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# Assessment of Gene Action for Agronomy Characters in Segregating Generation of Soybean [*Glycine max* (L.) Merr.]

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# Abstract

Gamma ray irradiation is one of way to improve the plant genetic diversity. Seeds of Anjasmoro variety was treated with 100 Gy, 200 Gy and 300 Gy doses of Gamma-rays. The gene action for the agronomy characters in the mutated segregating generation was found out based on the frequency distribution of characters through measurement of skewness and kurtosis value. The frequency distribution for the agronomy characters viz., time of flowering, plant height, number of primary branches, seeds weight per plant and weight of 100 seeds were obtained. The skewness and kurtosis estimate were calculated to study the gene action. The number of primary branches recorded positive skewness value in all the three irradiated doses. The others characters have positive skewness value but different characters of each irradiated doses. This indicates the presence of complementary epistatic gene action for these traits and if selection will be made intensively in the segregating generations the gain will be faster of each characters in the three irradiated doses.

Keywords: gene action, segregating generation, soybean

# Background

Soybean is not a native plant from Indonesia, but it is introduction plants that originated from China. Soybean is self-pollinated plants that are kleistogami and soybean genetic diversity in Indonesia is still low (Adie and Krisnawati 2007). To increase the genetic diversity of soybean plants can be done through mutation breeding to improve desired characters of plants. Mutation breeding is a way to obtain genetic diversity of characters quantitative and qualitative in plants (Manjaya and Nandawar 2007; Kavithamani *et al.* 2010).

Mutations with high dose irradiation, usually leads to genetic instability (Van Harten 1998). The micro mutations change the quantitative characters derived from seeds irradiated and more beneficial for breeders. Micro mutations caused little damage although these mutations were difficult to detect. Micro mutations can increase the diversity on yield, protein content, plant height, time of flowering, pod production, seed weight and other results related to the quantitative inherited characters (Sakin 2002; Tah 2006). The irradiation dose is different for each cultivar and soybean varieties. In general, the dose of gamma irradiation for legumes ranged from 100 Gy to 200 Gy (Bhatia *et al.* 2001).

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Superior varieties obtained through plant breeding to the improvement of yield and crop adaptation. The new varieties require a population base which has a high genetic diversity and gene action that influence it.  $M_2$  population is a segregation population after gamma-ray irradiation, in which each individual of the population have the possibility randomly mutated genes so that the genetic diversity in each character different from irradiation genotype population. The objective of this study is to identifying the gene action of agronomy characters in soybean by studying the segregating  $M_2$  population.

#### **Materials and Methods**

Irradiation treatment was performed at BATAN (National Atomic Energy Agency) and field research was conducted at the University of Sumatra Utara, Medan. Soybean seed varieties of Anjasmoro were treated with 100, 200, 300, 400, 500, 600, 700, 800, 900 and 1000 Gy of gamma irradiation derived from irradiator gamma chamber. The effect of irradiation on germination was observed. Based on the observations the LD<sub>50</sub> value for germination to gamma rays was arrived at 425,416 Gy for seed soybean of Anjasmoro. Hence, the treatment doses viz., 100 Gy, 200 Gy and 300 Gy were chosen for conducting the field experiment. A total of 100 seeds (M<sub>1</sub>) planted with a spacing 40 x 20 cm<sup>2</sup>. For the M<sub>1</sub> generation, in each plant at each treatment dose, 10 pods per plant then were harvested (restricted bulk) and grown as an M<sub>2</sub> generation. Then 1500 seedlings of M<sub>2</sub> seeds were planted for each dose treatment with spacing of 40 x 20 cm<sup>2</sup>, and the variability in agronomic characters viz., time of flowering, plant height, number of primary branches, seeds weight per plant and weight of 100 seeds were evaluated. treatment. Based on the observations the Skewness and Kurtosis estimates to study the gene action.

# Results

Genetic variation and heritability of Anjasmoro soybean variety at different irradiation doses can be seen in Table 1.  $M_2$  plants are expected to show segregation at the genetic locus that has mutation. Genetic variety can be observed in  $M_2$  generation. In this study observations focused on agronomic characters like time of flowering, plant height, and yield components.

Character	Gamma Dosage	Coefficient	of variability	Heritability Value
		Genetic	Phenotype	
Time of flowering	100 Gy	1.33	2.13	1.00
	200 Gy	7.24	7.51	93.00
	300 Gy	8.32	6.33	95.00
Plant height	100 Gy	10.80	12.87	61.00
	200 Gy	6.97	11.34	38.00
	300 Gy	16.93	19.25	77.00
Number of primary branches	100 Gy	16.80	20.18	7.00
	200 Gy	12.05	27.63	35.00
	300 Gy	7.20	39.11	43.00
Seed weight per plant	100 Gy	18.98	25.43	27.00
	200 Gy	16.00	42.30	46.00
	300 Gy	51.84	62.66	21.00
Weight of 100 seeds	100 Gy	8.46	13.79	38.00
-	200 Gy	24.45	27.66	78.00
	300 Gy	48.86	50.16	95.00

#### Table 1. Variance and heritability for agronomic characters in M<sub>2</sub> generation of Anjasmoro soybean

Based on data in Table 1, the character seed weight per plant and weight of 100 seeds having coefficient variation genetic that ranged from low to high, while for the other characters observed coefficient variation genetic ranged from low to medium. The range of heritability values ranged from 1.00 to 95.00 on all the characters are observed.

Character	Gamma Dosage	Skewness	Kurtosis	
Time of flowering	100 Gy	0.25	-1.04	
	200 Gy	-0.33	6.09	
	300 Gy	0.69	-0.87	
Plant height	100 Gy	-0.09	-0.69	
	200 Gy	-0.28	-0.10	
	300 Gy	-0.31	-0.83	
Number of primary branches	100 Gy	0.06	-0.38	
	200 Gy	1.68	5.42	
	300 Gy	0.39	-0.19	
Seed weight per plant	100 Gy	0.07	0.73	
	200 Gy	-0.21	0.15	
	300 Gy	-0.19	-1.29	
Weight of 100 seeds	100 Gy	0.23	0.36	
	200 Gy	-0.97	2.64	
	300 Gy	1.63	8.43	

Table 2: Skewness and kurtosis value for agronomic characters in M<sub>2</sub> generation of Anjasmoro soybean

Table 2 shows that the positive skewness value found in the parameter number of primary branches in three doses of irradiation in the population was observed. Positive kurtosis value found in weight of 100 seeds characters in three population's irradiation was observed. In other parameters, skewness and kurtosis varied, ranging from negative and positive value

#### Discussions

The approach to estimating gene action for the quantitative traits in the mutated segregating generations was found out based on the frequency distribution of characters. Skewness describes the degree of departure of a distribution from symmetry or it shows the action of genes that control a character. Kurtosis characterizes the peakedness of a distribution or it estimates the number of genes (Roy 2000). The positive skewness indicated the influence of additive gene with the presence of complementary epistatic gene action for that character. The negative skewness indicated the influence of additive gene with the presence of duplicate epistatic gene action (Roy 2000). Kurtosis will occur if either a few genes are contributing to the phenotypic distribution. Traits (characters) showing leptokurtic distribution are usually under the control of few segregating genes and traits showing a platykurtic distribution usually represent characters that are controlled by many genes. The positive values of kurtosis indicated leptokurtic curve and negative kurtosis indicated platykurtic curve.

Genetically, the diversity of agronomic characters in M<sub>2</sub> populations of soybean irradiated by gamma rays due to the segregation of genes within loci that have mutations in the M<sub>1</sub>. The diversity that occurs as a result of segregation genes from affected population irradiation caused the diversity of quantitative characters on M<sub>2</sub> generation (Van Harten 1998; Tah 2006; Manjaya and Nandawar 2007; Pavadai *et al.* 2010). Previous researchers have reported hereditary changes in the desirable characters in crop plant by using gamma rays as a physical mutagen, which has been used to develop 64 % of the radiation-induced mutant varieties (Ahloowalia *et al.* 2004). High expectation value of broad sense heritability was found in the observation variable such as time of flowering, plant height and weight of 100 seeds. Selection for improvement of these characters can be done to produce genotypes with the desired time of flowering, plant height and production. For other characters, the estimated expectation value of heritability range from low to moderate. Sakin (2002) who observed wheat found that heritability for some mutant population depends on the characters observed.

The characters number of primary branches had positive skewness values in all the three irradiated doses (Table 2). This indicates the presence of complementary epistatic gene action for this character and if selection will be made intensively in the segregating  $M_2$  generations for number of primary branches. Selection can be done in early generations, until it can be obtained the better of selection progress later.

The kurtosis values estimate for the weight of 100 seeds had positive values in all the three treatments indicated that the character is controlled by few segregating genes only. Based on Jayaramachandran *et al.* (2010) the characters panicle length and 100 grain weight controlled by few segregating genes confirms that the genes actions are disturbed by irradiation.

# Conclusions

The variability of agronomic characters of soybean after irradiation was due to genetic factor. The highest heritability values menunjukkan adanya pewarisan genetik dan seleksi bisa dilakukan pada generasi awal dari karakter yang diinginkan. Skewness and kurtosis positive value indicates that the additive gene action and complementary epistatic gene plays a role determining the selection process and the progress of the selection that will be done later.

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