



Genetic diversity of character agronomy population single seed descent

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Abstract

Selection of the population F3 and F4 by method single seed descent was to obtain information about the genetic diversity character agronomy and yield components. The experiment was conducted at experimental field of the Agency for Biotechnology and Genetic Resource, Bogor start October 2012 to May 2013. The genetic material were F3 and F4 population derived from single seed descent. The result showed that mean of the population F4 higher than the population F3 to all characters. Components variability of phenotype, environment and genetic population F4 higher of the population F3 for almost all the characters except number of branches and 100 seed weight characters. The heritability estimates for population F3 and F4 were classified as moderate to high. The heritability estimates for population F3 only 100 seeds weight character were classified as moderate, while the heritability estimates for population F4 character of number of vacuum pods, seeds weight per plant, 100 seeds weight and sink size were classified as moderate. The genetic diversity coefficient for population F3 and F4 character of number of branches, number of vacuum pods, seeds weight per plant, and 100 seed weight were classified as narrow, while the genetic diversity coefficient for character of plant height, number of book, total number of pods, number of pithy pods and sink size were classified as broad.

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Introduction

The availability of varieties soybean adaptive and capable of producing high is the key major in the effort to soybean in Indonesia. This effort intended to meet the needs of soy and reduce dependence on were imported. Genotype soybeans having the characteristics of hope be in accordance with introduction followed by study adaptation and genetic recombination with crossing or mutation. Indonesia has several varieties superior soybean as Tanggamus, Ratai, Nanti, Sibayak and Rajabasa. The varieties were result of the activities breeding done in indonesia (Deptan, 2012).

The formation of program varieties soy adaptive in dry acid soil has been started in 1995 (Arsyad, 2007). Research activities covering evaluation germ plasm, the formation of the population breeding through crossing, step of lines formation and selection, evaluation of the preliminary and advanced of yield and test many place.

The success of formation varieties soybean adaptive to agroecosystem Indonesia determined by the availability of a source of genetics and genetic variability was broad, as well as the awareness about control and the pattern of genetic segregation characters that being the aim of improving. Genetic source of soybean that can be used as the base to produce expected varieties can be obtained through the introduction and crossing. Broad genetic variability can be estimated through characterization the introduction and crossing of varieties. Genetic control and analysis of pattern segregation agronomy character obtained through crossing design and analysis next generation of crossing. The understanding of genetic control of the characters that the purpose of repair be used as basis in determining the time and method of selection accurate in breeding population.

Selection in selfing plants can be divided into several methods, namely mass selection, pure line selection, pedigree selection, bulk and single seed descent selection (SSD) (Syukur *et al.* 2009).

Commonly, the method of bulk and SSD used to selection of quantitative character or heritability character was classified as low to moderate. Selection on two methods was conducted in the said (Roy, 2000; Chahal and Gosal, 2003). Single seed descent selection is method of selection devoted to keep genetic diversity during the segregant population of one generation to the next generation by not adding room and area for planting. The choice of expected genotypes done when already fixation optimal between alleles characterized in continued generation. Commonly, method of selection is used for the study genetic relating to mapping the locus character quantitative (Falconer and Mackay, 1996).

This research began with crossed two parent and obtained generation F₁ and F₂. Generation F₂ continued until F₄ with single seed descent method. Single seed descent method done by planting only one seed of one plant in one generation. Single seed descent method was easier maintain the mean and higher diversity of the population compared with bulk method (Srivastava, 1989). The principle of single seed descent method is an individual plant chosen from crossing at F₂ and then grown only one seed of one plant in one generation. Commonly, this way performed to generation 5th (F₅). This research aims to obtain information about the genetic diversity agronomy and yield character of F₃ and F₄ genotypes with single seed descent method.

Materials and methods

The experiment was conducted at experimental field of the Agency for Biotechnology and Genetic Resource, Bogor start October 2012 to May 2013. The genetic material were F₃ and F₄ population derived from single seed descent. Seed planted with the distance 30 cm x 20 cm one seed per hole by given treat inoculum rhizobium about 5g for 1kg seeds to help the formation of pustule roots.

The cultivation until ready planting done two weeks before planting. Plants given fertilizer base with doses 50 kg ha⁻¹ urea, 100 kg ha⁻¹ SP36 and 100 kg ha⁻¹ KCl. Maintenance and pest disease/weed done according to the conditions of plant.

Agronomy characters observed were plant height, number of the productive branch, number of pods pithy, number of vacuum pods, number of productive books, seeds weight per plant, 100 seed weight and sink size.

Note :

- h^2_{bs} = broad sense heritability
- V_P = phenotype variance
- V_G = genotype variance
- CVG = coefficient of genetic variability

All data were obtain, analyzed with Program Minitab 16. The data obtained was analyzed to count components variance, analysis genetic diversity, and heritability estimated use formula as follows:

$$VE = KTe/r$$

$$VG = Ktg - KTe$$

$$VP = VG + VE$$

$$h^2_{bs} = \frac{VG}{VP}$$

$$CVG = \sqrt{VG/\bar{X}}$$

Results and discussion

Success in genetic improvement plants strongly determined by genetic diversity. The results of the analysis components variance, heritability and CVG shown in Table 1 show that there is variation variance of the phenotype, genetic, environment, heritability and the CVG in the population F3 and F4. Differences in environment in the same location caused by the differences conditions of micro environmental which includes factors physical and chemical soil.

Table 1. Analysis variance component. coeffisien variance genetic dan broad sense heritability agronomy character in two generation.

CHARACTER	Number of individual		Mean		σ^2_p		σ^2_e		σ^2_g		h^2_{bs}		CVG	
	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄	F ₃	F ₄
Plant height	261	166	40.0	62	115.9	137	41.2	41.7	74.6	95	64.4	69.5	21.7	15.6
													(broad)	(broad)
Number of branch	261	166	4.1	7	10.1	6	2.5	2.3	7.6	4	75.0	62.1	67.9	29.3
													(narrow)	(narrow)
Number of book	261	166	24.5	55	108.1	387	48.0	111.6	60.1	275	55.6	71.2	31.7	30.0
													(broad)	(broad)
Number total of pods	261	166	89.3	160	2321.4	4906	421.4	1352.1	1899.9	3554	81.9	72.4	48.8	37.2
													(broad)	(broad)
Number of pithy pods	261	166	85.4	156	2120.1	4687	386.8	1242.7	1733.0	3444	81.8	73.5	48.8	37.6
													(broad)	(broad)
Number of vacuum pods	261	166	4.0	4	20.1	15	6.1	7.5	14.0	7	69.6	48.5	95.3	62.6
													(narrow)	(narrow)
Seed weight per plant	261	166	14.7	28	62.5	159	14.3	103.7	48.2	55	77.1	34.9	47.1	26.8
													(broad)	(broad)
100 seed weight	261	166	9.1	10	3.7	4	2.8	2.5	0.9	1	23.8	34.2	10.3	11.7
													(narrow)	(narrow)
Sink size	261	166	17.1	34	95.5	214	17.0	121.3	79.5	93	82.4	43.4	52.3	28.8
													(broad)	(broad)

Keterangan : σ^2_p = variance phenotype; σ^2_e = variance environment; σ^2_g = variance genetic; h^2_{bs} = broad sense heritability;

CVG = coefficient variance genetic; broad, narrow = classification score of CVG.

Number of population in F3 and F4 generation

The results of the experiment number of the population in F3 and F4 showed decreasing. It is estimated that happened because of the sprouts genotype F4 was decrease by around 36,4%,

where population of F3 there were about 261 genotypes while population F4 only there were about 166 genotypes, whereas previously the number of genotype of population F2 were about 512 so happened decreasing about 47,8% in the population F3.

The minimum number of population could be accomplished for the next generation (F5 and F6), if number of early population namely F2 population reckoned.

Based on the research done so suggested to planted around 1000 genotypes F2 that can be obtained about 650 genotypes F3,

about 500 genotypes F4 and about 350 genotypes F5 so that it will obtained 200 genotypes F6.

Reduction in the number of genotypes in F4 caused by the death toll from natural selection of the climate condition. The diminishing number individual in the population F4 can also caused by inability plant produced seeds (Fehr, 1987).

Table 2. Value skewness, gene action and value kurtosis F3 and F4 population by crossing Argomulyo with Tanggamus in optimum condition.

Character	Skewness		Gene Action	Kurtosis	
	F3	F4		F3	F4
Plant height	-0.13	-0.32	Additive+ epistasis duplicate	-0.12	0.71
Number of branch	6.67	0.73	Additive+ epistasis complementary	77.18	0.83
Number of book	0.29	0.39	Additive+ epistasis complementary	-0.19	0.40
Number total of pods	0.73	0.43	Additive+ epistasis complementary	0.50	-0.02
Number of pithy pods	0.69	0.40	Additive+ epistasis complementary	0.46	-0.02
Number of vacuum pods	1.95	1.28	Additive+ epistasis complementary	4.51	1.79
Seed weight per plant	0.77	1.05	Additive+ epistasis complementary	1.02	2.07
100 seed weight	0.88	1.64	Additive+ epistasis complementary	2.69	4.81
Sink size	0.89	0.81	Additive+ epistasis complementary	1.05	1.42

The mean population in the F3 and F4

The studies genetic control agronomy character known that almost all agronomy characters learned on this experiment in is controlled by polygenic with additive gene action and duplicate epistasis or complementary.

The additive epistasis gene action found on almost all the characters, so that need more individuals segregant planted in the next generation to increase the amount of expected segregant. According to Barona *et al.* (2012), the influence of epistasis complementary and duplicate not inheritable to next generation.

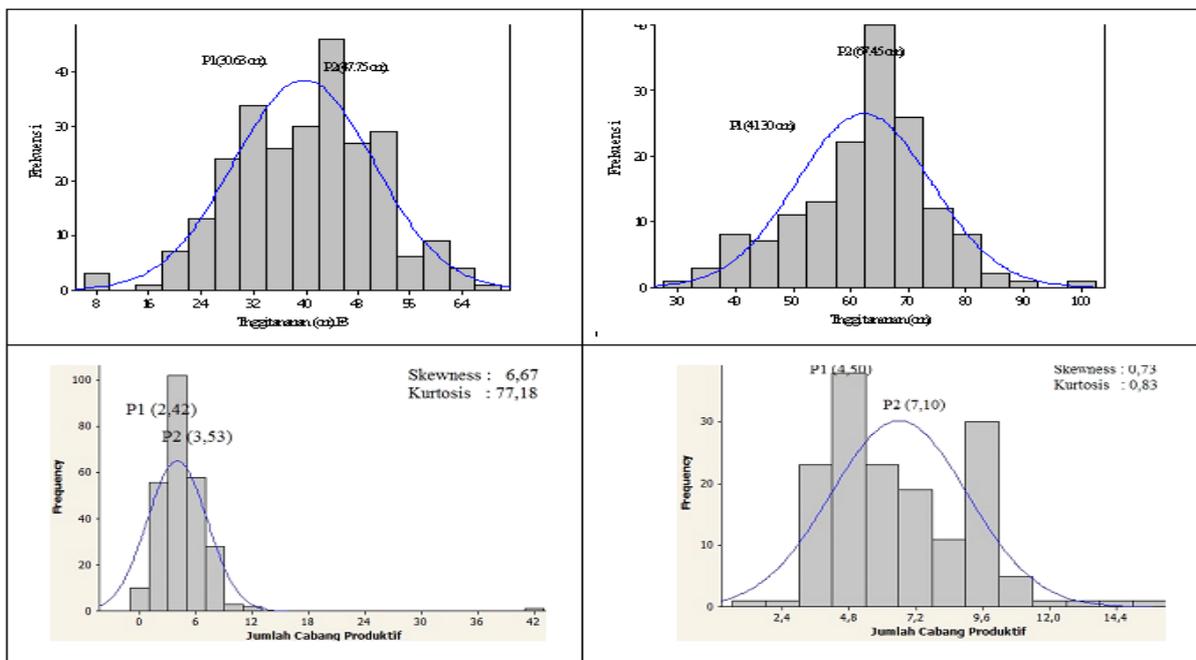


Fig. 1. Charts distribution of plant height and number of productive branch F3 and F4 population in optimum condition.

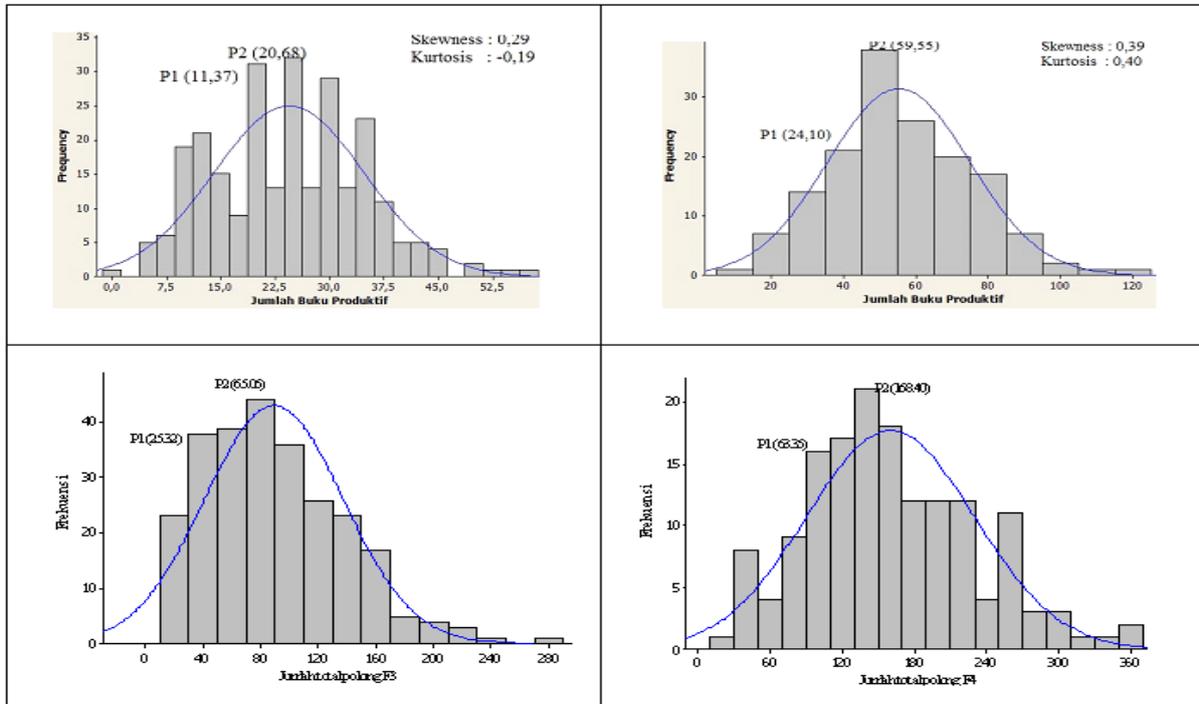


Fig. 2. Charts distribution of number of productive book and number total of pods F3 and F4 population in optimum condition.

Based on the results of the analysis shows that estimated the mean F4 population higher than the F3 population to all the observed characters although not done selection only done selection by self pollination.

An increase in the mean all the characters is allegedly because the action of genes that occurs an action of genes additive epistasis complementary on all character except plant height character that is additive epistasis duplicate.

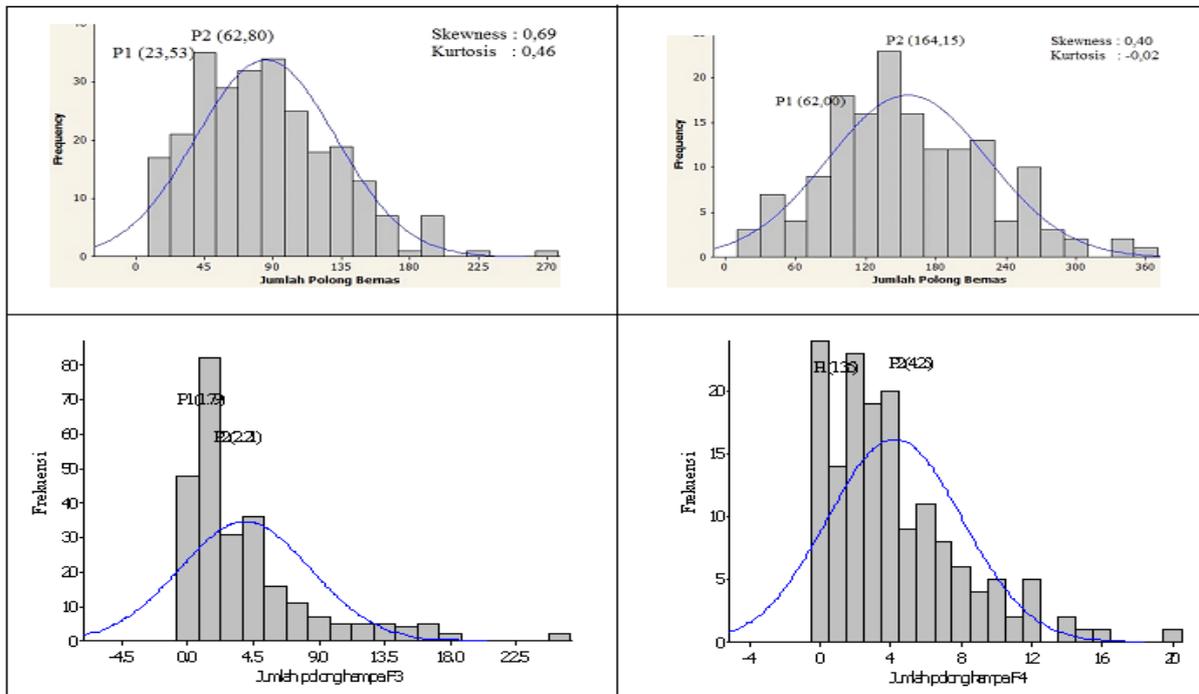


Fig. 3. Charts distribution of number of pithy pods and number of vacuum pods F3 and F4 population in optimum condition.

The epistasis duplicate to the plant height show that to get expected segregant should be more many segregants planted. Theoretically influence epistasis will decreases for the continued generation selection (Roy, 2000).

In the population F3 and F4 has happened fixation genes additive that causes the mean F4 population higher than F3 population and in the F4 is estimated homozygous had been high ($\pm 90\%$) (Riaz *et al.* 2003).

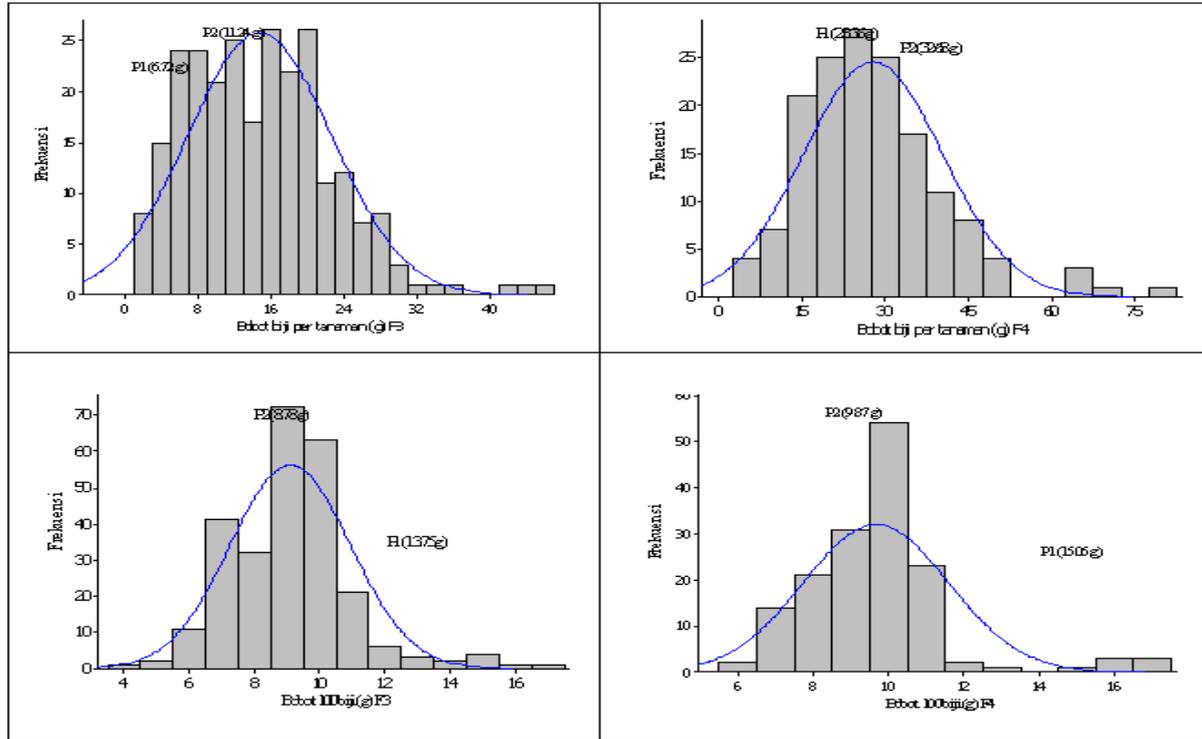


Fig. 4. Charts distribution of seed weight per plant and 100 seeds weight F3 and F4 population in optimum condition.

Variance value of the population in the F3 and F4

Based on the research done in the population F3 and F4 shows that variance of all the observed characters higher in the population F4 except character of number of branches and the number of vacuum pods. Hayward (1990) said that diversity this F4 population can increase caused by seed planted is derivated seed of F4 still segregation by the action of genes additive and epistasis complementary, because of the not action genes additive are not inheritable and be dissipated in the process to make lines (selfing). The results of estimated skewness value. The action of gene and value kurtosis population F3 and F4 seen in Table 2.

An analysis of a pattern to scatter to the whole character observed there are in Figure 1 to Figure 5. The action of genes in the F3 and F4 population unchanged.

Almost all the observed characters in the F3 and F4 population having pattern to scatter to be continuous. This shows that all the observed characters estimated controlled many genes and epistasis complementary, except plant height character who was suspected to be controlled in polygenic by the action of genes additive and epistasis duplicate. Different type epistasis can cause distinction expression and phenotype. The epistasis complementary that controls agronomy character also reported Nazeer *et al.* (2010).

Value heritability population in the F3 and F4

Heritability show inheritance of the nature of tolerance soybean to aluminum in the acid soil. Based on the research done information was obtained that in the F3 population all the observed characters has value broad sense heritability classified were high only 100 seeds weight classified were low, while value broad sense heritability F4 population to the seeds weight per plant and 100 seeds weight.

This means that for all the characters observed in the F3 and F4 is controlled more by genetic factors than environmental factors (Poehlman and Slepper, 1996).

Value broad sense heritability F4 population higher than F3 population to the characters of plant height, number of books and 100 seeds weight,

while value broad sense heritability F3 population higher than F4 population to the characters of number of branch, number total of pods, number of pithy pods, number of vacuum pods, seeds weight per plant although not done selection, but selection natural to can occur.

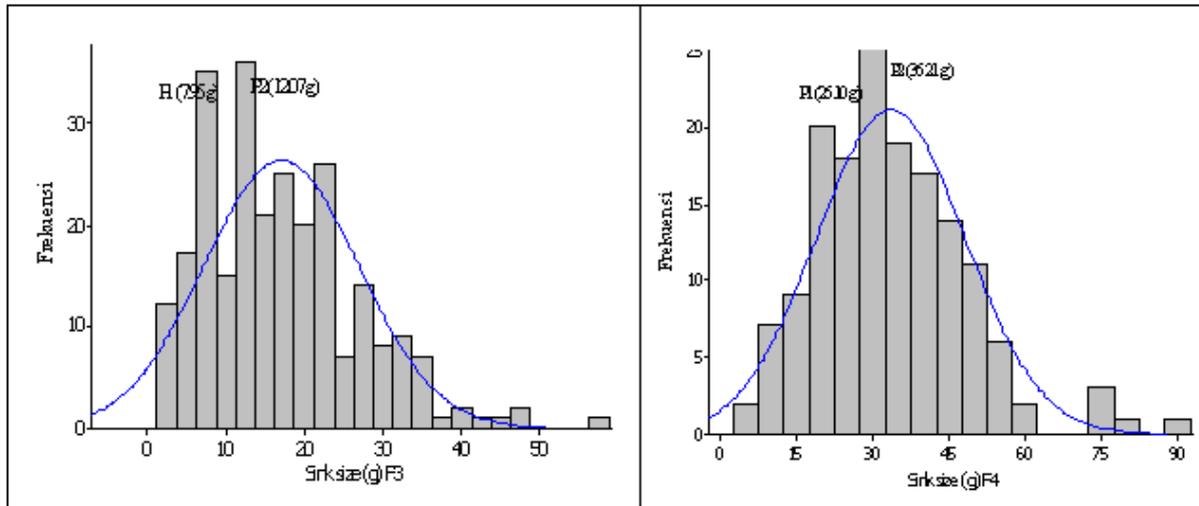


Fig. 5. Charts distribution of sink size F3 and F4 population in optimum condition.

Coefficients of genetic variability (CVG) in F3 and F4 population

The coefficient of genetic variability (CVG) all of the observed characters in the F3 and F4 fixed (unchange) namely are narrow and broad. Almost all of the observed characters having the CVG are broad, except character of number of branches, number of vacuum pods and 100 seeds weight having the CVG are narrow. The character of CVG is broad indicates that progress genetic is high. The value estimated genetic progress was high on a character indicates that appearance such characters is controlled more by genetic factors (Suprpto *et al.* 2007).

Conclusion

The mean F4 population higher than F3 population to all of the characters. Variance components of the phenotype, environment and genetic F4 population higher than F3 population for almost all the characters except character of number of branches and 100 seeds weights.

In the F3 and F4 population value heritability classified are moderate to high. In F3 population only character weight 100 seeds value heritability classified are moderate, while in F4 population character of number of vacuum pods, seeds weight per plant, 100 seeds weight and sink size value heritability classified are moderate.

In the F3 and F4 population value of the CVG are narrow to characters of number of branches, number of vacuum pods, seeds weight per plant and 100 seeds weights, while value of the CVG are broad to the characters of plant height, number of books, total number of pods, number of pithy pods, and sink size.

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