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Identification and molecular characterization of downy mildew resistant gene candidates in maize (*Zea mays* subsp. *Mays*)

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Abstract

Downy mildew (DM), caused by several species in the *Peronosclerospora* and *Sclerophthora* genera, is a major maize (*Zea mays* L.) disease in tropical or subtropical regions. DM is an obligate parasite species in the higher plants and spreads by oospores, wind, and mycelium in seed surface, soil, and living hosts. Owing to its geographical distribution and destructive yield reduction, DM is one of the most severe maize diseases among the maize pathogens. Positional cloning in combination with phenotyping is a general approach to identify disease resistant gene candidates in plants; however, it requires several time-consuming steps including population or fine mapping. Therefore, in the present study, we suggest a new combination strategy to improve the identification of disease resistant gene candidates. Downy mildew (DM) resistant maize was selected from five cultivars using the spreader row technique. Positional cloning and bioinformatics tools identified the DM resistant QTL marker (*bnlg1702*) and 47 protein coding genes annotations. Eventually, 5 DM resistant gene candidates, including *bZIP34*, *Bak1*, and *Ppr*, were identified by quantitative RT-PCR without fine mapping of the *bnlg1702* locus. Specifically, we provided DM resistant gene candidates with our new strategy, including field selection by the spreader row technique without population preparation, the DM resistance region identification by positional cloning using bioinformatics tools, and expression level profiling by quantitative RT-PCR without fine mapping. As whole genome information is available for other crops, we propose applying our novel protocol to other crops or for other diseases with suitable adjustment. Keyword: downy mildew, maize, positional cloning, spreader row technique

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