**GENETIC PARAMETERS CHARACTER YIELD OF COMPONENT 20 SELECTED GENOTYPES F4 SOYBEAN (*Glycine max* L.) PEDIGREE SELECTION**

**ABSTRACT**

The character having the parameter character can be used as a good genetic selection. The study is done to obtain a genotype that has a high production. The research was done in augmented, which is the methodology that does not use repetition for the F4 generation but makes repetition for both parents. The all plant was planted on a plot. Twenty seeds of the F4 genotype (planted as 40 plants for every genotype), Argomulyo, and Tanggamus were planted as 60 plants with 3 times repeated. Character component of yield examined is the number of branches per plant, the number of pods per plant, seed weight per plant, and the weight of 100 seeds. The calculation used to calculate the heritability, the genetic variability coefficient (GVC), and the skewness, kurtosis, and correlation. The research results obtained genotype hopes were high evenF4.5.82.87.104=G7 because gene action was governed by additive complementary epistasis and a small number of genes. A great significant positive correlation between the number of branches with the number of pods per plant.

**Keywords:** Additive, character, epistasis, kurtosis, skewness.

**INTRODUCTION**

Superior varieties are expected at high soy because soy is one of the sources of protein and the availability of soya must be high among the public. Almost all Indonesian people consume soybeans as a food. Soybean production can be improved by planting varieties superior to their soil condition because every variety of soybean responds to different soil conditions (Deviona et al., 2021).

Assembly of the soybean plant varieties superior technique can be done using conventional plants in breeding and biotechnology. Breeding plants to produce plants are expected to be able to adapt to environmental factors that affect a phenotype plant. Based on this expectation plant breeders need to use good breeding techniques, right, effective, and efficient to produce the varieties expected (Pardal, 2015).

Technique breeding plant often done to the increased production of plants to conduct a cross between plant producing high with the plant adaptive grows in nearly all locations planting (Ardiarini et al., 2022). Improvement outcomes and the quality of the outcome through plant breeding is a selection process, selection directly to good the selection concerned and indirectly through secondary character. Characterizing the number of pods per plant and seed weight per plant character selection is often used both such characters as the principal character to determine crop production (Sitompul et al., 2015).

Character the number of pods per plant and seed weight per plant can be used as a character selection if such value of the character parameter genetic has been good. Improved yields and the quality of the outcome through breeding plants can be achieved by a selection process, good selection directly to the character itself, or selection indirectly through secondary character. Some parameters that can be used as a genetic selection that genetic variability is effective and efficient, heritability, and the effects of correlation characters that were closely related to the yield (Yakub et al, 2013)

One of the methods widely used selection pedigree selection is the method. The pedigree selection method is one method of the selection process in the breeding of plants to the spiritual character. The selection is very much determined by the diversity, and the relationship between the heritability selection for the effective and accurate.

A cross between Argomulyo with Tanggamus varieties. Of the nature of seed varieties Argomulyo is large but does not hold acid soil, and the character of varieties Tanggamus has small seed, many branched and hold on acid soil. A cross between Argomulyo with Tanggamus produces 20 plants F1 grown and lined to generation F2, and then it would be selected using two methods the selection method pedigree and single seed selection descent. The result of pedigree selection was used in this study.

The genotype used in the research has high F3 genetic diversity in the selection so done in a selection of pedigree. The selection results were obtained in a pedigree of around 50 genotypes selected, but in research, only 20 genotypes selected were used. The objective of this research was to obtain high-yield genotypes.

**METHODE**

This study was conducted at a site at the Agriculture Faculty of Simalungun University Pematangsiantar with an elevation place ± 500 m above sea level and pH of soil 4.5 - 5.5. The research was conducted from February to April 2021. The research was done in an augmented method which is a methodology that does not use repetition for the F4 generation but make repetition for both parent.

The all plant was planted on a plot. Twenty seeds of F4 (F4.5.82.87.181=G1, F4.5.82.87.123=G2, F4.5.82.87.196=G3, F4.5.82.87.113=G4, F4.5.82.87.166=G5, F4.5.82.87.162=G6, F4.5.82.87.104=G7, F4.5.82.87.39=G8, F4.5.82.87.69= G9, F4.5.82.87.200=G10, F4.5.82.87.227=G11, F4.5.82.87.70=G12, F4.5.82.87.221=G13, F4.5.82.87.221=G13, F4.5.82.87.63=G14, F4.5.82.87.128=G15, F4.5.82.87.15=G16, F4.5.82.87.99=G17, F4.5.82.87.52=G19, F4.5.82.87.184=G20).

F4 genotypes (planted as 40 plants for every genotype) and both Argomulyo and Tanggamus planted as 60 plants with 3 times repeated. Doses fertilizer used 50kg/ha Urea, 100kg/ha SP36, and 75 kg/ha KCl. The treatment plant is irrigation, weeding, pest, and disease done optimally by the need.

The parameter character component of yield examined is the number of branches per plant, the number of pods per plant, seed weight per plant, and the weight of 100 seeds. The calculation used to calculate the heritability, the genetic variability coefficient (GVC), and the skewness, kurtosis, and correlation.

Broad heritabilty (h2) calcuted with:

 h2bs = (σ2g)/ (σ2p)

notice:

 h2bs : broad heritability

 σ2 g : varian genetic

σ2 p : varian fenotype

 The criteria of broad heritability as follow Singh dan Chaudry dengan ketentuan sebagai berikut: h2 < 0,20 = small heritability, 0,20 < h2 > 0,50 = midlle heritability, h2 > 0,50 = high heritability,

The genetic variability coefficient (GVC) was calculated using the following formulas:

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 Criteria GVC according to Knight (1979) in (Wulandari & Yulianah, 2016): namely narrow (0-10%), moderate (10-20%) and wide (>20%).

Estimating the gene's action is done based on value kurtosis. Kurtosis shows the height of the population curve. If kurtosis is positive then the graph is leptocurtic which indicates the character is controlled by a few genes whereas if kurtosis is negative then the graph is platycurtic which indicates that the character is controlled by many genes.

Skewness shows the form of the sloping curve of a population. If skewness = 0, the character is controlled by the action of additive genes, skewness > 0 then the character is controlled by the action of additive genes with the effect of complementary epistasis; conversely, if skewness <0, it is suspected that the action of the gene is additive with the effect of duplicate epistasis (Darbeshwar, 2000). Value skewness and kurtosis are calculated using a program of 15.0 SPSS (Sulistyowati et al., 2016)

**RESULTS AND DISCUSSION**

 Based on the results of the test which has been selected to do 20 genotypes generation F4 genetics obtained, and the phenotype coefficient and genetic diversity and value heritability a wider sense as table below.

Table 1 shows that the heritability of 20 genotypes selected generation F4 soybean to all the character components the results are criteria high, namely 1.93 until 19.4 so that all character components the results can be used as character selection. Hi, this shows that genetics has more of a role in the neighborhood (Aryana et al., 2019).

Table 1. Value of Varian Genetic (σ2g), Varian Fenotype (σ2p), Broad Heritability (h2bs) and Genetic Variability Coefficient for Character of Yield Component 20 genotypes F4 of Soybean

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Character |  σ2g |  σ2p | h2bs | Criteria | KKG | Criteria |
| The number of branches per plant |  1.47 |  0.22 | 6.68 | Height | 27% | wide |
| The number of pod per plant |  7.88 |  2.08 | 3.79 | Height | 6% | Narrow |
| Seed weight per plant |  5. 27 |  2.73 | 1.93 | Height | 12% | Moderate |
| Weight 100 seeds |  3.88 |  0.20 | 19.4 | Height | 15% | Moderate |

Value the genetic variability coefficient (GVC) to the number of branches per plant is a broad criterion, but not supported by the amount of per pod plant, the value of the GVC is a narrow criterion. It is not in line with the theory that many of the branches will amount to pods. Research analysis 20 genotypes selected this to the value of the GVC the number of pods per plant can be used as a selection criterion. According to the research of Fadli et al., (2021), the number of pods per plant was many on genotype have the day of harvest longer.



P2=119,90

P1=52,08

P2=5,11

P1=4,42

Figure 1. Frequency distribution the number of branches per plant and the number of pod per plant 20 Genotypes of F4 Generation Soybean

Figure 1 and 2 shows that each other genotype F4 has spreading normally to the character of the number of branches per plant and seed weight per plant. Each other genotype F4 has many segregant transgenic because the middle value of each other genotype exceeds that of the middle value of both parents. As for the character of the number of pods per plant only genotype F4 (F4.5.82.87.184 = G20) who have an individual segregant transgenic because the value of each other individuals for the character of the number of pods per plant genotype F4.5.82.87.184 = G20 more than both parents. The character of the weight of 100 seeds in Figure 2 shows that the spread of nothing normal about each other individuals from selected, Twenty genotypes just the spread of individuals genotype F4.5.82.87.166 = G5 who spread abnormally.



P1=25,04

P2=12,18

P1=14,18

P2=32,17

Figure 2. Frequency distribution seed weight per plant and weight 100 seeds 20 Genotypes of F4 Generation Soybean

Based on figure 2 found that each other genotype individuals from having 20 selected each other individuals segregant because the value of the individual mean exceeds the value of both parents. According to Maryono et al., (2019), when the curve does not spread abnormally and the middle value of a population exceeds both parents many segregant transgenic to selected and planted in the next generation

Table 2 the results of the analysis value skewness shows that character the number of branches per plant genotype F4.5.82.87.181 = G1, F4.5.82.87.123 = G2, F4.5.82.87.113 = G4, F4.5.82.87.104 = G7, F4.5.82.87.227 = G11 and F4.5.82.87.221 = G13 is the action of genes additive epistasis duplicate, while other genotype is the action of genes additive complementary epistasis.

The character of number of the pods per plant is an additive epistasis complementary to all genotypes. The seed weight per plant there was as many as three genotypes (F4.5.82.87.162 = G6, F4.5.82.87.15 = G16 and F4.5.82.87.52 = G19 ) additive duplicate epistasis, while another genotype additive complementary epistasis.

The results of the analysis show that for skewness to weigh 100 seeds, 10 genotypes are the action of genes epistasis additive complementary and 10 genotypes are the additive epistasis duplicate gene. Character is the action of genes epistasis additive used as complementary character selection because the characters controlled the number of many genes can be used as selection criteria and should be continued in the selection (Nurhidayah et al., 2017).

Based on the result analysis of kurtosis (Table 2) character how many branches of a plant controlled by few genes genotype at all, except the genotype F4.5.82.87.181 = G1 and F4.5.82.87.196 = G3 controlled by many gen. character the pods per plant controlled by many genes for nearly all of its genotype only F4.5.82.87.162 = G6, F4.5.82.87.39 = G8, and G4.5.82.87.99 = G17 gen. controlled a little

Character per seeds controlled by the heavy plant of many genes for six genotypes (F4.5.82.87.181 = G1, F4.5.82.87.123 = G2, F4.5.82.87.196 = G3, F4.5.82.87.39 = G8, F4.5.82.87.200 = G10, F4.5.82.87.63 = G14), and 14 genotypes controlled and a few other heavy gen. Characters 100 seeds controlled a few genes to almost all genotype only genotype F4.5.82.87.227 = G11 controlled many genes controlled gen. when a few genes, this means individual genes make a huge difference on a character, genes controlled and many genes so any gene influential to the small observed (Narwiyan et al., 2018).

Based on the result analysis correlates obtained in Table 3 show that the number of branches has a negative correlation not significant on the number of pods per plant only genotype F4.5.82.87.196 = G3 and F4.5.82.87.166 = G5, while another genotype is positive, not significant. The number of branches is negative not significant seed weight per plant to almost all except F4.5.82.87.166 = G5, Genotypes are positively significant and genotype F4.5.82.87.99 = G17 has a negative correlation significant. The number of branches has a negative correlation not significant with weight 100 seeds into 9 genotypes is genotype F4.5.82.87.196 = G3 having a positive significant correlation genotype and 10 other not significant having a negative correlation between the fronds with weight 100 seeds.

Correlation value positive significant and large (0.582\*) genotype F4.5.82.87.166 = G5 shows that if there increase the number of branches per pod plant is increased. The correlation significant between the character fronds with the number of per pod plant shows that there is entanglement between the governed by the same genetic system (Rawdhah et al., 2019) and (Felice et al., 2018).

The number of branches per plant has a negative correlation not significant and large (-0.635ns) with weight seed of per plant shows the number of branches per plant of character increase and will result in a decrease in weight of character (inversely) character or in other words the number branches per plant with weight seed per plant associate not closely (Prabowo et al., 2014).

Table 4 shows that the pods per plant correlate negatively and not significantly with seed weight per plant in eight genotypes while in 12 genotypes others have had a positive not significant correlation between the number of pods per plant with seed weight. per plant. The number of pods per plant is positively correlated not significant and of little worth (-0.028 until 0.472) against weight 100 seed for five genotypes, while the other 15 genotypes negative not significant between the number of pods per plant with weight 100. Seeds. The research is in research similar to Karyawati & Puspitaningrum, (2021) That every increase in the number of pods per plant did not increase the weight of 100 seeds.

Correlation value genotype F4.5.82.87.99 = G17 between characters the number of branches per plant with the number of pods per plant positive value having not significant (0.332ns), the number of branches per plant with weight seeds per plants are positive significant (0.610\*), and the number of branches per plant with weight 100 seeds having positive correlation value significant (0.662\*). Research is by research Kuswantoro et al., (2017) and (Pamulatsih & Waluyo, 2019) Who stated that the number per pod plant with heavy 100 seeds has a clear positive correlation to improve the result.

Small and negative correlation values not significant between one character with the other character show that contact between characters is small. The results of the analysis correlation already done to the character components to 20 of its genotype and get genotype selection has done the best genotype F4.5.82.87.99 = G17 having heritability high value, value the genetic variability coefficient (GVC) the number of branch per plants is broad, seed weight per plants and weight 100 seed is heavy, character per pods and the number of plants is narrow (Sundari & Artari, 2018)

The result analysis of a correlation between seed weight per plant with the weight of 100 seeds in Table 5 shows that seed weight per plant is positively correlated not significant and small to three genotypes (F4.5.82.87.181 = G1, F4.5.82.87.70 = G12 and F4.5.82.87.63 = G14), while other 17 genotypes positively correlate real and great value (0.877\*) especially in the genotype F4.5.82.87.99 = G17. This shows that every improvement in seed weight per plant will improve the weight of 100 seeds in the genotype F4.5.82.87.99 = G17.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Genotipe | The number of branch per plant | The number of pods per plant | Seed weight per plant | Weight 100 seeds |
| Skewness | Gene Action | Kurtosis | Number of Gene | Skewness | Gene Action | Kurtosis | Number of Gene | Skewness | Gene Action | Kurtosis | Number of Gene | Skewness | Gene Action | Kurtosis | Number of Gene |
| F4.5.82.87.181= G1 | -0.58  | Additive duplicate epistasis | 1.09 | Many | 0.97  | Additive ccomplementary epistasis  | 2.03 | many | 0.97 | Additive ccomplementary epistasis  | 2.03 | many | -0.11  | Additive duplicate epistasis | -1.01 |  little |
| F4.5.82.87.123=G2 | -0.14  | Additive duplicate epistasis | -0.89 |  Little | 1.35  | Additive ccomplementary epistasis  | 2.90 | many | 1.35 | Additive ccomplementary epistasis  | 2.90 | many | -0.14  | Additive duplicate epistasis | -1.14 |  little |
| F4.5.82.87.196= G3 | 0.19  | Additive ccomplementary epistasis  | 0.27 | Many | 1.45  | Additive ccomplementary epistasis  | 3.01 | many | 1.45 | Additive ccomplementary epistasis  | 3.01 | many | 0.23  | Additive ccomplementary epistasis  | -0.95 |  little |
| F4.5.82.87.113= G4 | -0.33  | Additive ccomplementary epistasis  | -1.32 |  Little | 0.94  | Additive ccomplementary epistasis  | 2.31 | many | 0.30 | Additive ccomplementary epistasis  | -1.11 | little | 0.29  | Additive ccomplementary epistasis  | -1.18 |  little |
| F4.5.82.87.166= G5 | 0.06  | Additive ccomplementary epistasis  | -1.10 |  Little | 0.91  | Additive ccomplementary epistasis  | 0.39 | many | 0.39 | Additive ccomplementary epistasis  | -0.93 | little | 0.82  | Additive ccomplementary epistasis  | -0.56 |  little |
| F4.5.82.87.162= G6 | 0.25  | Additive ccomplementary epistasis  | -0.61 |  Little | 0.62  | Additive ccomplementary epistasis  | -0.46 | little | -0.06 | Additive duplicate epistasis | -1.10 | little | 0.02  | Additive ccomplementary epistasis  | -0.92 |  little |
| F4.5.82.87.104= G7 | -0.25  | Additive duplicate epistasis | -0.45 |  Little | 0.93  | Additive ccomplementary epistasis  | 2.00 | many | 0.16 | Additive ccomplementary epistasis  | -1.32 | little | -0.04  | Additive duplicate epistasis | -1.03 |  little |
| F4.5.82.87.39= G8 | 0.85  | Additive ccomplementary epistasis  | -0.02 |  Little | 0.16  | Additive ccomplementary epistasis  | -0.94 | little | 0.87 | Additive ccomplementary epistasis  | 0.17 | many | -0.23  | Additive duplicate epistasis | -0.90 |  little |
| F4.5.82.87.69= G9 | 0.18 | Additive ccomplementary epistasis  | -0.66 |  Little | 1.16  | Additive ccomplementary epistasis  | 3.30 | many | 0.82 | Additive ccomplementary epistasis  | -0.22 | little | -0.03  | Additive duplicate epistasis | -1.23 |  little |
| F4.5.82.87.200= G10 | 0.66 | Additive ccomplementary epistasis  | -0.12 |  Little | 2.30  | Additive ccomplementary epistasis  | 6.06 | many | 0.90 | Additive ccomplementary epistasis  | 0.74 | many | -0.31  | Additive duplicate epistasis | -0.76 |  little |
| F4.5.82.87.227= G11 | -0.25 | Additive duplicate epistasis | -1.05 |  Little | 0.96  | Additive ccomplementary epistasis  | 0.17 | many | 0.45 | Additive ccomplementary epistasis  | -0.93 | little | 0.83  | Additive ccomplementary epistasis  | 0.37 |  little |
| F4.5.82.87.70= G12 | 0.10 | Additive ccomplementary epistasis  | -0.68 |  Little | 1.02  | Additive ccomplementary epistasis  | 0.14 | many | 0.60 | Additive ccomplementary epistasis  | -0.39 | little | 0.11  | Additive ccomplementary epistasis  | -0.79 |  little |
| F4.5.82.87.221= G13 | -0.61 | Additive duplicate epistasis | -0.40 |  Little | 1.32  | Additive ccomplementary epistasis  | 0.64 | many | 0.00 | Additive ccomplementary epistasis  | -0.87 | little | -0.32  | Additive duplicate epistasis | -1.13 |  little |
| F4.5.82.87.63= G14 | 0.57 | Additive ccomplementary epistasis  | -0.58 |  Little | 2.84  | Additive ccomplementary epistasis  | 8.50 | many | 0.83 | Additive ccomplementary epistasis  | 0.31 | many | -0.55  | Additive duplicate epistasis | -0.82 |  little |
| F4.5.82.87.128= G15 | 0.26 | Additive ccomplementary epistasis  | -1.18 |  Little | 2.65  | Additive ccomplementary epistasis  | 10.83 | many | 0.36 | Additive ccomplementary epistasis  | -0.71 | little | 0.31  | Additive ccomplementary epistasis  | -1.14 |  little |
| F4.5.82.87.15= G16 | 0.34 | Additive ccomplementary epistasis  | -0.80 |  Little | 2.46  | Additive ccomplementary epistasis  | 6.86 | many | -0.14 | Additive ccomplementary epistasis  | -1.27 | little | 0.08  | Additive ccomplementary epistasis  | -1.23 |  little |
| F4.5.82.87.99= G17 | 0.36 | Additive ccomplementary epistasis  | -0.92 |  Little | 0.07  | Additive ccomplementary epistasis  | -0.22 | little | 0.31 | Additive ccomplementary epistasis  | -0.17 | little | -0.07  | Additive duplicate epistasis | -1.41 |  little |
| F4.5.82.87.66=G18. | 0.31 | Additive ccomplementary epistasis  | -0.63 |  Little | 2.21  | Additive ccomplementary epistasis  | 5.27 | many | 0.33 | Additive ccomplementary epistasis  | -0.74 | little | -0.27  | Additive duplicate epistasis | -1.09 |  little |
| F4.5.82.87.52= G19 | 0.35 | Additive ccomplementary epistasis  | -0.89 |  Little | 1.07  | Additive ccomplementary epistasis  | 0.46 | many | -0.06 | Additive ccomplementary epistasis  | -1.28 | little | -0.04  | Additive duplicate epistasis | -0.60 |  little |
| F4.5.82.87.184= G20 | 0.19 | Additive ccomplementary epistasis  | -1.20 |  Little | 0.83  | Additive ccomplementary epistasis  | 0.27 | many | 0.10 | Additive ccomplementary epistasis  | -1.19 | little | 0.07  | Additive ccomplementary epistasis  | -1.08 |  little |

Table 2. The Score of Skewness and Kurtosis Character of Yeild Component on 20 Genotypes of F4 Population

Table 3. Fenotype Correlation is The Number of Branches per Plant to Character of The Number of Pods per Plant, Seed Weight per Plant and Weight of 100 seeds on 20 Genotype of The F4 Population

|  |  |  |
| --- | --- | --- |
| **Genotype**  | **Character** | Character |
| **The number of branch/plant** | **The number** **of pods/plant** | **Seed** **Weight/plant** | **Weight 100 seeds** |
| F4.5.82.87.181= G1 | **The number of branches per plant** | 1 | 0.275ns | -0.008ns | -0.175ns |
| F4.5.82.87.123=G2 | 1 | 0.063 ns | -0.285 ns | -0.224 ns |
| F4.5.82.87.196= G3 | 1 | -0.068 ns | -0.125 ns | -0.202 ns |
| F4.5.82.87.113= G4 | 1 | 0.222 ns | -0.404 ns | -0.441 ns |
| F4.5.82.87.166= G5 | 1 | -0.002 ns | 0.582\* | 0.660\* |
| F4.5.82.87.162= G6 | 1 | 0.667\* | -0.443 ns | -0.565\* |
| F4.5.82.87.104= G7 | 1 | 0.537 ns | -0.225 ns | -0.347 ns |
| F4.5.82.87.39= G8 | 1 | 0.350 ns | -0.564 ns | -0.650\* |
| F4.5.82.87.69= G9 | 1 | 0.285 ns | -0.471 ns | -0.633\* |
| F4.5.82.87.200= G10 | 1 | 0.548 ns | -0.141 ns | -0.275 ns |
| F4.5.82.87.227= G11 | 1 | 0.463 ns | -0.375 ns | -0.480 ns |
| F4.5.82.87.70= G12 | 1 | 0.439 ns | -0.435 ns | -0.614\* |
| F4.5.82.87.221= G13 | 1 | 0.375 ns | -0.027 ns | -0.411 ns |
| F4.5.82.87.63= G14 | 1 | 0.427 ns | -0.189 ns | -0.642\* |
| F4.5.82.87.128= G15 | 1 | 0.310 ns | -0.583 ns | -0.531\* |
| F4.5.82.87.15= G16 | 1 | 0.364 ns | -0.391 ns | -0.651\* |
| F4.5.82.87.99= G17 | 1 | 0.322 ns | -0.610\* | -0.662\* |
| F4.5.82.87.66=G18. | 1 | 0.550 ns | -0.343 ns | -0.635 ns |
| F4.5.82.87.52= G19 | 1 | 0.369 ns | -0.568 ns | -0.615\* |
| F4.5.82.87.184= G20 | 1 | 0.028 ns | -0.640 ns | -0.654\* |

Table 4. Fenotype Correlation the Number of Pods per Plant to The Character of The Number of Branches per Plant, Seed Weight per Plant and Weight of 100 Seeds on 20 Genotype of The F4 Population

|  |  |  |
| --- | --- | --- |
| **Genotype**  | **Character** | **Character** |
| **The number of branch/plant** | **The number** **of pods/plant** | **Seed** **Weight/plant** | **Weight 100 seeds** |
| F4.5.82.87.181= G1 | **The number of pods per plant** | 0.275ns | 1 | 0.037ns | -0.131ns |
| F4.5.82.87.123=G2 | 0.063 ns | 1 | -0.432 ns | 0.472 ns |
| F4.5.82.87.196= G3 | -0.068 ns | 1 | -0.066 ns | -0.180 ns |
| F4.5.82.87.113= G4 | 0.222 ns | 1 | -0.048 ns | -0.028 ns |
| F4.5.82.87.166= G5 | -0.002 ns | 1 | 0.420ns | 0.289ns |
| F4.5.82.87.162= G6 | 0.667\* | 1 | -0.023 ns | -0.314ns |
| F4.5.82.87.104= G7 | 0.537 ns | 1 | 0.080 ns | -0.181 ns |
| F4.5.82.87.39= G8 | 0.350 ns | 1 | 0.309 ns | -0.016ns |
| F4.5.82.87.69= G9 | 0.285 ns | 1 | 0.212 ns | -0.102ns |
| F4.5.82.87.200= G10 | 0.548 ns | 1 | -0.048 ns | -0.020 ns |
| F4.5.82.87.227= G11 | 0.463 ns | 1 | -0.130 ns | -0.421 ns |
| F4.5.82.87.70= G12 | 0.439 ns | 1 | 0.323 ns | -0.253ns |
| F4.5.82.87.221= G13 | 0.375 ns | 1 | 0.551 ns | 0.031 ns |
| F4.5.82.87.63= G14 | 0.427 ns | 1 | 0.549 ns | -0.050ns |
| F4.5.82.87.128= G15 | 0.310 ns | 1 | 0.254 ns | 0.037ns |
| F4.5.82.87.15= G16 | 0.364 ns | 1 | 0.370 ns | -0.073ns |
| F4.5.82.87.99= G17 | 0.322 ns | 1 | -0.143ns | -0.087ns |
| F4.5.82.87.66=G18 | 0.550 ns | 1 | 0.223 ns | -0.119 ns |
| F4.5.82.87.52= G19 | 0.369 ns | 1 | -0.098 ns | -0.212ns |
| F4.5.82.87.184= G20 | 0.028 ns | 1 | 0.201 ns | 0.141ns |

Table 5. Fenotype Correlation of Seed Weight per Plant Character to The Character of The Number of Branches per Plant, The Number of Pods per Plant and Weight of 100 Seeds on 20 Genotypes of The F4 Population

|  |  |  |
| --- | --- | --- |
| **Genotype**  | **Character** | **Character** |
| **The number of branch/plant** | **The number of pods/plant** | **Seed weight/plant** | **Weight 100 seeds** |
| F4.5.82.87.181= G1 | **Seed weight per plant** | 0.037ns | 0.037ns | 1 | 0.331ns |
| F4.5.82.87.123=G2 | -0.432 ns | -0.432 ns | 1 | 0.749\* |
| F4.5.82.87.196= G3 | -0.066 ns | -0.066 ns | 1 | 0.813\* |
| F4.5.82.87.113= G4 | -0.048 ns | -0.048 ns | 1 | 0.827\* |
| F4.5.82.87.166= G5 | 0.420ns | 0.420ns | 1 | 0.852\* |
| F4.5.82.87.162= G6 | -0.023 ns | -0.023 ns | 1 | 0.657\* |
| F4.5.82.87.104= G7 | 0.080 ns | 0.080 ns | 1 | 0.859\* |
| F4.5.82.87.39= G8 | 0.309 ns | 0.309 ns | 1 | 0.718\* |
| F4.5.82.87.69= G9 | 0.212 ns | 0.212 ns | 1 | 0.738\* |
| F4.5.82.87.200= G10 | -0.048 ns | -0.048 ns | 1 | 0.613\* |
| F4.5.82.87.227= G11 | -0.130 ns | -0.130 ns | 1 | 0.626\* |
| F4.5.82.87.70= G12 | 0.323 ns | 0.323 ns | 1 | 0.438ns |
| F4.5.82.87.221= G13 | 0.551 ns | 0.551 ns | 1 | 0.604\* |
| F4.5.82.87.63= G14 | 0.549 ns | 0.549 ns | 1 | 0.547ns |
| F4.5.82.87.128= G15 | 0.254 ns | 0.254 ns | 1 | 0.737\* |
| F4.5.82.87.15= G16 | 0.370 ns | 0.370 ns | 1 | 0.755\* |
| F4.5.82.87.99= G17 | -0.143ns | -0.143ns | 1 | 0.877\* |
| F4.5.82.87.66=G18. | 0.223 ns | 0.223 ns | 1 | 0.777\* |
| F4.5.82.87.52= G19 | -0.098 ns | -0.098 ns | 1 | 0.782\* |
| F4.5.82.87.184= G20 | 0.201 ns | 0.201 ns | 1 | 0.791\* |

**CONCLUTION**

Based on the research done so can be concluded that the selection of genotype which is expected to produce high, especially genotype F4.5.82.87.104 = G7 because out of the action of genes had played a role is additive epistasis complementary and the number of genes a little and correlation value large, positive real between the number of fronds with the number of pods per plants

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