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CLONAL VARIATION IN THE INTENSITY OF POWDERY MILDEW (*OIDIUM HEVEAE* STEINM.) DISEASE OF *HEVEA*

Alice John, Annakutty Joseph, T. Meenakumari, C.K. Saraswathyamma and Y. Annamma Varghese.

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Twenty genotypes representing gene pools of diverse origin were screened in the nursery with the objective of identifying sources of resistance against *Oidium heveae* Steinm. causing powdery mildew incidence. An attempt was also made to understand the pattern of response of the genotypes in different years. Clonal variation for the intensity of powdery mildew was highly significant. Among the 20 genotypes studied, eight genotypes viz., RRIC 52, AC/S/12 42/186, PR 261, RO/CM/10 44/7, RRIM 703, AC/S/12 42/59, PB 86 and IAN 45-873 possessed high degree of tolerance combined with stability in their response to disease intensity.

Key words: Disease intensity, *Hevea*, Powdery mildew, Response pattern, Stability.

Alice John (for correspondence), Annakutty Joseph, T. Meenakumari, C.K. Saraswathyamma and Y. Annamma Varghese, Rubber Research Institute of India, Kottayam–686 009, India (e-mail : rrii@vsnl.com).

INTRODUCTION

The ideal method of disease control is development and cultivation of varieties of plants that are resistant/tolerant. Assortative mating and vegetative propagation have, in effect, narrowed down the genetic base in *Hevea* causing erosion of many genes like those conferring resistance to various diseases. The relative susceptibility of many clones to diseases could be due to such genetic erosion. This situation demands extensive breeding programmes in *Hevea* for the development of high yielding clones with disease tolerance.

Powdery mildew caused by *Oidium heveae* Steinm. is one of the major leaf diseases causing considerable yield drop in rubber plantations in India (Jacob *et al.*, 1992). Complete drying up of the affected young rubber plants of two to three years growth has been reported (Edathil *et al.*, 1988). Though effective control measures are available to manage this disease, except for cultivation of resistant varieties, all other measures are recurring and hence costly and cumbersome. Therefore use of resistant varieties is by far the most effective, most economical and the least hazardous of disease control measures.

Resistance to a particular disease is not acquired or created *de novo*. Genes for resistance/susceptibility are already present in some varieties or wild relatives. Identification of the sources of resistance is one prerequisite for breeding for disease resist-

ance. In this context the present study was envisaged to identify and define sources of resistance and to understand their response pattern over different years so as to incorporate them in future breeding programmes.

MATERIALS AND METHODS

Twenty clones (Table 1) representing gene pools of diverse origin were selected for the study. The experiment was conducted at Rubber Research Institute of India (RRII), Kottayam employing RBD with three replications. Each clone was planted in one row of ten plants at a spacing of 1 x 1m. Spreader rows of a susceptible clone PB 5/51 were planted to create natural epiphytotics in the field. The plants were cut back to ensure uniform growth stage of the leaf and thereby to negate the possibility of escape. Disease assessment was carried out for three consecutive years at the peak disease season when the inoculum potential was high. The disease intensity was evaluated by scoring 10 leaves from each plant on a 0-5 scale and expressed as per cent disease intensity (PDI) as per Horsfall and Heuberger (1942). Since the occurrence of disease during one year was very mild the data from the other two years was considered for statistical analysis. Individual as well as combined analysis of variance were carried out. Shukla's stability variance, $\hat{\sigma}^2$ (Shukla, 1972) was worked out to study the stability of clones with respect to intensity of powdery mildew under varying weather conditions (Fig. 1) in different years.

Table 1. **Details of clones screened for tolerance to *Oidium heveae***

Clone	Parentage
Indian	
RRII 5	Primary clone
RRII 105	Tjir 1 X Gl 1
Malaysian	
RRIM 600	Tjir 1 X PB 86
RRIM 703	RRIM 600 X RRIM 500
PB 5/51	PB 56 X PB 24
PB 28/59	Primary clone
PB 86	Primary clone
PB 217	PB 5/51 X PB 6/9
PB 235	PB 5/51 X PB S/78
PB 260	PB 5/51 X PB 49
PB 311	RRIM 600 X PB 235
Sri Lankan	
RRIC 52	Primary clone
RRIC 102	RRIC 52 X RRIC 7
Indonesian	
PR 255	Tjir 1 X PR 107
PR 261	Tjir 1 X PR 107
GT 1	Primary clone
Brazilian	
AC/S/12 42/59	Primary clone
AC/S/12 42/186	Primary clone
RO/CM/10 44/7	Primary clone
IAN 45-873	PB 86 X F 1717

RESULTS AND DISCUSSION

None of the clones used in the study was free of the disease. The intensity of disease varied in different years. During 1997 the incidence was slightly higher than in 1999 (Table 2). Analysis of variance revealed highly significant clonal differences in disease intensity with a wide range of variation among the clones in both the years. The disease incidence during 1997 ranged from 21.27 to 76.57 per cent. The clone PB 235 appeared to be the most susceptible followed by PB 5/51 and PB 311. The lowest percentage of disease intensity was recorded in the clone PB 86 (21.27) followed by RRIC 102 (28.27), RO/CM/10 44/7 (28.43) and RRIC 52 (33.34). Among the 20 genotypes screened

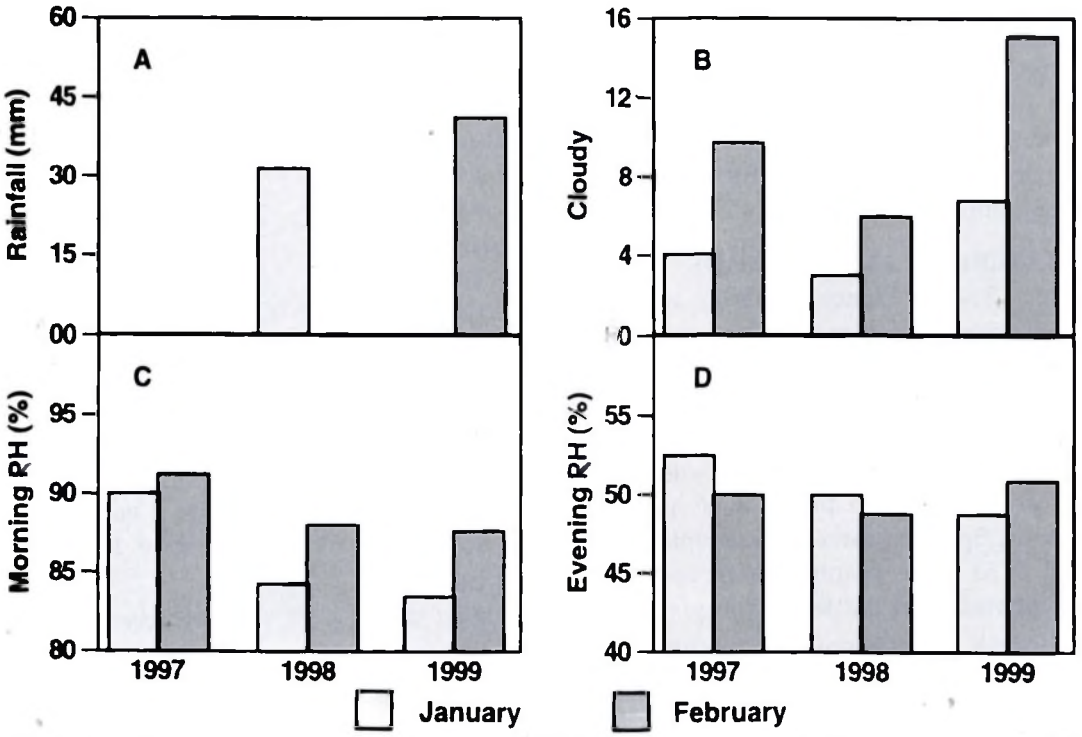

Fig. 1. Weather parameters at RRII, Kottayam; A. Rainfall; B. Cloudy days; C. Relative humidity (morning); D. Relative humidity (evening)

12 clones exhibited significantly lower PDI than the general mean.

Clones, in general, showed fluctuation of PDI during the second year (1999) of screening. Variation in disease intensity year after year in certain clones was also reported earlier (Rajalakshmi *et al.*, 1997). Clone PB 86 remained the most tolerant one followed by RO/CM/10 44/7, IAN 45-873, RRIC 52 and RRIM 703. PB 5/51 exhibited the highest disease intensity during 1999. The combined analysis showed highly significant clonal variation confirming the relatively satisfactory resistance and susceptibility of clone PB 86 and PB 5/51 respectively (Table 2). This observation corroborates earlier reports (Young 1950, Yu *et al.*, 1992). The existence of significant interaction between genotype and year component of variance for disease incidence revealed the presence of genetic differences among the genotypes for their response to varying environment.

The best method to understand the pattern of response of different genotypes over a range of environments would be to attempt stability analysis. For this purpose Shukla's stability variances were worked out (Shukla, 1972). The genotype that is most stable is the one that minimises the statistic. The estimates and ranks assigned to each clone, based on stability variance along with PDI in the descending order is presented in Table 2.

Out of the 20 clones screened, four clones showed significant estimates of stability variance ($\hat{\sigma}^2$). The clones RRIC 52, AC/S/12 42/186, PR 261,

Table 2. **Stability of clones for the intensity of powdery mildew disease during different years**

Clone	Per cent disease intensity			Stability variance	Rank
	1997	1998	Mean	($\hat{\sigma}^2$)	
PB 5/51	66.13	65.47	65.80	9.90	11
PB 311	63.73	59.87	61.80	-0.86	3
PB 235	76.57	45.91	61.24	355.63**	20
PB 260	50.37	47.80	49.08	2.11	4
RRII 105	52.25	40.66	46.45	20.07	14
RRIM 600	47.50	42.00	44.75	-1.96	1
PB 28/59	51.90	33.47	42.69	93.95**	19
RRII 5	40.83	41.50	41.16	17.72	13
PB 217	39.17	40.80	39.98	24.59	16
GT 1	38.93	40.41	39.67	23.45	15
AC/S/12 42/186	41.33	33.15	37.24	2.65	5
PR 255	34.34	39.83	37.09	62.54**	17
AC/S/12 42/59	38.90	29.51	34.20	7.35	9
RRIM 703	38.47	29.20	33.84	6.81	8
PR 261	34.20	32.23	33.22	4.12	6
IAN 45-873	36.73	26.62	31.67	10.92	12
RRIC 102	28.27	34.10	31.19	66.67**	18
RRIC 52	33.33	27.33	30.33	-1.71	2
RO/CM/10 44/7	28.43	26.60	27.52	4.65	7
PB 86	21.27	20.43	20.85	8.99	10
Mean	43.13	37.84	40.49		
Variance ratio	10.55**	3.43**	7.74**		
CD (P=0.05)	12.10	17.22	12. 00		

** Significant at $P \leq 0.01$

RO/CM/10 44/7, RRIM 703, AC/S/12 42/59, PB 86 and IAN 45-873 had small and non significant stability variances coupled with low PDI. Though clone RRIC 102 exhibited comparatively lower intensity of powdery mildew, the highly significant stability variance revealed its instability over environments. This means that under conducive climatic conditions for the inoculation and dissemination of the fungus, there are chances of this clone becoming susceptible. The inherent susceptibility of clones PB 311, PB 260 and PB 5/51 were evident from the high PDI values and the low and non significant stability variances. Clone RRIM 600 remained moderately tolerant with the highest stability of response to infection.

It is a proven fact that high yield and disease resistance are heritable characters in *Hevea* (Peries, 1974). The susceptible clones PB 235 and PB 260 had PB 5/51, a highly susceptible clone as one of their parents while PB 311 had PB 235 as one parent. RRIC 52 is a medium yielding clone, extremely vigorous and tolerant to most of the leaf diseases of *Hevea*. Reports also reveal that it is a good clone for breeding as it transmits its desirable characters to its progeny and has combined well with high

yielding characters of other clones, to produce some of the valuable clones of RRIC 100 series, which are high yielding and disease resistant (Fernando, 1972). The present study also revealed that RRIC 52 had high and stable tolerance to *Oidium* infection. Hence this clone could be selected as a parent in breeding for disease resistance as also reported earlier (Fernando, 1972; Yu *et al.*, 1992).

Generally resistance to diseases is available in primitive non-commercial strains which lack desirable quality attributes of commercially grown cultivars. Three wild genotypes AC/S/12 42/59, AC/S/12 42/186 and RO/CM/10 44/7 included in the present study exhibited good resistance coupled with stability. High resistance to *Oidium* in these genotypes has been reported earlier (Qiong, 1992).

The current observations lead to a tentative conclusion that clonal variation for the intensity of powdery mildew was significant and was highly influenced by the climatic conditions. Absolute resistance to *Oidium* was not exhibited by any of the clones studied. Among the 20 clones studied eight clones *viz.*, RRIC 52, AC/S/12 42/186, PR 261, RO/CM/10 44/7, RRIM 703, AC/S/12 42/59, PB 86 and IAN 45-873 possessed high degree of tolerance combined with stability in response to the disease reaction. These clones have the potential for use in future breeding programmes. However, further confirmation on the degree of resistance of the clones is required before drawing a conclusive inference.

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