



Mining the alfalfa genome for diterpenoid-related genes

Diterpenoids are a class of small, specialized molecules which help the plants to communicate with their environment and to deal with challenging conditions. In other crops, like corn and switchgrass, it has been shown that diterpenoids are for example produced under drought stress and to communicate with the plants' microbiome. While alfalfa (*Medicago sativa*) is an important crop for regenerative agriculture, the occurrence of diterpenoids in alfalfa is still unexplored. Eventually the knowledge about diterpenoid synthesis and function will allow us to modify terpenoid networks towards engineering of future-proof alfalfa lines and a sustainable crop production.

In this project, you will mine the recently released alfalfa genome for genes that encode for diterpene synthases and make predictions about their functionality by visualizing publicly available gene expression data.



Methods:

Mining, analysis and visualization of genomic and transcriptomic data

Further reading:

Tiedge *et al.* (2022). Comparative transcriptomics and metabolomics reveal specialized metabolite drought stress responses in switchgrass (*Panicum virgatum* L.). *New Phytol*, doi: [10.1111/nph.18443](https://doi.org/10.1111/nph.18443)

Medina *et al.* (2021). Pan-transcriptome identifying master genes and regulation network in response to drought and salt stresses in Alfalfa (*Medicago sativa* L.). *Sci Rep*, doi: [10.1038/s41598-021-96712-x](https://doi.org/10.1038/s41598-021-96712-x)

Staff member: Kira Tiedge
Daily supervisor: Kira Tiedge
Expertise group: GREEN

Contact: k.j.tiedge@rug.nl
Contact: k.j.tiedge@rug.nl

Type of project: Bioinformatics Fieldwork Laboratory Theoretical Data analysis
MSc program: Biology Ecology and Evolution Marine Biology
 Biomedical Sciences Behavioural and Cognitive Neurosciences
ECTS: 30 40 **Language:** Dutch English

Start date: Flexible

Location: Linnaeusborg and remotely