

### TEs as a major driver of genomic variation in trees? Jumping MITEs in common beech revealed by TIPs and eccDNA

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BORATOIRE

t **D**EVELOPPEMEN

des **PLANTES** 

# TEs as a major driver of genomic variation in trees ? Jumping MITEs in common beech revealed by TIPs and eccDNA

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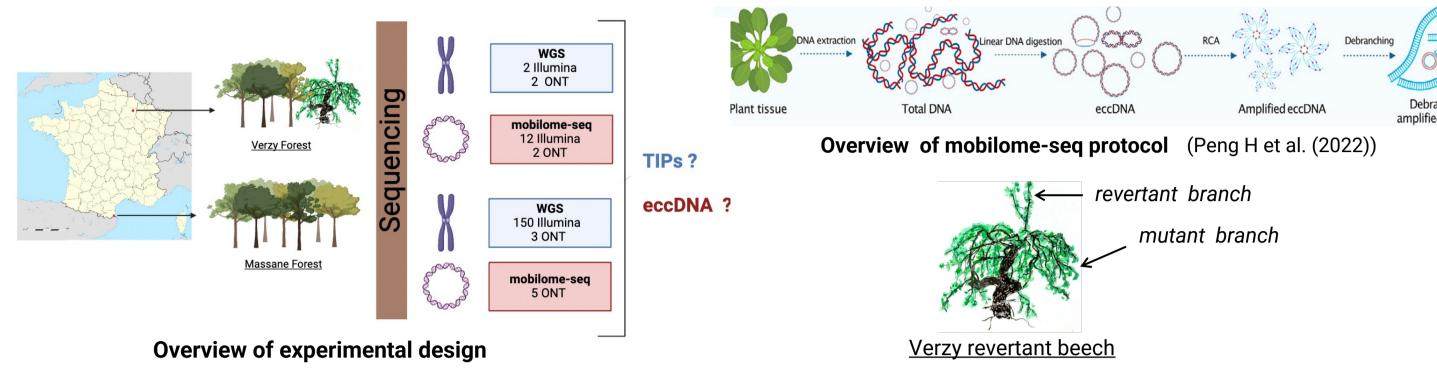
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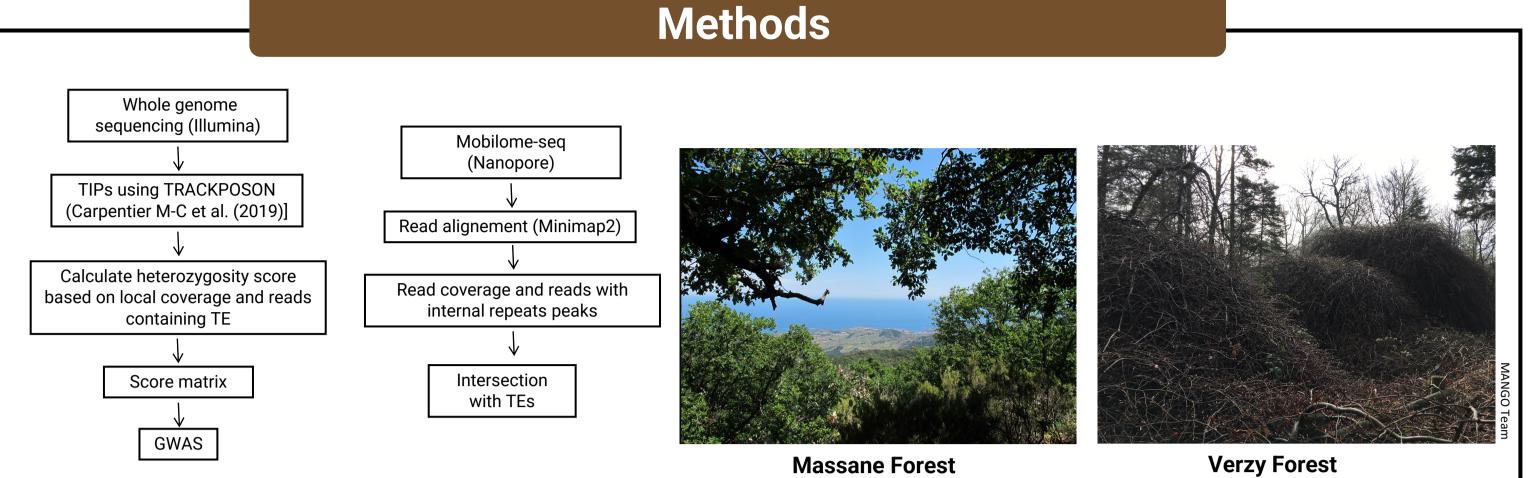


Transposable elements (TEs) are predominant in most plant genomes but their impact and activity has been mostly studied in annual species. Beech trees (Fagus sylvatica) make up most of European forests and are highly threatened by drought and climate change. We sought the investigation of the genomic diversity caused by TEs and their adaptive potential in this long-living species. We aimed at characterizing Transposable Element Insertion Polymorphisms (TIPs) playing key roles in genome evolution by analysing TIPs in a single population of 147 common beech trees, using 672 Long Terminal Repeats Retrotransposons (LTR) and 558 Miniature Inverted Transposable Elements (MITEs) families. We further analysed somatic structural variants (SV) generated by TEs. Given the high level of very recent TE activity in common beech, we investigated ongoing TE mobility using extrachromosomal circular DNA (eccDNA) sequencing or mobilome-seq, eccDNA being a useful proxy for identifying active TEs.

### **Experimental design**

We analysed trees from both the Massane and the Verzy forest. The Massane forest is a natural reserve in free evolution for more than 150 years. The Verzy forest is the largest ressource of tortuous beech or mutants tree which present an unstable phenotype.

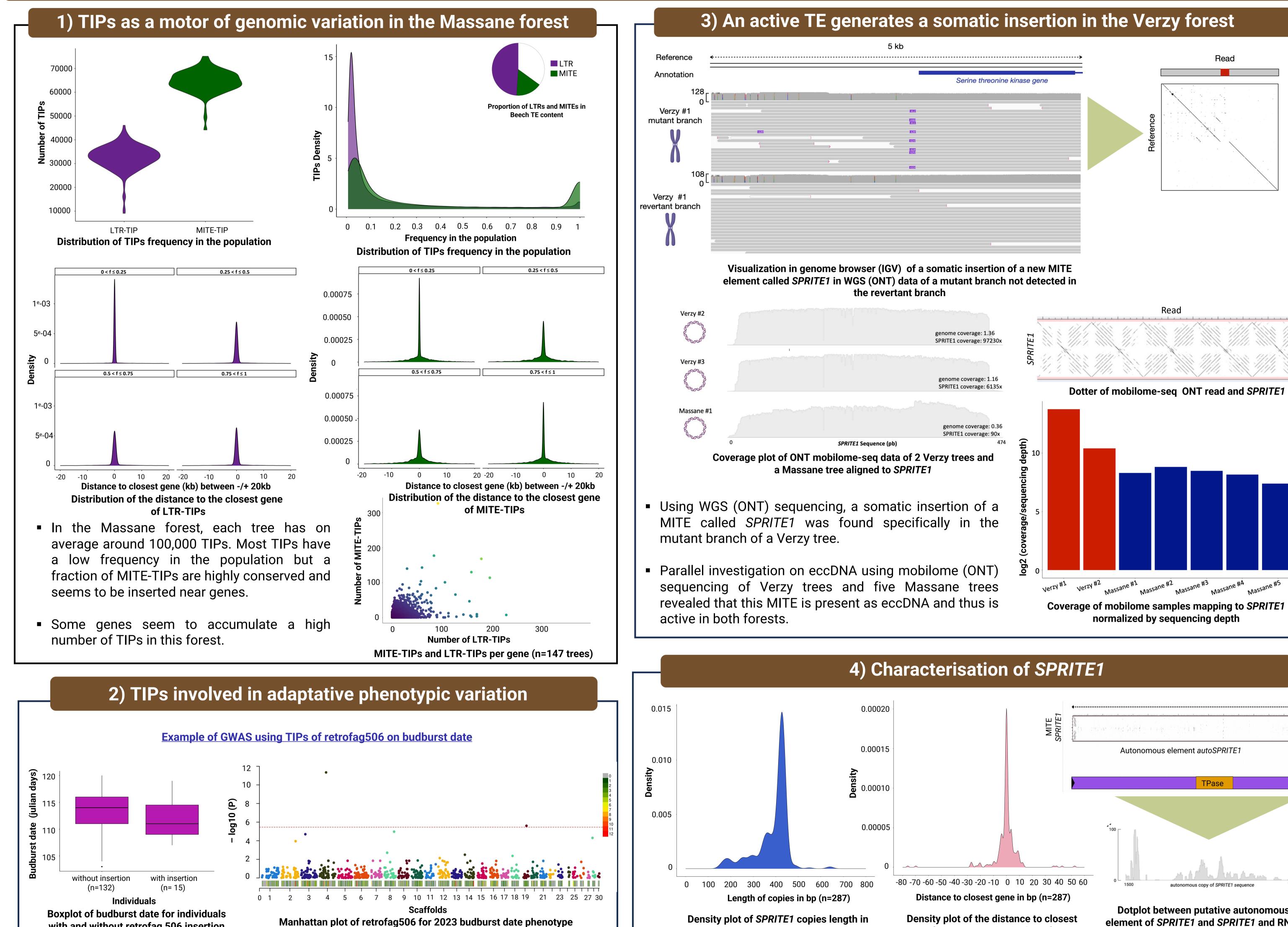


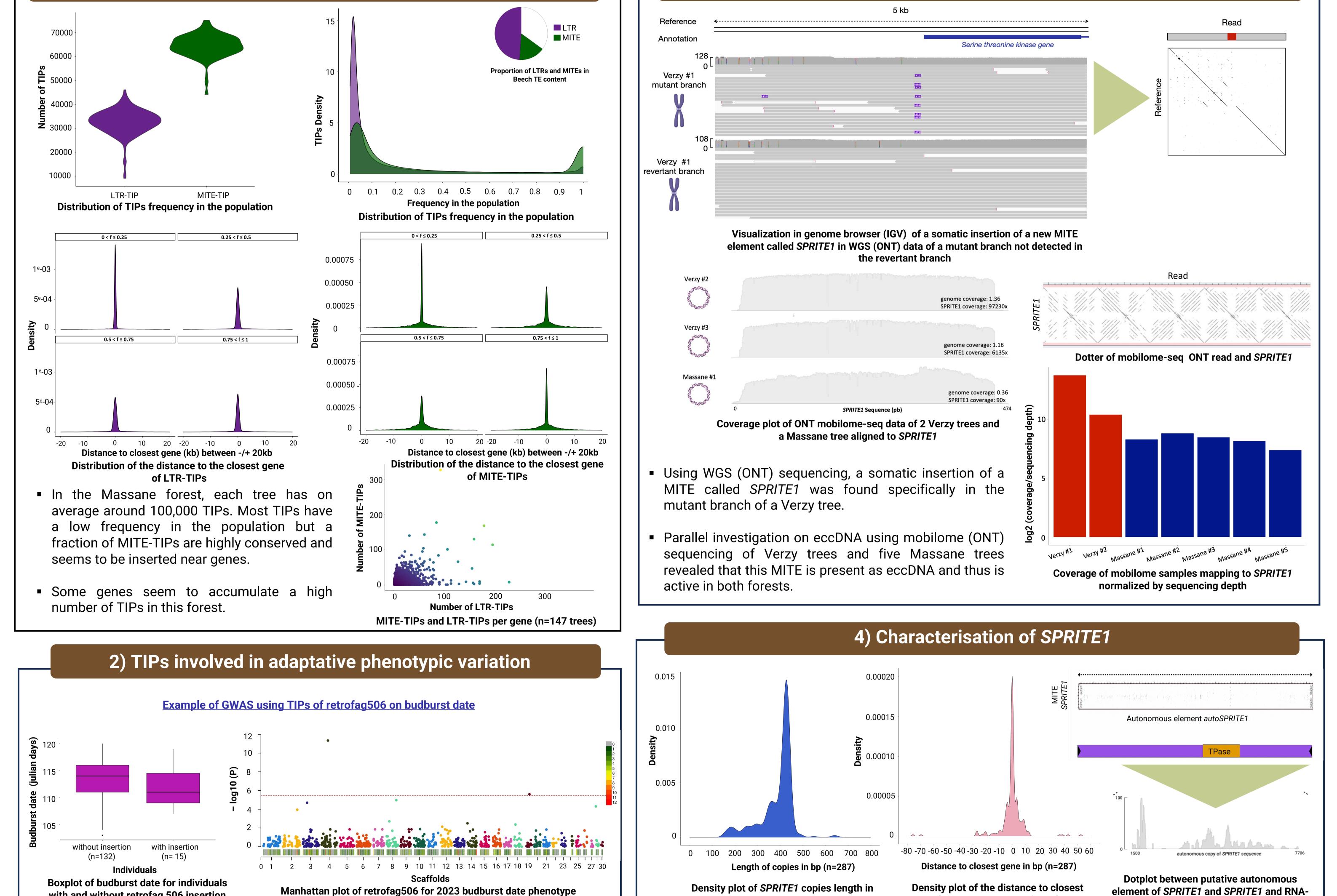


### **Overview of TIPs-GWAS** method

**Overview of mobilome-seq** data analysis method

### RESULTS





- with and without retrofag 506 insertion
- Using matrices of LTR-TIPs for 672 families, we performed 17,472 GWAS using a dataset of 26 phenological traits obtained in the Massane forest. An insertion of retrofag506 on scaffold 4 was found linked with 2023 budburst date. This insertion was found in 15 individuals and is present 145 pb upstream a candidate gene encoding for a membrane protein.
- gene of SPRITE1 copies in the reference the reference genome seq mapping to autonomous element genome
- SPRITE1 is a 474 bp Mutator MITE element with 179 bp long TIRs with A/T rich 7/8 bp TSDs. Most SPRITE1 copies size range between 100 and 800 bp and are inserted in gene rich regions, as generally described for MITEs (Feschotte, et al. (2002)).
- Homology based analyses on TIRs has allowed identification of a putative autonomous element that could enable SPRITE1 mobility and seems to be expressed at least in buds.

## CONCLUSION

- In our study, using a population of 147 beech trees, we identified around 100,000 TIPs on average in each tree generated by 1230 LTRs retrotransposons and MITEs families. We showed that most of the TIPs are low frequency possibly representing recent insertions. We also identified an potentially adaptive insertion in Massane.
- Using trees with somatic phenotypic variation from Verzy, we identified an active MITE called SPRITE1 causing somatic mutation. Using eccDNA as a proxy, we found that this MITE is still active in 2 very distinct forests. This study sheds light on how TEs could impact genome evolution and adaptation in perenials non model species such as woody trees.



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