What epigenetics can bring to (plant) physiologists and ecologists in a climate change context

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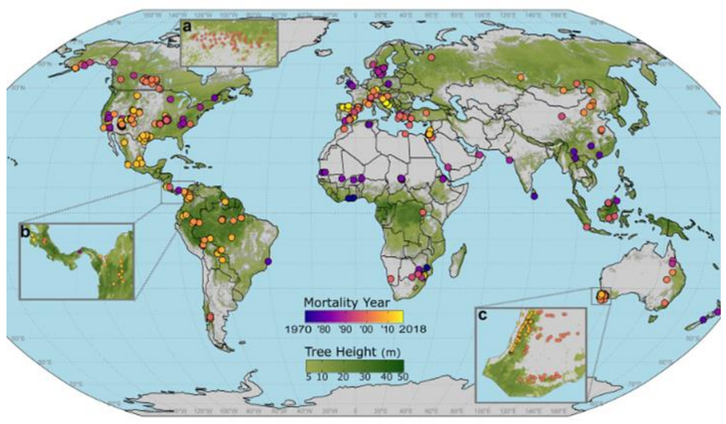
Context & Objective

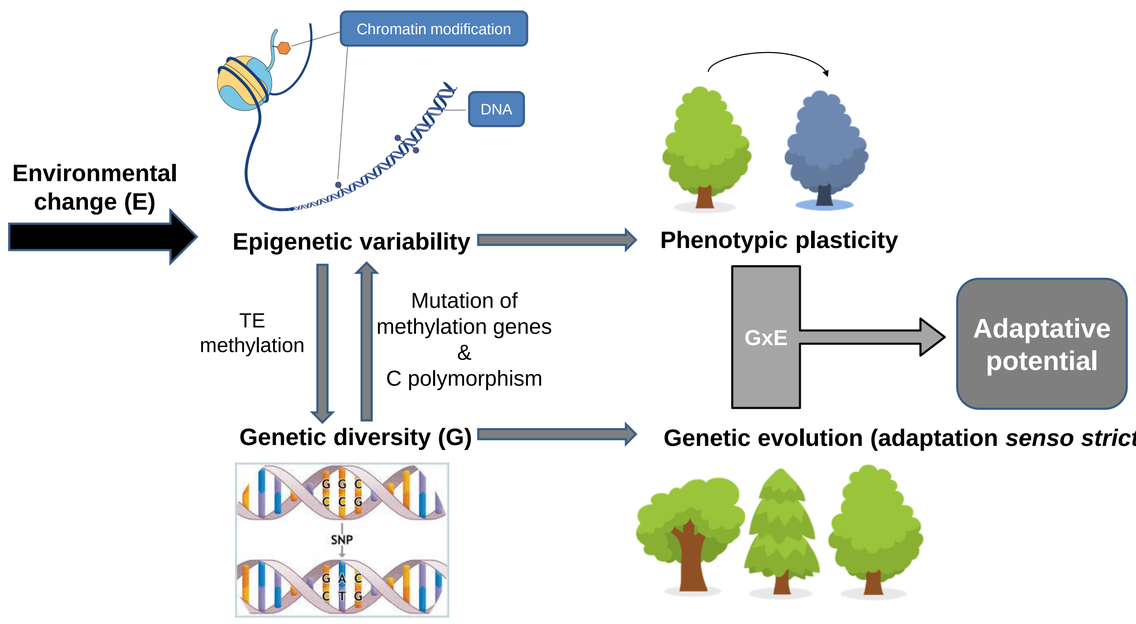
Living organism are subjected to fast and extreme climate changes, how their adaptative potential, individual plasticity could help them to survive? and can we predict their response for the next years?



Hammond et al. 2022 Nature

Forest decline due to climate change

Over the last decades, **widespread forest die-off** due to drought and/or heat constraints has been observed **around the world for all forest** biomes and is predicted to increase **with ongoing climate change**.



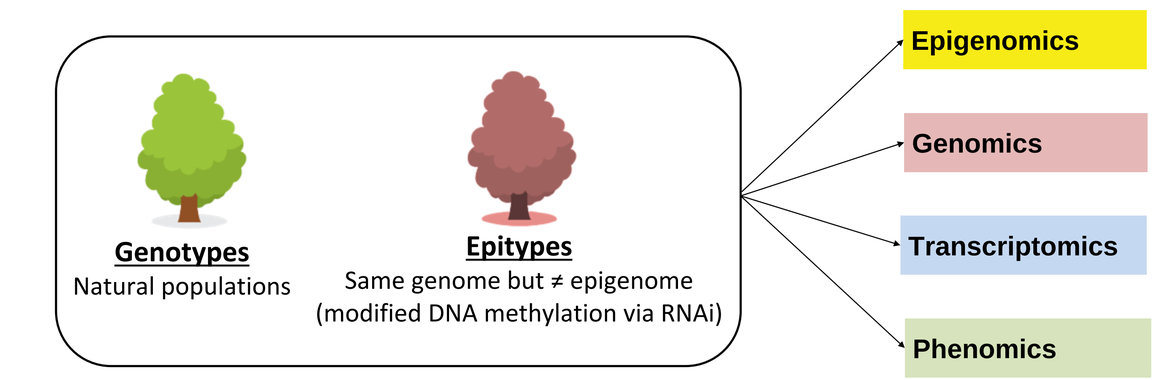
Black Poplar as a model tree

- Perennial and sessile
- Small genome: 485 ± 10Mb
- Diploid (19 Chromosomes)
- Cloning by cuttings
- Genetic transformation

Black poplar (*P. nigra*) is present in a large geographic range in Eurasia and is considered as **an indicator of the dynamic of the biodiversity**.

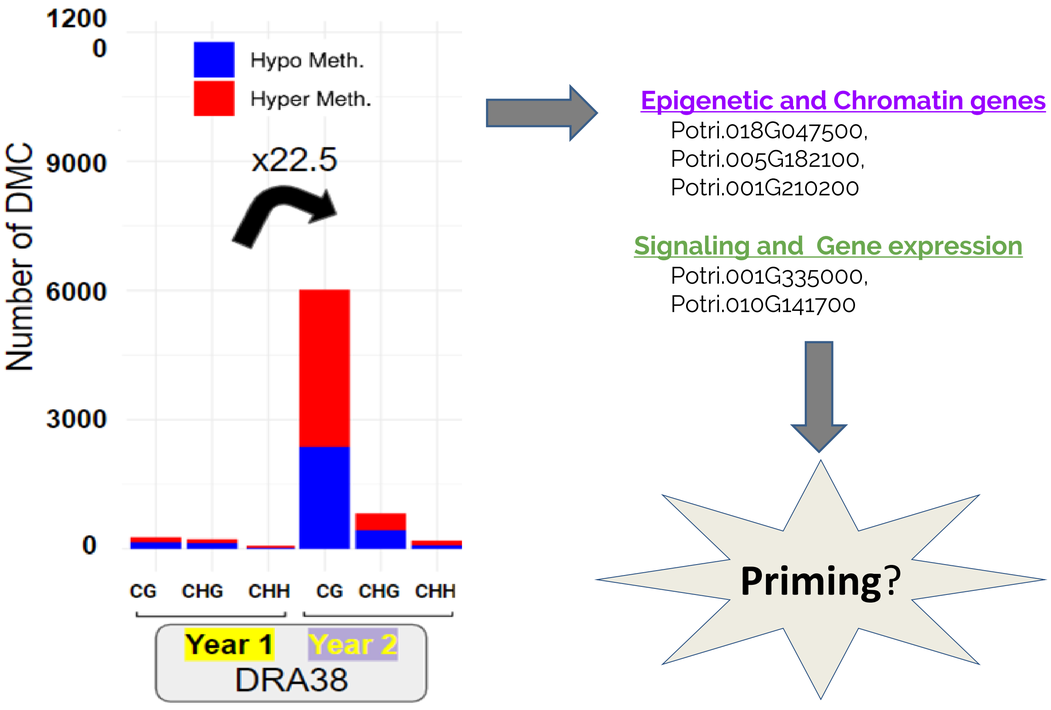
In this context, it's urgent to better understand the **mechanisms underlying adaptation and plasticity** of trees to better optimize genetic resources management. The study of the genetic bases of tree adaptation has mainly focused on the contribution of standing structural variation (genetic) to local adaptation. **Epigenetic mechanisms remain largely unstudied** while they can be extremely important for long-lived organisms as they allow rapid phenotypic modifications in reaction to changing environmental conditions ('priming effect'). Our objective (ANR EPITREE 2018-2023) is to characterize the importance of epigenetics in adaptation [1], plasticity [2][3] and memory-priming [4] of trees and to evaluate the **use of epigenetic data in predictive models.**

Ecological epigenetic memory in trees?



Experimental setup for drought rewatering experiments. Variations of the relative extractable water (REW) content over weeks for drought treatment on poplar in greenhouse.

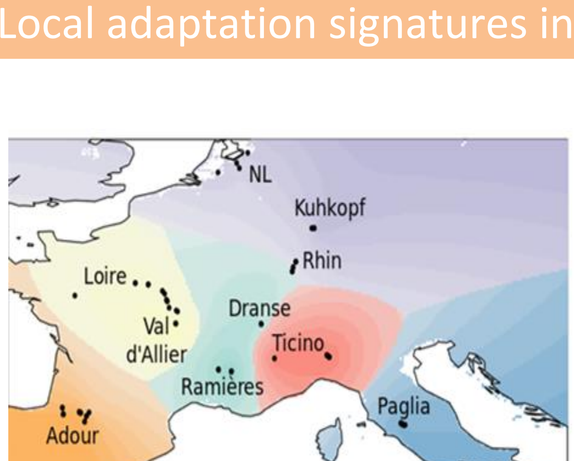
Natural and methylation-mutant poplar plants were placed in a greenhouse under drought conditions (WD = Water deficit; WW = Well-Watered) for 5 weeks, then re-watered (ReW= Re-Watering) for one week and sampled after recovery (memory?). Here the goal is to study short-term somatic memory and to identify a potential epigenetic control using Whole Genome Bisulfite Sequencing (WGBS). One year later, the trees were subjected to a second drought-watering cycle. The aim was to study inter-annual somatic memory and the corresponding epigenetic control.



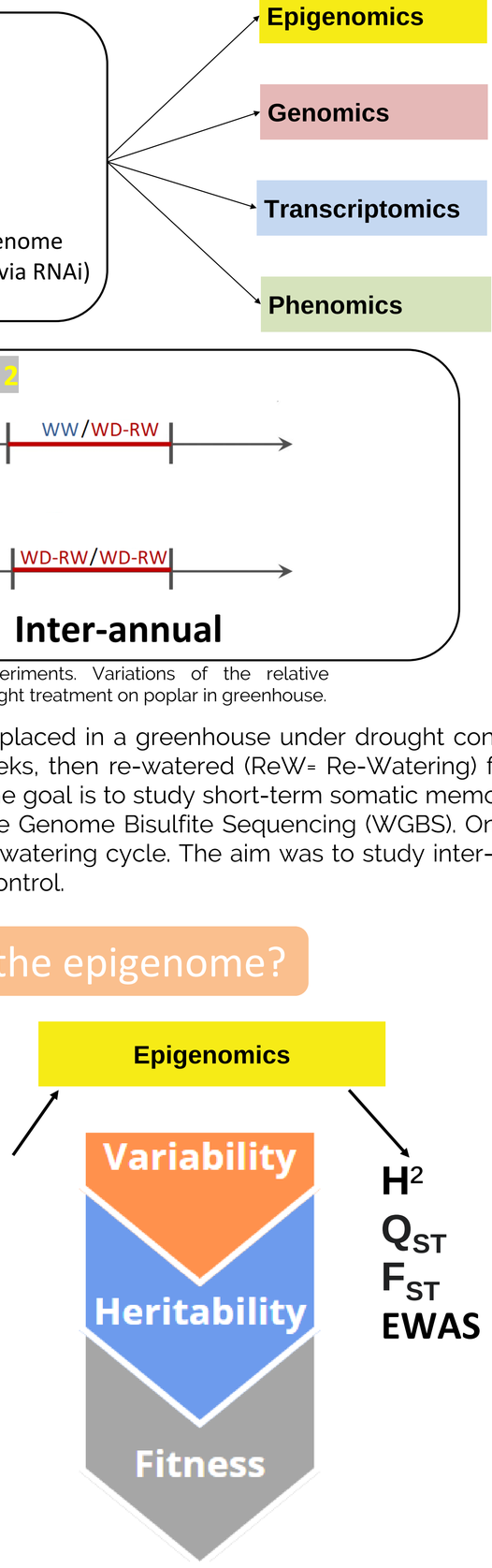
Numbers of differentially methylated cytosine (DMC) detected in the 3 methylation contexts (CG, CHG, CHH) in short-term and inter-annual memories in the DRA38 genotype (*Populus nigra*).

Results of WGBS analysis showing **DNA methylation variations associated to short-term (year 1) and inter-annual (Year 2) somatic memories in the DRA38 genotype**. These modifications are associated to variations in gene expression involved in epigenetic and chromatin organization and signaling. The ability of these somatic memories to induce priming effects (better response during a second challenge) is under evaluation (Duplan et al, in prep).

Local adaptation signatures in the epigenome?

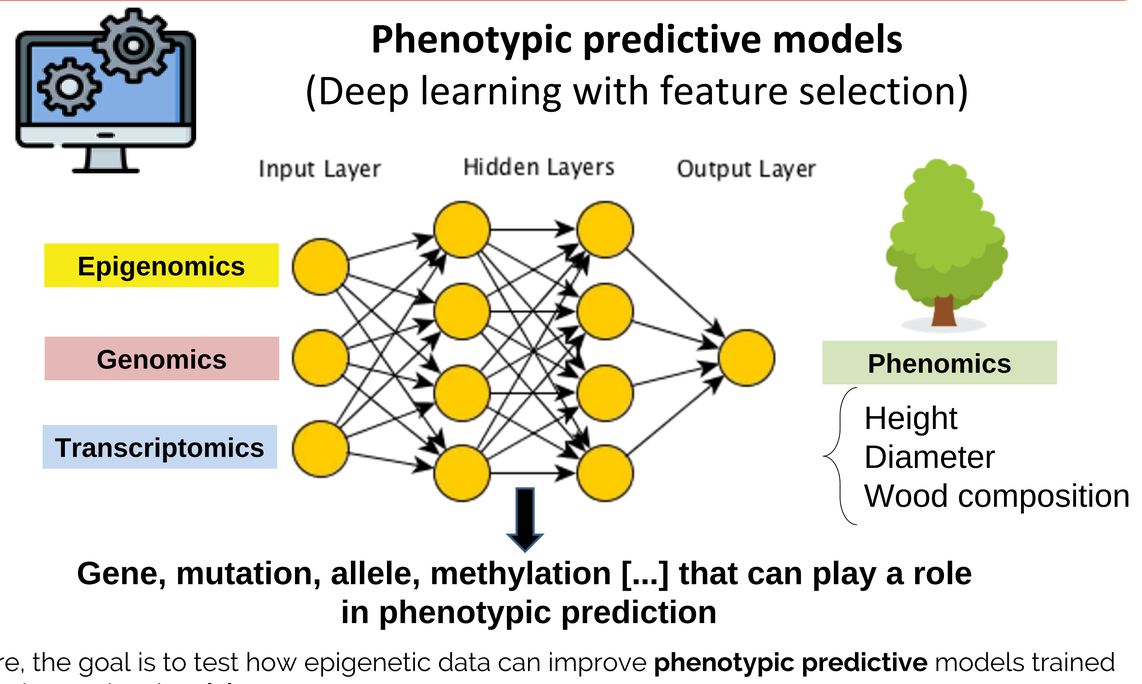


Distribution area of the 241 black poplar genotypes covering 11 metapopulations



We have analyzed **241 black poplars** originating from 11 natural populations in Europe and installed in a common garden (Orléans). We have obtained multi-omics data: **epigenetic**, genomic, transcriptomic and phenomic. Our goal is to identify signatures of potential local adaptation at the epigenetic level. A preliminary study by our consortium (ANR EPITREE) on 20 genotypes have already unravel epigenetic adaptative signature on disease resistant genes [1].

How to use epigenetic data associated to phenotype for predictive models?



Here, the goal is to test how epigenetic data can improve **phenotypic predictive** models trained by other omics data [5].

Bibliography : [1] Sow et al. 2023; [2] Lafon-Placette et al. 2018, Journal of Experimental Botany; [3] Sow et al. 2021, New Phytologist; [4] Le Gac et al. 2018, Journal of Experimental Botany; [5] Wade et al. 2022, BMC Genomics

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