ShT-05.4-1
Developing insect sex pheromone production in plants with the support of transcriptomic data

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Use of insect sex pheromones has become an important part of integrated pest management in agriculture as they provide a species-specific control of insect pests and contribute to reduction in conventional insecticide use. Despite of the great potential, their widespread use is still limited due to unsustainable and not cost-effective manufacturing by chemical synthesis. A green alternative, biomanufacturing in plants, is a goal of the SUPSHIRE project, which aims to upgrade the current proof-of-concept pheromone producing plant lines, called the SexyPlants, which successfully synthetize moth (Lepidoptera) pheromones. Our goals are twofold: to improve the plant chassis by removing molecular bottlenecks that cause growth penalty in lines with high pheromone yields and to develop new biosynthetic pathways, enabling synthesis of unique and chemically complex monoterpenoid pheromones of insects from the Coccoidea family. So far, we have used transcriptomic data to identify differentially expressed genes between the high and low producing SexyPlants, which where visualised in the MapMan tool and used for gene set enrichments analysis. This enabled us to pinpoint the cellular processes that are most affected by higher pheromone production, e.g. gibberellin synthesis. We are now working on network analysis to more specifically identify key molecular pathways and genes that lead to growth arrest. To develop the new biosynthetic pathway for production of Coccoidea pheromones, we have generated RNA-seq expression data from citrus mealybug (*Planoccoccus citri*) and combined it with functional predictions of contigs in the prepared *de novo* transcriptome assembly to extract candidate genes responsible for key conversions in the sex pheromone synthesis. Genes with confirmed desired enzymatic activity are used as baits in coexpression network analysis to find the full synthetic pathway that could be implemented in the plant chassis.

ShT-05.4-2
Investigation of the antioxidant effects of glycyrrhizin-containing nanoemulsion formulations in streptozotocin-induced diabetic rats

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Diabetes Mellitus (DM), which has a prevalence and high mortality rate worldwide, is a chronic and metabolic disease. Interest in natural antidiabetic compounds is increasing due to the adverse effects of oral hypoglycemic agents used in the treatment of type 2 diabetes. It is known that glycyrrhizin, one of the main components of licorice root, has a potential therapeutic effect in the treatment of diabetes. The aim of this study is to investigate the antioxidant effects of nanoemulsion formulations (NE) containing GLY (GLY-NE) in streptozotocin (STZ)-induced diabetic rats. Sixty rats were divided into 12 groups with 5 rats in each group (control groups and experimental groups). To induce the diabetic model in rats, 40 mg/kg (single dose) of STZ solution in freshly prepared citrate buffer (0.1 M, pH 4.5) kept on ice was administered intraperitoneally to fasted rats. 72 hours after STZ treatment, the blood glucose levels of the rats were measured, with a range of above 200 mg/dL considered diabetic. GLY-NE or pure GLY at different doses (10, 20 and 40 mg/kg b.w.) was administered orally to diabetic rats for 21 days. At the end of the experiment, alanine aminotransferase (ALT) and aspartate aminotransferase (AST) levels were measured in the serum samples of the rats. Superoxide dismutase (SOD) activity, glutathione (GSH) and malondialdehyde (MDA) levels were determined in liver tissues of the rats. It was determined a significant decrease in serum glucose, AST and ALT levels in diabetic rats treated with GLY-NE ($P < 0.05$). Besides, SOD activity and GSH levels increased, while MDA levels decreased in diabetic rats treated with GLY-NE compared to the control group ($P < 0.05$). As a result, GLY-NE has been effective in reducing oxidative stress seen in diabetes, thus the use of GLY-NE in the treatment of diabetes may be a potential and beneficial approach. This study was supported by Ataturk University (Project number: TDK-2019-7211).

Tuesday 6 July
9:00–11:00, Marmorna Hall B

Immunotherapy

S-06.1-1
The role of the gut microbiota in drug response and toxicity

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Individuals vary widely in their drug responses, which can be dangerous and expensive due to significant treatment delays and adverse effects. Growing evidence implicates the gut microbiome in this variability, however the molecular mechanisms remain mostly unknown. Using antiviral nucleoside analogues and clonazepam as examples, we recently reported experimental and computational approaches to separate host and gut microbiota contributions to drug metabolism and toxicity. The resulting pharmacokinetic models identified measurable physiological, microbial and chemical parameters that dictate host and microbiome contributions to the metabolism of xenobiotics. To systematically map the drug metabolizing capacity of the gut microbiota and assess its potential contribution to drug metabolism, we further measured the ability of 76 diverse human gut bacteria to metabolize each of 271 oral drugs. We found that two thirds of these drugs are chemically modified by at least one of the tested microbes. Through combination of high-throughput bacterial genetics with mass spectrometry, we systematically