Assessment of Genetic Variability, Heritability and Genetic Advance for vegetative, yield and yield component traits in tomato (*Solanum lycopersicum* L.) in Burkina Faso

.

ABSTRACT

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| In Burkina Faso, tomatoes have a significant portion in vegetable production and play a major socio-economic impact within rural populations. To meet the increased demand for fresh tomatoes, the development of improved tomato varieties is one of the important strategies for which studies on variability and association studies are essential to carry out selection within the population to improve different traits. To understand the genetic variability, heritability, and genetic advance in tomato, a study was conducted at Farako-Bâ research station from April 2023 to March 2024. Thirty (30) hybrids and their six (06) parents, were evaluated in a completely randomized design with one plant as experimental unit repeated 10 times. Plant height (PH, cm), principal stem diameter (PSD, mm), number of primary ramification (RAM), days to first flowering (DFLO) and fruit maturity (DMAT), total number of fruits per plant (TNFP), fruit yield per plant (YIELD, g), as well as equatorial fruit diameter (EFD, mm) and individual fruit weight (IFW, g) were recorded. The results showed that for all traits, PCV was slightly higher than GCV, indicating that variations are slightly influenced by the environment. TNFP and IFW recorded high PCV and GCV, with high genetic gain as per mean (GAM), indicating the presence of significant variability and the effect of additive genes action. Simple selection based on the observation of the phenotype allows for the improvement of these traits. Vegetative and cycles parameters showed moderate to low PCV and GCV with moderate to low GAM. Improving these parameters requires to enhance the genetic base of the population, following by recurrent selection. Heritability was high for all traits and coupled with high GAM for fruit yield and its components; moderate / low for vegetative and cycle parameters. Thus, yield and its components are less influenced by the environment, hence the effectiveness of direct selection, while vegetative and cycle parameters are under non-additive genes action. Exploiting heterosis, dominance and epistasis effects, and single plant selected would be a necessity to improve these parameters. PSD and TNFP would be the major component of yield given their strong positive correlation, while earliness would be in detriment of yield. These results would be of great helpful for the selection of high-performing genotypes in this population derived from the diallel. |

*Keywords: PCV, GCV, Heritability, Genetic Advance, Tomato, Burkina Faso.*

1. INTRODUCTION

Tomato (*Solanum lycopersicum* L., 1753.), as well as the other species of the Lycopersicon genus, is diploid. Its karyotype is 2n = 24 chromosomes with a genome size of 950 MB, composed of 77% heterochromatin and 23% euchromatin (Peterson *et al.,* 1996). Tomato is one of the most important vegetable crops that belong to the solanaceae family including the economically important crops such as, potato, eggplant, pepper. It is an annual to perennial prostrate self-pollinated crop in general, however, it is possible to create genetic variability through hybridization.

In Burkina Faso, tomatoes play an important role in vegetables production both in terms of areas devoted and quantity produced (MAAH, 2017; MAAHA, 2020). To meet the increased demand for fresh tomato, the development of improved tomato varieties is a good option to increase productivity (Gallais, 2025). It well knows that success in plant breeding depends on the availability of genetic variability either naturally realized in the population or created by plant breeders. Analyzing variability among traits is critical for the development and chosen of a successful breeding strategy (Roka *et al.,* 2024). For a given trait, the higher the variation presents the greater the scope for its improvement. To better understand the extent of variation and its potential for genetic improvement, the estimate of phenotypic and genotypic coefficient of variation (PCV, GCV), heritability (h²) and genetic advance (GA) appear useful. PCV measures the variation in traits that can be observed in a population, taking into account both genetic and environmental factors, while GCV measures the variation in traits due to genetic differences among individuals, excluding environmental effects (Roka *et al.,* 2024). In the assessment and selection of quantitative traits, high PCV can help to identify traits with high variability. These characters may be more influenced by environmental factors, requiring stable conditions when breeding or fixed stables varieties at different environments. Thus, a high value of GCV for a trait indicates a high potential for genetic improvement through selection, given that the variation is mainly of genetic origin. So, genetic variability along with heritability should be considered for assessing the maximum and accurate effect of selection as suggested by Burton, (1952).

The GA estimates the expected improvement in a trait from one generation of selection, assuming selection intensity and heritability are known. It’s providing an estimate of the potential gain from selection for a specific trait. Higher value of GA indicates greater efficiency in breeding programs, as more substantial improvements can be expected in subsequent generations. As a further benefit, GA values can be used to compare and prioritize traits during selection (Johnson *et al.,* 1955; Jilo *et al.,* 2018).

Heritability is the measures of the proportion of the total variation in a trait that is attributable to genetic factors as opposed to environmental ones. Understanding heritability helps breeders to predict the response to selection and design effective breeding programs. However, alone, heritability estimation is not enough to make efficient selection in segregating generation and needs to be associated to a substantial amount of genetic advance (Johnson *et al.,* 1955; Jilo *et al.,* 2018; Jajar *et al.,* 2023; Roka *et al.,* 2024).

The correlation coefficient measures the extent and direction to which two variables are associated and related (Baye *et al.,* 2020). In plant breeding, the correlation coefficient is a statistical measure that quantifies the degree of relationship between two variables. His intensity, indicated as 'r,' is range from -1 to +1 and is independent of the unit of character measured (Ullah, 2025). The magnitude of correlation coefficient is often used to understand the relationship between different parameters, such as growth parameters, yield and its component, or disease resistance, etc. Pleiotropy can create correlations between traits, and the coefficient of correlation provides a way to measure and understand these relationships. Eventually, path coefficient analysis is an effective tool to aids correlation studies (Islam *et al.,* 1991; Mc Giffen *et al.,* 1994). This information is crucial in plant breeding for making effective selections and achieving desired outcomes. The knowledge of association among character plays an important role in plant breeding by showing how changes in one character will bring simultaneous changes in the expression of another one. It also helps to select genotypes simultaneously when multiple traits of interest are desired. (Roka, 2024). As well as yield is dependent on many components, it would be desirable to consider the relative magnitude of various characters (Meitei *et al.,* 2014; Namdev & Dongre, 2018, Ullah, 2025). So, correlation studies can aid to schematize an efficient breeding program for improving the yield potential via its components (Frageria *et al.,* 1997, Ullah, 2025).

The core objective of the present study was to estimate the phenotypic (PCV) and genotypic (GCV) coefficients of variation, genetic advance (GA), and genetic advance as a percentage of the mean (GAM), as well as to establish the relationships between different studied characters in order to discuss genetic variability, the effects of genic action, identify the major components of fruit yield, and determine the best methods for improvement.

2. material and methods

 **2.1. Plant material**

Six (06) variety lines were used as parents: P1 = FBT1; P 2 = FTB2; P 3 = FBT3; P 4 = Buffalo; P 5 = CLN 2366 A; and P 6 = USDA 97L66. P1, P2, and P3, are improved varieties developed and released by INERA. They are suitable for production in hot and humid seasons (Rouamba *et al.,* 2013). Variety (P4) ''Buffalo'', is one of the most common commercial tomato varieties in Burkina Faso due to its high yield, deep red color, and oblong fruit shape. Parents P5 and P6 were collected from World vegetable Center and U.S. Department of Agriculture, respectively. These varieties are particularly rich in beta-carotene (Stommel, 2001). These six varietal lines are crossed in a full diallel crossing design to obtain thirty (30) hybrids. Table 1 shown the list of hybrids and their parents used in evaluation trial

Table 1: Plant materials list

|  |  |  |
| --- | --- | --- |
| N° | Crossed name | Source |
| 1 | FBT1 X FBT2 | Farako-Bâ |
| 2 | FBT1 X FBT3 | Farako-Bâ |
| 3 | FBT1 X BUFFALO | Farako-Bâ |
| 4 | FBT1 X CLN2366 A | Farako-Bâ |
| 5 | FBT1 X L66 | Farako-Bâ |
| 6 | FBT2 X FBT1 | Farako-Bâ |
| 7 | FBT2 X FBT3 | Farako-Bâ |
| 8 | FBT2 X BUFFALO | Farako-Bâ |
| 9 | FBT2 X CLN2366 A | Farako-Bâ |
| 10 | FBT2 X L66 | Farako-Bâ |
| 11 | FBT3 X FBT1 | Farako-Bâ |
| 12 | FBT3 X FBT2 | Farako-Bâ |
| 13 | FBT3 X BUFFALO | Farako-Bâ |
| 14 | FBT3 X CLN2366 A | Farako-Bâ |
| 15 | FBT3 X L66 | Farako-Bâ |
| 16 | BUFFALO X FBT1 | Farako-Bâ |
| 17 | BUFFAO X FBT2 | Farako-Bâ |
| 18 | BUFFALO X FBT3 | Farako-Bâ |
| 19 | BUFFALO X CLN2366 A | Farako-Bâ |
| 20 | BUFFALO X L66 | Farako-Bâ |
| 21 | CLN2366 A X FBT1 | Farako-Bâ |
| 22 | CLN2366 A X FBT2 | Farako-Bâ |
| 23 | CLN2366 A x FBT3 | Farako-Bâ |
| 24 | CLN2366A X BUFFALO | Farako-Bâ |
| 25 | CLN2366 A X L66 | Farako-Bâ |
| 26 | L66 X FBT1 | Farako-Bâ |
| 27 | L66 X FBT2 | Farako-Bâ |
| 28 | L66 X FBT3 | Farako-Bâ |
| 29 | L66 X BUFFALO | Farako-Bâ |
| 30 | L66 X CLN2366 A | Farako-Bâ |
| 31 | FBT1 | Farako-Bâ |
| 32 | FBT2 | Farako-Bâ |
| 33 | FBT3 | Farako-Bâ |
| 34 | BUFFALO | Commercial variety, Techmisem |
| 35 | CLN2366 A | Worldveg, Taïwan |
| 36 | USDA, 97L66 | USDA, Research Service, Vegetable Laboratory. |

 **2.2. Methods**

*Experimental site:* The experimentation is carried out at Farako-Bâ research station. This station is located in the western part of Burkina Faso, between isohyets 800 and 1200 mm, at 405 m of altitude, 4°20'W of longitude and 11°06'N of latitude. Soils are lexisols with low clay and organic matter content, with a notable deficiency in nitrogen and phosphorus (Bado, 2002). Climate is South Sudanian type. Table 2 show the characteristic of soil and compost used to prepare planting substrate.

Table 2: Characteristics of soil and compost mixed and used as substrate in this study

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | pH water | OC(g.kg-1) | Total-N (g.kg-1) | C/N | Total-P (mg.kg-1) | P-available(mg. kg-1) | Total -K (g.kg-1) | K-available(mg.kg-1) |
| Soil  | 5.34 | 3.29 | 0.31 | 10.7 | 92.24 | 4.35 | 0.01 | 73.01 |
| Compost | 7.67 | 242 | 15.7 | 15.42 | 10884 | - | 7.22 | - |

*Legend: OC: organic carbon, OM: organic magnesium, N: Nitrogen, P: Phosphorus, K: Potassium*

*Experimental design and cultural practice*: The seeds of each genotype (Six parents and 30 hybrids) were sown during 2023 and conducted according to Rouamba et al. (2013), recommendation nursing. Transplantation was done on 27th November 2023 in the completely randomization design (CRD) with vigorous plants. Each plant is planted in a pot of 16 liters filled with sterile potting soil composed to 2/3 soil and 1/3 compost. The characteristics of soil and compost used is given in table 2. The experimental unit consisted of one plant per genotypes replicated ten (10) times. Transplanting was done in the afternoon, in order to limit heat stress to plants and promote their good and fast recovery. Mineral fertilization consisted of 300 kg/ha NPKB (14-23-14-6) applied two times at 150 kg/ha two weeks after transplanting and at blooming. At the second application, 50 kg / ha of urea 46% is mixed to NPKB. For plant protection, Mancozeb 80 WG at 2 kg/ha against fungi and Lambda-cyhalothrin + Acetamiprid 215 EC, at 1 L/ha was applied to control caterpillars, aphids and white flies. Manual weeding and plant tutoring were conducted on demand throughout the experiment time.

*Data collection*: Data were recorded on three parameters groups. The first one is vegetative parameters, as plant height (PH, cm); principal stem diameter (PSD, mm) and number of primary ramification (RAM). The second group is cycle parameter, represented by the days to first flowering and maturity (DFLO and DMAT) expressed at number of days after transplanting. The third group is yield and its components viz., as total number of fruits per plant (TNFP), fruit yield per plant (Yield, g), equatorial fruit diameter (EFD, mm) and individual fruit weight (IFW, g). All data are collected according to “descriptors for tomato” actual Bioversity International (IPGRI, 1996).

*Data analysis*: Data was obtained from individual plants and genetics parameters were calculated in Excel according to the following formula:

The values of genotypic (Vg=σ²g) and phenotypic (Vp=σ²p) variance were calculated, using the following formula as suggested by Wricke and Weber, 1986.

$σ²g=\frac{MSG-MSE}{r}$ $σ²p=\frac{MSG}{r}$ $σ²e=\frac{MSE}{r}$ where:

MSG: Genotypic mean sum of square, MSE: Error mean sum of square, r number of replication

Broad sense heritability: $h^{2}=\frac{σ^{2}g}{σ^{2}p}$ (Allard 1999)

Expected Genetic Advance (GA) and Genetic Advance per cent of mean (GAM) was calculated by using the formula of Shukla et al. (2006).

Genetic advance $GA=k x h²x σp$ Genetic advance as per cent of mean: $GAM=\frac{GA}{x̄}$

Where: k: constant (2.06) standardized selection differential; h²: broad sense heritability; σp: phenotypic standard deviation

Phenotypic (PCV) and genotypic (GCV) coefficients of variation were calculated by using the following formula suggested by Singh and Chaudhary (1985).

$PCV=\left(\frac{σp}{\bar{x}}\right)x100$ $GCV=\left(\frac{σg}{\bar{x}}\right)x100$ where σp, σg: phenotypic, genotypic standard deviation; x̄: mean of the respective traits.

Pearson correlation matrix at 5% threshold, between trait is also establish using XLSTAT 2016.02.27444 software.

3. results and discussion

3.1. Genetic variability

The phenotypic coefficient of variation (PCV) was greater than their respective genotypic coefficient of variation (GCV) for all traits under study (Table 3, Fig. 1), which indicated that the apparent variation is not only due to genotype, but also due to the influence of environment. Therefore, selection for such traits sometimes might be misleading (Saleem *et al.,* 2013). The same observation is true for phenotypic and genotypic variance.

According to the categorization proposed by Sivasubramanian and Madhavamenon (1973) on the value of estimate variability, phenotypic coefficient of variation (PCV) was high for total number of fruits harvested (23.23%) following by individual mean fruit weight (22.16%). PCV for equatorial fruit diameter (14.62%), fruit yield per plant (13.95%) and plant height (10.12%) are classified moderate and the lowest value of PCV are registered on principal steam diameter (5.62%), number of primary ramification (8.05%), day to first maturity (8.59%) and day to first flowering (9.66%). High genotypic coefficient of variation (GCV) value was found for total number of fruits harvested (21.69%) following by individual mean fruit weight (21.40%). Moderate value of GCV was recorded on equatorial fruit diameter (14.52%) and fruit yield per plant (12.49%). Principal steam diameter (4.92%), number of primary ramifications (6.49%), Day to first maturity (8.54%) and flowering and plant height (9.82%) (table 3, fig.1) showed low GCA.

The highest values of phenotypic (PCV) and genotypic (GCV) coefficients of variation for a character indicate significant variability, which suggests that improvement through simple selection is possible. However, moderate/low values of PCV and GCV indicate low/moderate genetic variability. Shankar *et al.,* (2013) reported that to improve in this case, it is necessary first to broaden the genetic base of the starting population either by incorporating other genotypes or through interspecific crossings and then self-fertilizing the descendants up to the F2 generation, followed by recurrent selection to increase gene flow and fix favorable alleles.

In our study, parameters with high value of PCV and GCV are yield and its component as individual fruit weight; and total number of fruits harvested. These results are in accordance with those of Shankar et al. (2013), Meena et al. (2018), Sushma *et al.,* (2020), Meena *et al.,* (2023) and Dwary *et al.,* (2023). However, these authors also found in their studies a low/moderate value of genetic variability for cycle parameters. PCV and GCV value for yield and its component for these authors are less than our finding, mean that our material is more variable for these traits. Mahurtale *et al.,* (2023) and Narolia *et al.,* (2012) observed very high value of PCV and GCV for number of fruits per plant (142.69 and 142.54 % for the first authors; 130.62 and 130.06% for the second) and average fruit weight (75.29 and 74.82% for the first author’s; 105.74 and 105.22% for the second). Dwary *et al.,* (2023), also observed high value of PCV and GCV for number of primary branches/plant (23.21 and 20.08%); plant height (30.69 and 30.63%); fruit yield expressed in kg/plant (40.79 and 39.95%); fruit yield expressed in kg/plot (40.69 and 40.04%) and average fruit weight (32.35 and 32.13%). Meaning that their material is highly variable for these yield components

The slightly higher of PCV than their respective GCV, denoting that environment factors have a little influence one the expression of these characters to some degree or other. This little higher difference (< 1) between PCV and GCV values for DMAT, EFD and DFLO, mean that these traits were less influenced by environment hence, they could be improved using phenotypic selection like directional, disruptive and stabilized selection as reported by Dwary *et al.,* (2023), Shankar et al. (2013) and Narolia et al. (2012).

3.2. Heritability and Genetic Advance

The estimation of broad sense heritability value and genetic gain are given in table 3. According to classification made by Johnson et al. (1955), heritability in this study is high for all the characters and ranges from 0.65 to 0.99 (table 3, Fig. 2). The highest heritability (> 90%) was recorded for day to first maturity (0.99), equatorial fruit diameter (0.99), day to first flowering (0.97), plant height (0.94) and individual fruit weight (0.93). Total number of fruits per plant and yield per plant showed 0.87 and 0.80 respectively. The lowest value observed was 0.65 for number of primary ramifications. In tomato, high heritability is generally found for number of fruits per plant; individual fruit weight; individual fruit diameter; total fruit weight harvested Theses finding are in accordance with Shankar et al. (2013), Islam *et al.,* (2022), Rasheed *et al.,* (2023).

Estimating heritability is a key step in genetics and breeding programs because it indicates how much of the observed variation in a trait is due to genetic factors, rather than the environment. Understanding heritability helps breeders decide whether selection will be effective and which breeding method to use. The estimation of heritability permits to predict response to selection; to choose effective breeding strategies to estimate genetic advance and to understand trait stability. In the case of highest value of heritability (> 60%), traits of interest exhibit additive gene action suggested the greater effectiveness of selection due to the less influence of environment and improvement to be expected for these parameters in future breeding program. These traits can be improved by simple selection by observation of the performance of offspring. Similar results were also reported by Shankar *et al.,* (2013), Sushma *et al.,* (2020), Meena *et al.,* (2023) and Dwary *et al.,* (2023). Moderate heritability suggest that phenotype is equally due to the influence of genotype and environment. Selecting based on the performance of progenies could be done but need more generation. In case of low heritability, (<20%), traits of interests exhibit dominant and epistasic (non-additive) gene action. Influence of environmental factors is strong for their expression and genotype selection based on these characters may be postponed to the later generations (Savaranan *et al.,* 2019). Indirect selection; recurrent selection; exploiting heterosis; development of synthetic variety or backcross breeding are more efficient methods to select characters with low heritability.

Expected genetic advance (GA) is range from 0.73 for the number of primary ramifications to 366.65 g/plant for fruit yield per plant. The lowest GA values are recorded from vegetative and cycles parameters respectively 0.73 for RAM; 1.06 mm for PSD, 4.89 DAT for DFLO and 6.80 DAT for DMAT. The medium value is recorded from plant height (12.61 cm) and fruits calibrations (11.70 mm for EFD and 16.74g for IFW). The highest values of GA are for TNFP (25.66 fruits per plant) and fruit yield per plant 366.65 g.

Genetic advance as per cent of mean (GAM) is ranges from 8.85 to 42.55% (table 3, Fig. 2). The highest value is recorded from yields and its component with successively 42.55% for IFW, 41.73% for TNFP, 29.69% for EFD and 23.05% for fruit yield per plant. These values of GAM are classified to be high. Moderate values were found in vegetative and cycles parameters with 19.62% for plant height (PH), 19.26% for day to first flowering (DFLO) 17.49% for day to first maturity (DMAT) and 10.78% for the number of primary ramification (RAM). The lowest value of GAM is 8.85%, recorded from principal stem diameter (PSD) (Johnson *et al.,* 1955).

The expected genetic advance (GA) indicates the actual expected gain for a parameter. Coupled with high value of mean, it was a good tool for selecting trait in a breeding program (Pooja *et al.,* 2022). In Burkina Faso, the recommended cultural practice in tomato production in field transplant at 0.8 m x 0.5 m planting spacing which correspond to 25,000 plants per ha (Rouamba *et al.,* 2013). The expected genetic gain in fruit yield per plant of 366.65 g in this study would correspond to an increase in fruit yield of more than 9 t/ha, which represent more than 50% of actual fruit yield product per ha (MAAHA, 2020). According to Johnson *et al.,* (1955), high heritability coupled with high genetic advance as per cent of mean (GAM) were more useful than heritability alone in the prediction of the resultant effect during selection of best individual genotype (Eppakayala *et al.,* 2021). It also indicates the presence of additive gene effects (Tena *et al.,* 2022) which may be utilized for improvement through phenotypic selection for trait of interest (Roka *et al.,* 2024). Moreover, Wanga *et al.,* 2021 suggested that the selection at an early segregating generation will be advantageous for selecting superior varieties. This is the case of fruit yield and its principal components like total number of fruits per plant (TNFP), individual fruit weight (IFW) and equatorial fruit diameter (EFD). Thus, simple selection based on the phenotypic performance of these traits would be more effective (Shankar *et al.,* 2013; Meitei *et al.,* 2014). In our study, GAM for fruit yield and its components are classified high as the finding of Meitei *et al.,* (2014); Rasheed *et al.,* (2023) and Dwary *et al.,* (2023).

High heritability and low or moderate genetic advance as per mean (GAM) indicates the presence of non-additive gene action and considerable influence of environment in the expression of these characters as reported by Nadaranjan *et al.,* (2005); Shankar *et al.,* (2013) Soliman et al., (2023) and Roka *et al.,* (2024). These traits could be exploited trough manifestation of dominance and epistatic components through hybridization or heterosis breeding (Adhikari et al., 2018), however, using direct selection methods to improve these characters would be unproductive and should be avoid (Bartaula et al., 2019). This is the case for the vegetative and cycles parameters in our study in consonance with Mitra *et al.,* (2024) who observed for days to 50% flowering high heritability (h²=76.54%) and moderate GAM (15.25%). Al-Aysh et al. (2012), found that high heritability coupled with low genetic advance for days to maturity (h²= 78.08% and GAM = 5.04%) indicate that our material is easier to improve for earliness.

In the extreme case of both low value of heritability and genetic advance as per mean, further crossing is obligatory to create desired variations (Behera *et al.,* 2020). This case is not found in our study.

Table 3: Estimation of variability, heritability and genetic advance for different characters studies.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Characters | Range | Mean ± Sem | *Vp* | *Vg* | *Ve* | *Hb (%)* | *PCV (%)* | *GCV (%)* | *GA* | *GAM (%)* |
| PH (cm) | 54.00-76.60 | 64.29 ± 8.05 | 39.83 | 42.33 | 2.50 | 0.94 | 10.12 | 9.82 | 12.61 | 19.62 |
| PSD (mm) | 10.81-13.02 | 11.97 ± 1.19 | 0.35 | 0.45 | 0.11 | 0.76 | 5.62 | 4.92 | 1.06 | 8.85 |
| RAM (number) | 5.90-8.10 | 6.78 ± 1.12 | 0.19 | 0.30 | 0.10 | 0.65 | 8.05 | 6.49 | 0.73 | 10.78 |
| DFLO (DAT) | 21.42-31.20 | 25.42 ± 2.81 | 5.83 | 6.03 | 0.19 | 0.97 | 9.66 | 9.50 | 4.89 | 19.26 |
| DMAT (DAT) | 33.40-48.40 | 38.85 ± 3.67 | 11.00 | 11.13 | 0.12 | 0.99 | 8.59 | 8.54 | 6.80 | 17.49 |
| TNFP (number) | 32.80-88.80 | 61.48 ± 20.71 | 177.84 | 203.89 | 26.06 | 0.87 | 23.23 | 21.69 | 25.66 | 41.73 |
| Yield (g/plant) | 971.10-2064.40 | 1590.55 ± 367.36 | 39496.68 | 49243.53 | 9746.85 | 0.80 | 13.95 | 12.49 | 366.65 | 23.05 |
| EFD (mm) | 17.59-47.16 | 39.4 ± 6.08 | 32.71 | 33.19 | 0.48 | 0.99 | 14.62 | 14.52 | 11.70 | 29.69 |
| IFW (g) | 25.42-58.91 | 39.35 ± 11.24 | 70.88 | 76.05 | 5.17 | 0.93 | 22.16 | 21.40 | 16.74 | 42.55 |

Legend: Vp= Phenotypic variance; Vg = Genotypic Variance; Ve = Environmental variance; *H*b= Broad sense heritability; PCV= Phenotypic coefficient of variation; GCV = Genotypic coefficient of variation; GA = Genotypic advance. GAM = Genotypic advance as per cent of mean.

Table 4: Correlation between characters

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Variables | PH | PSD | RAM | DFLO | DMAT | TNFP | Yield | EFD | IFW |
| PH (cm) | **1** |   |   |  |  |   |   |   |   |
| PSD (mm) | -0.300 | **1** |  |  |  |  |  |  |  |
| RAM (number) | -0.055 | **0.395** | **1** |  |  |  |  |  |  |
| DFLO (DAT) | **0.369** | **-0.586** | -0.195 | **1** |  |  |  |  |  |
| DMAT (DAT) | **0.429** | **-0.539** | -0.279 | **0.772** | **1** |  |  |  |  |
| TNFP (number) | -0.064 | **0.388** | 0.301 | **-0.377** | **-0.372** | **1** |  |  |  |
| Yield (g/plant) | -0.076 | **0.538** | 0.139 | **-0.562** | **-0.400** | **0.719** | **1** |  |  |
| EFD (mm) | 0.079 | -0.105 | -0.304 | 0.196 | 0.317 | -0.087 | 0.099 | **1** |  |
| IFW (g) | 0.162 | -0.151 | **-0.433** | 0.022 | 0.112 | **-0.360** | 0.018 | **0.398** | **1** |



Figure 1: Genotypic and phenotypic coefficient of variation of nine (09) characters in tomato



Figure 2: Heritability estimates and genetic advance as per mean for nine characters in tomato

3.3. Relationship between characters

Pearson correlation matrix in breeding aims to identify and quantify the strength and direction of linear relationships between multiple quantitative traits. This can help breeders to understand how different traits are related to each other, which is crucial for selecting desirable characteristics to improve in the case of simultaneous multiple traits. Overall, the Pearson correlation matrix is a valuable tool for optimizing the selection and breeding process to achieve better and more predictable results in breeding programs. Positive correlation between two characters (r close to +1) signifies that these parameters are interdependent and selecting for one is also for the second one. One the other hand, two parameters negatively correlate (r close to -1) are antagonistically connected and the improvement to increase one of theme, automatically decrease the others (Ullah, 2025). This situation can be benefit for selecting parameters where least value is appreciable as precocity (Acquaah, 2012) and resistance/tolerance to pest and diseases (Yustiana *et al.,* 2013). Correlation analysis among the quantitative traits in this study is presented in table 4. Plant height is significant and positively correlated to cycles parameters (+0.369 and +0.429 for days to first flowering and maturity respectively), while stem diameter has shown significant correlation in negative direction (-0.586 and -0.539). Stem diameter is also shown significant and positive correlation to yield (+0.538) and total number of fruits per plant (+0.388). Cycles parameters as DFLO and DMAT are positively and significantly correlated each other’s (0.772). They show significant and antagonist correlation with yield components viz., total number of fruits per plant (-0.377, -0.372 for DFLO and DMAT respectively) and fruit yield per plant (-0.562, -0.400 for DFLO and DMAT respectively). On other hand, total number of fruits harvested shown a positive correlation with yield (+0.719) and negative correlation with individual fruit weight (-0.360). Individual fruit weight is significant and negatively correlated to RAM (-0.433) and positively correlate to equatorial fruit diameter. Similar results were found by Al-Aysh et al. (2012), Saleem et al. (2013), Tembe et al. (2018), Namdev et al. (2018) and Traore et al. (2019). These correlations indicate that fruits are small size when productivity (number of flower per inflorescence and /or fruits per plant) is high. It means that, the higher the fruit number per plant, the smaller the individual fruit weight (Emami and Eivazi, 2013; Meitei *et al.,* 2014; Ullah *et al.,* 2015; Rahaman *et al.,* 2015; Traore *et al.,* 2019; Ullah, 2025). In tomato, yield is a compromise within plant density, number of fruits per inflorescence and fruit weight (Ullah, 2025). In this study, the positive correlation was observed between yield and stem diameter (+0.538); yield and TNFP (+0.719) indicting that these two parameters are a major component to yield. It also suggested that selection based on these characters would result in better genotypes with higher yield (Meitei *et al.,* 2014). Indeed, thick stems are better equipped to transport necessary nutrients and water to leaves and fruit, resulting in improved overall growth and better production (Tounsi-Hammami, 2024). However, the negative correlation between yield and cycle parameters (-0.562 for DFLO and -0.400 DMAT) indicate that earliness was in detriment to yield as reported by Ullah et al. (2015); Ullah, (2025)

4. Conclusion

The obtained results from the present study have given some important future line work. The genotypes were studies for only few important parameters grouped as vegetative, cycles, yield and its major’s components. It would be very important to characterize this material for the essentials characters in the descriptor of tomato and related to DUS test. This may take count not only qualitative parameters but also biochemical and nutritional value parameters, after elimination of duplicates by use of DNA marker. For all the characters studied, the phenotypic coefficient of variation is slightly greater than the genotypic one. Yield and its direct components as total number of fruits per plant, equatorial fruits diameter and individual fruit weight are more variable based on the value of their PCV and GCV. These characters show greatest values of genetic advance (GA) and the value of genetic advance as per mean (GAM) classified as high, while vegetative and cycles parameters show moderate or low value of GAM. All characters in this study are highly heritable so, fruit yield per plant, total number of fruit par plant, equatorial fruit diameter and mean fruit weight are under additives genes actions. Therefore, they are easily improved by simple selection. However, the others parameters as vegetative and cycles need to be improved by exploiting heterosis, recurrent or indirect selection. Regarding Pearson correlation matrix, interesting correlation are highlighted and permit to choose the way of improvement for characters of interest. Thus, stem diameter, days to first flowering and total number of fruits harvested are the most parameter to improve in order to attend earliness genotypes with good productivity. These results of the genetic parameters would be of great helpful for the selection of high-performing genotypes outcoming to this population derived from the diallel.

Disclaimer (Artificial intelligence)

Author(s) hereby declares that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.) and text-to-image generators have been used during the writing or editing of this manuscript.

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Definitions, Acronyms, Abbreviations

*INERA : Institut de l’Environnement et de Recherches Agricoles*

*USDA: United States Department of Agriculture*