Fig Mosaic

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This project was initiated in summer of 2005. We have applied for a second years funding to continue efforts along the lines described here, and have applied for funding from other agencies.



There is not much definitive work on fig mosaic. Results suggest that the causal agent is transmitted by the fig mite, *Eriophyes ficus*.

There are reports of various fig-associated viruses, but none have been characterized, or shown to be the causal agent of FM.

We tried to get a BARD grant with Israel collaborators, it was not funded.

We are still in consideration for a MERC grant, with collaborators from Palestine and Israel, we will hear in May.

We also applied for additional funds from the USDA Germplasm Resources program.

We are focussed now on identifying the virus(es) in California figs and assessing the similarity/differences from different regions. Detection and identification of viruses associated with fig mosaic is an important part of fig production and maintenance.

OBJECTIVES:

1. Identification and characterization of the causal agent associated with Fig Mosaic Disease.

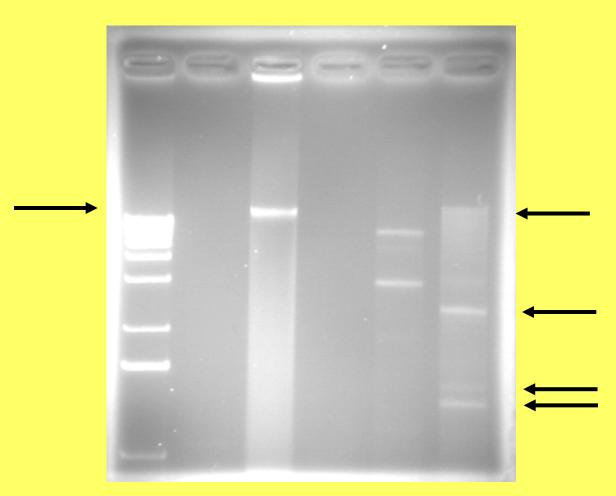
2. Determine the role and incidence of the fig mosaic virus(es) in California figs.

We used the following fig cultivars that used for dsRNA extraction in order to identify specific RNAs that may be associated with FM.

- 1. Caprica St Jean
- 2. Caprica Osborn Prolifig
- 3. Carica Genoa
- 4. Carica Caprio
- 5. Carica Flanders
- 6. Carica Genoa
- 7. Carica Aked
- 8. Carica Yellow Neche's
- 9. Carica Adriatic
- **10. Carica Ischiablack**
- **11. Carica Santa Cruz White**
- **12. Hybrid selection 341**

We extracted and purified double-stranded RNAs from 6 different FMV-affected figs. All showed very similar dsRNA patterns (lane 3).

1 2 3 4 5 6



Greater resolution suggests that in addition to the same dsRNA species, some different RNAs may be in different samples. There may be more than one virus.



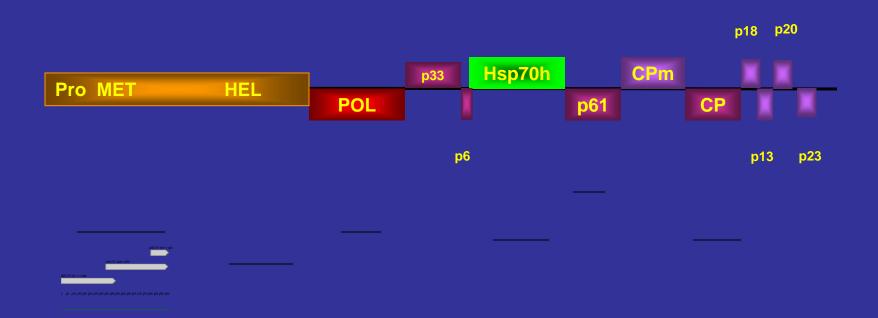
Rose 1 2 3 4 5 6 7 8 9

dsRNAs electropheresed through 6% polyacrylamide gel and stained with silver nitrate

cDNA cloning & sequence analysis

- > dsRNA was used as template for cDNA synthesis.
- CDNA was synthesized by using random primers and Oligo(dT).
- > 288 cDNA clones were screened, 144 were sequenced.
- Sequence data were analyzed using BLAST search programs of the NCBI.
- So far we have identified one virus and have significant sequence data.

We have identified nucleotide sequence for a virus that is a member of the virus family *Closteroviridae*. This family includes important viruses such as *Citrus tristeza virus* and *Beet yellows virus*, both of which are aphid-transmitted!



Schematic representation of the genome organization of CTV is above

Our virus shows some significant identity to a sequence from Italy for a virus called *Fig Leaf Mosaic-Associated Virus*.

RT-PCR detection

Primers were designed from positively identified clones.

> Total RNA from the virus-infected plants were used as templates.

> **RT-PCR** was performed to test the specificity of each pairs of primers.

> We can specifically detect FLMaV in figs.

Seed germination

•Seed of six fig cultivars, so far no germination.

Tissue culture media and sterile filter paper.

•Obtained seedlings of two hybrids from Malli Aradhya of the USDA Germplasm repository.

Testing them by RT-PCR

Some questions so far.

Closteroviruses don't typically cause mosaic symptoms.

Closteroviruses are transmitted by aphids, whiteflies or mealybugs, none are yet known to be mite-transmitted.

We don't as yet know if the virus we found is the causal agent of FM, or if other viruses are involved.

We are finishing the genomic RNA sequence and testing for similarity/variability among other affected figs.

Next Year

• Research objectives:

• <u>Objective 1.</u> To finish the genomic characterization of FLMaV.

• <u>Objective 2.</u> To determine the role and incidence of FLMaV in California figs.