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# GENETIC CHARACTERISTICS OF $F_2$ POPULATIONS OBTAINED THROUGH DOUBLE AND THREE-WAY CROSSES IN CAYENNE PEPPERS

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## SUMMARY

The enhancement in cayenne pepper (*Capsicum frutescens* L.) productivity is intently needed due to the ever-increasing demand, considered a vital vegetable commodity with complete nutrition and high economic value in Indonesia. Conventional plant breeding is one of the strategies to produce superior cultivars with increased yield. Thus, the latest research aimed to identify genetic diversity and gene inheritance patterns for selecting high-yielding $F_2$ populations of cayenne pepper made through double and three-way crosses. The said research employed an augmented design combined with a randomized complete block design as an environmental design. The research factors consisted of non-repeating cayenne pepper (*Capsicum frutescens* L.) lines with a limited number of seeds originating from 10 parental populations. The resulting 100 and 52 $F_2$ individual populations, obtained from double and three-way crosses, respectively, were evaluated in comparison with four control cultivars, i.e., Bara, Dewata, Ungara, and Katokkon. The non-repeated rows, divided into five blocks, included the control cultivars planted repeatedly in each block. The results indicated that almost all traits have high genetic diversity and heritability and have potential use as selection criteria. The traits plant habitus (0.135), stem diameter (0.202), number of productive branches (0.359), and fruit weight (0.171) have a direct utmost influence on yield compared with other traits; thus, these promising traits can serve as selection criteria along with yield.

**Keywords:** Cayenne pepper (*Capsicum frutescens* L.), double and three-way crosses, growth traits, heritability, path analysis

**Key findings:** Lines selection in $F_2$ populations is most important in developing cultivars in crop plants, including cayenne pepper (*Capsicum frutescens* L.). The results revealed that the genetic traits of plant habitus, stem diameter, number of productive branches, and fruit weight directly impact yield compared with other traits; thus, these distinct traits can be effective selection criteria, along with yield.

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## INTRODUCTION

Cayenne pepper (*Capsicum frutescens* L.) is a horticultural crop with high economic value and complete nutrition (Campestrini *et al*., 2019). According to current crop data, in 2020, the national chili productivity was 8.40 t/ha with a total production of 1.51 million t, which

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increased by 9.76% compared with the production in 2019 (1.37 million t) (Ministry of Agriculture - Indonesia, 2022). In South Sulawesi Province, Indonesia, in 2020, the cayenne pepper productivity was only 4.59 t/ha with a total production of 240,500 t, with a continued decline since the last five years of an average decrease of 18.85% per year. Therefore, it is necessary to enhance productivity, improving the quality of cayenne pepper.

Forming a base population with enhanced genetic diversity and developing high-yielding cultivars through different plant breeding programs can increase chili productivity. The higher the genetic diversity, the more efficient the selection progress. The base population formation can be through hybridization, which aims to bring together the superior genes from various parental genotypes (Karlinaningsih *et al*., 2019). The concept of hybridization is often combined with cross-design to optimize the combined potential of different parent cultivars used (Muthoni and Hussein, 2020). Crosses between hybrid cultivars can form double- and three-way cross populations with the highest potential for diversity. A double cross is a cross between two $F_1$ hybrids (from a single cross) that has superior traits. In contrast, a three-way cross is a cross between a single cross hybrid and a pure line, with the three lines unrelated; thus, the obtained individual will be genetically more different and diverse in appearance (Effendi *et al*., 2018).

Mainly, the $F_2$ populations with the highest heterozygosity and diversity showed more suitability for selecting promising lines than advanced generations (Maryono *et al*., 2019). Genetic variation in plant populations can be due to domestication, segregation, germplasm collection, plant introduction, hybridization, mutation, polyploidy, somaclonal variation, and genetic engineering (Abrham, 2019). Genetic information is essential for more efficient and effective plant selection.

Heritability and gene action are two principal genetic parameters, and their knowledge plays a vital role in the selection process (Priyanto *et al*., 2018). An increase in the predictive heritability value can result from a decrease in environmental variance or a significant increase in genetic variance. The heritability information allows the breeders to determine the extent to which the intense selection transpires to separate the environmental influences from the phenotype of the *Capsicum annuum* plants (Yudilastari *et al*., 2018). Combining heritability and gene action becomes crucial in determining the selection concept that the distribution becomes effective and directed (Anshori *et al*., 2018).

The correlation of agronomic traits with yield and even the correlation between each other and environmental influences on the expression of various features was significant in choosing a selection strategy (Chatterjee *et al*., 2018; Roy *et al*., 2019). Path analysis helps determine which attributes have more potential and are better used as benchmark traits in selection assessments (Amas *et al*., 2021). Path analysis also aids the breeders in developing appropriate strategies for selecting superior genotypes from various populations, such as chilies (Rohini and Lakshmanan, 2015), maize (Amas *et al*., 2021), and tomatoes (Fadhilah *et al*., 2022). Consequently, it is necessary to estimate genetic parameters, especially in $F_2$ populations of double and three-way crosses, to increase productivity as a step in selecting superior genotypes of cayenne pepper. Therefore, the presented research aimed to identify genetic diversity and gene inheritance patterns for selection in $F_2$ populations obtained through double and three-way crosses in cayenne peppers.

## MATERIALS AND METHODS

### Breeding material and procedure

The presented research ensued from May to September 2022 at the Experimental Farm of the Faculty of Agriculture, Hasanuddin University, Makassar City, South Sulawesi Province, Indonesia (5°7′40″ S, 119°28′59″ E). The research arrangement was in an augmented design combined with a randomized complete block design as its environmental scheme. Augmented design is well suited to populations with a limited number of seeds. The research factors consisted of non-repeating lines with a limited number of seeds originating from 10 parental populations of cayenne pepper (*Capsicum frutescens* L.). The resulting 100 and 52 $F_2$ individual populations obtained from double and three-way crosses, respectively, proceeded the comparison with four control (parental) cultivars, i.e., Bara (B), Dewata (D), Ungara (U), and Katokkon (K). The non-repeated rows had blocks divided into five, with the control cultivars planted repeatedly in each block. Therefore, each plant in these populations becomes an identical line as different from other lines.

Sowing of cayenne pepper ensued inside the greenhouse for easier management of the seeds, using soil, compost, and roasted husks, with a ratio of 1:1:1. Cayenne pepper seeds sown in seeding trays have previously germinated. Then, transfer of seedlings into polybags followed 14 days after sowing (DAS) applying AB mix solution at a dose of 5 ml $L^{-1}$. After three weeks of transplantation (WAT), seedlings planted on soil beds have a size of 9 m × 1 m with a spacing of 50 cm between the beds. The beds got covered with black silver mulch, with 10 cm diameter holes for planting with the chili seeds. The spacing was 50 cm × 60 cm, carrying 33 plants per bed. Spacing affects humidity level and nutrient absorption around the plant, the occurrence of pathogens, and sunlight reception intensity. A stake supported each chili plant for the plant not to break and collapse.

Plant maintenance comprises several activities, including watering in the morning and evening until the soil moistens. Replanting replaced plants that withered with abnormal growth and pests, and disease infestation at 14 days after planting (DAP) based on the same genotype and age. The fertilizer application used Mutiara NPK fertilizer (16:16:16) and $KNO_3$ with a concentration of 5 g $L^{-1}$, given three and six weeks after planting (WAP) in solution form applied around the plant roots. Pruning removes the small shoots on the lower stem for the chili growth to sprout on the main branch once a week. Immediate trimming of shoots that grow in the axils of the leaves prevent becoming branches. Weeding in the planting hole occurred manually, while herbicide application with active ingredients *Parakuat diklorida* (Gramoxone) at 2 g $L^{-1}$ water removed weeds that grew outside the beds. Measures to prevent and control pests and plant diseases also continued when pests and disease attacked plants. Employing pests and diseases control used the insecticide with active ingredients *Profenopos* (Curacron) at a dose of 2 cc $L^{-1}$ and fungicide with active ingredients *Propineb* and *zinc* (Antracol) at a dose of 2 g $L^{-1}$ by spraying on the plants surface. Harvesting transpired once a week for chilies that meet the ready-to-harvest criteria for six weeks for each genotype and individual plant around 70 DAP.

## Data recorded and analysis

Field observations carried out in each experimental plot obtained research data. The data recorded on parameters included plant height (in cm, measured from the soil surface to the highest growing point of the plant approaching harvest), dichotomous height (in cm, measured from the soil surface to the main branching when plant nears harvest), plant habitus (in cm, measuring the crown of the plant), stem diameter (in mm, measurement using a vernier caliper in the middle of the main stem), number of productive branches (branch measured by counting the number of branches that have fruit), flowering age (DAP, calculated from transplanting to flowering and full bloom for each plant), harvest age (DAP, calculated from transplanting until plants are ready for first harvest of each plant), fruit length (in cm, measured from the base of the fruit to the tip of the fruit), fruit diameter (in mm, measured at the center of the ripe fruit using a vernier caliper), fruit stalk length (in cm, measured from the base of the fruit stalk to the tip of the fruit stalk), fruit weight (in g, calculated by weighing all the fruit per plant and then averaged), and total yield (in g, calculated by adding up the fruit weight from the first harvest to the fifth harvest). All data underwent systematic analysis using several analytical concepts.

Observational data attained analysis of variance (ANOVA) according to the augmented design. The results of the ANOVA then become the basis for determining the heritability of each character. The heritability value is a principle in determining the character of selection (Kesumawati *et al*., 2022). Defining selection criteria were through correlation and path analysis. Traits showing significant results in the analysis of variance and having a very significant correlation with yield proceed for path analysis. The results of the path analysis become the basis for determining the selection criteria. Deciding the character as a selection criterion can be seen from the magnitude of the direct influence on the main character (Lelang, 2017). Each selection criterion gained analysis for action and the number of genes through the Z test for skewness and kurtosis values.

## RESULTS

Analysis of variance revealed that cayenne pepper (*Capsicum frutescens* L.) lines, check varieties, and their interaction significantly influenced all the traits except plant height and plant canopy. These were considerably affected only by the lines and their interaction with check cultivars, but cayenne pepper check cultivars showed no significant effect (Table 1).

**Table 1.** Mean square and heritability values for various traits in $F_2$ populations of cayenne pepper.

| Characters | (Lines) L | (Check) C | L x C | CV (%) | Vg | Vp | $H^2$ (%) |
|---|---|---|---|---|---|---|---|
| PH | 143.03* | 184.52ns | 581.43** | 15.15 | 21.95 | 35.76 | 61.38 |
| DH | 43.18ns | 201.34** | 64.03ns | 18.35 | 5.54 | 10.79 | 51.37 |
| PC | 275.26** | 233.02ns | 1451.12** | 15.57 | 50.77 | 68.81 | 73.77 |
| SD | 2.32** | 2.38* | 9.45** | 6.86 | 0.47 | 0.58 | 81.24 |
| NPB | 102.64** | 172.22** | 208.85** | 9.09 | 24.35 | 25.66 | 94.89 |
| FD | 1.38** | 111.34** | 413.39** | 0.53 | 0.33 | 0.35 | 96.84 |
| HD | 4.59** | 167.77** | 255.21** | 0.49 | 1.11 | 1.15 | 97.11 |
| FL | 0.50** | 2.41** | 2.29** | 6.76 | 0.11 | 0.13 | 89.02 |
| FS | 0.11** | 0.54** | 4.00** | 4.30 | 0.02 | 0.03 | 89.00 |
| FDM | 1.57* | 228.45** | 169.71** | 8.88 | 0.27 | 0.39 | 69.56 |
| FW | 0.04** | 6.26** | 14.27** | 3.77 | 0.01 | 0.01 | 93.92 |
| Y | 3274.10** | 2843.07** | 13178.31** | 17.35 | 717.31 | 818.52 | 87.64 |

Notes: ns: not significant, **: significant at α = 1%, *: significant at α = 5%, L: Lines, C: Check, L x C: interaction of Lines and Check, CV: Coefficient of variance, Vg: Variance of genotypes, Vp: Variance of phenotypes, H: Heritability, PH: plant height, DH: dichotomous height, PC: plant canopy, SD: stem diameter, NB: number of productive branches, FD: flowering days, HD: harvest day, FL: fruit length, FS: fruit stalk length, FDM: fruit diameter, FW: fruit weight, Y: yield.

The dichotomous height feature also had notable influence only from the check cultivars of cayenne pepper. Based on the heritability analysis, all the traits owned the highest heritability values (>50%) (Table 1). The traits recorded with the highest heritability values (>90%) were the number of productive branches (94.89%), flowering days (96.84%), harvest days (97.11%), and fruit weight (93.92%). The trait dichotomous height emerged with the lowest heritability value (51.37%).

The correlation analysis showed the traits, which significantly and positively correlated with the yield attributes, were plant height (0.40), plant canopy (0.59), stem diameter (0.43), number of productive branches (0.58), fruit length (0.24), fruit stalk length (0.20), fruit diameter (0.14), and fruit weight (0.12) (Table 2). The earliness traits, viz., days to flowering and harvesting, indicated a significantly negative correlation (-0.25) with the production characters.

The path analysis exhibited a determination value of 0.289 and a residual effect value of 0.506 for the model (Table 3). The traits, viz., plant canopy (0.222), stem diameter (0.161), number of productive branches (0.322), and fruit weight (0.193), have a substantial positive direct influence on yield compared with other traits. The variables, days to flowering (-0.152) and harvesting (-0.049), negatively affected the yield parameters. However, the traits plant height (0.040), fruit length (0.054), fruit stalk length (0.040), and fruit diameter (0.005) have a significant positive direct and relatively the same effect on yield attributes. Overall, traits that indirectly affect yield-related ones have a relative influence value almost the same for each character.

The image-based normality analysis revealed that the traits on fruit weight and yield have a relatively normal distribution (Figure 1). As for the plant canopy, stem diameter, and the number of productive branches traits, their curve has relative skewness toward the right. Skewness and kurtosis analysis showed that plant canopy had a nonsignificant effect, with many genes influencing each cross. Meanwhile, the trait number of productive branches appeared also influenced by many genes and almost showed a nonsignificant effect on every cross, except the double cross U/B//D/K (Zs = 3.202), which had a strong significant effect. The traits stem diameter, fruit weight, and yield showed a relevant positive effect on each cross and also were influenced by many genes, except for the double cross U/B//D/K, influenced by a few genes, and the three-way cross D/U//B also managed by a few genes for fruit weight and yield traits. In addition, the two types of cayenne pepper crosses (D/U//B and U/B//D/K) for each character also had additive gene effect and complementary epistasis, whereas for the three-way cross U/D//K for plant canopy traits had additive gene effect and complementary duplicates.

**Table 2.** Pearson correlation analysis for selected traits.

| Traits | PH | PC | SD | NPB | FD | HD | FL | FS | FDM | FW | Y |
|---|---|---|---|---|---|---|---|---|---|---|---|
| PH | 1.00 | | | | | | | | | | |
| PC | 0.68** | 1.00 | | | | | | | | | |
| SD | 0.34** | 0.47** | 1.00 | | | | | | | | |
| NPB | 0.36** | 0.60** | 0.28** | 1.00 | | | | | | | |
| FD | -0.06** | -0.18** | -0.14* | -0.24** | 1.00 | | | | | | |
| HD | -0.06** | -0.20** | -0.09ns | -0.27** | 0.69** | 1.00 | | | | | |
| FL | 0.19** | 0.25** | 0.19** | 0.14* | -0.15* | -0.13* | 1.00 | | | | |
| FS | 0.20** | 0.17** | 0.20** | 0.18** | -0.26** | -0.21** | 0.37** | 1.00 | | | |
| FDM | 0.07ns | 0.07ns | 0.14* | 0.14* | 0.40** | 0.23** | -0.04ns | -0.10ns | 1.00 | | |
| FW | 0.05ns | 0.05ns | 0.11* | 0.01ns | 0.51** | 0.38** | 0.05ns | -0.25** | 0.72** | 1.00 | |
| Y | 0.40** | 0.59** | 0.43** | 0.58** | -0.25** | -0.25** | 0.24** | 0.20** | 0.14* | 0.12* | 1.00 |

Notes: ns: not significant, **: significant at α = 1%, *: significant at α = 5%, PH: plant height, PC: plant canopy, SD: stem diameter, NPB: number of productive branches, FD: flowering days, HD: harvest day, FL: fruit length, FS: fruit stalk length, FDM: fruit diameter, FW: fruit weight, Y: yield.

**Table 3.** Path analysis for yield per plant based on the traits with the highest correlation with fruit yield in $F_2$ populations of cayenne pepper.

| Characters | Direct Effect | Indirect Effect | | | | | | | | | | Total Effect |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | PH | PC | SD | NPB | FD | HD | FL | FS | FDM | FW | |
| PH | 0.040 | | 0.150 | 0.054 | 0.114 | 0.010 | 0.003 | 0.010 | 0.008 | 0.000 | 0.009 | 0.397 |
| PC | 0.222** | 0.027 | | 0.076 | 0.194 | 0.028 | 0.010 | 0.014 | 0.007 | 0.000 | 0.010 | 0.586 |
| SD | 0.161** | 0.013 | 0.105 | | 0.089 | 0.021 | 0.005 | 0.010 | 0.008 | 0.001 | 0.020 | 0.431 |
| NPB | 0.322** | 0.014 | 0.134 | 0.045 | | 0.036 | 0.013 | 0.007 | 0.007 | 0.001 | 0.000 | 0.578 |
| FD | -0.152 | -0.003 | -0.040 | -0.022 | -0.076 | | -0.034 | -0.008 | -0.010 | 0.002 | 0.098 | -0.249 |
| HD | -0.049 | -0.002 | -0.045 | -0.015 | -0.088 | -0.105 | | -0.007 | -0.009 | 0.001 | 0.074 | -0.247 |
| FL | 0.054 | 0.007 | 0.056 | 0.031 | 0.044 | 0.023 | 0.006 | | 0.015 | 0.000 | 0.009 | 0.245 |
| FS | 0.040 | 0.008 | 0.037 | 0.033 | 0.057 | 0.039 | 0.010 | 0.020 | | -0.001 | -0.048 | 0.196 |
| FDM | 0.005 | 0.003 | 0.016 | 0.023 | 0.046 | -0.061 | -0.011 | -0.002 | -0.004 | | 0.138 | 0.141 |
| FW | 0.193** | 0.002 | 0.011 | 0.017 | 0.000 | -0.077 | -0.019 | 0.002 | -0.010 | 0.004 | | 0.116 |
| Residual | | 0.506 | | | | | | | | | | |

Notes: **: significant at α = 1%, PH: plant height, PC: plant canopy, SD: stem diameter, NPB: number of productive branches, FD: flowering days, HD: harvest day, FL: fruit length, FS: fruit stalk length, FDM: fruit diameter, FW: fruit weight.

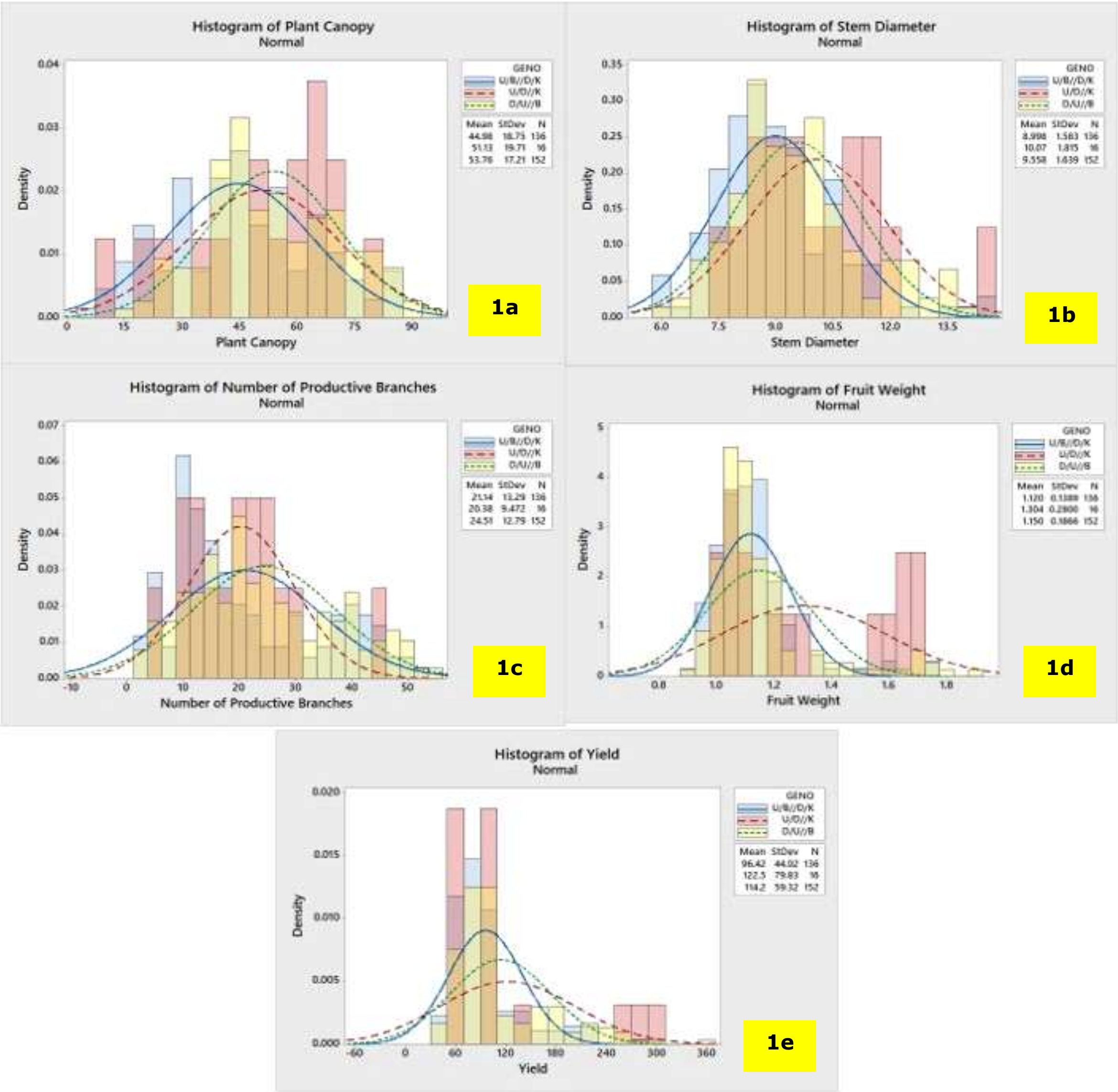

**Figure 1.** a) Distribution curve for plant canopy (PC), b) Stem diameter (SD), c) Number of productive branches (NPB), d) Fruit weight (FW), and e) Yield (Y).

## DISCUSSION

The analysis of variance showed that the cayenne pepper $F_2$ populations provided significant variations for almost all growth and production traits, esteemed as crucial factors in plant selection. These results resemble past findings, which revealed that high genetic diversity is essential in the plant selection process, increasing the chances of combining the desired traits (Priyanto *et al*., 2018). High heritability values for growth and production traits also support this idea. Growth and production traits with high heritability values have also resulted in past studies for plant height, fruit diameter, number of fruit per plant, fruit weight, and fruit weight per plant (Qasim *et al*., 2013); plant height, stem diameter, flowering age, harvest age, fruit length, and fruit diameter (Syukur and Rosidah, 2014); and stem diameter and fruit length in cayenne pepper populations (Rosmaina *et al*., 2016). Traits, such as, fruit length, diameter, and weight with the highest genetic variation and heritability should be considered reliable selection criteria for increasing chili yields (Sayekti *et al*., 2021).

High heritability values indicate that the influence of genetic factors was more significant and prevailing than environmental factors. The higher the heritability value, the more variability production traits gain influence by differences in genotypes and less by environmental variations. Traits with high heritability values will increase the effectiveness of selection because such attributes reflect the influence of genetic factors compared with environmental factors. Quantitative traits with high heritability will result in selection progress for the desired traits, with the lowest heritability showing less effectively in playing a vital role in selection (Bdr *et al*., 2020).

Natural diversity and high heritability indicate the inheritance of quantitative traits, and there are opportunities to increase selection progress in the next generation. Significant variance is the initial basis for determining the effectiveness of selection for a trait (Fellahi *et al*., 2018; Anshori *et al*., 2022). Selecting populations with high heritability proved more effective than the selection with low heritability. High heritability values indicated that most of the phenotypic variability resulted from genetic variability; hence, selection will experience genetic improvement (Sofian *et al*., 2019). Based on the analysis of variance and heritability, the selection process for the double- and three-way cross $F_2$ populations of cayenne pepper was effective.

Correlation analysis aims to evaluate the relationship between the traits and their association with yield (Akbar *et al*., 2019; Hastini *et al*., 2019). Therefore, correlation and path analyses can benefit trait selection. Estimating the genetic variability and determining the nature of the relationship among the variables is a significant step toward genotype selection and improvement programs (Ishaya *et al.*, 2020). The correlation analysis revealed that choosing almost all traits for use as selection criteria. However, in the selection process, using many attributes is not optimal because it reduces selection effectiveness hence, needing the main and supporting traits. These results were in line with the findings of Anshori *et al*. (2022), Fadli *et al*. (2022), and Farid *et al*. (2022). Thus, the effective selection criteria with the most influence on production traits are imperative in the selection process. Correlation analysis showed that the traits plant height, plant canopy, stem diameter, number of productive branches, fruit length, fruit stalk length, fruit diameter, and fruit weight have a significant positive correlation with production traits (Table 2).

The path analysis seeks to determine the direct and indirect effects of growth and morphological traits on yield parameters that correlate with productivity (Akbar *et al*., 2019). According to Abhilash *et al*. (2018), choosing productivity can directly serve as the main selection character. However, many factors affect productivity; therefore, it is better to use selection that correlates with productivity (Akbar *et al*., 2018; Al-kordy *et al*., 2019). The path analysis showed that plant canopy, stem diameter, number of productive branches, and fruit weight had a significant positive direct effect on production traits compared with other traits. Thus, these four traits can benefit as selection criteria along with production. However, these selection criteria need strengthening with the nature of gene action.

Gene action is one of the genetic parameters that determine the genetic control pattern of a trait and can also help provide information about the pattern and direction of selecting a crossing method (Farooq *et al*., 2019; Farid *et al*., 2022). Selecting those traits influenced by additive gene effects will be effective for trait improvement in the early generations ($F_2$–$F_3$) to develop superior genotypes (Saleem *et al*., 2013). Based on the results, genetic diversity with high heritability values significantly influenced all the traits, consequently determining the phenotypic pattern resulted from analysis of the number of genes and gene action. Therefore, further analysis ensued using the test of skewness and kurtosis values to see the action and number of genes in each character that affect production. The skewness and kurtosis tests on the $F_2$ populations of cayenne pepper showed that many genes dominantly controlled the traits, viz., plant habitus, stem diameter, number of productive branches, fruit weight, and yield, with additive gene effects and complementary epistasis for each cross.

The skewness and kurtosis values for each type of cross appear in Table 4. If the skewness and kurtosis tests are not significantly different from 0, then the distribution has a characteristic as normal. If the skewness test shows a significant z test, the population has additional actions, such as complementary epistasis (Zs is positive) and duplicative epistasis (Zs is negative). Kurtosis analysis determined the number of genes. A

**Table 4.** Estimation of gene action and gene count in double and three-way crosses.

| Crosses | Skewness | Kurtosis | Zs | Zk | Gene Action | Gene Count |
|---|---|---|---|---|---|---|
| Plant canopy (PC) | | | | | | |
| U/B//D/K | 0.132 | -0.632 | 0.635ns | -1.530ns | Additive, complementary epistasis | Many |
| U/D//K | -0.722 | -0.388 | -1.280ns | -0.356ns | Additive, complementary duplicate | Many |
| D/U//B | 0.181 | -0.653 | 0.919ns | -1.670ns | Additive, complementary epistasis | Many |
| Stem diameter (SD) | | | | | | |
| U/B//D/K | 0.995 | 1.638 | 4.784** | 3.966** | Additive, complementary epistasis | Few |
| U/D//K | 0.800 | 0.825 | 1.418tn | 0.756ns | Additive, complementary epistasis | Many |
| D/U//B | 0.645 | 0.112 | 3.274** | 0.286ns | Additive, complementary epistasis | Many |
| Number of productive branches (NPB) | | | | | | |
| U/B//D/K | 0.666 | -0.806 | 3.202** | -1.952ns | Additive, complementary epistasis | Many |
| U/D//K | 0.810 | 1.226 | 1.436ns | 1.123ns | Additive, complementary epistasis | Many |
| D/U//B | 0.381 | -0.725 | 1.934ns | -1.854ns | Additive, complementary epistasis | Many |
| Fruit weight (FW) | | | | | | |
| U/B//D/K | 2.173 | 6.950 | 10.447** | 16.828** | Additive, complementary epistasis | Few |
| U/D//K | 0.364 | -1.732 | 0.645ns | -1.588ns | Additive, complementary epistasis | Many |
| D/U//B | 2.098 | 4.246 | 10.650** | 10.859** | Additive, complementary epistasis | Few |
| Yield (Y) | | | | | | |
| U/B//D/K | 1.719 | 3.008 | 8.264** | 7.283** | Additive, complementary epistasis | Few |
| U/D//K | 1.563 | 1.031 | 2.771** | 0.945ns | Additive, complementary epistasis | Many |
| D/U//B | 1.505 | 1.983 | 7.640** | 5.072** | Additive, complementary epistasis | Few |

Notes: ns: not significant, **: significant at α = 1%, *: significant at α = 5%, PC: plant canopy, SD: stem diameter, NPB: number of productive branches, FW: fruit weight, Y: yield, Zs: skewness standardization, Zk: kurtosis standardization, Kurtosis >3: a few genes, Kurtosis <3: many genes.

kurtosis (Zk) value of more than 3 indicates that the character has a platykurtic distribution chart, with many genes in control. Conversely, a kurtosis value of less than 3 means that the character has a leptokurtic distribution chart and is managed by a few genes (Rahayu *et al*., 2018).

Based on skewness and kurtosis tests, the trait fruit weight provided with the additive gene action and complementary epistasis with a few genes, becoming a more stable character to serve as a selection criterion in the selection process in the double- and three-way cross chili $F_2$ populations for enhanced productivity. According to Maryono *et al.* (2019), a positive (+) skewness value indicates that the character has additive gene action in control and complementary epistasis. Conversely, if the skewness value is negative (-), the additive gene action controls the character with duplication epistasis. In crop plants, the distribution of quantitative traits that extends to the left or right indicates environmental influences, genotype-by-environment interactions, gene linkages, and epistasis. The heritability of a character is largely determined by the genetic potential of the cultivar, heritability, and the action of the genes that control the character. A trait that has a low broad-sense heritability value, controlled by additive gene action with complementary epistasis, means that the next generation can inherit the character. In contrast, other generations can inherit a character with a high broad-sense heritability value, and are controlled by additive gene action with complementary epistasis.

## CONCLUSIONS

The recent study developed an effective selection index on $F_2$ populations of double and three-way crosses of cayenne pepper. Traits of the plant canopy, stem diameter, number of productive branches, and fruit weight showed the best selection criteria with yield. The trait fruit weight with additive gene action and complementary epistasis with a few genes became a more stable character for use as a selection criterion in the selection process in the $F_2$ populations of double and three-way crosses of cayenne pepper for increased productivity.

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