

## Research article

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### Evaluation to Select Tomato Genotypes with Big Fruit and Verification of Genetic Advance

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#### Abstract

##### Keywords

index selection;  
selection progress;  
transgressive segregant

Selection progress is one of the parameters of success in a plant breeding program. Selection with a pedigree approach made in early generation is intended to increase the mean value and reduce the variance of the selected population. This study aimed to determine the selection response from F<sub>2</sub> to F<sub>3</sub> in different locations, and to obtain transgressive segregant genotypes. The study was conducted from August 2018 to April 2019 at the IPB Tajur II Experimental Field (300 m asl), Bogor, West Java, Indonesia. The results showed a positive response for flowering time, fruit length, harvest time, fruit diameter, fruit weight per plant, fruit weight, and numbers of fruits. There was a big difference between the estimated value and the real value of selection response and realized heritability, which was most likely due to differences in the location of the experiment. Transgressive segregant was found in each observed character, but no genotype showed transgressive segregant criteria for all characters. The most transgressive segregant criteria were found in the F<sub>3</sub>GH3-248 genotype, for five of the seven characters observed.

## 1. Introduction

Tomato represents one of the major fruit vegetables with an increasing global demand due to its popularity and health benefit effects [1, 2]. The optimum yield of tomato varieties is a character that is always considered to ensure its acceptance by the people in the world [3-5]. The optimum yield

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is defined by complex characters that are strongly influenced by the yield component character [6], so the selection is better if done based on several characters [7, 8]. Selection runs effectively if it is done using the right method.

Index selection is one of the selection methods for multiple characters commonly used in addition to tandem selection and independent culling [9, 10]. Hazel and Lush [11] and Lin [12] investigated the relative efficacy of tandem selection, independent culling levels, and index selection. They demonstrated that the most effective method was index selection. Additionally, Young and Tallis [13] and Finney [14] discovered that relative efficiency depends upon the number of traits selected, the relative economic value of the traits, heritabilities, phenotypic and genetic correlations between traits, and selection intensity. The use of index selection in the study of yield component character of tomato was reported [7, 15-17]. In the index selection, the breeder sets a weighted value for each character according to its economic value. This is intended to optimize the genetic advance of economic characters and other secondary characters [18-21].

Tomato is a self-pollinating plant, and the selection of tomatoes is intended to improve the mean value of the target character and reduce variety [22]. Transgressive segregant utilization can greatly help the selection program. Transgressive segregation produces a genotype of the segregated population that has a high level of homozygosity and character mean values [23, 24]. The use of a transgressive segregant can accelerate the selection program of up to two generations [25, 26]. Transgressive segregant utilization in selection has been carried out on many plants such as green beans [27], *Pisum sativum* [28], and chili [29-31].

Evaluating the selection program can be done by comparing the value of genetic advance and the expected genetic advance [21, 32-34]. This was to find out the achievement of genetic advances from all of genotypes we had. This experiment was carried out to obtain a transgressive segregants genotype candidate and to determine the response of the selection method for the character of the tomato yield components.

## 2. Materials and Methods

### 2.1 Study area

The study was conducted during August 2018-April 2019 at the PT Bisi International Tbk Experimental Field, Village Citapen (518 m above sea level) with maximum and minimum temperatures of 37.8°C and 17.6°C, as well as maximum and minimum air humidity of 99% and 37%, respectively, and at the IPB University Experimental Field, Tajur II (300 m asl), Bogor, West Java, Indonesia. The study included a selection program for the  $F_2$  population, expected genetic advance, and verification of genetic advance in the  $F_3$  population.

### 2.2 Plant materials

The plant material was the  $F_2$  population from the crossing of 99D X Tora in a previous experiment [35]. Three hundred individual plants were subsequently selected to obtain 10 seed genotypes of  $F_3$ . The selected seed genotypes of  $F_3$  were planted as families, where each family consisted of 10 plants. The Intan and Ratna varieties (unpollinated or non-hybrid) were used as comparison varieties. These were varieties that had been commercialized.

### 2.3 Procedures

The complete populations of  $P_1$ ,  $P_2$ , and  $F_1$  from each set of crosses were planted in a greenhouse. Greenhouse optimization was carried out with the following principles: (1) homogeneous microclimate, (2) anticipation of pest attacks, (3) minimization of wind movement, and (4) irrigation that minimized the evaporation so that soil moisture was maintained (watering once a week was sufficient). The greenhouse did not have any system automation. The three populations were allowed to self-pollinate to produce  $P_1$ ,  $P_2$ , and  $F_2$ . The seeds of  $F_2$  genotype were planted as an  $F_2$  population with 300 individual plants in each set. Each  $F_2$  population set was selected at 3% ( $i = 2.21$ ), so that 10 lines of  $F_2$  from the best cross sets were obtained. As many as 10 plants of each selected line of the  $F_3$  population were planted to observe genetic advance of character compared to the  $F_2$  population.

The verification of genetic advances was carried out in the lowlands at an altitude of 300 m above sea level. The  $F_2$  population was used to compare genetic advances with the  $F_3$  population. Planting was carried out in open fields using a system of two rows per single bed (double row) with a distance within  $0.5 \times 0.6 \text{ m}^2$  and a distance between beds of 1 m. The size of the bed was  $20 \times 1 \text{ m}^2$ , so that one bed consisted of 80 plants. The composition of fertilizer used per bed was 15 kg of manure, 2 kg of urea and KCl, 3 kg of SP-36, and 4 kg of dolomite lime, which was applied 7 days before planting. After being processed and given fertilizer, the beds were covered with black silver plastic mulch.

Plant upkeep consisted of fertilizer application, irrigation, and pest and disease control. Advantageous fertilizer was given at 2, 3, 4 and 5 weeks after planting in the form of NPK (16:16:16) solution at a concentration of  $15 \text{ g L}^{-1}$  by pouring 250 ml for every plant on a hole that was 8-10 cm from the base of the plant stem. Gandasil D and B fertilizers were applied once a week along with spraying pesticides according to the plant growth phase, with a concentration of  $2 \text{ g L}^{-1}$  from 2 to 5 weeks after planting. Weed control was done manually.

Observations were made on characters of flowering time, fruit length, harvest time, fruit diameter, fruit weight per plant, fruit weight, and the numbers of fruits per plant. The selection was carried out with a selection index based on the correlation between yield component character and fruit weight. The character that had the best correlation coefficient was chosen as the character in the index selection to determine the genotype that would carry over to the next generation. The calculation of the selection index was carried out using the following formula [36]:

$$I = a_1Z_1 + a_2Z_2 + a_3Z_3 + \dots + a_nZ_n, \quad (1)$$

Where  $Z_n = (x - \bar{x}) / (\sqrt{\sigma^2})$ , I: total index value of a phenotype, a: weighted value of each variable, Z: standardized phenotype value, x: mean of variables of a genotype,  $\bar{x}$ : mean of variables of all genotypes,  $\sigma^2$ : variance of  $F_2$  population

### 2.4 Data analysis

The data analysis was carried out in two stages. The first stage was an analysis of the  $F_2$  population and selected  $F_2$ , and the second stage was to compare the  $F_3$  population with the  $F_2$  population. The analyzes carried out included:

Expected genetic advance to predict the selection response in the next generation using the following formula [36]:

$$R = ih^2\sigma_p \quad (2)$$

Where R: expected genetic advance, i: selection intensity,  $h^2$ : narrow sense heritability,  $\sigma_p$ : phenotypic standard deviation.

Genetic advance to determine the difference in the mean value between the  $F_3$  population and the  $F_2$  population using the following formula [37]:

$$G = \bar{x}F_3 - \bar{x}F_2 \quad (3)$$

Where G: genetic advance,  $\bar{x}F_2$ : mean of  $F_2$  population,  $\bar{x}F_3$ : mean of  $F_3$  population.

Realized heritability of  $F_3$  population using the following formula [37]:

$$h_{ns}^2 = \frac{G}{S} = \frac{\bar{x}F_3 - \bar{x}F_2}{\bar{x}SF_2 - \bar{x}F_2} \quad (4)$$

Where  $h_{ns}^2$ : narrow sense heritability, G: genetic advance, S: selection differential,  $\bar{x}F_3$ : mean of  $F_3$  population,  $\bar{x}F_2$ : mean of  $F_2$  population,  $\bar{x}SF_2$ : mean of selected  $F_2$  population.

Phenotypic variance of  $F_3$  population to determine the value of variance within families and between families using the following formula [38]:

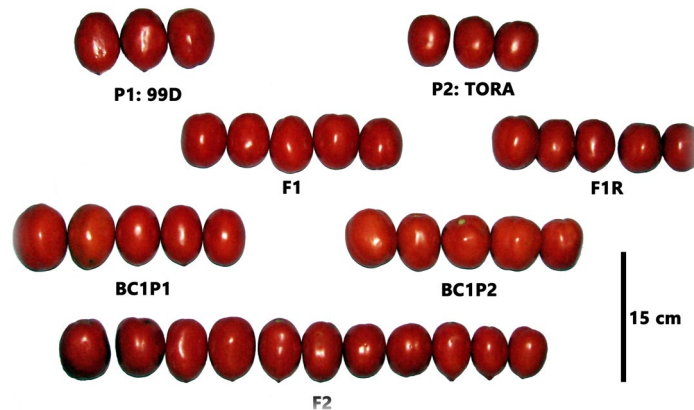
$$\sigma^2 = \frac{1}{N} \sum_{i=1}^N (x_i - \mu)^2 \quad (5)$$

Where  $\sigma^2$ : variance, N: total of  $F_3$  population,  $\mu$ : mean of  $F_3$  population,  $x_i$ : plant variable value related to trait i.

### 3. Results and Discussion

#### 3.1 Selection of tomato genotypes in $F_2$ 99D x Tora generation

Selection to obtain the superior segregants in this experiment was carried out on the  $F_2$  population from the 99D x Tora cross set (Figure 1). The selection was based on the best character that existed in the 99D x Tora cross set compared to the 97D x Tora such as genetic potential and adaptability. The results of the previous experiment [35] showed that although the two sets of crosses were equally affected by strong epistatic genes action, the proportion of additive genes in the 99D x Tora cross set was higher than the 97D x Tora cross set. This is indicated by the narrow sense heritability value.



**Figure 1.** The  $F_2$  population from the 99D x Tora cross set

As selection progresses, it was hoped that the additive gene frequency would replace the existing epistatic gene action [39]. In addition, the parents and the crossbreed population in the 99D x Tora set were relatively more resistant to high-temperature stress than the 97D x Tora set, so in this experiment, which was conducted at a lower altitude (compared to the previous experiment [35], the population of the 99D x Tora cross set was considered more suitable to be continued in the next generation.

The selection in this experiment was carried out using an index selection that had a weighted value. This meant that the target character was not only high fruit weight, but also productivity and early maturity. Index selection was very helpful in selecting several characters because the genetic advance of each character could be obtained proportionally according to its economic value [40, 41].

Character selection in determining the selection index must be supported by information about the correlation between characters and the main character. Significant correlation between characters in the development of selection criteria was studied using correlation and path analysis [7, 27, 42]. Table 1 shows the correlation coefficients of the yield component characters on the fruit weight. Characters that were highly significant and positively correlated were fruit diameter, fruit length, and fruit weight per plant. The character of flowering time was highly significant and negatively correlated, while the harvest time and the numbers of fruit did not show a significant correlation. A positive correlation value meant that it had a direct connection with fruit weight.

**Table 1.** Correlation coefficient values of yield component characters on tomato fruit weight in F<sub>2</sub> 99D x Tora population

No.	Characters	Correlation Coefficient
1	Flowering time (dap)	-0.26 **
2	Harvest time (dap)	0.07 ns
3	Fruit length (cm)	0.66 **
4	Fruit diameter (cm)	0.85 **
5	Fruit weight per plant (g)	0.36 **
6	Number of fruits	0.17 ns

ns: not significant; \*\*: significant at 1% level; \*: significant at 5% level according to the Pearson correlation test

The characters of harvest time, fruit diameter, fruit length, fruit weight per plant, and the number of fruits were still used in indexing. The character of the flowering time was not included because the correlation coefficient was already negative and significant. Early maturity criteria were represented by flowering time and harvesting time which showed genetic advance that was opposite (negative) to other characters, but these characters had different relationships to fruit weight, so for indexing the harvest time character was selected to be adjusted for its influence in selecting several characters.

The weighted value given to each character was: harvest time (-1), fruit diameter (1), fruit length (1), fruit weight per plant (5), and the number of fruit (1). Selection in the F<sub>2</sub> 99D x Tora generation was carried out with 3% ( $i = 2.21$ ), so that 10 genotypes were selected from 300 individuals in the F<sub>2</sub> population.

Table 2 shows the performance of the yield components of the selected genotypes. The ten selected genotypes had mean values of fruit weight character that were superior to their parents,

**Table 2.** Comparison of the mean value of yield component characters between the parental and the selected genotype from the index selection

No	Genotype	FLT	HVT	FRL	FRD	FRW	FWP	NFR
1	99D/Tora	22.40	73.03	6.65	4.51	85.28	3045.77	86.84
2	F <sub>2</sub> GH3-3	19.00	65.00	6.70	5.70	133.67	3262.00	52.00
3	F <sub>2</sub> GH3-241	23.00	65.00	5.90	5.03	103.00	4715.00	100.00
4	F <sub>2</sub> GH3-223	22.00	65.00	6.53	5.37	117.33	2857.00	84.00
5	F <sub>2</sub> GH3-59	24.00	68.00	6.73	4.43	89.67	4500.00	102.00
6	F <sub>2</sub> GH3-58	24.00	70.00	6.97	4.40	93.33	4270.00	87.00
7	F <sub>2</sub> GH3-6	24.00	68.00	6.57	5.07	101.00	3046.00	77.00
8	F <sub>2</sub> GH3-159	23.00	75.00	6.93	5.20	114.00	2751.00	80.00
9	F <sub>2</sub> GH3-248	27.00	70.00	6.77	5.03	111.67	2957.00	63.00
10	F <sub>2</sub> GH3-79	21.00	75.00	7.10	4.97	105.00	3088.00	72.00
11	F <sub>2</sub> GH3-123	21.00	75.00	6.87	5.13	118.33	2489.00	54.00

FLT: flowering time (dap); HVT: harvest time (dap); FRL: fruit length (cm); FRD: fruit diameter (cm); FRW: fruit weight (g); FWP: fruit weight per plant; NFR: number of fruits

99D or Tora, but for other characters, not all selected genotypes were superior. Four genotypes had mean values that were superior to parents on the character of flowering time, seven genotypes for the characters of harvest time and fruit length, eight genotypes for the character of fruit diameter, six genotypes for the character of fruit weight per plant, and three genotypes for the numbers of fruit characters.

Determination of index selection was also based on simulations that were carried out to compare index selection with selection using one character. Simulations were carried out with the same intensity. The results of the selection using a weighted index selection, fruit weight character, and fruit weight character per plant are shown in Table 3. Selection using one character was proven to be able to provide high potential for genetic advancement on target characters, but not on other characters. The results of selection using a weighted index selection show the potential for proportional advancement for each character, including fruit weight and weight per plant. This shows that selection using a weighted index selection was more suitable for selecting several characters [41, 43].

**Table 3.** Comparing the mean value of the selected population using index selection and selection with one character (fruit weight and fruit weight per plant)

Type of Selection	FLT	HVT	FRL	FRD	FRW	FWP	NFR
IS	23	70	6.71	5.03	108.70	3393.50	77.10
SFWP	23	69	6.27	4.78	91.93	4241.40	98.40
SFW	23	72	6.62	5.16	112.67	2694.80	60.20

IS: Index selection; SFWP: selection with fruit weight per plant character; SFW: selection with fruit weight character; FLT: flowering time (dap); HVT: harvest time (dap); FRL: fruit length (cm); FRD: fruit diameter (cm); FRW: fruit weight (g); FWP: fruit weight per plant; NFR: number of fruits

### 3.2 Genetic advance in F<sub>3</sub> generation

The genetic advance was calculated by comparing the mean of the selected populations F<sub>3</sub> and F<sub>2</sub>. The F<sub>2</sub> population in this experiment was a new population planted at the same time as the F<sub>3</sub> population, to reduce errors due to environmental influences between the previous experiment [35] and this experiment. Table 4 shows that the selected F<sub>3</sub> population had a higher mean value for all characters compared to the F<sub>2</sub> population. Comparable outcomes were likewise on the tomato yield component [44] and rice yield component [45]. Selection from F<sub>2</sub> to F<sub>3</sub> generations decreased the frequency of dominant gene action and increased additive gene action. This indicated that the additive genes in this population also contributed to increasing the mean value of each character.

The comparison between genetic advance and expected genetic advance showed a difference (Table 4), as well as between the narrow sense heritability in the previous experiment [35] and the realized heritability (Table 5). Realized heritability is a calculation using the selection response and selection differential, so the results reflect the diversity that is truly inherited in the next generation [37, 46, 47].

**Table 4.** Genetic advance on the yield component characters of the 99D x Tora population

No.	Characters	Mean		$\bar{G}$	Genetic Advance
		F <sub>2</sub>	F <sub>3</sub>		
1	Flowering time (dap)	30.74	29.27	2.33	1.47
2	Harvest time (dap)	70.69	70.43	4.48	0.26
3	Fruit length (cm)	6.56	6.77	0.66	0.21
4	Fruit diameter (cm)	4.79	4.87	0.43	0.08
5	Fruit weight (g)	75.13	79.88	24.38	4.75
6	Fruit weight per plant (g)	1627.27	1697.80	512.42	70.53
7	Number of fruits	40.01	44.45	0.34	4.44

$\bar{G}$ : expected genetic advance

**Table 5.** Comparison of F<sub>2</sub> heritability and realized heritability on the yield component characters of the 99D x Tora population

No.	Characters	$h^2_{ns} (\%)$	$h^2_{ns} (\%)$
		F <sub>2</sub> generation*	(Realized heritability)
1	Flowering time (dap)	-193.87	122.50
2	Harvest time (dap)	-165.17	9.59
3	Fruit length (cm)	72.50	22.90
4	Fruit diameter (cm)	72.41	13.49
5	Fruit weight (g)	72.61	14.15
6	Fruit weight per plant (g)	38.32	5.27
7	Number of fruits	1.96	25.64

\*: heritability of F<sub>2</sub> generation on the previous experimental [35]

The results of the expected genetic advance and heritability had a higher value than the real values for all characters except for the numbers of fruits. The numbers of fruits had a higher mean value than the expected genetic advance. The difference was caused by differences in environmental influences at the two experimental locations. The environmental stress in this experiment caused the

mean value of each character in the  $F_3$  population to be lower than the expected genetic advance. The different environmental conditions in the two experiments represented a shuttle breeding approach for exploring genes that were related to tolerance characters, especially high temperatures.

### 3.3 Verification of putative transgressive segregants

The verification of putative transgressive segregants for each character was carried out using genotypes that had lower variance and higher mean values than the pure lines. The characters of fruit length and fruit diameter were exceptions that were verified by their values of variance because they showed different fruit shapes between comparisons and selected genotypes. The  $F_3$  generation was a population that was still segregating, so that families of low diversity could be expected to have a high proportion of homozygous genotypes. The comparison used was a pure line variety, which meant that the level of homozygosity was close to the maximum for each character. This study did not use the source parents of the cross (99D and Tora) as a comparison because it was not possible for the two parents to be planted in this experimental location.

Table 6 shows the mean and variance characters of flowering time harvest time and fruit length between the comparison varieties (Intan and Ratna), with ten genotype families that were previously selected. There was one verified genotype of transgressive segregation in flowering time characters,  $F_3$ GH3-248. These genotypes had lower diversity and mean values than the two comparison varieties. The harvest time character also contained one transgressive segregant genotype,  $F_3$ GH3-248. There were six verified genotypes of transgressive segregant in fruit length character,  $F_3$ GH3-59,  $F_3$ GH3-6,  $F_3$ GH3-159,  $F_3$ GH3-248,  $F_3$ GH3-79, and  $F_3$ GH3-123.

**Table 6.** Mean value and variance of flowering time, harvest time, and fruit length characters in the  $F_3$  99D x Tora population

No.	Genotype	Flowering time (dap)		Harvest time (dap)		Fruit length (cm)*	
		Mean	Variance	Mean	Variance	Mean	Variance
1	Intan	27.82	11.76	68.18	10.36	4.44	0.43
2	Ratna	30.13	16.41	70.00	12.57	4.50	0.31
3	$F_3$ GH3-3	29.00	0.67	71.50	17.00	6.13	1.02
4	$F_3$ GH3-241	28.75	6.25	70.50	23.58	6.51	0.56
5	$F_3$ GH3-223	30.00	7.00	70.00	13.00	6.50	1.61
6	$F_3$ GH3-59	28.80	4.70	71.80	15.70	7.07	0.08
7	$F_3$ GH3-58	28.67	11.75	69.78	16.19	6.93	0.39
8	$F_3$ GH3-6	29.60	20.30	69.20	16.70	6.13	0.16
9	$F_3$ GH3-159	30.20	0.70	71.00	2.50	6.80	0.20
10	$F_3$ GH3-248	27.25	8.92	66.25	0.25	7.25	0.07
11	$F_3$ GH3-79	30.80	12.70	73.40	10.30	6.73	0.25
12	$F_3$ GH3-123	29.80	1.20	70.40	2.80	7.35	0.24

\*: comparison only to the value of variance

The mean and variance of fruit diameter and fruit weight characters between the comparison varieties and ten families of transgressive segregants are shown in Table 7. There were five transgressive segregants in fruit diameter characters,  $F_3$ GH3-6,  $F_3$ GH3-159,  $F_3$ GH3-248,



F<sub>3</sub>GH3-79, and F<sub>3</sub>GH3-123. The fruit weight characters contained four verified transgressive segregants, F<sub>3</sub>GH3-59, F<sub>3</sub>GH3-6, F<sub>3</sub>GH3-248, and F<sub>3</sub>GH3-79.

Table 8 shows the mean and variance of fruit weight per plant and numbers of fruit in both comparison varieties and ten selected genotype families. The character of fruit weight per plant contained four transgressive segregant genotype, F<sub>3</sub>GH3-241, F<sub>3</sub>GH3-223, F<sub>3</sub>GH3-79, and F<sub>3</sub>GH3-123, while the numbers of fruit character contained only one genotype, F<sub>3</sub>GH3-123. Transgressive segregants verified by comparing the mean and variance [47, 48] between selected genotype families and homozygous comparisons were also reported in *Pisum sativum* [28], and chili [29-31].

**Table 7.** Mean and variance of fruit diameter and fruit weight characters in the F<sub>3</sub> 99D x Tora population

No.	Genotype	Fruit diameter (cm)*		Fruit weight (g)	
		Mean	Variance	Mean	Variance
1	Intan	4.88	0.34	58.37	253.85
2	Ratna	5.48	0.73	52.36	296.78
3	F <sub>3</sub> GH3-3	4.55	0.60	70.34	860.80
4	F <sub>3</sub> GH3-241	5.11	0.48	80.49	516.76
5	F <sub>3</sub> GH3-223	4.99	0.92	80.63	1645.83
6	F <sub>3</sub> GH3-59	4.58	0.08	85.52	136.13
7	F <sub>3</sub> GH3-58	4.99	0.60	81.53	470.22
8	F <sub>3</sub> GH3-6	4.67	0.05	64.28	34.57
9	F <sub>3</sub> GH3-159	5.08	0.12	84.12	355.27
10	F <sub>3</sub> GH3-248	5.08	0.15	95.05	189.35
11	F <sub>3</sub> GH3-79	4.54	0.14	68.39	74.16
12	F <sub>3</sub> GH3-123	5.13	0.18	88.71	495.96

\*: comparison only to the value of variance

**Table 8.** Mean and variance of fruit weight per plant and number of fruits in the F<sub>3</sub> 99D x Tora population

No.	Genotype	Fruit weight per plant (g)		Number of fruit	
		Mean	Variance	Mean	Variance
1	Intan	1156.45	199122.27	31.45	92.07
2	Ratna	1168.25	219371.64	35.13	167.27
3	F <sub>3</sub> GH3-3	2206.75	1340545.58	41.75	301.58
4	F <sub>3</sub> GH3-241	1682.50	106941.67	60.50	433.67
5	F <sub>3</sub> GH3-223	2150.67	8986.33	57.33	400.33
6	F <sub>3</sub> GH3-59	1514.00	255342.50	38.00	123.50
7	F <sub>3</sub> GH3-58	1670.56	378434.03	40.33	141.00
8	F <sub>3</sub> GH3-6	1415.60	405234.30	42.20	261.70
9	F <sub>3</sub> GH3-159	1140.00	492850.00	32.00	950.00
10	F <sub>3</sub> GH3-248	2823.75	245356.25	64.50	174.33
11	F <sub>3</sub> GH3-79	1444.00	161417.50	45.40	266.30
12	F <sub>3</sub> GH3-123	1457.00	26045.00	37.60	18.30

Verification results (Table 9) show the number of genotypes verified by putative transgressive segregants for the characters of flowering time, harvest time, fruit length, fruit diameter, fruit weight, fruit weight per plant, and the numbers of fruit (1, 1, 6, 5, 4, 4, 1 genotypes, respectively) of the ten observed genotypes. There is a pattern that is close to the heritability value in the previous experiment [35]. This shows that the percentage of transgressive segregants was strongly influenced by the proportion of additive gene action in a character.

**Table 9.** Recapitulation of verified putative transgressive segregants from 10 families F<sub>3</sub> 99D x Tora

No.	Char.	Mean			Variance			Ver. (%)
		Intan	Ratna	PTS	Intan	Ratna	PTS	
1	FLT	27.82	30.13	27.25	11.76	16.41	8.92	10
2	HVT	68.18	70.00	66.25	10.36	12.57	0.25	10
3	FRL	4.44	4.50	6.13 - 7.35	0.43	0.31	0.07 - 0.03	60
4	FRD	4.88	5.48	4.54 - 5.13	0.34	0.73	0.05 - 0.18	50
5	FRW	58.37	52.36	64.28 - 95.05	253.85	296.78	34.57 - 189.35	40
6	FWP	1156.45	1168.25	1444.00 - 2150.67	199122.00	219371.00	8986.00 - 161417.00	40
7	NFR	31.45	35.13	37.60	92.07	167.27	18.30	10

Char.: characters; Ver.: verified transgressive segregant; PTS: putative transgressive segregants; FLT: flowering time (dap); HVT: harvest time (dap); FRL: fruit length (cm); FRD: fruit diameter (cm); FRW: fruit weight (g); FWP: fruit weight per plant; NFR: number of fruits

#### 4. Conclusions

This study showed the positive genetic advances for each character. Comparing the values of real genetic advance with the expected genetic advances showed the differences. The expected genetic advance had a higher value than the genetic advance for the characters of flowering time, harvest time, fruit length, fruit diameter, fruit weight, and fruit weight per plant, while the numbers of fruit had genetic advance exceeding the expected value. The transgressive segregation was contained in each of the observed characters, but no genotypes showed transgressive segregant criteria for all of the characters. The most transgressive segregant criteria were found in the F<sub>3</sub>GH3-248 genotype which was superior to the comparison varieties Intan and Ratna for five of the seven characters observed.

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