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Deep sequencing leads to the identification of eukaryotic translation initiation factor 5A as a key element in Rsv1-mediated lethal systemic hypersensitive response to soybean mosaic virus infection in soybean

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Rsv1, a single dominant resistance locus in soybean, confers extreme resistance to the majority of Soybean mosaic virus (SMV) strains but is susceptible to the G7 strain. In Rsv1-genotype soybean, G7 infection provokes a lethal systemic hypersensitive response (LSHR), a delayed host defense response. The Rsv1-mediated LSHR signaling pathway remains largely unknown. In this study, we employed a genome-wide investigation to gain insight into the molecular interplay between SMV G7 and Rsv1-genotype soybean. sRNA-seq, degradome-seq and transcriptome-seq analyses were used to identify differentially expressed genes (DEGs) and miRNAs (DEMs) in response to G7 infection. A number of DEGs, DEMs and miRNA targets and the interaction network of DEMs and their target mRNAs responsive to G7 infection were identified. Knock-down of one of the identified DEGs, the eukaryotic translation initiation factor 5A (eIF5A), diminished the LSHR and enhanced viral accumulation, suggesting the essential role of eIF5A in the G7-induced, Rsv1-mediated LSHR signalling pathway. This work provides an in-depth genome-wide analysis of high-throughput sequencing data and identifies multiple genes and microRNA signatures that are associated with the Rsv1-mediated LSHR.