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AUXIN EFFLUX TRANSPORTERS IN MAIZE: PHYLOGENETIC ANALYSIS AND GENE EXPRESSION STUDIES

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Auxin regulates many aspects of plant development, such as embryogenesis, leaf, flower and lateral root initiation, vascular tissues differentiation and tropisms. Auxin molecules can move over long distances through the vascular system via the phloem, from source tissues to the roots. However, it is well known that a polar cell-to cell transport is the main mechanism involved in the wide spectrum of auxin-related developmental processes. Multiple transport proteins are required to create and maintain directional auxin flows within organs and tissues: the resulting auxin concentration gradients are essential for the establishment and maintenance of polar growth and morphological patterning. A better understanding of auxin transporter role in mediating polar auxin transport (PAT) in maize is of outstanding importance for basic plant biology research and for crop improvement as well: shoot and root architectures, two of the main issues in determining crop yield, are indeed strictly regulated by PAT.

To date in Arabidopsis, three families of auxin transport proteins have been identified: AUXIN RESISTANT 1/LIKE AUX1 (AUX1/LAX) uptake symporters, P-GLYCOPROTEIN (MDR/PGP/ABCB) transporters and PIN-FORMED (PIN) efflux carriers.

In our group we identified the twelve members of the maize *PIN* gene family and two *PIN-like* genes. In this poster we report the characterization of the maize *PIN* and *PIN-like* genes the analysis of their expression patterns during pre- and post-embryonic development and their localization in different maize tissues during differentiation and development. Our results confirm the widening of monocots *PIN* family compared to dicots one (twelve maize *PINs* versus the eight Arabidopsis members) showing also in maize, as previously reported in rice and sorghum, the presence of three monocot-specific proteins, namely ZmPIN9, ZmPIN10a and ZmPIN10b. This indicates the fundamental role of PIN efflux-driven auxin accumulation for proper monocots development. Some *ZmPINs* show overlapping expression patterns, suggesting a certain degree of functional redundancy, whereas other family members, for example *ZmPIN9*, present peculiar expression domains. Given that, the preliminary data on possible molecular mechanisms regulating *ZmPIN9* expression will be illustrated.

Furthermore, to better elucidate the role of PAT in maize root architecture we are currently investigating the role of BR2, a maize MDR/PGP/ABCB efflux transporter expressed in internodes and roots, using a *br2* mutant. The mutant plants show a slow response to changes in the gravity vector, resulting in the formation of agravitropic primary roots.