



## A NEW WORLD VIRUS ALTERS BIOCHEMICAL PROFILING OF JUTE PLANTS (*CORCHORUS CAPSULARIS*) UPON INFECTION

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### ABSTRACT

The biochemical changes induced in jute (*Corchorus capsularis*) in response to a New World begomovirus (*Corchorus golden mosaic virus*) infection have been investigated. Changes in different biochemical components in infected plants were observed as compared to healthy plants. Assays of different enzymes, chlorophyll and total protein indicated that the causal agent altered the biochemical pathway of the infected jute plants.

**KEY WORDS:** Begomovirus, enzyme, jute, protein, whitefly

### INTRODUCTION

Plants respond to invasion by pathogens with an array of biochemical and genetic changes. Several mechanisms have been found to be involved in plant defense against bacterial and fungal invasion. The multi component defense responses include a burst of reactive oxygen intermediates (Lamb and Dixon, 1997), transcriptional activation of defense genes encoding phenyl propanoid pathway enzymes, lytic and antimicrobial pathogenesis (PR) proteins (Lamb *et al*, 1989) and development of the hypersensitive response (HR) (Keller *et al*, 1999). The outcome of HR is manifested by dry, necrotic lesion at the infection site that is clearly delimited from surrounding healthy tissue and is thought to contribute to the limitation of pathogen spread (Keen, 1990). In many cases, their protective mechanisms involve inducible defense system. The ability of plants to invoke such defense reactions is presumed to be mediated by an initial recognition process between plants and pathogens that involves detection of certain unique signal molecules of incompatible pathogens by receptor-like molecules in plants, with a subsequent resultant cascade of biochemical events that leads to the expression of resistance and susceptibility to a disease (Dixon *et al*, 1994; Ryals *et al*, 1994). Host-pathogen interactions are presumed to be generated signals that activate nuclear genes involved in plant defense responses leading to the induction of stress-related enzymes, differential expression of proteins and free amino acids and the associated accumulation of high levels of phenolic compounds. Antimicrobial phytoalexins such as sesquiterpinoid, isoflavanoid, coumarins, acetylenic and phenolic compounds also contribute to multilayered plant defense systems (Keen, 1992).

*Corchorus golden mosaic virus*, a New World virus occurring in Old World, Infecting is preceded with jute

plants (*Corchorus capsularis*, family *Tiliaceae*) and produce golden mosaic symptom. The occurrence of Golden mosaic disease of jute, a new entrant to disease scenario in India and Vietnam (Ghosh *et al*, 2008, Ha *et al*, 2008), was found in endemic form in different parts of India for the last few years and the disease spread with a faster rate causing greater reduction in fibre yield and thus assumed a major threat to the production of jute fibre. (Due to bann of polythene use for pollution people have shown interest to natural fibre like jute in their daily routine) Restricted use of synthetic fibre necessitates the search of its natural replacement, can be well accustomed with the properties like biodegradability of Jute. On the other hand, an accelerated decrease in production is documented due to several diseases caused by fungal, bacterial and viral pathogens. A severe mosaic disease has been reported to be the most limiting factor for its cultivation, causing loss of yield up to 20% (Ghosh *et al*, 2008). The disease was characterized by typical mosaic symptoms (Ghosh *et al*, 2008). The transmission, host range and etiological impact of the disease were studied, and the causal agent was identified as a whitefly-transmitted geminivirus related to *Corchorus golden mosaic virus* reported from Vietnam (Ha *et al*, 2008). There is an only few reports regarding biochemical changes with respect to begomovirus infection (Chatterjee and Ghosh, 2008). But the alterations of the biochemical components due to infection with this recently known *Begomovirus* pathogen in jute plants are still obscure. Hence, an attempt was made with the diseased plants to find out biochemical changes, if any and the results are presented.

## MATERIALS AND METHODS

Jute plants (*C. capsularis*, JRC 212) were raised through seeds in healthy condition under glasshouse. Artificial inoculation of healthy plants was done by viruliferous whiteflies, the natural vector of this disease. The inoculated plants were then maintained in an insect-proof glasshouse for symptom development along with their respective healthy controls. Plant samples consisted of pooling the first three fully expanded leaves from the terminal of each plant for further use.

Amount of chlorophyll in leaves from healthy and diseased mesta plants was determined using standard procedure (Sadasivam and Manickam, 1992). Total protein from healthy and diseased leaf samples of jute were estimated following Lowry et al. (Lowry et al, 1991). Activity assay of catalase (CAT) (Braber, 1980), esterase (EST) (Thimmaiah, 1999) and peroxidase (POD) (Malik and Singh, 1980).

Experimental design was completely randomized and consisted of three independent experiments. All tests for significance were conducted at the  $p \geq 0.001$  level using Genstat (GenStat Release 12.1) statistical programme.

## RESULTS AND DISCUSSION

Present investigation pointed out enormous changes in biochemical components in jute plants due to infection with *Corchorus golden mosaic virus* and it started with the gradual reduction in green pigments like chlorophyll (a, b and total) at different stages of pathogenesis (Table 1). The disease development in jute also altered the ratio between chlorophyll a and b and thus hampered photosynthetic efficiency as reported by Endo et al (Endo et al, 2000).

Estimation of total protein obtained from jute plant revealed that the protein content was low in diseased plants (56 µg/ml) over control (60 µg/ml).

**TABLE 1:** Biochemical alterations in leaves from infected and healthy jute

	Infected*	Control*
Chlorophyll (mg/g)		
a	1.31±0.01	1.92±0.03
b	0.53±0.03	0.93±0.06
Total	1.85±0.05	2.85±0.09
Total protein(µg/mg)	2.70±0.11	7.40±0.05
Catalase (U/min/mg)	0.091±0.009	0.038±0.006
Peroxidase (U/min/mg)	0.010±0.006	0.0015±0.0002
Esterase (U/min/mg)	0.80± 0.09	0.40± 0.03

\*Mean average of three replications ± SE

Observations on enzymatic activity indicated that the level of CAT and POD enzymes in diseased plants is higher as compared with healthy ones, whereas marked increase in levels of EST activity was found with diseased material than control (Table 1). Since the enzymes control biochemical reactions, and their syntheses is under the control of specific gene(s), any change in the activity of an enzyme would reflect in the pattern of gene expression and corresponding metabolic events in the cell. Hence, the enzymes can be used as tools to study the induced responses of plants showing disease symptom at the biochemical level (Neog et al, 2004). In the present investigation, changes in the activities of CAT, EST and POD along with total amount of protein have been studied in jute plants, to understand the fate of existing biochemical components in jute plants upon infection by *Corchorus golden mosaic disease*. The higher EST activity in diseased leaves indicated a probable mechanism of overcoming the stress situation developed due to virus infection. The lower activity of POD enzyme, a key enzyme for lignin biosynthetic pathway, in diseased plants probably focused on the lowering down of metabolic pathway for ligno-cellulosic bast fibre formation indicating a possible clue for reduction in fibre yield due to virus infection. Based on the differential ability POD to drive the oxidation and condensation of lignin precursors, it has been suggested that POD would be more likely to catalyze the reactions leading from olignols to highly condense macromolecular lignin (Sterjiades et al, 1993).

## CONCLUSION

The results demonstrated the value of studying viral infection and metabolic shift in plants. The present study may help in better understanding of the metabolic alterations during biotic stress in other plant species of agricultural and commercial importance.

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