

RICHARDSON, KELLEY L.* , JEFF WASSON, LINDA PAKISH, AND MARIA MEZA, USDA, Agricultural Research Service, 1636 E. Alisal Street, Salinas, CA 93905. **Identification and characterization of broad-spectrum sugar beet resistance to rhizomania, caused by *Beet Necrotic Yellow Vein Virus*.**

Rhizomania is a devastating disease of sugar beet (*Beta vulgaris* subsp. *vulgaris* L.) in production areas around the world. It is caused by *Beet Necrotic Yellow Vein Virus* (BNYVV) and vectored by *Polymyxa betae*. In the absence of effective control measures, infection results in 50-60% losses in root yield and negative effects on sugar yield and processing quality. Most control of rhizomania is achieved using resistant varieties. The most widely used source of resistance is the qualitative gene, *Rz1*. In the last 15 years, sugar beet fields around the world, planted with *Rz1*-resistant commercial varieties have been observed with severe rhizomania symptoms, suggesting *Rz1* is compromised. Novel sources of quantitative, multi-gene resistance must be identified to develop commercial sugar beet varieties with durable protection against rhizomania. Here, we report on evaluation of six rhizomania-resistance introgression lines, representing the five named genes (*Rz1-Rz5*) and a sixth, unnamed gene (*Rz?*) each introgressed into a susceptible background. The introgression lines and check entries were grown in soil infested with the *Rz1* resistance-breaking strain of BNYVV and virus titer was measured with ELISA and qPCR. Multiple individuals per line were evaluated and genotyped with 384 SNP. Individuals with *Rz1*, *Rz4*, or *Rz5* resistance genes showed the highest virus titers, and *Rz2*, *Rz3*, and *Rz?* had the lowest. qPCR results directly correlated with ELISA values. Population structure analysis grouped all *Rz1*, *Rz4*, and *Rz5* individuals together, in three respective groups, and all remaining individuals in a single group. Deeper analysis of remaining individuals put the *Rz?* individuals into one group, and *Rz2* and *Rz3* individuals in a second group.