

## RESUMOS DOS POSTERS

<p><b>P1. Expression of allergens in <i>Betula pendula</i> pollen under atmospheric pollution influence</b></p>	<p><b>P2. Unravelling the importance of FLA5 (Fasciclin-like Arabinogalactan Protein 5) in Arabidopsis reproduction</b></p>
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<p>Previous work showed an increase in allergen reactivity with patient sera in pollen exposed to different pollutants. <i>Betula pendula</i> pollen, exposed to atmospheric pollutants, was used to determine changes in intracellular accumulation and in the transcription of two major allergens, Bet v 1, a pathogenesis-related protein member of PR-10 family, and Bet v 2, a major pollen allergen, profilin. Allergens were located in pollen by immunofluorescence microscopy and transmission electron microscopy and labelling was most abundant in the cytoplasm and external wall. Differential gene expression was ascertained by Real-Time Quantitative Reverse Transcription PCR. These changes were observed after exposing the pollen to a controlled atmosphere in an environmental chamber system enriched with various levels of nitrogen dioxide (NO<sub>2</sub>) and ozone (O<sub>3</sub>, which are two of the most abundant aerosol pollutants in industrialized countries. Preliminary results suggest a possible influence of pollutants, particularly of ozone. The interaction between pollen allergens and gaseous pollutants seem to lead towards an increase in pollen's allergenic potential.</p>	<p>The fasciclin-like arabinogalactan proteins (FLAs) are a subclass of 21 members that belong to the arabinogalactan protein (AGP) family in Arabidopsis thaliana. FLAs are a heterogeneous group characterized by having one or two fasciclin-like domains and one or two AGP-like glycosylated regions in their polypeptide core. They are widely distributed in various cells and tissues and are implicated in plant growth and development, yet only few FLA genes in Arabidopsis have been identified and functionally characterized. This study is focused on fasciclin-like arabinogalactan protein 5 (FLA5). FLA5 has 2 PRO-rich domains flanking a fasciclin domain and a glycosylphosphatidylinositol (GPI) anchor. FLA5 is a target of the transcription factor SEEDSTICK, which regulates the development of the ovule and the seed. Since seeds are essential units for plant propagation and the first step in their development is the formation of ovules, it is very important to study the genes involved in the reproductive process. Therefore, to increase our knowledge about the role of FLA5, the objective of the present work was to study a fla5 RNA interference knock-down line and access its localization by GFP/GUS promoter analysis.</p>

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<p><b>P3. Characterisation of <i>Solanum lycopersicum</i> L. type 2 metallothioneins-encoding gene subfamily expression</b></p>	<p><b>P4. Morphological and physiological responses of strawberry to a biostimulant and calcium application</b></p>
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<p>Some heavy metals are highly reactive and consequently can be toxic to living cells when present at high levels. Metallothioneins (MT) are small cysteine-rich metal chelators proteins that participate in the transport, sequestration and homeostasis of metals. In plants, there are four MT types: 1; 2; 3 and 4, which differ in their Cys-residues distribution and preferred expression profiles. This study aimed to analyze the MT2 subfamily gene expression in <i>Solanum lycopersicum</i> L. in shoots and roots of plants grown exposed to different zinc and chromium concentrations (Zn treatment 1: 0.87 mM Zn for 4 weeks; Zn treatment 2: 0.87 mM Zn for the first 3 weeks, and then to 3.5 mM for one week; Zn treatment 3: 3.5 mM Zn for one week after 3 weeks of no high Zn treatment (T3 treatment; Cr treatment 1: 2.5 µM for 5 weeks; Cr treatment 2: 5 µM for 5 weeks). Based on the NCBI database, five MT2-encoding cDNA sequences were retrieved: MT2a, MT2b, MT2c, MT2d and MT2e and specific primer pairs were designed. Specificity of the designed primers was firstly tested using genomic DNA. MT2a-amplified sequences were sequenced and locally compared to those retrieved from NCBI confirming the specificity of the design primers for MT2a. MT2b, c, d and e will be sequenced in further steps. By comparing the expected sizes of the amplicons with the sizes obtained using genomic DNA in PCRs, it was possible to confirm that the amplified MT2a and MT2b sequences possess no introns while MT2c, MT2d, and MT2e have a higher number of base pairs than expected, proving the presence of introns. Specific RT-PCRs were then performed to verify the expression of the different MT2 family members genes in response to Zn or Cr exposure. Results showed that, in the zinc assays, MT2a, MT2b, MT2d and MT2e increased their expression with the increase in Zn concentration supplied; all MT2 subtypes raised their expression levels in all Cr assays. The obtained results prove the relationship between heavy metal stress and metallothioneins.</p>	<p>The use of biostimulants in agriculture has been growing in recent years due to increased demand for commercial products based on natural substances that enhance crop productivity and quality. Given the high cost of biostimulants it is of great importance to carry out studies in order to validate their positive effect at plant level and to optimize their application. Also calcium (Ca) is often applied to fruit crops during fruit development to increase postharvest fruit quality. This nutrient has been related to fruit firmness by strengthening the cell wall, which, in turn, improves shelf life. Through an integrated approach, where morphological, physical and nutritional parameters were evaluated, this work aimed to analyse the effect of a commercial seaweed-derived biostimulant (applied every 15 days via fertigation at a dose of 3.0 l/ha) and calcium (applied every seven days at a dose of 5 kg/ha<sup>-1</sup>) on yield and quality of four strawberry cultivars (cv. San Andreas, cv. Charlotte, cv. Portola and cv. Diamante) grown in soil under protected cultivation. In general, the application of biostimulant and calcium proved to be more effective in cv. Charlotte and cv. Portola resulting in higher cumulative productivity. The highest productivity found upon application of biostimulant was observed in Charlotte cultivar with a 33% increase compared to the control treatment. Although cv. San Andreas was the cultivar with the highest value of accumulated productivity during the total production cycle, taking into account the number of weeks in production, it was observed that cv. Portola showed the highest weekly production averages. As regards to the fruit firmness, there was no significant effect of biostimulant or calcium application, but significant differences were found between cultivars (with cv. Portola having fruits 55% more firm than the softer cultivar cv. Charlotte). The SPAD values showed a statistically significant effect of the plant nutrition as well as significant differences among cultivars. Plants that received biostimulant had a 9% higher chlorophyll content as compared to the control ones and the cvs. San Andreas showed a SPAD value up to 9% higher as compared to the other studied cultivars. Also in relation to the photosynthetic efficiency, cv. Portola had approximately 7% higher values, when compared with Charlotte, the cultivar with the lowest efficiency. This study shows the strong impact of biostimulants on strawberry productivity, but its extent depends on the cultivar. Higher photosynthetic activity as a result of higher chlorophyll content partly explains this effect. Fruit firmness seems to be more closely related to cultivar rather than by the biostimulant or calcium application.</p>