SAFE 2018

6th International Conference on
Sustainable Agriculture, Food and Energy.
October 19 - 21, 2018. MANILA, Philippines.

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6th International Conference on Sustainable Agriculture, Food and Energy.
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Inclusive Agri-food Energy Production for Community Empowerment in a Changing Climate

SAFE NETWORK

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SA/E-103

GENETIC ANALYSIS OF GRAIN YIELD OF F4 POPULATIONS FROM SINGLE CROSS LOCAL RICE VARIETIES FOR NEW TYPE UPLAND RICE

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Abstract— **High production of rice is closely related to high yield component characters namely the number of filled grains per panicle or the density of grains per panicle. The characters influence the rice yield components, which are controlled by many genes that are influenced by the plant environment. This research aims to analyze the genetic variety and the character inheritance system on rice yield grains of F4 populations and to result in the plant best genotype. The research conducted from November 2017 to April 2018 in Desa Semarang, Bengkulu Province, Indonesia". The materials in this research were F3 Generation Seed consisted of 190 numbers from the pedigree selection which divided into 24 field numbers were resulted from single crosses between local varieties (Bugis and Sriwijaya) with both IR7858-1 and N22 are tolerant to drought. The research applied the Augmented Design with the spaced planting system. The result shows that the grain yield of F4 populations is polygenic controlled by additive gene actions. The heritability value and genetic variety coefficient of grain yield of F4 populations are classified as middle and high. Selection intensity of 10% based on the grain weight/hill character increased the middle value of other observed characters, like panicle length of 20.9%, the total number of grain (48.4%), the filled grain number per panicle (59.7%), grain weight/hill of 40.9% and decreased percentage of empty grain/panicle by 87.6%. Selection on both grain weight and panicle length characters increased the grain weight/ hill of 69.5% with selection differential for the panicle length of 21.8% in the next generation.**

Keywords: grain yield, f4 population, single cross, heritability, genetic variability

SA/E-104

THE QUANTITY AND QUALITY OF ROBUSTA COFFEE BEANS HARVESTED FROM DIFFERENT SLOPE STEEPNESS AND POSITIONS FOR THREE CONSECUTIVE YEARS OF STUDIES

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Abstract—**Studies aiming to compare the quantity and quality of robusta coffee beans grown on three different slope steepness and positions have been conducted at three consecutive years of 2016 to 2018 in a high country region in Sumatera. Slope steeness of 13, 25 and 35% as well as positions at the upper, middle and lower slopes were used as independent factors under a randomized complete blocked design with three replicates of 2016-2018 observations. Results showed that the quantitative variables of coffee beans were significantly different among the slope factors as indicated by the weight of 100 wet beans, while significant differences in rendement values of coffee beans to powder products indicated the effects of slopes on the coffee bean quality. The best quantitative results were found at the middle and lower positions of 25% slopes steepness, while the beans-to-powder rendement values were highest for the lower part of 35% slope. The findings of three-years studies suggested that better quantitative and qualitative yields of coffee beans at the lower slope positions could probably due to the accumulation of soil water and nutrients at the slope toes.**

Keywords— **coffee beans; robusta coffee; slopes steepness and positions.**

SA/E-105

CROSS PROTECTION POTENTIAL OF *COLLETOTRICHUM LINDEMUTHIANUM* (SACC. & MAGN.) AGAINST ANTHRACNOSE PATHOGENS OF CHILI, TOMATO AND EGGPLANT

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Abstract— **Anthracnose disease caused by Colletotrichum spp. has been widely known as important disease of various crops such as mango, banana, avocado, papaya, eggplant, tomato, paprika, chili, strawberry, coffee, common bean etc. Different species of Colletotrichum might be associated with the same host, and the same species of the fungus can be associated with different host species of different families. Anthracnose of chilli has been identified to be associated with C. acutatum, C. capsici, C. gloeosporioides and C. coccodes. Anthracnose of eggplant has been reported to be associated with C. gloeosporoides f. sp. Melongenae, C. nigrum, C. capsici, and C. dematium. However, tomato anthracnose is known to be exclusively caused by single species, Colletotrichum coccodes. Bean anthracnose is also exclusive since the disease only caused by C. lindemuthianum and the pathogen can only infect leguminoceous crops such as mung bean (P. aureus), cowpea (Vigna sinensis), and broad bean (Vicia faba), but failed to infect plant species from other families. Being avirulent against other families suffering from infection of other species of Colletotrichum, C. lindemuthianum might have cross protection effect on non-host plants against anthracnose caused by their natural pathogens. Research on cross protection of C. lindemuthianum against anthracnose pathogens of chili, eggplant and tomato has been conducted to investigate the potential of using cross protection technique as part of biological control of the disease. The results showed that C. lindemuthianum could noticeably suppress the infection of natural pathogen of anthracnose on chili and eggplant but not on tomato.**

Keywords— **Cross protection, anthracnose, Colletotrichum, chilli, tomato, eggplant.**

GENETIC ANALYSIS OF GRAIN YIELD OF F_4 POPULATIONS FROM SINGLE CROSS OF LOCAL RICE FOR DEVELOPING NEW TYPE OF UPLAND RICE

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INTRODUCTION

- This study aims to study genetic diversity and the character inheritance pattern of grain yields in the F4 population and to get the best genotype from the selection.

MATERIALS AND METHODS

- These experiments were conducted from November 2017 to April 2018 in the Research Station of Department of Agriculture and Animal Husbandry of Bengkulu, Bengkulu Province, Indonesia.
- The materials in this research were F3 Generation Seed consisting of 190 numbers from pedigree selection which divided into 24 field numbers resulting from single crosses between local varieties namely Bugis and Sriwijaya with IR7858-1 and IR148+ both of which were drought tolerant (Sriwijaya/IR-148+, Sriwijaya/IR-7858-1, Bugis/IR-148+, and Bugis/IR-7858-1).
- The experiments applied an augmented design with a spaced planting system, with a planting space of 20 cm x 20 cm, and one seed in each hole in a head-to-row system. Each number was planted with six lines consisted of ± 800 populations.

- Observations were made on:
  - the length of panicles,
  - the total number of grains/panicles,
  - the number of filled grains/panicle,
  - the percentage of empty grains/panicle, and the weight filled grain/hill.
- The data were analyzed with Microsoft Excel and Minitab 15 statistical programs were:
  - **Variety and Heritability Components Estimation**
  - **Gene Action Estimation**
  - The selection differential estimation

RESULTS

- **Varian Analysis and Heritability**

Table 1. Genetic Analysis on the Grain Yield of F4 Populations in the Single Crossing of Local Rice Variety

Characters	$\sigma^2 g$	$\Sigma^2 p$	$\sigma^2 e$	KKG (%)	Criteria	HBS	Criteria
Panicle length	4.46	5.70	1.24	7.63	moderate	0.78	high
Total number of grains per panicle	2942.34	3025.00	82.66	25.51	broad	0.97	high
The number of filled grains per panicle	2588.42	2669.15	80.73	30.09	broad	0.97	high
Percentage of empty grain per panicle	159.74	162.58	2.84	62.46	broad	0.98	high
Grain weight per hill	1019.49	1021.41	1.91	51.49	broad	0.99	high

RESULTS

- **Skewness and Kurtosis Analysis**

Table 2. Estimation of Gene Action and Number of Genes of Grain Yield Character in F4 Population from Single Crossing of Local Rice Varieties

Characters	Skewness	$Z_{skewness}$	Gene Action	Kurtosis	$Z_{kurtosis}$	Number of Control Genes
Panicle length	0.11	0.05^{ns}	additive	2.86	1.35^{ns}	many
Total number of grains per panicle	0.49	0.01^{ns}	additive	2.84	0.05^{ns}	many
The number of filled grains per panicle	0.68	0.01^{ns}	additive	2.88	0.06^{ns}	many
Percentage of empty grain per panicle	0.97	0.08^{ns}	additive	3.03	0.24^{ns}	many
Grain weight per hill	0.41	0.01^{ns}	additive	2.34	0.07^{ns}	Many

kurtosis > 0 = a few gene, kurtosis < 0 = many genes (Roy 2000), ns= no significant at 5% level

RESULTS

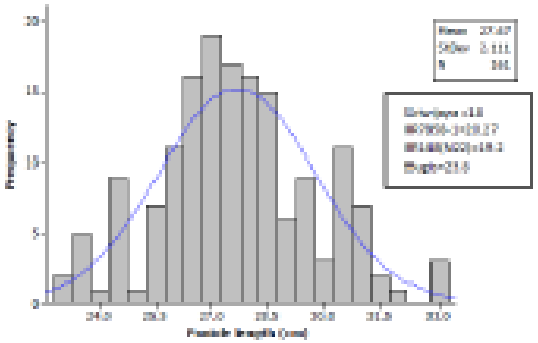

Figure 1. Distribution of panicle length from F4 populations

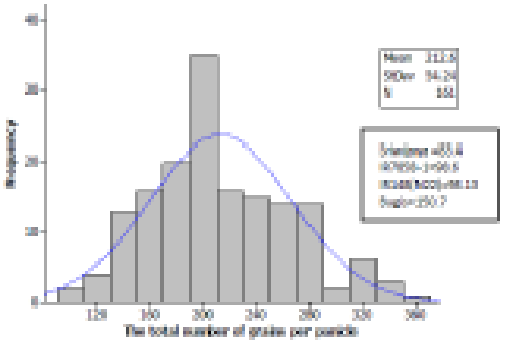

Figure 2. Distribution of the total number of grains per panicle from F4 populations

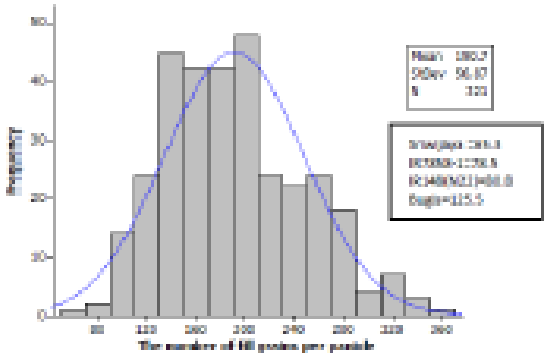

Figure 3. Distribution of the number of fill grains from F4 populations

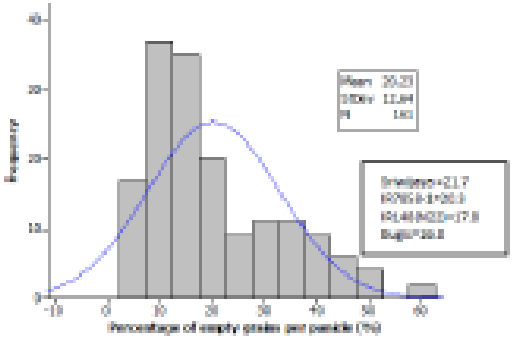

Figure 4. Distribution of percentage of empty grains per panicle from F4 populations

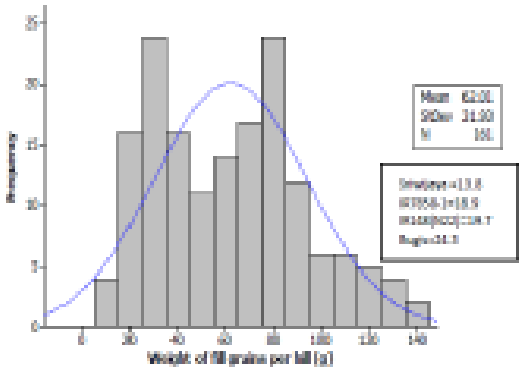

Figure 5. Distribution of weight of fill grains Per hill from F4 populations

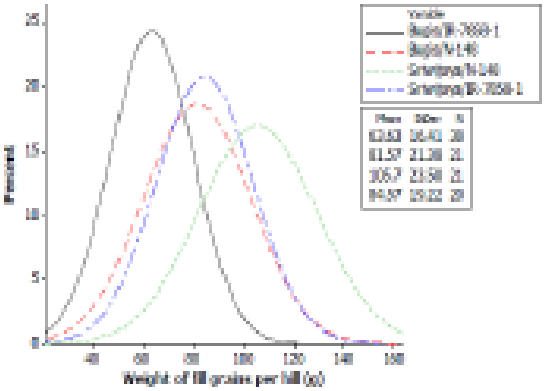

Figure 6. Percentage of population base on weight of fill grains per hill in defferent crossing

RESULTS

- **The F4 Population Selection Differential**

Table 3. The Selection differential based on grain weight/hill character in the F4 populations from a single cross of local rice variety for new type upland rice

Characters	Early population average	Selected population average	Selectional differential (%)
Panicle length	21.9	27.7	20.9
Total number of grains per panicle	109.8	212.6	48.4
The number of filled grains per panicle	68.1	169.1	59.7
Percentage of empty grain per panicle	37.97	20.2	-87.6
Grain weight per hill	36.63	62.0	40.9

Table 4. The selection differential based on grain weight/hill and panicle length character in the F4 populations from a single cross of local rice variety for new type upland rice

Characters	Early population average	Selected population average	Selection differential (%)
Panicle length	21.9	28.0	21.8
Total number of grains per panicle	109.8	246.2	55.4
The number of filled grains per panicle	68.1	215.6	68.4
Percentage of empty grain per panicle	37.97	12.2	-210.5
Grain weight per hill	36.63	120.2	69.5

CONCLUSION

- The genetic diversity coefficient of grain yield characters is moderate to broad ranges between 7.63 and 62.46. High heritability value estimation on the grain yield characters indicate as high which the ranges between 0.78-0.99.
- The grain yield character in the F4 population is polygenic controlled by the additive gene action. Heritability value and high genetic diversity coefficient of grain yield characters in the F4 population could be used for the selection goal not only by single selection but also by simultaneous selection.
- Selection with an intensity of 10% based on the grain weight/hill character increased the middle value of other observed characters, like panicle length of 20.9%, the total number of grain (48.4%), the number of filled grain per panicle (59.7%), grain weight/hill of 40.9% and decreased percentage of un-fill grain/panicle by 87.6%.
- Selection on both grain weight and panicle length characters increased the grain weight/ hill of 69.5% with selection differential value for panicle length of 21.8% in the next generation.
- Selection on filled grain numbers and dense panicle characters, no matter the panicles length, are significant to be considered for the new type upland rice with high yield rate.

THANK YOU