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Organization of a resistance gene cluster containing the rhizomania resistance locus (*rz1/rz2*) in sugar beet.

Genetic resistance to the sugar beet virus rhizomania has been in use for over 40 years, but characterization of the molecular basis for susceptibility and resistance has proved challenging. Here we describe the region around the *Rz1* and *Rz2* loci in the sugar beet genome using whole-genome sequencing, RNA sequencing, molecular markers, and resistance gene modeling. Nucleotide-binding leucine-rich-repeat-containing (NB-LRR) genes have been implicated in numerous gene-for-gene resistance interactions. Twenty tentative nucleotide-binding (NB) sequences were identified in 16 MB of Chromosome 3 encompassing the *Rz1* and *Rz2* loci. These NB-like sequences were identified using a hidden Markov model derived from resistance gene NB domains and provided tentative locations for NB-LRR loci. These sequences exhibit spatial clustering correlated with their phylogenetic clustering, which suggests evolution through gene duplication. Comparing two populations sharing a common parent, we describe variation at these 20 NB-ARC sequences. This includes the presence of segregating transposable elements in or adjacent to 16 of the 20 predicted NB-LRR sequences. Transcript evidence is given for the expression of eight of these NB loci in root tissue of the common parent C869, with trace transcript evidence for an additional seven (15 putatively expressed loci in total in C869).