*Line 1 – Plants biodiversity, Evolution and systematics*

FLORAL EVOLUTION OF NYMPHAEALES USING MADS-BOX GENES AS MARKERS

People involved: Barbara Baldan

Project description

The rapid and widespread domination of flowering plants all over the world was largely promoted by the evolution of fruits and flowers, a very successful mode of reproduction. The development of these crucial novel reproductive structures is mainly regulated by MADS-box transcription factors, that have been identified in nearly all groups of eukaryotes, where they are major regulators of development. The number of these genes has greatly expanded in plants, where their functions range from root development to floral organ specification and to fruit development. In most of the flowering plants, the MADS-box genes that are expressed in the floral buds during the flower development, act as homeotic selector genes specifying the different floral organs (sepals, petals, stamens, carpels), according to the ABC(D)E model. This model, developed for eudicots, is not perfectly applicable to basal angiosperms and, by inference, to the earliest angiosperms in general. Expression patterns of those genes in basal angiosperms are often broader than expected. The aim of this research project is the study of MADS-box genes that are expressed in the floral buds and in the reproductive structures of basal angiosperms that belong to the Nymphaeales order, with the purpose to better understand the MADS-box genes expression pattern involved in these species, thus contributing to an update of the 'ABC(D)E' model in the organisms object of the study. These studies are carried out by collaborations with Prof. L. Colombo (Milan), Prof.S. Masiero (Milan) and Dr. S. Cagnin (Padova).
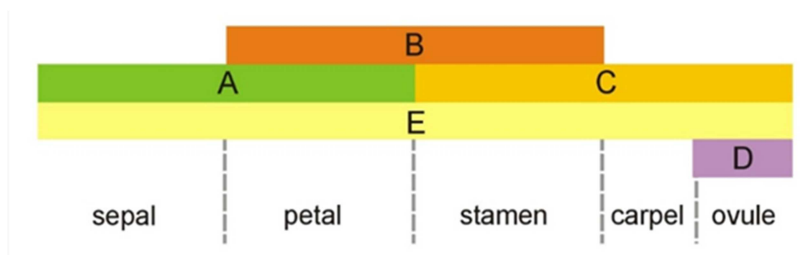
ABC(D) E model and flowers of *Nymphaea caerulea*