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Stability of Quantitative Traits through Analysis of Rice Diversity (Oryza Sativa L.) Mapan P-05 Variety with its Ratoon

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Abstract: Thisstudy aims to analyze the level of relationship between F1 Mapan P-05 rice plants and their ratoons based on quantitative characteristics. The Mapan P-05 rice variety that was tested was analyzed together with its queen using the kinship analysis method to understand the level of stability of the quantitative traits observed. The use of kinship analysis allows evaluating the genetic relationship between the Mapan P-05 variety and its queen, as well as evaluating the level of stability of the observed quantitative traits. The results showed that through kinship analysis, it was possible to understand the level of genetic relationship between the Mapan P-05 rice variety and its queen, as well as the stability of the observed quantitative traits. This research provides a deeper understanding of the genetic characteristics and stability of quantitative traits in the Mapan P-05 rice variety and its queen, which has important implications in the development and breeding of rice plants to support plant resilience and productivity.

Keywords: Quantitative; Ratoon; Stability.

Introduction

Population growth and environmental changes have had a significant impact on rice production in Indonesia, which is the main source of nutrition for the community. Climate change, including increasing temperatures and changes in rainfall patterns, as well as land conversion from rice fields to residential and industrial areas, has reduced the area of rice collection and has resulted in reduced rice production (Erdiman et al., 2013). In facing these challenges, ratoon rice cultivation has emerged as an innovation that can increase productivity by utilizing rice stalk residues, reducing the habit of burning straw, and increasing the number of harvests without re-cultivation (Ishaq et al., 2017).

Selection of the right plant variety is also an important factor in increasing rice production. Crossbred varieties such as Mapan P-05 have shown higher yield potential than other varieties such as Ciherang (Ruminta, 2016). Through research conducted, it was found that this crossbred variety can provide higher grain yields, which are very necessary in meeting the increasing food needs along with population growth (Karim and Aliyah, 2018). However, to understand more deeply about the genetic relationship in quantitative traits of rice plants, analysis of genetic diversity between the Mapan P-05 variety and its ratoons is an important step (Krismawati and Sugiono, 2016).

Analysis of genetic diversity between Mapan P-05 rice variety and its queens is a further step in improving the understanding of quantitative traits of rice plants. This study aims to identify the genetic relationship between major rice varieties and their queens, with the hope of providing deeper insight into the genetic potential of these varieties. With a better understanding of the genetic relationship between rice varieties and their queens, farmers and researchers can develop more effective plant breeding strategies to increase sustainable rice production in the face of climate change and population growth.

The rice plant, Oryza sativa L., has become a major food source for most of the world's population, especially in Asia. Native to Central Asia, the Himalayas, and surrounding areas, rice grows as grass with a root system that can absorb water and nutrients from the soil (Mubaroq, 2013). The stem consists of several parts separated by nodes and has round holes in it. Rice leaves are fragmented with a tongue between

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the sheath and the leaf margin. Rice flowers, which are usually white, produce grains protected by husks. Rice panicles have important branches that produce new tillers, becoming an important element in the plant's growth cycle (Wati, 2015).

The rice plant breeding process is key to producing superior varieties that can overcome environmental challenges and increase crop yields. Through conventional methods, rice varieties that have certain advantages are crossed to create more resilient and productive varieties. Germplasm diversity plays an important role in providing genetic resources for the breeding process, opening new potential in increasing plant resilience and productivity (Asmarani, 2017).

The genotype of rice plants plays an important role in determining phenotypic traits and adaptation to the environment. Through the process of natural selection and selective breeding, superior genotypes can be identified and utilized to produce plants that are stronger and more resistant to environmental stress (Suhartatik, 2008). The stability of rice production is a major concern in ensuring consistent food availability. Parametric and non-parametric analysis methods are used to understand and measure the level of genotype stability under various environmental conditions (Adimiharja, 2019).

Cluster analysis and genetic distance are important tools in understanding the relationship between diversity between rice genotypes and populations. By grouping similar data, cluster analysis helps in identifying patterns underlying plant genetic diversity (Hairmanis et al., 2005). On the other hand, genetic distance provides an overview of the level of genetic differences between species or populations, becoming an important guideline in selecting varieties for crossing and genetic improvement (Syukur et al., 2015). Thus, a deep understanding of rice genetics and stability is key in efforts to increase productivity and food security sustainably (Lestari et al., 2010).

Method

The research method used in this study is the Randomized Block Design (RAK) method with three replications. The study was conducted from November to June 2022 on farmers' land in Sumberharjo Village, Prambanan District, Sleman Regency, Yogyakarta. The research location was chosen because it has a type of semi-irrigated technical rice field with regosol (gray) soil type and dusty sandy soil texture, and a soil pH of around +6, which is in accordance with the growth needs of rice plants. In addition, the altitude of the place which reaches 116.8 meters above sea level is also an important consideration in choosing the research location. The tools and materials used include various agricultural equipment such as roll meters, stakes, scales, buckets, water pumps, pH meters, tarpaulins, sacks, as well as office equipment and technology such as laptops and cellphones for documentation and data processing.

The implementation of the experiment began with land preparation involving soil cultivation until loose and the creation of 7 plots that would be used for planting. Seed preparation and seedbeds were carried out carefully to ensure optimal seed quality. The process of transplanting plants was carried out manually by human power, while fertilization was carried out in two stages with different types of fertilizers. In addition, post-harvest handling is also an important part of this methodology, which involves several stages such as drying, turning straw, cleaning, packaging, and storage that pay attention to appropriate environmental conditions.

The variables observed in this study include various aspects of rice plant growth and yield such as the number of productive tillers, the weight of dry grain harvested per clump, per plot, and per hectare, and the weight of 100 grains. Data analysis was carried out using the cluster analysis method to evaluate similarities based on morphological and agronomic traits and using numerical metrics to show differences between quantitative data. The results of the cluster analysis are presented in the form of a dendogram, which shows the level of similarity between the rice plant accessions studied. Thus, the research method used provides a systematic and comprehensive framework for evaluating the growth performance and yield of certain rice plant varieties under specific environmental conditions.

Result and Discussion

Dendrogram Analysis

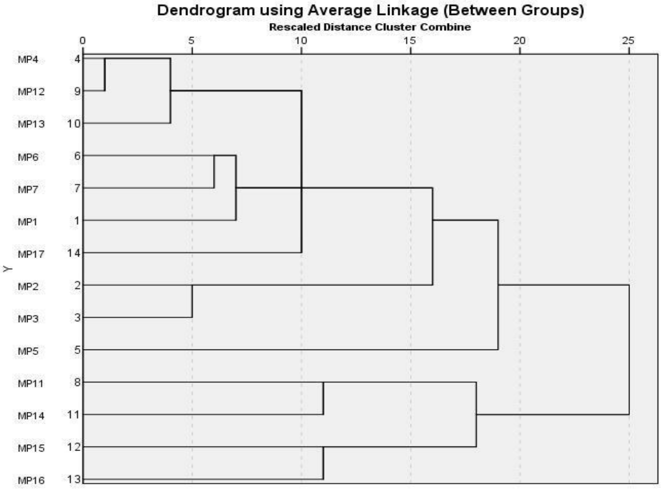

Figure 1. Dendogram of diversity in Mapan P-05 rice variety

The results of the analysis based on 14 objects using the Dendogram with the Average Linkage method show that from various rice varieties there are four clusters where each cluster has its own characteristics. The dendogram shows that there are adjacent objects, namely:

Table 2. Objects of the Mapan P-05 Rice Variety Formed by Dendogram Analysis with the Average Linkage Method

Cluster	Varieties
Cluster 1	MP4, MP12, MP13, MP6, MP7, MP1, MP17, MP2, MP3 and MP5
Cluster 2	MP8, MP11, MP12 and MP13

Table 1 shows that the grouping of Mapan P-05 rice variety objects into 2 clusters and in this case the codes MP1 to MP7 are the results of Mapan P-05 rice plant ratoons while the codes MP11 to MP17 are the results of F1 Mapan P-05 rice variety plants.

The dendogram in Figure 1 shows that the level of similarity between the first plant and its ratoon based on the observed research data ranges from 0-25. At a similarity level of 20%, two groups are formed. The first group starts from MP4, MP12, MP13, MP6, MP7, MP1, MP17, MP2, MP3 and MP5 (first group), MP8, MP11, MP12 and MP13 (second group). The similarity value of the molecular markers owned is proportional to the number of similarities, which indicates a closer diversity relationship. Conversely, the more differences in characters owned, the lower the similarity value, which indicates a further diversity relationship between the compared genotypes.

Each cluster formed has different quantitative characteristics. The quantitative characteristics that distinguish each cluster formed are the number of productive tillers, weight of dry harvested grain per clump, weight of dry harvested grain per plot, weight of dry harvested grain per hectare, weight of dry stored grain per clump, weight of dry stored grain per plot, weight of dry stored grain per hectare and weight of 100 grains.

According to Pinilih et al. (2015), genetic distance values between 0.01 and 0.37 indicate a relationship close and low genetic variability. The value of this genetic distance is very important for crossing. In cases where a pair of genotypes or varieties have a genetic distance value that is considered narrow, the crossing process is avoided. Crossing will not cause diversity in the offspring. Kover (2009) stated that high diversity will produce a large heterozygous population if several characters are combined from the results of crossing several parents for several generations. However, the dendogram value will be lower.

Pearson Correlation Analysis

Table 2. Results of the correlation test analysis of research variables

	JAP	GKPR	GKPP	GKPH	GKSR	GKSP	GKSH	B100
Number of Offspring Productive	1							
Dry Paddy Harvest of the Cluster	0.377	1						
Dry Paddy Harvest Per Plot	0.280	0.147	1					
Dry Grain Harvest Per hectare	0.441	0.605*	0.214	1				
Dry Paddy Save the Community	0.214	0.635*	0.369	0.763*	1			
Store Dry Paddy Perplot	0.166	-0.174	0.896**	0.092	0.087	1		
Dry Paddy Save Per Hectare	0.174	0.382	-0.237	0.752*	0.478	-0.259	1	
Weight 100 Item	0.215	0.684*	-0.220	0.301	0.260	-0.497	-0.213	1

Based on the table above, the results of the correlation analysis show a relationship between treatment factors, namely MP1 to MP7 and MP11 to MP17, to all observation variables including: number of productive tillers (JAP), weight of dry harvested grain per clump (GKPR), weight of dry harvested grain per plot (GKPP), weight of dry harvested grain per hectare (GKPH), weight of dry stored grain per clump (GKSR), weight of dry stored grain per plot (GKSP), weight of dry stored grain per hectare (GKSH), and weight of 100 grains (B100).

The JAP variable shows a very weak relationship to the GKSP and GKSH variables, weakly related to the GKPR, GKPP, GKSR, and B100 variables, moderately related to the GKPH variable. The number of productive tillers (JAP) of Mapan P-05 variety rice ranges from 17-

20. The number of plants will be maximized if the plant has good genetic characteristics coupled with environmental treatment that is in accordance with the growth and development of rice plants. The relationship between the JAP variable and GKPH (0.441) > r table (0.44) is significant, the correlation category is strong. While the relationship between GKPR (0.377), GKPP (0.280), GKSR (0.214), GKSP (0.166), GKSH (0.174) and B100 (0.215) < r table (0.44) is not significant, the grouping category is weak. In this case, dry grain produced from productive rice seedlings in rice fields measuring hectares will produce the maximum tonnage so that it can be maximized (Rahmad, et al., 2022).

The GKPR variable shows a very weak relationship to the GKPP and GKSP variables. It is weakly related to the GKSH variable, and strongly related to the GKPH, GKSR and B100 variables. The relationship between the GKPR variable and GKPP (0.605) and GKSR (0.763) and B100 (0.684)> r table (0.44) is significant, the correlation category is strong. While the relationship between GKPR and the GKPP variable (0.147), GKSP (-0.174), GKSH (0.382) <r table (0.44) is not significant, the correlation category is weak. This is because if the dry grain harvest per clump produced from the panicle in one clump will produce rice with good quality rice grain weight in terms of content and grain weight (Rudy, 2017).

The GKPP variable is weakly related to the GKPH, GKSR, GKSH and B100 variables, and is very strongly related to the GKSP variable. The relationship between the GKPP and GKSP variables (0.896) > r table (0.44) is significant, the correlation category is strong. While the relationship between GKPP and GKPH (0.214), GKSR (0.369), GKSH (-0.237) and B100 (-0.220) < r table (0.44) then it is not significant, weak correlation category.

GKPH variables are relatedvery weak with the GKSP variable, weakly related to the B100 variable, and strongly related to the GKSR and GKSH variables. The relationship between the GKPH variable and the GKSR (0.763) and GKSH (0.752) variables > r table (0.44) then significant, strong correlation category. While the relationship between GKPH and the GKSP (0.092) and B100 (0.301) variables < r table (0.44) then not significant, weak correlation category.

The GKSR variables are very closely related weak with the GKSP variable, weakly related to the B100 variable, and moderately related to the GKSH variable. The relationship between the GKSR variable and the GKSH variable (0.478) > r table (0.44) is significant, strong correlation category. While the relationship between GKSR and the GKSP variable (0.087) and B100 (0.260) < r table (0.44) is not significant, weak correlation category.

The GKSP variable is weakly related to the GKSH variable and moderately related to the B100 variable. The relationship between the GKSP variable and the B100 variable (-0.497) > r table (0.44) is significant, the correlation category is strong.

Whereas the relationship between the GKSP variable and GKSH (-0.259) < r table (0.44) is not significant, the correlation category is weak. While the GKSH variable is weakly related to the B100 variable. The relationship between the GKSH variable and the B100 variable (-0.213) < r table, so it is not significant, the correlation category is weak. The weight of 100 grains ranges from 22-25 grams. The weight of rice grain is closely related to the photosynthesis process that occurs in the leaves, a good photosynthesis process will increase the results of photosynthate transferred into the seeds (Azalika et al., 2018). The weight of 100 grains was observed to estimate the productivity of the rice plant.

Conclusion

The conclusion obtained from this study is that there is a relationship between the diversity of F1 rice plants of Mapan P-05 variety and its ratoons based on quantitative characters that are relatively close because of the similarity of characters and a maximum similarity of 20%. Dendogram analysis using the Average Linkage method on 14 objects of Mapan P-05 rice varieties shows that these varieties are divided into two main clusters. Cluster 1 consists of MP4, MP12, MP13, MP6, MP7, MP1, MP17, MP2, MP3, and MP5, while Cluster 2 consists of MP8, MP11, MP12, and MP13. The dendogram shows that the level of similarity between the first plant and its ratoons based on molecular markers is in the range of 0-25. These data illustrate that there are two large groups with high molecular similarity in the Mapan P-05 variety. High similarity values in clusters indicate closer diversity relationships. Conversely, greater differences in similarity values indicate more distant diversity relationships. Each cluster formed shows distinctive quantitative and qualitative characteristics. Quantitative characteristics include the number of productive tillers, dry grain weight per hill, dry grain weight per plot, stored dry grain weight per hill, stored dry grain weight per plot, and 100-grain weight. According to Pinilih et al. (2015), a genetic distance between 0.01 and 0.37 indicates a relationship between the varieties analyzed.

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Conflicts of Interest

The authors declare that there is no conflict of interest regarding the publication of this paper

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