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enzymes to the extracellular space with the likely purpose to interact with the transmitting tissue.

PS10. Post-translational Regulation of Starch Synthase IIa, a Key Enzyme of Starch Biosynthesis in Maize Endosperm. S. Mehrpouyan[1*], I.J. Tetlow[1] and M.J. Emes[1]. [1]*Department of Molecular and Cellular Biology, University of Guelph, Ontario, Canada, N1G 2W1.*

Starch is the most abundant storage carbohydrate in plants, providing 70% of human caloric intake and has many industrial applications. Starch biosynthesis involves the coordination of starch synthases (SSs), starch branching enzymes (SBEs) and debranching enzymes.
In cereals, some starch biosynthetic enzymes function via formation of multi-enzyme complexes, and protein phosphorylation plays a crucial role in their assembly. In maize, the isozyme SSIIa, forms the core of a heteromeric protein complex with SBEIIb and SSI, and is responsible for the localization of this complex in the starch granule. The catalytic activity of this particular protein complex is crucial for normal starch biosynthesis in maize. When maize amyloplast extracts were analysed by western blots, following non-denaturing PAGE, multiple bands of SSIIa were identified. The relative mobility and distribution of SSIIa bands was markedly different between samples treated with ATP or alkaline phosphatase, suggestive of major conformational changes and/or association with other proteins caused by protein phosphorylation. Results will be presented showing effect of phosphorylation on the catalytic activity of enodgenous and recombinant forms of SSIIa as well as on formation of enzyme complexes with other enzymes of starch biosynthesis. The sites of SSIIa phosphorylation have been investigated by site-directed mutagenesis and data on the amino acid residues involved will be discussed. The present study provides new insights into our understanding of the signal transduction system regulating amylopectin biosynthesis in plants. This work is of strategic importance and has the potential to identify novel genes for crop improvement.

PS11. Evolution and mechanism of the mitochondrial *cox1* intron horizontal transfer in Angiosperms. L.F. Ceriotti[1]*, L.E. García[1,2] and M.V. Sánchez-Puerta[1,2,3]. [1]Facultad de Ciencias Exactas y Naturales, UNCuyo, [2]Instituto de Biología Agrícola de Mendoza, CONICET-UNCuyo and [3]Facultad de Ciencias Agrarias, UNCuyo.

The most frequent case of horizontal gene transfer in angiosperms involves the group I intron in the *cox1* mitochondrial gene, originally acquired from a fungal donor and followed by more than 100 subsequent inferred plant-to-plant transfer events. This promiscuous behaviour is thought to be due to its encoded DNA *homing* endonuclease, whose cleavage site is in *cox1* intron-less alleles. The study of homologous introns in yeast suggests that intron insertion occurs through the double-strand break repair (DSBR) pathway without crossover, process called *intron homing*. So, this mechanism has been proposed to participate in angiosperms *cox1* intron propagation. However, other repair mechanisms supposed to occur in plant mitochondria could participate. These mechanisms can be distinguished because they are supposed to generate crossovers (CO) and/or non-crossovers (NCO) in different proportions. In order to detect possible alternative repair mechanisms involved in *cox1* intron propagation, we analyzed 139 angiosperm species with the intron. The analysis consisted in the identification of CO and NCO events comparing exon1, exon2 and intron phylogenetic relationships. When sequences were available the analyses was extended to intergenic regions flanking the exons. In contrast with original DSBR model, where COs and NCOs are expected to occur in similar proportions, only NCO events where detected in our analyses. We propose an alternative repair pathway called synthesis-dependent strand annealing (SDSA), which can only produce NCO results, as the most probable mechanism involved in the *cox1* intron propagation in angiosperms.

PS12. Identification of candidate *Fusarium graminearum* effectors during infection of *Arabidopsis thaliana* using biotin identification (BioID). M. G. Miltenburg[1]*, C. Rampitsch[2], M. Khan[3], D. Desveaux[3], R. Subramaniam[1]. [1]*Dept.*