



Genome-wide identification of Mlo gene family members in *Cicer arietinum* and *Medicago truncatula* and its comparative phylogenetics with *Glycine max*

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Powdery mildew (PM) is considered as one of the major diseases of crops, and breeding for PM resistance is one of the important objectives to minimize yield losses. The powdery mildew locus O (Mlo) function is necessary for infection by the PM pathogen, and the recessive allele, mlo, confers broad range resistance to the PM disease. The Mlo gene family is one of the largest known seven transmembrane domain protein encoding gene families in plants. The Mlo proteins are known to be associated with the plasma membrane, and seem to be involved in a variety of developmental and stress response functions. The identification of members of Mlo gene family may facilitate their molecular characterization leading to their use in breeding programs.

Chickpea is one of the important grain legumes, and *Medicago truncatula* is a model legume species. In this study, we have computationally identified genome-wide 13 CaMlo (*C. arietinum* Mlo) and 14 MtMlo (*M. truncatula* Mlo) members. The CaMlo and MtMlo genes exhibit homology in terms of their gene structure, protein sequence, topology and distinguishingly, their chromosomal distribution patterns. Most of the transmembrane domains in the Mlo proteins showed similar invariant/ conserved amino acid residues. The CaMlo and MtMlo proteins form four major clusters, with most of the orthologous members exhibiting one-to-one pair of closely related homologs. Further, the analysis of cis-acting elements in the promoter region of each CaMlo and PvMlo members using PlantCARE tool revealed the presence of pathogenesis as well as various hormonal and heat-stress response elements. The study also suggests that *M. truncatula* has undergone extensive chromosomal rearrangements following separation from its close relative *C. arietinum*. However, in both the species, Mlo gene family has been subjected to strong negative selection pressure, indicating their non-redundant and essential roles in plant function.

We have also attempted to investigate the comparative phylogeny of the Mlo gene families from *C. arietinum*, *M. truncatula* and *Glycine max* in order to propose a relative model for Mlo gene family lineage. The G. max genome encodes 39 GmMlo members, which is more than twice the number of members present in *C. arietinum* or *M. truncatula*. The Mlo proteins from these species also form four major clusters. As expected, the GmMlos are more divergent from the CaMlos and MtMlos, which are much closely related. In addition, one CaMlo, one MtMlo and two GmMlo members were clustered together. It appears that the number of Mlo gene family member in diploid dicot species ranges between 15 and 20.

Biography

Reena Deshmukh is currently pursuing PhD in Plant Biotechnology, from Banaras Hindu University under the supervision of Em. Prof. B.D. Singh. She completed her MSc (Ag) Biotechnology from Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur in 2008. At present she is working on the identification of disease resistance genes in crops, the comparative genomics and evolutionary phylogenetics. She has been also awarded with the Young Scientist Award in Agricultural Sciences by MP Council of Science and Technology. She has published four research papers in reputed journals.

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