

## REPRODUCTIVE BARRIERS IN ASTERACEAE SPECIES: AN OVERVIEW ON THE RELATIONSHIPS BETWEEN CROPS AND THEIR ALTERED MATING SYSTEMS

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*male sterility, self-incompatibility, phylogeny*

Plant breeding and the development of new varieties in crops is largely influenced by the reproductive strategies of the species. Different mating systems, as allogamy and autogamy, imply different strategies for the development and propagation of breeding lines. Controlled pollination can be achieved through reproductive barriers (RBs) and, in particular, exploiting male sterility (MS) and self-incompatibility (SI) systems. The present research deals with the RB identified and characterized thus far in the Asteraceae family.

We firstly reviewed all the genic loci, both mitochondrial and nuclear, involved in MS, assessing the availability of cytoplasmic male sterility (CMS) and nuclear male sterility (NMS) systems for breeding purposes. The orthologous genes of the aforementioned loci were searched in other species of agricultural interest belonging to the same family and the possibility to carry out gene-editing approaches to induce male sterility in Asteraceae species where RB are missing was evaluated. In many species, we highlighted the lack of effective protocols concerning the regeneration of edited plants. As regards SI, we tried to provide new insights into the phylogenetic evolution of this barrier within the family. A meta-phylogenetic analysis of the taxa belonging to Asteraceae was performed, by retrieving the main plastidial sequences used for DNA barcoding analyses. Multiple alignments, Maximum Likelihood clustering, as well as phylogenetic reconstruction of the considered taxa, were performed. The molecular analyses were then interpolated with the information deriving from the scientific literature and related to the presence of SI systems (both sporophytic and gametophytic) in the species under investigation. The aim

was to investigate whether the SI system within the Asteraceae family evolved from a common ancestor or it evolved multiple times following different developmental pathways. Our findings would support this latter hypothesis, as already proposed in other families. Moreover, an almost total lack of molecular data has emerged and the genomic loci controlling the self-incompatibility system remains thus far under-investigated.