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Genetic Studies of Leaf Disease Resistance in Hevea

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This paper highlights the major findings on the genetic studies of Hevea *leaf disease (*Colletotrichum, Corynespora *and* Oidium*) resistance using 18 selected genotypes and progenies from a five-parent diallel cross population. Results of the investigations showed that* Colletotrichum *and* Corynespora *resistance had moderate heritability estimates while* Oidium *resistance had relatively lower values. General combining ability (GCA) effects were important in controlling all the three disease resistance traits. Specific combining ability (SCA) effects were demonstrated to be important in accounting for the variation of* Corynespora *and* Oidium *resistance. Reciprocal effects were not detected for these diseases; and the relative magnitude of GCA to SCA was 37 (range: 25.6 – 40.0) for* Colletotrichum*; 4.6 (range: 1.4 – 11.1) for* Corynespora *and 2.0 (range: 0.5 – 4.8) for* Oidium *resistance.*

These findings are discussed in relation to Hevea *breeding.*

An understanding of the pattern of genetic inheritance for major economic traits is important in planning and execution of a breeding programme in any crop. In *Hevea*, although the breeding programme of the Rubber Research Institute of Malaysia (RRIM) started as early as 1928, attention on the need of some genetic understanding of the crop only began in the early 1970s when the breeders encountered some difficulties in the direction of yield improvement. This prompted genetic studies on major economic traits such as yield and vigour of the crop. No emphasis, however, was given to the genetic aspect of leaf disease resistance during that time. It was only until recent years when disease outbreak became more prominent and when there was global concern over the use of prophylactic measures for disease control in agriculture that some genetic studies relating to *Hevea* leaf diseases were initiated in the RRIM.

This paper highlights some results of the genetic study of three local leaf diseases, caused by *Colletotrichum gloeosporioides*, *Corynespora cassiicola* and *Oidium Hevea*. An attempt is also made to answer the following questions pertinent to the making of breeding decisions:

- Nature and extent of genetic variation
- Mode of genetic inheritance
- Relationship with other economic traits.

Implication of the findings will be discussed in relation to *Hevea* breeding.

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DATA SOURCE AND ANALYSES

The data used were derived from:

1. A sample of 18 selected genotypes (Tjir 1, GT 1, AV 157, AV 427, RRIM 501, RRIM 519, RRIM 600, RRIM 607, RRIM 614, RRIM 615, RRIM 623, PB 49, PB 86, PB 5/51, PB 5/63, PR 107, PR 255 and PR 261) of various degrees of leaf disease resistance.
2. Fifteen randomly selected progenies per family from a five-parent (RRIM 501, RRIM 600, AV 157, Tjir 1 and PB 49) diallel cross population[1].

Each of the above genotypes was represented by five buddings per plot in a randomised block design with three replications at a 1.07 m × 1.07 m planting distance. The nursery was at the RRIM Experiment Station, Kota Tinggi, an area which is conducive for the development of *Colletotrichum* leaf fall, *Corynespora* leaf blight and *Oidium* leaf fall diseases.

Screening for leaf disease resistance of the genotypes was made at appropriate times after artificial inoculation with *Colletotrichum* and natural infection of *Corynespora* and *Oidium* according to some adopted methods[2–4]. Two rounds of *Colletotrichum* disease screening and three rounds of *Corynespora* and *Oidium* disease screening were carried out.

The disease severity scores were obtained as follows:

- *Colletotrichum* infection was obtained by scoring the degree of spotting of the five middle leaflets for each of the three randomly selected leaf flushes per plant using scores 0 to 5.
- *Corynespora* infection was obtained by averaging the total number of lesions of nine middle leaflets for each of the three randomly selected leaf flushes per plant.
- *Oidium* infection was obtained by averaging the scores of six middle leaflets for each of the three randomly selected leaf flushes using scores 0 to 5 .

The above data, comprising individual and combined assessments from the different rounds of disease screening, were used for the estimation of heritability and combining ability analyses (*Method III*, *Model 1*) as outlined by Becker[5] and Griffing[6].

NATURE OF GENETIC VARIATION

Usually, variation of disease resistance of a crop can be observed in an environment where a particular disease is prevalent. The apparent difference in resistance of a sample population observed may suggest certain form of genetic control mechanism leading to the specific resistance. Basically, two broad categories of genetic variations can be recognised *viz* major gene and polygenic inheritance. While there are several characteristics to differentiate various forms of genetic mechanisms[7], one of the criteria is to monitor the distribution or variation pattern of a specific trait in a given population. A trait which shows continuous variation is often referred to as likely candidate for polygenic inheritance. On the other hand, a trait which demonstrates a discrete variation, giving only a few distinct phenotypic classes, has often been regarded as potential candidate for major gene inheritance. This major gene inheritance may be detected through the recognition of more than one physiological races of the pathogen for the particular disease.

The degrees of resistance to *Colletotrichum*, *Corynespora* and *Oidium* in the field, nursery or laboratory have shown a continuous form of variation (see Wastie[4], Lim[8] and Tan *et al.*[9]), implying polygenic inheritance.

In addition, there is a suggestion that the *Corynespora* resistance may also be governed by the major gene mechanism which exhibits hypersensitivity characteristic upon disease infection in certain genotypes such as RRIC 103 and KRS 21.

The above inference on the nature of genetic variation and possible genetic control is empirical to some extent. Further genetic investigations are therefore necessary.

EXTENT OF GENETIC VARIATION

To describe the extent of genetic variability with reference to *Colletotrichum*, *Corynespora* and *Oidium* resistance traits, the broad-sense heritabilities are estimated in the study population and are summarised as follows:

- The mean heritability estimates based on the 18 genotypes for *Colletotrichum*, *Corynespora* and *Oidium* resistance traits were 32.6% (28.9% – 37.7%), 38.5% (22.2% – 52.2%) and 23.3% (7% – 40.3%), respectively.
- The mean heritability estimates based on the diallel progenies were 31.2% (22.8% – 35.4%) for *Colletotrichum*, 21.1% (18.0% – 25.5%) for *Corynespora* and 12.4% (7.4% – 17.7%) for *Oidium*.

The results indicate that both the *Colletotrichum* and *Corynespora* resistance had moderately high heritability estimates while *Oidium* resistance had relatively lower values (*Tables 1* and *2*). It implies that there was a larger genetic variability for *Colletotrichum* and *Corynespora* resistance traits than that of *Oidium* resistance in the population studied. Selection for genotypes with *Colletotrichum* and *Corynespora* resistance would therefore be more effective than the selection for *Oidium* resistant genotypes.

TABLE 1. HERITABILITY ESTIMATES OF LEAF DISEASE RESISTANCE IN 18 GENOTYPES

Assessment	Heritability estimates (%)		
	Colletotrichum	*Corynespora*	*Oidium*
I	28.9	52.2	7.0
II	31.1	22.2	13.2
III	-	28.9	40.3
Overall[a]	37.7	50.6	32.5
Average	32.6	38.5	23.3

[a] Based on the overall disease scores from individual assessments.

TABLE 2. HERITABILITY ESTIMATES OF LEAF DISEASE RESISTANCE IN A FIVE-PARENT DIALLEL CROSS POPULATION

Assessment	Heritability estimates (%)		
	Colletotrichum	*Corynespora*	*Oidium*
I	22.8	18.0	7.4
II	35.4	25.5	14.6
III	-	19.5	17.7
Overall[a]	35.4	21.4	9.8
Average	31.2	21.1	12.4

[a] Based on the overall disease scores from individual assessments.

MODE OF GENETIC INHERITANCE

Combining ability analyses are useful for partitioning genetic variations due to additive, non-additive and reciprocal effects in polygenic inheritance study.

From a study of a five-parent diallel cross population, the following information was obtained (*Table 3*):

- Predominance of general combining ability (GCA) effects were generally demonstrated for *Colletotrichum, Corynespora* and *Oidium* resistance.
- Specific combining ability (SCA) effects were significant for *Corynespora* and *Oidium* resistance traits but not for *Colletotrichum* resistance.
- Reciprocal effects (RE) were not detected for all the disease resistance traits.

TABLE 3 COMBINING ABILITY ANALYSES FOR DISEASE RESISTANCE IN A FIVE-PARENT DIALLEL CROSS POPULATION

Source	Mean squares		
	Colletotrichum	*Corynespora*	*Oidium*
GCA	***	***	**
SCA	NS	**	**
RE	NS	NS	NS
GCA SCA[a]	37.0	4.6	2.0
	(25.8–40.0)	(1.4–11.1)	(0.5–4.8)

NS Not significant at $P<0.05$

**, *** $P<0.01$ and 0.001, respectively

[a] Mean square ratios of GCA and SCA expressed as mean and range from individual and overall assessments

The relative contribution of GCA and SCA effects, as reflected in their mean square ratios, indicates that GCA is more important than SCA for *Colletotrichum* resistance (mean = 37.0; range = 25.6 – 40.0) followed by *Corynespora* resistance (mean = 4.6; range = 1.4 – 11.1) and *Oidium* resistance (mean = 2.0; range = 0.5 – 4.8) in governing the genetic variations. A large part of the major genetic variation of the disease resistance, especially that of *Colletotrichum*, could be attributed to additive gene control. In addition, the non-additive gene control also plays a significant role in *Corynespora* and *Oidium* resistance.

GENERAL COMBINING ABILITY ESTIMATES

GCA values of parental clones can help in the choice of parents in a breeding programme. As GCA effects have been established to play an important role in governing the variation of the three disease resistance traits, the GCA values of the parents involved in the crosses were estimated and were compared with their phenotypic values (*Table 4*). A fairly good correspondence between the parental rankings, based on their phenotypic and genotypic values, was observed for *Colletotrichum* and *Corynespora* While certain correspondence in the parental rankings based on the two values was noted, there was discrepancy with the ranking of some parents (for example, RRIM 600) for *Oidium* resistance trait. It is possible that the SCA, being important in governing the variation, could have exerted its effect in crosses involving certain parents. In general, the phenotypic values of *Hevea* genotypes could be used as a basis for the choice of parents in the breeding programme. The phenotypic values, however, should preferably be complemented by the GCA values obtained from the genetic study to form a better guide for the selection of disease resistant parents

CORRELATION BETWEEN DISEASE RESISTANCE AND OTHER TRAITS

Correlations among the disease resistant traits in the sample population studied were generally shown to be non-significant. However, very low ($r < 15\%$ with $n = 250 – 299$) correlations were detected in a few instances. The results

TABLE 4. PHENOTYPIC AND GENOTYPIC VALUES OF PARENTAL GENOTYPES FOR LEAF DISEASE RESISTANCE IN A FIVE-PARENT DIALLEL CROSS POPULATION

Colletotrichum		*Corynespora*		*Oidium*	
Phenotypic	Genotypic	Phenotypic	Genotypic	Phenotypic	Genotypic
Tjir 1 1.076	AV 157 0.273	RRIM 600 0.242	RRIM 600 0.217	RRIM 600 0.106	Tjir 1 0.083
AV 157 0.806	Tjir 1 0.197	Tjir 1 0.031	RRIM 501 0.110	AV 157 0.096	AV 157 0.034
RRIM 501 –0.114	RRIM 600 0.168	AV 157 –0.012	Tjir 1 –0.024	Tjir 1 0.086	RRIM 501 –0.005
RRIM 600 –0.194	PB 49 –0.289	RRIM 501 –0.129	AV 157 –0.069	PB 49 –0.114	PB 49 –0.045
PB 49 –0.574	RRIM 501 –0.349	PB 49 –0.132	PB 49 –0.234	RRIM 501 –0.174	RRIM 600 –0.067
3.384*	3.400*	0.132*	0.280*	2.594*	2.510*

*General mean score

Both phenotypic and genotypic values are based on combined assessments.

indicated that there was no close genetic association among these traits.

The influence of disease resistance traits in relation to latex yield and vigour can be fairly evident in the field. From observations that selected high yielding and/or vigorous genotypes have varying degrees of disease resistance, adverse genetic association between disease resistance and the important economic traits is not evident.

IMPLICATION IN BREEDING

Breeding against *Microcycleus ulei*, a devastating pathogen causing South American Leaf Blight, is emphasised in Brazil. Over several decades of breeding efforts, no successful genotypes with durable resistance and acceptable latex yield have been produced[10–12]. A few factors may have hampered the success of the programme. First, the source of disease resistance appeared to have centred on major gene resistance. Second, disease resistance seems to be negatively associated with high yielding traits. Third, the pathogen has short life cycle and is capable of evolving new physiological races. Fourth, the host, *Hevea,* is a perennial tree crop.

From experience and history of breeding in agricultural crops, breeding for durable resistance, contributed by polygenic inheritance, is favoured as a current strategy[10–15]. In *Hevea*, *Colletotrichum*, *Corynespora* and *Oidium* are demonstrated to have this favourable genetic mechanism and there was also no evidence of adverse genetic association between the disease resistance traits and latex yield or vigour. In addition, sufficient genetic variability is available in the current breeding and germplasm populations. Thus, the enhancement and incorporation of durable disease resistance traits in the breeding populations should be favourable.

One of the main objectives of our breeding programme is to produce high (latex) yielding genotypes with acceptable secondary traits such as good immature vigour, vigour on tapping, virgin bark and bark renewal and disease tolerance. The breeding approach, based on additive principle, has shown considerable progress. The leaf disease resistance traits, which are polygenic and durable in nature, have also been built up in the breeding population. The present findings for the three leaf diseases therefore strongly support the current breeding strategy.

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