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

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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.

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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-