

Identification and molecular dissection of broad-spectrum recessive resistance genes against plant viruses

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Amongst plant pathogens causing severe damage to crops, plant viruses have peculiar way of life in which they depend on many host proteins to increase the viral genome in host plant cells. To manage plant virus diseases, due to lack of agrochemicals to plant viruses, the use of resistant crop cultivars is one of the most common and effective options. More than half of virus-resistant cultivars is based on recessive resistance, which is caused by recessively inherited mutations in a host gene essential for virus infection in most cases¹⁾. The most well-known class of recessive resistance genes encode the translation initiation factor eIF4E. However, the eIF4E-mediated recessive resistance is limited to potyviruses and other related viruses. Potexviruses are a group of approximately 40 species of plant viruses, to which no recessive resistance genes had been reported. Firstly, we identified an Arabidopsis mutant that confers a loss-of-susceptibility phenotype against a potexvirus, plantago asiatica mosaic virus (PLAMV), and successfully identified the responsible gene named *Essential for poteXvirus Accumulation 1 (EXA1)*²⁾. Although EXA1 is functionally unannotated in Arabidopsis, orthologous genes are found in a wide range of plant species. We found that *EXA1* deficiency robustly inhibits PLAMV infection at the initially infected cells, suggesting that *EXA1* is a potential genetic resource for recessive resistance against multiple potexviruses. EXA1 has a predicted functional motif that binds to eIF4E family proteins. This implies that translation initiation factors might also be essential for potexvirus infection. Among Arabidopsis mutants lacking plant *eIF4E* family genes, we found that the *nCBP* deficiency impaired PLAMV spread in inoculated leaves³⁾. In addition, the *ncbp* mutant compromised viral accumulation of two other potexviruses and one lolavirus, which is closely related to potexviruses. Our results suggest that *nCBP*-mediated resistance is also effective against multiple potexviruses, probably through inhibition of the translation of viral proteins required for viral spread. Our studies thus far identified *EXA1* and *nCBP* as novel genetic resources for recessive resistance and partly revealed their functions in potexvirus infection. In the future, genome editing technology will enable non-genetically modified recessive resistance-based antiviral crop breeding using these genetic resources, which could lead to the development of a crop cultivar with broad spectrum resistance.

References

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