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treated mutants. *AtCuAOδ* over-expressing plants showed an increase in stomatal closure level along with a detectable H_2O_2 production in guard cells under normal growth conditions. These data suggest that AtCuAOδ may play a role as H_2O_2 source in ABA-induced stomatal closure.

P6.6
Population traits shape the elevation effect on non-structural carbohydrates (NSC) and flavonoids of *Vaccinium myrtillus* stands in Alpine tundra

V. Casolo, F. Boscutti, E. Petrussa, A. Filippi, E. Buffon, M. Zancani, E. Braidot

Environmental stressors induce plants to acclimate by both morphological and physiological modifications. Along an elevation gradient (as a proxy for temperature stress), we demonstrated that changes of two ecophysiological stress indicators (NSC in underground stems and leaf flavonoids) of *Vaccinium myrtillus* were affected not only by altitude, which, in some cases, acts as secondary player. In particular, plant traits (age, width of xylem rings, length of stem shoot) of the populations and interspecific competition (shrub density) can shape the effect of elevation. Glucose content was positively correlated with altitude, but negatively with competition. Instead, sucrose decreased at high altitude and in older populations. Starch content increased along with ring width and decreased with high shrub density. Flavonoid content was mainly related to elevation and plant trait of the population. NSC and flavonoids exhibit different patterns with respect to elevation and plant traits. In conclusion, we suggest that bulk NSC can not be considered as indicators of stress and that plant traits would represent modulators of species response.

P6.7
Expression Analysis of Stress-Related genes involved in the response of Durum wheat to salinity and high light

L. F. Ciarmiello, P. Woodrow, A. Mirto, F. Conte, V. S. De Lucia, E. Dell'Aversana, L. D'Amelia, L. De Simone, A. Fuggi, P. Carillo
Dipartimento di Scienze e Tecnologie Ambientali Biologiche e Farmaceutiche (DISTABIF)- Seconda Università degli Studi di Napoli (SUN)- Caserta, Italia

The study of stress-related genes is critical to understand the molecular mechanisms of stress tolerance in plants. Several studies have demonstrated the important role of asparagine synthetase, glutamate decarboxylase and Δ^1-pyrroline-5-carboxylate synthase genes signalling in response to environmental stresses. In order to investigate the expression changes of these genes in durum wheat under salinity and high light, a semi-quantitative RT-PCR analysis was performed. High light increased the gene expression level of *TdAsn1* alone (2.6 fold) and in combination with salinity (2 fold) in comparison with the control at low light. The isoforms *TdAsn2* was expressed at low levels compared to *TdAsn1* and the transcript was present only in leaves in control conditions or simultaneous stresses . A trend similar to that of *TdAsn1* was observed for *P5CS* expression. On the contrary, *GAD* expression was decreased by salinity and high light (1.1 and 1.5-fold, respectively) and even more under the two combined stresses (3.7 fold) compared to control. The expression levels were compared to the respective enzymatic activities. Our expression data confirmed the pivotal role of the studied genes in the response to abiotic stresses in *durum wheat.*

P6.8
Metabolic engineering of the phenylpropanoid pathway in *S. lycopersicum* using CRISPR/Cas9 mediated genome editing

F. D'Orso[1,2], T. Lawrenson[1], W. Harwood[1], Y. Zhang[1], J. Li[1], L. Tomlinson[3], G. Morelli[2], C. Martin[1]
[1]John Innes Centre, Norwich Research Park, Colney, Norwich, UK, [2]Food and Nutrition Research Centre, Council for Agricultural Research and Economics, Rome, Italy, [3]The Sainsbury Laboratory, Norwich Research Park, Norwich, UK

CRISPR/Cas9 system is a powerful tool enabling efficient and precise genome editing in many organisms and with many applications in several fields, including metabolic engineering. In plants one of the most important secondary metabolic pathways is the phenylpropanoid pathway that produces many nutraceutical compounds. To modify this pathway, we edited the *SlHQT* gene involved in the biosynthesis of caffeoylquinic acids (CQAs), the most abundant polyphenols in many plant species. We induced mutagenesis of the *SlHQT* gene at two different positions directing the cas9 cut in the *SlHQT* genomic sequence. Undertaking full genotypic analysis of a large number of T0 transformed tomato plants, we observed a very high mutation frequency but also considerable variability in terms of the number of alleles and types of mutations in any one plant; this variability correlated very well with the CQA accumulation. Here we show that the CRISPR/cas9 system can be used successfully for metabolic engineering of the phenylpropanoid pathway affecting the caffeoylquinic acid biosynthesis and possibly altering the production of other phenolic compounds with pontential impacts on nutritional value.

P6.9
Subcellular localization analyses of a *Hordeum vulgare* P2-G6PDH isoform by transient expression of reporter fusion proteins

A. De Lillo[1], M.C. Lutterbey[2], H. Lansing[2], A. von Schaewen[2], V. Paradisone[1], S. Esposito[1]
[1]Dept. of Biology – University of Napoli "Federico II" – Naples, (Italy), [2]Institute for Plant Biology and Biotechnology (IBBP) - Münster, (Germany)

In plants different glucose 6-phosphate dehydrogenases (G6PDH) exist. Among them, plastidic P2 isoforms are considered an essential source of NADPH in heterotrophic plastids. Barley P2-G6PDH displays an unusually long plastidic transit peptide (>95aa), considering these sequences generally comprise less than 60aa. We investigated the subcellular localization of *Hv*P2-G6PDH reporter fusions in Arabidopsis protoplasts and tobacco leaves; specifically, whether this protein may be directed to heterotrophic plastids only, or to other compartments as well. The results obtained in protoplasts suggest that *Hv*P2-G6PDH with GFP fused to the C-terminus may localize to chloroplasts. However, upon Agrobacterium infiltration, the fusion protein was detected in heterotrophic plastids of the epidermis and in the cytosol of mesophyll cells. Interestingly, with GFP fused to the N-terminus, the fusion protein partially co-localised with peroxisomes, indicating presence of a peroxisomal targeting signal. Moreover, initial co-expression experiments suggest interaction with inactive *Hv*P0-G6PDH. Further studies are needed to confirm the P2-P0 interaction, and to specify localization of the heterodimers.

P6.10
Transgenerational responses to nitrogen deprivation in *Arabidopsis thaliana*

M. Massaro[1], L. Zanin[1], N. Tomasi[1], E. De Paoli[1], M. Morgante[1,2], R. Pinton[1]
[1]Dept Agricultural, Food, Environmental and Animal Sciences, University of Udine, Udine, Italy, [2]Istituto di Genomica Applicata, Udine, Italy

Nitrogen deprivation represents one of the major stresses to which plants are exposed. As plants respond to this stress, it would be profitable to retain a *memory* of the response to prime following generations. Therefore, an experimental setup considering successive generations of control or stressed *Arabidopsis* plants was used to evaluate the establishment of a transgenerational memory of N-deficiency stress response. Results demonstrated a faster induction of a high nitrate uptake capability as a result of multigenerational stress exposures. This behaviour was paralleled by changes in the expression of nitrate responsive genes. Transcriptional analyses revealed an enduring modulation of genes in downstream generations, despite the lack of stress stimulus in these plants. Using genome-wide detection of DNA methylation we could