THE MAIZE PIN GENE FAMILY OF AUXIN EFFLUX CARRIERS: EVOLUTIONARY RELATIONSHIP AND EXPRESSION ANALYSIS

FORESTAN C., VAROTTO S.
Department of Environmental Agronomy and Crop Science, University of Padova, Viale dell’Università 16, 35020 Legnaro (PD), Italy

auxin, PIN family, polar auxin transport, Zea mays

The plant hormone auxin (IAA) controls many central developmental processes of plants, including cell division, cell elongation, vascular tissues differentiation, root initiation, apical dominance, and tropic growth responses to environmental stimuli. Auxin is synthesized primarily in meristematic regions at the shoot apex and is then intercellularly transported in a polar fashion to the whole plant. The Chemiosmotic Hypothesis, formulated in the mid 1970s to explain the polar auxin transport (PAT), predicted the existence of specific auxin influx and efflux carriers. Because the chemical properties of IAA suggested that auxin efflux is the limiting step, the isolation of auxin efflux carriers became the main objective of scientists. The molecular characterization of the pin1 mutant allowed the identification of the first member of PIN-FORMED gene family. Subsequently, seven other genes similar to PIN1 were found in Arabidopsis genome and PIN proteins have been shown to play a rate-limiting role in the catalysis of auxin efflux from cells, determining the direction of cell-to-cell auxin flow and, as a consequence, creating the auxin gradients that regulate plant development.

Genes homologous to the Arabidopsis PIN are present in genomes throughout the plant kingdom, from the model moss Physcomitrella patens to all vascular plants, and the relatively high amino acid identity between PIN proteins suggests that all the PIN genes diverged from a single ancestral sequences. Phylogenetic analysis of PIN sequences from Oryza sativa and Triticum aestivum revealed that the monocot PIN family is wider and divergent than dicots one, with three or four genes homologous to one Arabidopsis PIN gene. On the other hand, the identification of wheat and rice proteins that do not clusterize with any dicot sequence suggests the presence of monocot-specific PIN proteins.

To identify genes member of the maize PIN family we screened several biological databases. Preliminary phylogenetic analysis using the detected ZmPIN proteins plus rice and Arabidopsis PINs confirmed the widening of monocots PIN family compared to dicots one. We identified at least three orthologs of AtPIN1, called ZmPIN1a, ZmPIN1b and ZmPIN1c and we mapped them respectively on the chromosomes 9, 5 and 4. In addition we identified two genes closely related to AtPIN2 (ZmPIN2a and ZmPIN2b) and a putative orthologs of AtPIN4 (ZmPIN4). As previously reported in rice, also in maize three putative orthologs of PIN5 (ZmPIN5a, ZmPIN5b and ZmPIN5c) have been isolated, while, at the moment, only one monocot-specific protein (ZmPIN10) has been identified. Semiquantitative RT-PCR expression analysis revealed that newly identified ZmPIN genes are differentially expressed during maize embryonic, vegetative and reproductive development. To better understand the role of these genes in controlling seed and plant development we are determining their expression patterns by in situ hybridization.