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DEVELOPMENT OF POTATO HYBRIDS VIA TRUE POTATO SEED, NOVEL POTATO BREEDING APPROACH AIMING FOOD SECURITY IN PAKISTAN

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Abstract

The main aim of modern potato breeding programs is to introduce and develop potato hybrids via true potato seed, a novel and innovative approach compared to traditional vegetative propagation methods. Experimental material including twenty eight potato hybrids, five parental cultivars and a check variety were evaluated in three diverse environments namely Abbottabad, Battakundi and Kaghan, during 2021-23. Randomized complete block design was employed with three replications. Analysis of variance revealed significant ($p<0.01$, 0.05) differences among the studied traits, signifying a substantial level of genetic variability. The lower coefficient of variation across varied sites, confirmed the good precision of the experiments. The highest phenotypic coefficient of variation highlighted the significant influence of environmental factors on the expression of the traits under study. Moderate to high heritability (47.19% to 94.31%) and low to high genetic advance (9.34% to 55.77%) for studied characters, confirmed the role of additive gene action. The observed positive and significant correlations among potato traits have provided valuable insights for breeding programs. The results concluded that genotypes, G23 (TPSSMC65) and G17 (TPSSMR41) excelled in performance and selected as promising genotypes with potential to be released as potato hybrids. It is worth mentioning that high genetic variability, heritability and strong genetic potential of studied hybrids could play a significant role in increasing potato cultivation, and production. Further evaluation and testing of these hybrids under different environments could reveal ultimate potential for resilience, yield, and yield attributing traits in future breeding strategies, hence, significantly contributing to food security and sustainable agriculture, globally.

Keywords: Additive gene action, Battakundi, Genetic advance, Heritability, True potato seed.

Introduction

Potatoes (*Solanum tuberosum* L.) play a critical role in global food security due to their versatility, nutritional value, and wide range of uses. Potatoes are enrich with vitamin C, antioxidant and essential micronutrients (Luitel *et al.,* 2020). They are considered a staple food, globally due to their ability to provide a significant portion of daily energy requirements. With over 200 tuber-bearing species within the Solanum genus, potatoes offer a diverse range of varieties suitable for different growing conditions and culinary purposes (Brittanica, 2023). Potato production occurs on a large scale, with varying yields depending on factors such as climate, soil conditions, and agricultural practices. According to FAO data, global potato production reached about 376 million tons harvested from an area of approximately 18.1 million hectares (Anon., 2023). In Pakistan, potatoes are cultivated on around 341 thousand hectares, with an average production of 8,319 thousand tons (Anon., 2022-23).

Genetic analysis is a powerful tool in potato breeding that provides insights into the genetic variations between progeny and their ancestors. By utilizing genetic information, breeders can improve the precision, efficiency, and speed of breeding programs, leading to the development of potato varieties with improved traits, such as higher yield, better disease resistance, and better quality. It also helps ensure the sustainability of breeding efforts by maintaining genetic diversity and allowing for the selection of varieties that can adapt to changing environmental conditions. Genetic analysis in potato breeding involves a range of tools and concepts that are crucial for selecting and maintaining new potato hybrids and varieties. These tools and concepts help breeders identify desirable traits, optimize selection processes, and ensure the development of robust, high-yielding, and disease-resistant potato varieties. Among these tools; heritability (H2), genetic advance (GA), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), phenotypic variance (VP), genotypic variance (VG) and environmental variance (VE) are the most important.Heritability is the sum of the genetic effects contributing to the phenotypic variation, which typically includes additive genetic effects and dominance genetic effects (Tessema *et al.,* 2022).High heritability means that a significant portion of the observed variation in a trait is due to genetic factors, rather than environmental influences.This is a critical piece of information for potato breeding programs, as it suggests that the trait is more likely to be passed on to subsequent generations through selective breeding (Ney *et al.,* 2016). Quantifying heritable variation more accurately is crucial for making informed decisions in breeding programs, as it directly informs breeders about the potential for genetic improvement (Dalumu*et al.,* 2109).

The high nutritional value, versatility, and global production of potatoes make them a crucial component of efforts to meet the food requirements of a growing global population (Anon., 2023).Continued research and development in potato cultivation, breeding, and processing will further enhance their contribution to food security and agricultural sustainability. The main goal of any plant/potato breeding program is to develop new cultivars/hybrids that exhibit high yield and quality characteristics to meet the demands of specific regions, worldwide. However, potato breeding is a lengthy process that often takes around a decade to develop new hybrids. Additionally, the genetic variability in potatoes, driven by additive, dominance, and epistatic gene actions, plays a key role in shaping the inheritance and expression of traits. Understanding how these genetic mechanisms work enables breeders to design more effective and precise breeding strategies (Ene *et al.,* 2016). This variability allows breeders to select individuals with desired traits and combine them through systematic breeding programs. Through this process, undesirable genes or alleles transferred during hybridization can be eliminated over time, even it can take decades to achieve the desired outcomes (Bonierbale*et al.,* 2020).

True potato seed (TPS) is a promising breeding approach with worth significance, especially in high-altitude like northern sites of Pakistan where lack of quality seed potato production, absence of improved potato varieties, identification of suitable growing conditions (Majeed *et al.,* 2017a), and non-availability of true-to-type and disease free certified seed which can result in low potato production, and quality meet products. True potato seed (TPS) method produce new varieties/hybrids with broader genetic diversity, better tuber-yielding with disease resistance, and with improved genetic variability. Additionally, TPS could easily be stored with longer shelf life, a significant aspect in regions with limited storage facilities and infrastructure. One of the most important aspect and novelty of TPS breeding strategy is to bring true-to-type and disease free seed potato production in region like Pakistan where substantial resources are spent on importing seed potato, annually. By using TPS, productivity of the crop could be increased with lower production cost, and less dependency on imported seed. Most importantly, ultimate benefits of TPS are the introduction and selection of high-yielding, and disease resistance potato genotypes based on yield attributing traits that are adaptable and well-suited to local conditions in the region, therefore, encouraging food security, and sustainable agriculture, especially in Pakistan.

Therefore, keeping in view the importance of potato breeding, particularly through true potato seed (TPS) breeding approach, the current potato breeding program was initiated in high-altitude region of Hazara division Khyber Pakhtunkhwa Pakistan, where genetic tools were applied to evaluate the performance of potato hybrid clones in their early generations. This evaluation involves assessing various yield attributing traits to identify superior hybrids for further selection and advancement. By utilizing genetic tools and rigorous selection criteria, current study was designed with the aim to develop and select potato hybrid clones in their early generations based on performance of yield attributing traits, that not only meet domestic food requirements but also have the potential for broader adaptation, and commercial success. This approach underscores the importance of continuous research, particularly through true potato seed (TPS), and innovation in potato breeding to address the evolving needs of agricultural production and food security in future, providing valuable insights into the adaptation and productivity of the tested genotypes across varied agro-climatic conditions in Khyber Pakhtunkhwa, Pakistan.

Materials and Method

Study site overview: The study was investigated in three different potato growing environments namely Abbottabad (34°10'7.5036"N, 73°13'17.3892"E); Battakundi (34°56'0"N, 37°46'0"E), and Kaghan (34°32'30"N, 73°21'0"E), in Hazara division Khyber Pakhtunkhwa, Northern Pakistan. Experiments were conducted atHazara Agriculture Research Station Abbottabad, Seed Potato Research and Multiplication Farm Battakundi, and Summer Agriculture Research Farm Kaghan, situated at the height of 1256 m, 2812 m, and 2510 m, respectively. Recorded data for annual rainfall was 1532, 1500, and 1489 mm with annual temperature of 15.9, 3.9 and 4.3°C, for three different environments, respectively. Mostly, soil in studied sites was acidic with pH ranges from 5.0 to 6.3. Experimental trials was conducted during the planting seasons, spanning from 2021 to 2023.

Description of experimental materials: Initially, crosses were conducted among diverse potato parents to produce a wide ranges of genetic variations at Seed Potato Research and Multiplication Farm Battakundi, during the 2021, summer season. Potato berries (containing true potato seed) were collected from successful cross combinations. The extracted seed from berries was planted in nurseries to grow new potato plants, where the most promising plants were selected for tuber production, and other desirable agronomic traits for further evaluation and testing under varying environments to select adaptable and stable potato varieties/hybrids. The selected experimental material used in the present study were consisted of twenty eight potato genotypes, five parental cultivars, and a check variety, as presented in Table 1. The pedigree of the parents involved during hybridization is provided in Table 2, which likely include information about their genetic background, traits of interest, and breeding history. This information is essential for understanding the genetic composition and potential of the progenies resulting from the crosses.

Experimental design and layout: The experimental design employed was randomized complete block (RCB) design with three replications, ensuring robustness and reliability of the results. Planting density was optimized with row-to-row distance set at 0.75 meters and tuber-to-tuber distance at 0.25 meters. Each plot was consisted of two rows with 24 tubers, covering a plot size of 4.5 square meters. Both randomization and replication can play a significant role in controlling the environmental error, to reduce the bias with distribution of unknown variations, and to increase reliability and precision of an experiment.

Management of experimental field: Experimental plots were set after proper plough and soil bed raising. Healthy and well sprouted seed tubers were planted, manually. Fertilizers applied were DAP, SOP and Urea at the rate of 220, 260 and 180 kg ha^{-1}, respectively. Standard agronomic practices including irrigation and fungicides were applied according to recommended rates. Harvesting was also performed manually, ensuring consistent, and accurate data collection. All the other necessary pre- and post-cultural practices including spraying, hoeing, and weeding were applied, uniformly and timely to maintain crop health and vigor throughout the experiment.

Table 1. Potato genotypes evaluated in different environments of Khyber Pakhtunkhwa.

Code	Hybrids	Parents		Code	Hybrids	Parents	
		♀	♂			♀	♂
G1	Sarpomira			G18	TPSSMR42	SM	R42
G2	Burna			G19	TPSCLR51	CL	R51
G3	Coroda			G20	TPSCLR52	CL	R52
G4	Rocco			G21	TPSCLR53	CL	R53
G5	Cardinal			G22	TPSCLR54	CL	R54
G6	TPSCB11	C	B11	G23	TPSSMC65	SM	C65
G7	TPSCB12	C	B12	G24	TPSSMC66	SM	C66
G8	TPSCB13	C	B13	G25	TPSSMC67	SM	C67
G9	TPSCB14	C	B14	G26	TPSRSM73	R	SM73
G10	TPSCLB21	CL	B21	G27	TPSRSM74	R	SM74
G11	TPSCLB22	CL	B22	G28	TPSRSM75	R	SM75
G12	TPSCLB23	CL	B23	G29	TPSRSM76	R	SM76
G13	TPSCR31	C	R31	G30	TPSCSM86	C	SM86
G14	TPSCR32	C	R32	G31	TPSCSM87	C	SM87
G15	TPSCR33	C	R33	G32	TPSCSM88	C	SM88
G16	TPSCR34	C	R34	G33	TPSCSM89	C	SM89
G17	TPSSMR41	SM	R41	G34	**Check**	UOH100	

Table 2. Pedigree's of potato parents used for Hybridization in Battakundi.

S. No.	Hybrid	Parentage	Origin	Year release/ Code
1.	Sarpomira	76.PO.12.14.268 × D187	Hungry	2003 / 87.4.120
2.	Roko	ALWARA × MA 81-536	Austria	1998 / NO 89-2525
3.	Cardinal	TULNER/DEVRIES54-30-8 × SVP55-89	Holland	1972 / BRANDS 60-51
4.	Coroda	AR 76-199-3 × KONST 80-1407	Holland	1998 / KK83-216
5.	Burna	KARDAL × SPOLIA	Germany	2007 / UP6.434/2

Source: www.hars_atd@yahoo.com

Data collection and measurements: Collecting data on various agronomic traits such as the number and weight of tubers of different sizes is crucial for assessing the performance of potato hybrids. Data were collected for several agronomic traits. These traits include number of small tubers plot^{-1}, number of medium tubers plot^{-1}, number of large tubers plot^{-1}, weight of small tubers plot^{-1}, weight of medium tubers plot^{-1} and weight of large tubers plot^{-1}, respectively, according to described data protocols (Cabello *et al.,* 2020). On harvesting, potato tubers were divided into three different categories based on their size i.e. small (31.5 ± 2.5 g), medium (57 ± 2.5 g), and large tubers (77.5 ± 2.5 g), respectively (Asnake *et al.,* 2023).

The selected tuber size were separated, counted, and weighted in each plot across three environments, individually, as well as collectively. Weight of seed-sized tubers used in each category was uniform where maximum weight difference among seed tubers was about ± 2.5 g.These traits provide valuable insights into the yield and size distribution of tubers, which are important considerations for potato breeding and production.

Additionally, Relative humidity (%) and temperature (°C) data were also collected as given in Fig. 1. Monitoring these environmental factors helps assess their impact on the growth and development of potato plants and different tubers size. Understanding how environmental conditions influence agronomic traits can inform management practices and breeding strategies to optimize yield and quality under different growing conditions.

Broad-sense heritability (%): Total genotypic variance to total phenotypic variance among diverse genetic population is termed as heritability. It provide an indication about the extent to which genetic factors contribute to the observed variation in a trait. Broad sense heritability was calculated using following formula (Khan *et al.,* 2017).

$$H^2_{(BS)} = VG/ VP \times 100 \ldots\ldots\ldots\ldots\ldots\ldots \text{Eq. 1}$$

where,
$VG = MSG - MSE / r$
$VP = MSG / r$
$VE = MSE / r$

Meanwhile,
HBS = Broad sense heritability; VG = Genotypic variance; VP = Phenotypic variance; VE = Environmental variance; MSG = Mean square for genotype; MSE = Mean square for error and r = Replication

Heritability percentage was categorized into low, medium and high (Tessema *et al.,* 2022).

where,
Low = 0 to 30%, 30 to 60% = Moderate and > 60% = High

Genetic advance (%): Percent gain for a trait delivered under certain applied pressure is generally considered as genetic advance. It represents the expected increase in the mean value of the trait due to selection within a single generation. Genetic advance is often expressed as a percentage of the population mean. It was measured by using following formula (Khan *et al.,* 2017).

EGA = isph …………………………..………….. Eq. 2
GA % = GA/ × 100 ……………………..……..…. Eq. 3

where,
EGA = Expected genetic advance; i = Standardized selection differential; sp = Phenotypic standard deviation, whereas, selection intensity was applied at 5% (2.06).

Genetic advance percentage was categorized into low, medium and high (Tessema *et al.,* 2022).

where,
Low = 0 to 10%, 10 to 20% = Moderate and > 20% = High

Genetic variability (%): Genetic variability was measured in term of genotypic coefficient of variation and phenotypic coefficient of variations while genotypic variance, phenotypic variance and environmental variance were also studied. These measures could help to quantify the degree of variation present in a trait and provide insights into the genetic and environmental factors contributing to this variation. Formula used for measuring genetic variability is given below (Khan *et al.,* 2017).

PCV $= (^{\delta}p/x) \times 100$ ……………….……….. Eq. 4
GCV $= (^{\delta}g/x) \times 100$ ……………………...…... Eq. 5

where,
PCV = Phenotypic coefficient of variation; GCV = Phenotypic coefficient of variation; $^{\delta}p$ = Phenotypic standard deviation; $^{\delta}g$ = Genotypic standard deviation and X = Grand mean.

Phenotypic and genotypic coefficient of variation percentage was categorized into low, medium and high (Tessema *et al.,* 2022).

where,
Low = 0 to 10%, 10 to 20% = Moderate and > 20% = High

Statistical analysis

The recorded data was subjected to analysis of variance (ANOVA) to assess the significance of differences present among treatment means for each environment individually, as well as combined analysis for all the environments, by using Statistix 8.1 model. Based on mean data generated from Statistix 8.1, and heritability performance of traits in diverse environments, genetic variability was computed for studied traits of potato genotypes. Following ANOVA, least significant differences (LSD) Fisher test ($p \leq 0.05$) was also applied to compare, and differentiate between treatment means. LSD is a post-hoc test used to determine which treatment means was significantly different from each other in studied environments. A correlation plot was developed to study the correlation between different characters/ traits. Correlation analysis helps to identify the strength and direction of relationships between studied variables. Positive correlation indicates that two variables tend to move in the same direction with positive effect on each other, while negative correlations indicate they move in opposite directions. By employing these statistical methods, the study aim to comprehensively analyze the data, identify significant differences among treatment means, and explore relationships between different traits. This rigorous analysis provides valuable insights into the performance and interactions of potato hybrids across diverse environments, which can facilitate in selection and advancement of superior genotypes for breeding programs.

Results

Analysis of variance: The potato hybrids developed through true potato seed (TPS) breeding, excelled in their mean performance and exhibited significant variability for yield-contributing traits tested in different environments, as presented by analysis of variance (ANOVA). Observed significant differences $p<0.01$, $p<0.05$ for studied traits in different environments was indicative of presence of significant variations across different environments (Table 3).The wide ranges observed in mean values of studied traits showed that substantial amount of genetic variability was present among the potato hybrids across different environments. In the present study, among potato genotypes, G17 and G23 exhibited highest total number of tubers plot^{-1} (258.668 and 254.000) and total tubers weight plot^{-1} (17.276 and 17.444 Kg), whereas among parental cultivars, Sarpomira performed excellent with highest number of total tubers (227.78) and weight (15.956 Kg) plot^{-1}, respectively (Table 3). It is worth mentioning that total number of tubers plot^{-1} and total tuber weight plot^{-1} was calculated from small, medium and large number and weight of tubers per plot as presented in Table 3.

Genotypic, phenotypic and environmental variances: Considerable amount of genotypic, phenotypic and environmental variances were recorded for the traits under consideration in diverse ranges of multiple environments. Number of small tubers plot^{-1} showed highest values for genotypic, phenotypic, and environmental variance. The values observed was; Vg = 425.94, Vp = 480.48, and Ve = 54.54 under the climatic conditions of Battakundi followed by Kaghan (Vg = 384.84, Vp= 421.78 & Ve = 36.94), and Abbottabad (Vg = 61.45, Vp = 130.21 & Ve = 68.76), respectively, as presented in Fig. 2.

Broad sense heritability (%): In case of broad-sense heritability, moderate to high heritability was observed in agro-climatic conditions of Abbottabad, Battakundi and Kaghan. The observed estimates of broad sense heritability for different traits were; 47.19, 88.64 & 91.24% (number of small tubers plot^{-1}); 88.59, 94.31 & 64.49% (number of medium tubers plot^{-1}); 76.24, 87.85 & 57.42% (number of large tubers plot^{-1}); 48.76, 77.69 & 89.81% (weight of small tubers plot^{-1}); 78.32, 90.54 & 86.59% (weight of medium tubers plot^{-1}) and 57.01, 84.85 & 60.37% (weight of large tubers plot^{-1}) in Abbottabad, Battakundi and Kaghan, respectively (Fig. 3).

Genetic advance (%): Low to highest genetic advance mean was measured for studied traits in different environments. Observed estimates of genetic advance mean for different traits were, 9.34, 26.76 & 25.86% (number of small tubers plot^{-1}); 47.63, 55.77 & 20.93% (number of medium tubers plot^{-1}); 34.68, 38.59 & 18.79% (number of large tubers plot^{-1}); 11.32, 20.13 & 35.33% (weight of small tubers plot^{-1}); 35.55, 38.85 & 29.94% (weight of medium tubers plot^{-1}) and 25.29, 35.05 &

21.93% (weight of large tubers plot^{-1}), in diverse environmental conditions of Abbottabad, Battakundi and Kaghan, respectively (Fig. 3). High heritability's percentage (≥70%) and genetic advance (≥20%) means suggested that these traits were heritable with potential to vigorous response to selection in breeding program.

Genetic variability: Genotypic and phenotypic coefficient of variations are the two basic components used to measure genetic variability within a population. Low to moderate phenotypic and genotypic coefficient of variations were observed for studied traits. Phenotypic coefficient of variation (PCV) was found higher than genotypic coefficient of variation (GCV). Observed values of GCV for different yield-attributing characters were, 6.61, 13.83 & 12.14% (number of small tubers plot^{-1}); 24.57, 28.02 & 12.65% (number of medium tubers plot^{-1}); 19.27, 20.08 & 12.03% (number of large tubers plot^{-1}); 7.86, 11.11 & 18.09% (weight of small tubers plot^{-1}); 19.50, 19.93 & 15.62% (weight of medium tubers plot^{-1}), and 16.27, 28.50 & 13.69% (weight of large tubers plot^{-1}) in different climatic zones. While values observed for PCV include; 9.61, 14.69 & 13.76% (number of small tubers plot^{-1}); 26.09, 28.86 & 15.75% (number of medium tubers plot^{-1}); 22.07, 21.42 & 15.88% (number of large tubers plot^{-1}); 11.27, 12.59 & 19.09% (weight of small tubers plot^{-1}); 22.04, 20.94 & 16.78% (weight of medium tubers plot^{-1}), and 21.52. 20.08 & 17.63% (weight of large tubers plot^{-1}) in agro-ecological conditions of Abbottabad, Battakundi and Kaghan, respectively (Fig. 4).

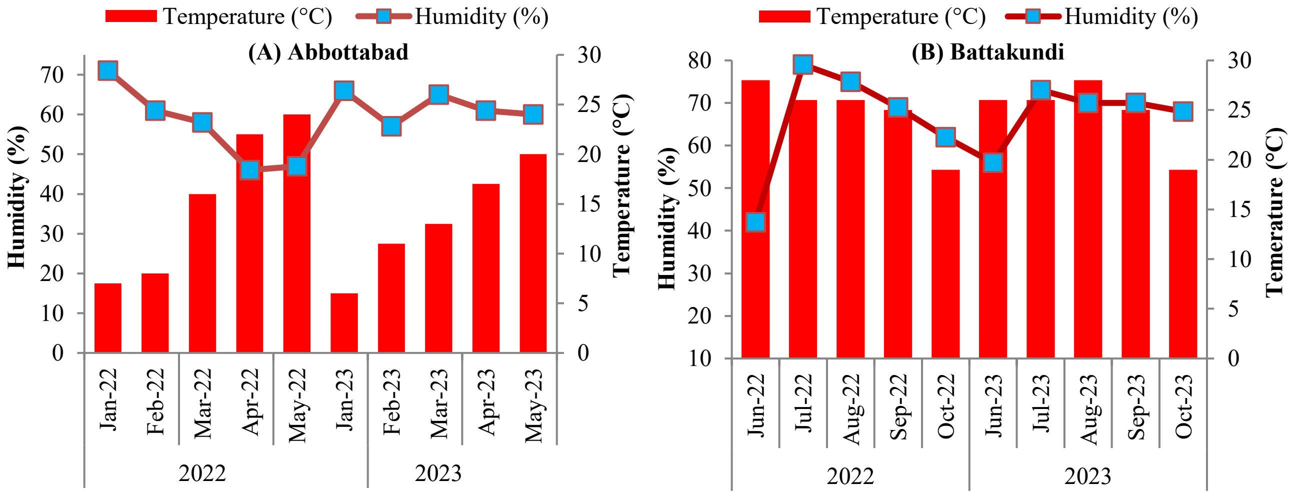

Fig. 1. Annual mean temperature (°C) and humidity% for studied environments.

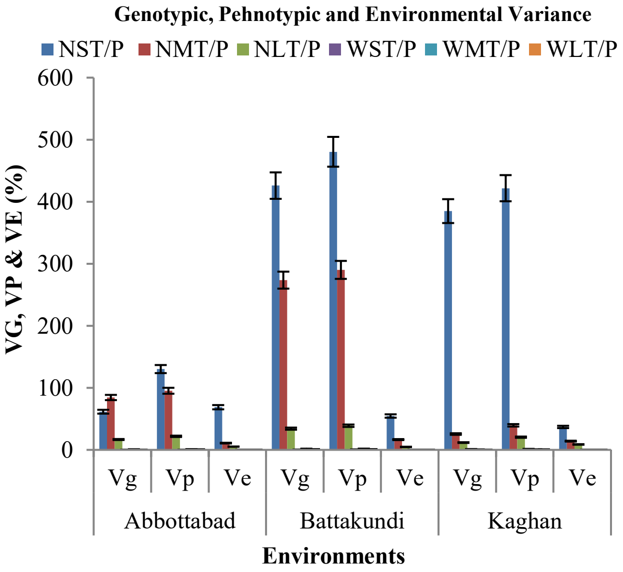

Fig. 2. Genotypic variance (Vg), phenotypic variance (Vp), and environmental variance (Ve) fordifferent studied traits evaluated in Abbottabad, Battakundi and Kaghan.

NST/P: Number of small tubers plot^{-1}, NMT/P: Number of medium tubers plot^{-1}, NLT/P: Number of large tubers plot^{-1}, WST/P: Weight of small tubers plot^{-1}, WMT/P: Weight of medium tubersplot^{-1}, and WLT/P: Weight of large tubers plot^{-1}. Vertical bars showing Vg, Vp and Ve values with error mean bar.

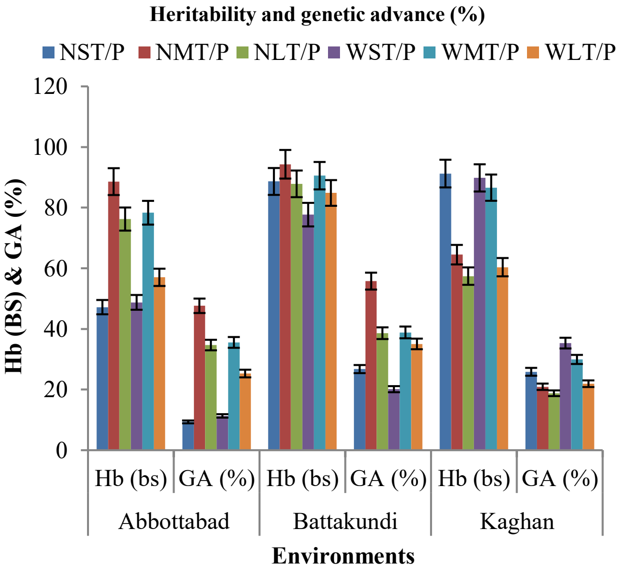

Fig. 3. Broad senses heritability % and genetic advance % for studied traits in Abbottabad, Battakundi and Kaghan.

NST/P = Number of small tubers plot^{-1}, NMT/P = Number of medium tubers plot^{-1}; NLT/P = Number of large tubers plot^{-1}; WST/P = Weight of small tubers plot^{-1}; WMT/P = Weight of medium tubers plot^{-1}; and WLT/P = Weight of large tubers plot^{-1}. Vertical bars showing broad sense heritability and genetic advance mean values with error mean bar.

Table 3. Mean performance and coefficient of variation for number and weight of small, medium and large tubers plot-^{1} in 34 potato genotypes.

Hybrid codes	Potato hybrids	Number of small tubers plot^{-1}	Number of medium tubers plot^{-1}	Number of large tubers plot^{-1}	Weight of small tubers plot^{-1}	Weight of medium tubers plot^{-1}	Weight of large tubers plot^{-1}
	Potato parents						
G1	Sarpomira	154.333^{abcd}	45.667^{abcdefg}	27.778^{abcde}	6.022^{abcd}	4.956^{abcdefg}	4.978^{abcde}
G2	Burna	133.111^{cde}	34.556^{defg}	24.111^{abcde}	5.289^{cd}	4.222^{efgh}	3.967^{cdefg}
G3	Coroda	130.222^{cde}	28.889^{g}	20.778^{de}	5.189^{cd}	3.3^{h}	3.091^{g}
G4	Rocco	146.111^{bcde}	41.889^{bcdefg}	20.556^{e}	6.011^{abcd}	4.856^{bcdefgh}	3.533^{fg}
G5	Cardinal	124.222^{e}	33.889^{defg}	27.111^{abcde}	5.478^{bcd}	3.956^{gh}	4.544^{abcdef}
	Potato hybrids						
G6	TPSCB11	128.778^{de}	56.444^{abc}	25.333^{abcde}	5.9^{abcd}	6.422^{a}	4.267^{bcdefg}
G7	TPSCB12	136.222^{cde}	56.444^{abc}	26^{abcde}	5.667^{abcd}	6.122^{ab}	3.878^{defg}
G8	TPSCB13	142.444^{bcde}	54.778^{abc}	26.444^{abcde}	5.722^{abcd}	5.944^{abcd}	4.2^{bcdefg}
G9	TPSCB14	142.778^{bcde}	55.111^{abc}	24.333^{abcde}	5.578^{abcd}	5.989^{abc}	3.733^{efg}
G10	TPSCLB21	140.111^{cde}	46^{abcdef}	26.333^{bcde}	5.489^{bcd}	5.856^{abcd}	4.889^{abcde}
G11	TPSCLB22	133.444^{cde}	48^{abcde}	29.111^{abcde}	5.6^{abcd}	5.322^{abcdefg}	5^{abcde}
G12	TPSCLB23	131.778^{cde}	43.778^{bcdefg}	30.333^{ab}	5.611^{abcd}	5.367^{abcdefg}	5.278^{abc}
G13	TPSCR31	136.444^{cde}	41.111^{bcdefg}	26.778^{abcde}	5.278^{cd}	4.556^{cdefgh}	4.467^{abcdef}
G14	TPSCR32	135.556^{cde}	41.444^{bcdefg}	26.556^{abcde}	5.167^{d}	4.667^{bcdefgh}	4^{cdefg}
G15	TPSCR33	131.889^{cde}	53^{abc}	24.111^{abcde}	5.456^{bcd}	5.2^{abcdefg}	4.233^{bcdefg}
G16	TPSCR34	125.889^{e}	44.222^{bcdefg}	24.444^{abcde}	5.156^{d}	4.9^{abcdefg}	4.456^{abcdef}
G17	TPSSMR41	170.556^{ab}	61.556^{a}	26.556^{abcde}	6.833^{ab}	5.933^{abcd}	4.4^{abcdefg}
G18	TPSSMR42	157.111^{abc}	57.556^{ab}	28.111^{abcde}	6.633^{abc}	5.756^{abcde}	4.556^{abcdef}
G19	TPSCLR51	149.556^{abcde}	56.444^{abc}	26.444^{abcde}	6.111^{abcd}	6^{abc}	4.456^{abcdef}
G20	TPSCLR52	147.889^{bcde}	54.222^{abc}	23.556^{abcde}	5.8^{abcd}	5.589^{abcdef}	4.111^{bcdefg}
G21	TPSCLR53	139^{cde}	54.778^{abc}	23^{bcde}	5.889^{abcd}	5.589^{abcdef}	4.344^{abcdefg}
G22	TPSCLR54	141.889^{cde}	50.444^{abcd}	25.667^{abcde}	5.967^{abcd}	5.333^{abcdefg}	4.622^{abcdef}
G23	TPSSMC65	176.889^{a}	45.222^{abcdefg}	31.889^{a}	7^{a}	4.811^{bcdefgh}	5.633^{a}
G24	TPSSMC66	145.444^{bcde}	42.778^{bcdefg}	30.111^{abc}	5.833^{abcd}	4.422^{defgh}	5.178^{abcd}
G25	TPSSMC67	140.778^{cde}	43.111^{bcdefg}	31^{ab}	6.167^{abcd}	4.878^{abcdefg}	5.378^{ab}
G26	TPSRSM73	137.111^{cde}	41.556^{bcdefg}	21.556^{cde}	6.044^{abcd}	5.278^{abcdefg}	3.7^{efg}
G27	TPSRSM74	138.778^{cde}	40.889^{bcdefg}	26.556^{abcde}	5.956^{abcd}	5.489^{abcdefg}	4.767^{abcdef}
G28	TPSRSM75	131.889^{cde}	41.889^{bcdefg}	30.556^{ab}	5.856^{abcd}	5.144^{abcdefg}	5.2^{abc}
G29	TPSRSM76	134.667^{cde}	41.889^{bcdefg}	30.222^{ab}	5.322^{cd}	5.522^{abcdef}	5.367^{ab}
G30	TPSCSM86	126.333^{de}	43.889^{bcdefg}	26.333^{abcde}	5.167^{d}	5.589^{abcdef}	4.478^{abcdef}
G31	TPSCSM87	122.222^{e}	41^{bcdefg}	24.333^{abcde}	5.367^{cd}	5.467^{abcdefg}	4.1^{bcdefg}
G32	TPSCSM88	133.111^{cde}	39.667^{cdefg}	23.222^{bcde}	5.033^{d}	5.067^{abcdefg}	4.256^{bcdefg}
G33	TPSCSM89	133.444^{cde}	31.889^{efg}	29.222^{abcd}	5.333^{cd}	4.2^{efgh}	5.344^{ab}
	Check cultivar (Sarpomira)						
G34	Check	128.222^{de}	30.778^{fg}	23.667^{abcde}	5.377^{bcd}	4.122^{fgh}	4.133^{bcdefg}
LSD (0.05)		28.190*	16.901*	8.578**	1.463*	1.560*	1.317*
SE		14.119	8.4651	4.2965	0.7329	0.7817	0.6599

LSD = Least significant difference; SE = Standard error; ** = Highly significant, * = Significant

Table 4. Pearson correlations among different studied traits of potato genotypes.

	NST/P	NMT/P	NLT/P	WST/P	WMT/P
NMT/P	0.4782**				
NLT/P	0.4942**	0.3038**			
WST/P	0.8768**	0.4510**	0.5119**		
WMT/P	0.4086**	0.8846**	0.3014**	0.4056**	
WLT/P	0.4175**	0.3544**	0.8789**	0.4188**	0.3752**

NST/P = Number of small tubers plot^{-1}, NMT/P = Number of medium tubers plot^{-1}; NLT/P = Number of large tubers plot^{-1}; WST/P = Weight of small tubers plot^{-1}; WMT/P = Weight of medium tubers plot^{-1}; and WLT/P = Weight of large tubers plot^{-1}. **: Highly significant, *: Significant

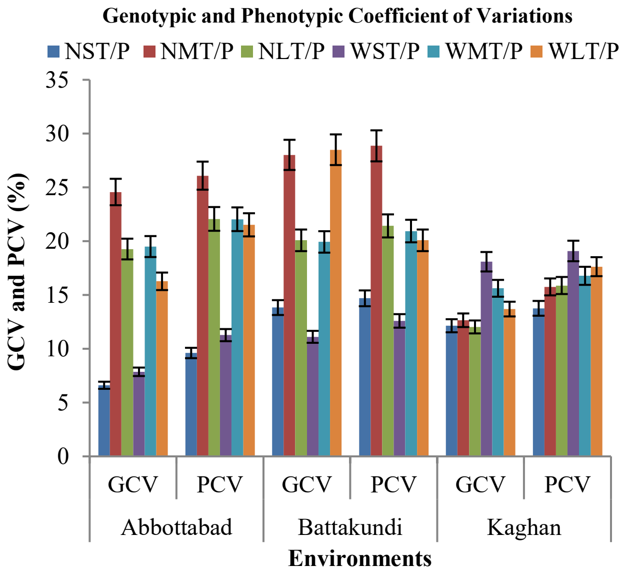

Fig. 4. Genotypic and phenotypic coefficient of variations for studied traits in Abbottabad, Battakundi and Kaghan.
NST/P = Number of small tubers plot^{-1}, NMT/P = Number of medium tubers plot^{-1}; NLT/P = Number of large tubers plot^{-1}; WST/P = Weight of small tubers plot^{-1}; WMT/P = Weight of medium tubers plot^{-1}; and WLT/P = Weight of large tubers plot^{-1}. Vertical bars showing GCV and PCV values with error mean bar.

Correlation: Positive and highly significant correlations among different studied characters were promising findings, especially when they contribute to increased tuber yield production (Table 4).

Discussion

Achieving high tuber yield, disease resistance, and improving yield-attributing traits are the primary objectives in potato breeding program. However, achieving this goal can be challenging, particularly due to presence of adverse factors like disease, that can significantly affect yield and quality traits (Malik *et al.,* 2021). The distinctive performance of the potato genotypes for their mean performance indicates that certain hybrids may excel in particular traits compared to others. The focus on maximizing the number and weight of small, medium, and large tubers in potato breeding and production is crucial for increasing overall potato yield and quality, ultimately contribute and promote food security and agricultural sustainability, worldwide. The significant genetic variability observed among potato genotypes develop through TPS breeding, underscore the potential for further genetic improvement in yield-attributing and quality traits, ultimately contribute to promote advance potato varieties with better agronomic traits. In the same way, significant genetic variability and parallel mean performance were also proposed by Subedi *et al.,* (2021); Zeleke *et al.,* (2021); Ebrahim *et al.,* (2018); Hafiz(2015); Ozturk &Yildrim (2014) and Fiakdo*et al.,* (2013), where they proposed similar findings. The higher phenotypic variance compared to genotypic variance indicates that environmental factors play a significant role in influencing these traits. This suggested that much of the variation observed in the traits is due to environmental conditions rather than genetic differences. The existence of variability within breeding material provide an opportunities to select and promote individuals with desired traits for further improvement (Khayatnezhad*et al.,* 2011).

Seedling selection is very important in potato breeding as it directly affectthe traits like yield and disease resistance, with high heritability. Initially, seedling selection was ignored however, focusing on viable seedlings and suitable variety selection, increases the chances to develop enviable traits (Melo *et al.,* 2011). Selection is one of the important method for variety/hybrid development during breeding strategies. The opportunity for selection of superior varieties with desired traits during a breeding program can be effective if a population with large genetic diversity is available (Baffi *et al.,* 2016).Meanwhile, diversity among genotypes could be effected by environmental factors i.e. temperature, rainfall and soil, besides genetic factors (Baffi *et al.,* 2016). Heritability was considered as one of the most important and valuable tool (Ney *et al.,* 2016) in potato breeding due to presence of additive, epistatic, and dominance gene actions (Tessema *et al.,* 2022). Heritability can expose the sum of effects of either environmental factor or genetic factors on different traits, during potato breeding. While genetic advance can also provide a direct measure of genetic improvement and contribute to the accuracy, and productivity of breeding efforts (Dalumu*et al.,* 2019), hence declared as a prolific tool to guide breeders in selection program during early generation (Ahmed *et al.,* 2017). The consistency of moderate to high broad sense heritability and genetic advance across multiple environments in the present investigation indicated the robustness and stability of the genetic factors influencing the traits, regardless of the environmental conditions which can promote and broad the scope of potato breeding in future. If heritability and genetic advance were found high, meant trait is under the influence of genetic factors which can be utilized for an effective selection, especially in early generations of potato (Afuape*et al.,* 2015; Dewi *et al.,* 2021).

Both genotypic and phenotypic coefficient of variations are the essential tools to assess genetic variability in potato breeding (Hajam *et al.,* 2018). High PCV in present study suggested that trait was under the influence of environmental factors rather than genetic factors and vice versa (Demelie & Aragaw, 2016; Rahajeng & Rahayuningsih, 2016). Differences between PCV and GCV for studied traits showed that these traits are substantially influenced by the growing environments (Tessema *et al.,* 2022). High heritability for number of marketable/large tubers in the present study was also proposed by Benavides *et al.,* (2017), Rahman (2015) and Ortiz *et al.,* (2021). Meanwhile, high heritability, genetic advance and genetic variability for tuber size i.e. below and above 40 mm were also highlighted in the study conducted by Seid *et al.,* (2020) and Subedi *et al.,* (2021). The presence of additive gene action can significantly contribute to different aspects of plant breeding i.e. high heritability, genetic advance, genotypic and phenotypic coefficient of variations, with high genetic potential, also proposed by Zeleke *et al.,* (2021) and Mishra *et al.,* (2017).

The presence of high genetic variability among the evaluated potato genotypes in the present study identified and presented breeding lines that could used, effectively, as parental materials in future potato breeding for further improvement and advancement based on yield and yield-attributing traits. The potato genotypes G12, G18, G17, G23 and G25 excelled in their mean performance. However, G23 and G17 was identified and selected as promising hybrids based on superior mean performance and high-yielding attributes in multiple environments whereas Battakundi was identified as an idyllic environment for potato cultivation, and for future breeding strategies. Adapted, stable and superior genotypes with broad genetic diversity and consistent production can be identified by genotype × environment interaction while testing in wide ranges of environment during any breeding program both locally, and globally (Ortiz *et al.,* 2023). Therefore high values of heritability, genetic advance, phenotypic and genotypic variation for studied characters confirmed the presence of genetic variations in potato genotypes under evaluated environments which provide an ideal opportunity for promotion, development and improvement of potatohybrids (Chaurasia *et al.,* 2012), and for selection of specific environment in future. Positive association between numbers of large (marketable) tubers plot^{-1} with all other characters hadalso been determined by Luitel *et al.,* (2020) and Mallick *et al.,* (2021).

In Northern Pakistan, predominantly in areas like Battakundi, the high-altitude, mega-environment conditions, and favorable factors proposed several advantages for off-season potato production. These factors include cooler temperatures, reduced disease pressure, and optimal light conditions, which are not only crucial for growing high-quality seed potatoes production but also improve yield-attributing traits like tuber size with high quantity, which can contribute to food security. While efficient employment of these conditions can also meet local food needs with potential to support regional food requirements by producing true-to-type and disease-free seed potato which can enhance and promote local seed production, and enable surplus exports, worldwide. The present study showed significance with broad genetic diversity for genetic improvement in future breeding program. Genetic factors was found responsible for traits expression, ensuing in availability of substantial genetic potential among new released potato genotypes/hybrids in future breeding strategies under different environments. Selection of evaluated potato genotypes based on yield attributing traits could contribute towards improvement of potato yield, crop resilience, and could compete with adverse effects of climatic change to meet domestic food requirements and food security, globally. Therefore, enhanced focus and devotion in selection process by studying more agronomic and yield-attributing traits in future potato breeding strategies will not only impact livelihood of smallholder farmers, consequences of malnutrition, and shortage of food but also promote food security with sustainable agriculture practices, both in Pakistan, and worldwide.

Conclusions

Substantial amount of genetic variability, broad sense heritability and genetic advance confirmed the role of additive gene action, in shaping trait expression and genetic progress in breeding programs. Presence of genetic variability and positive correlation between different character is crucial for upcoming breeding strategies, and for selection of enviable and better-quality hybrids for their advancement, and further utilization. Results concluded that genotypes, G23 and G17 was selected as the most promising hybrids with potential for release as commercial potato hybrids. Battakundi is selected as an ideal environment for potato cultivation, high tuber production, and for continuing of potato breeding in future. By focusing genetic potential and selecting superior hybrids allows breeders to increase potato production, adapt to changing conditions, and address evolving needs of both growers and consumers. The present findings recommended that continuing the potato breeding efforts particularly through true potato seed (TPS) is beneficial to develop robust and high-yielding hybrids with desired agronomic and yield-attributing traits, well suited to high-altitude environments like Battakundi. By utilizing True Potato Seed (TPS) in Pakistan, farmers can potentially enhance potato yield, resilience, and quality meet products and can also reduce dependency on seed tuber, and production cost by improving genetic diversity and sustainable agriculture practices in challenging environments.

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References

Afuape, S.O., I.I.M. Nwankwo, R.A. Omodamiro, J.C. Njoku, C.L. Ogbonna and D.C. Uzuegbu. 2015. Targeted breeding for sweet potato-based Enterprises: variability, genotype-by- environment interaction, heritability and correlation studies of important sweet potato root processing quality traits. *Int. J. Plant Breed. Genet.,* 9(4): 206-217.

Ahmad, M., M. Iqbal, B.A. Khan, Z.U. Khan, K. Akbar, I. Ullah, M. Shahid and A. Rehman. 2017. Response to selection and decline in variability,heritabilty and genetic advance from F2 to F3generation of tomato (*Solanum lycopercicum*). *Int. J. Plant Res.*, 7(1): 1-4.

Anonymous. 2022-23. Pakistan Bureau of Statistics. http://www.pbs.gov.pk

Anonymous. 2023. FAOSTAT. *Food and Agriculture Organization of the United Nations FAOSTAT Database*; FAOSTAT: Rome, Italy, 2023.

Asnake, D., M. Alemayehu and S. Asredie. 2023. Growth and tuber yield responses of potato (*Solanum tuberosum* L.) varieties to seed tuber size in northwest highlands of Ethiopia. *Heliyon*., 9: 1-11. e14586.

Baafi, E., K. Ofori, E.T. Blay, V.E. Gracen, J.M. Aduening and E.E. Carey. 2016. Exploitation of genetic potential of sweet potato for end-user traits improvement. *Afr. Cr. Sci. J.*, 24(4): 377-387.

Benavides, M.A.G., L. Diaz, G. Burgos, T.Z. Felde and M. Bonierbale. 2017. Heritability for yield and glycoalkaloid content in potato breeding under warm environments. *Open Agri.,* 2: 561-570.

Bonierbale, W.M., W.R. Amoros, E. Salas and W.de Jong. 2020. Chapter 06: Potato Breeding. *Int. Pot. Cent. Lima, Peru*., pp: 163-217.

Briitannica, T. 2023. Editors of Encyclopaedi. potato. Encyclopedia Britannica.

Cabello, R., D. Cevallos, I. De Souza, R. Gutierrez, E. Farfa, F. Lozano, R. Eyzaguirre, A. Khan, R. Schafleitner and Bonierbale, M. 2020. Procedures for standard evaluation and data management of advanced potato clones. Practical guide to assessing potato clones for drought tolerance under field conditions. International cooperators guide. *Int. Pot. Cent. Lima, Peru.*, pp. 1-42.

Chaurasia, A.K., P.K. Rai and A. Kumar. 2012. Estimation of genetic variability, heritability and genetic advance in aromatic fine grain rice. *Rom. J. Biol.,* 57(2): 99-104.

Dalamu, J., S. Sharma, V. Kumar, S.K. Sharma, A.K. Luthra and V.K. Dua. 2019. Mineral content of red skinned potatoes of Eastern India. *J. Hort. Sci.*, 14(1): 79-82.

Demelie, D. and A. Aragaw. 2016. Genetic variability of sweet potato on yield and yield related traits at were Agricultural Research Center Ethiopia. *Elect. J. Plant Breed.,* 362-370.

Dewi, R., S.D. Utomo, M. Kamal, P.B. Timotiwu and S. Nurdjanah. 2019. Genetic and phenotypic diversity, heritability, and correlation between the quantitative characters on 30 sweet potato germplasms in Lampung, Indonesia. *Biodiversity*, 20(2): 380-386.

Ebrahim, S., M. Wasu and A. Tesfaye. 2018. Genetic variability in potato (*Solanum tuberosum* L.) genotypes for tuber quality, yield and yield related traits at Holetta, Central Highlands of Ethiopia. (MSc. Thesis, Haramaya University).

Ene, C.O., P.E. Ogbonna, C.U. Agbo and U.P. Chukwudi. 2016. Studies of phenotypic and genotypic variation in sixteen cucumber genotypes. *Chilean J. Agri. Res*.,76(30): 307-313.

Fikadu, A., Y. Petros and H. Zelleke. 2013. Genetic variability and association between agronomic characters in some potato (*Solanum tuberosum* L.) genotypes in SNNPRS, Ethiopia. *Int. J. Biodiv. Conserv.,* 5(8): 523-528.

Hafiz, M. 2015. Participatory variety selection and variability of potato (*Solanum tuberosum* L.) varieties at Jimma Zonne, Southwest Ethopia. M. Sc Thesis. School of Graduate Studies, Jimma University College of Agriculture and Veterinary Medicine

Hajam, M.A., T.A. Bhat, A.M. Rather, S.H. Khan, L. Reyaz, M.A. Shah and S. Paul. 2018. Genetic variability, heritability and genetic advance for various qualitative characters of potato. *Int. J. Crop Sci.,* 6(6): 518-522.

https://www.britannica.com/plant/potato

Khan, B.A., S.F. Mehboob, M. Ahmad, M. Iqbal, I. Ullah, M. Saleem, A. Rehman and M. Shaid. 2017. Genetic analysis of F2 population of tomato for studying quantitative traits in the cross between Coldera x KHT5. *Int. J. Plant Res.*, 7(4): 90-93.

Khayatnezhad, M.R., B.R. Shahriari, R.G. Gholamin, S. Jamaati-e-Somarin and R. Zabihi-e-Mahmoodabad. 2011. Correlation and path analysis between yield and yield components in potato (*Solanum tubersum* L.). *J. Sci. Res.,* 7: 17-21.

Luitel, B.P., B.B. Bhandari1 and B. Thapa. 2020. Evaluation of potato genotypes for plant and yield characters in field at Dailekh. *Nepal J. Sci. Tech.*, 19(2): 16-24.

Majeed, A., Z. Muhammad, Z. Ullah, R. Ullah and H. Ahmad. 2017a. Late blight of potato (*Phytophthora infestans*): Fungicides application and associated challenges. *Turk. J. Agric. Food Sci. Tech.,* 5(3): 261-266.

Mallick, S.R., A.K.M. Quamruzzaman, Md. A. Hossain, M.M. Rahman, Md.A. Hoque and Md.R. Islam. 2021. Diversity of potato varieties in Bangladesh. *Europ. J. Agri. and Food Sci.,* 3(3): 55-61.

Melo, D.S., C.A.B.P. Pinto, L.S. Peixouto, D.G. Neder and J.C. Assis. 2011. Early selection of full-sib potato families. *Ciencia e Agrot, Lav.*, 35(6):1101-1109.

Mishra, S., J. Singh and P.K. Sharma. 2017. Studies on parameters of genetic variability for yield and its attributing traits in potato (*Solanum tuberosum* L.). *Biosci. Biotech. Res. Asia.,* 14: 489-495.

Namugga, P., J. Sibiya, R. Melis and A. Barekye. 2020. Combining ability analysis of yield and resistance to late blight disease caused by *Phytophthora infestans* in Uganda.*Aust. J. Crop Sci.,* 14(10): 1637-1644.

Ney, V.G., L.R. Terres, G.O. Silva and A.S. Pereira. 2016. Expected response to early-generation selection for yield and tuber appearance traits in potatoes. *Agron.,* 37(5): 2849-2858.

Ortiz, R., F. Reslow, J. Crossa and J. Cuevas. 2021. Heritable variation, genetic and phenotypic correlations for tuber traits and host plant resistance to late blight for potato breeding in Scandinavian testing sites. *Agric.,* 11(1287): 1-10.

Ortiz, R., F. Reslow, J. Huicho, R. Vetukuri and J. Crossa. 2023. Optimizing multi environment testing inpotato breeding: Using heritability estimates to determine number of replications, sites, and years for field trial. *Euphyata*, 219: 48.

Ozturk, G. and Z. Yildrim. 2014. Heritability estimates of some quantitative traits in potatoes. *Turk. J. Field Crops*, 19(2): 262-267.

Rahajeng, W. and S.A. Rahayuningsih. 2016. Potensi genetik klon-klon ubijalar berdasarkan karakter agronomi. Prosiding seminar Nasional Hasil Penelitian Tanaman Aneka Kacang Dan Umbi Tahun. pp. 588-595.

Rahman, M. 2015. Character association and genetic diversity of potato (*Solanum tuberosum* L.). Department of genetics and plant breeding Sher-E-Bangla Agricultural University Dhaka -1207, (MSc. Thesis), Bangladesh.

Seid, E., W. Mohammed and T. Abebe. 2020. Genetic variability, heritability and genetic advance in potato (*Solanum tuberosum* L.) for processing quality, yield and yield related traits. *Int. J. Plant Breed Crop Sci.*, 7: 928-936.

Subedi, S., N. Tripathi, S. Neupane and P. Bastakoti. 2021. Enhancing genetic gain in potato clones through phenotyping late blight resistance. *Indo. J. Agric. Res.*, 04(02): 105-117.

Tessema, G.L., A.W. Mohammed and D.T. Abebe. 2022. Genetic variability studies for tuber yield and yield attributes in Ethiopian released potato (*Solanum tuberosum* L.) varieties. *Peer J.*, 10: e12860.

Zeleke, A.A., T.D. Abebe and B.B. Getahun. 2021. Estimation of genetic variability, heritability and genetic advance in potato (*Solanum tuberosum* L.) genotypes for tuber yield and yield related traits. *Turk. J. Agric. Food Sci. Tech.,* 9(12): 2124-2130.

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