

Using gas chromatography and mass spectrometry (GC-MS) for the detection of drought stress effects on the metabolome of *Solanum tuberosum* varieties

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Introduction

Potato (*Solanum tuberosum* L.) is among the highest-yielding staple crops worldwide, making its resilience to abiotic stress a critical factor in global food security. Yet, the potato yield is strongly dependent on many abiotic factors. Pressing matters like climate change urge to understand plant stress response to abiotic factors, such as drought. This knowledge will be essential in **breeding more adaptable crop varieties to maintain food security**. Previous studies showed changes in plant stress-related metabolites [1,2].

Materials & Methods

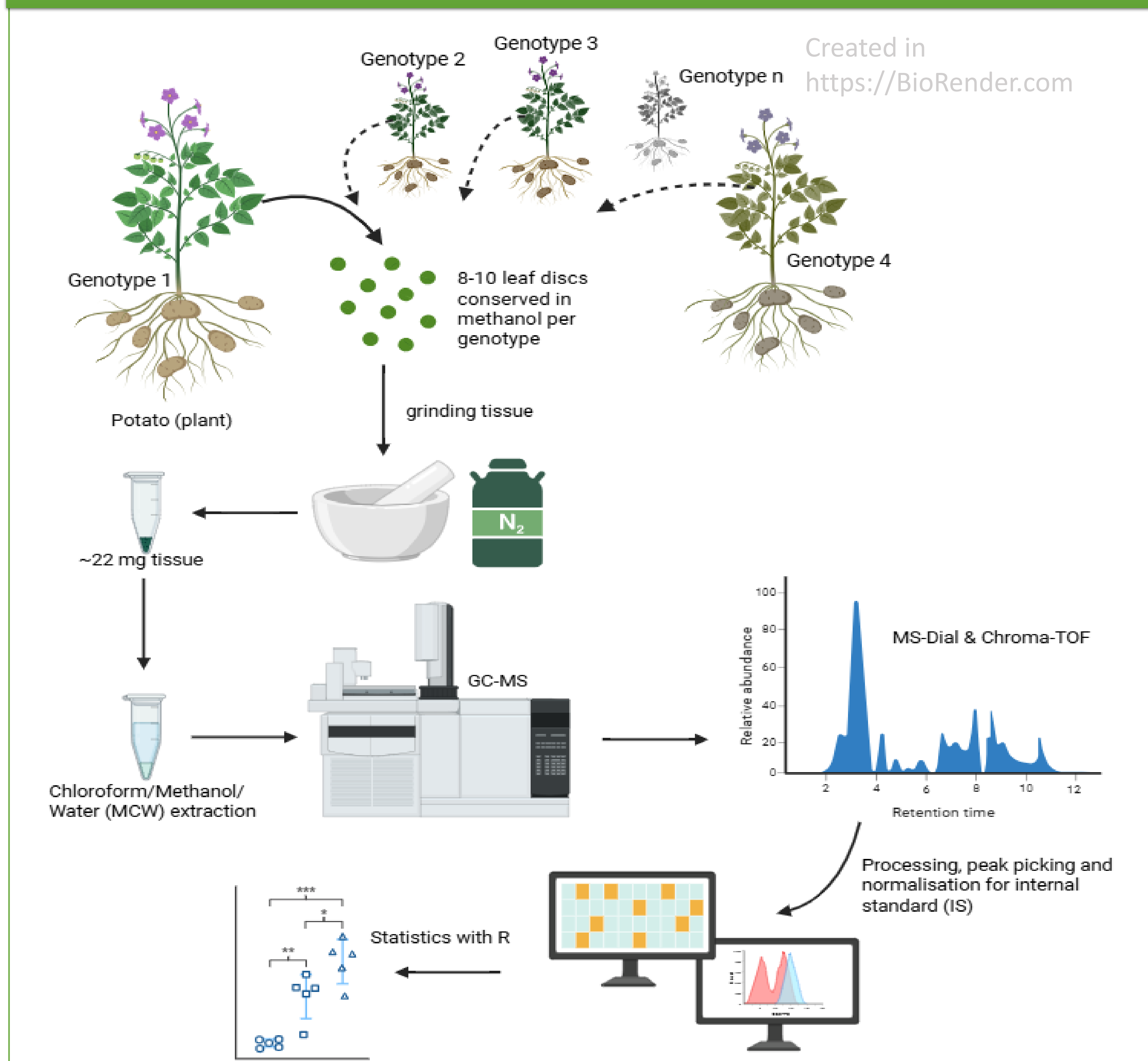


Figure 1: Workflow overview of plant tissue processing for metabolomics using multiple varieties of *Solanum tuberosum*. Field trials were implemented by AGES within the ESKLIEB project, funded by BIOS Science.

Discussion and Outlook

The results of the metabolomic analysis are in line with the physiological data gathered in the field trial. As described before [1,2] the **increase of the sugars** involved in the raffinose synthesis as well as **proline** are strong indicators of drought stress. While amino acids like tyrosine are involved in plant hormone signaling. Drought **decreased almost all the organic acids** during the treatment which have versatile roles in abiotic stress responses. **Comparison of significantly changed metabolites with the spectrometric data** (PolyPen RP 410 & ASD FieldSpec) **shows correlations**, potentially hinting at a metabolite set to detect drought stress. Further comparison between the genotypes will show the genotype that was most insensitive to the drought stress.

Combined with transcriptomics and proteomics data this might give us a more detailed insight into the mechanisms of this genotype to achieve a fast adaption to the drought stress under the specific experimental conditions.

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Results

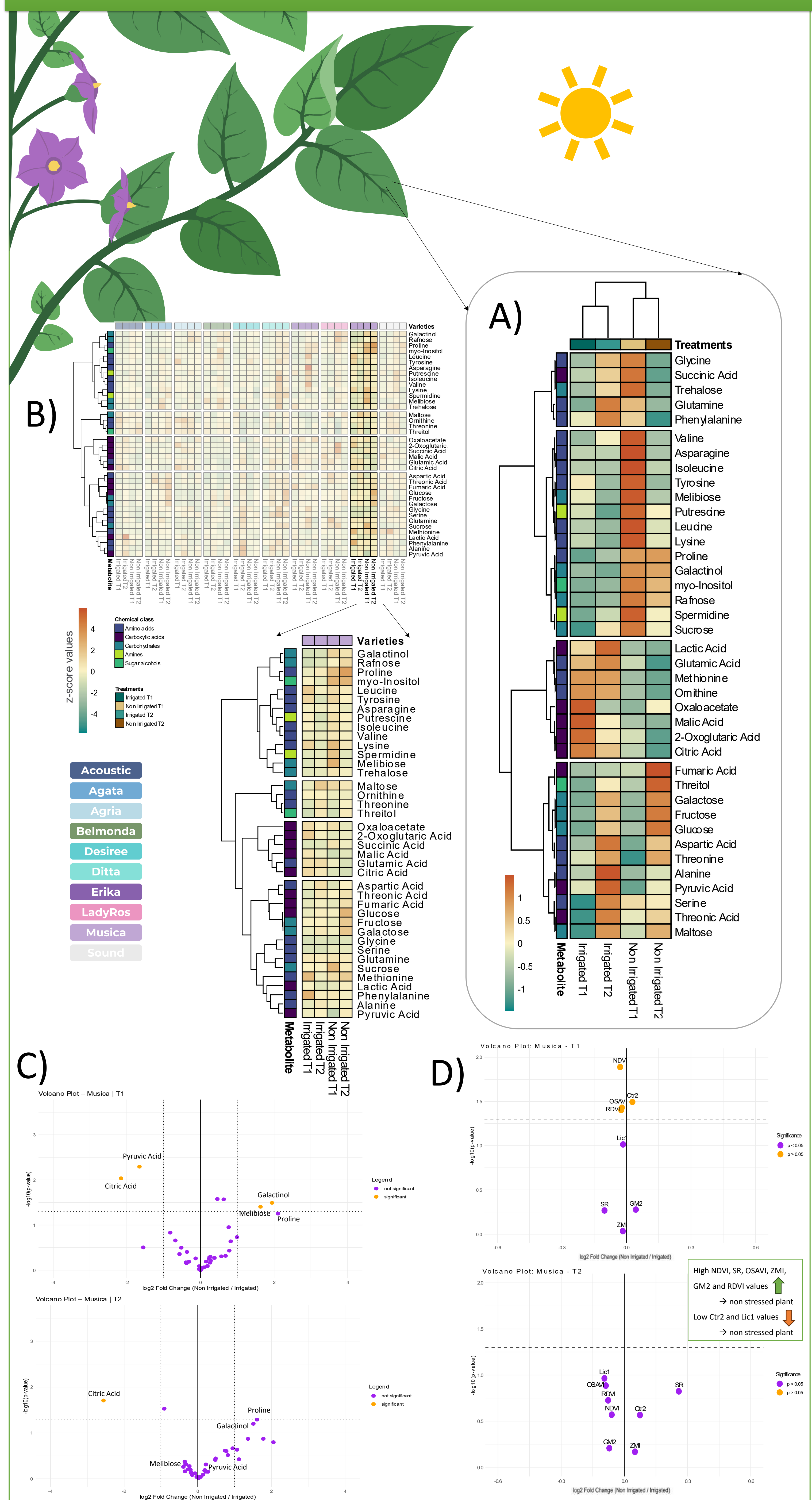


Figure 2: Preliminary analysis after the absolute quantification of the metabolites. A) A clustered heatmap comparing metabolite abundance between the conditions (average of all genotypes) and the two timepoints. B) Heatmap showing genotype dependent changes in metabolite abundance. Highlighted here is the genotype Musica because of its representative changes in metabolites. C) Volcano plots for Musica depict the log₂ fold change of metabolites between the conditions. D) Physiological changes of Musica could also be captured by the PolyPen II data. OSAVI, Lic1, RDVI, NDVI, GM2, ZMI, SR are indices of chlorophyll content.

References

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2. Ghatak, A., Chaturvedi, P., & Weckwerth, W. Metabolomics in plant stress physiology. *Plant genetics and molecular biology*, 187-236 (2018).

