

Errata

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The following abstracts were not published in the "Abstracts of APS Presentations at the 1992 APS/MSA Joint Meeting" but were presented at the meeting.

A1111

HOST-MODULATED ACCUMULATION AND ENCAPSIDATION OF DI- RNAs OF BROAD BEAN MOTTLE VIRUS

J. Romero, Q. Huang, J. Pogany and J.J. Bujarski, Plant Molecular Biology Center, Northern Illinois University, DeKalb, IL 60115.

Several strains of broad bean mottle virus (BBMV) encapsidate defective-interfering RNAs (DI-RNA) which exacerbate the severity of symptoms when inoculated on pea seedlings. In order to understand the molecular function of DI-RNA in the virus infection, we have studied the accumulation and encapsidation of DI-RNAs in various BBMV hosts. Our results demonstrated that DI-RNAs can accumulate in broad bean, tobacco, bean, peas and soybean plants but were encapsidated only in virus preparations isolated from broad bean, *Nicotiana benthamiana* and *Nicotiana clevelandii*. Those hosts which did not encapsidate DI-RNAs did not further transmit DIs when the virus was reinoculated on its natural broad bean host. These results suggest a host-mediated inhibition of DI-RNA encapsidation.

A1112

SYSTEMIC SPREAD AND SYMPTOM FORMATION OF COWPEA CHLOROTIC MOTTLE VIRUS IN SOYBEAN AND COWPEA PLANTS MAP TO THE RNA-3 COMPONENT. H. Shang, and J. J. Bujarski, Plant Molecular Biology Center and the Department of Biological Sciences, Northern Illinois University, DeKalb, IL 60115

S strain of cowpea chlorotic mottle virus (CCMV) causes necrotic lesions on soybean, cv. Bragg and mild mottling on cowpea, cv.

Blackeye, whereas D and N strains cause systemic mottling on soybean and severe mottling on cowpea. To map these CCMV features, four CCMV pseudorecombinants were constructed by mixing gel-separated RNAs 1 and 2 from one strain and RNA3 from another. On soybean, S₁S₂D₃ caused systemic mosaic and distortion similar to D strain and S₁S₂N₃ caused a systemic mosaic similar to N strain. D₁D₂S₃ and N₁N₂S₃ produced local lesions on soybean. On cowpea, S₁S₂D₃ and S₁S₂N₃ caused severe mottling whereas D₁D₂S₃ and N₁N₂S₃ caused mild mottling. Pseudorecombinant variants were confirmed by sequencing of progeny RNA. Our results demonstrate that the RNA3 component plays an important role in CCMV systemic spread and in symptom formation.

A1113

REMOVAL AND DE NOVO GENERATION OF DEFECTIVE INTERFERING RNAs IN BROAD BEAN MOTTLE VIRUS STRAINS. Q. Huang, J. Romero, and J.J. Bujarski, Plant Molecular Biology Center, Northern Illinois University, DeKalb, IL 60115.

Symptom-modulating defective-interfering RNAs (DI-RNA) have been found encapsidated in several strains of broad bean mottle virus (BBMV). We report here that these DI-RNAs can be removed from progeny virus by passing through bean plants. *De novo* generation of DI-RNAs has been observed after subsequent serial passages of BBMV strains through broad bean plants. Some of the *de novo* DI-RNAs were similar to originally-observed DIs whereas the other differed considerably in size. Cloning, sequencing and biological characterization of the *de novo* formed DI-RNAs are in progress.

The following is the complete abstract for presentation A577, printed on page 1123 of "Abstracts of APS Presentations at the 1992 APS/MSA Joint Meeting."

A577

GENETIC SIMILARITY AMONG RACES OF *USTILAGO HORDEI* AND *USTILAGO NIGRA*. D.D. Pope, Department of Plant Pathology, University of Georgia, Athens, Georgia, 30602.

The genetic similarity of 13 races of *Ustilago hordei* and nine races of *Ustilago nigra*, the causal agents of covered and false loose smut of barley, respectively, was determined using random amplified polymorphic DNAs (RAPDs) generated by the polymerase chain reaction (PCR). Seven oligomer primers, 10 bases long, amplified a total of 65 different anonymous fragments from genomic templates. Levels of intra- and interspecific variation were low. Results from unweighted pair group mean analysis suggest a high degree of genetic similarity among isolates of both species. No single fragment or simple banding pattern distinguished the species. However, race 6 isolates of both species were genetically identical and were readily distinguished from all other races. Differences among the other races were not as clear cut.

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