PERFORMANCE OF PEANUTS *(Arachis hypogaea* L.*)* LINES FROM SELECTION OF TRANSGRESSIVE SEGREGANTS

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ABSTRACT

Superior variety is one of the main technology components that play an important role in the program of increasing peanut production. The improved varieties have some advantages over the local varieties that still dominate today's peanut crops, for example in terms of productivity, age, and tolerance to biotic and abiotic stress. The performance of the F5 generation lines showed that G113 genotype has the shortest plant height. Genotype of G99 has the highest pod number with higest fresh pod weight ang highest dry kernel weight also, so it has the potential to be developed in the following season. Characters of plant height, fresh stover weight, shell pod weight, dry kernel weight, and pods number were significantly correlated with fresh pod weight which represent the yield. Plant height character showed a direct effect to the fresh pod weight with the negative value so that it can be indicated that high plants will produce a low fresh pod weight. The fresh stover weight shows the highest direct effect on the fresh pods weight. Cross sectional analysis can show the height character of the plant, the weight of the fresh stover, the weight of the shell pods, the weight of dry kernels and the number of pods as the character of selection to obtain new varieties with the ideal character of short height and high fresh pod weight.

Keywords: correlation, fresh pod weight, path analysis, pod number

INTRODUCTION

Peanuts are plants originated in South America with a wide adaptability in subtropical and tropical areas. According to Wang *et al*. (2012), peanuts rank on the fourth position as a source of vegetable oil and the 13th as a worldwide important food planted widely in more than 80 countries. According to Janina *et al.* (2013), peanuts are planted more than 24 million hectares in the world. Sumarno (1993) explained that this plant is widely planted in Indonesia, particularly in the region of East Java, Central Java, and West Java. Peanut productivity ranges from 0.5 tons ha^{-1} of dry pods. America and Australia are the countries with the highest productivity ranging from 3 tons to 5 tons ha^{-1}. Meanwhile, tropical country productivity is only about 0.7 to 1.3 tons ha^{-1} of dry pods. Sumarno (1993); Adisarwanto (2001); Yudiwanti *et al.* (2008) explained that low productivity is probably affected by various factors such as cultivation technology, agroclimatic characteristics, pest, varieties, harvest age, and farming system.

The increasing demands of the protein and fat with the increasing of world population causes the demand for peanut also continues to increase. Furthermore, each country tries to meet the sufficiency of peanuts in their country (Sumarno, 1993). Naeem-ud-Din *et al.* (2012) reported that Pakistan has a peanut variety BARI 2011 with the potential yield of 2.5-6.3 tons of dry pods as well as tolerant to drought stress, leaf spots, and root rot disease. Domestic peanut varieties released from 1995 to 2014 amounted to 34 varieties with a low productivity of 1.2-3.0 ton of dry pods (Kasno & Harnowo, 2014). The low yield has not been able to meet the needs of the country so that the assembly of superior varieties with high productivity still needs to be done in order to meet the community demands for peanut.

High yield is a major goal in the development of plant genetics (Wang *et al.,* 2012). One of the steps taken in plant breeding is a selection (Sa'diyah *et al.,* 2009), an important stage in peanut yield (Smith & Simpson 1995). However, there are several factors to consider in the plant selection-based phenotype such as diversity, heritability, and its correlation to agronomic characteristics that can improve the peanuts yield (Sa'diyah *et al.* 2009; Jogloy *et al.,* 2011).

The effectiveness of the selection is influenced by the availability of diversity in the population to be selected. The greater the population diversity affects on higher effectiveness to choose the desired character (Sa'diyah *et al.*, 2009). In addition to diversity, another factor that determines the effectiveness of a selection is heritability, a genetic parameter to measure the extent of genotype inherits traits possessed by a plant. Moreover, the information of the relationship between characters can be calculated by correlation analysis to determine how far the relationship between characters. Furthermore, competition between characters can lead to negative correlations between characters. Genetic factors that can cause the correlation between characters is the linkage and pleiotropy (Falconer, 1989).

Genetic correlations can be utilized for indirect selection when the main characters selected have high heritability. The existence of a correlation between two characters can be influenced by pleiotropy and linkage events. Pleiotropy is a phenomenon occurs when one gene in a locus or a set of genes in some locus controls two or more different characters. If part of the locus controlling character A and B, then both characters are considered to be genetically correlated. The linkage is the phenomenon of the presence of two or more genes that control twoor more different characters located on the same chromosome unit. Both of the characters tend to be inherited together as the control of the gene lies on the same chromosome of which the presence of character A is regularly followed by the character B (Sa'diyah *et al.,* 2009). According to Kotzamanidis (2006), the character and quality of the yield can be improved by utilizing the phenomenon of transgressive segregation in Virginia and Spanish crosses. Jambormias (2014) reported that the phenomenon of transgressive segregation in green beans reached 18-24% transgressive segregation families.

Various methods have been conducted by researchers from research institutes as well as from genetics and plant breeding of IPB in producing superior varieties of peanut. One of them is the utilization of transgressive segregation phenomenon by selecting of transgressive segregants that can accelerate the fixation of genes until the F5 generation thereby affecting the time effectiveness.

This research aimed to (1) obtain information on the peformace of F5 generation of peanut derived from trangressive segregation selection, and (2) study the correlation among quantitative characters and the path of those which directly affect the yield to determine the selection characters.

MATERIALS AND METHODS

Time and Place

The study was conducted from March to June 2017 in the experimental farm of Biotrop, Ciawi, Bogor. The calculation of the component results was conducted in Seed Laboratory, Department of Agronomy and Horticulture, Bogor Agricultural University.

Materials and Tools

The test material consisted of 35 families of F5 generation from 5 biparental populations (Jerapah/GWS79A1, GWS79A1/Zebra, GWS79A1/Jerapah, Zebra/GWS79A1, and Zebra/GWS18) and 4 commercial varieties (Gajah, Jerapah, Sima, dan Zebra) as comparison varieties. Other materials used were phonska fertilizer with a dose of 200 kg ha^{-1} and lime fertilizer with a dose of 500 kg ha^{-1}. Tools used were cultivation equipments, plant stake, scissors, plastic strap, meter, label, digital scales, and digital cameras.

Research Procedure

The experiments were prepared using a Completely Randomized Design (CRD) with a factor of peanut lines. In this experiment, each genetic materials were planted as a line of the family with 30-plant spread across 3 experimental replications. Each line was replicated while the commercial variety was also randomized as a comparison in replication.

Before planting, the soil was processed first and then divided into 35 plots. At the time of planting, the planting spacing used was 40 cm x 20 cm with one seed per hole. Phonska, Furadan and lime fertilizers were applied at planting time. Maintenance consisted of embroidery, irrigation, weeding as well as pests and diseases control in accordance with the level of attacks. Plants were harvested at 105 DAP (days after planting) by removing the plants and then separating each strain. The harvest time was characterized by real streaks on the pod's skin, fully loaded pods, and inner skin pods turned to brown. The process of drying pods was done by drying ± 8 hours per day in sunny weather for 3 days. The observation of agronomic character in 6 plant samples per unit of experiment included: plant height (cm), fresh stover weight per plant (g), branch number per plant, shell pod weight per plant (g), dry kernel weight per plant (g), 100 kernels weight (g), harvest index, pod number per 6 plants (g), and fresh pod weight per 6 plant (g).

Data Analysis

The data obtained were analyzed by calculating variance components at α 0.05. The use of proc mixed in SAS in CRD was randomized treatment and block (Santos *et al.*, 2002). If the tested treatment had a significant effect on the observed character, then it continued with Tukey test at α 0.05 using SAS 9.1.3 software. The normality on assumptions of the model of information of family and its comparison was tested with the Kolmogorov-Smirnov test while the homogeneity of the variance was tested with the Levene and Bartlett tests.

The analysis of simple linear correlation coefficient values was calculated based on the Pearson correlation formula (Gomez & Gomez, 2007) as follows:

$$r = \frac{\sum x_1 \, x_2}{\sqrt{(\sum x_1^2)(\sum x_2^2)}}$$

Where:
r = correlation coefficient
x1 and x2 = the observed variables

The closeness of relationship between characters was analyzed using Pearson correlation analysis followed by path analysis based on the simultaneous equation as follows (Singh and Chaudhary 1979):

$$\underbrace{\begin{bmatrix} r_{11} & r_{12} & \cdots & r_{1p} \\ r_{21} & r_{22} & \cdots & r_{2p} \\ \cdots & \cdots & \cdots & \cdots \\ \cdots & \cdots & \cdots & \cdots \\ r_{p1} & \cdots & \cdots & r_{pp} \end{bmatrix}}_{R_x} \underbrace{\begin{bmatrix} C_1 \\ C_2 \\ \cdots \\ \cdots \\ C_p \end{bmatrix}}_{C} = \underbrace{\begin{bmatrix} r_{1y} \\ r_{2y} \\ \cdots \\ \cdots \\ r_{py} \end{bmatrix}}_{R_y}$$

Based on the above equation, the value of C can be calculated using the formula:

$$C = R_x^{-1} R_y$$

Where:
Rx = Correlation matrix between independent variables
Rx^{-1} = Inverse of matrix-Rx
C = Vector coefficient of the trajectory showing the direct effect of an independent variable that has been standardized to the dependent variable
Ry = Vector of correlation coefficients between the independent variables xi (i = 1, 2, …, 11) with dependent variables-y

RESULTS AND DISCUSSION

The development of peanut breeding is aimed at getting character improvements according to the idiotype expected by consumers. The idiotype based on consumer demand is as follows: productivity per hectare, number of pods per plant, number of branches, the weight of pod, weight of 100 grain, and velocity of 50% flowering time. Recapitulation of genotype signification on some quantitative characters of peanut in this research were listed in Table 2.

Based on the variance analysis, there were highly significant different characters for plant height, branches number, fresh stover weight, pod number, fresh pod weight, shell pod weight, dry kernel weight, and harvest index. Only 100 kernels weight that showed no significant different (Table 2).

Table 2. Recapitulation of genotype signification on some quantitative characters of peanut

Characters	Pr > F	CV (%)
Plant height (PH)	<.0001**	8.19
Branches number per plant (BN)	0.0001**	13.93
Fresh stover weight per plant (FSW)	0.0001**	28.19
Fresh pod weight per 6 plants (FPW)	0.0001**	28.67
Pod number per 6 plants (PN)	0.0001**	21.97
Shell pod weight per plant (SPW)	0.0005**	25.11
100 kernels weight (100K)	0.0778ns	19.45
Dry kernel weight per plant (DKW)	<.0001**	24.66
Harvest Index (HI)	<.0001**	26.93

Table 3. Recapitulation of further test for 35 peanut genotypes on vegetative characters

Genotype	Plant height (cm)	Branch number	Fresh stover weight (g)
G13	48.51 abcdef	6.1 ab	41.94 abc
G14	48.80 abcdef	5.0 ab	36.27 abc
G21	58.99 defghij	6.4 b	25.13 ab
G29	64.13 hij	6.8 ab	35.30 abc
G31	57.87 cdefghij	4.8 ab	28.84 ab
G33	63.41 ghij	5.8 ab	45.46 abc
G37	47.17 abcde	4.8 ab	54.90 abc
G39	47.96 abcde	5.1 ab	53.42 abc
G41	44.14 abc	4.3 ab	50.49 abc
G53	55.73 abcdefghij	4.7 ab	34.18 abc
G54	56.63 abcdefghij	5.1 ab	37.99 abc
G66	52.14 abcdefghi	4.3 ab	47.49 abc
G76	60.69 efghij	6.1 ab	31.48 abc
G83	50.22 abcdefgh	3.9 a	41.07 abc
G84	51.16 abcdefgh	4.4 ab	58.92 bc
G87	55.60 abcdefghij	6.1 ab	32.37 abc
G96	57.64 bcdefghij	4.7 ab	19.58 a
G99	43.91 abc	4.6 ab	68.53 c
G100	50.93 abcdefgh	4.3 ab	51.55 abc
G113	42.90 a	5.5 ab	56.03 abc
G126	49.19 abcdefg	5.3 ab	44.42 abc
G133	68.09 j	4.8 ab	30.97 abc
G142	59.40 defghij	6.0 ab	38.17 abc
G144	52.71 abcdefghi	4.3 ab	50.08 abc
G159	46.18 abcde	5.6 ab	36.91 abc
G188	66.17 ij	4.7 ab	37.42 abc
G190	59.73 defghij	4.0 a	37.88 abc
G193	59.49 defghij	4.8 ab	19.35 a
G199	43.20 ab	4.3 ab	36.58 abc
G205	55.41 abcdefghij	6.1 ab	32.52 abc
G209	55.90 abcdefghij	4.3 ab	54.67 abc
G219	45.29 abcd	4.9 ab	41.63 abc
G234	60.03 efghij	5.1 ab	30.87 abc
G236	62.77 fghij	5.1 ab	41.66 abc
G237	50.51 abcdefgh	4.9 ab	52.21 abc

Values followed by the same letters in each variable show no significant different based on Tukey-test at α 0.05

Table 4. Recapitulation of further test for 35 peanut genotypes on yield characters and harvest index

Genotype	PN	FPW	SPW	DKW	100K	HI
G13	118.0 abc	41.94 abc	6.07 abc	13.64 abcde	42.33 a	9.64 a
G14	110.0 abc	36.27 abc	4.08 ab	9.95 abc	36.70 a	10.36 a
G21	103.0 abc	25.03 ab	3.72 ab	9.11 ab	32.30 a	11.62 ab
G29	109.3 abc	35.30 abc	5.36 abc	12.59 abcde	25.43 a	16.28 ab
G31	111.7 abc	28.80 ab	4.27 abc	8.18 a	35.17 a	8.14 a
G33	174.3 bc	45.46 abc	7.64 abc	21.98 cde	46.57 a	19.57 ab
G37	161.0 bc	54.87 abc	6.12 abc	14.37 abcde	28.30 a	13.77 ab
G39	133.3 abc	53.42 abc	6.25 abc	20.45 bcde	41.07 a	20.77 ab
G41	93.3 ab	49.99 abc	4.47 abc	14.32 abcde	34.80 a	10.94 ab
G53	162.7 bc	32.01 abc	5.12 abc	14.67 abcde	35.03 a	21.04 ab
G54	113.3 abc	37.99 abc	6.12 abc	16.21 abcde	39.87 a	15.19 ab
G66	124.7 abc	46.01 abc	5.36 abc	15.85 abcde	38.57 a	18.95 ab
G76	120.0 abc	28.36 ab	4.52 abc	14.68 abcde	46.90 a	16.22 ab
G83	122.7 abc	39.26 abc	5.13 abc	14.33 abcde	35.07 a	20.10 ab
G84	168.7 bc	58.37 bc	7.81 abc	17.25 abcde	31.17 a	18.88 ab
G87	140.0 abc	32.37 abc	4.61 abc	10.19 abc	28.97 a	11.83 ab
G96	68.3 a	19.56 a	3.35 a	7.47 a	32.57 a	9.76 a
G99	191.3 c	68.53 c	8.23 bc	23.38 e	39.60 a	17.54 ab
G100	152.7 abc	51.52 abc	8.75 c	22.49 de	40.27 a	21.17 ab
G113	148.7 abc	55.83 abc	7.10 abc	17.07 abcde	31.70 a	14.77 ab
G126	113.7 abc	44.43 abc	4.86 abc	13.62 abcde	34.63 a	16.28 ab
G133	118.7 abc	30.97 abc	6.27 abc	14.18 abcde	41.60 a	17.98 ab
G142	103.0 abc	33.02 abc	5.68 abc	13.39 abcde	40.60 a	13.39 ab
G144	104.7 abc	49.24 abc	6.69 abc	19.16 abcde	38.37 a	24.13 b
G159	156.3 abc	36.91 abc	6.04 abc	15.13 abcde	38.87 a	10.46 a
G188	91.0 ab	36.21 abc	4.42 abc	10.94 abcd	39.73 a	12.96 ab
G190	130.7 abc	39.24 abc	7.03 abc	18.54 abcde	44.97 a	24.44 b
G193	87.0 ab	20.66 ab	4.35 abc	8.13 a	34.90 a	12.24 ab
G199	119.7 abc	36.58 abc	5.94 abc	16.18 abcde	40.03 a	19.10 ab
G205	142.3 abc	32.48 abc	5.67 abc	13.87 abcde	39.03 a	14.75 ab
G209	123.7 abc	55.35 abc	6.92 abc	17.54 abcde	35.77 a	13.73 ab
G219	150.7 abc	41.63 abc	5.79 abc	13.03 abcde	29.30 a	12.25 ab
G234	151.3 abc	30.87 abc	5.25 abc	15.68 abcde	38.00 a	24.43 b
G236	109.3 abc	41.66 abc	5.60 abc	12.98 abcde	36.60 a	12.81 ab
G237	146.3 abc	52.14 abc	8.23 bc	18.10 abcde	32.67 a	17.73 ab

PN (pod number), FPW (fresh pod weight), SPW (shell pod weight), DKW (dry kernel weight), 100K (100 kernels weight), HI (harvest index); values followed by the same letters in each variable show no significant different based on Tukey-test at α 0.05

The character that shows very significant different were then followed by a further test of Tukey. The highest plant height was 68.09 cm in genotype G133, the highest fresh stover weight was 68.53 in genotype G99 while the lowest in genotype G193, the highest number of branches was in genotype G21 of 6.4 and the highest fresh pod weight was in genotype G99 of 68.53 (Table 3, 4).

The highest shell pod weight characteristic was obtained by the genotype G100 which reached 8.75, the highest dry kernel weight was found in genotype G99 with 23.38, the highest harvest index was obtained by genotype G190 which reached 24.22 and the highest pod number per 6 plants was in genotype G99 of 191.3, or approximately 30 pods pe plant (Table 4).

The selection of ideal characters in a population can be preceded by correlation analysis for some samples (Meehl & Waller, 2002). Selection through correlation analysis can be aimed at productivity character per hectare, number of pods per plant, number of branches, weight of pods, and weight of 100 seeds. The weight of seeds per plant showed the highest positive significance with the total number of pods per plant, pod size and 50% flowering time (Zaman *et al.*, 2011). High heritability is found in the character of productivity per hectare, number of pods per plant, number of branches, weight of pod, and weight of 100 seed, it is very effective to be used as a character of selection in the development of peanut plant breeding. Relationship of the character of fresh pod weight (FPW) on plant height (PH), fresh stover weight (FSW), branches number (BN), shell pos weight (SPW), dry kernel weight (DKW), 100 kernels weight (100K), harvest index (HI) and pods number (PN) are shown in Table 5.

Table 5. Pearson's correlation coefficient among quantitative characters of peanut

	FSW	BN	SPW	DKW	100K	HI	PN	FPW
PH	-0.34**	0.16	-0.13	-0.18	0.14	0.09	-0.25**	-0.34**
FSW		-0.03	0.67**	0.69**	0.04	0.10	0.44**	0.99**
BN			-0.01	-0.10	0.03	-0.35**	0.07	-0.02
SPW				0.85**	0.17	0.36**	0.63**	0.68**
DKW					0.34**	0.56**	0.55**	0.69**
100K						0.25**	0.05	0.05
HI							0.28**	0.10
PN								0.45**

**significantly correlated at α 0.01, PH (plant height), FSW (fresh stover weight), BN (branch number), SPW (shell pod weight), DKW (dry kernel weight), 100K (100 kernels weight), HI (harvest index), PN (pod number), FPW (fresh pod weight)

Correlation analysis can be used as a basis for selecting the characters of pod and yield. The productivity of the yield can be due to the polygon and the environmental factors. A character may be inherited if the predicted value of the correlation coefficient is high compared with the phenotypic coefficient. The yield component characteristics of pod productivity can be affected by weight of peanut skins, weight of peanut skin percentage and weight of 100 seed (John *et al.*, 2015). The weight of dry pods was positively correlated with weight of peanut skin, the number of pods per plant and weight of 100 seeds (Rao *et al.*, 2014). The weight of 100 seeds and harvest index are important in identifying yield per plant (Korat *et al.,* 2010; Zaman *et al.,* 2011). Based on the result of observation in Table 5, the characteristic of plant height, fresh stover weight, shell pod weight, dry kernel weight and pod number significantly positively correlated with fresh pod weight. Correlations can be negative as in plant height with weight of fresh pods (-0.34) so it can be indicated that high plants will produce a low weight of fresh pods (Table 5). Zaman's *et al.* (2011) reported a negative correlation between the character of the harvest time and the weight of pods per plant.

Significant correlation coefficients between two characters may not necessarily indicate that the two characters are related to each other (Majumder *et al.*, 2012) as well as how big the relationship is (Meehl & Waller, 2002), so it is necessary to conduct cross-sectional analysis, or path analysis, to explain causal relationships and levels of closeness between characters. The coefficient of cross-sectional analysis is a simple regression standard by dividing the correlation coefficients to determine the direct and indirect effects (Majumder *et al.*, 2012). The relationship of direct and indirect effects on weight of fresh pods in the population of F5 peanut generation is shown in Figure 1.

Based on the result of the path analysis, the character that gives a direct influence to fresh pod weight is plant height, fresh stover weight, dry kernel weight, and pod number. The number of mature pods per plant showed a positive direct effect on productivity per hectare and followed by pod size, the percentage of weight of peanut skins, and 50% flowering (Zaman *et al.*, 2011). Path analysis can be used to obtain direct influence of the characters of the number of pods within the 3rd generation (Luz *et al.*, 2011). Path analysis shows that the number of pods per plant is an important character to the increase of productivity (Rao *et al.*, 2014; Luz *et al.* 2011; Zaman *et al.* 2011).

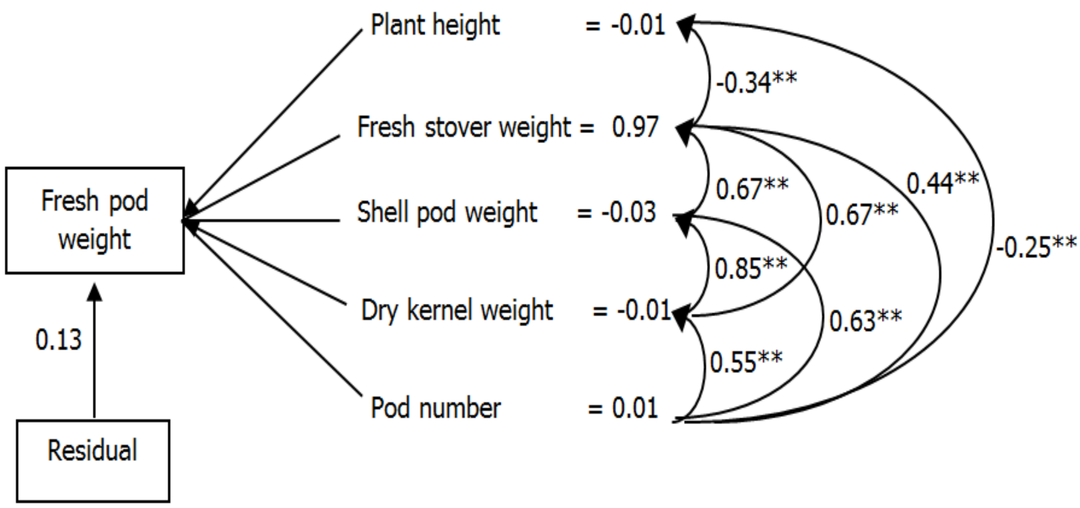

Figure 1. Diagram of path analysis of the fresh pod weight with plant height, fresh stover weight, shell pod weight, dry kernel weight, and pod number of peanut

The character of fresh stover weight shows the highest direct effect (0.97) on the fresh pod weight, the greater the fresh stover weight impact on greater of fresh pod weight. However, the characters of fresh stover weight, shell pods weight, dry kernel weight require the initial measurement then furtherly be a selection characters, thus it requires other previous activities such as weighing. Selection character will be good if it is easily observed visually in the field. The character of plant high can be used as a selection character to estimate the fresh pods weight. Based on the results of the analysis (Figure 1), the plant height character showed a direct effect with a negative value which indicated that the high plant will produce a low-weight of fresh pod. The genotype G199 has the shortest plant height (43.20 cm) and G113 (42.90 cm), and the potentially producing high fresh pod weight are genotypes G199 (36.58) and G113 (55.83).

CONCLUSION

The character of plant height, fresh stover weight, shell pod weight, dry kernel weight and pods number were significantly correlated with thefresh pod weight. The cross-sectional analysis can show the character of plant height, fresh stover weight, shell pods weight, dry kernel weight and pods number as the characters of selection to obtain new varieties with ideal character of plant namely short plant with a high fresh pods. The genotypes G199 (43.20 cm) and G113 (42.90 cm) reveals the shortest plant height while that potentially producing high fresh pod weight are genotypes G199 (36.58) and G113 (55.83). Peanut genotype G99 also has the potential to be developed in the following season as it has a lot of pods compared to other genotypes.

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