

MIK2 IS THE CANDIDATE FEMALE DETERMINANT OF THE SPOROPHYTIC SELF-INCOMPATIBILITY (SSI) LOCUS IN CHICORY (CICHORIUM INTYBUS, ASTERACEAE)

DRAGA S.*, PALUMBO F.*, MAGON G.*, GABELLI G.*, SORIA GARCIA F.*, VANNOZZI A.*, FARINATI S.*, SCARIOLO F.*, LUCCHIN M.*, BARCACCIA G.*

*) University of Padova

MDIS1 INTERACTING RECEPTOR LIKE KINASE 2, pollen–stigma recognition, AT4G08850, chicory, self-incompatibility

The *Cichorium* genus offers a unique opportunity for the investigation of the sporophytic self-incompatibility (SSI) system. This genus consists of species that exhibit highly effective self-incompatibility, such as *C. intybus*, and complete self-compatibility, like *C. endivia*. In order to explore this further, we utilized the newly released chicory genome to map seven markers previously associated with the SSI locus. Consequently, the S-locus region was confined to a window of approximately 4 million base pairs on chromosome 5. Within this region, one particular gene, *MDIS1 INTERACTING RECEPTOR LIKE KINASE 2* (*ciMIK2*), showed great potential as a candidate for SSI. Its ortholog in *Arabidopsis* (*atMIK2*) plays a role in pollen-stigma recognition reactions, and its protein structure has similarities with the S-receptor kinase (SRK), a crucial component of the SSI system in the Brassica genus. By amplifying and sequencing *MIK2* in chicory and endive accessions, we observed two contrasting scenarios. In *C. endivia*, *MIK2* remained fully conserved, even when comparing different botanical varieties such as smooth and curly endive. In *C. intybus*, 387 polymorphic positions and 3 INDELS were identified when comparing accessions of different biotypes, all of which belonged to the same botanical variety (i.e. radicchio). The distribution of polymorphisms across the gene was uneven, with hypervariable domains predominantly located in the LRR-rich extracellular region, which was predicted to be the receptor domain. The gene seemed to be under positive selection, as the number of nonsynonymous mutations was more than double that of synonymous mutations (dN/dS = 2.17). A similar pattern was also observed in the analysis of the first 500 base

pairs of the *MIK2* promoter: no single nucleotide polymorphisms (SNPs) were found among the endive samples, whereas 44 SNPs and 6 INDELS were detected in the chicory samples. An analysis of expression kinetics was carried out on leaf (used as a control) and flower tissues at various phenological stages to monitor the accumulation of *MIK2* transcripts. Further investigations are required to validate the role of *MIK2* in SSI and to determine whether the 23 species-specific nonsynonymous SNPs in the coding sequence (CDS) and/or the species-specific 10 base pair-INDEL discovered in a CCAAT box region of the promoter are responsible for the divergent sexual behaviors exhibited by chicory and endive.