Somatic mutation may contribute to the genetic diversity of the tropical tree population

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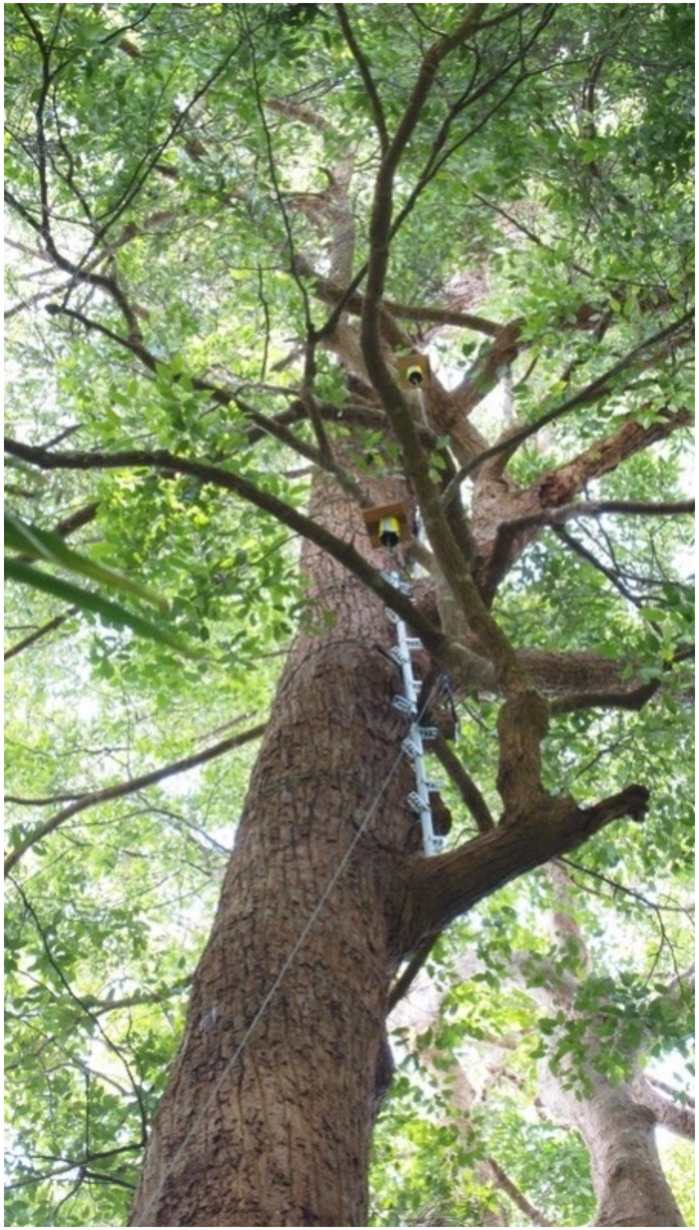


Trees have long-life span

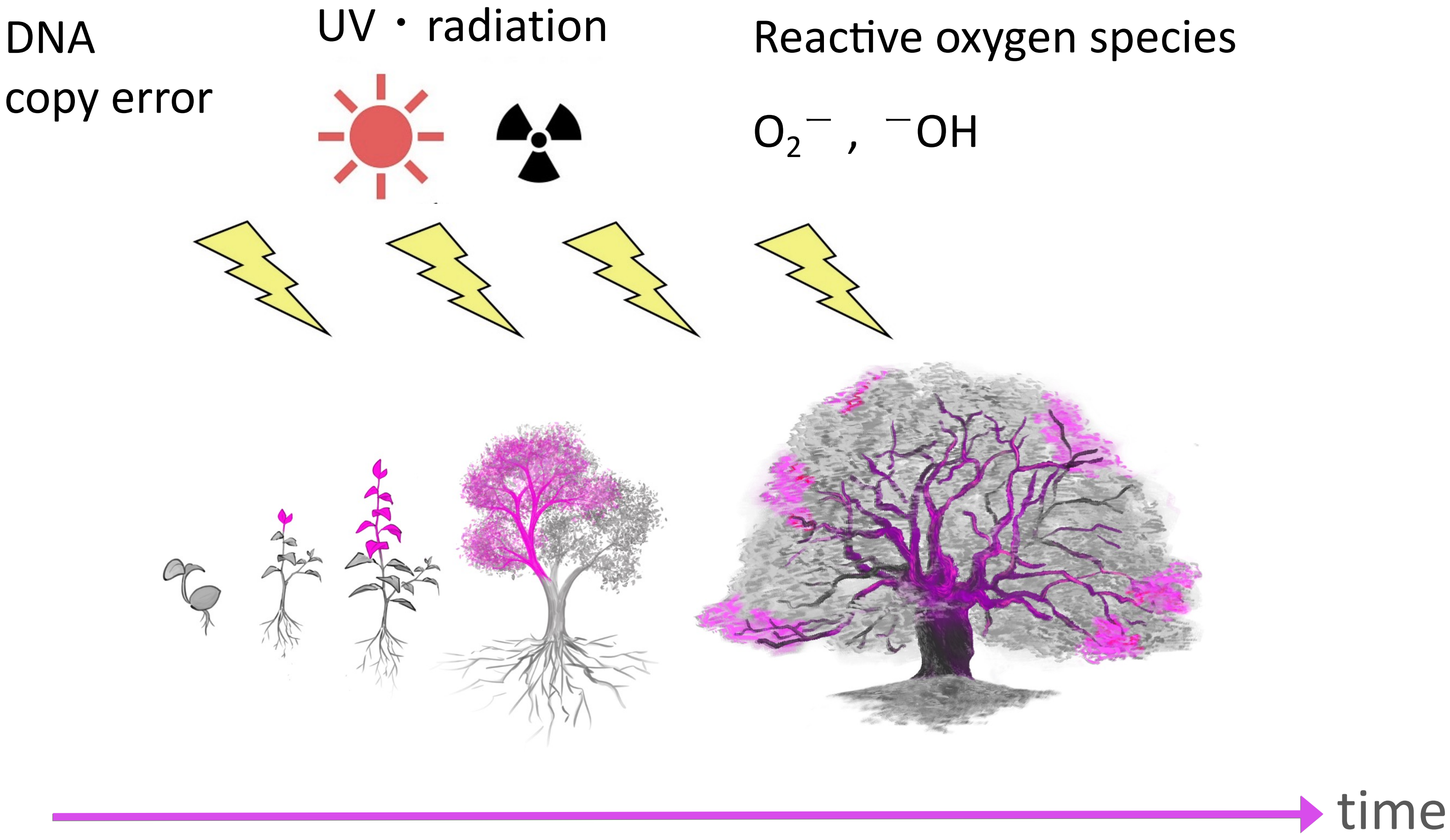
Japanese cedar in Yakushima (aged 2200)

Bristlecone pine (aged 4700)

Distribution of long-lived trees seems to biased to places where those have been least affected by human impacts (Piovesan and Biond 2020)

http://yoshida-bigtree.tokyo/gallery/bristlecone_pine/bristlecone.html,
http://www.yakusugi-museum.com/data-yakushima-yakusugi/204-kyojyu.html,

Longevity of trees result in the accumulation of somatic mutations



DNA
copy error

UV・radiation

Reactive oxygen species

O_2^- , ^-OH

time

Gill et al. 1995 *Ann. Rev. Ecol. Syst.* 26; Burian 2021 *Front. Plant Sci. 12*

Somatic mutations accumulated in trees passed on to the descendants

Animals

Somatic mutations
NOT passed to descendants

Plants

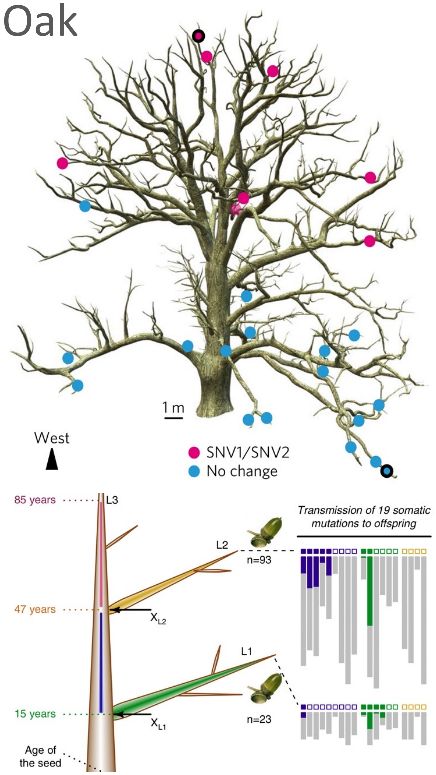
Genetically diverse
descendants are produced

Somatic mutations within trees may contribute to genetic diversity of the tree population

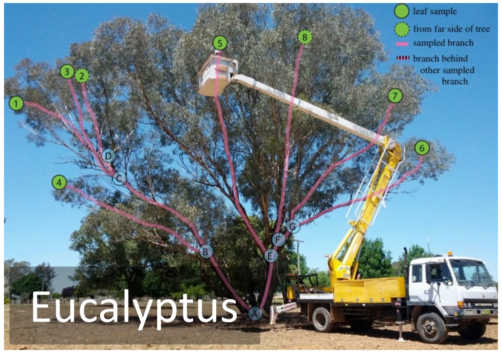
Whitham 1981 *Oecologia*; Sutherland and Watkinson 1986 *Nature*

Empirical studies verified accumulation of somatic mutations

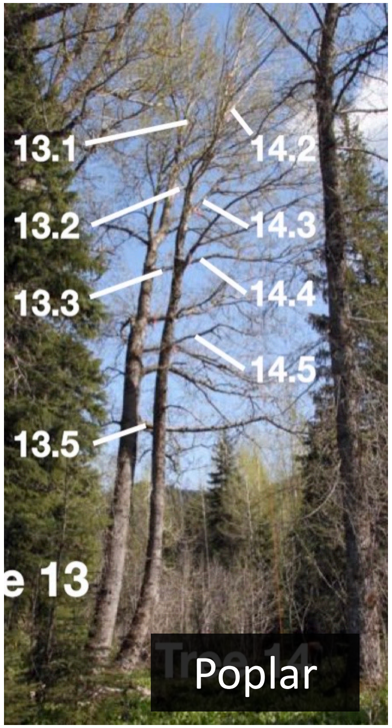
Oak



Peach



Eucalyptus



Poplar

Conifer

Thanks to the development of NGS,
many studies reported the accumulation of somatic mutations
in long-lived tree species

Schmid et al. 2017; Plomin et al. 2018; Wang et al. 2019; Hanlon et al. 2019; Orr et al. 2020; Hofmeister et al. 2020

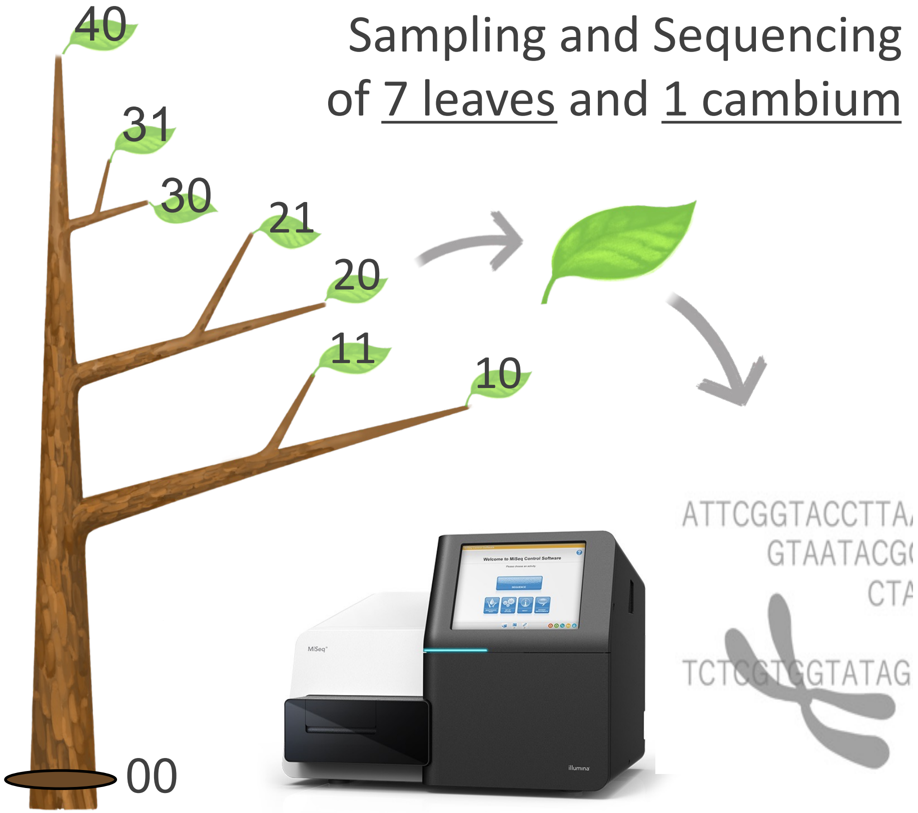
Investigation of Somatic mutations on tropical trees, *Shorea*, with different growth rate

S. laevis
(slow growing)

aged | 325
187

S. leprosula
(fast growing)

aged | 79
54



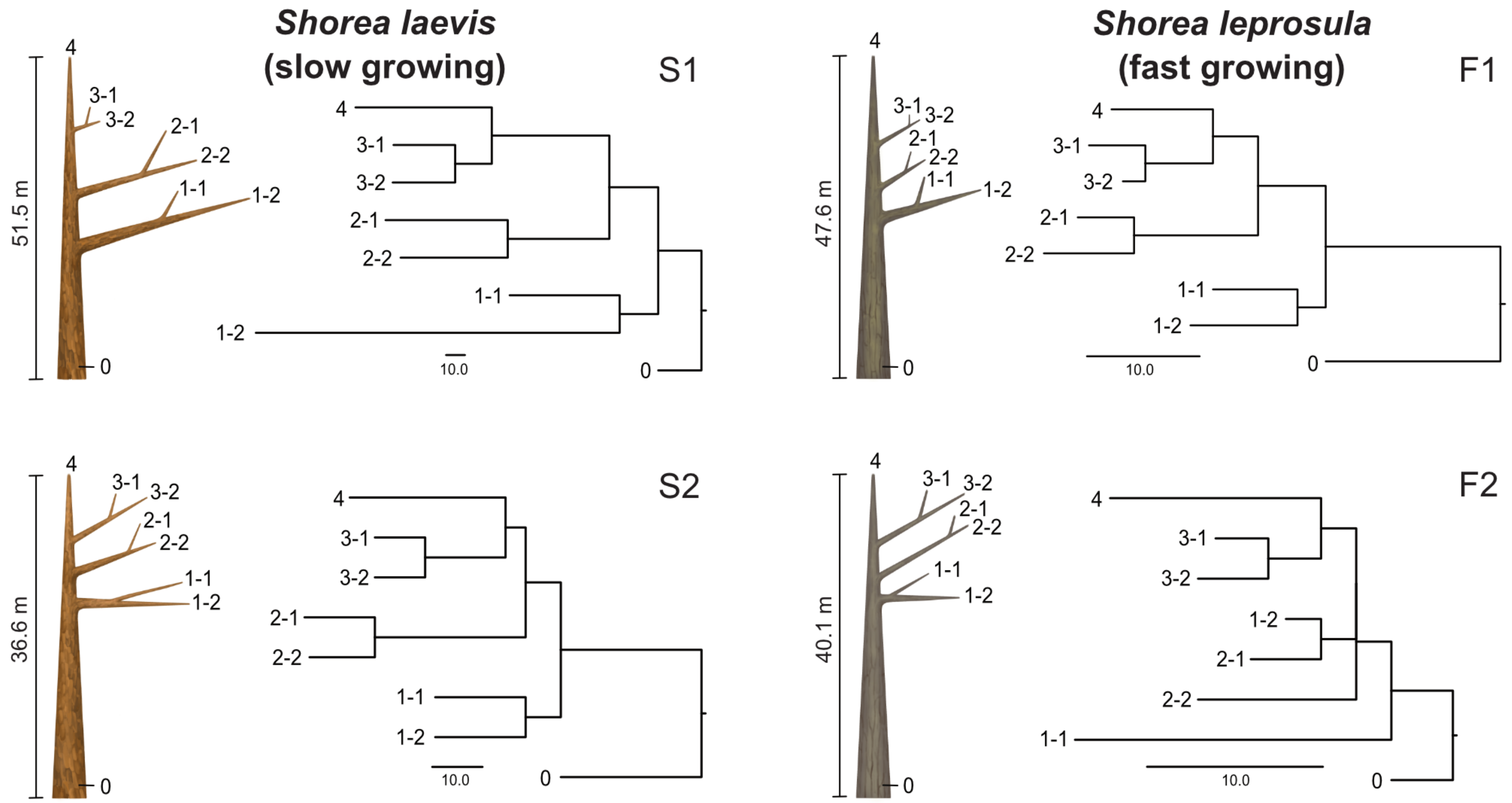
Sampling and Sequencing
of 7 leaves and 1 cambium

Next **G**eneration **S**equencer

How accumulation of Somatic mutations differs between slow- and fast-growing species with different lifespans

https://www.biolabtech.com.ua/en/products/ngs-cekvenator-miseq.html#

Phylogenetic tree based on somatic mutations perfectly congruent with the physical tree architectures

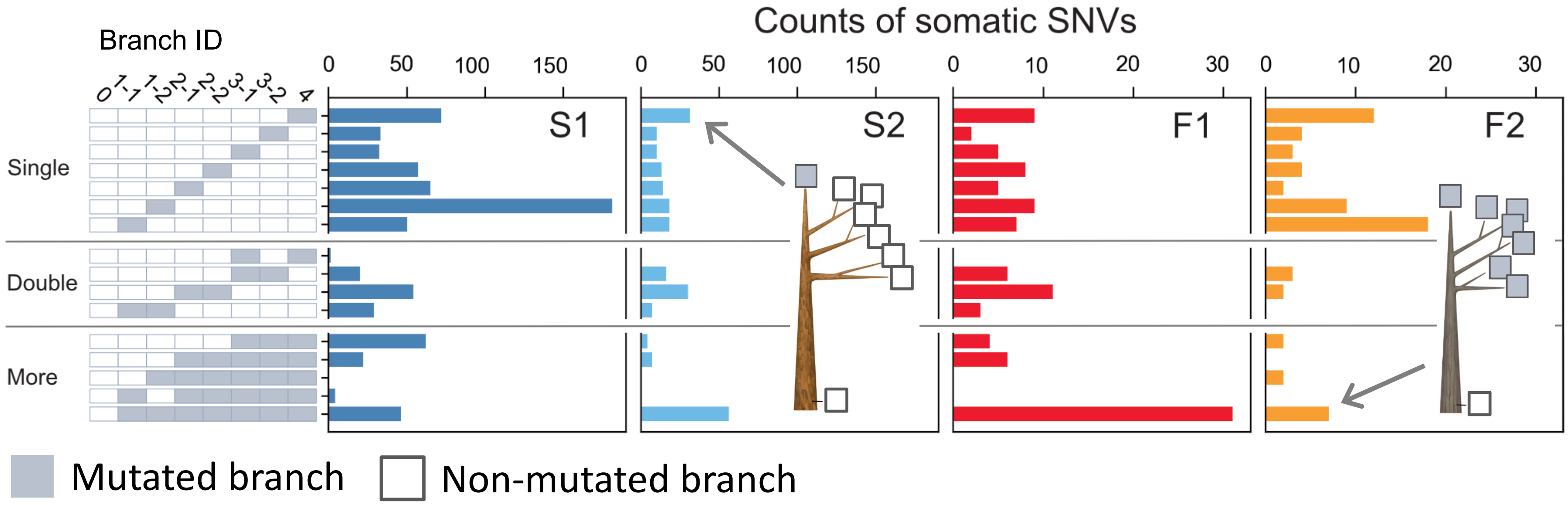


***Shorea laevis* (slow growing)**

***Shorea leprosula* (fast growing)**

This strong concordance suggests the reliability of the somatic mutation detection

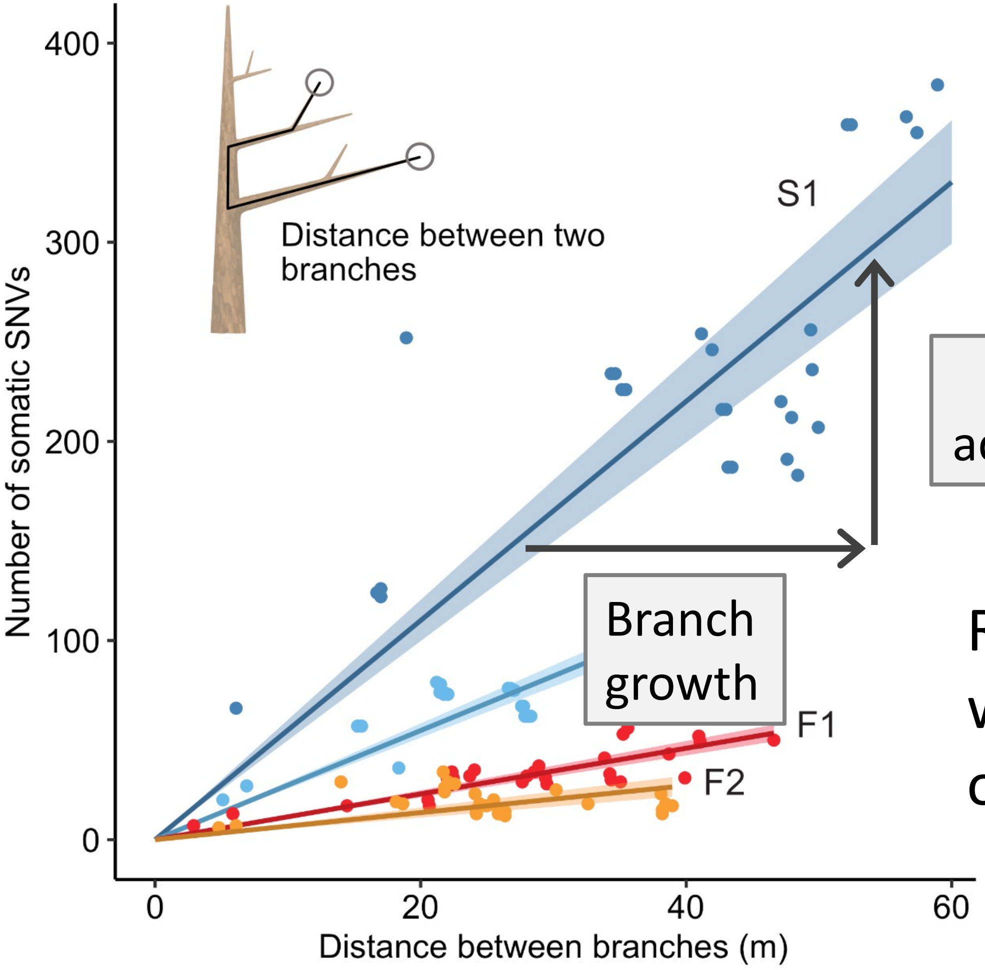
Distribution of somatic mutations across branches within a tree architecture



Although some mutations were shared by multiple branches,

The majority of somatic mutations were unique to a single branch, resulting in genetic mosaicism among branches.

Somatic mutations accumulate in association with growth of branch



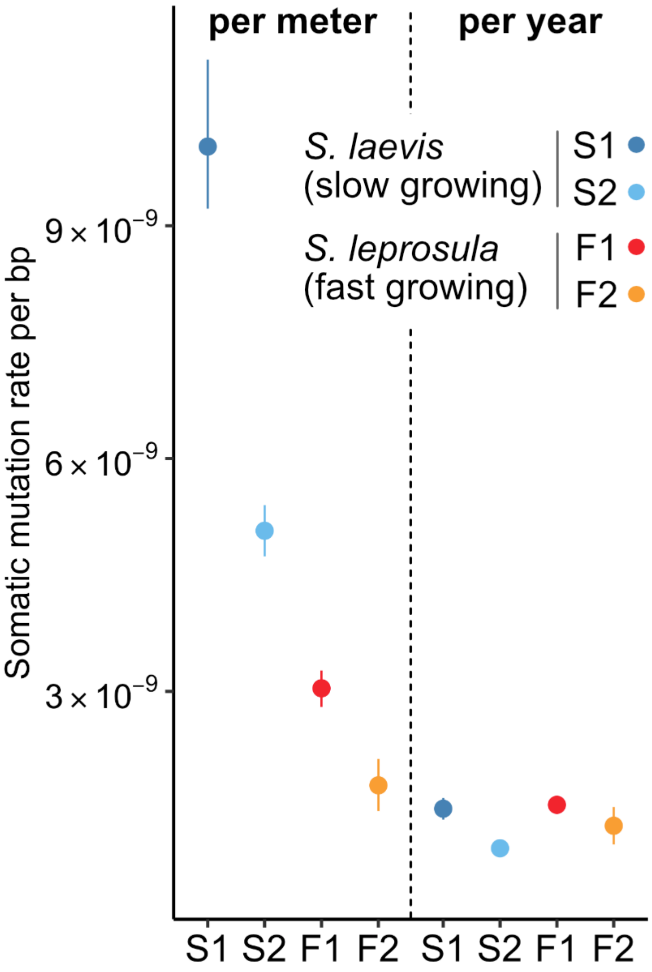
Branch growth

Mutations accumulation

Number of somatic mutations increases linearly,
as the physical distance between branches increases.

Rate of somatic mutation was determined by the slope of the linear regression line

Estimated Rate of Somatic mutations per growth and per time



- **per meter** rate

  × 3.16 higher in Slow- than Fast-growing sp.

However,

- **per year** rate

  Similar between Slow- and Fast-growing

i.e. Somatic mutation accumulates in a clock-like manner as trees age, regardless of their growth

Somatic mutation Rate in tropical trees

1.24–1.40 × 10^{-9} /site/yr

much higher than in temperate trees

Somatic mutations are stored within an individual tree as a source of genetic diversity for tree population

Genetically diverse descendants may be produced from each of branches in a single old-standing tree,

contributing to the genetic diversity of the tree population.

By cutting down a long-lived tree, we also lose the genetic diversity that has accumulated within the individual tree over a long period of time

Schoen and Schultz 2019 *Annu Rev Ecol Evol Syst*

Take home message

- Large amounts of Somatic mutations accumulate during the long-life span of tropical trees

- Accumulation of Somatic mutations are associated with the age of tree, rather than its height

- Genetic diversity of tree population is also stored among branches within a single long-lived tree

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