



Cover page: The Synthetic Lethal Rosette

Aberrant mitotic phenotype found in BRCA1-deficient cells treated with the PLK1 inhibitor Volasertib. Cells become giant and multinucleated and acquire a flower shape, with nuclei arranging in a circular disposition around a cluster of centrosomes. Blue (DAPI: nuclei), Green (FITC-phalloidin: actin cytoskeleton), Red (γ -Tubulin: centrosomes).

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in terms of protein and oil content. This work constitutes a starting point in order to detect metabolic differences that explain the different levels of reserve compounds and will help us identify molecular components involved in oil and/or protein biosynthesis, including enzymes, transporters, transcription factors, and other proteins.

PL-P36

NITROGEN METABOLISM IS ALTERED IN *ARABIDOPSIS* PLANTS WITH MODIFIED POLYAMINE LEVELS SUBJECTED TO NITROGEN DEFICIENCY

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Nitrogen (N) is one of the most important nutrients in plant growth and is a constituent of many stable compounds such as amino acids, proteins, and polyamines (PAs). In *Arabidopsis thaliana*, where the PA putrescine (Put) is produced exclusively through the arginine decarboxylase (ADC) pathway, two genes encode ADC (*ADC1* and *ADC2*). The objective of this work was to study the interrelation between N and PAs metabolisms in *Arabidopsis* plants under N deprivation. Leaves of wild type plants (WT), a line defective in Put biosynthesis (*adc1*) and a line overexpressing ADC (7.2) were used. Plants were grown in a Hoagland basal nutrient media containing normal (C) or reduced (Low N) total nitrogen content, in hydroponics for 21 days. In C media, free Put content in *adc1* and 7.2 lines was 35% lower and 2.5-fold higher, respectively, than in WT line, whereas in low N medium, Put content decreased close to 30% in WT and *adc1* plants but did not change in 7.2. Spermine content was greatly increased in *adc1* respect to WT plants in both media. The mutant *adc1* has a slightly higher fresh biomass and protein content in N7 medium but seemed to be the more affected one when grown under N deprivation in terms of growth, protein or chlorophyll content and showed different behavior in some aspects of N metabolism respect to WT, in basal and deficient media. Nitrate reductase activity was lower in the *adc1* line and slightly changed in 7.2 line compared to WT in C medium, while in low N medium, its activity decayed in WT and *adc1*, but it maintained its level in 7.2. Ammonium and nitrate levels were reduced in low N respect to C at a comparable rate in all lines, but the decay was less pronounced in 7.2. The amino acids glutamate, glutamine, arginine, proline, and GABA were higher in C respect to low N media in the three studied lines. However, *adc1* showed elevated levels of the five compounds respect to WT in C, but all compounds decreased in the mutant line compared to WT in low N media. In 7.2 line, only GABA and glutamate showed higher levels, respect to the WT in C medium. Altogether, these results suggest that N depletion affected PAs or nitrogenated metabolites formation differently in WT, mutant or transgenic plants, highlighting the importance of N intermediates flux through the major network of nitrogen-metabolizing pathways in plants under N deficiency.

PL-P37

INTERACTION BETWEEN *PSEUDOMONAS STUTZERI* MJL19 AND SOYBEAN PLANTS IN SALINE STRESS

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Root surrounding is a highly complex ecosystem influenced by roots secretions and by microbial activity in the soil. During colonization and adaptation to life in the rhizosphere, bacteria modify gene expression affecting metabolism, mobility, chemotaxis, EPS synthesis, and secretion. The interaction of the bacterium *Pseudomonas stutzeri* MJL19 with soybean root was studied by RT-qPCR transcriptional analysis of genes potentially related to colonization and abiotic stress response. We analyzed the expression of genes involved in root colonization (*algA*, *bcsA*, *oprF*, *clpP*, *bcsA*, *putA*, and *putP*) and genes coding for chaperones responsible for the proper folding of stress-damaged proteins, superoxide dismutase and production of protective osmolites (i.e., *dnaJ*, *proC*, and *sodC*). We found higher expression of *clpP*, *oprF*, *algA*, *bcsA*, *putA*, and *putP* when MJL19 was attached to soybean root in saline conditions compared with MJL19 growing in the absence of the plant. In the case of *clpP* and *oprF*, the difference in root expression was about 5-fold greater in the saline condition with respect to the non-saline one. In contrast, NaCl in the absence of soybean roots did not generate significant changes in the expressions. The expression of genes related to abiotic stress, *dnaJ* and *proC*, showed greater expression in populations of MJL19 attached to the soybean root in saline stress, meanwhile *sodC* decreased its expression under this condition. In *P. stutzeri* MJL19 genes related to colonization and formation of biofilms such as *oprF*, *clpP*, *algA*, and *bcsA* are expressed in the presence of soybeans roots exposed to saline stress, indicating that the bacterium is prone to grow as a biofilm when it is in the presence of the soybean root. Expression of the gene involved in the proline biosynthesis (*proC*) and expression of the chaperone DnaJ (*dnaJ*) are low when MJL19 is in the presence of soybean in non-saline conditions. However, when MJL19 is in contact with soybean roots in saline conditions, the expression of both genes is substantially enhanced.