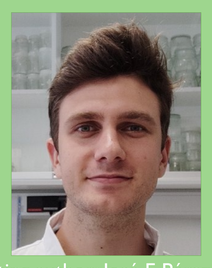
Effect of environmental factors on wild strawberry primary metabolic profile



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Introduction

Climate factors such as temperature and precipitation vary significantly over continental scales, resulting in species differently adapted either genetically or plastically to cope with their local climate. However, climate change will likely alter these biomes, which might lead to changes in the distribution of plants leading to novel patterns of local adaptation and maladaptation. We aim to study how plant traits vary with latitude and in response to different temperature and drought conditions in order to find genetic determinants of climate adaptation. For that purpose, we use the **woodland strawberry** (*Fragaria vesca*) as the model organism. We have analyzed **16 different genotypes** that have been grown in **3 common gardens** located in Belgium (Gontrode), Sweden (Alnarp) and Finland (Ruissalo), in which **drought treatments** were also performed. Here, we present the **chemical analysis** (primary metabolism) in leaves of these genotypes in order to better understand how environmental factors can alter the primary metabolic profiles of *F. vesca* accessions grown in different locations.

Work flow

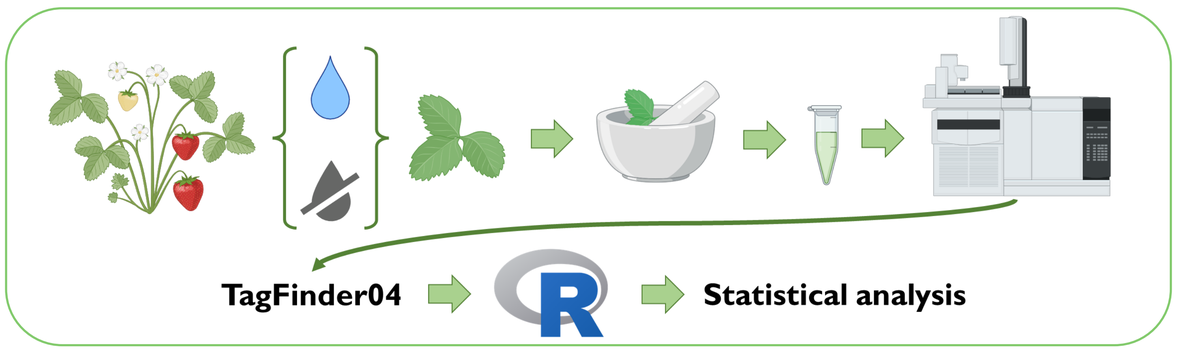

Figure 1. Work flow scheme. *F. vesca* plants are grown under two different conditions (control and drought). Leaves are collected to extract primary metabolites, that are analyzed using GC-MS technique. Lectures are processed using TagFinder04 software. Once obtained results, they are treated using R to perform statistical analysis.

Geolocalization affects primary metabolic profile

Leaf samples from **Belgium**, **Finland** and **Sweden** were taken with the aim of determining their **primary metabolic profiles**. **Metabolomic** assays were performed, and the results were used to carry out **PLS-DA** analysis.

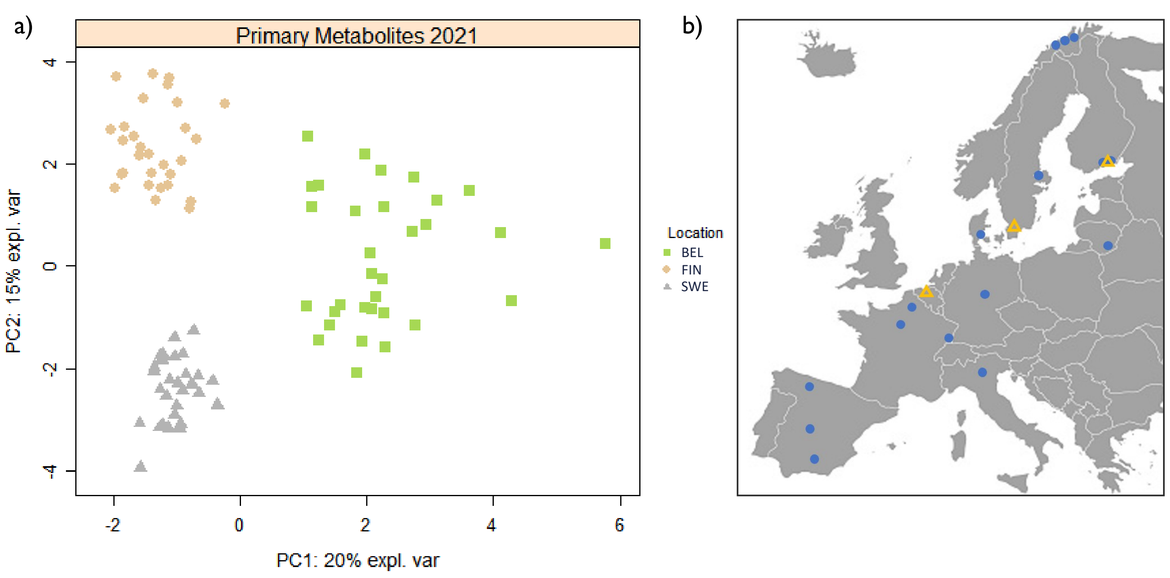

Figure 2. Approach to the whole population. a) Partial least squares discriminant analysis (PLS-DA) scores scatter plot of the primary metabolites analysis identified in the 3 different common gardens populations. There are stablished 3 different clusters attending to the location where plants were grown. b) Origins of the 16 plant genotypes (blue dots) and locations of the 3 common gardens (yellow triangles).

Drought affects primary metabolic profile

According to the previous results, **3 groups** were made based on the **location** where plants were grown. These ones were used to perform **PCA** analysis individually, with the aim of determining those **genotypes** whose variance affects more relevantly to the whole group.

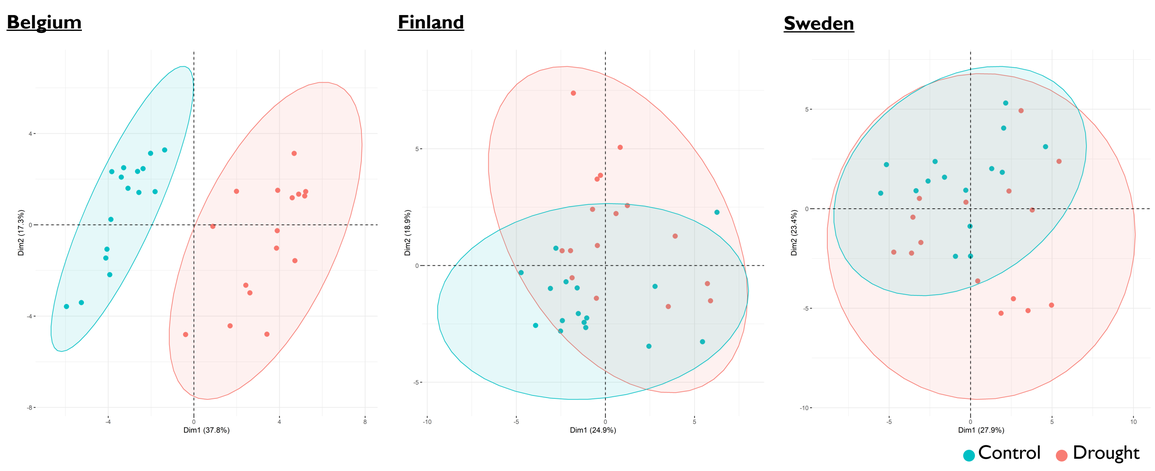

Figure 3. Primary component analysis (PCA) plot of the 2 principal components based on the metabolomic data attending to different individuals.

Relevant differences are found among drought related metabolites levels

Finally, these data were used to plot **heatmaps** with the intention of identifying **significant differences** between **treatments** and **genotypes** among each single location. Special attention is paid for metabolites whose levels change more relevantly in these samples.

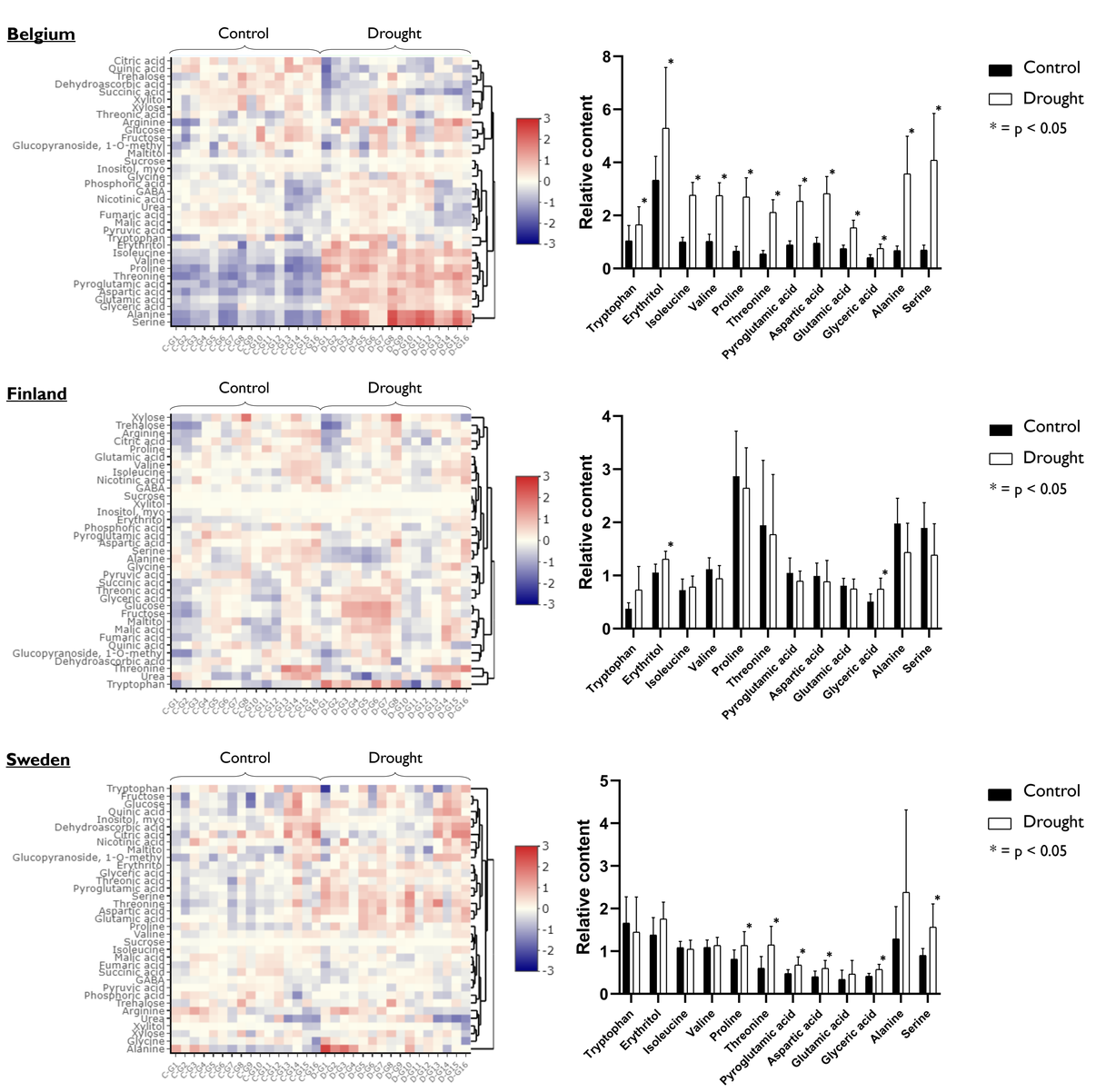

Figure 4. Analysis of the primary metabolic profiles of 2021 harvest from the 3 common gardens. Heatmaps visualizations (left) are shown for each location. Each value represents the normalized (median-centered and $\log_2$-transformed) mean of the 10 biological replicates, with red and blue color denoting relatively high and low intensities. Maximum linkage clustering is used to order metabolites. Bar plot is represented (right) for 12 selected metabolites whose levels are expected to change relevantly when plants are exposed to drought stress. Statistical significance between control and drought samples has been determined using the Holm-Sidak method.

Conclusions

- **PLS-DAs** and **PCAs** analysis evidence that there are significant **differences** not only among **populations**, but between **treatments**.

- There are established **patterns** of primary metabolites expression that are maintained depending on whether we observe plants exposed to **control** conditions or **drought stress**, such as most **amino acids** (valine, proline, threonine…). This situation is much more noticeable in samples from Belgium.

Future perspectives

- Determine **secondary metabolic profiles** of these samples.

- **Repeat** the assay with samples obtained from **different harvests**.

- Use these results to make **conclusions** about how **environmental factors** can **alter** the primary metabolic profiles of *F. vesca*.

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