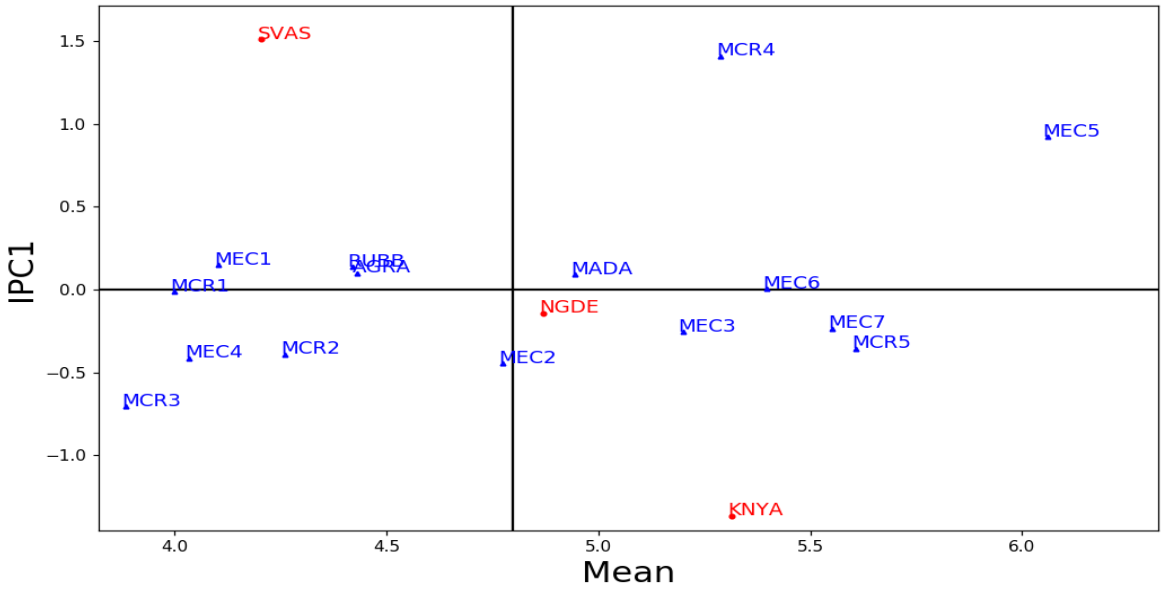

Figure 4.4. Biplot analysis of interaction principal component axis (IPCA-1) with mean of stem number per plant (NSP) of potato genotype evaluated across three different environments. Note: MCR1 =MACAR1402.10, MCR2 = MACAR1402.11, MCR3 = MACAR1406.04, MCR4 = MACAR1406.07, MCR5 = MACAR1409.09, MEÇ1 = MEÇ1402.07, MEC2 = MEÇ1402.09, MEC3 = MEÇ1405.06, MEC4 = MEÇ1407.05, MEC5 = MEÇ1407.08, MEC6 = MEÇ1407.17, MEC7 = MEÇ1411.06, AGRA = AGRIA, MADA = MADELEINE, RUBB= RUSSET BURBANK; KYNA = Konya, NGDE = Nigde, SVAS = Sivas

4.3 Plant Height

The analysis of variance for plant height (PH) reveals that genotypes, environments and the genotype by environment interaction (GEI) have highly (P≤0.001) significant effect on the potato genotypes for the general ANOVA and the AMMI ANOVA (Table 4.9 and Table 4.10). The grand mean of the potato plant height was 65.3 at the CV of 5.4. There was also a significant difference for the IPC1 and the residual (P<0.001) and the

block/environment (P<0.05). Of the total sum of squares, 93.26% was explained by the treatments of which the environment accounted for 76.98% of the treatment sum of squares than the genotypes and the genotype by environment interaction. The IPC1 also constituted 66.12% of the GEI sum of squares while the residual effect accounted for 33.88% of the GEI sum of squares.

Table 4.9. ANOVA of plant height for 15 genotypes grown in three different environments

Source	DF	SS	MS	F	P-value
Genotype (G)	14	5786.9	413.4	33.2	0.000***
Environment (E)	2	36638.1	18319.1	1471.26	0.000***
G x E	28	5171.2	184.7	14.83	0.000***
Error	135	1680.9	12.5		
Total	179	49277.2			
CV		5.4			

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** p≤0.001

Table 4.10 AMMI analysis of variance for plant height (PH) of 15 potato genotypes grown in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	179	49271	275.26			
Treatment	44	47591	1081.6***	93.26		
Genotype	14	5786	413.3***		12.16	
Environment	2	36634	18317***		76.98	
G x E	28	5171	184.69***		10.87	
IPC1	15	3419	227.96***		(7.18)	66.12
Residual	13	1752	134.77***		(3.68)	33.88
Error	135	1680	12.444	6.74		
Blocks/Env	9	87.7	9.744*			
Pure Error	126	1592	12.637			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sun of squares *p≤0.05, *** p≤0.001

The mean comparison in Table 4.11 shows that MEÇ1407.08 (77.2cm) and Russet Burbank(56.5cm) respectively recorded the highest and lowest mean plant height (PH) among the genotypes while the mean PH among the environments, Konya recorded the highest PH of 83.9cm followed by Sivas with 63.8cm and the lowest PH was found in Nigde with 49.2cm with statistical significance existing between the highest and lowest PH of the genotypes within and across the environment. The highest PH; in Nigde was found in Agria (60.5cm), while MEÇ1407.08 recorded the highest PH in Sivas of 76.2cm

and Konya of 97.0 cm. On the other hand, the lowest PH was found in Russet Burbank(40.1cm) in Nigde, MEÇ1407.17 (46.6cm) in Sivas, and MEÇ1407.05 (68.7cm) in Konya. These differences in the ranks of the genotypes for the PH across environment is can be associated with the presence of crossover type of GEI or due to differences in the environmental input.

Table 4.11. Two-way table of plant height (PH) for 15 potato genotypes grown in three different environments*

GEN	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	42.5 *st*	68.6 *hi*	89.4 *bcd*	66.8
MACAR1402.11	43.3 *rst*	60.4 *lmno*	91.5 *bc*	65.0
MACAR1406.04	47.5 *qr*	62.3 *jklm*	84.8 *de*	64.9
MACAR1406.07	45.2 *qrs*	55.6 *op*	76.2 *f*	59.0
MACAR1409.09	57.1 *nop*	71.9 *fg*h	83.0 *e*	70.7
MEÇ1402.07	45.5 *qrs*	67.0 *hij*	91.9 *bc*	68.2
MEÇ1402.09	42.9 *rst*	54.5 *p*	89.3 *bcd*	62.2
MEÇ1405.06	54.0 *p*	63.5 *jkl*	73.9 *fg*	63.8
MEÇ1407.05	48.8 *q*	65.6 *ijk*	68.7 *hi*	61.0
MEÇ1407.08	58.5 *mnop*	76.2 *f*	97.0 *a*	77.2
MEÇ1407.17	56.3 *nop*	46.6 *qrs*	86.2 *de*	63.0
MEÇ1411.06	54.0 *p*	60.8 *klmn*	71.2 *gh*	62.0
AGRIA	60.5 *lmno*	75.6 *fg*	94.1 *ab*	76.7
MADELEINE	42.1 *st*	58.1 *mnop*	87.6 *cde*	62.6
RUSSET BURBANK	40.1 *t*	55.5 *op*	73.8 *fg*	56.5
Mean	49.2	62.8	83.9	65.3

*: Different letters within a row and column indicate significance at p≤0.05 in Duncan test

Table 4.12. Stability estimation of plant height of potato breeding lines grown in three different environments

Genotype	Mean PH	Finlay & Wilkinson	Eberhart& Russel	Shukla	Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ2	CV	KR	IPC1
MACAR1402.10	66.8	1.32	5.66	55.4	35.16	15	1.14
MACAR1402.11	65.0	1.4	0.28	53.02	37.55	15	1.14
MACAR1406.04	64.9	1.07	0.00	-1.63	28.92	9	0.32
MACAR1406.07	59.0	0.9	0.29	1.07	26.75	18	-0.37
MACAR1409.09	70.7	0.73	2.06	30.59	18.43	9	-1.37
MEÇ1402.07	68.2	1.32	1.04	37.56	34.05	12	1.32
MEÇ1402.09	62.2	1.36	4.12	59.49	38.76	22	1.85
MEÇ1405.06	63.8	0.57	0.25	63.92	15.56	20	-1.99
MEÇ1407.05	61.0	0.54	7.49	102.09	17.52	27	-2.37
MEÇ1407.08	77.2	1.10	0.64	2.54	24.96	6	0.35
MEÇ1407.17	63.0	0.95	43.09	171.39	32.75	24	0.55
MEÇ1411.06	62.0	0.5	0.00	86.04	13.97	25	-2.24
AGRIA	76.7	0.96	0.35	-1.64	21.96	3	-0.24
MADALEINE	62.6	1.32	0.3	33.91	36.91	17	1.49
R. BURBANK	56.5	0.96	0.47	-1.15	29.87	18	-0.26

IPC1, interaction principal component analysis axis 1; AMMI, Additive Main Effects and Multiplicative Interaction

The stability estimation for the PH in Table 4.12 shows that MACAR1406.04, MACAR1406.07, MEÇ1407.17, AGRIA, and RUSSET are stable for the Finlay and Wilkinson regression coefficient (bi). The Eberhard BURBANK and Russel analysis revealed that MACAR1406.04, and MEÇ1411.06, were stable genotypes for PH. For the Shukla stability variances, MACAR1406.04, MACAR1406.07, and AGRIA were identified to be stable of PH. There is some similarity between the Eberhard and Russel analysis and the Shukla stability variances. However, Francis & Kannenberg failed to identify any stable genotype for PH while Kang Rank Sum identified AGRIA as a stable genotype in terms of PH. For the AMMI model stability estimation, genotypes with IPC1 scores less than 0.5 were considered stable. In this regards, MACAR1406.04, MACAR1406.07, MEÇ1407.08, AGRIA, and RUSSET BURBANK were stable genotypes for the AMMI model.

The regression analysis of the plant height (PH) (Figure 4.5) considering the relationship of genotypes adaptation (regression coefficient "bi") and the mean PH showed that MEÇ1402.07, MACAR1402.10, and MEÇ1407.08 are well adaptable favourable environment whereas MACAR1409.09 is well adapted to an unfavourable environment which depicted specific adaptability (stability). On the other hand, MEÇ1402.09, MACAR1402.11, and MADELEINE are poorly adapted to favourable environment whiles MACAR1406.07, MEÇ1411.06, MEÇ1407.05, and MEÇ1405.06 are poorly adapted to unfavourable environmental conditions. Contrarily to these, MEÇ1407.17, RUSSET BURBANK, and MACAR1406.04 are poorly adaptable to all environments whereas AGRIA is well adapted to all environmental conditions in terms of plant height. This shows that genotypes that are well adapted to unfavourable environment are tolerant genotypes whiles genotypes that are poorly adapted to unfavourable environment are sensitive to environmental conditions.

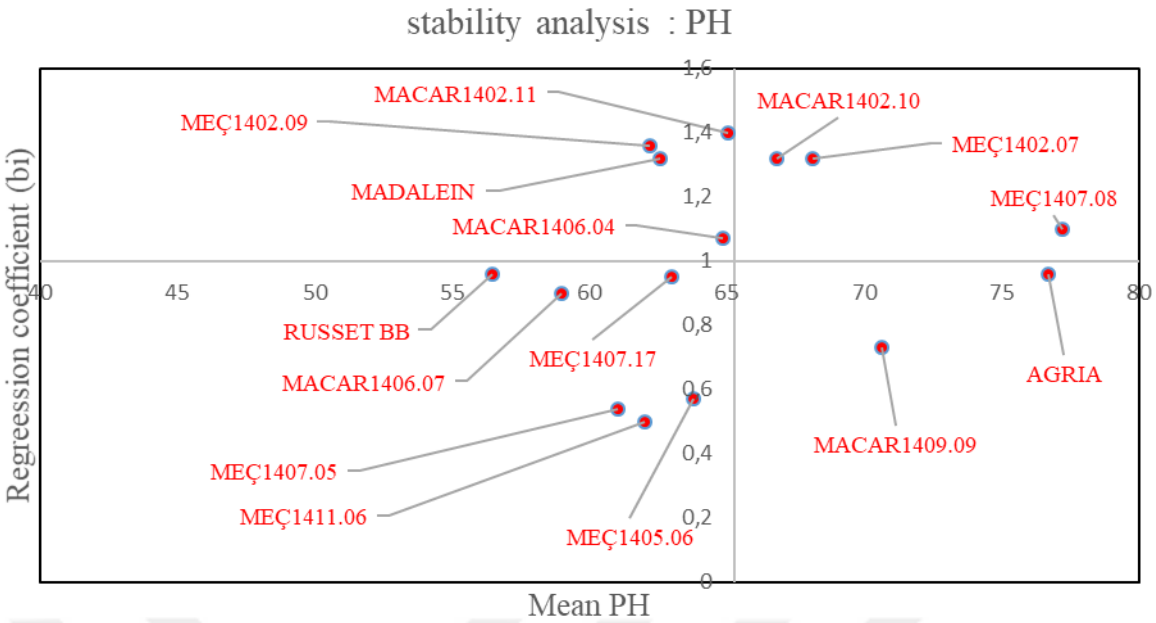

Figure 4.5. Relationship of genotype adaptation (regression coefficient 'bi') and mean plant height (PH) of 15 potato genotypes grown in three diverse environments

Comparatively, the AMMI biplot shows that RUSSET BURBANK, MACAR1406.07, AGRIA, MEÇ1407.08, MACAR1406.04, MEÇ1407.17 are less influenced by environmental input with RUBB, MACAR1406.07, MACAR1406.04, and MEÇ1407.17 having below-average stability whiles AGRIA and MEÇ1407.08 have above-average stability. The rest of the genotypes are however having high G*E interaction and specifically adapted to either favourable or unfavourable environments. The environments are highly scattered across, with Konya (KNYA) and Nigde (NGDE) highly unstable whiles Sivas (SVAS) is potentially an ideal environment for most genotype which is closer to the mean and IPC1 origin.

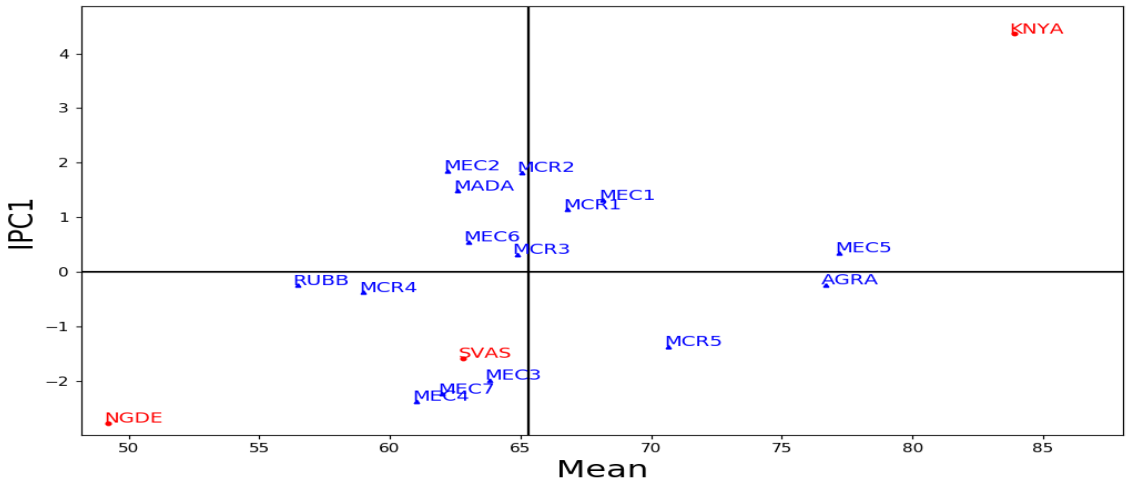

Figure 4.6. AMMI biplot analysis of interaction principal component analysis (IPCA-1) with mean of plant height (PH) of potato genotype evaluated across three different environments. Note: MCR1 =MACAR1402.10, MCR2 = MACAR1402.11, MCR3 = MACAR1406.04, MCR4 = MACAR1406.07, MCR5 = MACAR1409.09, MEÇ1 = MEÇ1402.07, MEC2 = MEÇ1402.09, MEC3 = MEÇ1405.06, MEC4 = MEÇ1407.05, MEC5 = MEÇ1407.08, MEC6 = MEÇ1407.17, MEC7 = MEÇ1411.06, AGRA = AGRIA, MADA = MADELEINE, RUBB = RUSSET BURBANK; KYNA = Konya, NGDE = Nigde, SVAS = Sivas

4.4. Total Plant Yield

The general ANOVA and AMMI ANOVA for the total plant yield (TPY) revealed highly significant ($p < 0.001$) differences among the environments, genotypes, and the genotype by environment interaction (Table 4.13 and Table 4.14) indicating the high effects of the genotypes and environments on the yield of the potato breeding lines and the standard genotypes. The CV among the genotypes and the environments were found to be 11.33 and the grand mean yield of 744.29. 75.35% of the total sum of squares was explained by the treatment of which 28.31%, 60.70%, and 10.99% of the treatment sum of squares were respectively accounted for by the genotypes, the environments, and the genotype by environment interaction effects while 24.65% of the total sum of squares was attributed to experimental errors. There was also a significant difference for the IPC1 ($P<0.001$) which explained 74.55% of the GEI sum of squares and the residual ($P<0.05$) which constituted 25.45% of the GEI sum of squares.

Table 4.13 ANOVA of total plant yield for 15 genotypes grown in three different environments

Source	DF	SS	MS	F	P
Genotype (G)	14	3970464	283605	39.91	0.000***
Environment (E)	2	8750810	4375405	615.65	0.000***
G x E	28	1476318	52726	7.42	0.000***
Error	135	959436	7107		
Total	179	1.52E+07			
CV	11.3				

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** p≤0.001

Table 4.5. AMMI analysis of variance for total plant yield (TPY) of 15 potato genotypes grown in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	179	1.50E+07	84651.6			
Treatment	44	1.30E+07	304587***	75.35		
Genotype	14	3793624	270973***		28.31	
Environment	2	8135012	4067506***		60.7	
G x E	28	1473184	52613.7 ***		10.99	
IPC1	15	1098301	73220.1 ***		(8.2)	74.55
Residual	13	374883	28837.1 *		(2.8)	25.45
Error	135	1750810	12969	24.65		
Blocks/Env	9	146957	16328.6 ns			
Pure Error	126	1603852	12729			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, *p≤0.05, *** p≤0.001 ns= not significant

In Table 4.15, the mean total plant yield (TPY) ranges from Russet Burbank (400.08 t/ha) to MEÇ1407.17 (967.03 t/ha) among genotypes, while among environments; Nigde (545.6), Sivas (1087.17), and Konya (529.47) which are significantly different among the genotypes and environments. Crossover type of GEI was observed which led to different genotype ranking across the environments. Yan and Tinker (2006), Atnaf et al. (2013), Mwiiga et al. (2020), and Bhartiya et al. (2017) also states that the presence of crossover type GEI necessitate stability analysis. The highest TPY in Nigde was found in MEÇ1407.17 (869.2 t/ha), in Sivas, the highest TPY was found in MEÇ1407.05 (1315.2 t/ha), while in Konya, the highest TPY was found in MACAR1402.10 (885.2 t/ha) whereas Russet Burbank recorded the lowest TPY in Nigde 226.6 t/ha, and in Sivas of 523.5t/ha while MACAR1406.04 recorded the lowest TPY in Konya of 451.7 t/ha. Though Russet Burbank recorded the lowest TPY in both Nigde and Sivas environments, there was a difference in the yield quantity which explained that the greater variation in

the TPY between genotypes is due to environmental fluctuations more than the genotypic differences. The contribution of the total sum of squares due to the genotypes can be attributed to the differences in the crossing parents of genotypes which brings about different significant responses with the environments.

Table 4.6. Two-way table of total plant yield (TPY) for 15 potato genotypes grown in three different environments*

GEN	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	483.1 *op*	996.6 *de*	885.2 *efg*	788.3
MACAR1402.11	417.8 *p*	799.6 *ghi*	692.8 *ijk*	636.7
MACAR1406.04	490.3 *op*	1199.2 *ab*	451.7 *op*	713.7
MACAR1406.07	452.2 *op*	1073.3 *cd*	546.6 *lmno*	690.7
MACAR1409.09	484.4 *op*	1220.6 *ab*	695 *ijk*	800.0
MEÇ1402.07	465.3 *op*	981.4 *def*	618.1 *klmn*	688.2
MEÇ1402.09	474.4 *op*	888.4 *efg*	515.4 *nop*	626.1
MEÇ1405.06	566.7 *lmno*	1261.1 *ab*	661.4 *jkl*	829.8
MEÇ1407.05	736.4 *hij*	1315.2 *a*	729.4 *ijk*	927.0
MEÇ1407.08	711.4 *ijk*	1270.3 *a*	660.9 *jkl*	880.9
MEÇ1407.17	869.2 *fg*	1152.2 *bc*	879.7 *efg*	967.0
MEÇ1411.06	743.3 *hij*	1203.7 *ab*	730.8 *hijk*	892.6
AGRIA	293.2 *q*	847.5 *gh*	472 *op*	537.6
MADELEINE	636.8 *jklm*	1011.3 *d*	707.3 *ijk*	785.2
RUSSET BURBANK	226.2 *q*	523.5 *mnop*	452.6 *op*	400.8
Mean	545.6	1087.2	529.47	744.3

*: Different letters within a row and column indicate significance at p≤0.05 in Duncan test

The *bi* stability analysis revealed that MEÇ1402.07, MEÇ1402.09, MEÇ1411.06, and AGRIA were stable for TPY. The Eberhart & Russel (1966) and Shukla (1972) stability have different paterns of stability estimation that could not identify any stable genotypes. This partially agrees with the findings of Caliskan et al. 2007 in which they found a similar pattern of stability estimates between Eberhard & Russel (1966) and Shukla (1972) stability models for the total tuber yield of sweet potato but both failed to identify stable genotypes Also, the Francis & Kannenberg CV analysis recorded high CV values and so failed to identify any desirable genotype for TPY. However, the Kang's Rank (KR) sum identified MEÇ1411.06 as a stable genotype due to its lower KR value (Table 4.16). Contrarily, the AMMI stability model identified AGRIA as a stable genotype for TPY. The differential yield traits expression of the genotypes in the varying environment is based on three impacts; the expression of the gene in the environment, the suppressing of the gene in the environment, or the codominance (neutrality) of the gene responsible for the trait (Bailey-Serres et al. 2019). An environment may favour or impede the expression

of the phenotypic traits of interest which lead to different stability levels of the genotypes (Kang *et al*. 2004).

Table 4.7. Stability estimation of total plant yield of potato breeding lines grown in three different environments

Genotype	Mean TPY	Finlay & Wilkinsin	Eberhard & Russel	Shukla	Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ^2	CV	KR	IPC1
MACAR1402.10	788.29	0.81	7325.92	31711.2	34.27	20	-7.57
MACAR1402.11	636.75	0.62	3206.31	24335.6	30.94	24	-8.39
MACAR1406.04	713.70	1.51	3121.97	33534.4	58.97	24	11.22
MACAR1406.07	690.71	1.24	128.82	4264.72	48.46	15	4.59
MACAR1409.09	800.00	1.4	239.36	13475.4	47.4	16	5.17
MEÇ1402.07	688.24	0.98	152.24	-368.2	38.51	12	-0.53
MEÇ1402.09	626.08	0.84	196.19	1924.66	36.43	16	-0.79
MEÇ1405.06	829.74	1.39	252.03	12878.2	45.39	14	7.02
MEÇ1407.05	926.98	1.22	1477.49	8911.15	36.27	9	6.02
MEÇ1407.08	880.82	1.2	2491.52	12562.1	38.39	12	-1.72
MEÇ1407.17	967.02	0.59	216.69	14255.1	16.59	12	-4.28
MEÇ1411.06	892.61	0.97	1062.29	3330.41	30.19	7	2.24
AGRIA	537.55	1.04	308.54	370.4	52.63	16	0.02
MADALEINE	785.16	0.74	8.43	4803.52	25.35	14	-2.92
R. BURBANK	398.50	0.46	2312.14	33085.8	38.29	29	-10.06

CV, coefficient of variation; IPC1, interaction principal component analysis axis 1; AMMI, Additive Main Effects and Multiplicative Interaction

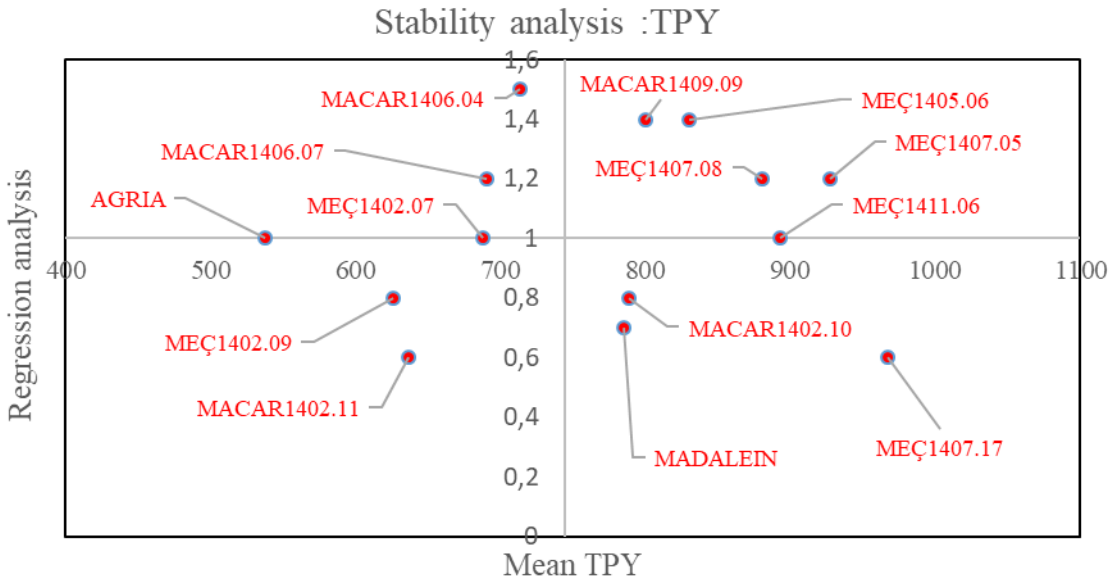

Figure 4.7. Relationship of genotype adaptation (regression coefficient 'bi') and mean total plant yield (TPY) of 15 potato genotypes grown in three diverse environments

Figure 4.7 characterized the genotypes into six levels of adaptability for the total plant yield using the bi model. AGRIA and MEÇ1402.07 are poorly adapted to all

environments, whereas MEÇ1411.06 is very well adapted to all environments. On the other hand, MEÇ1402.09 and MACAR1402.11 are poorly adapted to unfavourable environments whiles, MACAR1406.07 and MACAR1406.04 are poorly adapted to favourable environments. On the contrarily, genotypes; MEÇ1407.17, MACAR1402.10, and MADELEINE are very well adapted to unfavourable environments and thus are tolerant genotypes whiles, MEÇ1405.06, MEÇ1407.06, MEÇ1407.08 and MACAR1409.109 are ideal genotypes and so very well adapted to favourable environment.

In Figure 4.8 AGRIA, MEÇ1402.07, and MEÇ1402.09 though averagely low yielding, are generally adapted to a large spectrum of environments. Among all the genotype, Russet Burbank was the most highly adaptive to a specific environment with no association with the other genotype. MADELEINE, MEÇ1405.06 MEC 4, MEÇ1407.08, MEÇ1407.17, MEÇ1411.06, MACAR1409.09 were high yielding genotypes with general adaptability. The environments were widely interactive more than the genotypes with Sivas being the most interactive and best environment while Nigde and Konya being very much sensitive (Figure 4.8).

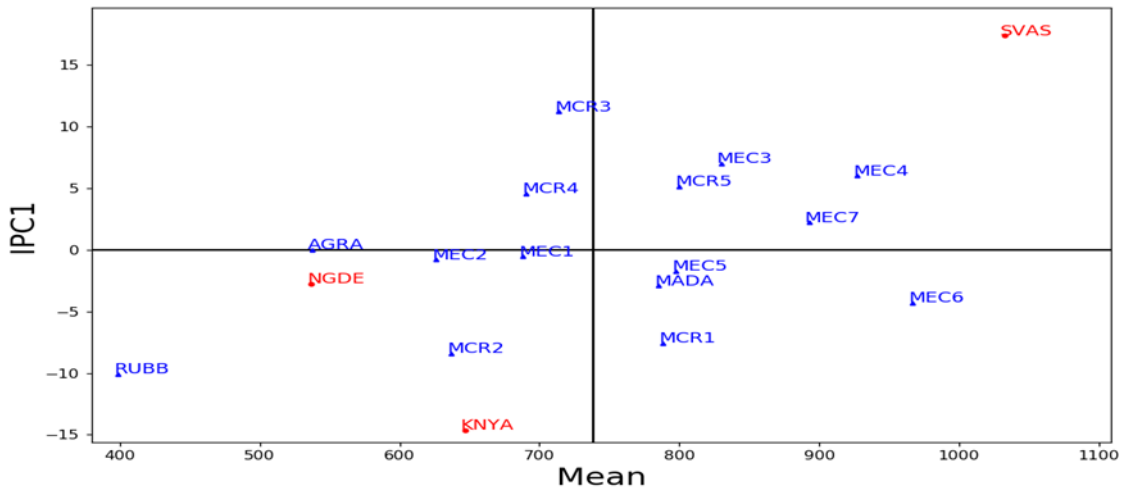

Figure 4.8. Biplot analysis of interaction principal component axis (IPCA-1) with mean of total plant yield (TPY) of potato genotype evaluated across three different environments. Note: MCR1 =MACAR1402.10, MCR2 = MACAR1402.11, MCR3 = MACAR1406.04, MCR4 = MACAR1406.07, MCR5 = MACAR1409.09, MEÇ1 = MEÇ1402.07, MEC2 = MEÇ1402.09, MEC3 = MEÇ1405.06, MEC4 = MEÇ1407.05, MEC5 = MEÇ1407.08, MEC6 = MEÇ1407.17, MEC7 = MEÇ1411.06, AGRA = AGRIA, MADA = MADELEINE, RUBB = RUSSET BURBANK; KYNA = Konya, NGDE = Nigde, SVAS = Sivas

4.5 Total Tuber Yield (TTY)

The results of the total tuber yield (TTY) revealed that there were highly significant ($p < 0.001$) effects on the potato yield caused by the genotypes, environments, and the genotype by environment interaction for both the standard ANOVA and AMMI ANOVA (Table 4.17, Table 4.18) with the CV among the genotypes and the environments of 3.8 and the grand mean yield of 31.41. The IPC1 and the residual component of the GEI also revealed a highly significant ($P<0.001$) effect with the IPC1 constituting 77.44% while residual accounting for 22.56% of the GEI sum of squares. Of the total sum of squares, the treatment explained 99.08% with 31.6%, 52.9%, and 15.3% respectively attributed to genotype, environment, and GEI. It can be deduced that; a negligible error was observed on the tuber yield of the potato and so is not responsible for the yield differences among the genotypes. Greater differences in the yield can be stated to be environmentally induced more than genetically induced and the genotypic differences is attributed to the differences in the crossing parents of the cultivar which confers different responses with the environments and led to the significant difference in the yield of the genotypes.

Table 4.8. ANOVA of total tuber yield (TTY) for 15 genotypes grown in three different environments

Source	DF	SS	MS	F	P-value
Genotype (G)	14	7986	570.43	400.27	0.000***
Environment (E)	2	13368.2	6684.09	4690.24	0.000***
G x E	28	3915.9	139.85	98.14	0.000***
Error	135	192.4	1.43		
Total	179	25462.5			
CV	3.8				

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** $p \leq 0.001$

The crossover GEI observed in the TPY also influenced the total tuber yield (TTY) of the genotypes. The TTY of the genotypes ranges from Russet Burbank(17.033t/ha) to MEÇ1407.17 (41.77t/ha) whiles among environment; Nigde (24.24t/ha), Sivas (44.56t/ha), and Konya (26.45t/ha) (Table 4.19) with statistically significant yield differences between the highest and lowest yield of the genotypes and with the rest of the genotypes. There was a differential ranking of the genotypes across the environments. The highest TTY across the environments was found in MEÇ1407.17 (41.01 t/ha) in

Nigde, MEÇ1407.05 (56.69 t/ha) in Sivas, and MACAR1402.10 (35.52 t/ha) in Konya. On the other hand, the lowest TTY in Sivas was found in MACAR1402.11 (21.06 t/ha), while Russet Burbank was recorded the lowest TTY of 10.47 t/ha and 19.09 t/ha respectively in Nigde and Konya.

Table 4.18. AMMI analysis of variance for total tuber yield (TTY) of 15 potato genotypes grown in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	179	25462.5	142.249			
Treatment	44	25270.1	574.321***	99.08		
Genotype	14	7986.02	570.43***		31.6	
Environment	2	13368.2	6684.09***		52.9	
G x E	28	3915.94	139.855***		15.5	
IPC1	15	3032.54	202.169***		(12)	77.44
Residual	13	883.401	67.954***		(3.5)	22.56
Error	135	192.39	1.425	0.92		
Blocks/Env	9	29.529	3.281*			
Pure Error	126	162.861	1.293			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, *** $p \leq 0.001$

Biru (2017) reported a highly significant effect of genotype, environments, and G×E on the yield and yield component imply that the genetic variability among genotype, and the segregating possibility for selecting stable. Raja et al. (2018), Rymuza et al. (2015), and Wassu, (2017) reported that the genetic difference among potato genotypes account for the difference in marketable tuber yield, total tuber yield.

Table 4.19 Two-way table of total tuber yield (TTY) for 15 potato genotypes grown in three different environments*

GEN	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	19.74 *vwx*	43.07 *fg*	35.52 *j*	32.77
MACAR1402.11	18.28 *x*	21.06 *stuv*	28.09 *op*	22.48
MACAR1406.04	21.55 *stu*	51.83 *c*	19.42 *vwx*	30.93
MACAR1406.07	20.46 *tuvw*	45.43 *e*	22.59 *s*	29.49
MACAR1409.09	21.99 *st*	51.67 *c*	28.36 *op*	34.00
MEÇ1402.07	20.40 *tuvw*	41.65 *gh*	24.97 *r*	29.00
MEÇ1402.09	21.93 *st*	37.51 *i*	20.39 *tuvw*	26.61
MEÇ1405.06	25.69 *qr*	51.58 *c*	27.16 *pq*	34.81
MEÇ1407.05	33.14 *kl*	56.69 *a*	28.15 *op*	39.33
MEÇ1407.08	31.92 *lm*	53.91 *b*	27.97 *op*	37.93
MEÇ1407.17	41.01 *h*	49.40 *d*	34.90 *j*	41.77
MEÇ1411.06	34.41 *jk*	48.15 *d*	29.44 *no*	37.33
AGRIA	13.55 *y*	35.73 *j*	20.01 *uvw*	23.10
MADELEINE	29.13 *no*	43.70 *f*	30.70 *mn*	34.51
RUSSET BURBANK	10.47 *z*	21.55 *stu*	19.09 *wx*	17.04
Mean	24.24	44.56	26.45	31.75

*: Different letters within a row and column indicate significance at p≤0.05 in Duncan test

The AMMI IPC1 score mode of stability estimation states that the closer the IPC1 score values are to zero, the more stable the genotypes are to their testing environments (Purchase, 1997). In this research, the IPC1 score values of MEÇ1402.07, MEÇ1402.09, MEÇ1411.06, and AGRIA are closer to zero and so imply that they are more in the three test environments (Nigde, Sivas and Konya) for TTY. The Francis & Kannenberg CV and Kang Rank Sum (KR) methods did not identify any stable genotype as a result of their large CV and large KR. For the Shukla stability variance, MEÇ1402.07, MEÇ1402.09, and AGRIA were identified as stable genotypes while for the Eberhard and Russel deviation from the regression method, MACAR1406.07, MEÇ1405.06, and MADALEINE were revealed to be stable for TTY. More so, Finlay and Wilkinson regression coefficient (bi) revealed MACAR1402.10, MEÇ1402.07, MEÇ1402.09, MEÇ1411.06, and AGRIA as stable genotypes for TTY (Table 4.20).

Table 4.9. Stability estimation of total tuber yield of potato breeding lines grown in three different environments

Genotype	Mean TTY	Finlay & Wilkinson	Eberhart & Russel	Shukla	Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ2	CV	KR	IPC1
MACAR1402.10	32.777	0.918	13.659	53.335	36.32	20	-1.03
MACAR1402.11	22.477	-0.067	7.161	172.576	22.495	29	-3.32
MACAR1406.04	30.933	1.695	2.49	69.386	58.605	23	2.12
MACAR1406.07	29.493	1.311	0.042	9.912	46.935	15	0.84
MACAR1409.09	34.003	1.473	0.706	28.947	45.963	16	1.02
MEÇ1402.07	29.007	1.054	0.363	-0.844	38.561	12	0.01
MEÇ1402.09	26.61	0.882	0.878	2.652	35.592	14	-0.09
MEÇ1405.06	34.813	1.375	0.175	16.141	41.763	12	1.05
MEÇ1407.05	39.323	1.392	4.685	36.028	38.768	13	1.48
MEÇ1407.08	37.933	1.284	3.325	21.115	36.845	11	1.13
MEÇ1407.17	41.77	0.592	3.974	34.722	17.428	11	-0.59
MEÇ1411.06	37.333	0.858	3.403	13.645	25.959	10	0.05
AGRIA	23.097	1.063	1.222	2.753	49.391	16	-0.08
MADALEINE	34.51	0.758	0.001	4.862	23.174	10	-0.61
R. BURBANK	17.037	0.411	4.296	59.254	34.152	28	-1.96

CV, coefficient of variation; IPC1, interaction principal component analysis axis 1; AMMI, Additive Main Effects and Multiplicative Interaction

For the level of genotype adaptability, the Finlay and Wilkinson regression model characterized the genotypes into four levels of adaptability for the total tuber yield (TTY) (Figure 4.9). MACAR1406.04, MACAR1406.07, AGRIA, and MEÇ1402.07 were identified as having poor adaptability to favourable environments while RUSSET BURBANK, MEÇ1402.09, and MACRA1402.11 have poor adaptability to unfavourable environments. On the other hand, MACAR1409.09, MEÇ1407.05, MEÇ1405.06, and MEÇ1407.08 were identified as genotypes adapting favourably to favourable environment whiles MEÇ1411.06, MEÇ1407.17, MACAR1402.10, and MADELEINE as tolerant and very well adapted to unfavourable environments.

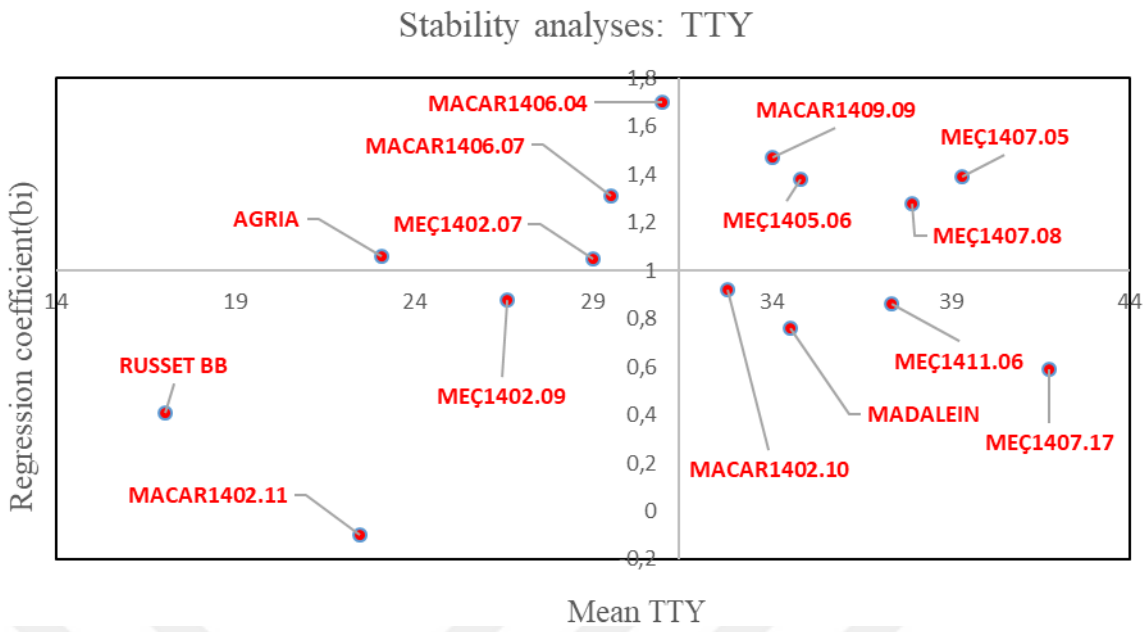

Figure 4.9. Relationship of genotype adaptation (regression coefficient 'bi') and mean total tuber yield (TTY) of 15 potato genotypes grown in three diverse environments

Also, the AMMI IPC1 biplot against mean TTY group the genotypes into general stability or specific stability, and high or low yielding genotypes. The degree of adaptability of a genotype to the environment is determined by the distance of the genotype IPC1 scores to the IPC1 axis. In, Figure 4.10, AGRIA, MEÇ1402.09, MEÇ1402.07, MEÇ1411.06 are stable genotypes and broadly adapted to a wide range of environments with only MEÇ1411.06 high yielding while MACAR1406.04 and MACAR1406.07 are low yielding and very much interactive with favourable environmental conditions. On the other hand, MACAR1409.09, MEÇ1405.06, MEÇ1407.08, and MEÇ1407.05 are high yielding genotypes and highly interactive with favourable environmental conditions. Furthermore, MACAR1402.11 and Russet Burbank are low yielding genotypes and highly sensitive to unfavourable environmental conditions while MACAR1402.10, MEÇ1407.17, and MADELEINE are high yielding and highly interactive to adverse environmental fluctuations. The environments are widely interactive more than the genotypes with Sivas being the most interactive and best environment while Nigde and Konya being very much sensitive (Figure 4.10).

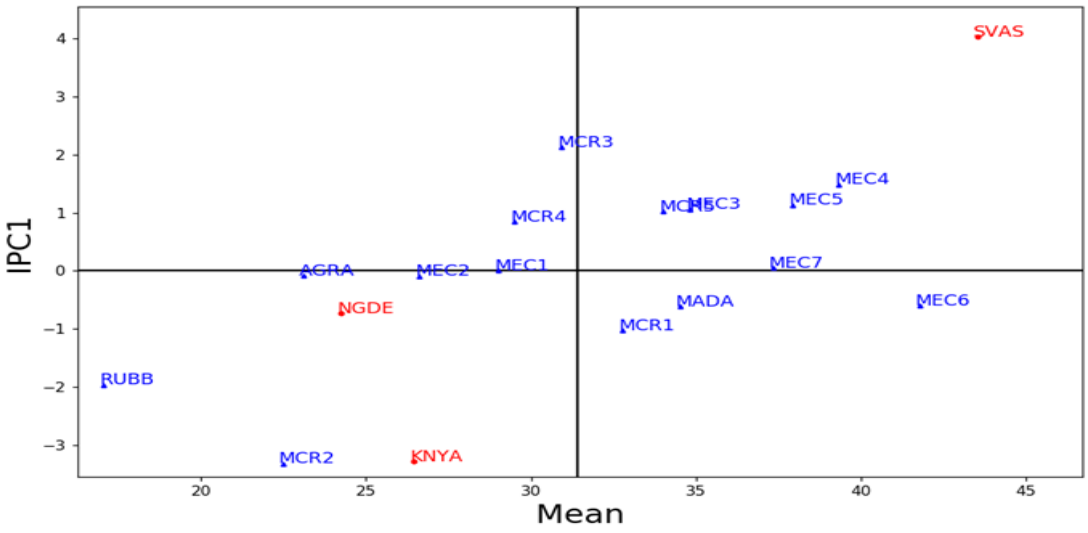

Figure 4.10. AMMI biplot analysis of interaction principal component axis (IPCA-1) with mean of total tuber yield (TTY) of potato genotype evaluated across three different environments. Note: MCR1 = MACAR1402.10, MCR2 = MACAR1402.11, MCR3 = MACAR1406.04, MCR4 = MACAR1406.07, MCR5 = MACAR1409.09, MEÇ1 = MEÇ1402.07, MEC2 = MEÇ1402.09, MEC3 = MEÇ1405.06, MEC4 = MEÇ1407.05, MEC5 = MEÇ1407.08, MEC6 = MEÇ1407.17, MEC7 = MEÇ1411.06, AGRA = AGRIA, MADA = MADELEINE, RUBB = RUSSET BURBANK; KYNA = Konya, NGDE = Nigde, SVAS = Sivas

4.6 Marketable Tuber Yield

The analysis of variance for the marketable tuber yield (MTY) revealed that there were highly significant ($p < 0.001$) effects of the genotypes, environments, and the genotype by environment interaction on the potato yield for the general ANOVA and the AMMI ANOVA (Table 4.21 and Table 4.22). The CV among the genotypes and the environments were found to be 3.87 and the grand mean yield of 31.21. The IPC1 and the residual component of the GEI also revealed highly significant ($P<0.001$) with the IPC1 constituting 77.62% while residual accounting for 22.38% of the GEI sum of squares. The treatment explained 99.04% of the total sum of squares with 28.58%, 52.49%, and 15.52% respectively attributed to genotype, environment, and GEI. This indicates that genotype, environment, and GEI have a great influence on the marketable tuber yield of the potato. The greater differences in the yield can be stated to be environmentally induced more than genetically induced. The significant differences in the genotypes are attributed to the differences in the crossing parents of these breeding lines and their different responses to environmental fluctuations.

Table 4.21. ANOVA of Marketable tuber yield (MTY) for 15 genotypes grown in three different Environments

Source	DF	SS	MS	F	P-value
Genotype	14	8053.9	575.28	394.03	0.000***
Environment	2	13215.3	6607.66	4525.88	0.000***
G x E	28	3907.1	139.54	95.58	0.000***
Error	135	197.1	1.46		
Total	179	25373.4			
Grand Mean	31.212				
CV	3.87				

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** p≤0.001

Table 4.22. AMMI analysis of variance for marketable tuber yield (MTY) of 15 potato genotypes grown in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	179	25373.4	141.751			
Treatment	44	25176.3	572.189***	99.04		
Genotype	14	8053.86	575.276***		28.58	
Environment	2	13215.3	6607.66 ***		52.49	
G x E	28	3907.15	139.541 ***		15.52	
IPC1	15	3032.77	202.184 ***		(12.05)	77.62
Residual	13	874.383	67.26 ***		(3.47)	22.38
Error	135	197.096	1.46	0.96		
Blck/Env	9	29.181	3.242*			
Pure Error	126	167.915	1.333			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, *p≤0.05, *** p≤0.001 ns= not significant

The effect of the crossover GEI was also realized in the marketable tuber yield (MTY) of the potato genotypes. The mean MTY of the genotypes ranges from 16.66 t/ha to 41.60 t/ha which was found in Russet Burbank and MEÇ1407.17 respectively. Among the environments; Nigde (24.00 t/ha), Sivas (43.25 t/ha), and Konya (26.38 t/ha) (Table 4.23). Across the environments, different genotypes occupy different ranks with MEÇ1407.17 (40.70 t/ha), MEÇ1407.05 (56.52 t/ha), and MACAR1402.10 (35.5 t/ha) recording the highest MTY respectively in Nigde, Sivas, and Konya whereas Russet Burbank recorded the lowest MTY for all the three environments with 10.14t/ha, 20.92 t/ha and 18.91 t/ha respectively in Nigde, Sivas and Konya. The difference in yield may also be attributed to the differences in the nutrients supply and other environmental conditions.

Table 4.23. Two-way table of marketable tuber yield (MTY) for 15 potato genotypes grown in three different environments

GEN	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	19.51 *vwx*	42.74 *fg*	35.50 *j*	32.58
MACAR1402.11	18.12 *x*	20.97 *stuv*	27.96 *op*	22.35
MACAR1406.04	21.41 *stu*	51.54 *c*	19.40 *vwx*	30.79
MACAR1406.07	20.22 *tuvw*	45.19 *e*	22.51 *s*	29.30
MACAR1409.09	21.74 *st*	51.50 *c*	28.32 *op*	33.85
MEÇ1402.07	20.29 *tuvw*	41.42 *gh*	24.92 *r*	28.88
MEÇ1402.09	21.65 *st*	37.24 *i*	20.37 *tuvw*	26.42
MEÇ1405.06	25.48 *qr*	51.21 *c*	27.10 *pq*	34.60
MEÇ1407.05	32.92 *kl*	56.52 *a*	28.11 *op*	39.18
MEÇ1407.08	31.60 *lm*	53.62 *b*	27.80 *op*	37.67
MEÇ1407.17	40.70 *h*	49.22 *d*	34.88 *j*	41.60
MEÇ1411.06	34.22 *jk*	47.96 *d*	29.43 *no*	37.20
AGRIA	13.23 *y*	35.41 *j*	19.92 *uvw*	22.85
MADALEIN	28.84 *o*	43.32 *f*	30.64 *mn*	34.26
RUSSET BURBANK	10.14 *z*	20.92 *stuv*	18.91 *wx*	16.66
Mean	24.00	43.25	26.38	31.21

*: Different letters within a row and column indicate significance at p≤0.05 in Duncan test

The difference in the mean yield performance (Table; 4.16, 4.19, 4.23, and 4.27) of the genotypes within and across environment was expected in this study as the genotypes differed genetically from the crossing parents as reflected in the high significant differences ($p \leq 0.01$) in the genotypes, environment and their interaction for the TPY, TTY, MTY, and NTP. Effect of genotype, environment, and their interaction on NTP, MTY, TTY (Eaton *et al.*, 2017), and TPY can be explained by the variation in their biological vigour of the genotypes, and probably due to the variation in favourable environmental conditions at the study's locations and management practices. Sivas performed the highest MTY and it was followed by Konya and Nigde. Thus, potato responds favourably to better environments, and hence subject to the strong influence of genotype, environment, and genotype by environment interaction (Bai *et al.*, 2014). It is stated that a significant interaction of cultivar x location indicates instability of expression of these traits in different cultivars across locations and seasons as these quality traits are genetically controlled (Wassu, 2017). GEI has a significant impact on the potato breeding lines assessed in these environments; Nigde, Konya, and Sivas, which confirms Bradshaw's (1997) study in that interactions of potato genotypes to macro-environments and microenvironment lead to yield and traits fluctuations. This implies that the breeding lines differ in their yield quality and stability strength, varied resistibility or susceptibility to environmental fluctuations due to different genetic factors that explained the existence

of difference in the ranking of the genotypic means and the various stability estimates used in this research. Raja et al. (2018) stated that the phenotypic expression of any trait is greatly influenced by genotype and growing location, whiles Haydar et al., (2009) and Flis et al., (2014) shows that cultivar yield is significantly affected by environment, as it confirmed in the present research.

Table 4.10 Stability estimation of marketable tuber yield of potato breeding lines grown in three different environments

Genotype	Mean MTY	Finlay & Wilkinson	Eberhart & Russel	Shukla	Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ^2	CV	KR	IPC1
MACAR1402.10	25.62	2.081	0.025	4.167	14.245	16	-1.04
MACAR1402.11	21.49	1.158	0.061	0.279	9.662	20	-3.29
MACAR1406.04	21.89	0.751	0.102	0.574	6.594	19	2.11
MACAR1406.07	22.83	1.047	0.001	-0.044	8.021	6	0.85
MACAR1409.09	23.60	1.044	0.009	-0.01	7.774	6	1.04
MEÇ1402.07	21.49	0.814	0.098	0.462	7.159	20	0.01
MEÇ1402.09	22.45	0.935	0.004	-0.023	7.301	9	-0.10
MEÇ1405.06	22.25	0.824	0.00	0.056	6.474	13	1.04
MEÇ1407.05	21.52	1.089	0.17	0.661	9.545	21	1.50
MEÇ1407.08	23.68	1.495	0.001	0.812	11.037	14	1.14
MEÇ1407.17	22.64	1.234	0.007	0.164	9.548	13	-0.59
MEÇ1411.06	23.00	0.896	0.012	0.031	6.863	8	0.05
AGRIA	19.15	0.396	0.076	1.536	4.507	28	-0.09
MADALEINE	19.44	0.912	0.028	0.085	8.362	20	-0.63
RUSSET BB	19.99	0.324	0.118	2.032	4.284	27	-2.00

CV, coefficient of variation; IPC1, interaction principal component analysis axis 1; AMMI, Additive Main Effects and Multiplicative Interaction

In Table 4.24, the Finlay and Wilkinson regression coefficient depicted that genotypes MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1407.05, MEÇ1411.06, and MADALEINE were stable with bi values equal to or close to 1. The Eberhard and Russel stability model also depicted MACAR1402.10, MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1405.06, MEÇ1407.08, MEÇ1407.17, MEÇ1411.06, and MADALEINE as stable genotypes. Also, the Shukla stability variance identified MACAR1406.07, MACAR1409.09, MEÇ1405.06, MEÇ1411.06, and MADALEINE to be stable. Thus, different stability models identified different stable genotypes with MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1411.06 and MADALEINE been identified by Finlay and Wilkinson regression model, Eberhart and Russel stability model, and Shukla stability model as stable genotypes. However, the Francis & Kannenberg CV and Kang Rank Sum (KR) failed to identify any desirable genotype for

MTY while the AMMI IPC1 score revealed MEÇ1402.07, MEÇ1402.09, MEÇ1411.06, and AGRIA as stable genotypes for MTY.

Figure 4.11 characterized AGRIA, MEÇ1402.09, and MEÇ1402.07 as poorly adaptable genotypes to all environmental conditions whiles MEÇ1402.10 was well adaptable to all environments. Furthermore, MACAR1402.11, and Russet Burbank were highly sensitive to unfavourable environmental conditions while MACAR1406.04 and MACAR1406.07 were poorly adaptable to favourable environments. On the other hand, MEÇ1407.17, MEC1411.06, and MADELEINE were high yielding and very well adapted to unfavourable environmental conditions whiles MACAR1409.09, MEÇ1405.06, MEÇ1407.05, and MEÇ1407.08 were very well adaptable to favourable environmental conditions.

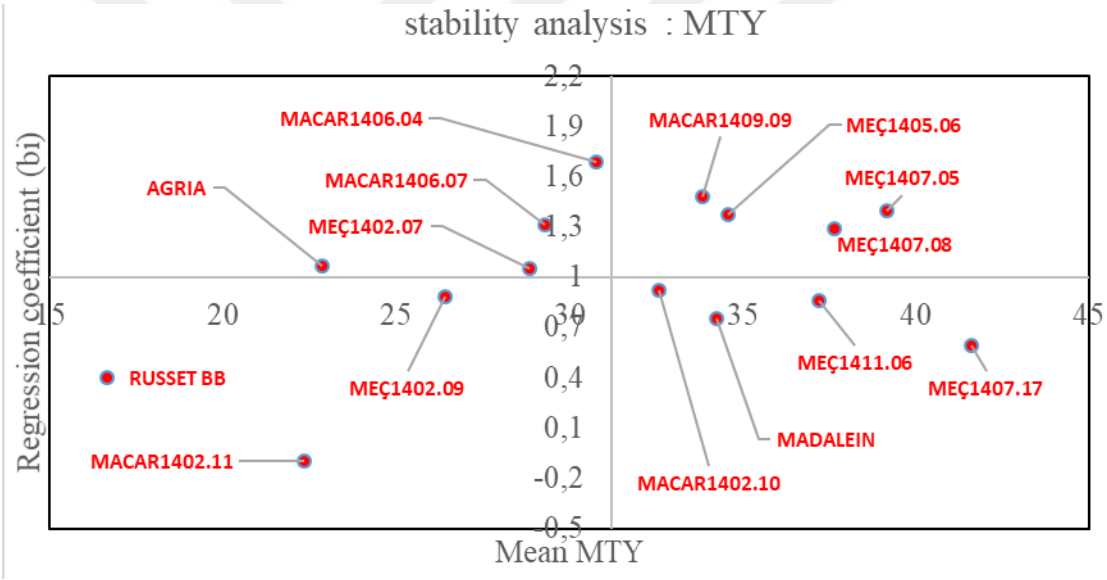

Figure 4.11. Relationship of genotype adaptation (regression coefficient 'bi') and mean marketable tuber yield (MTY) of 15 potato genotypes grown in three diverse environments

The AMMI biplot analysis of the genotype for MTY (Figure 4.12) showed that AGRIA, MEÇ1402.09, MEÇ1402.07, and MEÇ1411.06 had general adaptation regardless of the environmental influences which are similar to the genotype characterization in Figure 4.11. Genotype partitioned closed to each other had a positive correlation, thus the genotypes in this biplot were generally segregated into three groups; Russet Burbank and MACAR1402.11 forming one group, AGRIA, MEÇ1402.09, MEÇ1402.07,

MACAR1406.07, and MACAR1406.04 forming one group, and MACAR1402.10, MADELEINE, MEÇ1411.06, MEÇ1407.17, MEÇ1407.08, MEÇ1407.05 MACAR1409.09, and MEÇ1405.06 also forming one group. The environments, on the other hand, were scattered and relatively forming two groups: Nigde (NGDE) and Konya (KNYA) on one site and Sivas (SVAS) on the other site. This similarity in the grouping of genotype may be associated with genetic similarities between cultivars and the similarity in the environment is predictively due to environmental inputs. Nigde (NGDE) environment was relatively stable whiles Konya (KNYA) and Sivas (SVAS) environments were highly unstable for marketable tuber yields for the genotype.

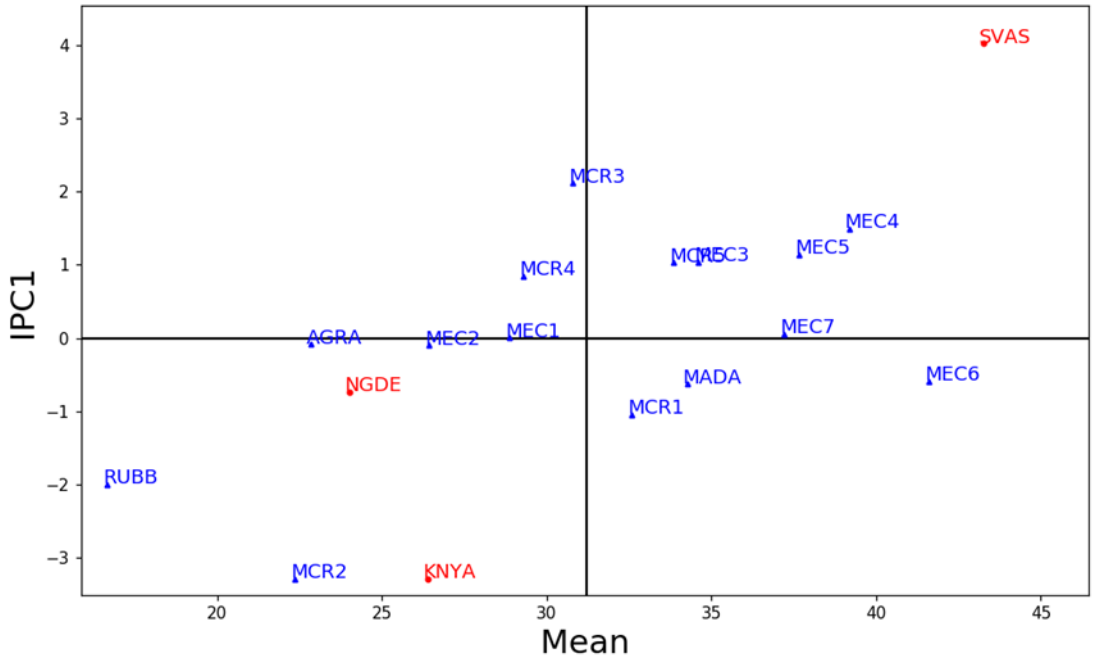

Figure 4.12. AMMI biplot analysis of interaction principal component axis (IPCA-1) with mean of marketable tuber yield (MTY) of potato genotype evaluated across three different environments. Note: MCR1 =MACAR1402.10, MCR2 = MACAR1402.11, MCR3 = MACAR1406.04, MCR4 = MACAR1406.07, MCR5 = MACAR1409.09, MEÇ1 = MEÇ1402.07, MEC2 = MEÇ1402.09, MEC3 = MEÇ1405.06, MEC4 = MEÇ1407.05, MEC5 = MEÇ1407.08, MEC6 = MEÇ1407.17, MEC7 = MEÇ1411.06, AGRA = AGRIA, MADA = MADELEINE, RUBB = RUSSET BURBANK; KYNA = Konya, NGDE = Nigde, SVAS = Sivas

4.7. Number of Tuber Per Plant

Highly significant ($p < 0.001$) effect of the genotypes, environments, and the genotype by environment interaction on the number of tubers per plant(NTP) was observed in the ANOVA results (Table 4.25 and Table 4.26). The CV among the genotypes, and the environments were found to be 7.76 and the grand mean yield of 6.08. The IPC1 and the residual component of the GEI also revealed highly significant ($P<0.001$) with the IPC1

constituting 77.44% while residual accounting for 22.56% of the GEI sum of squares. The treatment explained 95.23% of the total sum of squares with 39.53%, 41.47% and 19% respectively attributed to genotype, environment and GEI. This indicates that genotype, environment, and GEI have a great influence on the tuber number per plant.

Table 4.25 ANOVA OF Number of tubers per plant for 15 genotypes grown in three different Environments

Source	DF	SS	MS	F	P-value
Genotype	14	273.017	19.501	87.59	0.000***
Environment	2	287.544	143.772	645.79	0.000***
G x E	28	132.194	4.721	21.21	0.000***
Error	135	30.055	0.223		
Total	179	722.81			
CV	7.8				

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** p≤0.001

Table 4.26 AMMI analysis of variance for number of tubers per plant (NTP) of 15 potato genotypes grown in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	179	726.826	4.06			
Treatment	44	696.411	15.828 ***	95.23		
Genotype	14	275.307	19.665 ***		39.53	
Environment	2	288.783	144.391 ***		41.47	
G x E	28	132.322	4.726 ***		19	
IPC1	15	97.921	6.528 ***		(14.06)	77.44
Residual	13	34.401	2.646 ***		(4.94)	22.56
Error	135	30.415	0.225	4.77		
Blocks/Env	9	2.007	0.223 ns			
Pure Error	126	28.408	0.225			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, *p≤0.05, *** p≤0.001 ns= not significant

The lowest and highest mean NTP among genotypes was respectively MACAR1402.11 (4.1tubers) and MEÇ1405.06 (9.2tubers), whiles across environments, Sivas (7.9 tubers) recorded the highest NTP followed by Konya (5.3 tubers) and Nigde (5.1 tubers), recorded the least (Table 4.27). The highest number of tubers per plant within the environments were recorded in MEÇ1407.17 (7.3 tubers) in Nigde, for MEÇ1405.06 (13.7 tubers) in Sivas, and for MEÇ1405.06 (8.1 tubers) in Konya while the lowest number of tubers per plant within the environments was recorded for Russet Burbank (3.4 tubers) in Nigde, MACAR1402.11 (3.7 tubers) in Sivas, and MACAR1406.04 (3.4

tubers) in Konya. Greater differences in the NTP are environmentally induced more than genetically induced and can be due to agronomic practices and nutrient input. This confirms that agronomy, nutrients (phosphate, potassium, and calcium) and varietal potential influenced the numbers of potato tubers produced per potato plant (Delgado *et al.* 2016).

Table 4.11 Two-way table of tubers per plant (NTP) for 15 potato genotypes grown in three different environments*

GEN	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	4.7 *opqrs*	7.7 *ef*	7.0 *ghi*	6.5
MACAR1402.11	3.8 *tuvw*	3.7 *uvw*	4.7 *opqrs*	4.1
MACAR1406.04	5.2 *no*	7.2 *fgh*	3.4 *w*	5.3
MACAR1406.07	5.4 *lmn*	7.7 *efg*	4.8 *nopqr*	6.0
MACAR1409.09	4.5 *pqrs*	7.2 *fgh*	4.3 *rst*	5.4
MEÇ1402.07	4.1 *stuv*	6.9 *hi*	4.9 *nopqr*	5.3
MEÇ1402.09	5.4 *lmn*	7.6 *efg*	4.7 *opqrs*	5.9
MEÇ1405.06	6.0 *jkl*	13.7 *a*	8.1 *de*	9.2
MEÇ1407.05	5.1 *nopq*	7.8 *ef*	5.1 *nop*	6.0
MEÇ1407.08	6.6 *ij*	9.9 *b*	5.4 *lmn*	7.3
MEÇ1407.17	7.3 *fgh*	8.9 *c*	6.8 *hi*	7.7
MEÇ1411.06	6.0 *jkl*	8.5 *cd*	6.0 *jkl*	6.8
AGRIA	3.5 *vw*	8.0*de*	4.3 *rstu*	5.2
MADELEINE	5.9 *klm*	6.4 *ijk*	5.3 *mno*	5.8
RUSSET BURBANK	3.4 *w*	7.0 *ghi*	4.4 *qrst*	4.9
Mean	5.1	7.9	5.3	6.1

*: Different letters within a row and column indicate significance at p≤0.05 in Duncan test

The genotype characterization for NTP based on the Finlay and Wilkinson regression analysis showed that MEÇ1402.09, MEÇ1402.07, MEÇ1407.05, MACAR1406.04, MACAR1406.07, and MACAR1409.09 were poorly adaptable to all environmental conditions whiles MEÇ1411.06 was well adaptable to all environmental conditions. More so, MACAR1402.11, and MADELEINE were highly sensitive and poorly adaptable to unfavourable environmental conditions while AGRIA and RUSSET BURBANK were poorly adaptable to favourable environments. On the other hand, MEÇ1407.17 and MACAR1402.10 were high yielding and very well adapted to unfavourable environmental conditions whiles, MEÇ1405.06 and MEÇ1407.08 were very well adaptable to favourable environmental conditions (Figure 4.13).

The AMMI biplot for the NTP (Figure 4.14) shows that, MACAR1409.09, MEÇ1402.07, MEÇ1407.05, MACAR1406.07, MACAR1402.10, MEÇ1411.06, MEÇ1407.17 and

Russet Burbank were less influenced by environmental interactions due to their small IPC1 values and so were generally stable. MEÇ1405.06 was the highest performing genotype for tuber number per plant but also highly unstable, and thus had specific adaptation. MACAR1402.11 gave off good tuber number in the poor environment and had high G*E interactions. MACAR1402.10, MEÇ1407.08, MEÇ1407.17, and MEÇ1411.06 were the suitable genotypes which were generally stable and had above-average yield performance. Generally, the genotypes had average yield performance for tuber number per plant and stability except for MEÇ1405.06 and MACAR1402.11 which were unstable and segregated to the good environments and poor environments, respectively.

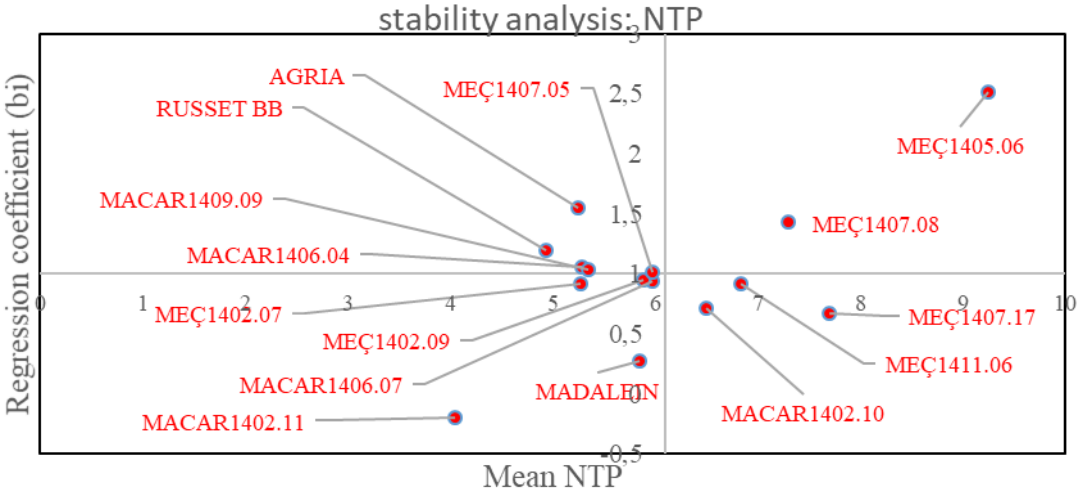

Figure 4.13. Relationship of genotype adaptation (regression coefficient 'bi') and mean number of tubers per plant (NTP) of 15 potato genotypes grown in three diverse environments

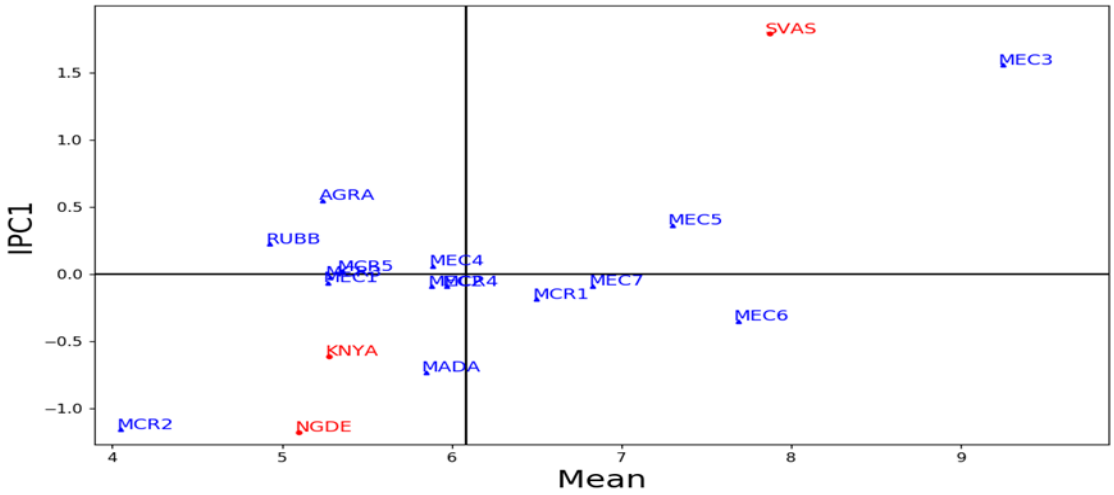

Figure 4.14. AMMI biplot analysis of interaction principal component axis (IPCA-1) with mean tubers per plant (NTP) of potato genotype evaluated across three different environments. Note: MCR1 =MACAR1402.10, MCR2 = MACAR1402.11, MCR3 = MACAR1406.04, MCR4 = MACAR1406.07, MCR5 = MACAR1409.09, MEÇ1 = MEÇ1402.07, MEC2 = MEÇ1402.09, MEC3 = MEÇ1405.06, MEC4 = MEÇ1407.05, MEC5 = MEÇ1407.08, MEC6 = MEÇ1407.17, MEC7 = MEÇ1411.06, AGRA = AGRIA, MADA = MADELEINE, RUBB = RUSSET BURBANK; KYNA = Konya, NGDE = Nigde, SVAS = Sivas

4.8 Tuber Grading

4.8.1 Big Tuber (> 50mm) Yield

The ANOVA for the big tubers (> 50mm) yield showed that, there was highly significant ($p < 0.001$) effects on the big potato tuber yield caused by the genotypes, environments, and the genotype by environment interaction (Table 4.28; Table 4.29). The CV among the genotypes and the environments were also found to be 1.69 and the grand mean yield of 87.06.

Table 4.12 ANOVA of Big Tuber (> 50mm) Yield (number) for 15 genotypes grown in three different Environments

Source	DF	SS	MS	F	P-value
Genotype	14	5565.8	397.56	183.14	0.000***
Environment	2	2848.4	1424.18	656.05	0.000***
G x E	28	3554.1	126.93	58.47	0.000***
Error	135	293.1	2.17		
Total	179	12261.3			
CV	1.69				

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** p≤0.001

Table 4.13 AMMI Analysis of variance of for big tuber (> 50mm) Yield (number) for 15 potato genotypes grown in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	179	12264.9	68.519			
Treatment	44	11971.6	272.081***	98.29		
Genotype	14	5571.99	397.999***		46.54	
Environment	2	2849.91	1424.96***		23.81	
Genotype x Environment	28	3549.66	126.774***		29.65	
IPC1	15	3003.04	200.203***		(25.08)	84.6
Residual	13	546.62	42.048 ***		(4.57)	15.4
Error	135	293.31	2.173	1.71		
Blocks/Env	9	15.022	1.669ns			
Pure Error	126	278.293	2.209			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, *** p≤0.001 ns= not significant

The IPC1 and the residual component of the GEI also revealed highly significant (P<0.001) with the IPC1 constituting 84.6% while residual accounting for 15.4% of the GEI sum of squares. The treatment explained 98.29% of the total sum of squares of which 46.54%, 23.81%, and 29.65%, respectively attributed to genotype, environment and GEI. This indicates that genotype has much influence on the big tuber size than the environment and GEI. The environmental effect may be due to temperature and nutrient disparities among the various environments which led to different responses of the genotypes with the environment.

Crossover interaction occurred among genotypes from one environment to another difference in yield. MEÇ1407.05 (94.4 tubers) and MEÇ1405.06 (72.5tubers) respectively recording the highest and lowest mean performance of the big (>50mm) potato tubers. Across environments, Nigde (81.5 tubers) recorded the least t mean yield for the big tuber, followed by Sivas (88.9 tubers) with the highest mean yield recorded in Konya (90.5tubers) (Table 4.30). Also, the differences in yield may be attributed to the differences in the nutrients supply, differences in parental origin and other environmental conditions (Sogbohossou et al. 2019).

Table 4.14. Two-way table of big tubers (>50mm) yield (BTN) for 15 potato genotypes grown in three different environments*****

GEN	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	74.1 *v*	87.9 *jklmn*	94.0 *bcdefg*	85.3
MACAR1402.11	84.6 *op*	96.4 *a*	94.4 *abcde*	91.8
MACAR1406.04	86.8 *lmn*	93.9 *cdefg*	94.6 *abcde*	91.8
MACAR1406.07	79.0 *r*	87.6 *klmn*	78.7 *r*	81.8
MACAR1409.09	86.0 *nop*	91.7 *hi*	95.0 *abc*	90.9
MEÇ1402.07	89.1 *jk*	89.8 *ij*	88.7 *jkl*	89.2
MEÇ1402.09	77.5 *rst*	86.5 *mno*	84.3 *p*	82.7
MEÇ1405.06	74.8 *uv*	65.9 *w*	76.7 *stu*	72.5
MEÇ1407.05	93.4 *cdefgh*	95.3 *abc*	94.7 *abcd*	94.4
MEÇ1407.08	81.7 *q*	89.3 *jk*	89.0 *jk*	86.7
MEÇ1407.17	88.5 *jklm*	89.1 *jk*	92.0 *gh*	89.9
MEÇ1411.06	92.6 *efgh*	92.2 *fgh*	92.2 *fgh*	92.3
AGRIA	75.8 *tuv*	92.2 *fgh*	92.8 *defgh*	86.9
MADELEINE	78.5 *rs*	92.9 *defgh*	96.0 *ab*	89.2
Russet Burbank	59.8 *x*	87.6 *klmn*	94.2 *bcdef*	80.5
Mean	81.5	88.9	90.5	87.1

*: Different letters within a row and column indicate significance at p≤0.05 in Duncan test

For the stability estimates, Finlay and Wilkinson regression analysis revealed MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1407.05, MEÇ1411.06, and MADALEINE as stable genotypes. Genotypes, MACAR1402.10, MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1405.06, MEÇ1407.08, MEÇ1407.17, MEÇ1411.06, and MADALEINE were also identified to be stable by Eberhard and Russel's stability model, while the Shukla's stability model identified MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1411.06, and MADALEINE as stable genotypes (Table 4.31). There was a similar pattern of stability ranking of genotypes between the Eberhard and Russel's stability model and Shukla's stability model which confirms the results of Caliskan et al., (2007)

Table 4.31. Stability estimation of big tuber number of potato breeding lines grown in three different environments

Genotype	Mean BTN	Finlay & Wilkinson	Eberhart & Russel	Shukla	Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ^2	CV	KR	IPC1
MACAR1402.10	25.623	2.081	0.025	4.167	14.245	16	
MACAR1402.11	21.487	1.158	0.061	0.279	9.662	20	
MACAR1406.04	21.887	0.751	0.102	0.574	6.594	19	
MACAR1406.07	22.833	1.047	0.001	-0.044	8.021	6	
MACAR1409.09	23.597	1.044	0.009	-0.01	7.774	6	
MEÇ1402.07	21.493	0.814	0.098	0.462	7.159	20	
MEÇ1402.09	22.450	0.935	0.004	-0.023	7.301	9	
MEÇ1405.06	22.247	0.824	0.00	0.056	6.474	13	
MEÇ1407.05	21.523	1.089	0.17	0.661	9.545	21	
MEÇ1407.08	23.680	1.495	0.001	0.812	11.037	14	
MEÇ1407.17	22.643	1.234	0.007	0.164	9.548	13	
MEÇ1411.06	23.003	0.896	0.012	0.031	6.863	8	
AGRIA	19.153	0.396	0.076	1.536	4.507	28	
MADALEINE	19.437	0.912	0.028	0.085	8.362	20	
Russet Burbank	19.990	0.324	0.118	2.032	4.284	27	

CV, coefficient of variation; IPC1, interaction principal component analysis axis 1; AMMI, Additive Main Effects and Multiplicative Interaction

4.8.2 Medium Tuber (30-50 mm) Yield

The ANOVA for the medium (between 30mm and 50 mm**)** tubers yield showed that there was highly significant ($p < 0.001$) effects of genotypes, environments, and the genotype by environment interaction on the medium tuber yield of the potato (Table 4.32; Table 4.33). The CV among the genotypes and the environments were also found to be 11.46 and the grand mean yield of 12.2 tubers.

Table 4.32. AVONA of medium tuber (30-50mm) yield for 15 genotypes grown in three different environments

Source	DF	SS	MS	F	P-value
Genotype	14	5199	371.35	189.36	0.000***
Environment	2	2409.3	1204.66	614.28	0.000***
G x E	28	3331.3	118.98	60.67	0.000***
Error	135	264.7	1.96		
Total	179	11204.3			
CV	11.5				

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** $p \leq 0.001$

The treatment explained 98.35% of the total sum of squares of which 47.53%, 21.99% and 30.48% respectively attributed to genotype, environment, and GEI. The IPC1 and the residual component of the GEI also revealed highly significant (P<0.001) with the IPC1 constituting 84.53% while residual accounting for 15.45% of the GEI sum of squares.

Table 4.33. AMMI Analysis of variance of medium tuber (30-50mm) yield for 15 potato genotypes grown in three environments

Source	DF	SS	MS	%TSS explained	% TRT SS explained	%GEI SS explained
Total	179	11197.7	62.557			
Treatment	44	10933	248.476 ***	98.35		
Genotype	14	5196.69	371.192***		47.53	
Environment	2	2404.42	1202.21***		21.99	
G x E	28	3331.84	118.994***		30.48	
IPC1	15	2817.08	187.805***		(25.77)	84.55
Residual	13	514.76	39.597 ***		(4.71)	15.45
Error	135	264.73	1.961	1.65		
Blocks/Env	9	10.67	1.185 ns			
Pure Error	126	254.06	2.016			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, *** p≤0.001 ns= not significant

The mean comparison of the medium tuber yield shows that significant difference occurred among the genotypes and the environment which depicted crossover interaction among genotypes from one environment to another. This resulted in MEÇ1407.05 (6.0 tubers), MACAR1402.11 (3.1 tubers), and MEÇ1407.05 respectively in Nigde, Sivas and Konya for recording the lowest medium size number of tubers, while Russet Burbank (37.1 tubers), MEÇ1405.06 (33.4 tubers), and MEÇ1405.06 (23.1 tubers) recorded the highest medium tuber number respectively in Nigde, Sivas, and Konya. Furthermore, Nigde (18.2 tubers) recorded the highest mean medium tuber yield followed by Sivas (10.4 tubers) and Konya (8.1tubers) being the least across locations. Among the genotypes, the highest and lowest mean yield for the medium tuber yield was recorded in MEÇ1405.06 (27.0 tubers) and MEÇ1407.05 (5.2 tubers) (Table 4.34) respectively. Also, it can be attributed to the differences in the nutrients supply and other environmental conditions.

Table 4.34. Two-way table of medium tuber (30-50mm) yield for 15 potato genotypes grown in three different environments*

GENOTYPES	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	24.7 *c*	11.3 *jklm*	6.0 *qrstu*	14.0
MACAR1402.11	14.5 *hi*	3.1 *w*	5.2 *stuv*	7.6
MACAR1406.04	12.6 *ijk*	5.6 *rstuv*	5.3 *stuv*	7.8
MACAR1406.07	19.8 *f*	11.8 *jkl*	20.9 *ef*	17.5
MACAR1409.09	12.9 *ij*	8.0 *nop*	4.8 *uvw*	8.5
MEÇ1402.07	10.3 *lm*	9.7 *mn*	11.1 *jklm*	10.4
MEÇ1402.09	21.3 *def*	12.8 *ij*	15.6 *gh*	16.6
MEÇ1405.06	24.5 *c*	33.4 *b*	23.1 *cd*	27.0
MEÇ1407.05	6.0 *qrstu*	5.2 *stuv*	4.5 *uvw*	5.2
MEÇ1407.08	17.3 *g*	10.2 *lm*	10.4 *lm*	12.6
MEÇ1407.17	10.8 *klm*	10.6 *lm*	7.9 *nop*	9.8
MEÇ1411.06	6.9 *pqrs*	7.5 *opqr*	7.8 *nopq*	7.4
AGRIA	21.8 *de*	6.9 *pqrs*	6.8 *pqrst*	11.9
MADELEINE	20.5 *ef*	6.2 *pqrstu*	3.8 *vw*	10.2
RUSSET BURBANK	37.1 *a*	9.4 *mno*	4.9 *tuvw*	17.1
Mean	18.2	10.4	8.1	12.2

*: Different letters within a row and column indicate significance at $p \leq 0.05$ in Duncan test

Table 4.35 Stability estimation of the medium size tubers of potato breeding lines grown in three different environments

Genotype	Mean MTN	Finlay & Wilkinson	Eberhard & Russel	Shukla	Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ^2	CV	KR	IPC1
MACAR1402.10	25.6	2.08	0.03	4.17	14.25	16	
MACAR1402.11	21.5	1.16	0.06	0.28	9.66	20	
MACAR1406.04	21.9	0.75	0.10	0.57	6.59	19	
MACAR1406.07	22.8	1.05	0.00	-0.04	8.02	6	
MACAR1409.09	23.6	1.04	0.01	-0.01	7.77	6	
MEÇ1402.07	21.5	0.81	0.10	0.46	7.16	20	
MEÇ1402.09	22.5	0.94	0.00	-0.02	7.30	9	
MEÇ1405.06	22.3	0.82	0.00	0.06	6.47	13	
MEÇ1407.05	21.5	1.09	0.17	0.66	9.55	21	
MEÇ1407.08	23.7	1.50	0.00	0.81	11.04	14	
MEÇ1407.17	22.6	1.23	0.01	0.16	9.55	13	
MEÇ1411.06	23.0	0.90	0.01	0.03	6.86	8	
AGRIA	19.2	0.40	0.08	1.54	4.51	28	
MADALEINE	19.4	0.91	0.03	0.09	8.36	20	
RUSSET BURBANK	20.0	0.32	0.12	2.03	4.28	27	

CV, coefficient of variation; IPC1, interaction principal component analysis axis 1; AMMI, Additive Main Effects and Multiplicative Interaction

4.8.3 Small Tuber (< 30mm) Yield

The ANOVA for the small tubers (<30mm) yield showed that, there was a highly significant ($p < 0.001$) effects of genotypes, environments, and the genotype by environment interaction on the potato tuber yield by the (Table 4.36, Table 4.37). There was a high CV among the genotypes and the environments of 39.63 and the grand mean yield of 0.72. The treatment explained 82.64% of the total sum of squares of which 54.66%, 29.15%, and 16.18%, respectively attributed to genotype, environment, and GEI. The IPC1 and the residual component of the GEI also revealed highly significant ($P<0.001$) with the IPC1 constituting 70.52% while residual accounting for 29.48% of the GEI sum of squares. This indicates that genotype has much influence on the tuber grading than environment and GEI. The environmental effect may be due to temperature and nutrient disparities among the various environments which led to different responses of the genotypes with the environment.

Table 4.36. ANOVA for small tubers (<30mm) for 15 genotypes grown in three different environments

Source	DF	SS	MS	F	P-value
Genotype	14	43.7598	3.1257	38.33	0.000
Environment	2	23.5048	11.7524	144.14	0.000
G x E	28	12.8419	0.4586	5.62	0.000
Error	135	11.0075	0.0815		
Total	179	91.1139			
Grand Mean	0.7206				
CV	39.63				

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** $p \leq 0.001$

Table 4.15. AMMI Analysis of variance of small tuber size (<30mm) for 15 potato genotypes grown in three environments

Source	DF	SS	MS	%TSS explained	% TRT SS explained	%GEI SS explained
Total	179	89.609	0.501			
Treatment	44	78.919	1.794 ***	82.64		
Genotype	14	43.139	3.081 ***		54.66	
Environment	2	23.007	11.504 ***		29.15	
G x E	28	12.773	0.456***		16.18	
IPC1	15	9.007	0.6 ***		(11.41)	70.52
Residual	13	3.765	0.29 ***		(4.77)	29.48
Error	135	10.69	0.079	17.36		
Blocks/Env	9	0.677	0.075 ns			
Pure Error	126	10.013	0.079			

Statistically significant differences occurred among the genotypes and the environment for the STN which suggested crossover interaction among genotypes from one environment to another. The highest and lowest mean yield for STN (<30mm) were respectively recorded in Russet Burbank (2.4 tubers) and MEÇ1411.06 (0.3 tuber) among genotypes whiles across environments, mean yield were Nigde (1.2 tubers) recorded the highest followed by Sivas (0.7 tuber) and Konya (0.3 tuber) recording the least (Table 4.38.

Table 4.38. Two-way table of small tuber (<30mm) yield for 15 potato genotypes grown in three different environments*

GENOTYPES	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	1.2 *cd*	0.8 *fghij*	0.1 *q*	0.7
MACAR1402.11	0.9 *defghi*	0.5 *jklmnop*	0.5 *jklmnop*	0.6
MACAR1406.04	0.6 *hijklm*	0.6 *ijklmno*	0.1 *pq*	0.4
MACAR1406.07	1.2 *cde*	0.6 *ijklmn*	0.4 *klmnopq*	0.7
MACAR1409.09	1.2 *cdef*	0.3 *mnopq*	0.2 *opq*	0.5
MEÇ1402.07	0.6 *ijklmn*	0.6 *ijklmno*	0.2 *opq*	0.4
MEÇ1402.09	1.3 *c*	0.7 *ghijkl*	0.1 *pq*	0.7
MEÇ1405.06	0.8 *efghij*	0.7 *ghijkl*	0.2 *nopq*	0.6
MEÇ1407.05	0.7 *ghijklm*	0.3 *mnopq*	0.2 *opq*	0.4
MEÇ1407.08	1.1 *cdefg*	0.6 *ijklmno*	0.6 *ijklmn*	0.7
MEÇ1407.17	0.8 *ghijk*	0.4 *lmnopq*	0.1 *q*	0.4
MEÇ1411.06	0.6 *ijklmn*	0.4 *klmnopq*	0.1 *q*	0.3
AGRIA	2.4 *b*	0.9 *defghi*	0.5 *jklmnop*	1.3
MADELEINE	1.0 *cdefg*	0.9 *defghi*	0.2 *nopq*	0.7
Russet Burbank	3.2 *a*	3.0 *a*	1.0 *cdefgh*	2.4
Mean	1.2	0.7	0.3	0.7

*: Different letters within a row and column indicate significance at p≤0.05 in Duncan test

Table 4.39. Stability estimation of the small tuber number (STN) of potato breeding lines grown in three different environments

Genotype	Mean STY	Finlay & Wilkinsin Regression	Eberhart & Russel (1966)	Shukla (1972)	Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ^2	CV	KR	IPC1
MACAR1402.10	25.62	2.08	0.03	4.17	14.25	16	
MACAR1402.11	21.49	1.16	0.06	0.28	9.66	20	
MACAR1406.04	21.89	0.75	0.10	0.57	6.59	19	
MACAR1406.07	22.83	1.05	0.00	-0.04	8.02	6	
MACAR1409.09	23.60	1.04	0.01	-0.01	7.77	6	
MEÇ1402.07	21.49	0.81	0.10	0.46	7.16	20	
MEÇ1402.09	22.45	0.94	0.00	-0.02	7.30	9	
MEÇ1405.06	22.25	0.82	0.00	0.06	6.47	13	
MEÇ1407.05	21.52	1.09	0.17	0.66	9.55	21	
MEÇ1407.08	23.68	1.50	0.00	0.81	11.04	14	
MEÇ1407.17	22.64	1.23	0.01	0.16	9.55	13	
MEÇ1411.06	23.00	0.90	0.01	0.03	6.86	8	
AGRIA	19.15	0.40	0.08	1.54	4.51	28	
MADALEINE	19.44	0.91	0.03	0.09	8.36	20	
R. BURBANK	19.99	0.32	0.12	2.03	4.28	27	

CV, coefficient of variation; IPC1, interaction principal component analysis axis 1; AMMI, Additive Main Effects and Multiplicative Interaction

MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1407.05, and MADALEINE were stable genotypes for the regression analysis while almost all the genotypes were stable for Eberhart & Russel model (Table 4.35 and Table 4.39). Also, Shukla's stability model revealed MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1405.06, MEÇ1411.06, and MADALEINE as stable genotypes. Whereas Francis and Kannenberg model and KR sum models failed to identify desirable genotypes for medium size tuber number.

4.9. Marketable Tuber Weight (MTW)

The general ANOVA and combined AMMI ANOVA results of the MTW revealed highly significant ($p < 0.001$) effects of the genotypes, environment, and their interaction on the marketable tuber weight with a grand mean weight of 122.27kg at a CV of 3.06 among the genotypes, and the environments of 3.06 (Table 4.40; Table 4.41). The genotypes, environment, and the genotype by environment interaction treatment explained 94.75% of the total sum of squares of which 50.53%, 25.46%, and 24.02% respectively accounted

for genotype, environment, and GEI. The IPC1 and the residual component of the GEI also revealed highly significant (P<0.001) with the IPC1 constituting 70.8% while residual accounting for 29.2% of the GEI sum of squares.

Table 4.40. ANOVA of marketable tuber weight for 15 genotypes grown in three different environments

Source	DF	SS	MS	F	P-value
Genotype	14	81636	5831.2	415.45	0.000***
Environment	2	38730	19364.8	1379.66	0.000***
G x E	28	32452	1159	82.57	0.000***
Error	135	1895	14		
Total	179	154713			
Grand Mean	122.27				
CV	3.06				

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** p≤0.001

The high significant effects observed in Table 4.40 and Table 4.41 reflect the significant difference between genotypes across environments (Table 4.42) which shows that, MACAR1402.11 (159.83kg) recorded the highest mean weight whiles Russet Burbank(81.65kg) recorded the lowest with the environmental mean tuber weight of 141.54kg, 123.04kg, and 102.23kg respectively for Nigde, Sivas, and Konya. In Nigde, the highest tuber weight was recorded in MEÇ1407.05 (145.9 kg), in Sivas, MACAR1402.11 (222.7kg) while in Konya, MACAR1409.09 (161.1kg). On the other hand, the lowest tuber weight in Nigde and Sivas was found in Russet Burbank of 67.7kg and 74.5kg respectively while in Konya the lowest tuber weight was found in MEÇ1405.06 (82.1kg). There was crossover GEI from one environment to another and statistical significance differences occurring between the highest and lowest mean weight of the genotypes across and within the environments which confirms Caliskan et al. 2007 finding on sweet potato.

Table 4.16. AMMI analysis of variance of MTW for 15 potato genotypes grown in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	179	160149.3	894.689			
Treatment	44	150978.9	3431.34 ***	94.75		
Genotype	14	76288.46	5449.176***		50.53	
Environment	2	38432.21	19216.11***		25.46	
G x E	28	36258.27	1294.938***		24.02	
IPC1	15	25672.19	1711.479***		(17)	70.8
Residual	13	10586.08	814.314***		(7.01)	29.2
Error	135	9170.322	67.928	5.25		
Blocks/Env	9	650.73	72.303 ns			
Pure Error	126	8519.592	67.616			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, *** p≤0.001 ns= not significant

Table 4.42. Two-way table of marketable tuber weight (MTW) for 15 potato genotypes grown in three different environments*

GEN	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	101.7 *t*	129.0 *ghij*	126.2 *ijk*	119.0
MACAR1402.11	109.5 pqr	222.7 a	147.3 *e*	159.8
MACAR1406.04	94.1 *uopq*	165.9 *bc*	132.5 *gh*	130.8
MACAR1406.07	83.5 *wx*	140.0 *f*	113.6 opq	112.4
MACAR1409.09	107.4 *rs*	169.2 *b*	161.1 *cd*	145.9
MEÇ1402.07	114.5 *nop*	142.7 *ef*	127.5 *hij*	128.2
MEÇ1402.09	87.9 *vw*	116.9 *mno*	110.7 *pqr*	105.2
MEÇ1405.06	94.9 *u*	92.3 *uv*	82.1 *x*	89.7
MEÇ1407.05	145.9 *e*	169.1 *b*	143.7 *ef*	152.9
MEÇ1407.08	108.6 *qr*	128.4 *hij*	121.4 *klm*	119.5
MEÇ1407.17	119.0 *lmn*	129.5 *ghi*	128.4 *hij*	125.6
MEÇ1411.06	124.0 *jkl*	142.2 *ef*	121.5 *klm*	129.2
AGRIA	84.0 *wx*	106.2 *rst*	110.9 *pqr*	100.4
MADELEINE	108.5 *qr*	158.8 *d*	134.1 *g*	133.8
Russet Burbank	67.7 *z*	74.5 *y*	102.9 *st*	81.7
Mean	141.5	123.0	102.2	122.2

*: Different letters within a row and column indicate significance at p≤0.05 in Duncan test

The genotype MTW stability estimation in Table 4.43 revealed that none genotypes were stable based on the Finlay & Wilkinsin (1963) Regression model, Eberhart & Russel (1966) model, Shukla (1972) model, Francis & Kannenberg CV, Kang Rank Sum and AMMI Model. Figure 4.15 categorised AGRIA, Russet Burbank, MEÇ1402.09, MEÇ1405.06, MACAR1402.10, and MEÇ1407.08 as poorly adaptable to unfavourable

environmental conditions whiles MACAR1406.07 was categorised to be poorly adaptable to favourable environmental conditions. MEÇ1402.07, MEÇ1407.05, MEÇ1407.17, and MEÇ1411.06 on the other hand were very well adapted to unfavourable environments whereas on the contrarily, MACAR1406.04, MACAR1409.09 MACAR1402.11, and MADELEINE were very well adapted to favourable environmental conditions

Table 4.43. Stability estimation of marketable tuber weight (MTW) of potato breeding lines grown in three different environments

Genotype	Mean MTW	Finlay & Wilkinson	Eberhart & Russel	Shukla	Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ^2	CV	KR	IPC1
MACAR1402.10	118.97	0.79	6.89	22.2	12.6	13	-0.80
MACAR1402.11	159.83	3.08	75.05	1891.95	36.07	16	6.33
MACAR1406.04	130.82	2.00	1.15	352.68	27.47	17	2.80
MACAR1406.07	112.36	1.57	0.74	102.82	25.18	18	1.61
MACAR1409.09	145.89	1.78	29.78	325.4	23.02	14	1.72
MEÇ1402.07	128.23	0.78	1.14	0.22	11.05	8	-0.55
MEÇ1402.09	105.19	0.83	3.26	1.72	14.52	14	-0.63
MEÇ1405.06	89.73	-0.11	12.16	483.1	7.58	27	-2.80
MEÇ1407.05	152.87	0.60	23.51	131.58	9.23	10	-0.39
MEÇ1407.08	119.46	0.56	0.17	50.09	8.46	14	-1.26
MEÇ1407.17	125.64	0.30	1.04	162.79	4.59	18	-2.01
MEÇ1411.06	129.19	0.47	16.26	148.41	8.75	15	-1.18
AGRIA	100.36	0.66	18.28	93.81	14.3	19	-1.27
MADALEINE	133.77	1.39	1.33	40.77	18.78	8	1.14
RUSSET BURBANK	81.65	0.28	92.08	539.96	22.86	29	-2.70

CV, coefficient of variation; IPC1, interaction principal component analysis axis 1; AMMI, Additive Main Effects and Multiplicative Interaction

The AMMI biplot analysis of the potato tuber weight (Figure 4.16) showed that MACAR1406.07 had a large positive IPC1 value and low weight tubers below the grand weight of the genotypes and so was moderately susceptible to environmental conditions. Russet Burbank, AGRIA, MACAR1402.10, MEÇ1407.08, MEÇ1402.09, and MEÇ1405.06 produced low weighted tubers and had large negative IPC1 values, making them susceptible and highly interactive to environmental condition and thus unstable. MACAR1406.04, MACAR1402.11, MADELEINE, and MACAR1409.09 produce above-average weighted tubers, with high IPC1 scores, making them unstable due to their high interaction with the environments. On the other hand, MEÇ1402.07, MEÇ1411.06, MEÇ1407.05, and MEÇ1407.17 had high IPC1 scores which depicted high GEI and unstable in tuber weight in unfavourable environmental conditions.

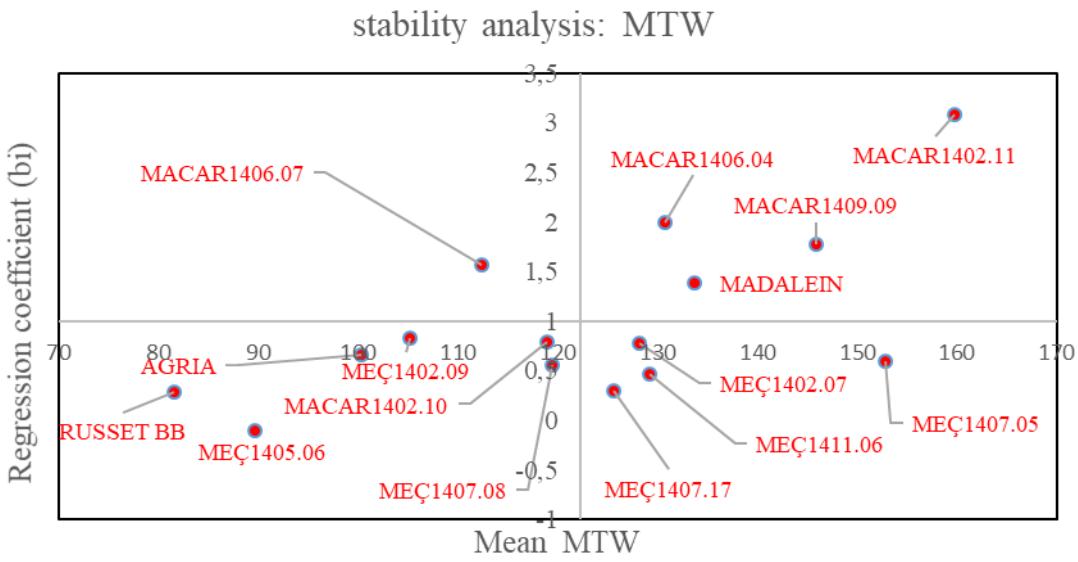

Figure 4.15. Relationship of genotype adaptation (regression coefficient 'bi') and mean marketable tuber weight (MTW) of 15 potato genotypes grown in three diverse environments

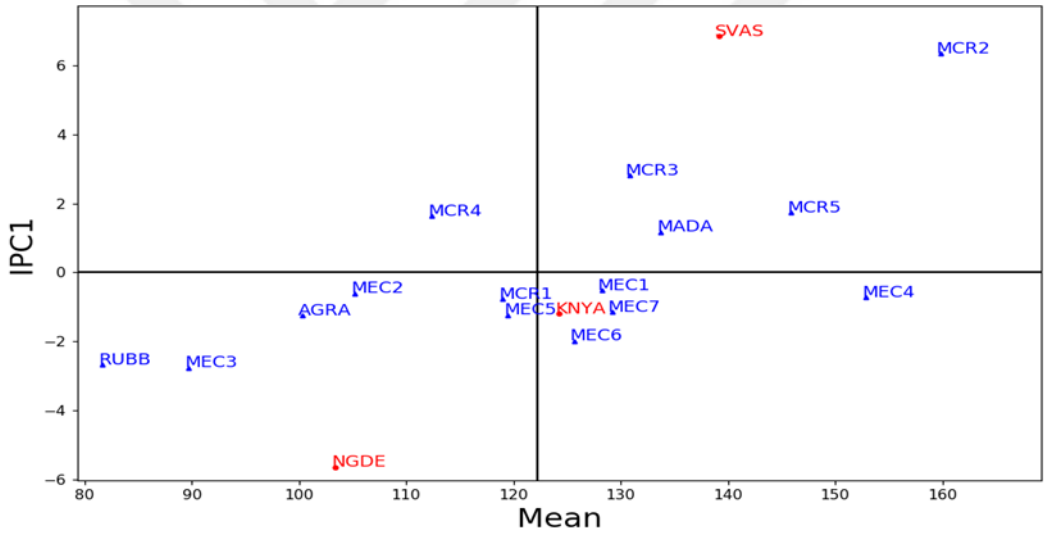

Figure 4.16. AMMI biplot analysis of interaction principal component axis (IPCA-1) with mean marketable tuber weight (MTW) of potato genotype evaluated across three different environments. Note: MCR1 =MACAR1402.10, MCR2 = MACAR1402.11, MCR3 = MACAR1406.04, MCR4 = MACAR1406.07, MCR5 = MACAR1409.09, MEC = MEÇ1402.07, MEC2 = MEÇ1402.09, MEC3 = MEÇ1405.06, MEC4 = MEÇ1407.05, MEC5 = MEÇ1407.08, MEC6 = MEÇ1407.17, MEC7 = MEÇ1411.06, AGRA = AGRIA, MADA = MADELEINE, RUBB = RUSSET BURBANK; KYNA = Konya, NGDE = Nigde, SVAS = Sivas

4.10 Dry Matter Content (%)

The general ANOVA and combined AMMI ANOVA revealed highly significant ($p < 0.001$) effects of the genotypes, environments, and the genotype by environment interaction on the dry matter content (DMC) (Table 4.44; Table 4.45) with a grand mean DMC of 22.1% at a CV among the genotypes, and the environments of 1.89 (Table 4.44). A 93.96% of the total sum of squares was explained by the treatments of which genotypes, environments, and genotype by environment constituted 51.95%, 39.4%, and 8.65% of the total sum of squares, respectively. The high contribution of the treatment sum of squares by genotypes and environment than the genotype by environment interaction depicts that the variation in the DMC of the potato genotypes is largely due to genotypic differences followed by the environments than the GEI component. The IPC1 and the residual component of the GEI also revealed highly significant ($P<0.001$) with the IPC1 constituting 75.53% while residual accounting for 24.47% of the GEI sum of squares.

Table 4.44. ANOVA for dry matter content (DMC) for 15 genotypes grown in three different environments

Source	DF	SS	MS	F	P-value
Genotype	14	483.443	34.532	199.11	0.000***
Environment	2	366.738	183.369	1057.31	0.000***
G x E	28	80.457	2.873	16.57	0.000***
Error	135	23.413	0.173		
Total	179	954.052			
CV	1.89				

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** $p \leq 0.001$

Table 4.45. AMMI Analysis of variance of dry matter content (DMC) for 15 potato genotypes grown in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	179	954.052	5.3299			
Treatment	44	930.639	21.1511***	93.96		
Genotype	14	483.443	34.5317***		51.95	
Environment	2	366.738	183.369***		39.41	
G x E	28	80.4573	2.87347***		8.65	
IPC1	15	60.767	4.05114***		(6.53)	75.53
Residual	13	19.6902	1.51463***		(2.12)	24.47
Error	135	23.4131	0.17343	6.04		
Blocks/Env	9	1.83286	0.20365 ns			
Pure Error	126	21.5803	0.17127			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, *** $p \leq 0.001$ ns= not significant

In Table 4.46, the mean DMC comparison revealed that the highest mean % DMC was observed in MACAR1402.10 (25.62) whiles the lowest mean DMC was observed in AGRIA (19.15) among the genotypes. The highest mean DMC among the environments was observed in Sivas (23.41%) followed by Konya (22.71%) and the least observed in Nigde (20.09%). Across environments revealed, MACAR1402.10 recorded the highest DMC in Sivas and Konya of 28.157 and 27.273 respectively while MACAR1409.09 recorded the highest DMC in Nigde. On the other hand, AGRIA recorded the lowest DMC for all the environments of 18.245, 19.235, and 19.972 respectively for Nigde, Sivas, and Konya.

The differences in the dry matter content of the potato breeding lines might be due to agro-ecological disparities. Differences in evaporative demand due to high global solar radiation flux density, low relative humidity, and/or high wind speed cause closure of stomata leading to reduction in photosynthesis accompanied with restriction of CO2 uptake, thus resulting in light intensities outside the required optimum for maximum dry matter production (Stark and Love, 2003). The differences in altitude of the study areas might also have a contributory factor in the disparities in the dry matter content as a result of air and soil temperature differences as shown in Table 3.2 which have been ascribed to have varietal effect on specific gravity of the potato tubers causing differences in the dry matter concentration of the potato tubers (Pereira et al 2008).

Potato dry matter concentration is important in the food processing industry, especially for French fries or chips. Dry matter content of >20% gives good chips quality (Kabira and Berg, 2003; CIP 2007). Again, the Acquisition and Distribution Unit of CIP (2009) distinctively categorized that, DMC of >23% is termed as high, DMC from 20 to 23% as medium and DMC <20% as low according to the CIP (CIP, 2009). Wassu (2017) stated that, the industrial use of potato is dependent on tuber dry matter concentration and starch and that tubers with 20 to 24% dry matter concentration are ideal for French fries and crisps processing. In the study, MACAR1402.10, MACAR1409.09, MEÇ1407.08, and MEÇ1411.06 had high DMC (>23%); MACAR1402.11, MACAR1406.04, MACAR1406.07, MEÇ1402.07, MEÇ1402.09, MEÇ1405.06, MEÇ1407.05, and MEÇ1407.17 had medium DMC (20 to 23%) whilst Agria, Madeleine and Russet Burbank had low DMC (<20%). All potato breeding lines in this study had DMC >21%

as compared to the check cultivars and thus making them ideal for the French fries and chips industry.

Table 4.46. Two-way table of dry matter content (DMC) for 15 potato genotypes grown in three different environments*****

GENOTYPES	NIGDE	SIVAS	KONYA	Mean
MACAR1402.10	21.4 *no*	28.2 *a*	27.3 *b*	25.6
MACAR1402.11	19.1 *v*	22.6 m	22.7 *lm*	21.5
MACAR1406.04	20.5 *qrs*	23.4 *hij*	21.7 *n*	21.9
MACAR1406.07	20.7 *pqr*	24.2 *efg*	23.6 *hi*	22.8
MACAR1409.09	21.5 *n*	24.8 *d*	24.5 *d*e	23.6
MEÇ1402.07	20.0 *stu*	23.1 *ijklm*	21.4 *no*	21.5
MEÇ1402.09	20.6 *qr*	23.8 *fgh*	22.9 *jklm*	22.5
MEÇ1405.06	20.6 *qr*	23.3 *hijk*	22.8 *klm*	22.2
MEÇ1407.05	19.6 *uv*	23.6 *ghi*	21.4 *no*	21.5
MEÇ1407.08	20.7 *pqr*	25.7 *c*	24.6 *de*	23.7
MEÇ1407.17	20.2 *rst*	24.4 *de*	23.3 *hijkl*	22.6
MEÇ1411.06	21.3 *nop*	24.4 *def*	23.3 *hijk*	23.0
AGRIA	18.2 *w*	19.2 *v*	20.0 *stu*	19.2
MADELEINE	17.6 *x*	20.4 *qrst*	20.4 *qrst*	19.4
RUSSET BURBANK	19.2 *v*	19.9 *tu*	20.9 *opq*	20.0
Mean	20.1	23.4	22.7	22.1

*: Different letters within a row and column indicate significance at p≤0.05 in Duncan test

Table 4.47. Stability estimation of DMC of potato breeding lines grown in three different environments

Genotype	Mean DMC	Finlay & Wilkinsin Regression	Eberhart & Russel (1966)	Shukla (1972)	Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ^2	CV	KR	IPC1
MACAR1402.10	25.623	2.081	0.025	4.167	14.245	16	1.33
MACAR1402.11	21.487	1.158	0.061	0.279	9.662	20	0.17
MACAR1406.04	21.887	0.751	0.102	0.574	6.594	19	-0.28
MACAR1406.07	22.833	1.047	0.001	-0.044	8.021	6	0.06
MACAR1409.09	23.597	1.044	0.009	-0.01	7.774	6	0.05
MEÇ1402.07	21.493	0.814	0.098	0.462	7.159	20	-0.2
MEÇ1402.09	22.45	0.935	0.004	-0.023	7.301	9	-0.07
MEÇ1405.06	22.247	0.824	0.000	0.056	6.474	13	-0.22
MEÇ1407.05	21.523	1.089	0.170	0.661	9.545	21	0.15
MEÇ1407.08	23.68	1.495	0.001	0.812	11.037	14	0.62
MEÇ1407.17	22.643	1.234	0.007	0.164	9.548	13	0.3
MEÇ1411.06	23.003	0.896	0.012	0.031	6.863	8	-0.12
AGRIA	19.153	0.396	0.076	1.536	4.507	28	-0.78
MADALEINE	19.437	0.912	0.028	0.085	8.362	20	-0.13
RUSSET BB	19.99	0.324	0.118	2.032	4.284	27	-0.88

CV, coefficient of variation; IPC1, interaction principal component analysis axis 1; AMMI, Additive Main Effects and Multiplicative Interaction

The stability estimates in Table 4.47 revealed that MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1407.05, MEÇ1411.06, and MADALEINE were stable for based on *bi* model while almost all the genotypes were stable based on S^2d model. On the other hand, except MACAR1402.10, MACAR1402.11, MACAR1406.04, AGRIA, and Russet Burbank, the rest of the genotypes were stable based on Shukla (1972) model. The IPC1 scores also revealed that except MACAR1402.10, MEÇ1407.08, AGRIA, and Russet Burbank, the rest of the genotypes were stable for DMC.

According to the Finlay and Wilkinson regression model, MACAR1409.09, MACAR1406.07, and MEÇ1402.09 were well adapted to all environmental conditions, while MEÇ1405.06, and MEÇ1411.06 were well adapted to unfavourable environmental conditions making them tolerant to unfavourable environmental fluctuations. Also, MACAR1402.10, MEÇ1407.08 and MEÇ1407.17 very well adapted to favourable environmental conditions while MACAR1402.11, and MEÇ1407.05 were poorly adapted to favourable environmental conditions. Contrarily, MACAR1406.04, MEÇ1402.07, MADELEINE, AGRIA, and Russet Burbank were very much sensitive and are poorly adapted to unfavourable environmental conditions.

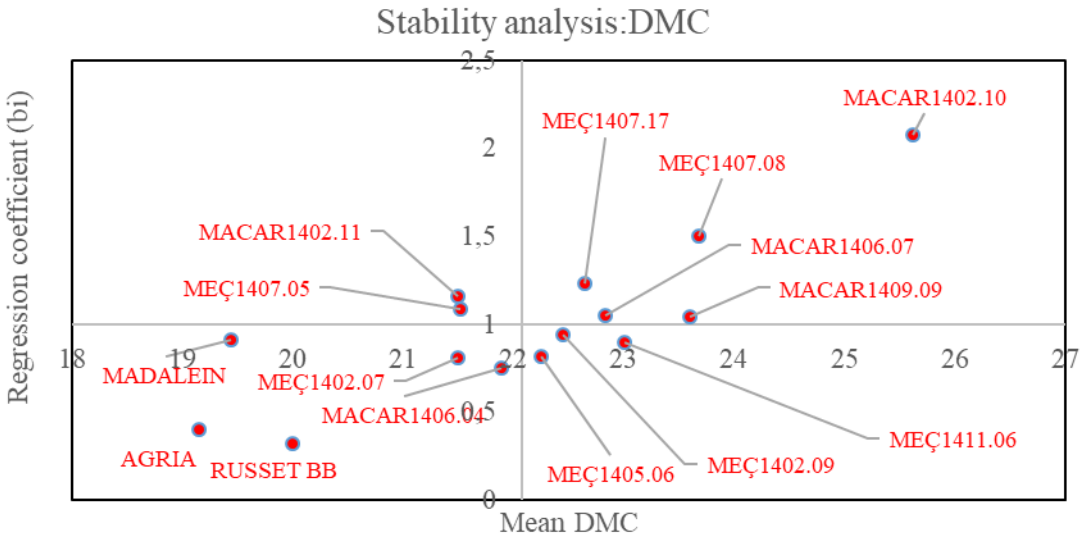

Figure 4.17. Relationship of genotype adaptation (regression coefficient 'bi') and mean number of Dry Matter Content (DMC) of 15 potato genotypes grown in three diverse environments

The AMMI biplot analysis (Figure 4.18) also revealed that MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1405.06, and MEÇ1411.06 had high DMC and

were less influenced by environmental conditions due to their small IPC1 score making them generally stable whilst MACAR1402.11, MACAR1406.04, MEÇ1402.07, MEÇ1407.05, and MADELEINE had low DMC below the grand mean but generally stable due to their small IPC1 scores. Contrarily, MACAR1402.10, MEÇ1407.08, and MEÇ1407.17 on the other hand had very high DMC and high IPC1 scores which is an indication of high GEI making them unstable whereas AGRIA and RUSSET BURBANK were very susceptible to environmental condition and so highly unstable for DMC and so have specific adaptability. The environments were grouped in to two mega environments which are highly heterogeneous and unstable with large IPC1 values for DMC. Konya and Sivas were positively correlated and produced high DMC whilst they were negatively correlated with Nigde environment. Konya environment was ideal for the majority of the genotypes in terms of DMC.

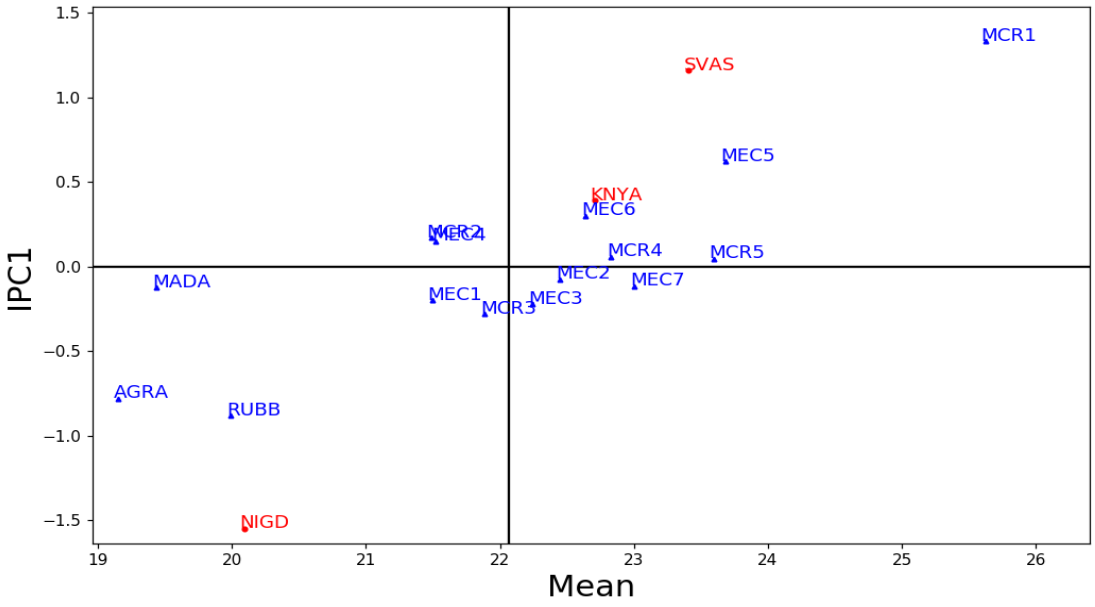

Figure 4.18. AMMI biplot analysis of interaction principal component axis (IPCA-1) with mean of dry matter concentration (DMC) of potato genotype evaluated across three different environmentsNote: MCR1 =MACAR1402.10, MCR2 = MACAR1402.11, MCR3 = MACAR1406.04, MCR4 = MACAR1406.07, MCR5 = MACAR1409.09, MEÇ1 = MEÇ1402.07, MEC2 = MEÇ1402.09, MEC3 = MEÇ1405.06, MEC4 = MEÇ1407.05, MEC5 = MEÇ1407.08, MEC6 = MEÇ1407.17, MEC7 = MEÇ1411.06, AGRA = AGRIA, MADA = MADELEINE, RUBB = RUSSET BURBANK; KYNA = Konya, NGDE = Nigde, SVAS = Sivas

4. 11 Specific Gravity (SG)

It was revealed by the ANOVA results (Table 4.48, Table 4.49) that, genotypes, environments, and the genotype by environment interaction had a highly significant ($p <$

0.001) effects on the SG of the potato tubers with a grand mean SG of 1.089 and a CV 0.19 among the genotypes, and the environments (Table 4.48). A 93.16% of the total sum of squares was explained by the treatments of which genotypes, environments, and genotype by environment constituted 53.4%, 38.83%, and 9.71% of the total sum of squares respectively. This shows that SG is genetically induced more than the environmentally and GEI induced. The IPC1 and the residual component of the GEI also revealed highly significant ($p < 0.001$) with the IPC1 constituting 50% of the GEI sum of squares. The significant G, E, and G x E interaction effects on the DMC, SG, MTW in the genotypes indicate that they vary in their genetic constitution (genotype main effect), environmental fluctuations and the GEI which greatly influenced the quality traits. Several potato scholars separately reported that, DMC (Tesfaye et al. 2013; Habtamu et al. 2016b; Wassu, 2016) and SG are influenced by genetic varietal difference and environmental conditions (Tessema et al. 2020). This confirms Arinaittwe et al. (2018) reporting that GEI has a significant effect on the yield and quality traits of potato cultivars which is reflected in the significant difference in the studied traits between genotype and in environments.

Table 4.48 ANOVA of Specific Gravity (SG) for 15 genotypes grown in three different environments

Source	DF	SS	MS	F	P-value
Genotype	14	0.01052	7.51E-04	174.61	0.000***
Environment	2	0.00831	0.00415	965.85	0.000***
G x E	28	0.00176	6.29E-05	14.63	0.000***
Error	135	0.00058	4.30E-06		
Total	179	0.02117			
Grand Mean	1.089				
CV	0.19				

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** $p \leq 0.001$

Table 4.49. AMMI Analysis of variance of specific gravity (SG) for 15 potato genotypes grown in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	179	0.0212	0.0001			
Treatment	44	0.0206	0.0005 ***	93.16		
Genotype	14	0.011	0.0008 ***		53.4	
Environment	2	0.008	0.0042 ***		38.83	
G x E	28	0.002	0.0001 ***		9.71	
IPC1	15	0.001	0.0001 ***		(4.85)	50
Residual	13	0	0.0000 ***			
Error	135	0.001	0.00	6.84		
Blocks/Env	9	0	0.0000 ns			
Pure Error	126	0.001	0			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, *** $p \leq 0.001$ ns= not significant

It is observed in Table 4.50 that, the highest mean SG among the genotypes was found in MACAR1402.10 (1.106) whiles the lowest SG was found in AGRIA (1.076), with Nigde recording the least mean SG of 1.080, followed by Konya of 1.092 and Sivas recording the highest SG of 1.095, which were significantly different from each other. It was also observed that, all the breeding lines have higher SG than the commercial genotypes (AGRIA, Russet Burbank, and MADELEINE). MACAR1402.10 recorded the highest SG across the all environments making it superior over all the other genotypes in terms of SG whereas AGRIA recorded the lowest SG in Sivas and Konya while in Nigde, MADELEINE recorded the lowest SG. Though MACAR1402.10 was superior to all other genotypes, there were different SG values across the environments thus indicating crossover GEI. Potato SG is key a parameter in the food processing industry especially for French fries or chips (Kabira and Berg, 2003; CIP, 2007; Wassu, 2017). For French fry and potato chips, CIP (2007) set the minimum acceptable levels of potato tubers with a specific gravity of ≥1.080, which reduces the amount of oil uptake by potato chips and French fries during frying and enhanced texture and yield quality of finished products. In this study, all the breeding lines have SG >1.081 gcm^{-3} as compared to the check cultivars (AGRIA, Madeleine, and Russet Burbank) which have less than 1.08 gcm^{-3} SG and so all the breeding lines are ideal for French fries and chips.

Table 4.50. Two-way table of specific gravity (SG), for 15 potato genotypes grown in three different environments*

Genotype	Nigde	Sivas	Konya	Mean
MACAR1402.10	1.087 *mn*	1.118 *a*	1.114 *b*	1.106
MACAR1402.11	1.075 *wx*	1.092 *l*	1.092 *l*	1.086
MACAR1406.04	1.082 *pqrs*	1.095 *hijk*	1.088 *m*	1.088
MACAR1406.07	1.083 *pqr*	1.099 *efg*	1.096 *hij*	1.093
MACAR1409.09	1.087 *mn*	1.103 *d*	1.100 *de*	1.096
MEÇ1402.07	1.079 *stu*	1.094 *ijkl*	1.086 *mno*	1.086
MEÇ1402.09	1.082 *pqrs*	1.097 *fgh*	1.093 *jkl*	1.091
MEÇ1405.06	1.082 *qrs*	1.095 *hijk*	1.092 *kl*	1.089
MEÇ1407.05	1.077 *uvw*	1.096 *ghi*	1.086 *mno*	1.086
MEÇ1407.08	1.083 *opq*	1.106 *c*	1.101 *de*	1.097
MEÇ1407.17	1.080 *rst*	1.100 *def*	1.095 *hijk*	1.092
MEÇ1411.06	1.083 *pqr*	1.100 *def*	1.096 *hi*	1.093
AGRIA	1.072 *x*	1.076 *w*	1.079 *stu*	1.076
MADELEINE	1.069 *y*	1.081 *qrst*	1.082 *qrs*	1.077
RUSSET BURBANK	1.076 *vw*	1.079 *tuv*	1.085 *nop*	1.080
Mean	1.080	1.095	1.092	1.089

*: Different letters within a row and column indicate significance at $p \leq 0.05$ in Duncan test

In Table 4.51, MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1407.05, and MEÇ1411.06 were identified by the *bi* stability model to be stable. Based on the S^2d and σ^2 models all the genotypes were revealed to be stable. Also, almost all the genotypes were classified to be stable based on the IPC1 scores, but according to the Francis & Kannenberg and Kang Rank Sum models, no genotype was identified to be stable. The differences in the stability levels for the MTW, DMC, and SG of the genotypes can be attributed to the difference in genotypic constitutions and environmental fluctuations which led their different forces of interactions.

Table 4.51. Stability estimation of specific gravity of potato breeding lines grown in three different environments

Genotype	Mean SG	Finlay & Wilkinson	Eberhart & Russel	Shukla	Francis & Kannenberg	Kang Rank Sum	AMMI Model
		bi	S^2d	σ^2	CV	KR	IPC1
MACAR1402.10	1.106	2.036	0.000	0.000	1.524	16	0.097
MACAR1402.11	1.086	1.167	0.000	0.000	0.903	18	0.009
MACAR1406.04	1.088	0.731	0.000	0.000	0.598	19	-0.017
MACAR1406.07	1.093	1.029	0.000	0.000	0.778	7	0.003
MACAR1409.09	1.097	1.029	0.000	0.000	0.776	2	0.001
MEÇ1402.07	1.086	0.845	0.000	0.000	0.691	9	-0.012
MEÇ1402.09	1.091	0.937	0.000	0.000	0.712	11	-0.002
MEÇ1405.06	1.09	0.823	0.000	0.000	0.625	13	-0.013
MEÇ1407.05	1.086	1.073	0.000	0.000	0.875	11	0.038
MEÇ1407.08	1.097	1.463	0.000	0.000	1.103	12	0.016
MEÇ1407.17	1.092	1.257	0.000	0.000	0.953	12	0.021
MEÇ1411.06	1.093	1.075	0.000	0.000	0.813	7	0.009
AGRIA	1.076	0.344	0.000	0.000	0.326	28	-0.062
MADALEINE	1.077	0.847	0.000	0.000	0.671	21	-0.013
R. BURBANK	1.08	0.345	0.000	0.000	0.424	27	-0.064

CV, coefficient of variation; IPC1, interaction principal component analysis axis 1; AMMI, Additive Main Effects and Multiplicative Interaction

The *bi* values and mean SG biplot categorized MACAR1409.09 as well adapted to all environmental conditions, while MACAR1406.07 is poorly adapted to all environmental conditions. MACAR1402.10 and MEÇ1407.08 were well adapted to favourable environmental conditions. On the contrarily, MEÇ1411.06, MEÇ1407.17, MEÇ1407.05, and MACAR1402.11 were poorly adapted to favourable environmental conditions while MEÇ1402.09, MEÇ1405.06, MACAR1406.04, MEÇ1402.07, MADELEINE, AGRIA, and Russet Burbank were very much sensitive and were poorly adaptable to unfavourable environmental conditions (Figure 4.19).

The AMMI biplot of SG (Figure 4.20) revealed that MACAR1406.07, MACAR1409.09, MEÇ1402.09, MEÇ1405.06, and MEÇ1411.06 had high SG with less interaction with environmental influences making them generally stable whilst MACAR1402.11, MACAR1406.04, MEÇ1402.07, MEÇ1407.05, and MADELEINE had low SG and generally stable. Contrarily, MACAR1402.10, MEÇ1407.08, and MEÇ1407.17 on the other hand, had very high values of SG and high IPC1 scores indicating a high GEI making them unstable whereas AGRIA and Russet Burbank were very susceptible to environmental condition and so highly unstable for SG and so had specific adaptability. The environments were highly heterogeneous with large IPC1 values and were unstable for SG. Averagely, Konya environment was ideal for the majority of the genotypes in

terms of SG. Overall, 8 of the 15 genotypes had SG above grand mean and 7 (47 %) genotypes had SG below the grand mean of 1.089. Also, 53% of the genotypes have positive IPCA1 whilst 47% of the genotypes had negative IPCA1 values. Larger IPC1 scores and larger *bi* values of the genotypes indicate higher instability and specific adaptability of the genotypes to the environment due to higher interaction (Temesgen *et al*. 2015).

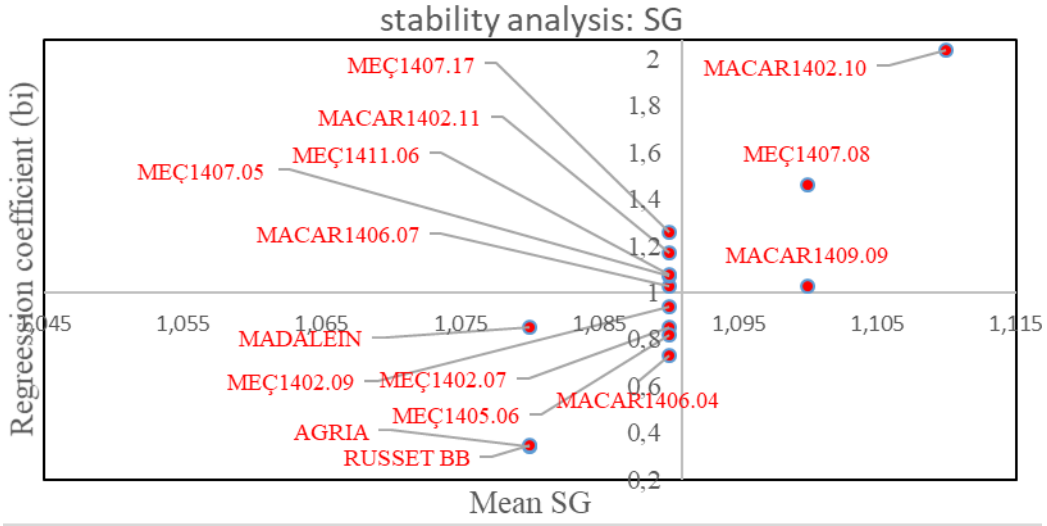

Figure 4.19. Relationship of genotype adaptation (regression coefficient 'bi') and mean specific gravity (SG) of 15 potato genotypes grown in three diverse environments

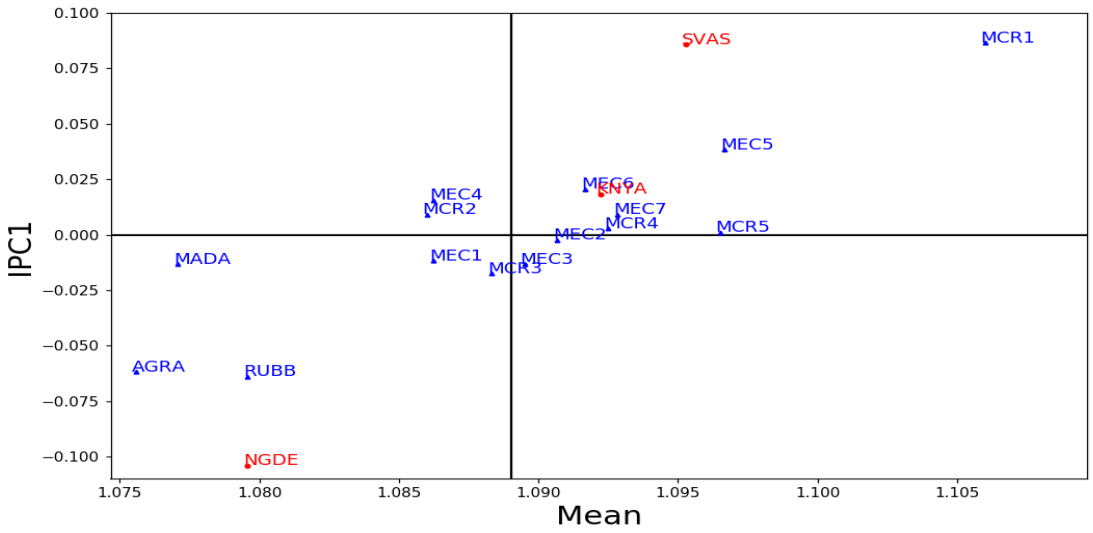

Figure 4.20. AMMI biplot analysis of interaction principal component axis (IPCA-1) with mean of specific gravity (SG) of potato genotype evaluated across three different environments

Note: MCR1 =MACAR1402.10, MCR2 = MACAR1402.11, MCR3 = MACAR1406.04, MCR4 = MACAR1406.07, MCR5 = MACAR1409.09, MEÇ1 = MEÇ1402.07, MEC2 = MEÇ1402.09, MEC3 = MEÇ1405.06, MEC4 = MEÇ1407.05, MEC5 = MEÇ1407.08, MEC6 = MEÇ1407.17, MEC7 = MEÇ1411.06, AGRA = AGRIA, MADA = MADELEINE, RUBB = RUSSET BURBANK; KYNA = Konya, NGDE = Nigde, SVAS = Sivas

4.12. Principal component analysis of variables

To determine the number of PCA to retain, the scree plot based on the eigenvalues was used. The PCA with an eigenvalue greater than or equal to 1 had a significant effect on the GEI and so was retained whilst those with eigenvalue less than 1 was discarded. The first four PCA (F1, F2, F3, and F4) had their eigenvalues greater than 1 which had a cumulative variability of 85.63% (Figure 4.21).

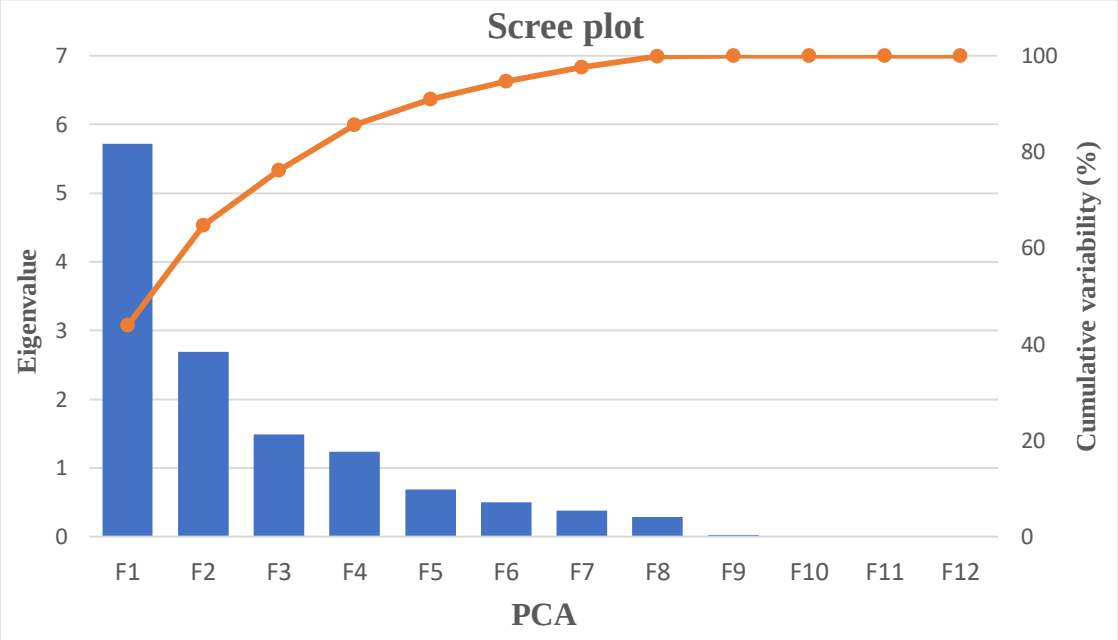

Figure 4.21. Scree plot of Eigenvalues against PCA with cumulative variability (%) for GEI of the studied traits, where F1 to F12 indicates IPCA1 to IPCA12

To avoid disturbance and complication in the analysis, the first two interaction principal component axes (IPCA1 and IPCA2), which explained 64.72% of total GEI, were used in the PCA analysis in constructing the biplot to evaluate the genotypes traits relationships and adaptation to the environments (Figure 4.22). The degree of GEI was proportional to the length of the vector of an environment from the biplot origin. Thus, the environments with longer vectors indicated strong forces of interaction whilst the environments with shorter vectors indicated weak forces of interaction. The PCA results of the genotypes by environment interaction effects on the traits show that number of tubers per plant (NTP), marketable tuber yield (MTY), total plant yield (TPY), dry matter concentration (DMC), and specific gravity (SG) moved in the same direction and so exhibited positive correlations. They also had longer vectored away from the PCA origin which depicted

that they had very high GEI. There was almost a 100% positive correlation between DMC and SG, and between MTY and TTY. N11, S1, S3, S4, S5, S6, S7, S8, S9, S10, S11, S12, S13, and S14 are observed to cluster around the same quadrant of the PCA axis which indicated that they had the same response in similar environmental conditions for NTP, MTY, TPY, TTY, DMC, and SG. This suggested that Sivas location was the best environment for TTY, TPY. MTY, NTP, SG, and DMC. This confirmed the Spearman's correlation analysis (Table 4.38).

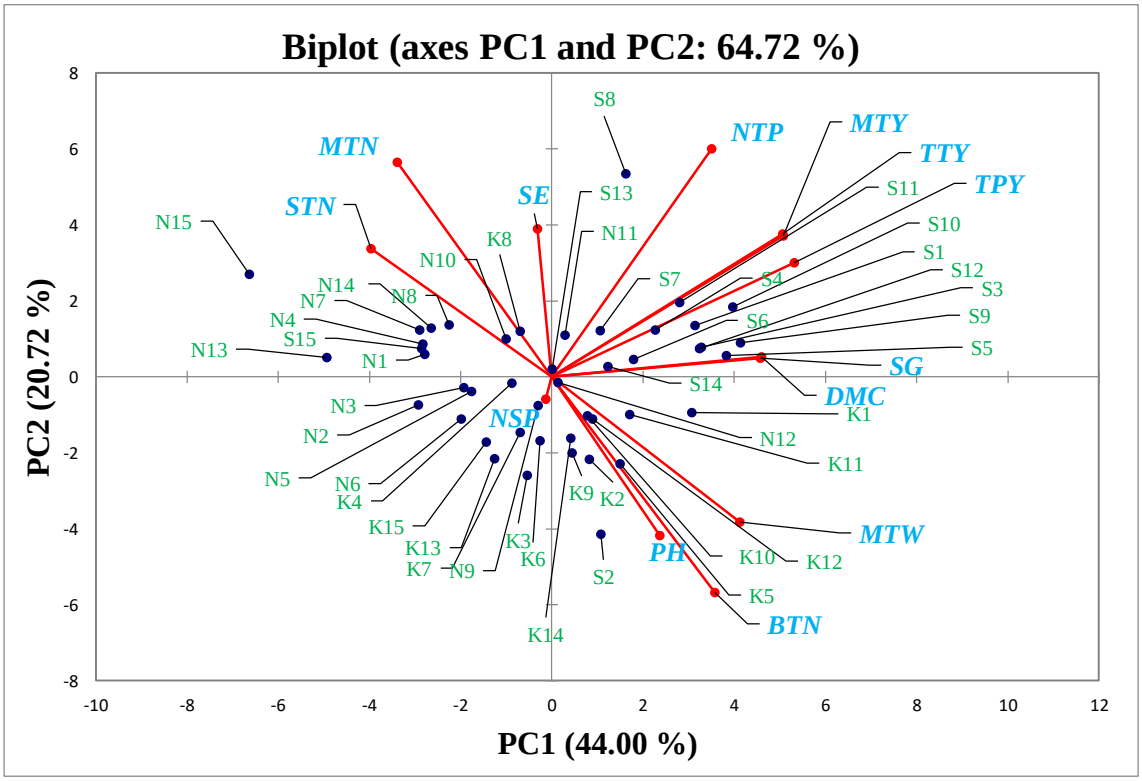

Figure 4.22. PCA1 and PCA2 biplot of genotype by environment interaction (GEI) relationship of the variables in the three different environments

Note: N1, N2, N3, …, N15, S1, S2, S3, …, S15 and K1, K2, K3, …,K15 respectively refers to genotype 1, 2, 3, …, and 15 interactions respectively with Nigde environment, Sivas environment, and Konya environment; N = Nigde, S = Sivas, K = Konya, 1 =MACAR1402.10, 2 = MACAR1402.11, 3 = MACAR1406.04, 4 = MACAR1406.07, 5 = MACAR1409.09, 6 = MEÇ1402.07, 7 = MEÇ1402.09, 8= MEÇ1405.06, 9= MEÇ1407.05, 10 = MEÇ1407.08, 11 = MEÇ1407.17, 12 = MEÇ1411.06, 13 = AGRIA, 14 = MADELEINE, 15 = RUSSET BURBANK; MTN= Medium tuber number, STN= small tuber number, SE=stand establishment, NTP= number of tuber per plant, MTY = marketable tuber yield, TTY = total tuber yield, TPY =total plant yield, SG=specific gravity, DMC=dry matter concentration, NSP=number of stem per plant

Genotype K1, K2, K5, K9, K10, K11, K12, K14, N12, and S2 were also clustered in the same quadrant of PCA axis which also indicated that they correlate positively in the same environmental conditions for MTW, PH, and BTN. The genotypes in this quadrant had yield above-average for MTW, PH, and BTN and thus were moderately tolerant. This

depicted that Konya environment was the best for PH, BTN, and MTW. On the contrarily, genotypes; N14, N15, N13, N4, N8, N10, N7, N1, S15, and K8 had similar field behaviour as they were clustered in the quadrant and were positively and strongly correlated with SE, STN, and MTN. Nigde environment was depicted to found in this quadrant which was moderately susceptible to unfavourable environmental conditions. It also had high GEI. Among all the variables, only NSP had less GEI though it was very susceptible to unfavourable environmental conditions. Genotype N3, N2, N5, N6, N9, K3, K6, K7, K3, K4, and K13 were segregated to be susceptible to unfavourable environmental fluctuations.

4.13 Spearman's Correlation analysis between the parameters

Table 4.52 presents the relations between the various traits using the spearman correlation techniques. It showed a very weak correlation between the SE, NSP, and PH and the plant yield (TPY, TTY, MTY, BTN, MTN, STN, NTP), and quality traits (MTW, DMC, and SG). Within and among the yield and quality traits, there exist moderate to strong correlations which was confirmed by the PCA results (Figure 4.22). There was a high correlation (above 70%) between NTP and the TPY, TTY, and MTY, but a weak correlation (below 50%) with DMC and SG. Within the yield and quality traits, there exist very high correlations above 90% between TPY, TTY, and MTY while with moderate correlation with DMC and SG. Whiles moderate correlations occurred between MTW and BTN, MTN, and STN.

Table 4. 17. Spearman Correlation analysis between parameters

Trait	SE	NSP	PH	NTP	MTW	BTN	MTN	STN	TPY	TTY	MY	DM	SG
SE	**1**	0.15	-0.09	0.17	-0.37	-0.13	0.12	0.22	0.05	0.23	0.23	-0.13	-0.13
NSP		**1**	0.24	0.00	-0.16	-0.01	0.02	-0.14	-0.11	-0.08	-0.08	0.06	0.06
PH			**1**	-0.01	0.26	0.45	-0.43	-0.51	0.11	0.06	0.07	0.41	0.42
NTP				**1**	0.01	-0.09	0.11	-0.16	0.80	0.81	0.81	0.46	0.45
MTW					**1**	0.71	-0.69	-0.56	0.57	0.47	0.48	0.41	0.41
BTN						**1**	-1.00	-0.57	0.35	0.30	0.31	0.28	0.27
MTN							**1**	0.52	-0.33	-0.28	-0.29	-0.25	-0.24
STN								**1**	-0.43	-0.38	-0.39	-0.50	-0.50
TPY									**1**	0.98	0.98	0.62	0.62
TTY										**1**	1.00	0.57	0.56
MTY											**1**	0.57	0.56
DMC												**1**	1.00
SG													**1**

SE= stem establishment, PH= plant height, NTP = tuber per plant, MTW = marketable tuber weight, NSP =stem per plant, BTN = big tuber (>50mm) Number, MTN = medium Tuber (>30mm and <50mm) number, STN = small size tuber (<30mm), TPY = total plant yield, TTY = total tuber yield, MTY = marketable tuber yield, DMC = dry matter, SG = specific gravity

4.14. Potato French fries

As in Table 4.53, the ANOVA of the French fries (FF) revealed highly significant ($p < 0.001$) differences among the genotypes (G) and the tested environments (E) for the lightness (L*), redness (a*) and the yellowness (b*), whiles GEI only have high significant ($P< 0.01$) effects on the redness (a*) but not on the lightness (L*) and yellowness (b*) ($P > 0.05$) of the FF. For the AMMI analysis, genotype had a highly significant ($P< 0.001$) effect on the French Fry's L*, a*, and b* which respectively accounted 50.86%, 52.72%, and 58.11%. The environmental effect was also significant ($P\leq 0.01$) for the L*, a*, and b* which respectively accounted 30.91%, 22.59%, and 12.67%. there was also a significant ($P< 0.01$) difference for IPC1 of the a* value which contributed 64.06% of the GEI sum of squares (Table 4. 54, 4.55, 4. 56). This result buttresses the findings of Rak et al. (2013) and Affleck et al., (2008) reporting that GEI had a great impact on the French fry colour during processing.

Table 4.53. ANOVA of French fries for 12 genotypes grown in three different environments

Source	DF	Lightness (L*)		Redness (a*)		Yellowness (b*)	
		SS	F>Pr	SS	F>Pr	SS	F>Pr
G	11	552.91	7.28***	159.48	8.79***	339.49	4.21***
E	2	335.98	24.34***	68.36	20.72***	74.02	5.04**
G*E	22	198.19	1.31ns	74.69	2.06**	170.67	1.06ns
Error	108	745.33		178.14		792.34	
Total	143	1832.42		480.67		1376.52	
GM		72.2		0.59		23.37	
CV		3.64		216.36		11.59	

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** p≤0.001

Table 4.54. AMMI Analysis of variance of French fries (lightness L*) for 12 potato genotypes evaluated in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	143	1832.424	12.814			
Treatment	35	1087.089	31.060***	59.33		
Genotype	11	552.911	50.265***		50.86	
Environment	2	335.986	167.993***		30.91	
G x E	22	198.192	9.009ns		18.23	
IPC1	12	158.407	13.201 ns		(14.57)	79.93
Residual	10	39.785	3.978 ns		(3.66)	20.07
Error	108	745.335	6.901	40.67		
Blocks/Env	9	55.956	6.217 ns			
Pure Error	99	689.379	6.963			

Table 4.55. AMMI Analysis of variance of French fries (redness a*) for 12 potato genotypes evaluated in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	143	480.668	3.361			
TRT	35	302.511	8.643***	62.94		
GEN	11	159.472	14.497***		52.72	
ENV	2	68.352	34.176***		22.59	
G x E	22	74.687	3.395***		24.89	
IPC1	12	47.841	3.987**		(15.81)	64.06
Residual	10	26.846	2.685		(8.87)	35.94
Error	108	178.157	1.650	37.06		
Blocks/Env	9	9.480	1.053ns			
Pure Error	99	168.677	1.704			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, **p≤0.01, *** p≤0.001 ns= not significant

Table 4.56. AMMI Analysis of variance of French fries (yellowness b*) for 12 potato genotypes evaluated in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	143	1376.516	9.626			
Treatment	35	584.178	16.691***	42.44		
Genotype	11	339.494	30.863***		58.11	
Environment	2	74.017	37.009**		12.67	
G x E	22	170.667	7.758ns		29.22	
IPC1	12	140.776	11.731ns		924.1)	82.49
Residual	10	29.891	2.989 ns		(5.12)	17.51
Error	108	792.338	7.336	57.56		
Blocks/Env	9	29.965	3.329 ns			
Pure Error	99	762.373	7.701			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, **p≤0.01, *** p≤0.001 ns= not significant

4.15 Potato Chips

The potato chips were fried and chroma-meter (Konica Minolta) measurements were taken for ANOVA analysis. The ANOVA results showed that there was high significant ($p<0.01$) effects of the environment on the potato chip but not the genotypes for the lightness (L*) whilst there was a high significant effect ($P < 0.01$) for the redness (a*) among the genotypes, but not the yellowness (b*) ($p > 0.05$) for the tested genotypes and environment. There was a significant effect ($P < 0.01$) of GEI on the potato chips a* but not on the L* and b* (Table 4.57). The grand mean a*, L*, b* values respectively were

4.41, 60.71, and 19.22 which occurred at a CV of 30.67, 4.41, and 92.69, respectively. The AMMI ANOVA for chips L* values showed that, only the environment had a significant ($P < 0.01$) effect on the chips whilst genotypes and GEI had no effect on the chips. For the a*, there was a significant ($P < 0.001$ and $P < 0.01$) effects caused by the genotypes and GEI but no significant effect was caused by the environment. IPC1 showed high significance ($P < 0.01$) which constituted 88.93% of the GEI sum of squares. On the contrarily, there was no significant effect of the treatments for the b* values (Table 4.58, 4.59, 60).

Table 4.57. Calorimetry assessment of potato chips for 12 genotypes grown in three different environments

Source	DF	Lightness (L*)		Redness (a*)		Yellowness (b*)	
		SS	F>Pr	SS	F>Pr	SS	F>Pr
Genotype (G)	11	138.7	1.54ns	102.34	5.08**	3095.3	0.89ns
Environment (E)	2	99.64	6.1**	4.777	1.3ns	632.5	1ns
G x E	22	187.98	1.05ns	92.005	2.28**	6535.5	0.94ns
Error	108	882.27		197.744		34275.2	
Total	143	1308.59		396.865		44538.5	
GM		60.71		4.41		19.22	
CV		4.71		30.67		92.69	

DF= degree of freedom, SS= sum of square, MS= mean square, CV= coefficient of variation, *** p≤0.001

Table 4.58. AMMI Analysis of variance of potato chips lightness (L*) for 12 potato genotypes evaluated in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	143	1308.596	9.151			
Treatment	35	426.326	12.181 ns	32.58		
Genotype (G)	11	138.703	12.609 ns		32.53	
Environment (E)	2	99.644	49.822**		23.37	
G x E	22	187.979	8.544 ns		44.1	
IPC1	12	154.318	12.860 ns		(36.2)	82.1
Residual	10	33.660	3.366 ns		(7.89)	17.91
Error	108	882.271	8.169	67.42		
Blocks/Env	9	90.351	10.039 ns			
Pure Error	99	791.920	7.999			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS=genotype by environment interaction sum of squares, **p ≤0.01, *** p≤0.001 ns = not significant

Table 4.59. AMMI Analysis of variance of potato chips redness (a*) for 12 potato genotypes evaluated in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	143	396.8684	2.7753			
Treatment	35	199.1224	5.68921***	50.17		
Genotype (G)	11	102.3387	9.30352***		51.4	
Environment (E)	2	4.77732	2.38866 ns		2.4	
G x E	22	92.00631	4.1821**		46.21	
IPC1	12	81.81696	6.81808**		(41.1)	88.93
Residual	10	10.18935	1.01893 ns	49.83	(5.12)	11.07
Error	108	197.746	1.83098			
Blocks/Env	9	25.69894	2.85544 ns			
Pure Error	99	172.0471	1.73785			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS=genotype by environment interaction sum of squares, **p≤0.01, *** p≤0.001 ns= not significant

Table 4.60. AMMI Analysis of variance of potato chips yellowness (b*) for 12 potato genotypes evaluated in three environments

Source	DF	SS	MS	% TSS explained	% TRT SS explained	%GEI SS explained
Total	143	737.0348	5.15409			
Treatment	35	234.5919	6.70263ns	31.83		
Genotype	11	81.37793	7.39799 ns		34.69	
Environment	2	21.12287	10.56143 ns		9	
Genotype x Environment	22	132.0911	6.00414 ns		56.31	
IPC1	12	110.376	9.198 ns		(47.1)	83.56
Residual	10	21.71514	2.17151 ns		(9.26)	16.44
Error	108	502.4429	4.65225	68.17		
Blocks/Env	9	39.63154	4.4035 ns			
Pure Error	99	462.8114	4.67486			

DF= degree of freedom, SS= sum of square, MS= mean square, TSS = total sum of squares, TRT SS = treatment sum of squares. GEI SS = genotype by environment interaction sum of squares, ns= not significant

CHAPTER V

CONCLUSION

The study of genotype by environment interactions in plant breeding has once again been proven to be essential for agronomists and plant breeders. The use of stability models such as Finlay and Wilkinson regression coefficient and the Additive main effect and multiplicative interactions (AMMI) are vital tools in establishing the stability levels of potato breeding lines. The study revealed that:

- There were significant genotypic, environmental and GEI effects on all traits, which shows the existence of high variabilities among the potato breeding lines due to the different parental sources and productivity of each environment.
- Crossover type of GEI was present which resulted in genotypes ranking differently in each environment.
- MEÇ1407.17, MEÇ1407.05, MEÇ1407.08 and MEÇ1411.06 were outstanding genotypes in respect to marketable tuber yield while the standard cultivars Agria, Russet Burbank and MACAR1402.11 were found as low yielding genotypes as average of three locations.
- Genotypes MEÇ1407.17, MEÇ1411.06, MADELEINE, MACAR1406.07, MEÇ1402.07, MEÇ1402.09, and Agria were more stable genotypes with broad adaptability to diverse environments.
- MEÇ1405.06, MEÇ1407.05, MEÇ1407.08, MACAR1409.09, MACAR1406.04, MACAR1402.10, MACAR1402.11 and Russet Burbank were unstable with specific adaptation.

- All the 12 breeding lines have DMC >20% and SG > 1.080, which are threshold levels for potato processing industries and are ideal for chips and French fries processing.
- Sivas location was found as the most productive environment for potato yield while the Niğde and Konya have similar performance.
- Our findings revealed that, AMMI model better explained the GEI and stability of genotypes comparing to the Finlay and Wilkinson model.
- They were difference in stability model models used in terms of genotype stability levels.
- The breeding lines MEÇ1407.17, MEÇ1407.05, MEÇ1407.08 and MEÇ1411.06 were identified as promising cultivar candidates due to their high tuber yield and stable performances across different environments

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CURRICULUM VITAE

Eric Kuopuobe NAAWE, a native of Kanguol-Piina in the Lambussie-Karni District of the Upper West Region of Ghana was born on November 14, 1990 in Piina to Mr. Cyprano NAAWE and Mrs. Agnes ZAATO. He attended his senior high education in Nandom Senior High Secondary School from 2009 to 2013 where he read General Science, and his undergraduate studies in University for Development Studies, Navrongo Campus, from 2013-2017 where he read Applied Biology and obtained B.Sc. Applied Biology. Eric did his one-year internship (National service) at the St John Bosco College of Education in Navrongo where he worked as a research assistant in many departments from 2017 to 2018. He afterwards gained admission at Niğde Ömer Halisdemir University, Nigde, Turkey, in the Graduate School of Natural and Applied Sciences, Department of Agricultural Genetic Engineering, for his Master studies under the Ayhan Şahenk Scholarship Foundation.