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group. No changes were observed concerning $CD80^+$ expressing B-lymphocytes. Interestingly, addition of either hCGu or hCGr induced a significant reduction in the total numbers of $CD19^+TNF\text{-}\alpha^+$ B cells as well as $CD4^+TNF\text{-}\alpha^+$ cells as compared to controls. Besides a slight increase, no significant differences were observed on IL-10 production by $CD4^+$ or $CD19^+$ B cells upon either hCG stimulation (data were analyzed by One-way ANOVA).

Overall, we demonstrated here that treatment with hCG *in vitro,* lowers the expression of the costimulatory molecule CD86 in B cells and also decreases the production of TNF-α, in both $CD4^+$ and $CD19^+$ B cells. These results highlight the potential use of this hormone for the treatment of MS.

Keywords: Multiple Sclerosis, hCG, immune suppression.

PLANT BIOLOGY 2

(828) **ADP-GLUCOSE PYROPHOSPHORYLASE IS POST-TRANSLATIONAL REGULATED BY PHOSPHORYLATION IN WHEAT SEEDS**

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ADPglucose pyrophosphorylase (ADPGlcPPase, EC 2.7.7.27), a heterotetramer comprised of two small (S) and large (L) subunits, catalyzes the first and rate-limited step of starch biosynthesis pathway. In plants, the activity of ADPGlcPPases is regulated allosterically by metabolites, by redox mechanisms and recently, phosphoproteomic and bioinformatic studies suggest its regulation by phosphorylation. In comparative studies along wheat (storing starch) and castor (storing triacylglycerides) seeds development, we found that ADPGlcPPase is phosphorylated only in wheat seeds at stages with increased ADPGlcPPase activity and higher starch accumulation. To study the effect of phosphorylation in wheat ADPGlcPPase, we used recombinant co-expression strategies in *Escherichia coli* to produce the subunits of wheat endosperm ADPGlcPPase, separately (*Tae*S, *Tae*L) or together (*Tae*SL). Also, we designed and produced different *Tae*S and *Tae*L Ser mutants located in putative phosphorylation sites. *In vitro* phosphorylation assays with ^{32}P-γ-ATP, wheat seed extracts (as kinases resource) or specific recombinant kinases (SnRK1, SOS2 and CDPK) showed that *Tae*ES, *Tae*EL and *Tae*ESL were phosphorylated. As well, all mutants were phosphorylated too, suggesting that *Tae*EADPGlcPPase is phosphorylated in other Ser/Thr residue or the occurrence of many phosphorylation sites. When we evaluated the effect of phosphorylation, the result showed a 4-fold increase of *Tae*SL activity. Altogether, the results point out that posttranslational regulation of *Tae*EADPGlcPPase by phosphorylation would increase the enzyme activity at specific stages of wheat seed development. This work describes a new posttranslational mechanism in the regulation of starch metabolism at the level of ADPGlcPPase, that will required further study to deeply comprehend the interplay with other regulation mechanism and explore possible biotechnological developments.

Keywords: starch, phosphorylation, seeds, wheat, castor oil seed

(840) **ARABIDOPSIS POLLEN EXTENSINS LRX ARE REQUIRED FOR CELL WALL INTEGRITY DURING POLLEN TUBE GROWTH**

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(1) INGEBI, (2) Fundacion Instituto Leloir.

Abstract: Polarized growth of pollen tubes is an oscillatory mechanism which involves high trafficking of vesicles to the tip where a constant remodeling of the cell wall occurs. To maintain the proper assembly of the cell wall is crucial the role of glycoproteins and homogalacturonans in the crosslinking. Here, we studied the function of four pollen specific LRX(8-11) (Leucine-Rich repeat Extensin-like) chimeric proteins which belong to the HRGP (Hydroproline-Rich Glycoprotein) family in *Arabidopsis thaliana*. These LRX proteins have an LRR (Leucine rich repeat) N-terminal domain followed by a cysteine rich region and a C-terminal domain extensin (EXT)-like with Ser-Pro repetitions. LRR domain might be involved in protein-protein interactions and the role of EXT domain might be to establish the crosslink on the cell wall allowing its integrity. Because we did not observe any obvious phenotype for the single mutants and to overcome a possible functional redundancy, we obtained multiple homozygous loss of function mutants. The triple *lrx9 lrx10 lrx11* mutant displayed the most severe pollen tube phenotype with an important reduction (60.7%) in pollen germination and a lower seed set (33% less compared to the WT). Moreover *in vitro*, semi *in vivo* and *in vivo* analyses revealed the presence of abnormal pollen tubes with widen tips and the emergence of bulges mostly near to the tube tip. To study the composition of the primary cell wall in the triple *lrx9 lrx10 lrx11* mutant, we analyzed the distribution of pectins, callose and cellulose using different dyes. Confocal and bright-field fluorescence microscopy revealed an altered deposition of pectin, callose and cellulose and thicker cell walls in the triple mutant. All together these results suggest that LRX8-11 have a structural role and are required for a proper cell wall assembly during polarized growth of pollen tubes.

Keywords: pollen tube, cell wall, extensin, polarized growth, LRX

(1253) ***Arabidopsis thaliana* ASPARTIC PROTEASES AND THEIR ROLE IN DROUGHT STRESS.**

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Plant aspartic proteases have been implicated in protein processing as well as in plant senescence, stress responses, programmed cell death and reproduction. In last years, it has been reported that they might have a role in the adaptation of plants to an environment with less water availability. In our laboratory we determined that an *A. thaliana* gene that encodes for an aspartic protease (*At1g11910*) that is expressed in guard cell, is induced under deficit water conditions.

The aim of this work was to study the role of *At1g11910* during the plant response to drought. We performed assays to compare the response of Col-0 and *At1g11910* mutant plants in a mild water deficit (MWD) condition. Seedlings of 14 days were putted in pots with an equal substrate quantity and were watered until saturation during 10 days. Then, treated plants were watered until reached a 26% of the maximum substrate capacity (0.13 g of water/g substrate) during the next 20 days. We evaluated the phenotype of each plant under stress conditions and quantified different hydric parameters as water content, consumption and loss.

Our results indicated that mutant plants were more susceptible than Col-0 to a MWD, showing a reduction in the total area leaf and in the apical length in a 60% and 40% respectively. On the other hand, we did not observed significant differences in chlorophyll content. We determine that mutant plants had a higher water loss (60%) and consumption (25%) but they presented lower water content (28%). These results allow us to suggest that *At1g11910 A. thaliana* gene would participate in the tolerance to drought. Currently we are completing the characterization of this gene and generating *At1g11910* overexpressing *A. thaliana* plants as a new biotechnological tool to face water deficit conditions.

Keywords: Aspartic Proteases, Drought, *A. thaliana*.

(1059) **CHARACTERIZATION OF A MAIZE FLAVONE SYNTHASE II**

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Flavones, a subtype of flavonoid, are widespread among the higher plants and have diverse physiological functions. There are two classes of flavone synthase (FNS) enzymes that catalyze the conversion of flavanones into flavones. The flavone synthase II comprises oxygen- and NADPH-dependent cytochrome P450 membrane-bound monooxygenases. We identified a gene encod-