REGULATORS OF FLOWERING AS CANDIDATE GENES FOR IMPROVING BIOMASS YIELD OF GIANT REED (ARUNDO DONAX)


*) Department of BioSciences, University of Milan, Via Celoria 26, 200133 Milano (Italy)
**) Agricultural Institute S. Michele all’Adige (IASMA), Trento (Italy)
***) CRA - Unità di Ricerca per la Floricoltura e le Specie Ornamentali, Corso degli Inglesi 508, 18038 Sanremo (Italy)
****) Istituto di Biologia e Biotecnologia Agraria del CNR, Via Bassini 15, 20133 Milano (Italy)

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The timing of flowering is dependent on the production of a flowering signal (florigen) in the leaves which is then translocated to the shoot apex where it stimulates the transition of the meristem from vegetative growth to inflorescence development. The florigen has been identified in Arabidopsis (FT protein) and rice (Hd3a) as a small protein of around 180aa. Similar genes have been identified in many species, some of which induce flowering, while other function as repressors. Work done in several species has demonstrated that prolonging the vegetative growth phase, by delaying flowering, is a promising strategy to increase plant biomass yield.

We present here a preliminary characterization of several members of the FT family from A. donax, identified both through PCR amplification with degenerated primers and through the analysis of RNAseq data.

We have identified so far at least 10 members/alleles of this family in A. donax and the data suggest that this species has probably many more isoforms than rice or sorghum, as expected for a putative allopolyploid plant with a high degree of heterozygosity due to the absence of sexual reproduction. A phylogenetic tree has been constructed allowing the identification of putative bona fide A. donax florigen genes.

On the base of the RNAseq data, we are recloning A. donax FT-like coding regions by PCR, to exclude polymorphism due to artefacts.

We plan to obtain stable transformants expressing different A. donax FT-like genes in order to test their role as florigen. We are therefore trying to improve the different steps of the process, namely: 1) use of different explants as a starting material, 2) set up efficient tissue culture and selection protocols, 3) identify suitable promoters.

We achieved callus formation from axillary buds and leaves which are available all year round. However, considering that plant regeneration from such tissue is still erratic, we set up a protocol for direct plantlets regeneration from inflorescence and flower meristems. In addition we are also testing different promoters to drive the expression of reporter genes.