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EVALUATING GENETIC VARIABILITY AND SELECTION CRITERIA IN SHALLOT M1V1 MUTANT INDUCED BY COLCHICINE TREATMENT

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SUMMARY

Knowing the estimated genetic parameters and the relationship between yield and associated traits is pivotal to successful shallot breeding. The study's objectives were to observe the effect of colchicine on the growth and yield characteristics of shallot (*Allium cepa*), investigate the genetic variability of shallot in the first generation, and determine the selection criteria for the shallot improvement program. The shallot bulbs received colchicine treatments ranging from 0, 100, 200, 300, and 400 ppm. The variance analysis revealed that colchicine treatments highly affected the shallot growth and yield characteristics in varying significance. It demonstrated that colchicine treatments were potent in inducing mutation and creating variability among populations of shallot; hence, it can be beneficial for shallot improvement. The highest values of the genotypic coefficient of variance, heritability, and genetic advance were evident in the 200-ppm population. Therefore, this study only recommends pursuing the 200-ppm population for the next generations. Path analysis exhibited that the trait of bulb fresh weight per clump had a high positive direct effect with bulb dry weight per clump, indicating its usefulness as a selection criterion for developing shallot genotypes with high-yielding next generations.

Keywords: Shallot (*Allium cepa*), colchicine, heritability, path analysis

Key findings: The 200-ppm population had a higher genotypic coefficient of variation, broad sense heritability, and genetic advance than other mutated populations in the shallot (*Allium cepa*). The bulb fresh weight per clump trait can serve as selection criteria for developing shallot genotypes with highyielding next generation having a high positive direct effect and heritability values.

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INTRODUCTION

Shallot (*Allium cepa var. ascolanicum* Becker) is one of the world's vegetable commodities with high economic value, after chilies and tomatoes. People use shallots as a cooking spice and medicine because shallot bulbs contain protein, carbohydrates, fat, potassium, phosphorus, thiamine, niacin, vitamin C, gibberellins, auxins, flavonoids, and saponins (Adeyemo *et al.,* 2023). In addition, shallot extract contains several polyphenolic compounds, including thiosulfinate, catechin, apigenin, kaempferol, quercetin, sapogenin, and gallic acid (Sittisart *et al.,* 2017) that are applicable as medicinal ingredients.

Limited fertile land is a primary problem for world agriculture in the future; thus, developing adaptive onion varieties for marginal land is necessary. Peatland is one of the marginal lands that can serve as cultivation areas, especially shallow peat. Indonesia is a country that has the broadest tropical peatland among tropical countries, at 24.6 million ha (MOEF, 2021). Until now, no shallot varieties have been adaptive in peatlands.

Mutation is one of the breeding strategies developed to expand the genetic diversity of shallots (Zulfahmi *et al.,* 2022). Mutation induction is an effort to change the allele arrangement of an organism to form new genetic diversity, which is beneficial in developing new varieties. Colchicine is a mutagen that prevents the formation of microtubules during the mitotic cycle to stop chromatid migration during anaphase, doubling the number of chromosomes (Samadi *et al.,* 2022). Many reports indicated the use of colchicine for shallot mutation (Ren *et al.,* 2018; Husain *et al.,* 2022). Colchicine is effective in inducing polyploid plants, changing the cell and morphological size of the plant to become more vigorous. Increasing ploidy in plants influences their ability to adapt to stressful environments (Harrison *et al.,* 2023).

Information on the population's genetic variability is pivotal since the higher the genetic variability, the more effective selection will be (Tesfaye, 2021). Genetic variability of the agronomic characteristics is crucial for improving yield components. Heritability

measures the phenotypic variance caused by genetic factors and has a predictive function in crop breeding. The relationship analysis between characters through correlation coefficients is vital in the early selection. However, the correlation study between traits does not clearly explain the relationships between characters, hence requiring path analysis. The path analysis provides detailed information on the effect of the trait involved in determining yield, which justifies the existence of positive and negative correlations and high and low magnitudes among the studied traits (Yogita *et al.,* 2023).

This research aimed to observe the effect of colchicine on the growth and yield characteristics of shallots, investigate their genetic variability in the first generation after applying several concentrations of colchicine, and determine the traits as selection criteria in the shallot improvement program.

MATERIALS AND METHODS

This research transpired at the experimental station of the Faculty of Agriculture and Animal Science, State Islamic University of Sultan Syarif Kasim Riau, Indonesia (latitude: 0° 28′ 6.17″, longitude: 101° 21′ 4.07″, altitude: 10 masl). Sakato variety shallots were samples used in this research. Healthy and uniformly sized shallot bulbs selected received colchicine treatments at several concentrations: zero, 100, 200, 300, and 400 ppm, with a soaking time of six hours. The selection of colchicine depended on the report by Foschi *et al.* (2013), who concluded that the effectiveness of using colchicine in several studies ranged from 0 to 500 ppm, while the determination of soaking time relied on the report by Kwon *et al.* (2013), who found that the most effective of soaking time for the induction of polyploidy was six hours, with a colchicine concentration of 500 ppm. Colchicine is highly toxic to plants; low doses with prolonged exposure are considerably reliable for reducing harmful effects and increasing shallot polyploidy. Planting patterns in the field had a randomized complete block design arrangement with three replications. The planting distance was 0.2 m \times

0.2 m, and all cultivation techniques, such as weeding, watering, fertilizing, and pest and disease control, ensued during the plant growth period, following the technical guidelines issued by Sumarni and Hidayat (2005).

The observed parameters comprised plant height (measured from the base to the extensive end of the leaf), the number of leaves, and the number of tillers, noted in the fourth week after planting. The number of bulbs, bulb diameter, bulbs weight per bulb, and bulb fresh weight per clump measuring occurred at harvest time, with the bulb dry weight per clump weighed two weeks after harvest and air-dried.

Data analysis

The data underwent analysis of variance, with the significant difference between the means of the treated and control population tested by the Duncan Multiple Range Test (DMRT) at a 5% significant level. Variance components, such as phenotype, genotypes, genotypic coefficient variance (GCV), phenotypic coefficient variance (PCV), heritability in a broad sense, genetic advance (GA), and genetic gain as a percent of the mean (GAM) of each colchicine concentration reached calculations. Genetic variability of M1V1 generation computation followed the formula below:

$$
\sigma^2 = \frac{(\sum x^2) - [(\sum x)^2/n]}{n-1}
$$

$$
\sigma^2 M_1 = \sigma^2 P
$$

$$
\sigma^2 P = \sigma^2 G + \sigma^2 E
$$

$$
\sigma^2 G = \sigma^2 P - \sigma^2 E
$$

$$
\sigma^2 G = \sigma^2 M_1 - \sigma^2 M_0
$$

Where:

 σ^2 = variance $\sigma^2 P$ = phenotypic variance $\sigma^2 G$ = genotypic variance $\sigma^2 E$ = environmental variance $\sigma^2 M_1$ = M1V1 population variation $\sigma^2 M_0$ = M0 population variance $n =$ number of population

GCV and PCV estimates

GCV and PCV estimations employed the formula of Mofokeng (2021) as follows:

$$
GCV = \frac{\sqrt{\sigma^2 G}}{\overline{X}} \times 100\%
$$

$$
PCV = \frac{\sqrt{\sigma^2 P}}{\overline{X}} \times 100\%
$$

Where: $\sqrt{\sigma^2 G}$ = genotypic standard deviation, $\sqrt{\sigma^2 P}$ = phenotypic standard deviation, and $X =$ grand mean of the character under evaluation.

Estimate of broad sense heritability (h²)

Heritability values calculation used the formula of Pranay *et al.* (2022) as follows:

$$
h^2 = \frac{\sigma^2 G}{\sigma^2 P} \times 100\%
$$

Estimate of GA

Determining the GA relied on the formula of Eliezah *et al.* (2021) as follows:

$$
GA = K x \sqrt{\sigma^2 P} \times h^2(b.s)
$$

Where K is a constant that represents the selection intensity, when k is 5%, the value is 2.06. $\sqrt{\sigma^2 P}$ = standard deviation of phenotypic, h^2 (b.s.) is the broad sense heritability.

Estimate of GAM

GAM determination engaged the formula of Eliezah *et al.* (2021) as follows:

$$
GAM = \frac{GA}{\bar{X}} \times 100\%
$$

Where GA is genetic advance, \bar{X} = grand mean of the character under evaluation.

Correlation and path analysis

Correlation analysis utilized the method of Negash *et al.* (2019), while path analysis employed the procedure by Karyawati and Puspitaningrum (2021). For the variance, correlation, and path analysis, the study used the SAS 9.1 software (SAS Institute, 2009).

RESULTS AND DISCUSSION

Growth performance

The colchicine treatment was highly significant in plant height and bulbs, significantly affecting the number of leaves, bulb fresh weight per clump, and bulb dry weight per clump characteristics (Table 1). Concentrations of 100 and 200 ppm colchicine substantially increased all parameters except the bulb diameter. Increasing the colchicine concentration to 300 and 400 ppm drastically reduced all parameters except for the number of tillers and bulbs (Figure 1). These results showed that colchicine of more than 200 ppm with a soaking time of six hours had inhibited the growth of shallot, as exhibited by the decrease in plant height, bulb weight, diameter, dry weight/clump, and fresh weight/clump.

Table 1. Mean square of variance analysis of each traits of shallot.

Note: ns = non-significant ($P \le 0.05$),*significant ($P \le 0.05$),** highly significant ($P \le 0.01$).

Figure 1. Percentage changes (increased or decreased) in several observed traits resulting from colchicine mutation induction.

However, an increase in the number of tillers and the number of bulbs occurred, but the bulb size was smaller. Rahmawati *et al.* (2024) also reported that increasing colchicine concentration and soaking time reduces plant height, bulb weight, and bulb diameter. Colchicine at the right concentration can boost growth, but at exorbitant amounts, it can inhibit growth (Yan *et al.,* 2022; Rosmaina *et al.,* 2021). The effectiveness of colchicine depends on the type of plant, concentration, length of exposure, and absorption of the compound (Cabahug *et al.,* 2022; Al-Jubouri and Alqaisi, 2023). Exposure and concentrations that are too high cause toxicity, damage cells, and even plant death (Chakraborty *et al.,* 2021; Arindyaswari *et al.,* 2021; Haring *et al.,* 2023).

Genetic variability of shallot

The mutation effect on the crop can be feasible by estimating the mean and genetic parameters in the mutagen-treated population. Estimated values of PCV, GCV, heritability, GA, and GAM are available in Table 2. At the population level, the GCV values ranged from 2.52% for the 300-ppm population to 52.38% for the 200-ppm population, while PCV values ranged from 61.14% for the 100-ppm population to 78.72% for the 200-ppm population (Table 2). According to Meena *et al.* (2017), PCV and GCV values greater than 20% are considerably high, scores between 10% and 20% are deemed medium, and less than 10% are relatively low. Based on the above criteria, all populations have high PCV, while

Table 2. The value of PCV, GCV, heritability, GA, and GAM per trait and population.

Doses	PH	NL	ΝT	NΒ	BD	BB	BFWC	BDWC	Mean
PCV									
Control	30.45	64.03	45.37	50.35	33.44	100.90	105.65	110.01	67.52
100 ppm	32.57	59.26	42.3	47.82	34.97	80.94	91.43	99.84	61.14
200 ppm	37.59	78.15	45.56	50.37	41.21	109.91	129.92	137.02	78.72
300 ppm	44.62	64.79	41.44	35.84	44.02	119.89	106.45	118.42	71.93
400 ppm	42.46	57.21	35.21	42.92	40.34	105.70	123.45	138.24	73.19
GVC									
100 ppm	14.18	25.83	12.39	11.07	8.73	0.00	0.00	27.29	12.44
200 ppm	23.01	54.87	16.06	24.69	22.93	55.17	106.73	115.59	52.38
300 ppm	20.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.52
400 ppm	23.41	26.96	0.00	24.18	0.00	0.00	0.00	32.87	13.43
Heritability (%)									
100 ppm	18.94	19	8.58	5.36	6.23	0.00	0.00	7.47	8.20
200 ppm	37.47	49.3	12.42	24.02	30.95	25.19	67.49	71.17	39.75
300 ppm	20.42	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.55
400 ppm	30.4	22.21	0.00	31.75	0.00	0.00	0.00	5.65	11.25
GA									
100 ppm	2.76	3.41	0.31	0.27	0.59	0.00	0.00	1.50	1.10
200 ppm	6.22	11.17	0.46	1.36	3.39	1.50	29.10	25.52	9.84
300 ppm	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.38
400 ppm	4.78	4.06	0.00	1.89	0.00	0.00	0.00	1.12	1.48
GAM									
100 ppm	12.71	23.19	7.48	5.28	4.49	0.00	0.00	15.37	8.56
200 ppm	29.01	79.37	11.66	24.93	26.28	57.05	180.62	200.88	76.22
300 ppm	18.77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.35
400 ppm	26.59	26.17	0.00	28.07	0.00	0.00	0.00	16.10	12.12

Note: PCV (phenotypic coefficient variance), GCV (genotypic coefficient variance), GA (genetic advance), GAM (genetic gain as a percent of the mean), PH (plant height), NL (number of leaves), NT (number of tillers), NB (number of bulbs), BD (bulb diameter), BB (bulbs weight/bulb), BFWC (bulb fresh weight per clump), BDWC (bulb dry weight per clump).

high GCV value was only apparent for the 200 ppm population. It exhibited that the 200-ppm population has the highest genetic variability compared with other mutated populations. A population with high GCV value provides opportunities for successful improvement efforts through selection (Rosmaina *et al.,* 2016; Tesfaye, 2021).

The GCV values ranged from 0.00% to 115.59% at the character level. The highest value of GCV appeared for the bulb dry weight per clump at the 200-ppm population (Table 2). The PCV values ranged from 30.45% for plant height in the control population to 138.24% for the bulb dry weight per clump at the 400-ppm population (Table 2). According to PCV and GCV values classified by Meena *et al.* (2017), PCV values of all characters in all populations were a high category. Similarly, a high GCV value was notable for the bulb dry weight per clump and number of leaves at 100-ppm population, all characters except for the number of tillers at the 200-ppm population, plant height at the 300-ppm population, and plant height, number of leaves, number of bulbs, and bulb dry weight per clump at the 400-ppm population. Moderate GCV value was evident for plant height, the number of tillers and bulbs in the 100-ppm population, and the number of tillers in the 200-ppm population.

Meanwhile, the rest of the characters have low GCV. High values of PCV and GCV indicated the existence of substantial variability for such characters, and selection may be effective based on these characters. Similar findings came from earlier researchers for bulb fresh weight, dried bulb weight, and number of leaves (Sinuraya *et al.,* 2019), for plant height, number of leaves, the number of tillers, bulb fresh weight, and dried bulb weight (Moeljani *et al.,* 2021; Billa *et al*., 2022; Maharijaya *et al*., 2023).

In this study, the PCV was relatively higher than the GCV for all traits and populations, indicating a significant contribution of environmental factors to the traits' expression. A similar finding resulted in the studies by Bhuiyan *et al.* (2022) and Venkatesan and Saravanan (2017) in Bhendi (*Abelmoschus esculentus*, L) with EMS and

colchicine treatments. Therefore, the above attributes need to be considered depending on the objectives of the shallot improvement program. The GCV provides information on the genetic variability present in quantitative characteristics in the base population, but estimating heritable variation with the help of GCV alone may be misleading. Eliezah *et al.* (2021) suggested that using the GCV with heritability estimates provides a better picture of the extent of heritable variation.

Heritability values help to predict the expected progress to succeed through the selection process. At the population level, the broad sense heritability estimates ranged from 2.55% to 39.75% for the 300-ppm population and 200-ppm population, respectively (Table 2). The heritability value category of the 200 ppm population was moderate, following Pranay *et al.* (2022). Meanwhile, the other population was low. It means that variability in the 200-ppm population revealed a balance between genetic and environmental effects, whereas variability has an ecological influence on the rest.

The broad sense heritability ranged from 0.00% to 71.17% at the character level. The highest value of heritability emerged for the bulb dry weight per clump at the 200-ppm population. Inversely, the lowest value of heritability was prominent for the bulb weight and bulb fresh weight per clump at 100-ppm population, bulb diameter, bulb weight, and bulb fresh weight per clump at 400-ppm population, and all traits at the 300-ppm population except for plant height (Table 2). According to Pranay *et al.* (2022), heritability values greater than 60% were high, from 30%–59% were medium, and scores less than 30% were low.

The bulb dry weight per clump and bulb fresh weight per clump characteristics at the 200-ppm population exhibited a high heritability category. The features with high heritability indicated a low contribution of environmental factors to the phenotype, and selection for such traits could be smooth due to a high additive effect. High estimates of heritability have also come from previous researchers for the leaf number, fresh weight of the bulb, dry weight of the bulb *(*Sinuraya *et* *al.,* 2019), bulb dry weight per plant, bulb, and leave diameter (Sari *et al.,* 2019).

Heritability alone does not indicate the amount of genetic improvement that results from the genotype selection. Hence, knowledge of heritability with genetic advancement will be more favorable (Zaki and Radwan, 2022). Genetic advance (GA) under selection refers to improving the genotypic value of characters for the new population compared with the base population under one selection cycle at a given selection intensity (Venkatesan and Saravanan, 2017). Furthermore, Terfa and Gurmu (2020) stated that genetic advances are essential in predicting the expected genetic gain from one selection cycle. Estimates of GA values for all populations and characters studied appear in Table 2.

The genetic advance value ranged from 0.38 to 9.84 for the 300-ppm and 200-ppm populations, respectively (Table 2). Estimates of the genetic advance value ranged from 0.00 to 29.10 at the character level. The highest value was notable for the bulb fresh weight per clump at the 200-ppm population, indicating that whenever one selects the best 5% highyielding genotypes as parents, the average bulb fresh weight per clump of the offspring could grow to a large of 29.10 g. That is, the average genotypic value of the new population for the bulb fresh weight per clump could be better from 16.11 to 45.21 g. In the same way, the bulb's fresh weight per clump could rise from 12.70 to 38.22 g.

Genetic advance as a percent of the mean (GAM) in this study ranged from 2.35% to 76.22% for the 300-ppm and 200-ppm populations, respectively (Table 2). The GAM value at the character level ranged from 0.00% to 200.88%. The highest GAM value appeared in the bulb dry weight per clump at 200-ppm population, followed by the bulb fresh weight per clump (180.62%). According to Meena *et al.* (2017), the value of GAM has three categories: low (< 10%), moderate (10%– 20%), and high (> 20%). The high GAM was evident for the number of leaves at 100-ppm population, plant height, the number of leaves and bulbs at 400-ppm population, and all traits at 200-ppm population except for the number of tillers. The moderate value of GAM occurred

for the bulb dry weight per clump at 400-ppm and 100-ppm populations, the number of tillers at the 200-ppm population, and plant height at the 100-ppm and 300-ppm populations.

Meanwhile, other characters have low GAM (Table 2). High heritability estimates with a high GAM are usually more helpful in predicting gains under selection than heritability alone (Meena *et al.,* 2016; *Mia et al.,* 2020). In the presented study, a high heritability with high GAM resulted in the bulb fresh weight per clump and bulb dry weight per clump at the 200-ppm population, reflecting the presence of an additive gene action for the expression of these traits, which is fixable for next generations. The selection of the next population based on this character would be ideal. Similar results also emerged from studies by Amir *et al.* (2023) and Tesfaye (2021). Rosmaina *et al.* (2016) reported high heritability combined with a high genetic advance for yield per plant.

A higher genotypic coefficient of variation accompanied by high heritability and a high genetic advance provides better clues than individual variables. Thus, populations with a high genotypic coefficient of variation, heritability, and genetic advance should be choices. In this study, the 200-ppm population had a higher genotypic coefficient of variation, heritability, and genetic advance. Therefore, we recommend that only a population of 200 ppm should continue in further generations.

Correlation and path analysis between traits

Besides the heritability characters used in selection, other information like the correlation coefficient and path analysis between characters also need detection. The correlation coefficient values between the growth and yield characters are accessible in Table 3. The results revealed a highly significant and positive correlation between the bulb dry weight per clump and the plant height *(r =* 0.773), number of leaves *(r =* 0.625), number of tillers *(r =* 0.403), number of bulbs *(r =* 0.413), bulb diameter *(r =* 0.781), bulb weight *(r =* 0.219), and bulb fresh weight per clump *(r =* 0.989). The bulb weight was significantly

Traits	PH	NL	NΤ	NΒ	BD	BВ	BFWC	BDWC	
PH									
NL	$0.576**$								
NT	$0.310**$	$0.543**$							
NB	$0.276*$	$0.543**$	$0.310**$						
BD	$0.820**$	$0.412**$	$0.123*$	0.043ns					
BB	$0.174*$	0.083ns	-0.002 ns	0.083ns	$0.232**$				
BFWC	$0.780**$	$0.638**$	$0.406**$	$0.412**$	$0.786**$	$0.224**$			
BDWC	$0.773**$	$0.625**$	$0.403**$	$0.413**$	$0.781**$	$0.219**$	$0.989**$		

Table 3. Correlation coefficient values between traits of shallots.

Note: PH (plant height), NL (number of leaves), NT (number of tillers), NB (number of bulbs), BD (bulb diameter), BB (bulbs weight/bulb), BFWC (bulb fresh weight per clump), BDWC (bulb dry weight per clump), ns = non-significant (*P* ≤ 0.05),*significant ($P \le 0.05$),** highly significant ($P \le 0.01$).

Table 4. Estimates of direct (bold-diagonal) and indirect effects of different traits on bulb dry weight per clump of shallots.

Traits	PH	NL.	NΤ	NΒ	BD.	BB	BFWC	Coefficient correlation with BDWC
PH		-0.00464 -0.00267	-0.00144 -0.00128		-0.0038	-0.00081	-0.00362	$0.773**$
NL	-0.01223		$-0.02123 - 0.01153 - 0.01153$		-0.00875	-0.00176	-0.01354	$0.625**$
NT	0.00363	0.00636	0.01171	0.00363	0.00144	-0.00002	0.00475	$0.403**$
NB	0.00593	0.01167	0.00666	0.02149	0.00092	0.00178	0.00886	$0.413**$
BD	0.02421	0.01217	0.00363	0.00127	0.02953	0.00685	0.02321	$0.781**$
BB.	-0.00077	-0.00037	0.00001	-0.00037	-0.00102	-0.0044	-0.00099	$0.219**$
BFWC	0.75686	0.61907	0.39395	0.39977	0.76268	0.21735	0.97033	$0.989**$

**: Significant at *P* ≤ 0.01. Residual effect = 0.146644, PH: plant height, NL: number of leaves, NT: number of tillers, NB: number of bulbs, BD: bulb diameter, BB: bulbs weight/bulb, BFWC: bulb fresh weight per clump, BDWC: bulb dry weight per clump.

and positively correlated with plant height *(r =* 0.174), bulb diameter *(r =* 0.232), and bulb fresh weight per clump *(r =* 0.786).

Waluyo *et al.* (2022) also reported a positive and significant correlation between plant height and the bulb dry weight per clump (yield) in shallot planted in several areas. Our results discovered that the plant height would increase bulb weight, which contradicts the report of Susilawati *et al.* (2018), who found no significant correlation between plant height and bulb weight/bulb. The number of leaves correlated with all characters except for bulb weight/bulb. This study's result aligned with Susilawati *et al.* (2018). The leaf organ produces photosynthate which is translocated to other organs. The correlation between growth and yield traits exhibited increasing plant photosynthesis capacity and dissemination of photosynthate to bulbs (Waluyo *et al.,* 2022).

Correlation analysis can only identify the degree of relationship between two characters but does not provide a reason for the relationship. Therefore, path analysis is pivotal for application. Path analysis can break down the total correlation coefficient into direct and indirect effect components (Khan *et al.,* 2022). The result of path analysis among characters on yield of shallot appears in Table 4. The bulb fresh weight per clump had the highest direct effect and positive value (0.97033), followed by the bulb diameter (0.02953), the number of bulbs (0.02149), and the number of tillers (0.0117). These characters significantly and positively correlated with the bulb dry weight per clump. It indicates that the correlation is a real relationship. A direct selection will be effective through this attribute because an increase in one of these features directly contributes to an upsurge in the yield. The path coefficient value

has five ranges: the coefficient value greater than one score as very high, the values between 0.30 and 0.99 are high, those between 0.2 and 0.29 are moderate, the values between 0.1 and 0.19 are low, and the values between 0.00 to 0.09 are negligible (Mubai *et al.*, 2020). Based on the above categories, only the characteristic of bulb fresh weight per clump had a high category of direct effect, and the rest were negligible. Therefore, bulb fresh weight per clump can be efficient as selection criteria for selecting genotypes with high bulb dry weight per clump due to having a high direct effect.

The plant height, the number of leaves, and bulb weight/bulb traits displayed negligible negative direct effects on yield (*P =* -0.00464, *P =* -0.02123, and *P =* -0.0044, respectively). These characters correlated significantly and positively with the bulb dry weight per clump, which indicated the indirect effect causing the correlation. This indirect effect needs more consideration. Such a result aligns with Singh *et al.* (2018) and Yogita *et al.* (2023). Raghuwanshi *et al.* (2016) found that the bulb diameter, number of leaves, and plant height characteristics had a direct negative influence but positively correlated with yield per plant. It suggests that indirect effects are causal correlates and are consequently simultaneous for selection.

The residual value of the path analysis was 0.1466; it indicates that characters included in the path analysis contributed 85.34% of the total variation in the yield, whereas other factors out of the model explained the 14.66%, such as environmental factors and cultural practices. The low residual values indicate that most of the crucial traits that contributed to the results have been included in this study (Raghuwanshi *et al.,* 2016). The residual value of this study was higher than the residual value of onion reported by Singh *et al.* (2018) and Yogita *et al.* (2023); but, it was lower than the residual value of onion reported by Visalakshi *et al.* (2018) and Waluyo *et al.* (2022).

CONCLUSIONS

The study concluded that the colchicine treatment induced varying effects on shallot, in which the population of 200 ppm of colchicine has the highest variability compared with other populations. The characteristic, bulb fresh weight per clump can benefit as a direct indicator selection, and the traits of plant height and the number of leaves can serve as indirect indicator selections in yield improvement of shallot.

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