Proceedings of the XLIX Italian Society of Agricultural Genetics Annual Congress
Potenza, Italy – 12/15 September, 2005
ISBN **88-900622-6-6**

Poster Abstract - B.05

PIN1 EXPRESSION STUDIES IN *ARABIDOPSIS THALIANA* AND *ZEA MAYS*

N. CARRARO*,**, C. FORESTAN*, J. TRAAS**, S. VAROTTO*

*) Dipartimento di Agronomia Ambientale e Produzioni Vegetali, Università di Padova, Viale dell'Università 16, 35020 Legnaro (PD), Italy - nicola.carraro@unipd.it
**) INRA, Laboratoire de Biologie Cellulaire, route de St.Cyr, 78026 Versailles, France - traas@versailles.inra.fr

auxin, phyllotaxis, PIN, maize, arabidopsis

Plant bodies are formed thanks to undifferentiated groups of cells called meristems. Here we focus on the shoot apical meristem (SAM) and the root apical mersitem (RAM). The SAM produces organs in a stereotypic fashion and follows a pattern which is highly regular. In this context, auxin is supposed to play a major role. Auxin is usually actively transported from cell to cell. This transport is established through influx membrane carriers (AtAUX family) and efflux membrane carriers (AtPIN family). Especially the efflux carriers are important for patterning at the SAM. Current hypotheses suppose that the PIN proteins create patterns of auxin gradients that, in turn, create patterns of gene expression and morphogenesis (Frîml et al., 2003). How these patterns of auxin fluxes are created and how they are interpreted in terms of growth and gene expression is unknown at present.

Orthologous genes encoding auxin transport regulators begin to be identified in other species such as rice, maize and members of the *Brassicaceae* family. We have used an antibody raised against a highly conserved site of AtPIN1 for immunolocalizations in sections of maize male and female inflorescences and embryos. We show that the antibody labels polarly localized proteins, confirming the conserved nature of auxin transport driven patterning. Several maize developmental mutants have been identified, so it would be desirable to analyse the expression of *PIN* genes in such individuals. At the moment we have identified three putative *PIN* sequences in the maize genome and produced probes for *in situ* hybridization. Preliminary experiments localize the putative *PIN* transcripts in the leaves tips, vascular bundles and root vascular tissues.