

**CHARACTERIZATION OF THE INFLUENCE OF *BET* SOIL-BORNE
MOSAIC VIRUS ON THE AGGRESSIVENESS OF *BET* NECROTIC
YELLOW VEIN VIRUS IN SUGARBEET**

Kathrin Bornemann^{1,2*}, Mark Varrelmann¹ and Melvin Bolton²

¹Institute of Sugar Beet Research, Holtenser Landstrasse 77, 37079 Goettingen, Germany
and ²USDA, Agricultural Research Service, Northern Crop Science Laboratory,
1605 Albrecht Blvd. N, Fargo, ND 58102

ABSTRACT

Beet necrotic yellow vein virus (BNYVV) strains with different levels of aggressiveness have spread to sugarbeet growing areas worldwide. As the *Rz1* resistance gene has been used in most of the commercial varieties since its identification, it had to be anticipated that resistance breaking variants would be selected. In the US and Europe, resistance breaking properties of some BNYVV strains causing high yield losses have been observed. The objective of the study was to identify the influence of (i) the sugar beet genotype, and (ii) *Beet soil-borne mosaic virus* (BSBMV) on the aggressiveness of BNYVV strains. Both viruses are vectored by the plasmodiophoromycete *Polymyxa betae* and occur in mixed infections in the field. Competition experiments with different BNYVV strains from Europe (Germany, France and Italy), and the US were performed under standardized greenhouse conditions. Infected roots of different sugarbeet genotypes (susceptible and resistant) were analyzed after five weeks of cultivation to determine virus titer (ELISA), and amino acid composition by means of “deep sequencing” of the viral pathogenicity factor. In a second experiment, the same BNYVV strains and the same sugarbeet genotypes were used in mixed infections with BSBMV. Additionally, another experimental approach was chosen to compare the aggressiveness of resistance breaking and wild type BNYVV strains in single and mixed infections with BSBMV. Therefore, the same vector population was loaded with both viruses, which also showed that the ability to overcome resistance was independent of the vector population. The results of the first experiment showed that, depending on the sugarbeet genotype, certain amino acids of the viral pathogenicity factor, which determine the resistance breaking properties of the virus strain, occur with a higher frequency. In *Rz1* plants, the resistance breaking variants out-competed the wild type variants, and mostly vice versa in susceptible plants, demonstrating a relative fitness penalty of resistance breaking mutations. The strong genotype effect supports the hypothesized *Rz1* resistance breaking strain selection with four RNAs suggesting a certain tetrad needs to become dominant in a population to influence its properties. Tetrad selection was not observed when a resistance breaking strain, with an additional P26 protein encoded by a fifth RNA, competed with a wild type strain supporting its role as second pathogenicity factor and suggesting reassortment of both types. At harvest, typical virus symptoms were observed in mixed infections with BNYVV and BSBMV. Further analysis remains to be done.