Crosstalk between arbuscular mycorrhizal fungi and host plants under drought stress

Drought stress is detrimental to plant growth and development. Nevertheless, plants have evolved mechanisms to cope with drought stress at cellular, tissue, and whole-plant levels. Plant physiological responses to drought stress are initiated and sustained by signal transduction pathways mediated by endogenous stimuli, for instance plant hormones. As a primary stress hormone, abscisic acid (ABA) helps to maintain plant water status by activating downstream stress-responsive genes.

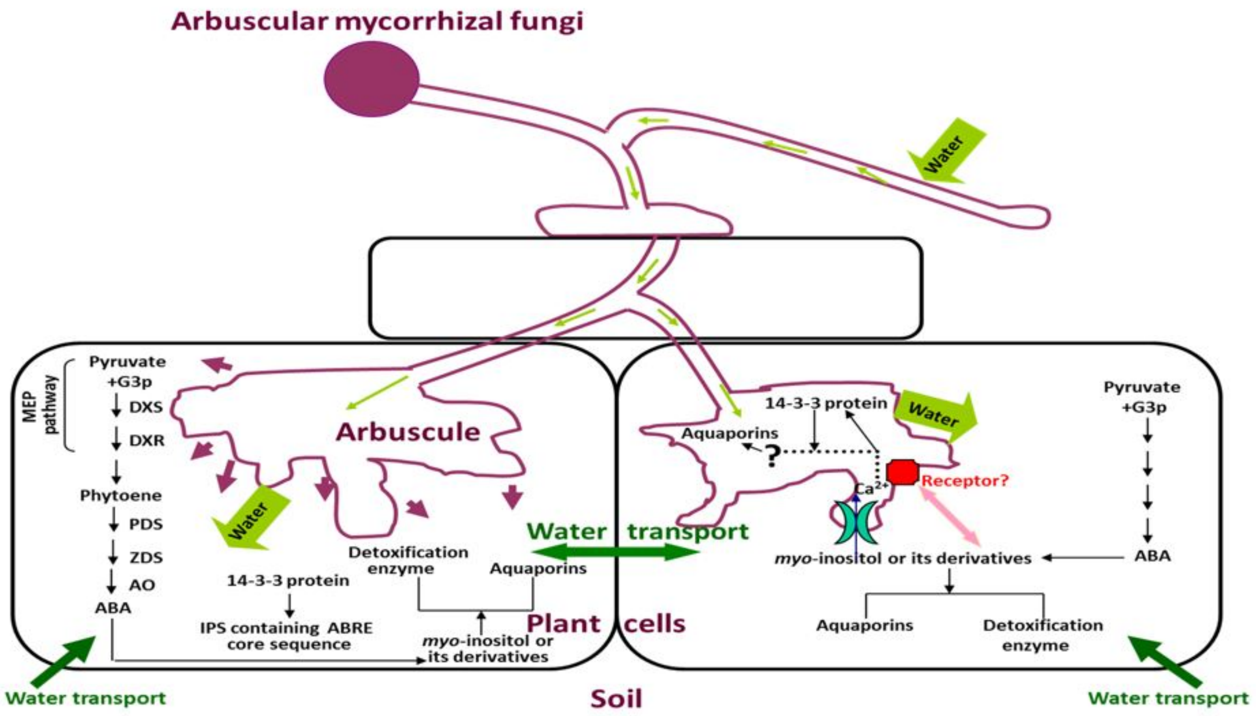

Fig. 1. Hypothesized crosstalk between AM fungus and host plant under drought stress.

On the other hand, arbuscular mycorrhizal (AM) symbiosis established between AM fungi (AMF) and roots of terrestrial higher plants, is known to stimulate plant resistance to various environmental stresses, including drought stress. Changes in plant ABA concentrations caused by AMF have been postulated to induce the expression of many stress related genes including aquaporin genes encoding membrane intrinsic proteins that facilitate transport of water and certain small molecules across biological membranes. Considering the specific role of ABA in the development of the arbuscule (interface between AM fungi and root cells) and its functionality during AM symbiosis, it is of special interest to study the putative influences of AM symbiosis on

ABA signaling pathway to improve plant drought tolerance. In this context, we performed a split-root experiment, in which two parts of the plant roots were subjected to independent treatments with drought stress and mycorrhizal inoculation. By comparing the impact of partial and overall inoculation on plant drought tolerance, we can elucidate whether the AMF *Rhizophagus intraradices* functions locally or systemically. Furthermore, we analyzed the effects of the heterogeneous drought stresses on the expression profiles of the genes from both roots and *R. intraradices* to shed light on the crosstalk between host plants and AMF.

In the experiment, we recorded plant physiological parameters including dry weight, relative water content, phosphorus (Pi) concentration, and root ABA concentration, and assessed expression of 15 genes from maize roots which are relevant to drought tolerance, including five genes involved in ABA biosynthesis, *IPS*, *14-3GF*, seven ABA-dependent PIPs and one gene encoding superoxide dismutase (SOD). In addition to the above-described plant genes, we took into account three AMF genes including a 14-3-3 gene (Ri14-3-3), and two fungal aquaporin genes, *GintAQPF1* and *GintAQPF*2.

Our study identified that mycorrhizal colonization can decrease root ABA concentration mainly by down-regulating aldehyde oxidase (AO) expression under drought stress. Consequently, *R. intraradices* improves plant water status by modulating ABA-mediated abiotic signaling pathway involving IPS and 14-3-3 proteins. Moreover, the study on the action mode of *R. intraradices* in enhancing plant drought tolerance under heterogeneous conditions reveals that when IPS and 14-3GF are co-expressed in the whole root system, the systemic regulation of plant drought tolerance by *R. intraradices* is activated. We propose that cooperation of IPS and 14-3-3 protein potentially is responsible for the crosstalk between maize and *R. intraradices*, which is crucial to AM-associated synergistic actions in improving plant drought tolerance.

Tao Li [1], ***Xin Zhang*** [1], ***Baodong Chen*** [1,2]
[1]*State Key Laboratory of Urban and Regional Ecology, Research Center for Eco-Environmental Sciences,*
Chinese Academy of Sciences, Beijing, China
[2]*University of Chinese Academy of Sciences, Beijing, China*

Publication

Potential role of D-myo-inositol-3-phosphate synthase and 14-3-3 genes in the crosstalk between Zea mays and Rhizophagus intraradices under drought stress.
Li T, Sun Y, Ruan Y, Xu L, Hu Y, Hao Z, Zhang X, Li H, Wang Y, Yang L, Chen B
Mycorrhiza. 2016 Nov