UNRAVELLING THE ENTRANCE/RELEASE OF ENDODORMANCY IN DECIDUOUS TREES
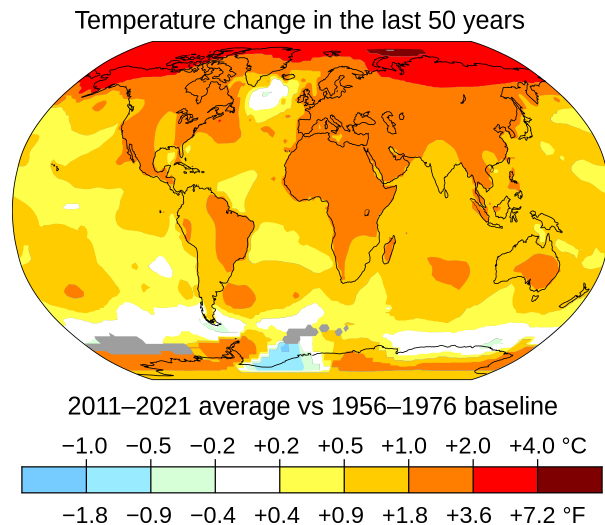
Temperature is rising globally

$\Rightarrow$ Has effect on all ecosystems

$\Rightarrow$ Temperate forests: 6% of global land surface and responsible for +- 13% of annual terrestrial carbon fixation

$\Rightarrow$ More moderate winters have an effect on the spring bud burst of deciduous trees (chilling requirement must be fulfilled) and therefore may impact the carbon uptake

Temperature change in the last 50 years

2011–2021 average vs 1956–1976 baseline

−1.0 −0.5 −0.2 +0.2 +0.5 +1.0 +2.0 +4.0 °C

−1.8 −0.9 −0.4 +0.4 +0.9 +1.8 +3.6 +7.2 °F

Endodormancy = "winter dormancy", inhibition of growth by internal bud signals. Buds need cold exposure to end the endodormancy

| (a) | (b) | (c) |
| Dormancy establishment | Endo-dormancy | Eco-dormancy | Growth resumption |
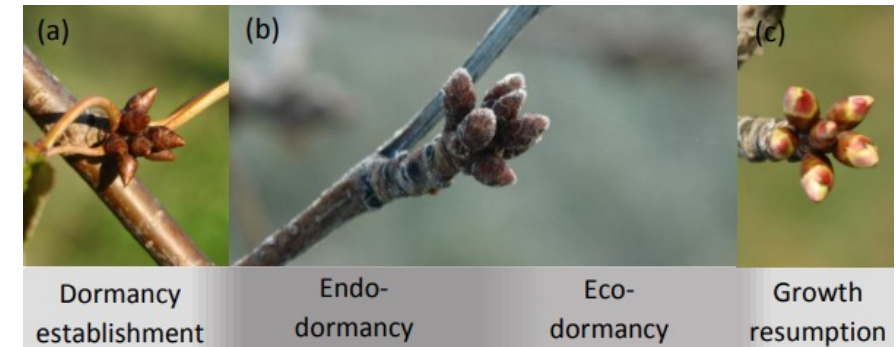
GOAL: we want to understand the genes and pathways responsible for the entrance and/or release of endodormancy and the effect of temperature and light on the endodormancy

- *Fagus sylvatica*
- *Populus nigra*

PHENOLOGY EXPERIMENTS

The trees were exposed to different temperature treatments to determine the effect of reduced chilling on the bud burst. In the last experiment different daylength treatments were applied to study its effect on the bud burst.

BD1	BD2: Temperature treatment in mid-late autumn	BD3: Temperature and light treatment
No treatment	Temperature treatment in climate-controlled greenhouses (reduce chilling): 10°C	Applied AFTER BD2: Different daylengths with 10°C in climate-controlled greenhouses - Long daylength = 2h longer - Short daylength = 2h shorter

Measurement and determination of phenological parameters:
- Chlorophyl index
  - CCI breakpoint
  - CCI50
- Dormancy peak
- Coloration
- Bud burst
- GGD
- Dormancy depth
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RNA extraction on dormant buds	**RNA extraction** on dormant buds	**RNA extraction** on dormant buds
Bio-informatic analysis - Transcriptomics	**Bio-informatic analysis** - Transcriptomics	**Bio-informatic analysis** - Transcriptomics

RAW DATA PROCESSING AND BIO-INFORMATICS ANALYSIS

Galaxy: raw data processing

- Mapping: HISAT2
- Quality control: fastQC
- Htseq-count
- DESeq2

Hierarchical clustering of differentially expressed genes

- MeV

Gene enrichment analysis and gene ontology

- OmicsBox

Determination of pathways and involved genes

- Biogrid
- Uniprot
- KEGG
- PLAZA
- TAIR
- …

Validation of results

- Transcriptomics
- Metabolomics

Your project
You will run bio-informatic analyses on the data and perform experiments to validate the results.

HOW TO APPLY?

Send your motivation to:

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IMPRES

Integrated Molecular
Plant Physiology
Research

Plants and Ecosystems