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GENETIC ANALYSIS FOR RESISTANCE TO ANTHRACNOSE CAUSED BY *Colletotrichum acutatum* IN CHILI PEPPER (*Capsicum annuum* L.) USING DIALLEL CROSSES

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SUMMARY

Anthracnose caused by *Colletotrichum acutatum* is one of the most destructive diseases of chili pepper in Indonesia. Genetic analysis for chili pepper resistance to anthracnose caused by *C. acutatum* was evaluated by full diallel analysis. The F_1 and parent plants were grown in randomized complete block design with four replications. Forty green chili pepper fruits obtained from each genotype were inoculated with *C. acutatum* PYK 04 isolate using the method developed by AVRDC then divided into four groups for replication purposes. Data from F1 generation and parents were analyzed using the Hayman and Griffing methods. Results indicated that epistasis effect was not significant for resistance to anthracnose. Additive genetic effects were larger than the dominant effects. IPB C15 genotype contained a high proportion of recessive alleles. Dominant genes outnumbered recessive genes in the parent populations. Narrow-sense and broad-sense heritability were medium. The selection for resistance to *C. acutatum* on chili pepper breeding programs should be conducted on later generations and the multiple crosses method with transgressive recombination is recommended.

Key words: chili pepper, resistance, anthracnose, *Colletotrichum acutatum*

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INTRODUCTION

Anthracnose disease is one of the major economic constraints to chili pepper production worldwide, especially in tropical and subtropical regions, including Indonesia (Kim *et al.*, 2008; Than *et al*, 2008). Anthracnose, caused by various species of *Colletotrichum* spp., cause significant damage to pepper, due to loss more than 35% of the total annual pepper production in Indonesia (Sastrosumarjo, 2003).

In Indonesia, the most common types of anthracnose infecting chili pepper plants are *C. capsici* (Syd and Bisb) and *C. gloeosporioides* (Penz) Sacc. *C. gloeosporioides* population is 5 – 6 times larger than *C. capsici* and causes more damage. Recently, however, the most commonly found species in Indonesia is *C. acutatum*. Based on information gathered by Widodo in 2006, from 13 *Colletotrichum* isolates collected in Bogor, Brebes, Bandung, Pasir Sarongge, Payakumbuh and Mojokerto, 7 isolates were *C. acutatum* (Syukur *et al.*, 2007).

Genetic information on resistance to anthracnose is required to obtain high-yielding varieties with anthracnose-resistant

characteristic. Understanding the genetic behavior of anthracnose-resistant controlling genes can be done by estimation of genetic parameters.

Some researches on anthracnose-resistant controlling genes have been conducted, but the results are still various. Cheema *et al*. (1984) reported that anthracnose-resistant is additive and recessive. Park *et al.* (1990), on the other hand, suggested that resistance to anthracnose is controlled by dominant genes. Other researchers reported that such resistance is partial dominance and polygenic (Cheema *et al*., 1984; Park *et al*., 1990). Syukur *et al.* (2007) confirmed that the resistance to *C. acutatum* anthracnose is controlled by many genes without maternal effects. There are eight genes in the minimum numbers of resistance effective factors (controlling genes). Resistance controlling genes are recessive and its dominance degree is partially recessive. Anthracnose-resistant controlling genes act on additive and dominance characteristics; additive variants are higher than the dominance variants.

One of the methods used for genetic parameter estimation is the diallel cross analysis. According to Johnson (1963), the method is experimentally systematic approach, whereas analytically, this is a comprehensive genetic evaluation beneficial in identifying the best selection potential for crossing at early generation.

Diallel cross analysis is beneficial in estimating the general combining ability (GCA) and specific combining ability (SCA). This analysis is also useful to estimate additive and dominance effects and for estimating genetic variance and heritability in a reference population (Roy, 2000). Combining ability can be analyzed by Griffing method (Griffing, 1956), while genes action, genetic component and heritability may could be estimated by Hayman method (Hayman, 1954). Both methods are often utilized simultaneously in the data interpretation and have been used in many plant species such as chili pepper (Sousa and Maluf, 2003; Geleta *et al.,* 2006; Sujiprihati *et al*., 2007; Daryanto *et al.,* 2010; Syukur *et al.,* 2010), wheat (Singh *et al*., 2003), barley (Kakani *et al*., 2007), tomato (Hannan *et al.* (2007) and peanut (Kalia and Sood, 2009). This article analyzed gene's action, genetic components, combining ability, and heritability of chili pepper plant resistance to anthracnose caused by *C. acutatum* using the Hayman and Griffing diallel analysis.

This study was to obtain information about the genetic parameter of chili pepper resistance to anthracnose caused by *C. acutatum* using full diallel analysis.

MATERIALS AND METHODS

Five lines of chili pepper (*Capsicum annuum* L.) genotype selected on the basis of resistance to anthracnose from 14 genotypes; *i.e*. IPB C2 (selfing from PSPT C-11 originated from Department of Agronomy and Horticulture (AGH)-IPB; highly susceptible to anthracnose), IPB C9 (selfing from ICPN 12#4 originated from AVRDC; susceptible to anthracnose), IPB C19 (selfing from Randu originated from Dept. AGH IPB; susceptible to anthracnose), IPB C15 (selfing from 0209-4 originated from AVRDC; resistant to anthracnose), IPB C8 (selfing from ICPN 7#3 originated from AVRDC; susceptible to anthracnose) (Syukur *et al.*, 2009). These lines were crossed in all possible combination including reciprocals. The five parents and their resulting 25 F1's were grown in a randomized complete block design with four replications at University Farm, Bogor Agricultural University, Tajur, Bogor, Indonesia. Silver-black plastic mulch and other standard cultural practices were used for chili pepper planting.

Purification, multiplication and preservation of fungus culture were conducted in the Plant Clinic Laboratory, Department of Plant Protection, Bogor Agricultural University. Inoculum originated from pure culture of *C. acutatum*, a collection of Plant Mycology Laboratory-Department of Plant Protection Bogor Agricultural University isolate PYK 04 collected from Payakumbuh-West Sumatera, was used in this study.

Inoculum preparation and incubation methods was performed with the procedure of Yoon (2003). Isolate *C. acutatum* was cultured in *Potato Dextrose Agar* (PDA) media and incubated for 7 days. The inoculum's density was then observed and counted using

haemacytometer and the value was adjusted to 5.0 x 10^5 conidia/ml.

A chili pepper resistance test to *C. acutatum* was conducted in Plant Breeding Laboratory, Department of Agronomy and Horticulture, Bogor Agricultural University. Forty green ripe fruits harvested from each genotype, divided into four replications, were surface sterilized with 70% alcohol by using cotton wipes and then rinsed with sterile distillated water. Inoculation was conducted by injecting 2 µl of conidia suspension in one and two spots for < 4 cm and > 4 cm in fruits length, respectively. The inoculated fruits then were put into a plastic basin layered with wire. Humidity inside the basin was kept by placing wet tissue paper at the bottom of the basin below the wire. Then, the basin was covered with black plastic and incubated at 25 ^oC for 5 days.

Disease incidence was observed 5 days after inoculation. Resistance score and criteria to anthracnose were based on estimated disease incidence using the modified Yoon method (2003). Disease incidence (DI) was calculated as proportion of number of fruits showing the symptom to total inoculated fruits in each replication. Fruits were considered to be infected when the necrotic diameter was greater than 4 mm (Table 1). Data analysis was conducted at 1 – Disease Incidence/100 using two approaches e.g. the Hayman and Griffing methods (Singh and Chaudhary, 1979).

Table 1. Red chili pepper resistance score and criteria to anthracnose based on disease incidence.

Score	Disease Incidence (%)	Criteria
1	$0 \leq x \leq 10$	Highly Resistant
2	$10 < x \leq 20$	Resistant
3	$20 < x \leq 40$	Moderate
4	$40 < x \leq 70$	Susceptible
5	$x > 70$	Highly Susceptible

Table 2. Mean Square of Disease Incidence[a)] of Chili Pepper Genotypes to PYK 04 isolate.

Source	df	Sum of square	Mean Square	F Value
Replication	3	0.874	0.291	6.769
Genotype	24	2.487	0.104	2.406**
Error	72	3.100	0.043	
Total	99	6.461		

Note: **: significantly different at $P < 0.01$, [a)]: Data analysis was conducted at 1 – Disease Incidence/100

RESULTS

The genetic parameter estimation using the diallel cross analysis can be done when clear differences occur among genotypes based on F test on resistance to anthracnose (Singh and Chaudhary, 1979). Highly significant differences in disease incidence to *C. acutatum* PYK 04 isolate were found among genotypes (Table 2). Therefore, the genetic parameter estimation to *C. acutatum* PYK 04 isolate can be determined.The gene interaction can be seen from b value (Wr, Vr). If b value is distinct to one, genes interaction occurs; on the contrary, if b value is not distinct to one, no genes interaction occurs (Roy, 2000; Sousa and Maluf, 2003). The result of b regression coefficient (Wr, Vr) was not distinct (Table 3); therefore, no genes interaction occurs in determining resistance to *C. acutatum* PYK 04 isolate on the chili pepper diallel population. The result showed that one of the diallel cross analysis assumption was met.

The additive effect (D) to *C. acutatum* PYK 04 isolate was apparent. The additive effect (D) of resistance to *C. acutatum* PYK 04 isolate was 0.036. The dominance effect (H_1) was indistinct to anthracnose-resistant (0.003) (Table 3). It indicates that resistance to

anthracnose on the diallel chili pepper population was affected more by additive gene action.

The gene distribution in parent can be seen from H_2 value. Determinant genes to *C. acutatum* PYK 04 isolate inheritance equally spread in parent, indicated by indistinct H_2 value (Table 3).

Positive genes proportion will be apparent from comparison of H_1 value to H_2. If $H_1 > H_2$, most genes were positive; on the contrary, if $H_1 < H_2$, negative genes were more than the positive ones. Most genes determining resistance to anthracnose PYK 04 isolate were positive genes, illustrated by the value of $H_1 > H_2$ (Table 3).

Dominance effect level was indicated by the value of $(H_1/D)^{1/2}$. The value of $(H_1/D)^{1/2}$ on *C. acutatum* PYK 04 isolate was less than one shows recessive partial (Table 3). According to Hayman (1956), when value of $(H_1/D)^{1/2}$ was more than one that indicates over dominance, whereas the value of $(H_1/D)^{1/2}$ between zero and one signifies partial dominance (partial dominance or partial recessive).

The number of dominance genes in parent was is reflected from the value of Kd/Kr. If Kd/Kr > 1, the dominance gene numbers are larger in parent. On the contrary, if Kd/Kr < 1, parent contains higher recessive genes (Singh and Chaudhary, 1979). Table 3 illustrates that Kd/Kr value > 1 (5,587), indicating more dominance genes in parent.

Sequence of parent dominance (based on Wr + Vr) reflects the number of dominant genes in parent. Smaller value of Wr + Vr means more dominance genes controlling certain characteristic. Dominance sequence was also illustrated from image showing relation between covariance (Wr) and variance (Vr). A Closer location of a point to zero means parent that containing the most dominant genes. On the contrary, the farther location between a point to zero means the most content of recessive genes in parent (Singh and Chaudhary, 1979; Sousa and Maluf, 2003).

Parent dominance sequence of resistance to *C. acutatum* PYK 04 isolate was IPB C2 (0.023) (Table 4). Parent IPB C15 contains most recessive genes, because its value was the farthest to zero. On the other hand, IPB C2 contains the most dominant genes, because value was the closest to zero.

Regression line on Wr – Vr diagram having intercept a value = 0.011 cuts across Wr axis above base point (0). The point of intersection position shows partial dominant genes action (Figure 1).

Table 3. Estimation of genetic parameter in chili pepper disease incidence[a)] to *C. acutatum* PYK 04 isolate using the Hayman method of diallel analysis.

Genetic Parameter	Disease Incidence to Antracnose
Covariance-variance regression coefficient (b(Wr, Vr))	0.415 ns
Additive effect (D)	0.036 **
Dominance effect (H_1)	0.003 ns
Proportion of dominance due to positive and negative effect of genes (H_2)	0.001 ns
F_r mean (F)	0.014 ns
F1 deviation from the average parent (h^2)	0.002 ns
Environment (E)	0.013 **
Mean degree of dominance ($(H_1/D)^{1/2}$)	0.285
Proportion of dominance genes to recessive genes ($H_2/4H_1$)	0.074
The proportion of dominant to recessive genes (Kd/Kr)	5.587
Number of groups of genes (h^2/H_2)	2.424
Coefficient of correlation (r) between $W_r + V_r$ and Y_r	0.667
Heritability in broad-sense (h^2_{bs})	0.475
Heritability in narrow-sense (h^2_{ns})	0.467
The highest limit if all the dominant genes assembled (Y_D)	0.442
The highest limit if all the recessive genes come together (Y_R)	0.478

**: significantly different at $P < 0.01$; ns : not significantly different, [a)] Data analysis was conducted at 1 – Disease Incidence/100

Table 4. Distribution Vr + Wr.

Genotype	Disease Incidence[a)] to Antracnose
IPB C2	0.023
IPB C8	0.027
IPB C9	0.030
IPB C15	0.041
IPB C19	0.033

[a)] Data analysis was conducted at 1 – Disease Incidence/100

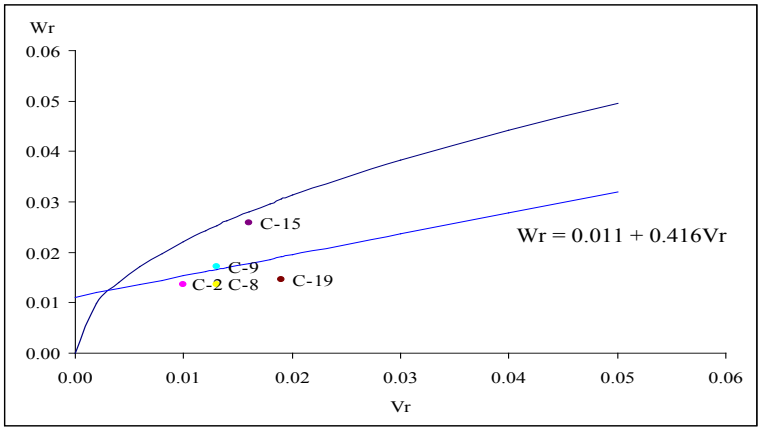

Figure 1. Correlation between covariance and variance of chili pepper disease incidence to anthracnose.

Resistance to *C. acutatum* PYK 04 isolate was controlled by recessive genes. Their numbers were reflected in the value of (h^2/H_2). The number of genes controlling resistance to *C. acutatum* PYK 04 isolate was divided into two controlling groups (Table 3).

The resistance estimation of broad-sense heritability (h^2_{bs}) and narrow-sense heritability (h^2_{ns}) to *C. acutatum* PYK 04 isolate was medium with the value of 0,475 and 0,467 respectively (Table 3). The additive effect to genetic variant can be seen from the proportion of h^2_{ns} to h^2_{bs}. The proportion of h^2_{ns} to h^2_{bs} was high, indicating that the genetic variant was determined more by the additive variance component. It shows high proportion of additive variance determining resistance level, which was in accordance with the previous explanation on distinct role of additive influence.

The highest limit of all homozygote dominance genes accumulated in an individual plant (YD) was 0.442. On the other hand, the highest limit of all homozygote recessive genes in an individual plant (YR) was 0.475 (Table 3). The YR value was considered low. For example, YR value 0.475 means maximum individual obtained was pure line to anthracnose (DI = 100 – 47.5% = 52.5%). Therefore, recommended crossing method was the reduplicative cross method with transgression separation or by introducing new gene source into population.

The general combining ability analysis applying the Griffing's method 1 shows effects of general combining ability that was distinct to resistance to *C. acutatum* PYK 04 isolate, whereas effects of reciprocal and specific combining ability were indistinct (Table 5). Parent IPB C15 (0.112) had the highest general combining ability compared to other parents. The mean of IPB C15 resistance to *C. acutatum* PYK 04 isolate was 0.825. IPB C9 had the lowest general combining ability (-0,018) (Table 6).

Table 5. Variance analysis of General Combining Ability (GCA) and Specific Combining Ability (SCA) in Chili Pepper Disease Incidence[a)] to *C. acutatum* PYK 04 Isolate.

Source	df	Mean squares
Replication	3	0.291
GCA	4	0.072 **
SCA	10	0.014 ns
Resiprocal	10	0.020 ns
Error	72	0.011

**: significantly different at $P < 0.01$, ns: not significantly different, [a)] Data analysis was conducted at 1 – Disease Incidence/100

Table 6. General combining ability (GCA) and specific combining ability (SCA) values in chili pepper disease incidence[a)] to *C. acutatum* PYK 04 isolate.

Genotype	Mean	GCA
IPB C2	0.416	0.048
IPB C8	0.447	0.047
IPB C9	0.250	-0.018
IPB C15	0.825	0.112
IPB C19	0.331	0.011
		SCA
IPB C2 x IPB C8	0.486	0.035
IPB C2 x IPB C9	0.575	0.030
IPB C2 x IPB C15	0.500	0.002
IPB C2 x IPB C19	0.625	0.118
IPB C8 x IPB C2	0.625	-0.069
IPB C8 x IPB C9	0.500	0.094
IPB C8 x IPB C15	0.775	-0.020
IPB C8 x IPB C19	0.250	-0.115
IPB C9 x IPB C2	0.450	0.063
IPB C9 x IPB C8	0.494	0.003
IPB C9 x IPB C15	0.450	-0.044
IPB C9 x IPB C19	0.300	0.036
IPB C15 x IPB C2	0.859	-0.180
IPB C15 x IPB C8	0.382	0.197
IPB C15 x IPB C9	0.582	-0.066
IPB C15 x IPB C19	0.597	-0.007
IPB C19 x IPB C2	0.575	0.025
IPB C19 x IPB C8	0.325	-0.038
IPB C19 x IPB C9	0.500	-0.100
IPB C19 x IPB C15	0.508	0.045

Note: [a)]: Data analysis was conducted at 1 – Disease Incidence/100

DISCUSSION

Resistance to anthracnose diseases caused by *C. acutatum* have been reported in various species including *Capsicum baccatum* (AVRDC, 1999; Yoon *et al*., 2006) and *C. chinense* (AVRCD, 1999; AVRDC, 2003). Nevertheless, the transfer of resistance genes from the species *C. baccatum* and *C. chinense* to *C. annuum* are not easy (Greenleaf, 1986) and undesirable traits of the species are difficult to remove. Therefore, exploration *C. annuum* containing genes for anthracnose resistance is being continued. AVRDC (2003) reported that three genotypes of *C. annuum* were resistant to anthracnose caused by *C. acutatum*. Three genotypes are 1430 PBC originally from Mexico, PBC 1439 from USA, and PBC 1478 from Australia, while one genotype (PBC 880 from Mexico) of the species *C. baccatum*.

In this study, one genotype were resistant to anthracnose caused by *C. acutatum*. The genotype was IPB C15 which was introduced from AVRDC (0209-4 code). According to Gniffke (2004), 0209-4 was BC3F6 of a cross between the species *C. annuum* (Susan's Joy) with *C. chinense* (PBC 932).

In this study, IPB C15 was used to study the inheritance of resistance to anthracnose disease as resistant genotypes. Resistance to diseases caused by *C. acutatum* is controlled by many recessive genes with partial recessive gene action (Syukur *et al*., 2007). This result was not in agreement to the results of Yoon *et al.* (2006), who reported that resistance to anthracnose caused by *C. acutatum* on interspecific hybridization of *C. annuum* (Habreno) with *C. baccatum* (PBC 81) controlled by a dominant major gene. Kim (2006) reported that resistance to anthracnose caused by *C. acutatum* on interspecific hybridization of *C. annuum* with *C. baccatum* (crosses HN 11' x 'AR) is controlled by a recessive major gene (a simple recessive gene), while the interspecific hybridization of *C. annuum* with another *C. baccatum* (crosses 'Golden-aji' x 'PI 594137') was controlled by a dominant major gene (simple dominant gene). These results indicated that the parent which carry different genes respond differently to the anthracnose resistance caused by *C. acutatum*. Resistance to anthracnose diseases caused by *C. gloesporioides* on interspecific hibridization between *C. annuum* with *C. frustescens* is controlled by one gene with recessive gene action (Amilin *et al.*, 1995). Resistance to anthracnose disease caused by *C. gloeosporioides* on chili interspecific hybridization of *C. annuum* (Jatilaba) with *C. chinense* (CC-27) is controlled by many genes with incomplete dominant gene action (Wusani, 2004). Pakdeevaraporn (2005) reported that resistance to anthracnose diseases caused by *C. capsici* in chili interspecific hibridization of *C. annuum* (Bangchang) with *C. chinense* (PBC 932) controlled by a single recessive gene with a pattern of 1 resistant to 3 susceptible at F2.

Inheritance studies using different species has several weakness such as differences in species provide different structure and morphology of chromosomes. These conditions will prevent the occurrence of chromosome pairing of the two parents. Genome differences in interspecific between *Capsicum annuum* x *C. baccatum* cause abnormalities in the pairing at meiosis, so that it appears the bridge and lagging (Yoon, 2003). A very real difference in size between *O. sativa* with *O. australiensis* will reduce the chances of the formation of hybrid embryos (Nezu *et al*., 1960; Li *et al.*, 1963). *O. australiensis* chromosomes are much bigger than (2-4 times) *O. sativa* chromosomes resulted incompatibility between the two species. Abnormalities of chromosome pairs during meiosis may cause biased estimate of genetic control of a character.

The general combining ability clearly affects and has a higher value compared to specific combining ability (SCA), indicating resistance to anthracnose that was controlled by additive genes. A higher level of general combining ability than specific combining ability reflects that the additive genes have a more important role in controlling the characteristic compared to non-additive genes (Sousa and Maluf, 2003; Geleta *et al.,* 2006).

On the contrary, a higher specific combining ability indicates a bigger role of non-additive genes in controlling certain characteristic compared to additive genes (Oliveira *et al.,* 1998; Cruz *et al.,* 2006). Roy (2000) suggests that the general combining

ability is an estimator to additive variant, whereas the specific combining ability is an estimator of non-additive variant (dominance and epistasis). According to Syukur *et al*. (2007), based on a combined scale test, the genes action controlling resistance to *C. acutatum*-triggered anthracnose adopts an additive-dominance model. The additive genes have bigger role than the dominance genes in determining resistance to anthracnose.

The additive genes variant is the main factor of similarity among families (between parent and filial). Variant is mean of genes effects: function of phenotype level changes due to selection. The dominance genetic variant is the main cause of family dissimilarity. It becomes the main basis of heterosis and specific combining ability (Roy, 2000).

CONCLUSION

There was no interaction among genes in determining resistance to anthracnose. Additive effect was apparent, whereas the dominance effect was indistinct. The additive effect was higher than the dominance effect. The recessive genes control resistance level. The dominance degree was categorized as incomplete recessive. IPB C15 genotype contained the most recessive genes. The broad-sense heritability and narrow-sense heritability were medium. Population development to create high-yielding chili pepper seeds resistance to *C. acutatum* may be done to enhance the generation applying reduplicative cross method with transgressive recombinant.

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