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Genomic regions responsible for rhizomania resistance in a mutagenic sugar beet line identified through graded-pool sequencing and transcriptome analysis.

Rhizomania in sugar beet caused by Beet necrotic yellow vein virus (BNYVV) vectored by the soilborne plasmodiophorid, *Polymyxa betae*, significantly reduces yield and sucrose content globally. Genetic resistance to rhizomania in commercial cultivars is obtained through the presence of *Rz1* and *Rz2*, resistant genes. Recently, *Rz* mediated resistance in commercial cultivars have shown some compromise under field evaluations. Through EMS mutation and genetic selection, sugar beet breeding line KEMS12 was developed, which is highly resistant (R) to rhizomania. KEMS12 when crossed with a rhizomania susceptible (S) line, KPS24, showed segregation of rhizomania resistance trait in the F2 population. We implemented a quantitative trait locus (QTL) mapping method, graded-pool sequencing, to rapidly map QTLs through whole-genome sequencing of graded-pool samples from F2 progeny using bulked-segregant analysis. Graded-pool whole genome sequencing combined with transcriptome analysis identified putative resistance associated QTLs primarily localized in chromosomes 2, 6, and 8. Candidate genes whose expression showed similar pattern between the highly R and S individuals in the segregating population and parents, included *Bevul.2G022500* (small nucleolar RNA-associated protein), *Bevul.2G022400* (spliceosome complex disassembly), and *Bevul.8G104700* (protein phosphatase inhibitor). The putative rhizomania resistance markers identified in KEMS12 will be greatly valuable for future trait introgression into commercial cultivars.