

Genetic Variability of *Benyviruses* Infecting Sugar Beets Nationwide

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BACKGROUND

Benyviruses are multipartite, rod-shaped, single stranded RNA viruses that are transmitted by soil fungi. Two of them, *Beet necrotic yellow vein virus* (BNYVV) and *Beet soil-borne mosaic virus* (BSBMV) are the predominant pathogens in most sugar beet (*Beta vulgaris* L.) producing regions of North America. BNYVV has a worldwide distribution and causes a disease known as “rhizomania,” which was introduced into the United States in 1982. By 1989, resistant varieties were released and 13 years later, resistant-breaking variants of BNYVV were detected. In California and Minnesota, the incidence of rhizomania in previously resistant genotypes has reached levels that compromised the economical value of this crop. Our working hypothesis is that the genetic composition of infecting virus populations, known as the quasispecies structure, and the genetic diversity among populations, will impact breeding programs and disease management strategies.



OBJECTIVES

1. Identify the genetic virus mutations that are associated with resistance-breaking variants.
2. Determine host conditions that promote emergence of resistance-breaking variants.
3. Determine the relationship between virus quasispecies structures and their capability to overcome plant resistance.

RESULTS AND BENEFITS

Root samples from asymptomatic and symptomatic resistant and susceptible sugar beet genotypes have been collected from Imperial Valley California and different locations of Minnesota. These samples were used to produce high fidelity PCR amplicons and plasmid clones of the highly variable viral RNA3, including the protein 25 (P25). Analysis of these sequences revealed the following:

- Californian versus Minnesotan isolates of BNYVV are consistently differentiated based on a single amino acid substitution in the P25.
- Californian resistant-breaking variants of BNYVV differ from the wild type virus in a single amino acid of a hyper-variable motif of P25.

Based on these preliminary results, the diagnosis of resistant-breaking variants using these polymorphic genetic markers seems possible in the near future.

Strain	amino acid position		
	67	68	135
Ch	V	L	E
Mag	V	L	E
DWe	V	L	E
Spr	V	L	E
Tam	V	L	E
Tae	V	C	E
WTC	A	L	E
B83	V	C	D
Cro	A	H	D
Gle	A	C	D
Wil	A	C	D
32H	A	H	D
WTM	A	C	D
WTT	A	C	D