

Genome-Wide Identification and Characterization of MLO Family Genes in Pumpkin (*Cucurbita maxima* Duch.)

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Abstract : Mildew resistance locus o (Mlo), a plant-specific gene family with seven-transmembrane (TM), plays an important role in plant resistance to powdery mildew (PM). PM caused by *Podosphaera xanthii* is a widespread plant disease and probably represents the major fungal threat for many Cucurbits. The recent *Cucurbita maxima* genome sequence data provides an opportunity to identify and characterize the MLO gene family in this species. Total twenty genes (designated CmaMLO1 through CmaMLO20) have been identified by using an in silico cloning method with the MLO gene sequences of *Cucumis sativus*, *Cucumis melo*, *Citrullus lanatus* and *Cucurbita pepo* as probes. These CmaMLOs were evenly distributed on 15 chromosomes of 20 *C. maxima* chromosomes without any obvious clustering. Multiple sequence alignment showed that the common structural features of MLO gene family, such as TM domains, a calmodulin-binding domain and 30 important amino acid residues for MLO function, were well conserved. Phylogenetic analysis of the CmaMLO genes and other plant species reveals seven different clades (I through VII) and only clade IV is specific to monocots (rice, barley, and wheat). Phylogenetic and structural analyses provided preliminary evidence that five genes belonged to clade V could be the susceptibility genes which may play the importance role in PM resistance. This study is the first comprehensive report on MLO genes in *C. maxima* to our knowledge. These findings will facilitate the functional analysis of the MLOs related to PM susceptibility and are valuable resources for the development of disease resistance in pumpkin.

Keywords : Mildew resistance locus o (Mlo), powdery mildew, phylogenetic relationship, susceptibility genes

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