Physiological performance of the soybean crosses in salinity stress

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Physiological performance of the soybean crosses in salinity stress

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Abstract. Plants grown in saline soils will experience salinity stress. Salinity stresses, one of which causes oxidative stress, that cause an imbalance in the production ROS compounds (Reactive Oxygen Species), antioxidants and chlorophyll. Where the reaction of this compound can affect plant growth and plant production. This study aims to inform performance and action gene to soybean physiological character that potential to tolerant from salinity soil that characterized by the presence of SOD and POD antioxidant compounds and chlorophyll. This research used a destructive analysis from crossbred (AxN) and (GxN). A = Anjasmoro varieties and G = Grobogan varieties as female elders and N = Grobogan varieties as male elders (N1,N2,N3,N4,N5) that have been through the stage of saline soil selection. Research result can be concluded that GxN cross is more potential for Inheritance of the offspring. This can be seen from the observed skewness of character SOD, POD compounds, Chlorophyll a and chlorophyll b.

1. Introduction

Soybean is a favorite crop food in Indonesia because of its high nutritional value. [1] BPS recorded soybean production in 2012 of 843.153 tons, in 2013 the production decreased by 779,992 tons. The next year 2014 soybean production increased by 954,997 tons and in 2015 the production is 963,099 tons. Despite increased by production but still not in line with the needs and the amount of public consumption. Therefore in Indonesia, this plant needs special attention.

In Indonesia, salinity-exploited agricultural land may be expanding, due to rising sea levels, sea water intrusion, waste pollution and excessive land exploitation, especially coastal areas [2]. [3] It is estimated that the area of agricultural land affected by salinity is 440,300 ha. The challenge is how the area of saline soils is used for a variety of competitive crops [4]. Salinity is an abiotic factor that limits the production of soybean crops worldwide, which is a limiting factor inhibiting growth and yield potential. Salinity causes depressed plants, where subsequent plants undergo structural changes that include changes in morphological, physiological and biochemical mechanisms.

The mechanisms of plant resistance to salinity depend on species and varieties, start from the sensitive to the level of tolelan. Response of plant to salt resistance is avoidance mechanism and those who do adapt mechanisms to be tolerant. One particularly effective way for plant breeders to overcome the decline in soybean production and saline expansion is through genetic improvement efforts by developing varieties of saline-resistant crops through crosses and adaptation selection. The
response of plants to salinity is of course important in efforts to improve the potential of this plant. This study aims to inform performance and action gene to soybean physiological character that potential to tolerant from salinity soil that characterized by the presence of SOD, POD compounds, Chlorophyll a and chlorophyll b.

2. Materials and Methods
This research was conducted at the screen house of the Faculty of Agriculture, University of North Sumatra and Physiology Laboratory of Sungai Putih. This research used a destructive analysis from crossbred seeds (AxN) and (GxN). A = Anjasmoro varieties and G = Grobogan varieties as female elders and N = Grobogan varieties as male elders (N1,N2,N3,N4,N5) that have been through the stage of saline soil selection.

Research methods that used is statistic descriptive analysis, where normality test data distribution and genotype frequency do to SOD, POD, chlorophyll a and chlorophyll b. Graph form for skewness and kurtosis value calculated with pearson theory, furthermore result obtained interpreted and characterized as follow (Table 1).

| Test Data Normality | Graphic Form      | Information                                           |
|---------------------|-------------------|-------------------------------------------------------|
| Skewness = 0        | Normal Distribution | Action gene additive                                  |
| Skewness < 0        | Abnormal Distribution | Action of additive gene with the effect of duplicate epistasis |
| Skewness > 0        | Abnormal Distribution | Action of additive gene with complementary epistatic effect |
| Kurtosis = 3        | Mesokurtik        |                                                       |
| Kurtosis < 3        | Platykurtik       | The characters are controlled by many genes           |
| Kurtosis > 3        | Leptokurtik       | Characters are controlled by few genes                |

3. Results and Discussion
3.1 Superoxide Dismutase Activity (SOD)
The observed Superoxide dismutase activity AxN crossover (figure 1.a.) shows result not normally distributed. The result of AxN crossing shows average activity of SOD 11.910 shows crossover result higher from elder N and lower than form elder A. The highest SOD actifity is 25.272 and lowest is 1.731. Action gene expected value for SOD activity (Table 2) skewness explain additive action gene with epistatic complemernter influence and kurtosis with playkurtik graph form explain character is controlled by many genes.

The observed Superoxide dismutase activity GxN crossover (figure 1. b.) shows result not normally distributed. The result of GxN crossing shows average activity of SOD 16.777 shows crossover result higher from elder N and G. The highest SOD actifity is 40.246 and lowest is 6.726. Action gene expected value for SOD activity (Table 2) skewness explain additive action gene with epistatic complemernter influence and kurtosis with playkurtik graph form explain character is controlled by many genes.

In the beginning phase of salinity stress, osmotic stress attributed by physiologist alteration, like membrane interference, unbalanced nutrition, disturb ability to oxygen reactive species (ROS) detoxification. First step during oxygen reduction is superoxide (O$_2^-$) establishment that can be converted to hydrogen peroxide (H$_2$O$_2$) with superoxide dismutation (SODs) action [5]. [6] Sopandie explained that plant develop detoxification system through enzymatic or non-enzymatic to face up ROS, so be able to protect cell from oxidative stress. SOD formed in plant very influential to some physiology phenomenon, including H$_2$O$_2$ lost, toxic reductant oxidation, biosynthesis and lignin
degradation in cell wall, auxin catabolism, self defense response against injury and some respiration process.

Figure 1. Grap of SOD activity distribution (unit/ mg protein) (a), AxN (b) and GxN crossover

3.2 Peroxide Activity (POD)

The observed peroxide activity AxN crossover (figure 2.a.) shows result not normally distributed. The result of AxN crossing shows average activity of POD 0.663 shows crossover result higher from elder N and lower than form elder A. The highest POD actifity is 1.643 and lowest is 0.094. Action gene expected value for POD activity (Table 2) skewness explain additive action gene with epistatic complementer influence and kurtosis with playkurtik graph form explain character is controlled by many genes.

The observed peroxide activity GxN crossover (figure 2. b) shows result not normally distributed. The result of GxN crossing shows average activity of POD 0.627 shows crossover result higher from elder N and G. The highest POD activity is 0.469 and lowest is 0.111. Action gene expected value for POD activity (Table 2) skewness explain additive action gene with epistatic complemenoter influence and kurtosis with playkurtik graph form explain character is controlled by many genes.

Figure 2. Grap of POD activity distribution (unit/mg protein) (a), AxN (b) and GxN crossover

Observed parameter result peroxide activity (figure 2.a,b) highest peroxide activity by AxN crosses result. Peroxide is antioxidant compound that can parry Hydrogen Peroxide (H\(_2\)O\(_2\)) compound, peroxide boost oxidation of some peroxide compound, especially H\(_2\)O\(_2\) that reduced to form water, enzyme that have active character, when in peroxide plant can help to minimize damage caused by stress factor [7]. Peroxide activity enhancement will increasing toxin product to pathogens so withstand infection. [8] Peroxide is a member of the reductase enzyme, isoenzyme that play a role in grow, differentation and defense. Peroxide catalyze H\(_2\)O\(_2\) to H\(_2\)O and O\(_2\) substrate feniline damin
compound like 3-amino-9-etil karbazole will oxidized with oxygen from reduction, that can be marked with formed a brownish red colored precipitate. [9] Other research mention that high enzyme peroxide activity can increase plant endurance to decease. In this research POD activity take effect to production, when POD enhancement parallel with number of plant escalation.

3.3 Chlorophyll a
The observed chlorophyll a AxN crossover (figure 3.a.) shows result not normally distributed. The result of AxN crossing shows average chlorophyll a 3.098 shows crossover result higher from elder n and lower than form elder a. The highest chlorophyll a value is 3.870 and lowest is 1.755. Action gene expected chlorophyll a (Table 2) skewness explain additive action gene with epistatic duplicate influence and kurtosis with playkurtik graph form explain character is controlled by many genes.

The observed chlorophyll a GxN crossover (figure 3.b.) shows result not normally distributed. The result of GxN crossing shows average chlorophyll a 1.652 shows crossover result lower from elder N and G. The highest chlorophyll a value is 3.492 and lowest is 0.525. Action gene expected chlorophyll a (Table 2) skewness explain additive action gene with epistatic complementer influence and kurtosis with playkurtik graph form explain character is controlled by many genes.

![Figure 3. Graph of chlorophyll a distribution (mg/g) (a), AxN (b) and GxN crossover](image)

3.4 Chlorophyll b
The observed chlorophyll b AxN crossover (figure 4. a) shows result not normally distributed. The result of AxN crossing shows average Chlorophyll b 2.910 shows crossover result higher from elder A and lower than form elder N. The highest chlorophyll b value is 3.786 and lowest is 1.851. Action gene expected chlorophyll b (Table 2) skewness explain additive action gene with epistatic duplicate influence and kurtosis with playkurtik graph form explain character is controlled by many genes.

![Figure 4. Graph of Chlorophyll b distribution (mg/g) (a), AxN dan (b) GxN crossover](image)

The observed chlorophyll b GxN crossover (figure 4. b) shows result not normally distributed. The result of GxN crossing shows average Chlorophyll b 1.777 shows crossover result lower from elder
N and G. The highest Chlorophyll b value is 2.943 and lowest is 0.554. Action gene expected chlorophyll b (Table 2) skewness explain additive action gene with epistatic complement influence and kurtosis with playkurtik graph form explain character is controlled by many genes.

Observed parameter result chlorophyll a and chlorophyll b (figure 3,a,b and 4,a,b) that potentially developed in salinity soil based highest chlorophyll value is result of crosses AxN. Chlorophyll is the main component of chloroplasts and chlorophyll positive correlated with photosynthesis rate. High content of chlorophyll in a plant shows that a plant potentially grow in salinity soil. Genotypically from observed result can be seen that chlorophyll a decreased if compared by chlorophyll b in salinity condition. According to Mane et al.[10] that content of chlorophyll a can be replaced by chlorophyll b, that have the same trend, from observed result obtained that in salinity condition chlorophyll a is more sensitive if compared by chlorophyll b. Chlorophyll decreased may be caused by obstacle of accumulation from the salts in biosynthesis chlorophyll process. [11] Salinity influence the strength from protein complex pigment liquid in chloroplasts structure. Chlorophyll decrease caused by photosynthesis decrease and cause decreased crop production, although plant tolerance level not only determined by one plant attribute. In this research prove that plant with high adaptation can defend the level of chlorophyll compared by sensitive plant or cant be able to adapt well. Other research [12] mention salinity stress inhibit chlorophyll syntetic on leaves as a result of decreased rate of photosynthesis and occurrence temperature enhancement and transpiration that cause chlorophyll disintegration.

Table 2. Action gene expected value for SOD and POD activity (unit/mg protein) through skewness and kurtosis value

| Crosses | SOD Activity | POD Activity | Chlorophyll a | Chlorophyll b |
|---------|--------------|--------------|---------------|---------------|
|         | Skewness     | Kurtosis     | Skewness      | Kurtosis      | Skewness     | Kurtosis     |
| Ax N    | 0.548        | 0.296        | 0.898         | -0.020        | -1.107       | 0.488        | -0.388       | 2.200         |
| GxN     | 0.766        | 0.640        | 1.654         | 2.522         | 0.518        | -0.452       | 0.035        | -0.712        |

Observed parameter SOD and POD activity, chlorophyll a and chlorophyll b have skewness > 0 means additives gene with epistatic complement influence, positive marked skewness means a character can be inherited to the offspring, epistatic complement influence means dominant gene occurs interaction that complete each other so it raises that character. Kurtosis < 3 platikurtik graph, means character is controlled by many genes. When character is controlled by many genes then possibility to inherit to the offspring became smaller. Skewness describes the slope level in distribution, the tendency to deviate a curve based on data centered relationship concept between average count, mode and median [13]. [14] Skewness also called slope measure can show symmetric curve form of a distribution. If frequency curve extends to the right means a positive value distribution pattern, if frequency extends to the left means a negative value distribution pattern, if symmetric data inclination means value of mode and mean are the same. Enlightenment of skewness and kurtosis normal distribution explain gene interaction of Mendel law deviation. [15] Skewness analysis potentially to inherit to the offspring is skewness with positive value that have action gene epistatic complementer with positis kurtosis indicated by leptokurtik graph where only few gene witch are involved in form a phenotype character[16]. [17] Between population, expected value gene action in all of peanut F2 population show different result between population, there are character that controlled by many gene and few gene with additive gene action, domination, duplicate epistatic as well complemen ter.

4. Conclusion
Research result can be concluded that Salinity can influence growth and plant production, plant response to salinity environment is generally cause by plant metabolism change. Physiology result from SOD, POD, Chlorophyll a and Chlorophyll b character dominated by GxN crosses are more
potential in inherit nature of descendants, it seen from observation result in distribution chart and skewness value, however to ensure soy genotype that potentially saline tolerant and high produce required more research and much more crops to development.

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