

Research activity

My research activity has been devoted to the molecular physiology of abiotic stress response in photosynthetic organisms, plants, mosses and algae, allowing counteracting adverse environmental conditions.

During their evolution, plants have developed mechanisms to cope with and adapt to different types of stress imposed by the frequently adverse environment.

Most of the vascular plants have evolved some anatomical adaptation mechanisms as vascular tissues, root system, cuticles, lignin and stomata control as well as complex integrated circuits at organismal level. In contrast to the complex plants, the less complex plants have very simple anatomical structure and fundamental mechanisms for environmental stress resistance at subcellular level.

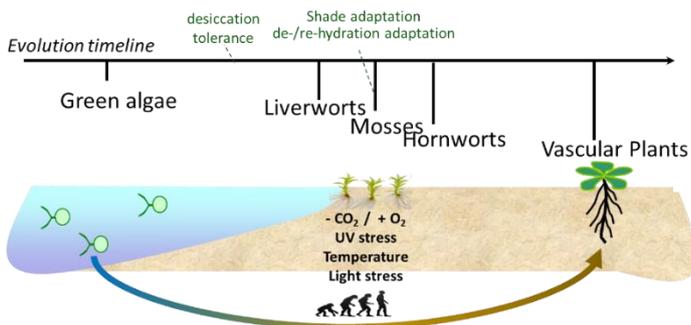
Instrumental to my research was the focus on a less complex plant such as the model moss system *Physcomitrella patens*.

Mosses are evolutionary intermediate between green algae and higher plants: they were the first organisms emerged from the water to the land environment characterized by more stressing conditions including increased level of oxygen, decreased availability of water, the sessile lifeform, UV stress and a lot of more light. Thus, thanks to the genome duplication, mosses developed new functions from pre-existing genes.

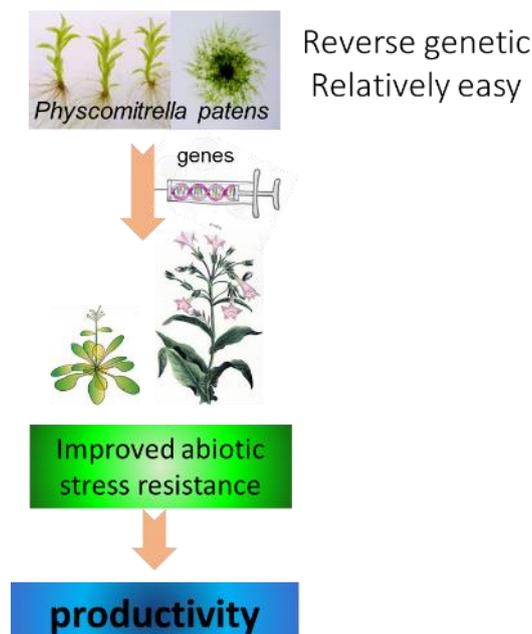
The goal of my research is using *P. patens* to study the molecular mechanisms of photosynthesis and photoprotection and identify stress resistance genes to be later expressed in crop species and verify the effect on stress resistance and overall productivity.

Research approach is multi-disciplinary in that crosses over various disciplines and made use of combined analytical approaches including molecular biology, physiology, biochemistry and biophysics. Scale of study is wide: from isolated pigment-binding proteins to organelles, intact cells and whole organisms.

The biological systems currently employed for this research are: *A. thaliana*, *N. tabacum*, *S. lycopersicum*, *P. patens*.



Scheme of plant evolution.



Working model to find out interesting *P. patens* genes: i) Identification of interesting genes through bioinformatic tools and literature; ii) “validation” of interesting genes making knock out in *P. patens*; iii) introduction of interesting *P. patens* genes in model higher plants (as *A. thaliana*) and crop plants (as *N. tabacum*, *S. lycopersicum*, etc) and phenotypic analysis of improved stress resistance and productivity in lab scale and in the field (outdoor).