

Deborah Fravel

National Program Leader

Plant Health



Grapevine yellows from New York to Virginia: Multilocus molecular genetic characterization of phytoplasmas affecting commercial vineyards



**Robert E. Davis,
Ellen L. Dally, Yan Zhao, Ing-Ming Lee,**

Tony K. Wolf, LeAnn Beanland,

Joseph A. Fiola,

Mark Chien,

Hans C. Walter-Peterson

USDA-Agricultural Research Service,

Virginia Tech,

University of Maryland,

Penn State University,

Cornell University

Grapevine Yellows Diseases -- WORLDWIDE

Europe

Flavescence doree,
Bois Noir (Legno Nero, Black Wood)

Australia

Australian grapevine yellows
Buckland Valley grapevine yellows

North America

North American grapevine yellows
Group 16Srl
Group 16SrIII

South America

Bois Noir

South Africa

Aster Yellows

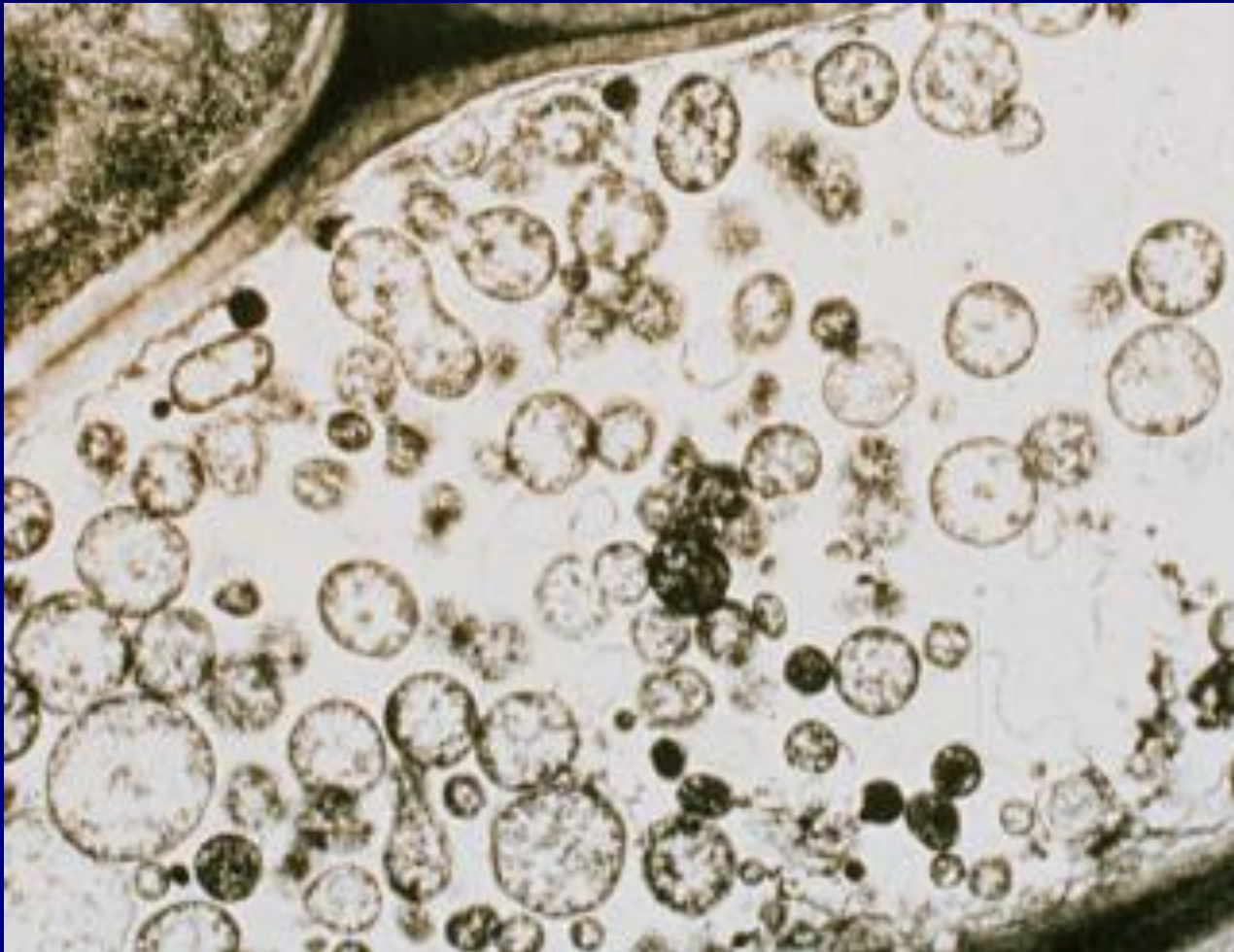
AN EXAMPLE – Bois Noir Disease in Sicily, Italy



CAUSE(S) of Grapevine Yellows

PHYTOPLASMA – a minute bacterium that lacks a cell wall

- cannot be isolated in pure culture
- reside in phloem tissue of plants



SPREAD of Grapevine Yellows

LEAFHOPPERS – feed in phloem tissue



The Region Covered by this Study

- New York State

Finger Lakes region

- Pennsylvania,

southern Pennsylvania

- Maryland

western Maryland, central Maryland,
and the eastern shore

- Virginia

western Virginia

ANALYSES OF PHYTOPLASMA GENES

16S rRNA *secY*, and ribosomal protein genes

Nucleotide sequence analyses / *In silico* translations

Taxonomic classification

Phylogenetic analyses

SNP identification / Design of NAGY strain

– specific detection & identification

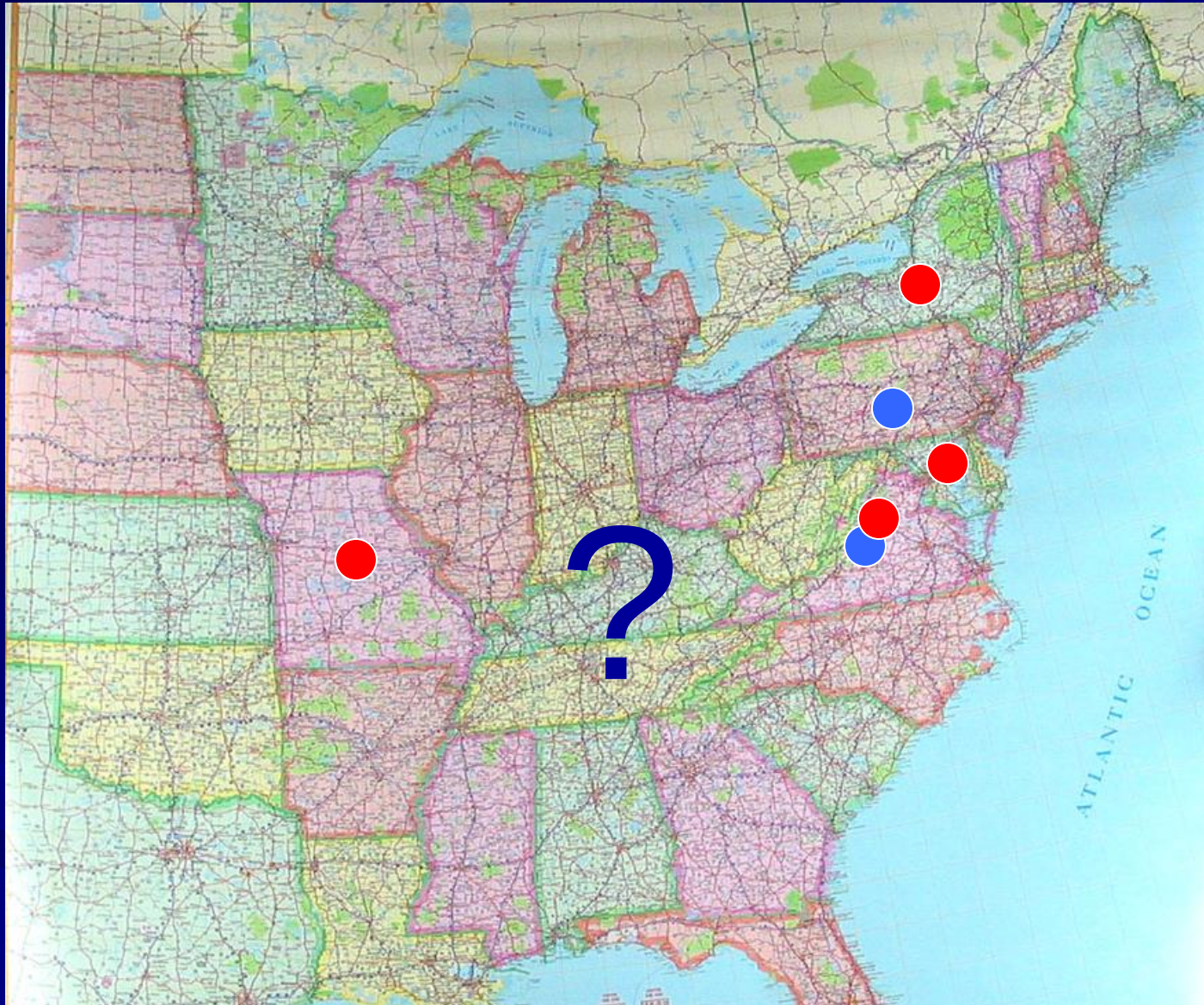
Grapevine Yellows - Diseased Cultivars

CULTIVAR	No. assayed	No. phytoplasma +
Chardonnay	34	34
Cabernet-Sauvignon	8	8
Viognier	1	1
Petit Manseng	1	1
Malbec	1	1
Pinot Gris	4	4
Black Malvesia	1	1
Pinot Noir	2	2
Chambourcin	1	1
Merlot	2	2
Cabernet-Franc	2	2
Syrah	2	1
TOTALS	59	59

Grapevine Yellows - PHYTOPLASMAS

CULTIVAR	16S rDNA RFLP	
	Group I	Group III
Chardonnay	3	25
Cabernet-Sauvignon	1	7
Viognier	0	1
Petit Manseng	0	1
Malbec	0	1
Pinot Gris	2	1
Black Malvesia	--	--
Pinot Noir	2	0
Chambourcin	--	--
Merlot	2	0
Cabernet-Franc	2	0
Syrah	1	0
TOTALS	13	36

Grapevine Yellows in North America



Maryland

Chardonnay

August 2011



Pennsylvania

Pinot Gris

August 26, 2011



Eastern Shore Maryland

Chardonnay

August 17, 2011



Pennsylvania

Pinot Gris

August 26, 2011



Western Maryland

Chardonnay

August 2011



Western Maryland

Chardonnay

August 2011



Pennsylvania

Pinot Gris

August 26, 2011



Pennsylvania

Pinot Gris

August 26, 2011



Pennsylvania F

Chardonnay

August 26, 2011



Pennsylvania H

Pinot Gris



Pennsylvania F

Pinot Noir



Pennsylvania F

Chambourcin



Pennsylvania F

Syrah

August 26, 2011



Maryland

Black Malvesia

August 2011



NAGY PHYTOPLASMAS: 2 different species

Group I

= Group 16SrI '*Candidatus Phytoplasma asteris*'-related

Group III

= Group 16SrIII, '*Candidatus Phytoplasma pruni*'-related



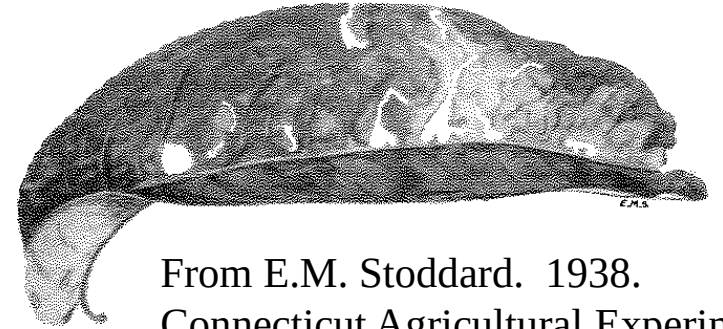
IMPLICATIONS –

the 2 NAGY phytoplasmas likely have different insect vectors
and
possibly different alternate plant hosts

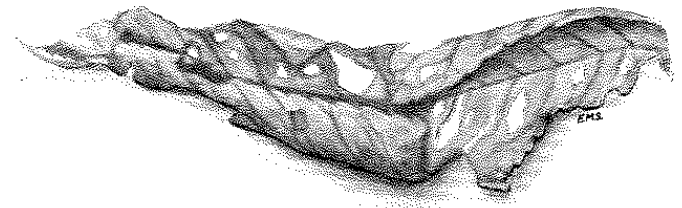
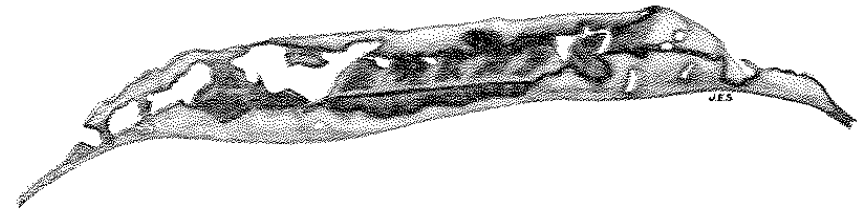
**NAGY Group III Phytoplasma
is Related to
the Phytoplasma Causing X-Disease of Stone Fruits**

**All 13 signature sequences
of '*Candidatus Phytoplasma pruni*'
are present in the Group III Strains Associated
with
North American Grapevine Yellows**

Peach X-Disease



From E.M. Stoddard. 1938.
Connecticut Agricultural Experiment
Station, New Haven. Circular 122.



Characteristic Leaf Symptoms of X Disease.

Do these phytoplasmas cross infect their agronomic hosts ?

Do the NAGY and X-disease phytoplasmas
cross infect grape and peach in nature ?



FUTURE

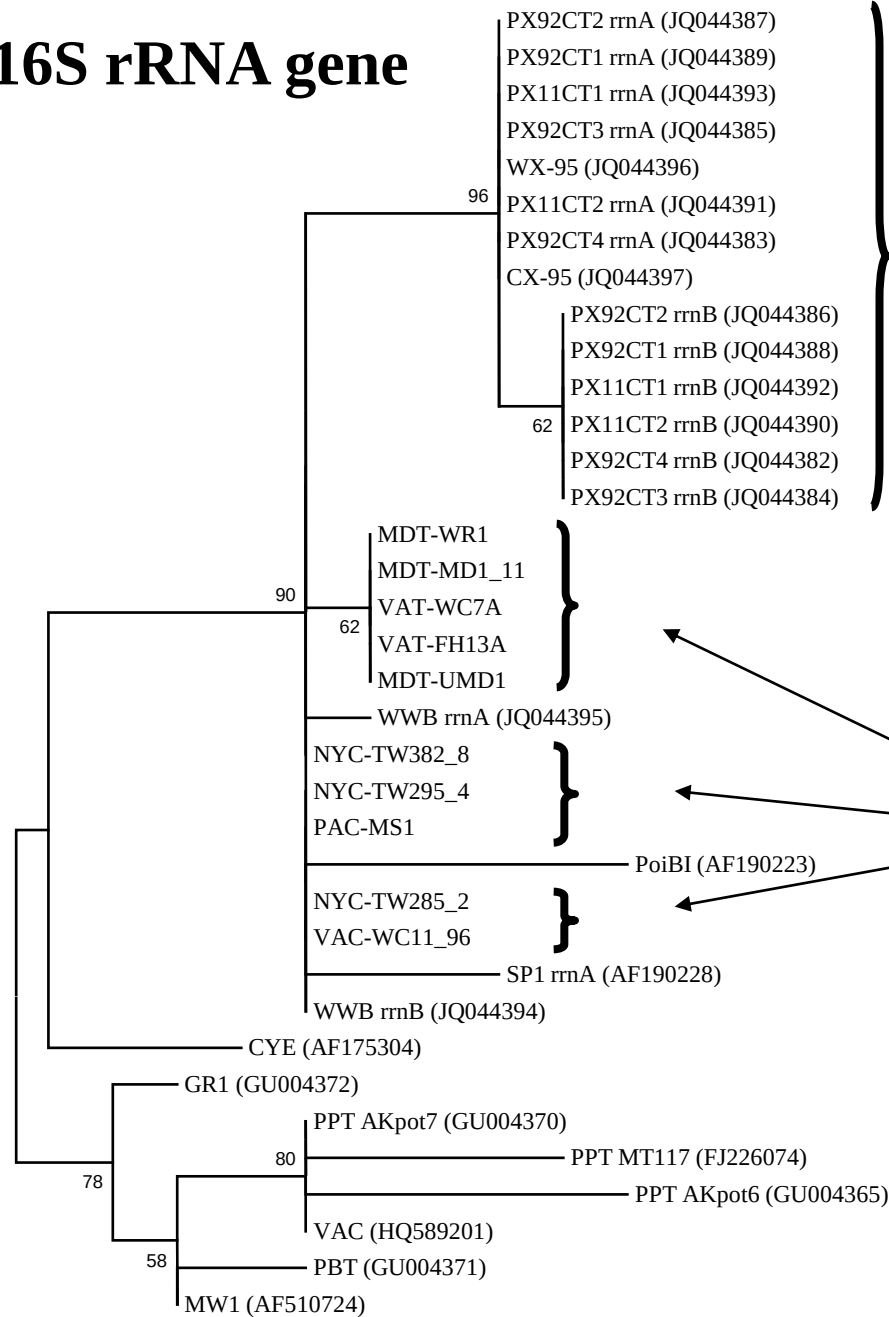
Insect transmission

coupled with

Molecular markers distinguishing the phytoplasma lineages

Phylogenetic analysis distinguishes NAGY strains from 'Ca. Phytoplasma pruni', cause of X-disease.

16S rRNA gene



Peach X-Disease

Grapevine Yellows (NAGY)

SNPs distinguish Grapevine Yellows Strains
from

X-disease Strains

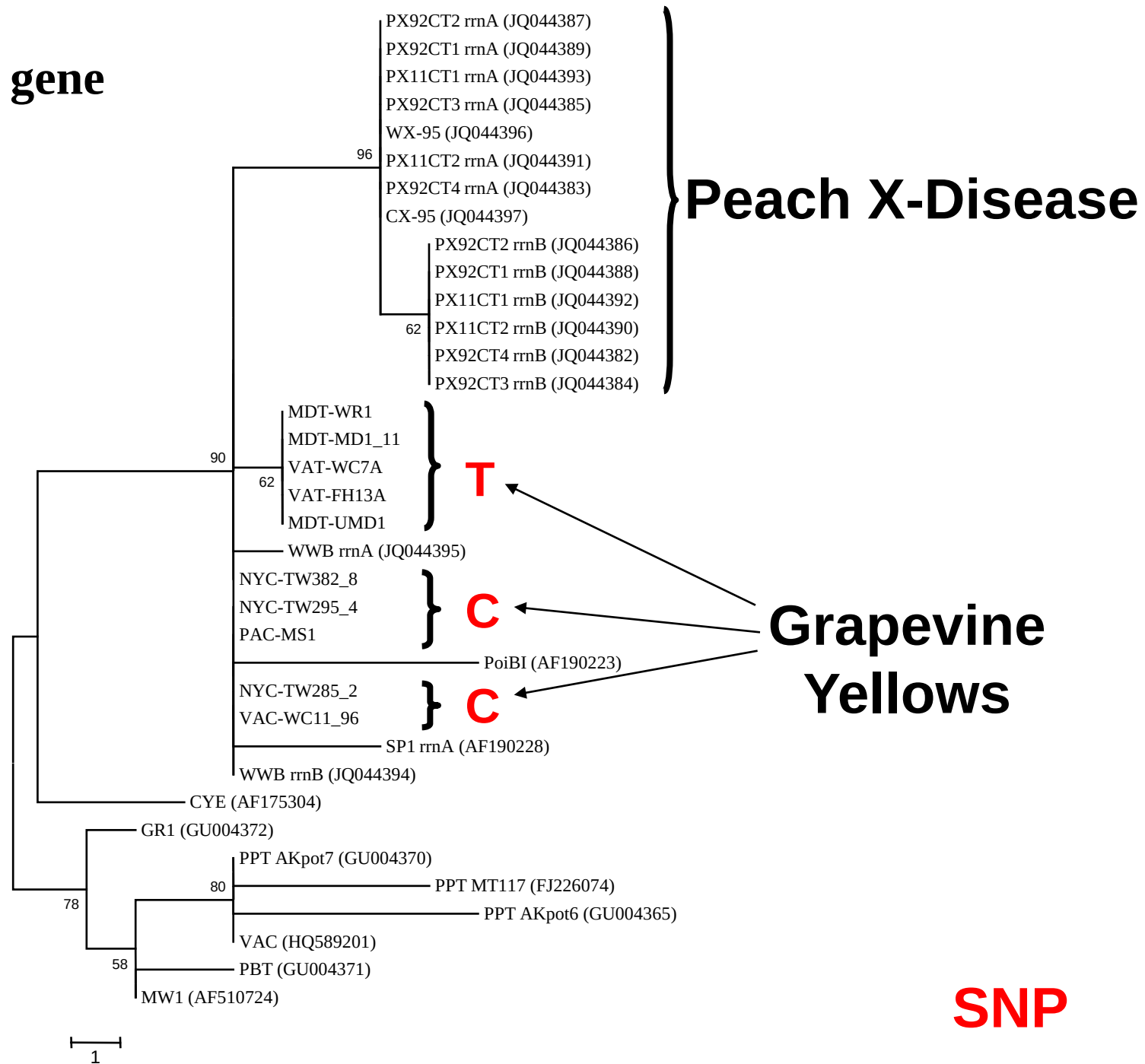


Design of pathogen – specific detection

ALSO

**SNPs distinguished 2 lineages
among strains causing NAGY.**

16S rRNA gene

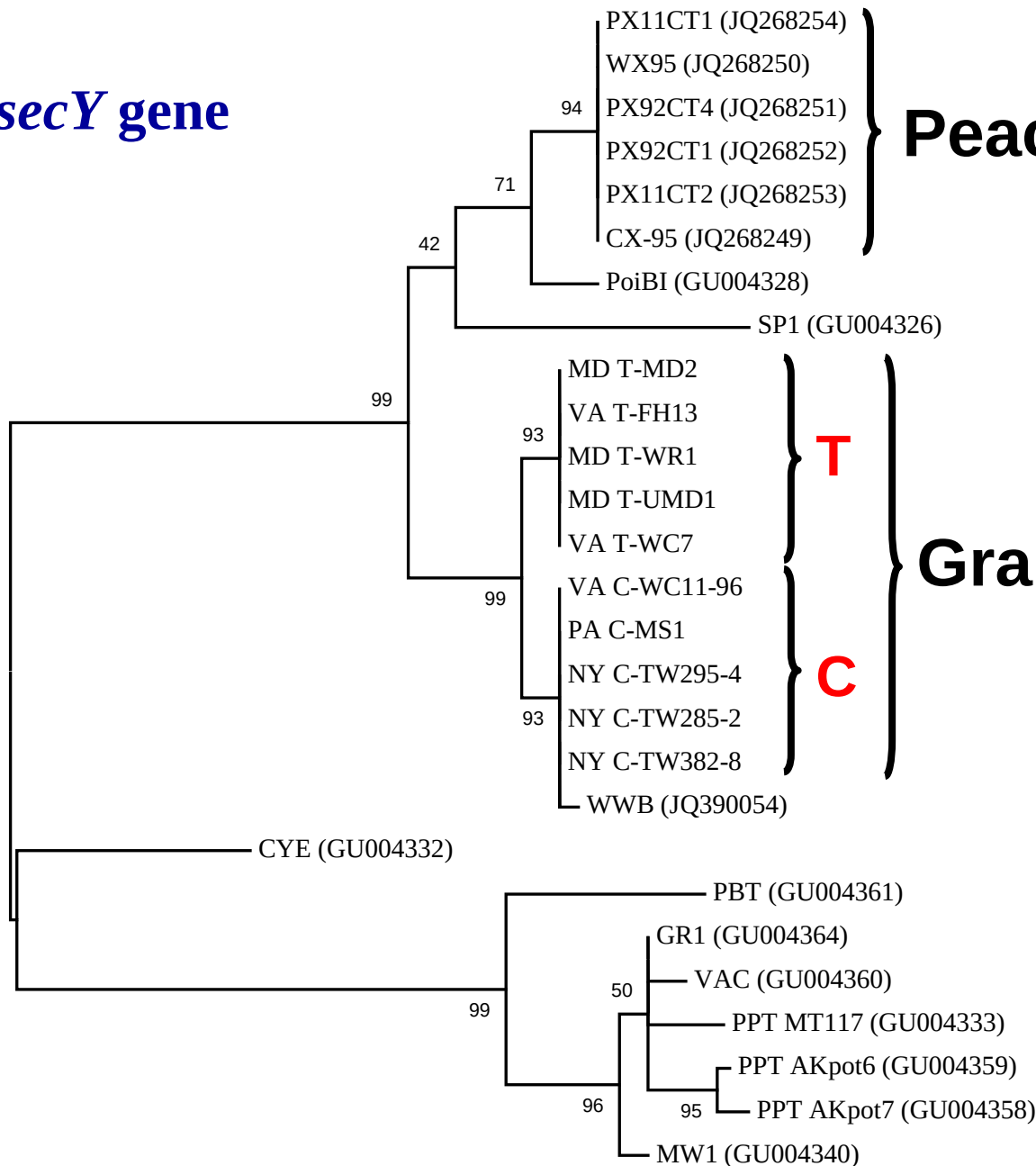


**SNP in 16S rRNA gene is a predictor
of lineage-specific divergence in other genes
among NAGY phytoplasma strains**

secY gene

Peach X-Disease

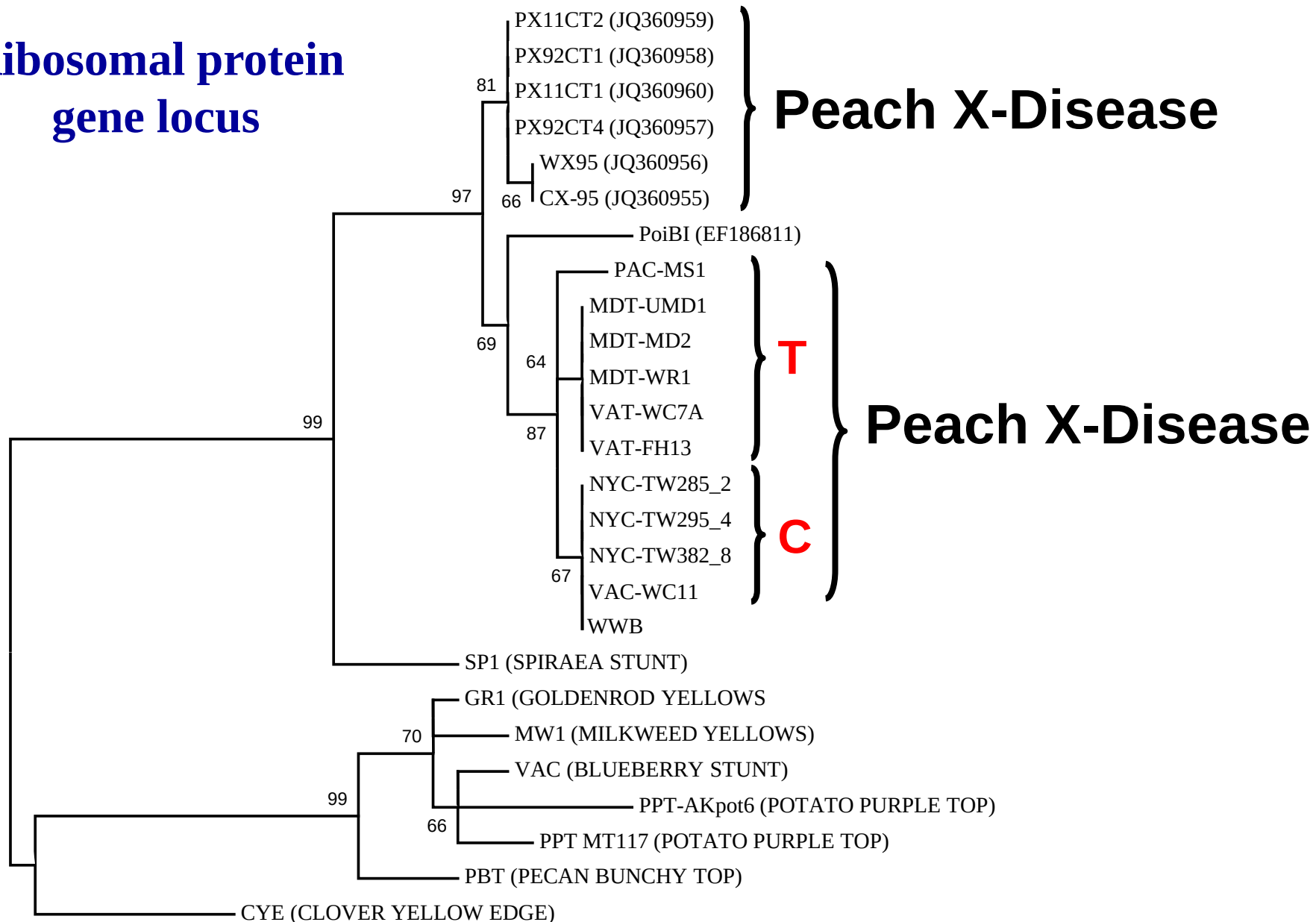
Grapevine Yellows



5

SNP in 16S rRNA gene

Ribosomal protein gene locus



5

SNP in 16S rRNA gene

This information will be used to develop rapid, specific, accurate diagnostic methods which will enable:

- Field diagnostics, clean plants, APHIS activities



The screenshot shows the homepage of the National Clean Plant Network (NCPN). The header features the NCPN logo on the left, the title "National Clean Plant Network" in the center, and a stylized plant icon on the right. Below the header is a navigation bar with tabs for "Berry", "Citrus", "Fruit Tree", "Grape", and "Hops". The main content area is titled "Grape Clean Plant Network" and includes three photographs: a group of people in a field, a man holding a sign, and two men in a vineyard. A sidebar on the left lists various links, and a footer at the bottom mentions "Grape CPN Board Members 2012".

National Clean Plant Network

Start clean, stay clean.

Our Clean Plant Networks:

- Berry
- Citrus
- Fruit Tree
- Grape
- Hops

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Grape Clean Plant Network

NCPN Home
About the NCPN
2007 Organizational Workshop
NCPN Governance
Tier 1 Governing Board
NCPN Berries
NCPN Citrus
NCPN Fruit Tree
NCPN Grape

■ Grape CPN Board Members 2012

NCPN tour to California grapevine nursery and vineyard in May 2010

..and will also enable:

- Epidemiology of two NAGY diseases
 - Identify insect vectors
 - Identify additional plant hosts
- Develop management strategies based on the epidemiological information

ACKNOWLEDGEMENTS

We are grateful to all the vineyard managers and owners who permitted us to enter their vineyards and collect leaf samples for this work.

Robert E. Davis, Ellen L. Dally, Yan Zhao, Ing-Ming Lee, Tony K. Wolf, LeAnn Beanland, Joseph A. Fiola, Mark Chien, and Hans C. Walter-Peterson

ARS research on grapes
continues with . . .



New virus-like disease in Oregon on Pinot Noir

Bob Martin, USDA, ARS, Corvallis



New virus-like disease in Oregon on Pinot Noir

Bob Martin, USDA, ARS, Corvallis



Symptoms on Cabernet Franc in Southern Oregon

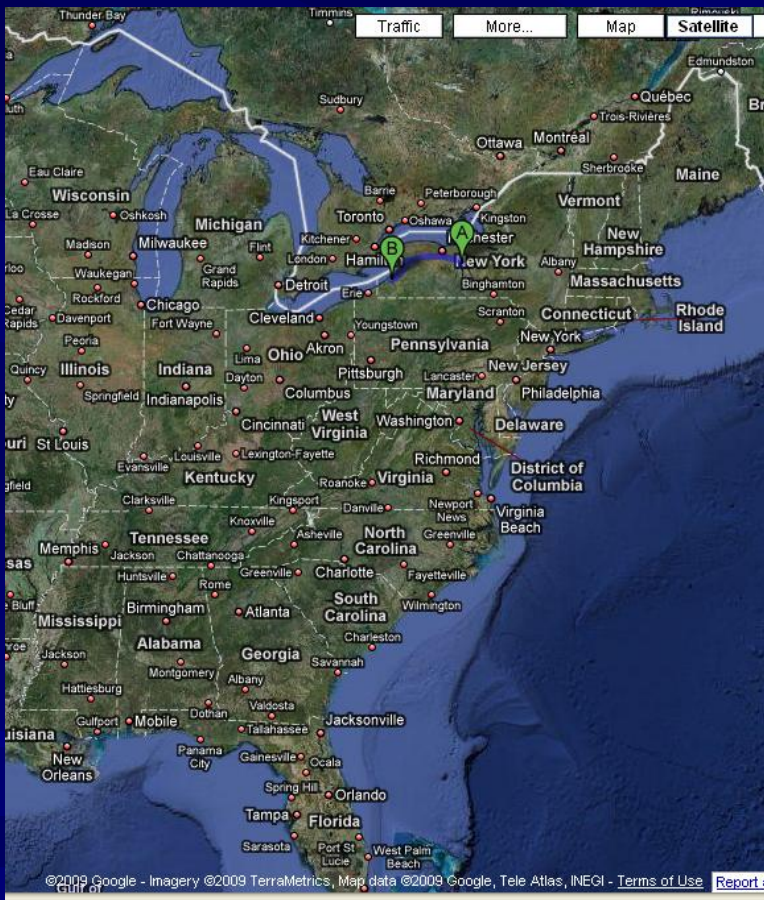
Bob Martin, USDA, ARS, Corvallis



Symptoms on Cabernet Franc in Southern Oregon

Bob Martin, USDA, ARS, Corvallis

Race-specificity: selection on local scale



Selection for powdery mildew virulence on *V. labrusca*

PI	ID		Geneva, NY	Fredonia, NY
588128	Vergennes	<i>V. labrusca</i>	0	7
588145	GBC 12	<i>V. labrusca</i>	2	5
588165	Alba	<i>V. labrusca</i>	0	4
588173	GBC 2	<i>V. labrusca</i>	2	5
588277	Jersey Muscat	<i>V. labrusca</i>	1	6
588307	Champagne	<i>V. labrusca</i>	1	6
588583	Grem-4	<i>V. labrusca</i>	6	7
594349	Alexander	<i>V. labrusca</i>	0	5
Average			1.3	5.5
			R	S



Race-specificity due to effector variation

Science

AAAS

Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism

Pietro D. Spanu, *et al.*

Science 330, 1543 (2010);

DOI: 10.1126/science.1194573

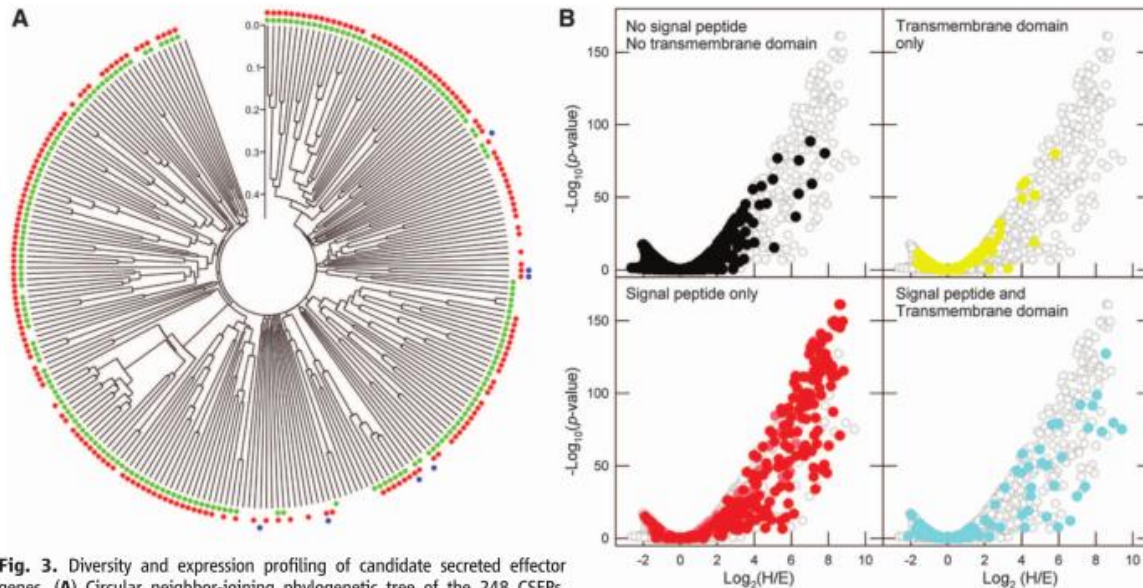
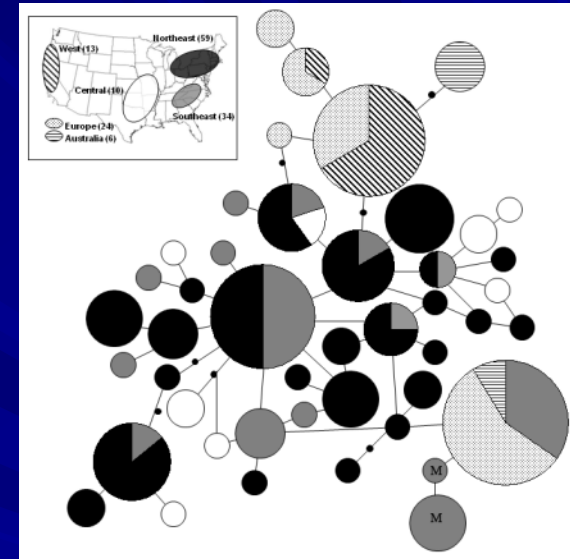


Fig. 3. Diversity and expression profiling of candidate secreted effector genes. **(A)** Circular neighbor-joining phylogenetic tree of the 248 CSEPs. Scale, amino acid substitutions per site; green, CSEPs harboring the YxC motif; blue, CSEPs conserved in *E. pisi* and/or *G. orontii*; red, CSEPs predominantly expressed in haustoria. **(B)** Global gene expression in haustoria (H) versus epiphytic structures (E). Relative abundance of each gene plotted versus the

p -value as a measure of the statistical significance. White circles, all gene models; black, no SP and no TM domain; yellow, TM only; red, CSEPs; pink, genes with BLASTP hits in the National Center for Biotechnology Information nr database and SP only; light blue, both SP and TM domains.

www.sciencemag.org **SCIENCE** VOL 330 10 DECEMBER 2010



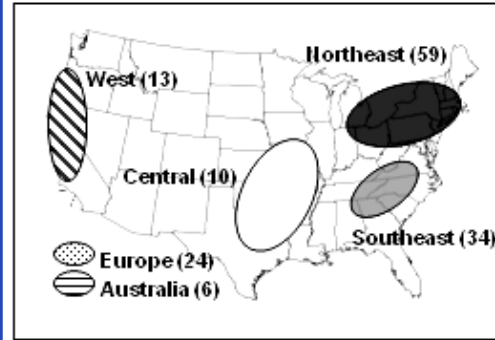
PM genetic diversity
Brewer & Milgroom



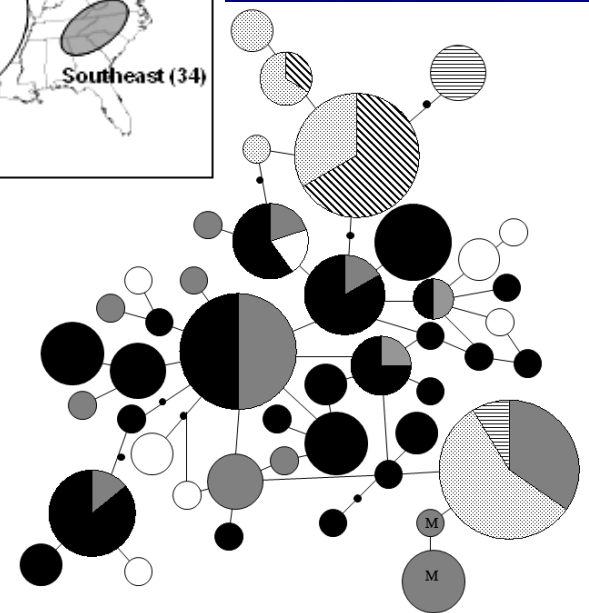
Natural variation in Geneva, NY: Heaven on Earth for powdery mildew genetics



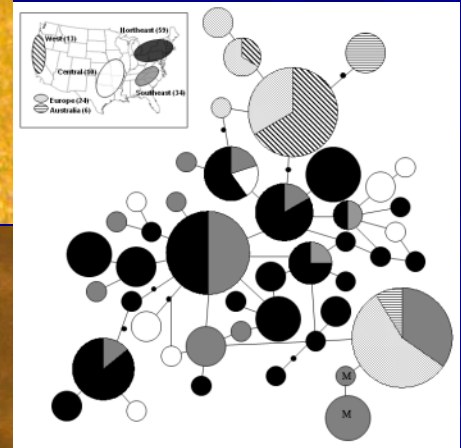
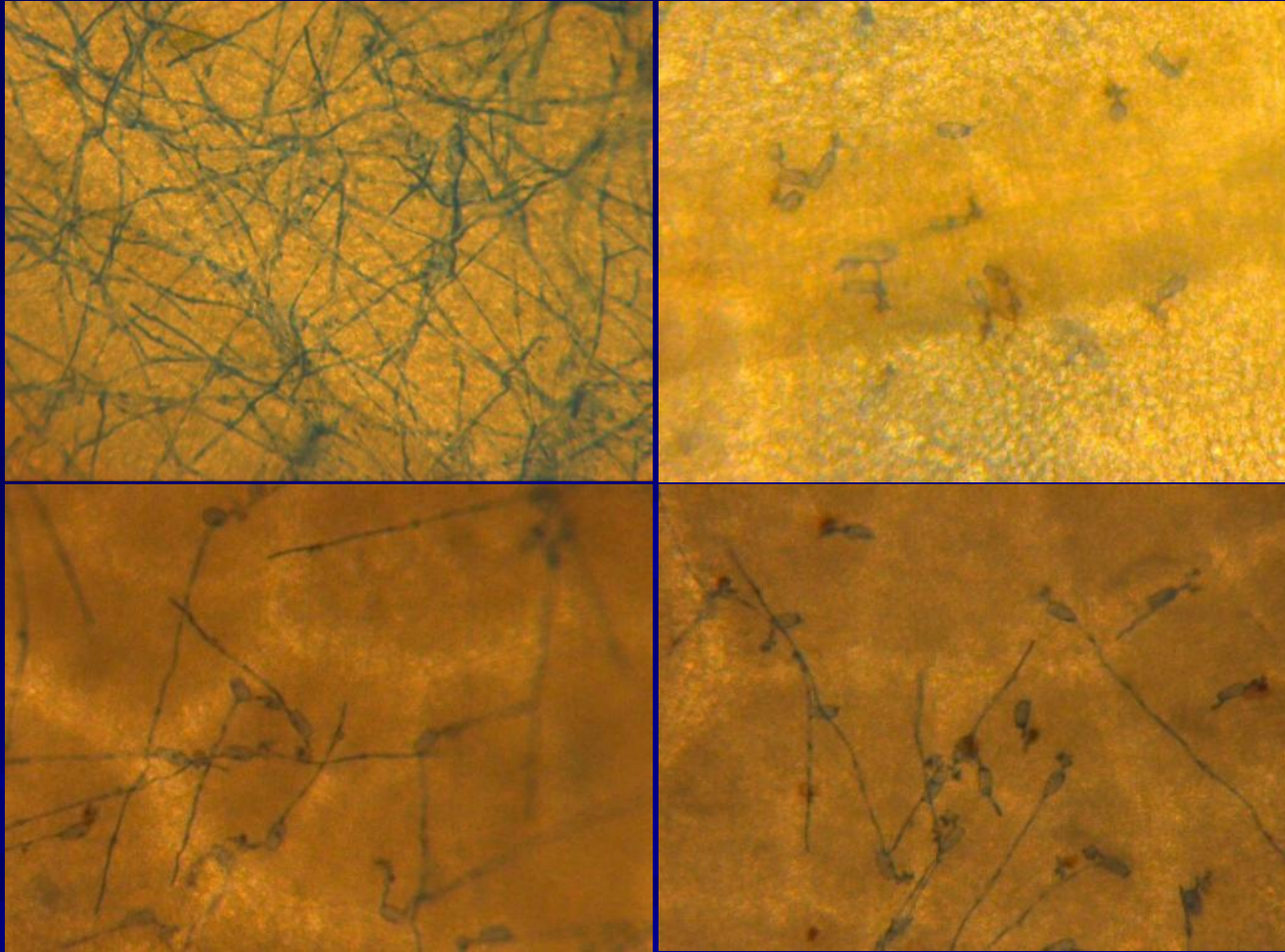
ARS-PGRU germplasm collection



PM genetic
diversity
Brewer &
Milgroom



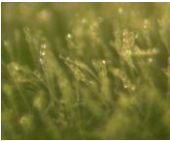
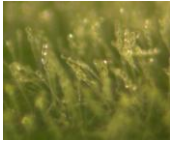
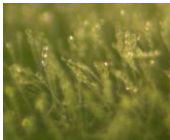
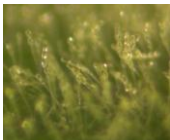
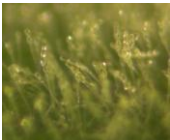
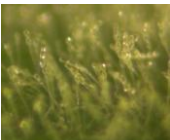
How far can you grow?



How far can you grow?

Different answer for different genotypes

Durable? →

		Powdery mildew genotype			
		Avr_1Avr_2	$Avr_1^{-}2$	$^{-}1Avr_2$	$^{-}1^{-}2$
Grapevine genotype	R_1R_2				
	$R_1^{-}2$				
	$^{-}1R_2$				
	$^{-}1^{-}2$				

??

