

**GENETIC ANALYSIS OF
COMMELINA YELLOW MOTTLE VIRUS (CoYMV)**

**A THESIS
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SUMMARY

Commelina yellow mottle virus (CoYMV) is the type member of the badnavirus group, a newly-recognized plant virus genus whose members have a circular noncovalently closed dsDNA genome encapsidated in non-enveloped bacilliform particles. The CoYMV genome is 7.4 kb in size and contains three open reading frames (ORF's), designated as ORF I, ORF II and ORF III, respectively. Only a portion of ORF III has a known function. Using site-directed mutagenesis, possible functions for ORF I, ORF II and the N-terminal portion of ORF III were investigated. Deletions at the beginning and at the end of ORF I did not have a significant effect on major virus functions (replication and movement). Deletion in the center of, or complete deletion of ORF I eliminated systemic infection. Since neither an insect (mealybug) transmissibility factor nor a cell-to-cell movement protein is likely to be encoded by ORF I, it was concluded that the latter two deletions were possibly affecting virus replication or assembly. The reduced mealybug retention and transmissibility observed in one ORF I mutant may be associated with changes in particle integrity. Mutations in ORF II and ORF III resulted in lack of systemic infection, suggesting an effect on virus replication and/or movement. The detection of virus particles in tissue culture experiments suggest that transcription and translation are not interrupted.