

Metabolomic responses of a native and nonnative shrub layer species to deer exclosure and herbivory in suburban forests

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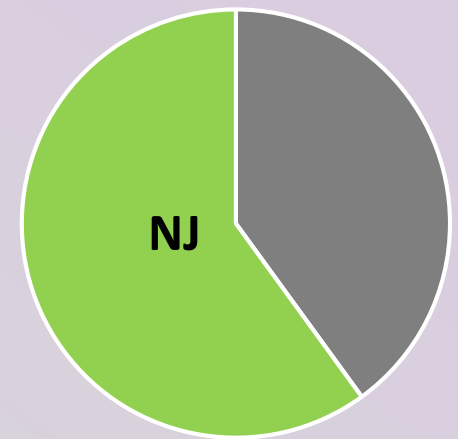
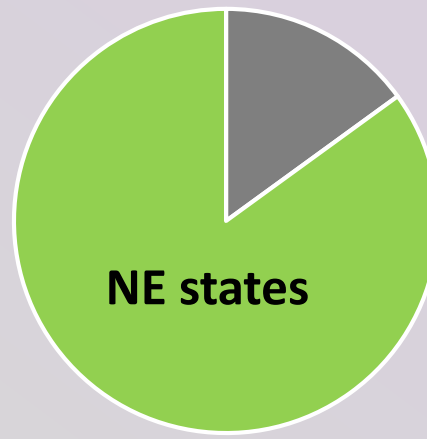
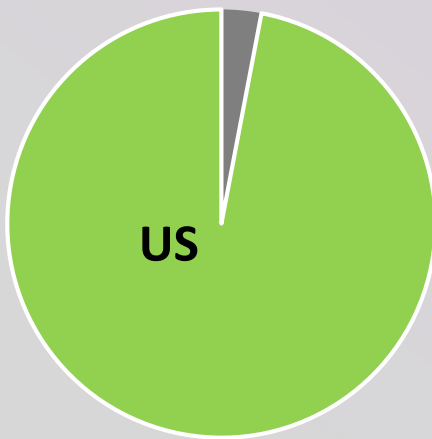


urban/suburban/exurban ecology



urban/suburban/exurban ecology

LAND (2010 US Census data):



■ urban ■ rural

suburban ecology



Charley Harper

overabundant deer



overabundant deer



Princeton, NJ:
45 deer / km²

Hopewell, NJ:
32 deer / km²



overabundant deer

Known consequences for plants of herbivory by deer

For individuals:

- Loss of winter buds
- Loss of flower buds and fruits/seeds
- Loss of foliage
- Death of seedlings
- Variation due to deer food preferences



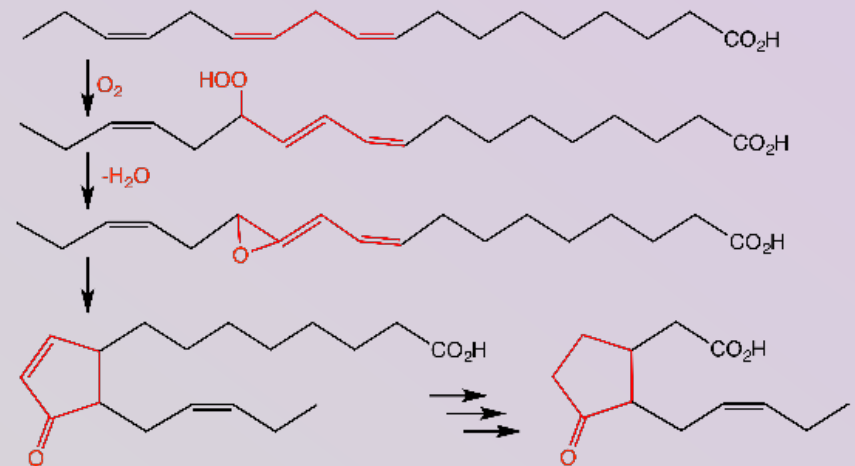
For communities:

- Reduced abundance in the understory vegetation
- Reduced diversity in the understory vegetation
- Shifts in understory community structure and potential for shifts in canopy species

... and consequences for higher trophic levels

overabundant deer

An unknown consequence for plants of chronic herbivory by deer: the metabolomic response



jasmonic acid biosynthesis (Wikimedia Commons)

plant metabolomics

- Plants produce thousands of phytochemicals, or secondary metabolites
- Many act as plant responses to stress and as defenses against herbivores, including
nitrogenous compounds: alkaloids, cyanogenic glycosides, glucosinolates, benzoxazinoids
terpenoids
phenolics
- The functions of many secondary metabolites are unknown
- With metabolomic techniques, we are now able to obtain a profile of the metabolites produced by a plant
- We can design experiments to investigate plants' production of metabolites to compare species, populations, or individuals under differing conditions related to herbivory



eco-metabolomics of woody plants living with chronic deer herbivory

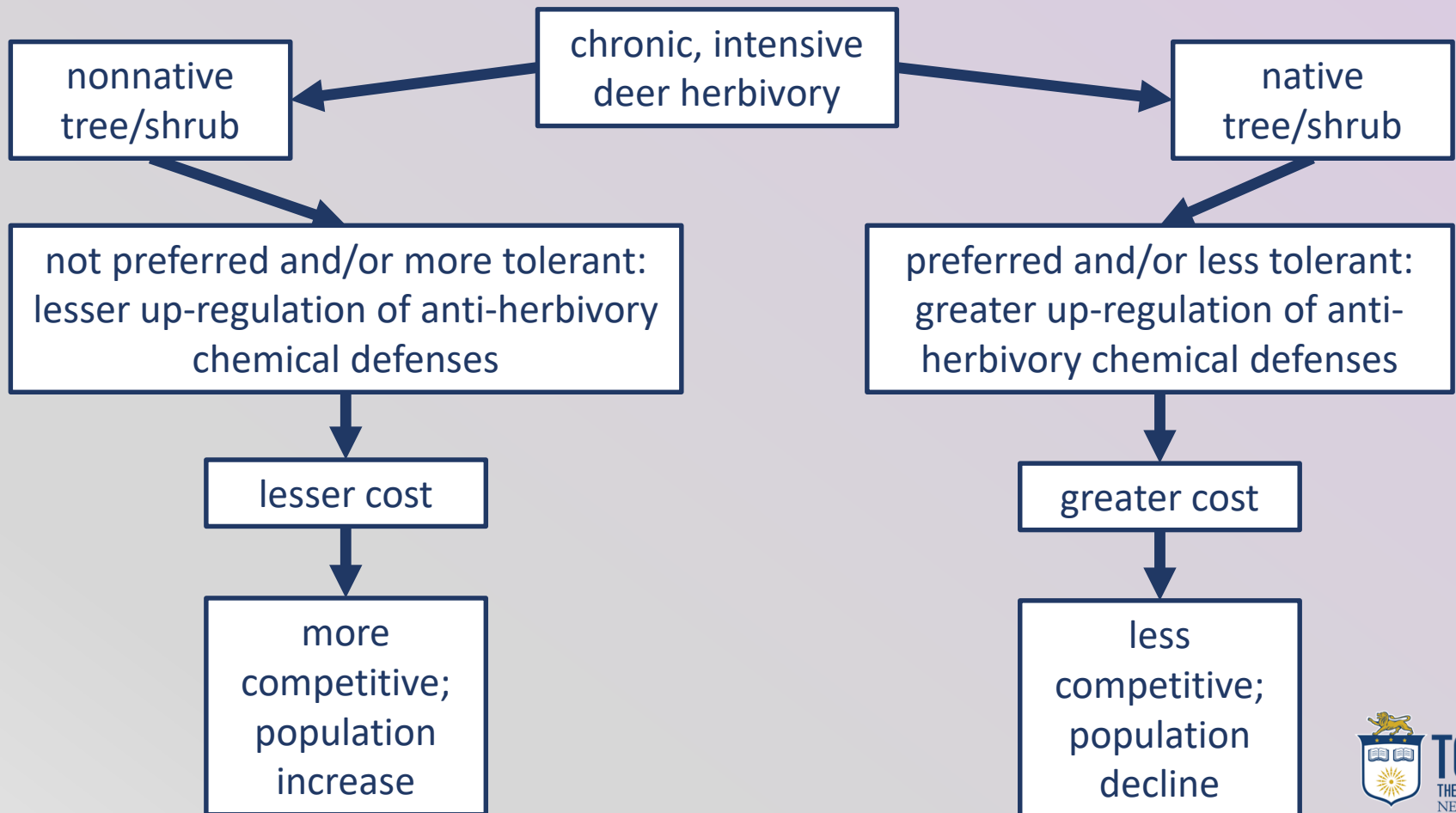
We can investigate the metabolomic profiles of plants under differing ecological conditions in natural communities

Research questions:

- Does exposure to overabundant deer alter woody plants' metabolomic profile?
- If so, does it indicate increased production of anti-herbivore chemical defenses, and which ones?
- Does the response differ among species, especially among native versus nonnative invasive species?

eco-metabolomics of woody plants living with chronic deer herbivory

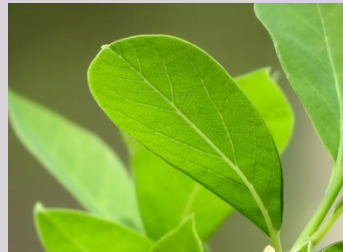
A conceptual model of potential implications for invasion ecology



eco-metabolomics of woody plants living with chronic deer herbivory

Our approach:

- One forest – Herrontown Woods Arboretum, Princeton, NJ
- A deer enclosure experiment:
 - 16 m² plots (37 total), half randomly assigned to a fencing treatment in spring 2013
- Two focal, woody species in a subset of the plots, both fenced and unfenced:
- A native – spicebush (*Lindera benzoin*)
- A non-native invasive – multiflora rose (*Rosa multiflora*)





collecting



- All foliage samples collected 27 July 2018
- From 12 or 14 plots per species
- Alternated fenced and unfenced plots
- Noted presence/absence of recent deer browse on unfenced plants
- Collected from three plants per plot, pooled the tissue
- Placed into liquid N within 30 sec
- Stored at -80 C until shipped to Boyce Thompson Institute on dry ice



extraction



- Ground tissue to fine powder in liquid nitrogen
- Vortex-mixed 100 mg of the powder with cold chloroform:methanol:water (1:2:1) buffer for 20 minutes
- Centrifuged at 15000g for 20 minutes
- Transferred clear supernatant to new tube
- Lyophilized until dry
- Resuspended in 70% methanol (in water, v/v)
- Centrifuged as above; retrieved clean supernatant

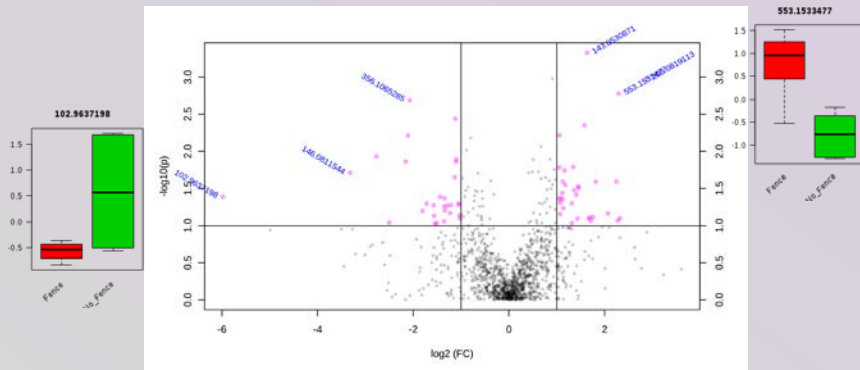


analysis

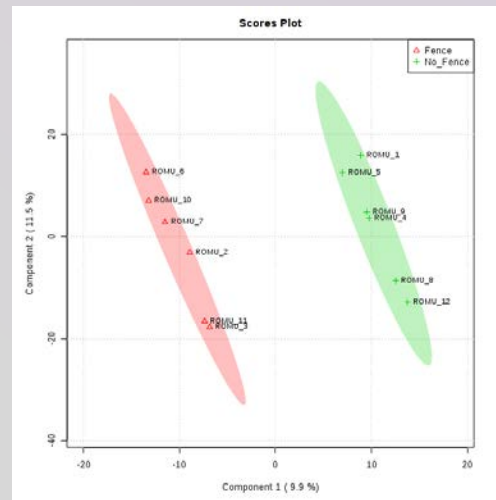
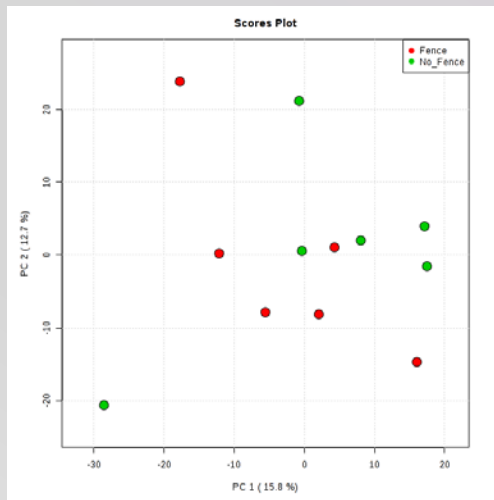


- Used the final supernatant
- Untargeted metabolomic analysis by LC-MS/MS (liquid chromatography mass spectrophotometry)
- Spectral data of ~6000 metabolites were converted to mzXML files and pre-processed using R packages XCMS and CAMERA
- Statistical analyses performed on Metaboanalyst

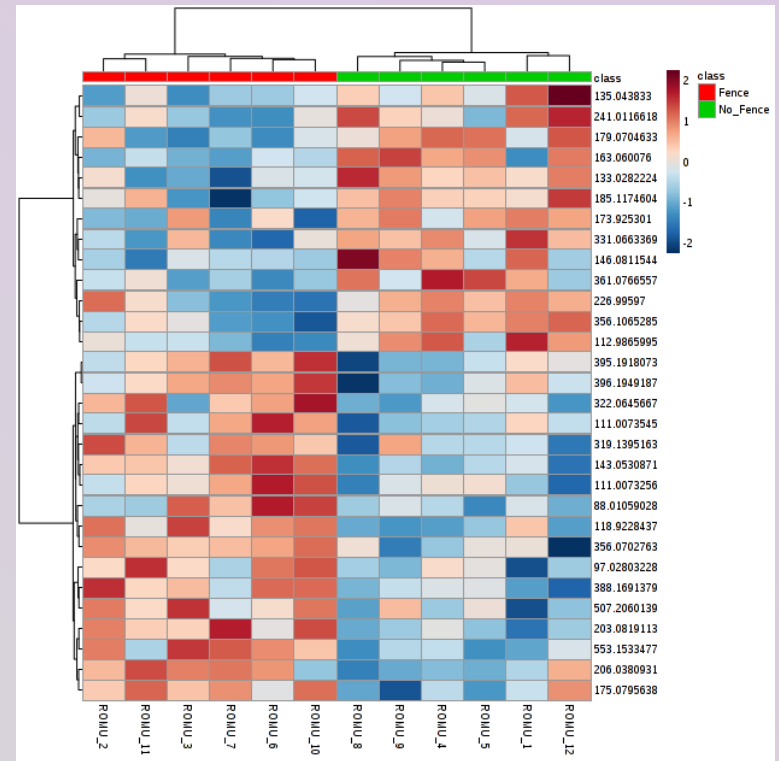
Rosa multiflora: fenced vs. unfenced



Volcano plot compares the metabolites in the two groups and identifies the metabolites that differed significantly and that had a fold change of 2 or more (colored dots)

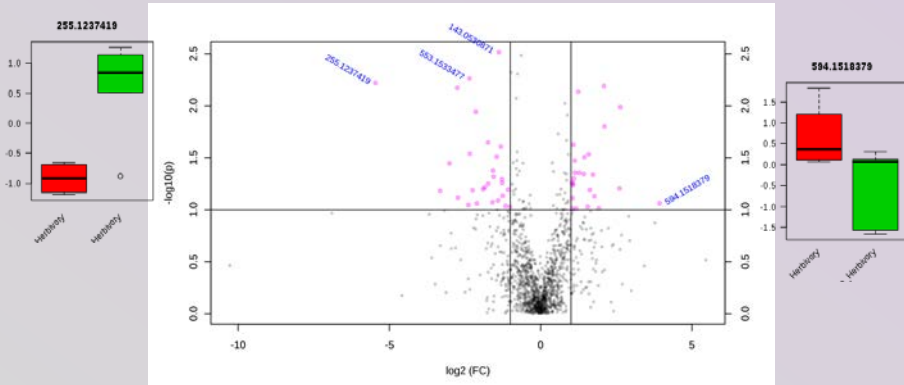


Principal Component Analysis (left) and **Partial Least Squares Discriminant Analysis** (PLS-DA) depict the the relationship among the samples based on all the metabolites. Samples that cluster together on these plots have more similar metabolite profile

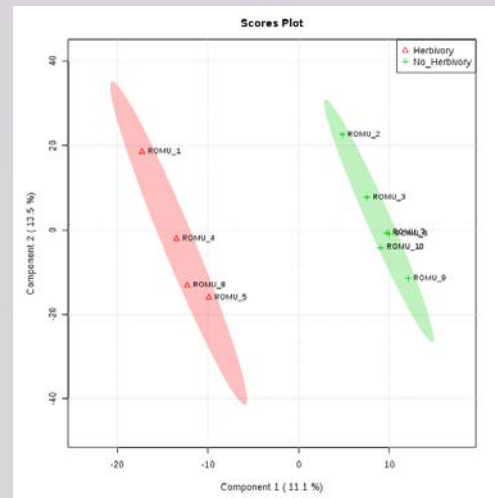
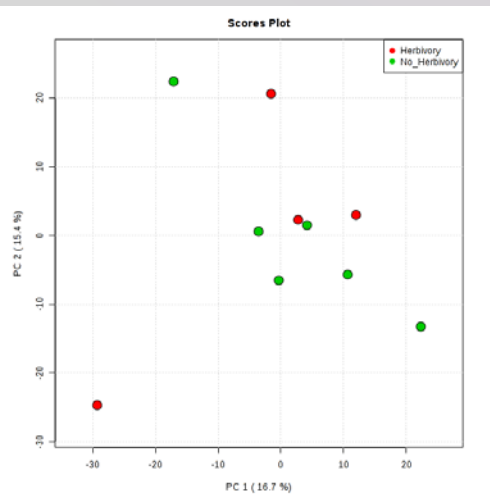


Heat map shows the pattern of accumulation of the top 30 significantly ($P < 0.01$) different metabolites among the samples. Note that, as expected, for each of these metabolites, the pattern observed here seem to agree with the results of the PLS-DA analysis. The numbers on the right are the masses of the metabolites.

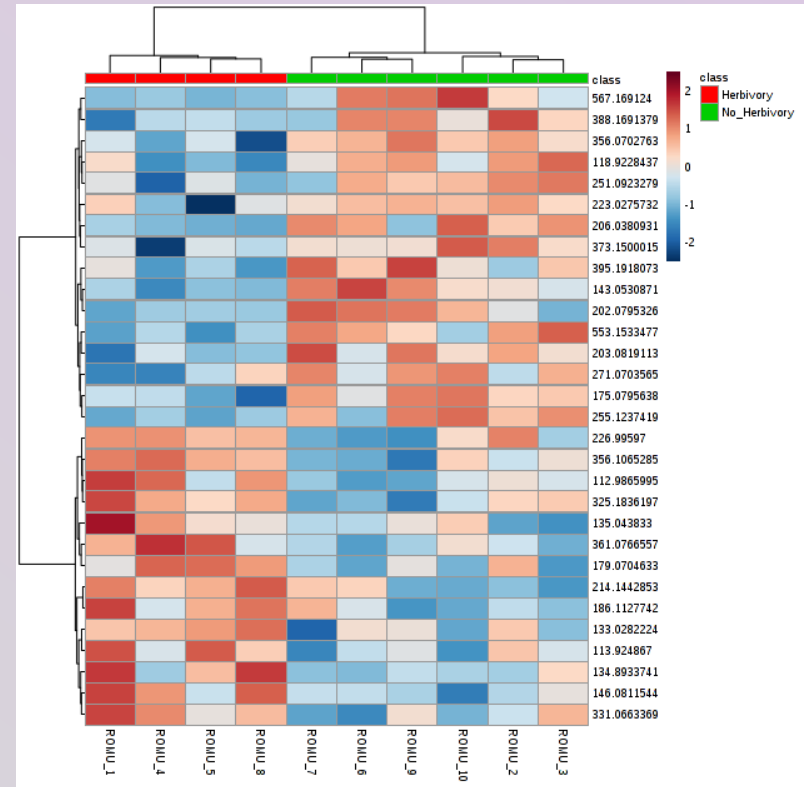
Rosa multiflora: fenced vs. browsed



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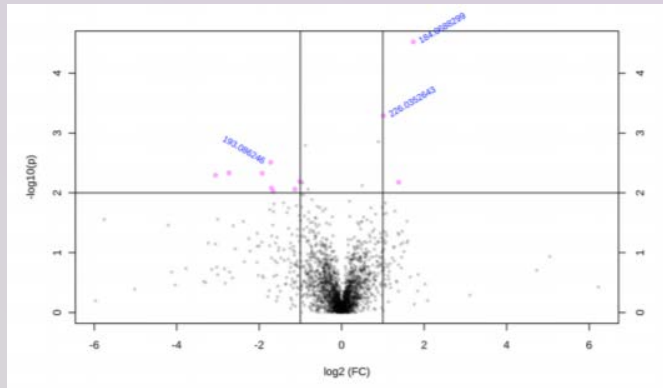


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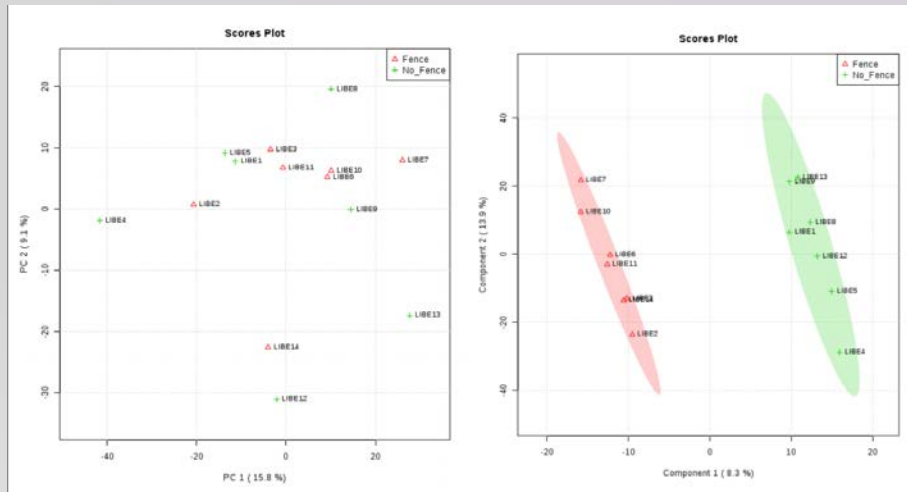


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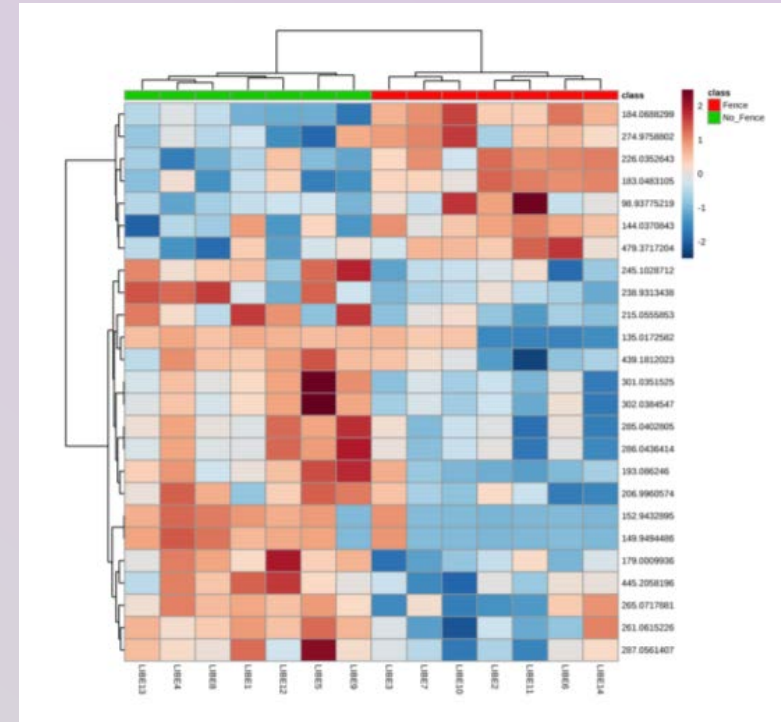
Lindera benzoin: fenced vs. unfenced



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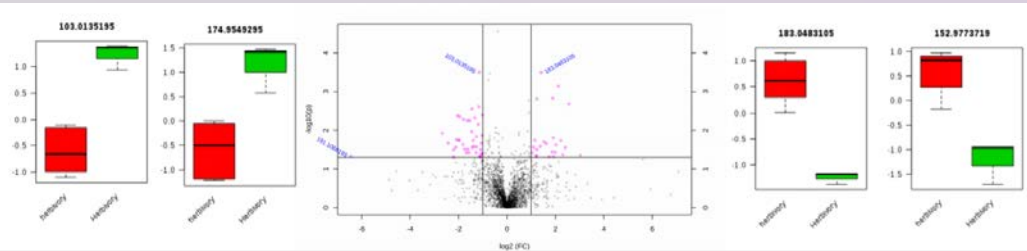


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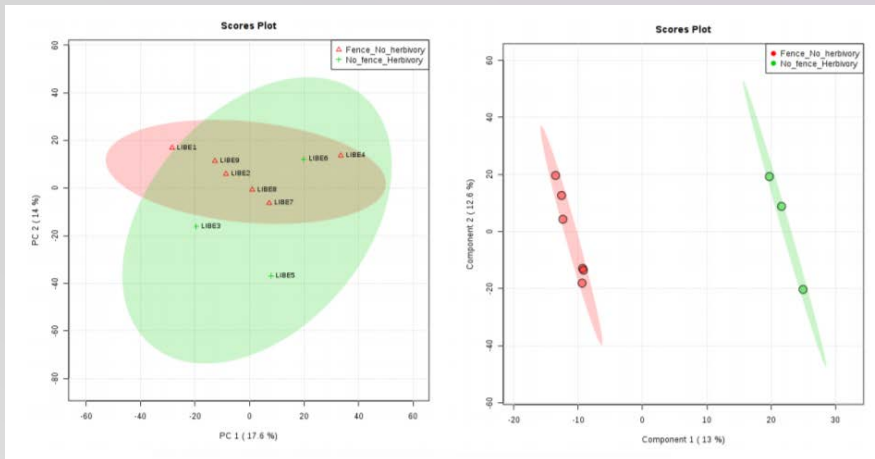


Heat map shows the pattern of accumulation of the top 30 significantly (P < 0.01) different metabolites among the samples. Note that, as expected, for each of these metabolites, the pattern observed here seem to agree with the results of the PLS-DA analysis. The numbers on the right are the masses of the metabolites.

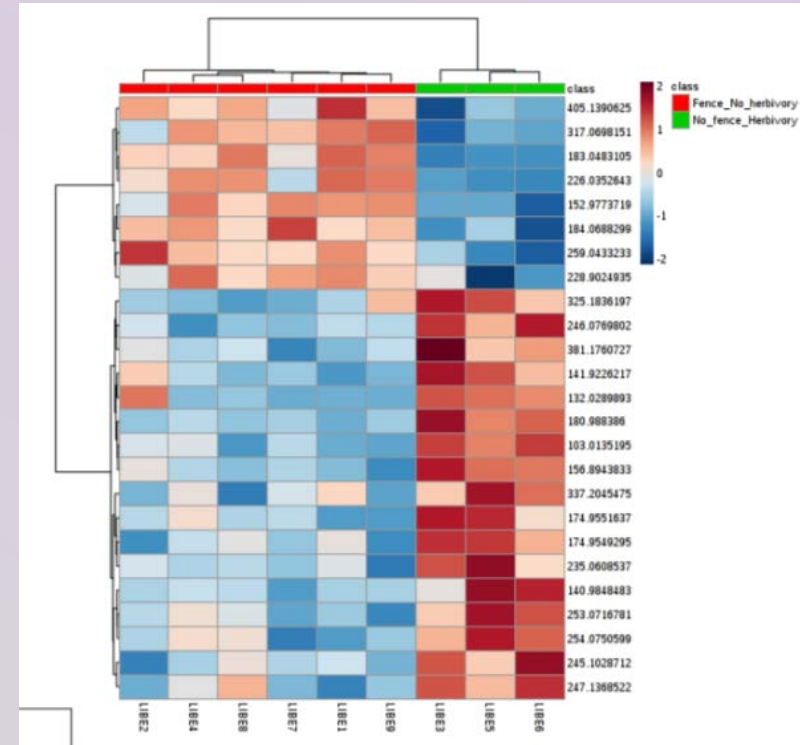
Lindera benzoin: fenced vs. browsed



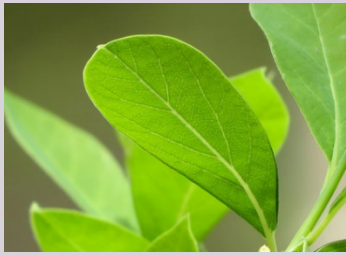
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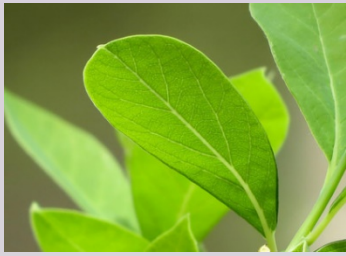
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conclusions



- For both, the metabolomic profiles were different between fenced vs. unfenced plots and for plants with and without browse.
- Despite the inherent qualitative difference in metabolite accumulation between species, we found responses predicted by common metabolic pathways, including the trans-farnesyl diphosphate (FPP) biosynthesis pathway, which plays an important role in sesquiterpene and sterol synthesis and affects jasmonic acid mediated defense responses.
- Chronic exposure to deer browse appears to cause metabolome-wide changes in plants, including defense-related metabolites.
- Further study is now needed to determine how common these changes are among species, and which metabolites are most affected.



thanks



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