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Poster Abstract – C.22

DIFFERENT RESPONSE TO S-STARVATION IN MAIZE INBRED LINES AND THEIR HETEROTIC HYBRID

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Heterotic maize hybrids are largely exploited in agriculture due to their increased productivity and resistance to stress conditions with respect to inbred lines. In fact, hybrids show intrinsic stability in sub-optimal growth conditions such as low macronutrient availability. Among these, sulfur is particularly important since it is essential for protein and stress-related metabolites biosynthesis. Sulfur assimilation is a multi-step pathway with several points of regulation. The first step consists in the uptake of inorganic sulfate from the soil. Early response to sulfate starvation is exclusively mediated by a high-affinity sulfate transporter (ST1:1). After uptake, sulfate is activated to adenosine 5'-phosphosulfate (APS) by ATP-sulfurylase. This compound subsequently is either reduced by APS-reductase (towards biosynthesis of cysteine) or phosphorilated by APS-kinase to 3'-phosphoadenosine-5'phosphosulfate (PAPS), the main source of organic sulfur for other compounds (flavonoids, glucosinolates, etc.).

The aim of this work is to relate transcription regulation and heterosis for sulfur assimilation. We set out to determine whether transcriptional levels of key enzymes (ST1:1 transporter, ATP-sulfurylase, APS-reductase and APS-kinase) was differently affected at specific time points after S-starvation by comparing their transcript abundance in two inbred lines and their heterotic hybrid by real time RT-PCR. Preliminary results indicate that the S-starvation induces variation of transcription level that is different among genotypes. In particular, one inbred line shows a decrease in mRNA levels, whereas the other inbred and the F_1 hybrid show an opposite behavior. Since ATP-sulfurylase sequence showed the presence of a target region for micro-RNA (Mir395), we also investigated the post-transcriptional processing of its messenger RNA. In fact, we were able to detect the presence of RNA cleavage products, indicating the involvement of micro-RNA-mediated transcriptional regulation of ATP-sulfurylase in roots.