Ne e i ance gene again mai e o gh d a fdi ea e iden ified in ce eal c op

We identi ed *ZmGLK36*, a resistance gene against rice black-streaked dwarf virus (RBSDV), in maize. *ZmGLK36* mediates resistance by regulating jasmonic acid (JA) biosynthesis and JA-mediated defence response; it also grants resistance to RBSDV to other cereal crops, such as rice and wheat.

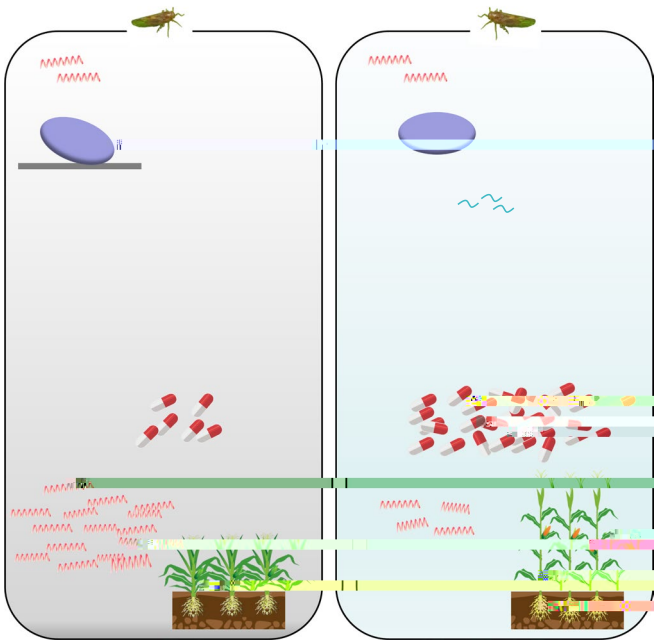
The mission

RBSDV[1] and maize rough dwarf virus (MRDV)[2] are closely related members of the *Fijivirus* genus in the *Reoviridae* family, and they can infect almost all major cereal crops (including maize, rice, wheat and barley) in Asia, Europe and South America. Whereas MRDV primarily infects maize in Europe and South America, RBSDV mainly infects maize in Asia, causing maize rough dwarf disease (MRDD). MRDD is characterized by dwarfing of plants; shortening of internodes, which are the lengths of the stem between two nodes (where buds, leaves or branches emerge); and thickened, short and stiff green leaves. MRDD ultimately results in heavy (30–100%) yield losses[2]. RBSDV is transmitted to plants via small brown grasshoppers, which act as a vector. Although adjustment of the sowing dates (so the crop planting time does not coincide with the grasshoppers' migration time) and insecticides (such as cypermethrin or γ-cyhalothrin) are commonly used to alleviate the disease and yield loss caused by RBSDV or MRDV, these practices are inefficient and harmful to the environment. Thus, identifying genes that confer resistance to RBSDV and breeding RBSDV-resistant cultivars (cultivated varieties) has remained the most effective and environment-friendly approach for MRDD management.

The solution

To fine map and clone *qMrdd2*, a previously reported major quantitative trait locus[3] (QTL, a DNA region associated with a specific phenotype) for RBSDV resistance in maize, we developed a pair of near-isogenic lines (NILs), one susceptible (NIL-S) and the other resistant (NIL-R) to RBSDV, and carefully examined MRDD symptoms in field conditions. Through de novo genome assembly, quantitative reverse transcription PCR and candidate gene association analyses, we pinpointed the candidate gene (*ZmGLK36*) and its causal (that is, resistance-associated) variation. Then, by using a suite of genetic (including overexpression and knockout mutant analyses), physiological and biochemical experiments (including yeast one-hybrid assay, transient expression assay in maize protoplasts and electrophoretic mobility shift assay), we dissected the molecular mechanisms of *ZmGLK36*-mediated resistance.

We show that *qMrdd2* includes a gene, *ZmGLK36* (which encodes a G2-like-transcription factor) that promotes resistance to RBSDV. RBSDV infection increases *ZmGLK36* expression and, in turn, ZmGLK36 promotes the transcription of *ZmJMT* (encoding jasmonate O-methyltransferase) and *ZmLOX8* (encoding linoleate 13S-lipoxygenase 8), which are involved in JA biosynthesis. This hormone mediates plant stress responses, including defence against pathogens[4]. We identified a 26-bp indel sequence located in the 5′UTR of *ZmGLK36* that is present in susceptible plants but absent in resistant plants and, therefore, contributes



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