GENETIC DIVERSITY IN PLANTED UK CONIFERS MANAGED UNDER CONTINUOUS COVER FORESTRY

Laura Guillardin - ForesTree Biology Group

OUTLINE

- Background
- Site Characterisation
- Genetic analyses

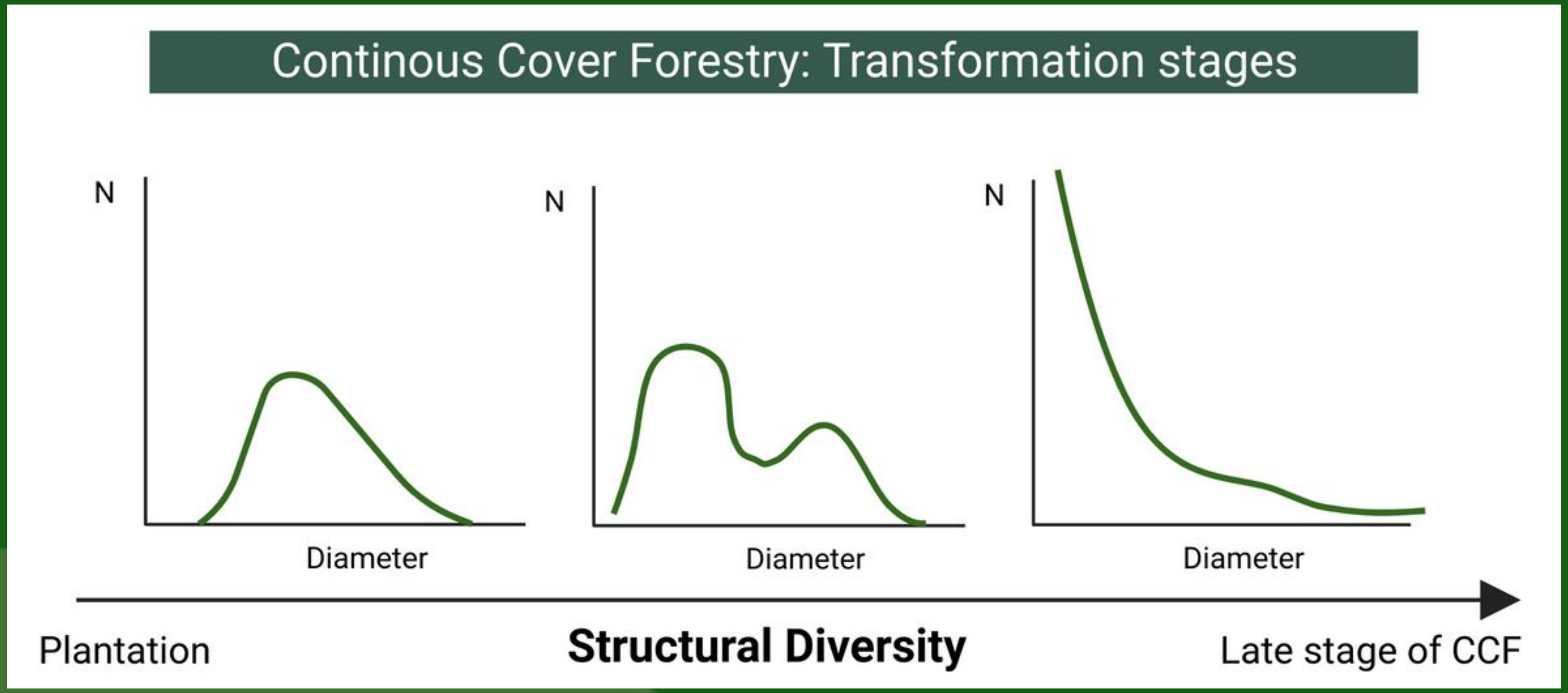
Transformation from plantations into CCF

why? Climate change context

Multi-purpose forest

how?

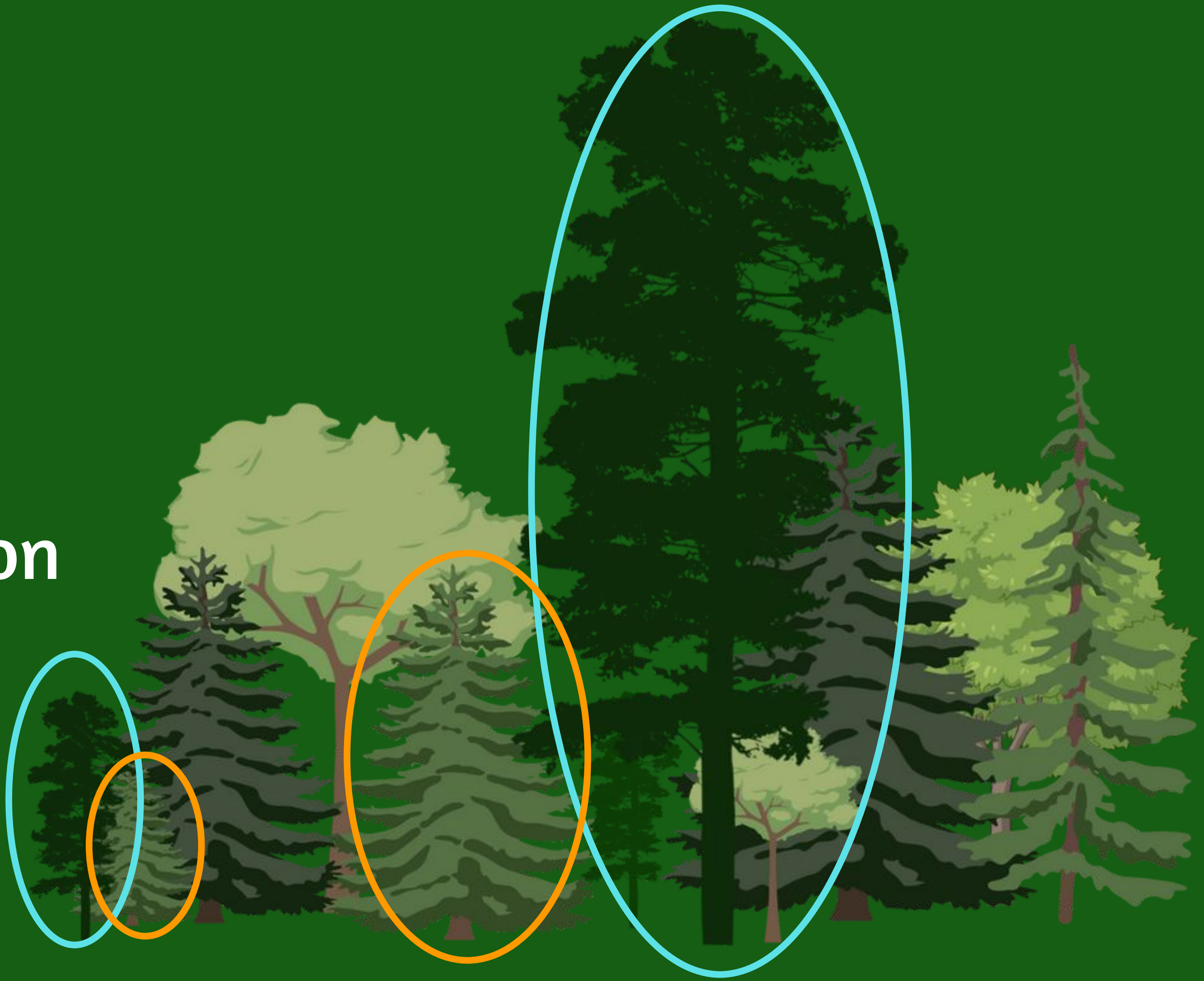
Timber production



Continous Cover Forestry: Transformation stages

Figure modified from Pommerening, A., & Murphy, S. T. (2004).

Our main objective is to study the genetic makeup of both the planted trees and their natural regeneration



Natural Regeneration

VS

Planted trees

how is genetic variation maintained in populations for making decisions about how to manage them in climate change context.

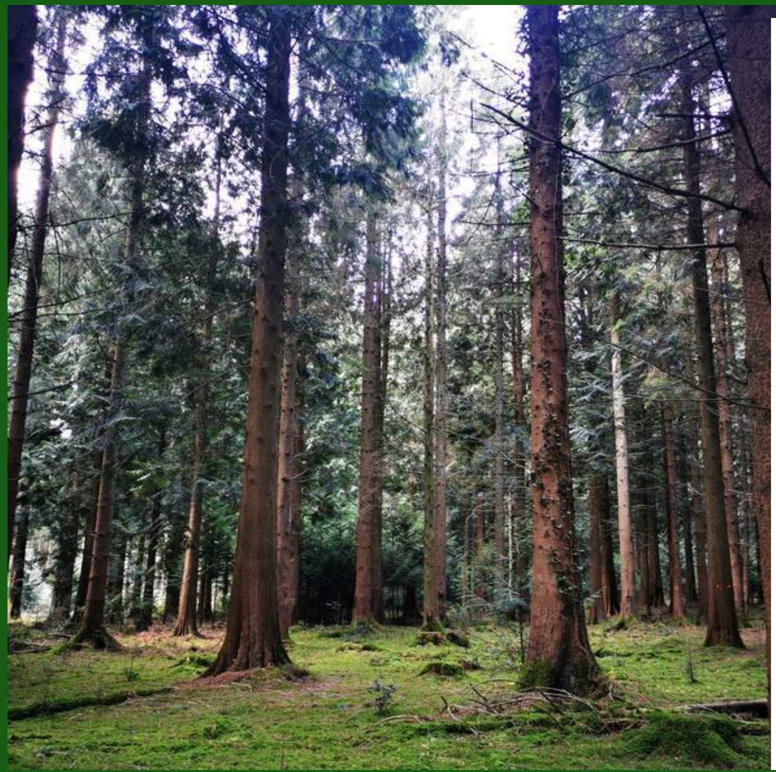
Two of the prefered planted species in the UK

Pseudotsuga menziesii (Pm)

PM

shows high level of genetic diversity both in its natural range and planted forests in Europe (Neophytou et al 2020)

Thuja plicata (Tp)



TP

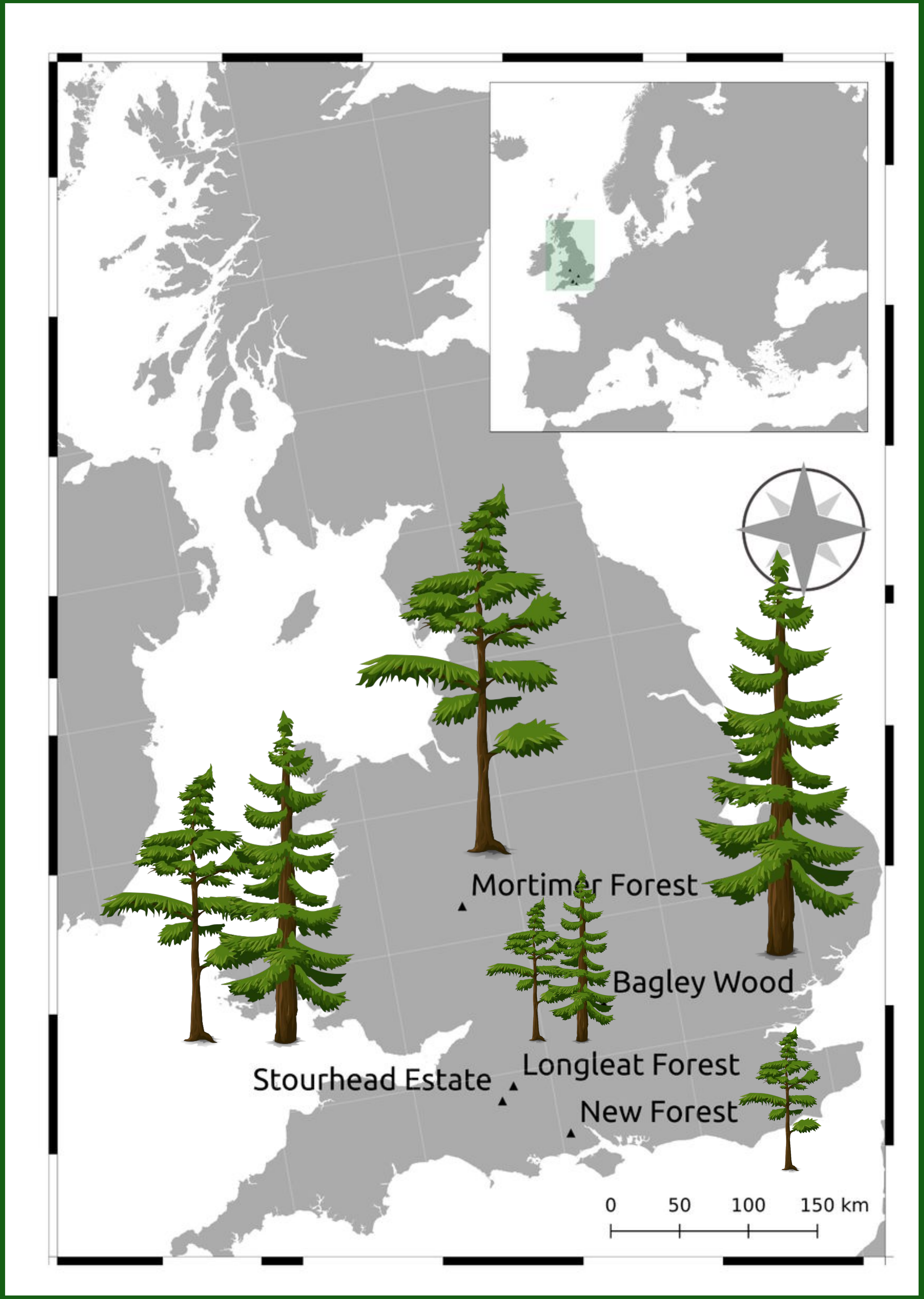
has naturally low outcrossing rates and self-fertilizes in nature (Shalev et al 2022)

Charalambos Neophytou and others, Genetic diversity in introduced Douglas-fir and its natural regeneration in Central Europe, Forestry: An International Journal of Forest Research, Volume 93, Issue 4, July 2020, Pages 535–544, https://doi.org/10.1093/forestry/cpz055
Shalev TJ, Gamal El-Dien O, Yuen MMS, Shengqiang S, Jackman SD, Warren RL, Coombe L, van der Merwe L, Stewart A, Boston LB, Plott C, Jenkins J, He G, Yan J, Yan M, Guo J, Breinholt JW, Neves LG, Grimwood J, Rieseberg LH, Schmutz J, Birol I, Kirst M, Yanchuk AD, Ritland C, Russell JH, Bohlmann J. The western redcedar genome reveals low genetic diversity in a self-compatible conifer. Genome Res. 2022 Oct;32(10):1952-1964. doi: 10.1101/gr.276358.121. Epub 2022 Sep 15. PMID: 36109148; PMCID: PMC9712635.

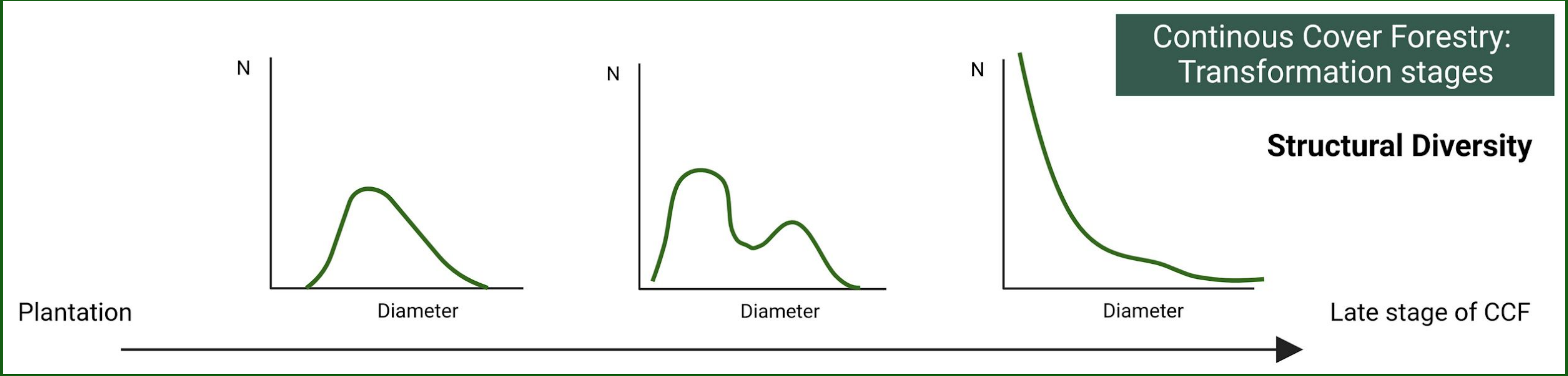
Five sites

Eight stands

	Trees/ha	Total N of trees
Longleat PM2	137.4	943.7
Stourhead PM2	92.0	1707.6
Mortimer PM	265.2	1413.8
Ringwood PM	79.6	717.4
Stourhead TP	237.3	1186.7
Stourhead TP2	21.2	394.1
Longleat TP	156.5	793.5
Bagley Woods TP	278.5	1038.0



Sites characterisation

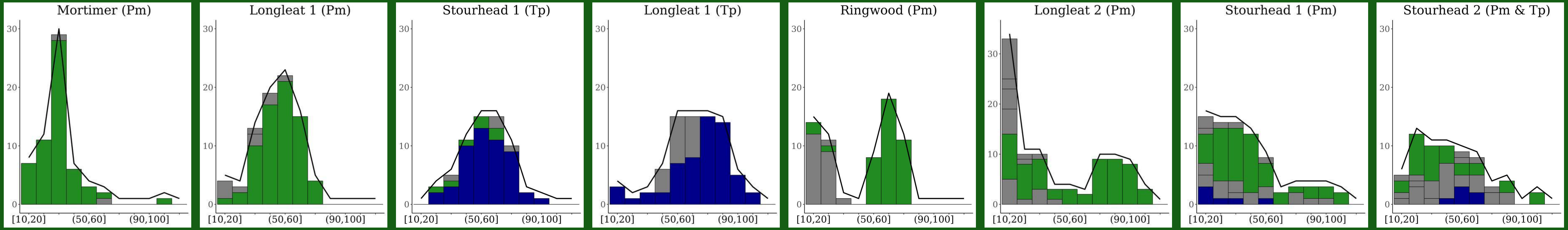


Continous Cover Forestry: Transformation stages

Structural Diversity

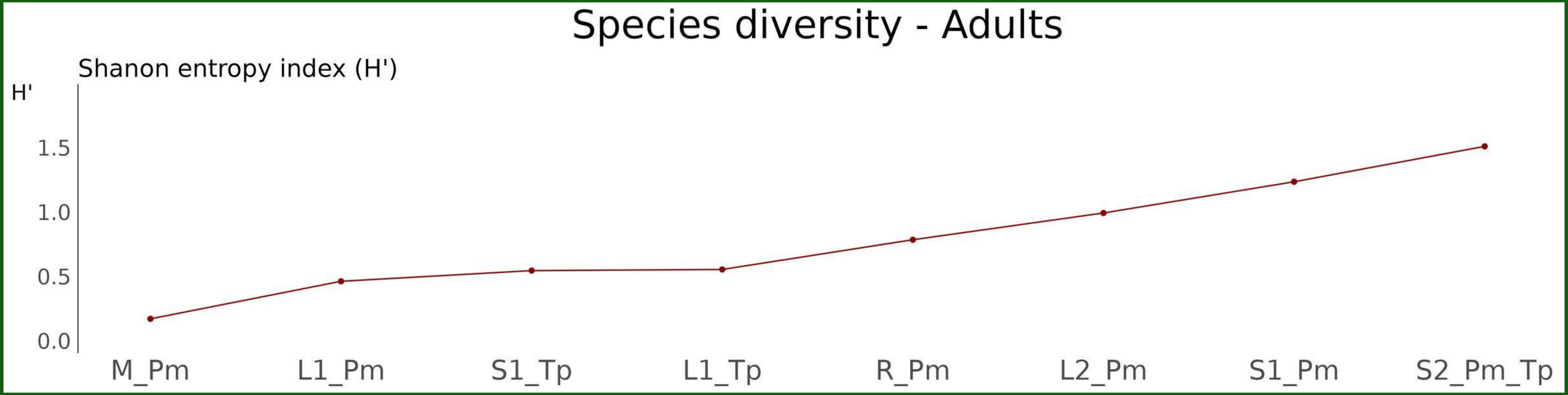
Plantation

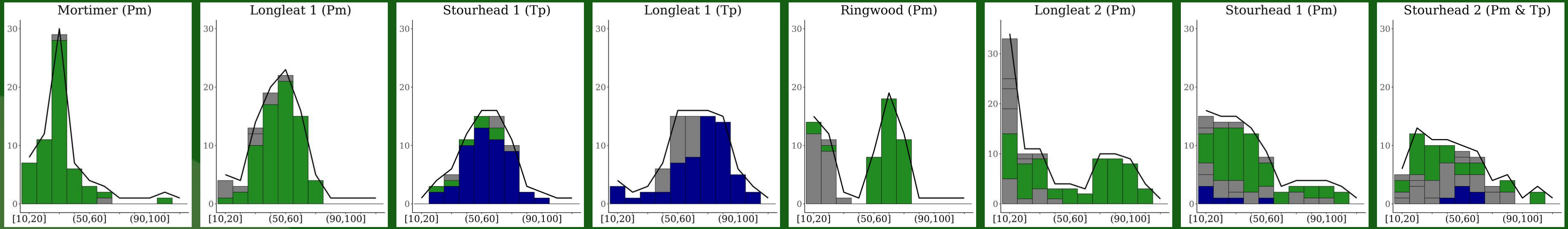
Late stage of CCF



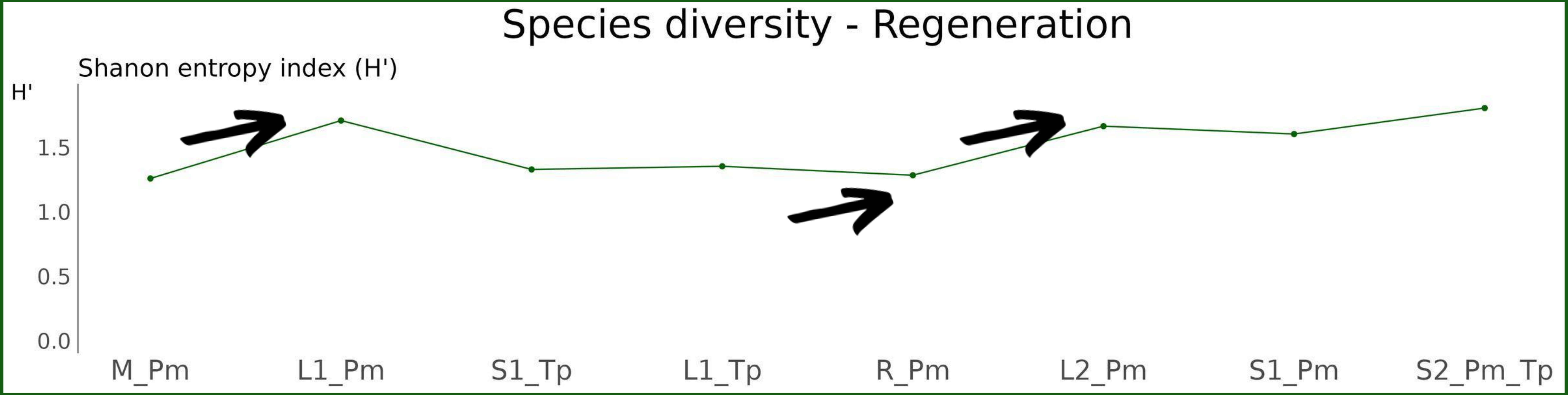
Sites characterisation

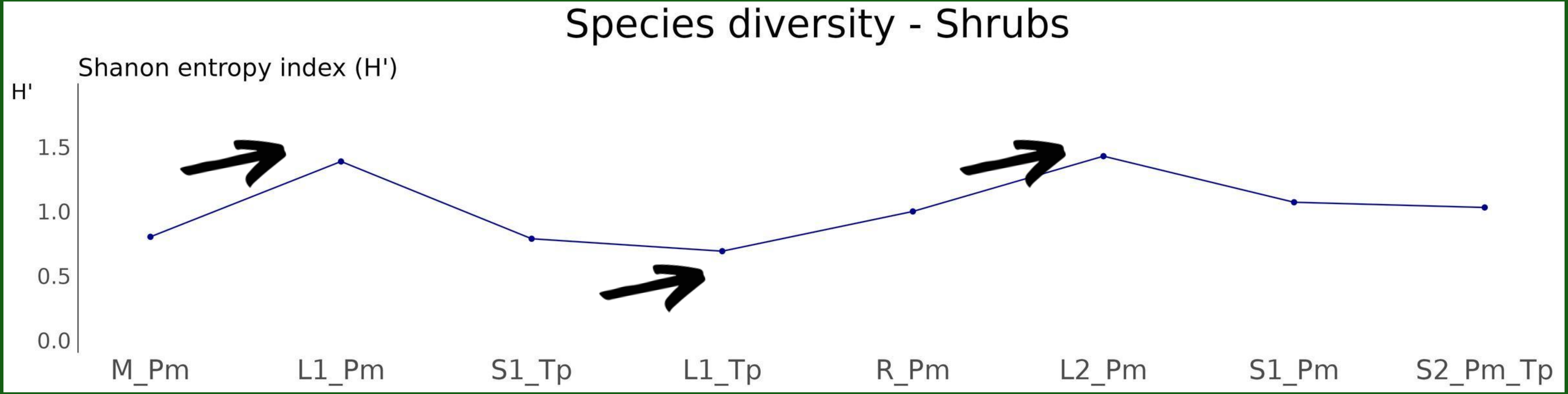
H' = represents the uncertainty with which we can predict which species will be one randomly selected individual in the community

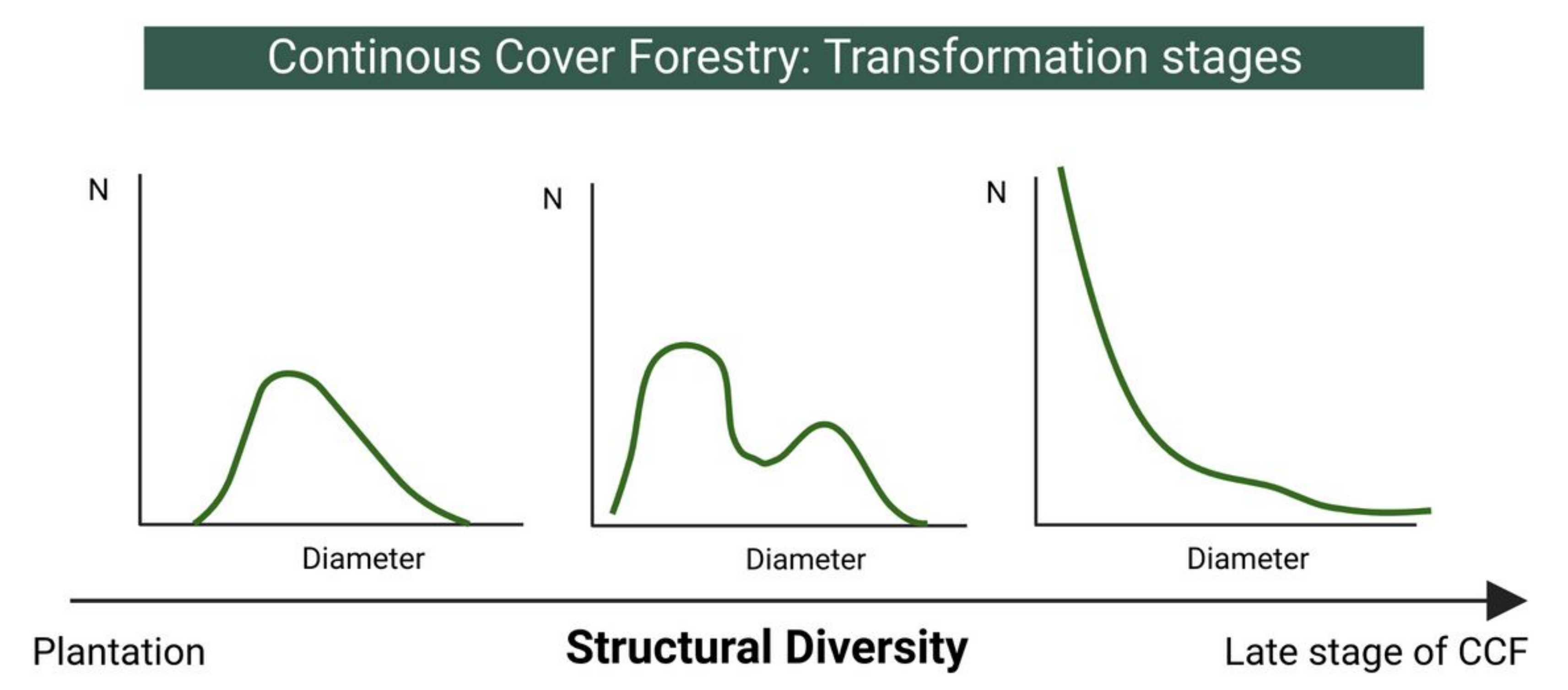


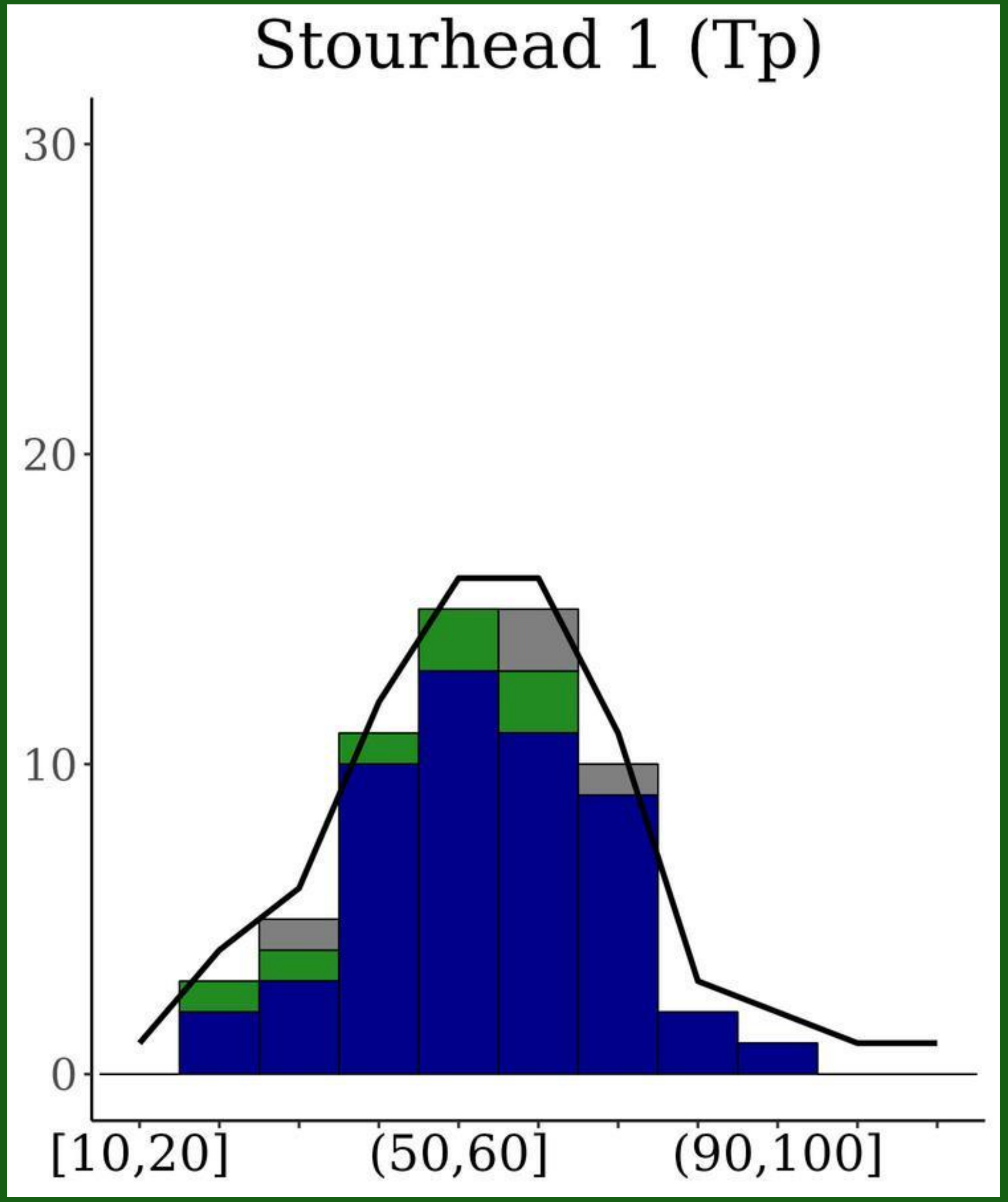


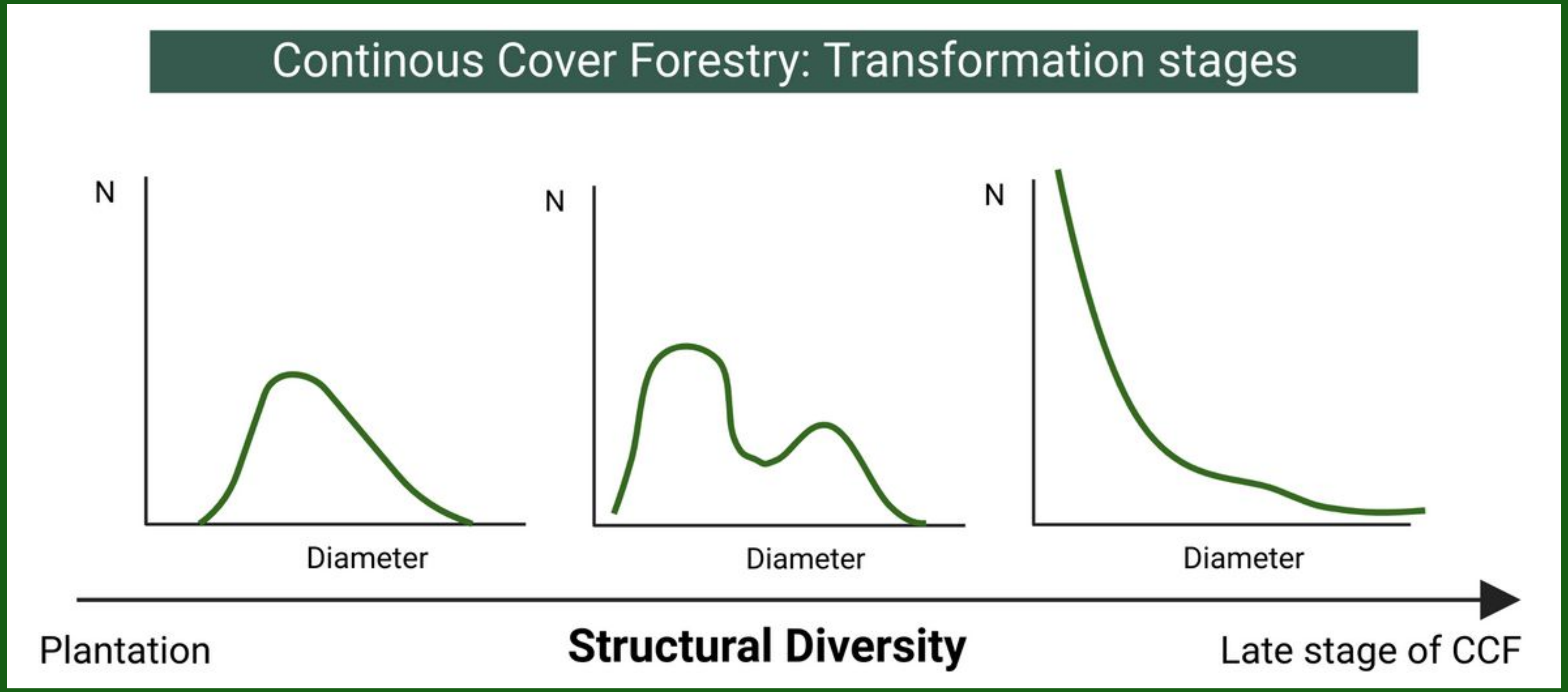
Sites characterisation






Continous Cover Forestry: Transformation stages
N
Diameter
N
Diameter
N
Diameter
Plantation
Structural Diversity
Late stage of CCF


Stourhead 1 (Tp)
30
20
10
0
[10,20]
(50,60]
(90,100]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Diameter
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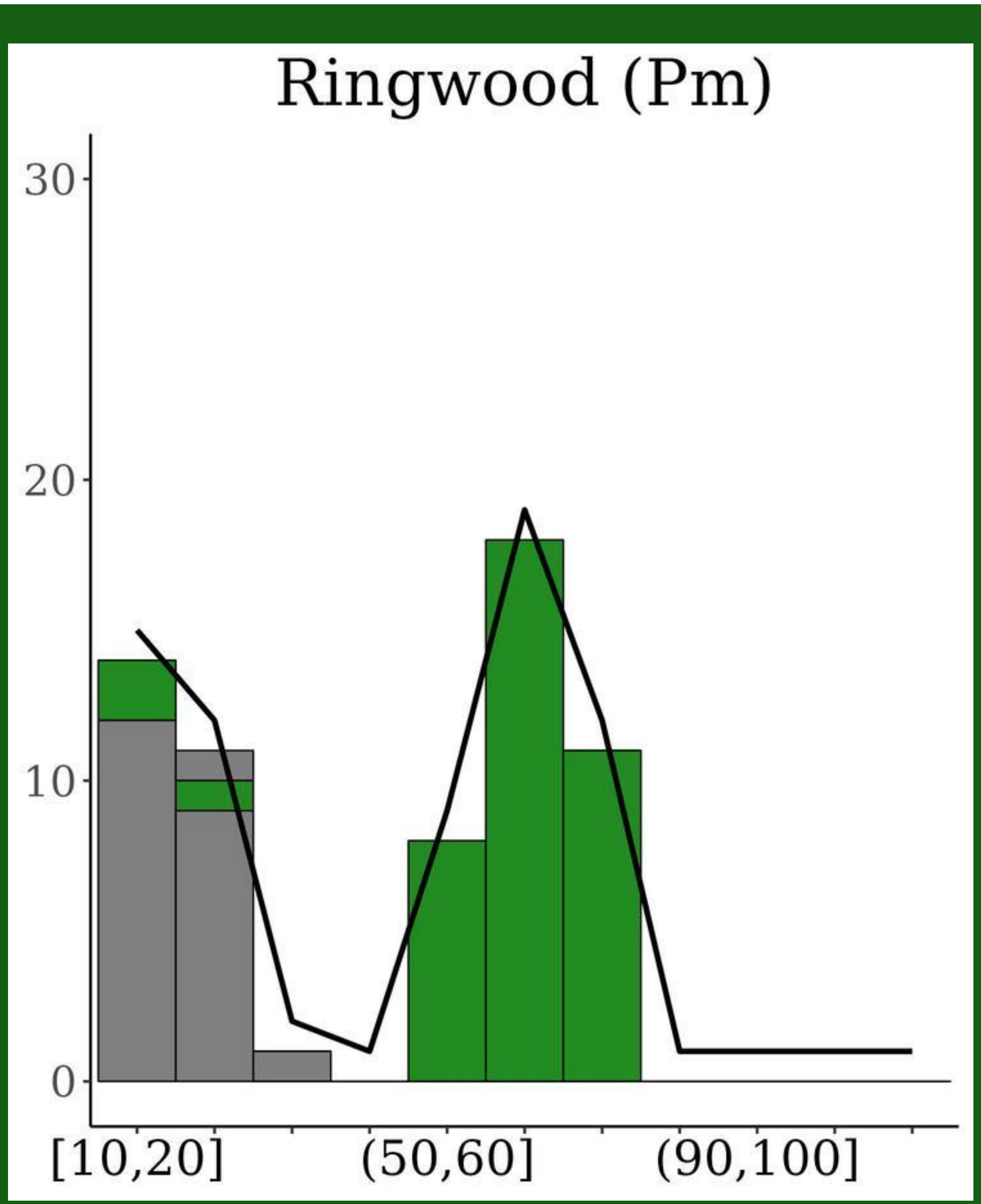
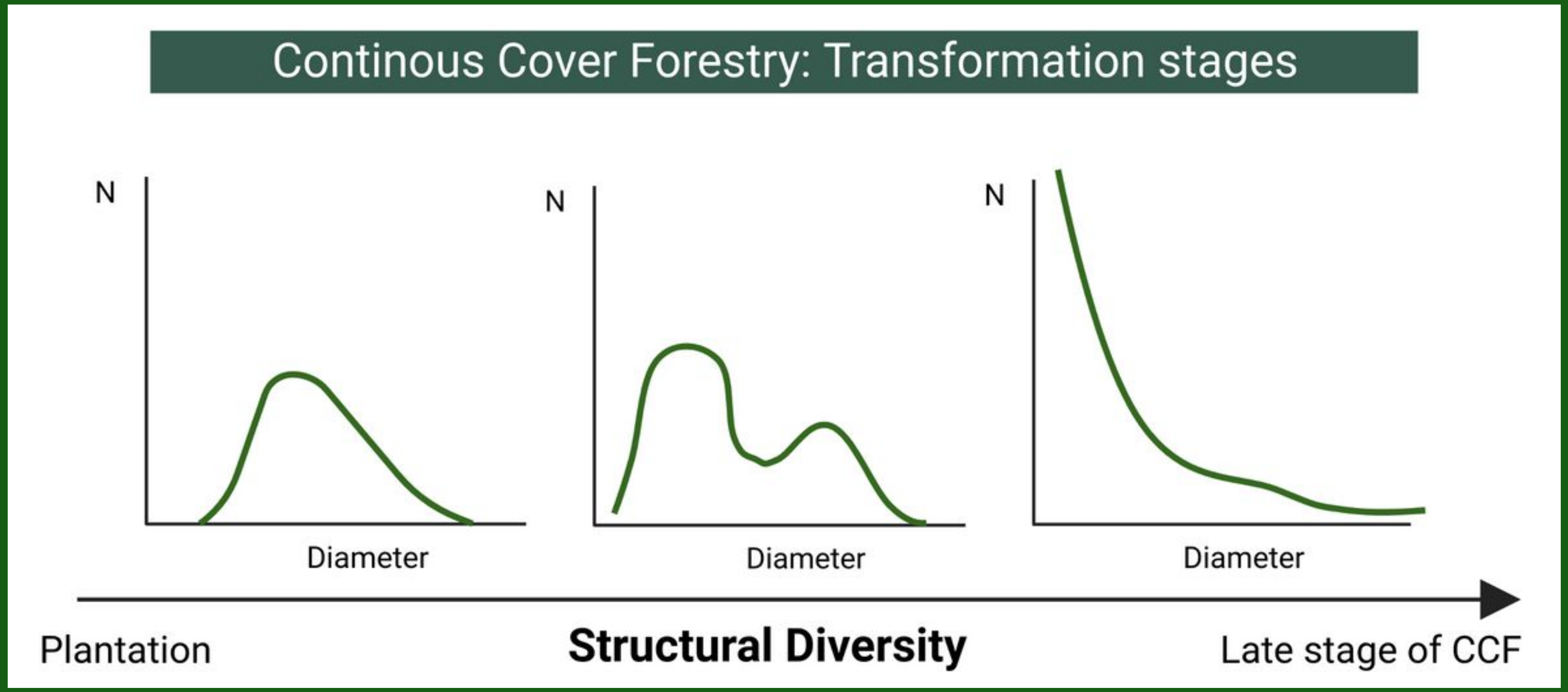

Ringwood (Pm)
30
20
10
0
[10,20]
(50,60]
(90,100]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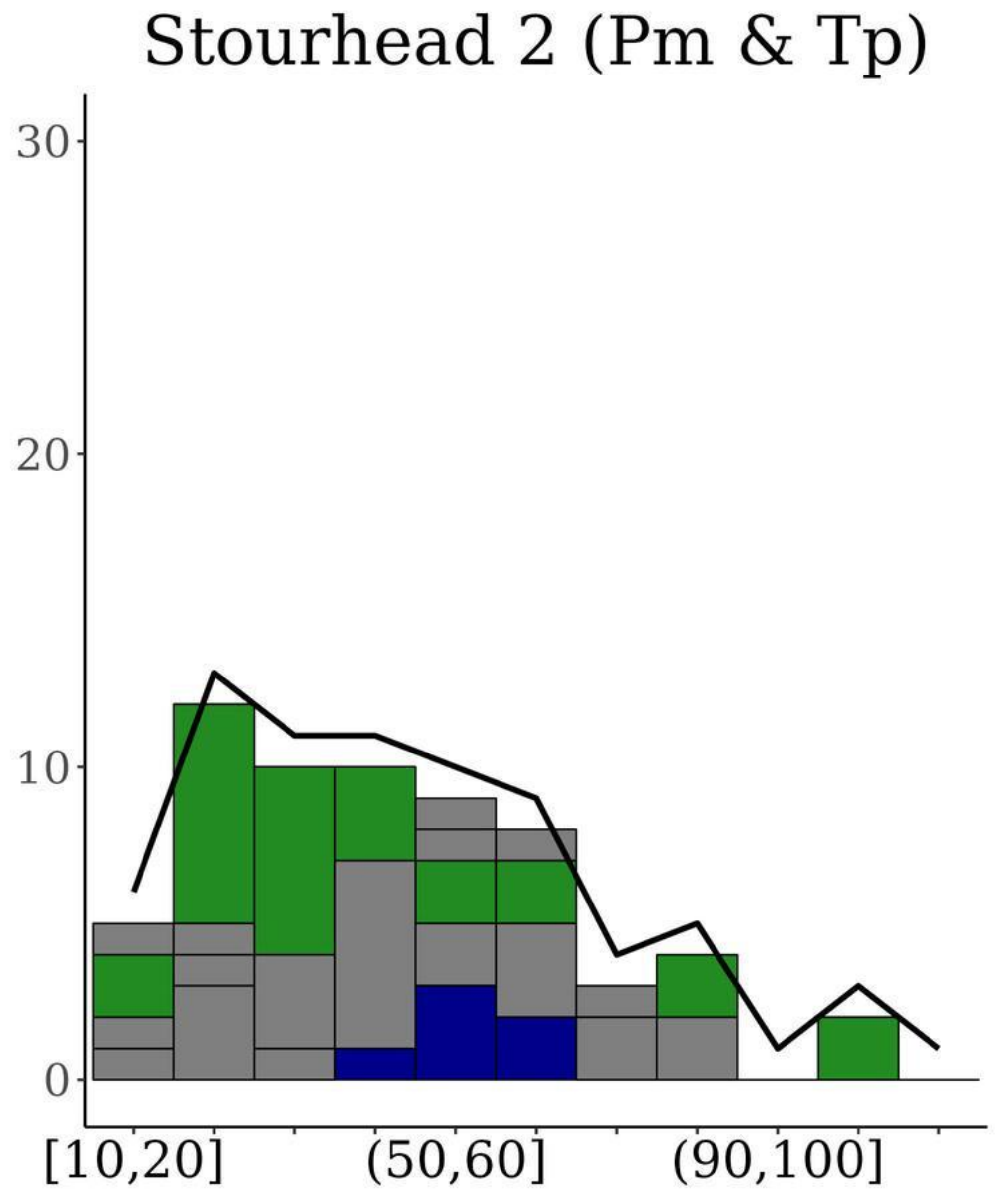
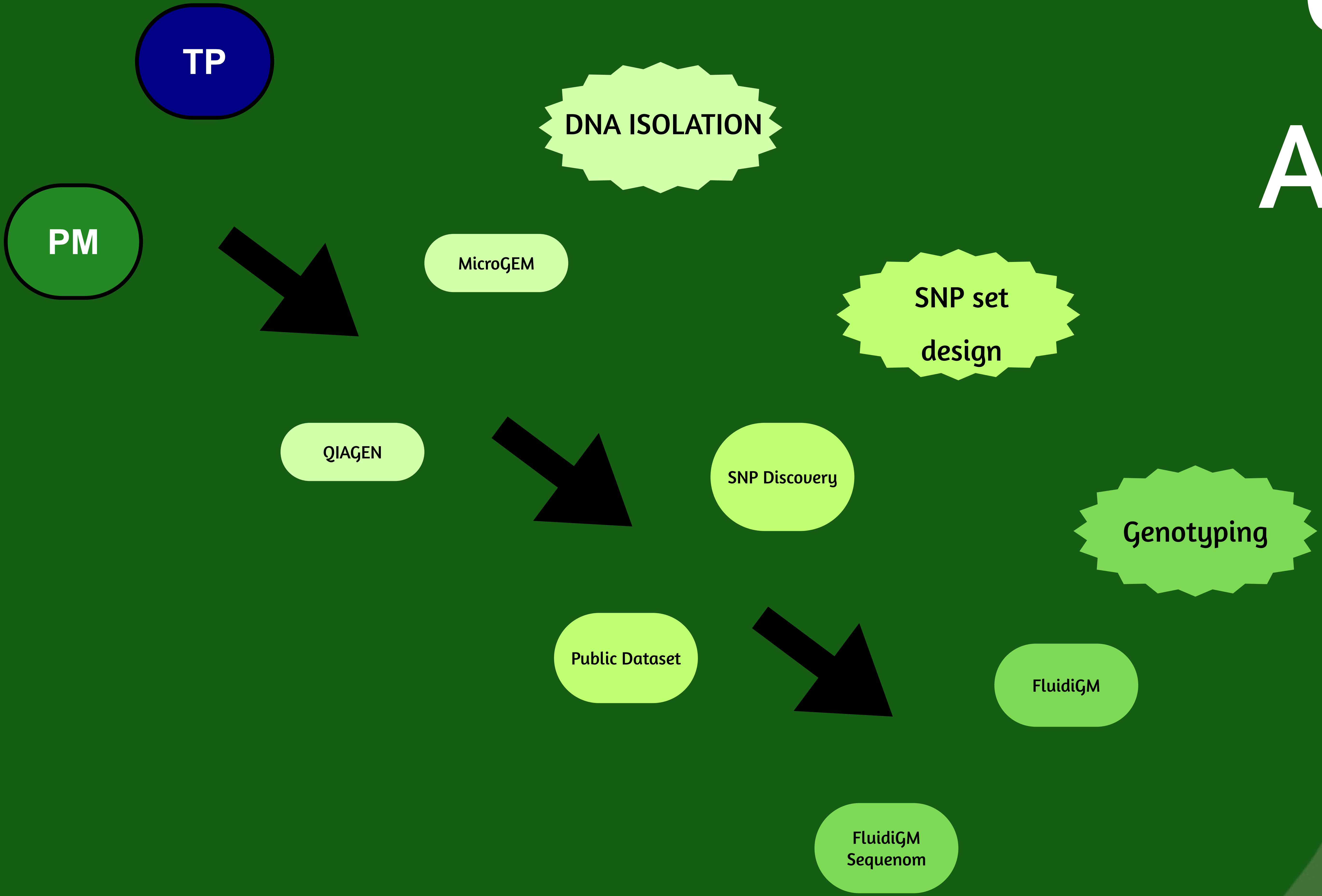

Stourhead 2 (Pm & Tp)
30
20
10
0
[10,20]
(50,60]
(90,100]

Genetic Analyses



TP

PM

DNA ISOLATION

MicroGEM

QIAGEN

SNP set design

SNP Discovery

Public Dataset

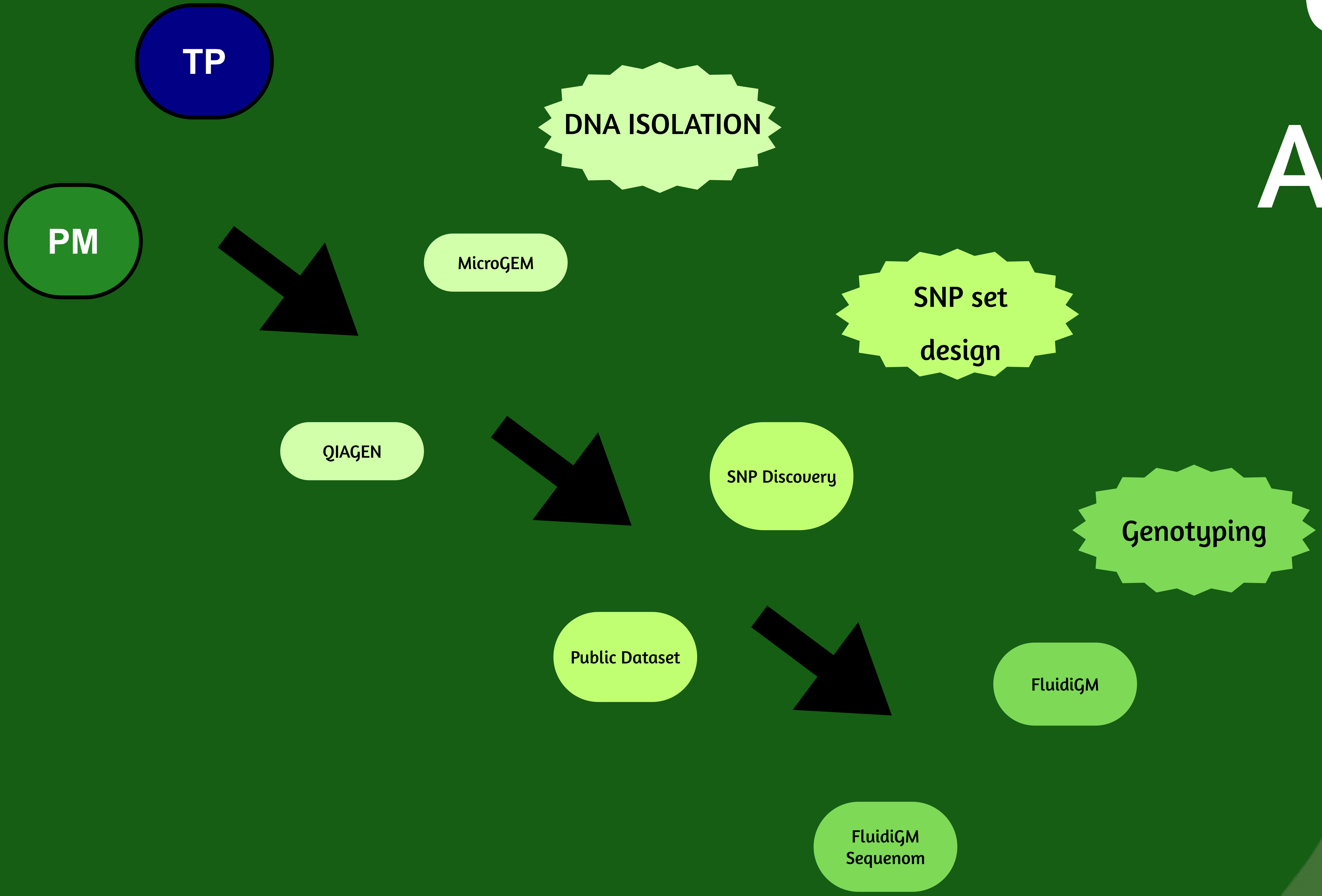
Genotyping

FluidiGM

FluidiGM Sequenom

50 Adults 50 Juveniles per site

Genetic Analyses



TP

PM

DNA ISOLATION

MicroGEM

QIAGEN

SNP set design

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Public Dataset

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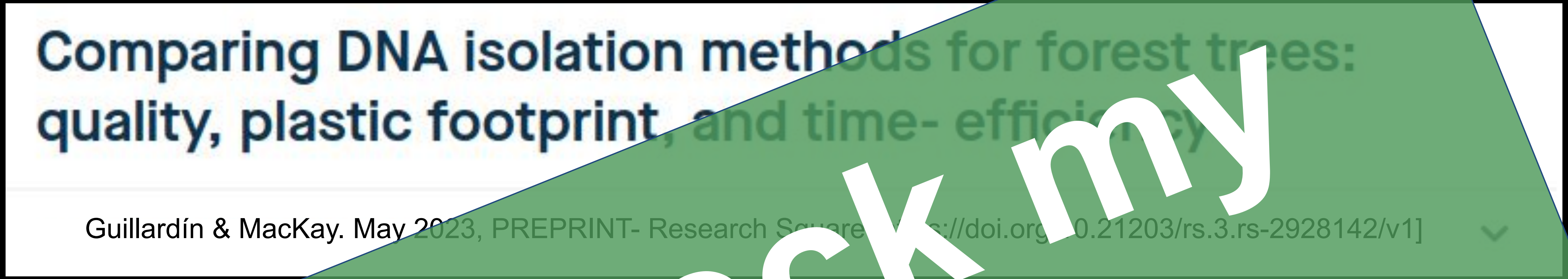
FluidiGM
Sequenom

Reducing plastic footprint of DNA isolations



Comparing DNA isolation methods for forest trees: quality, plastic footprint, and time- efficiency

Guillardín & MacKay. May 2023, PREPRINT- Research Square s://doi.org 0.21203/rs.3.rs-2928142/v1]

Optimization

Each method was tested and modified on three species

TP: **Thuja plicata**

PM: **Pseudotsuga menziesii**

Th: **Tsuga heterophylla**

DNA Quality

Analysed with DNA Barcoding techniques

Time needed

Measured for both methods

Plastic used

Measured for both methods

Come to check my poster out

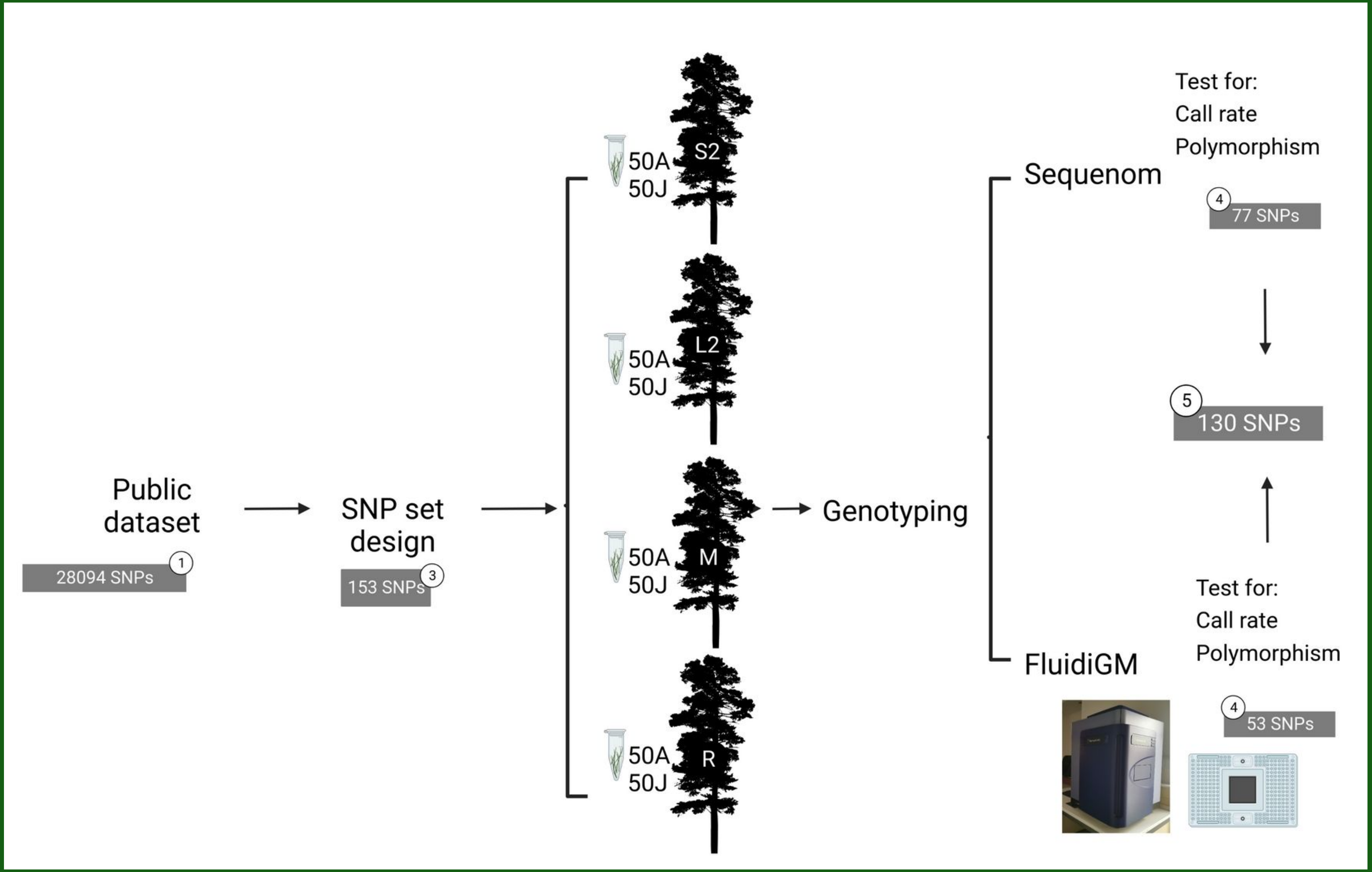
SNP set design

SNP Discovery

Genotyping

FluidiGM
Sequenom

PM



38400 PCRs

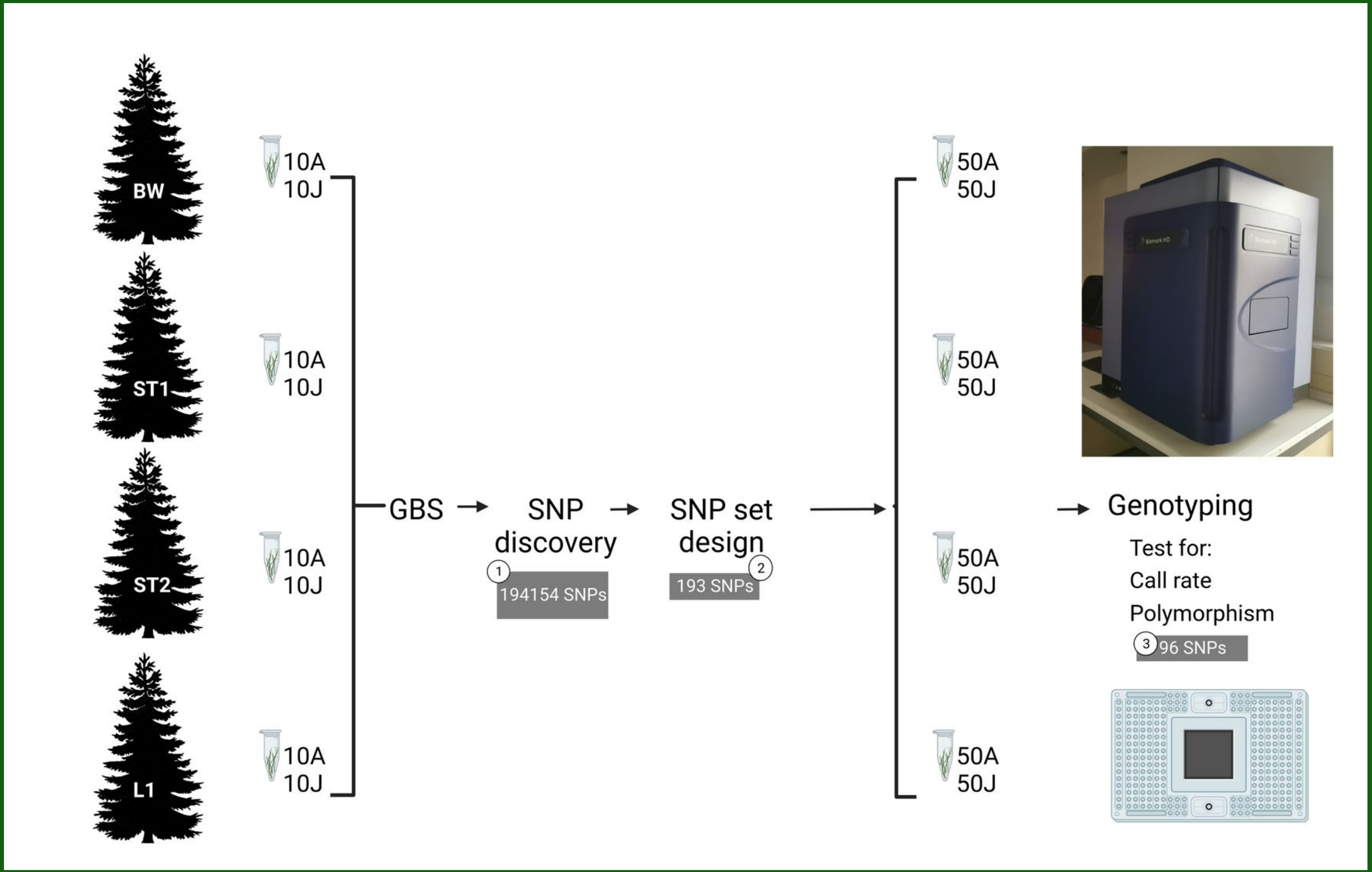
SNP set design

SNP Discovery

Genotyping

FluidiGM
Sequenom

TP



38400 PCRs

+ PM

76000 PCRs

Genetic diversity indicators

H: It is the proportion of individuals in a population that are heterozygous for at least one locus.

PM

pop	uHe
Stourhead2	0.485772
Longleat2	0.486062
Mortimer	0.483374
Ringwood	0.487052

Min: Mortimer

Max: Ringwood

* pval 0.014

High levels of g.d following what has been found before (Neophytou et al 2020).

Suggest broad genetic base in UK PM stands.

TP

pop	uHe
BagleyWoods	0.464572
Longleat	0.249361
Stourhead1	0.453969
Stourhead2	0.459056

Min: Longleat *

low levels of H can lead to g. drift and inbreeding depression

Genetic diversity indicators

H: It is the proportion of individuals in a population that are heterozygous for at least one locus.

pop	Adults	Juveniles
Stourhead2	=	
Longleat2	=	
Mortimer	=	
Ringwood	=	

PM

Stourhead2	Adults	Juveniles
BagleyWoods	=	
Longleat	↑	
Stourhead1	=	
Stourhead2		↑

Longleat: *

pval

0.001

Stourhead2: *

pval

0.005

TP

Genetic diversity indicators

Ne: size of an idealized population that shows the same value of g. drift as the real population

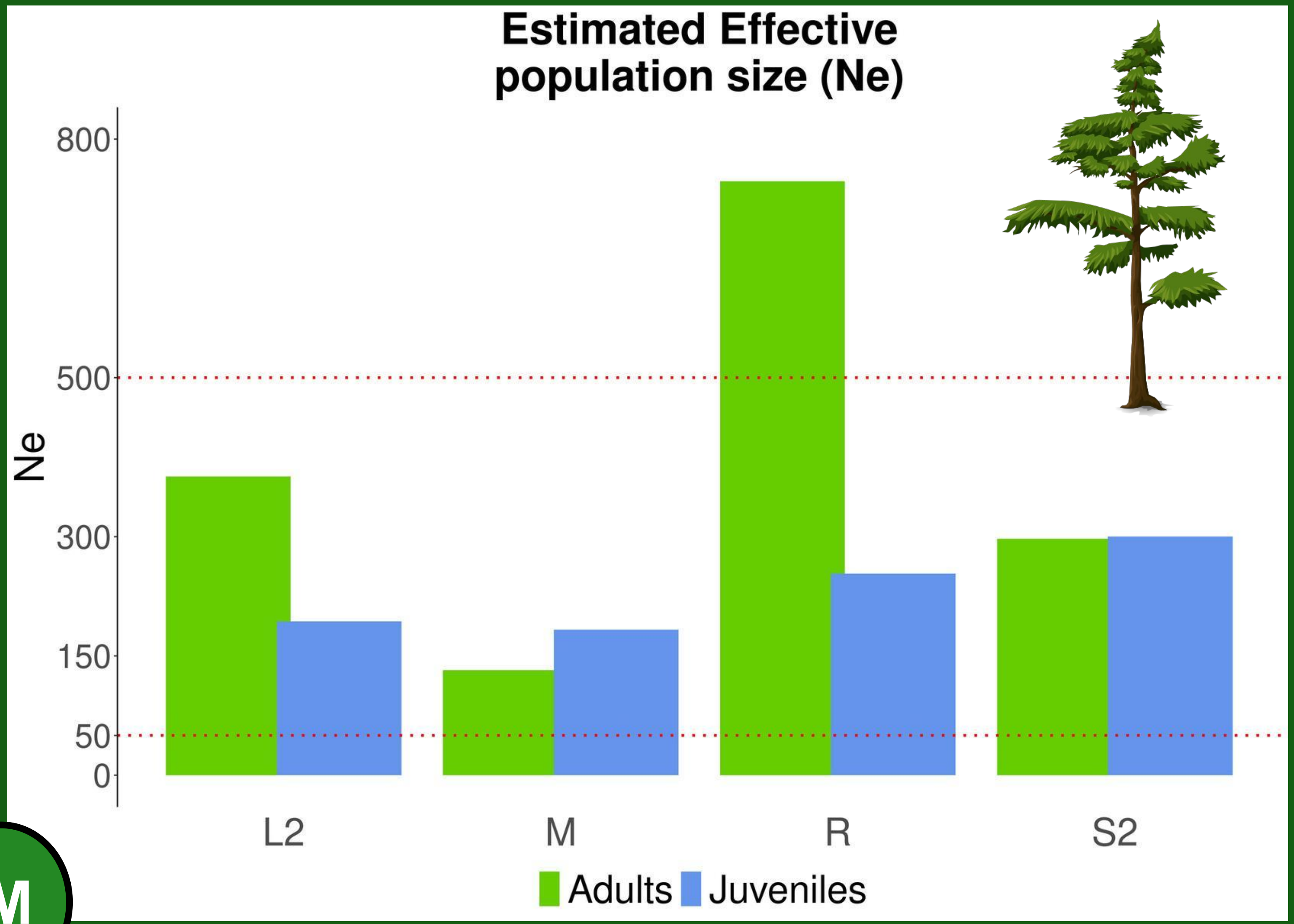
Seed orchards minimum Ne = 10

50/500 RULE

Ne>50 minimize short-term inbreeding

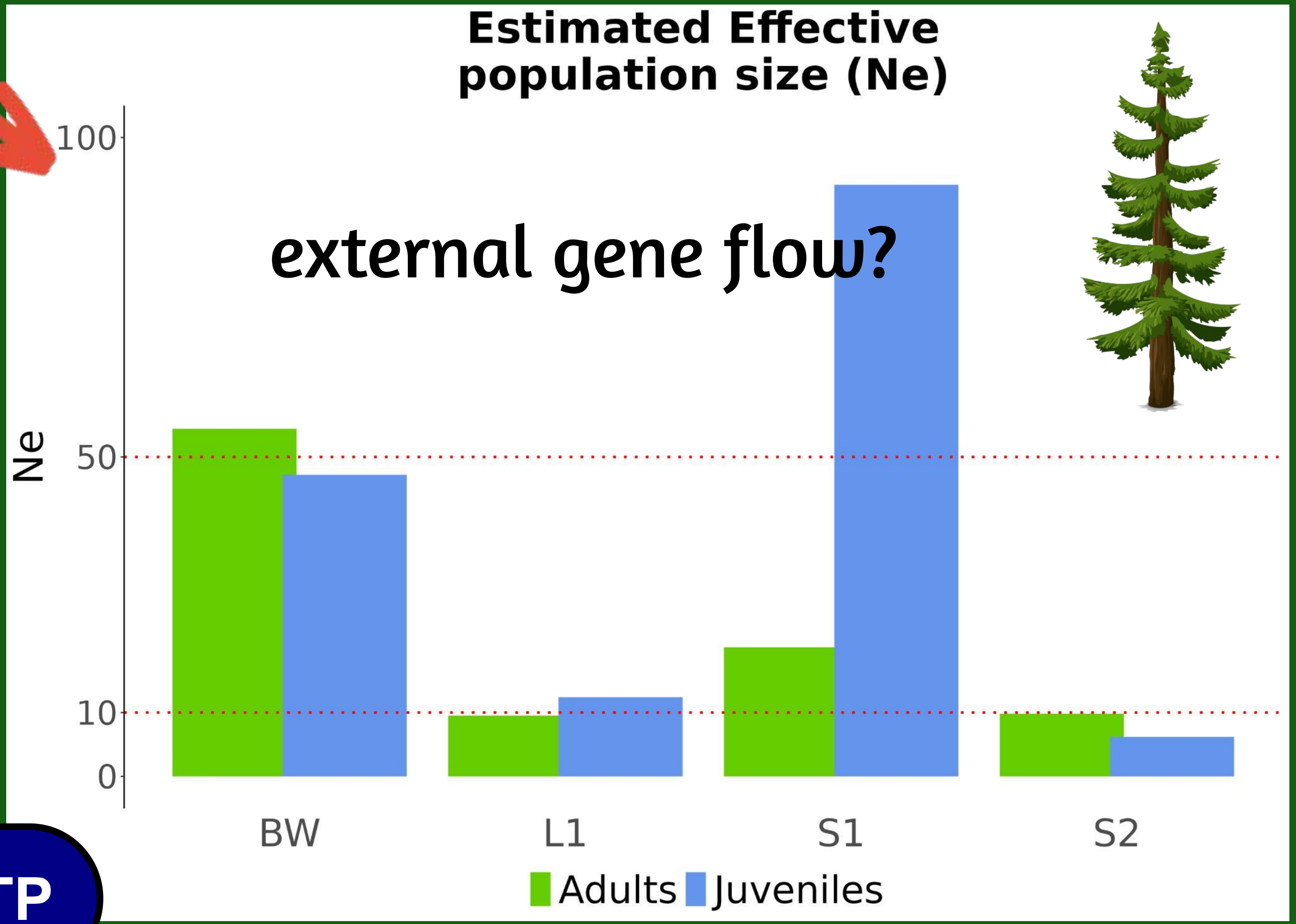
Ne>500 maintain genetic variance in long-term (COP15 new genetic conservation indicator)

< 50 → more difficult for the population to adapt to current/future conditions



PM

Different scale!



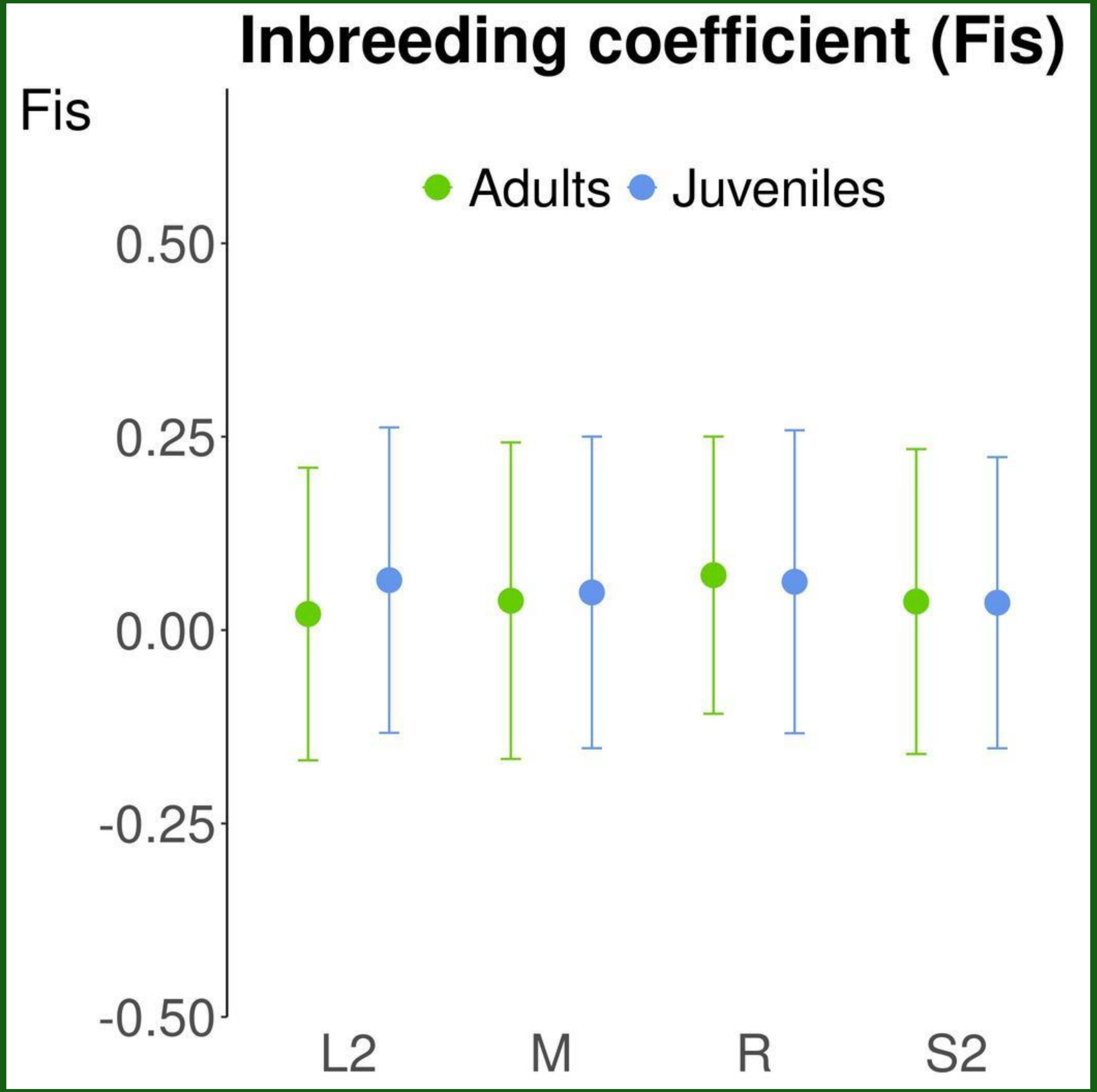
external gene flow?

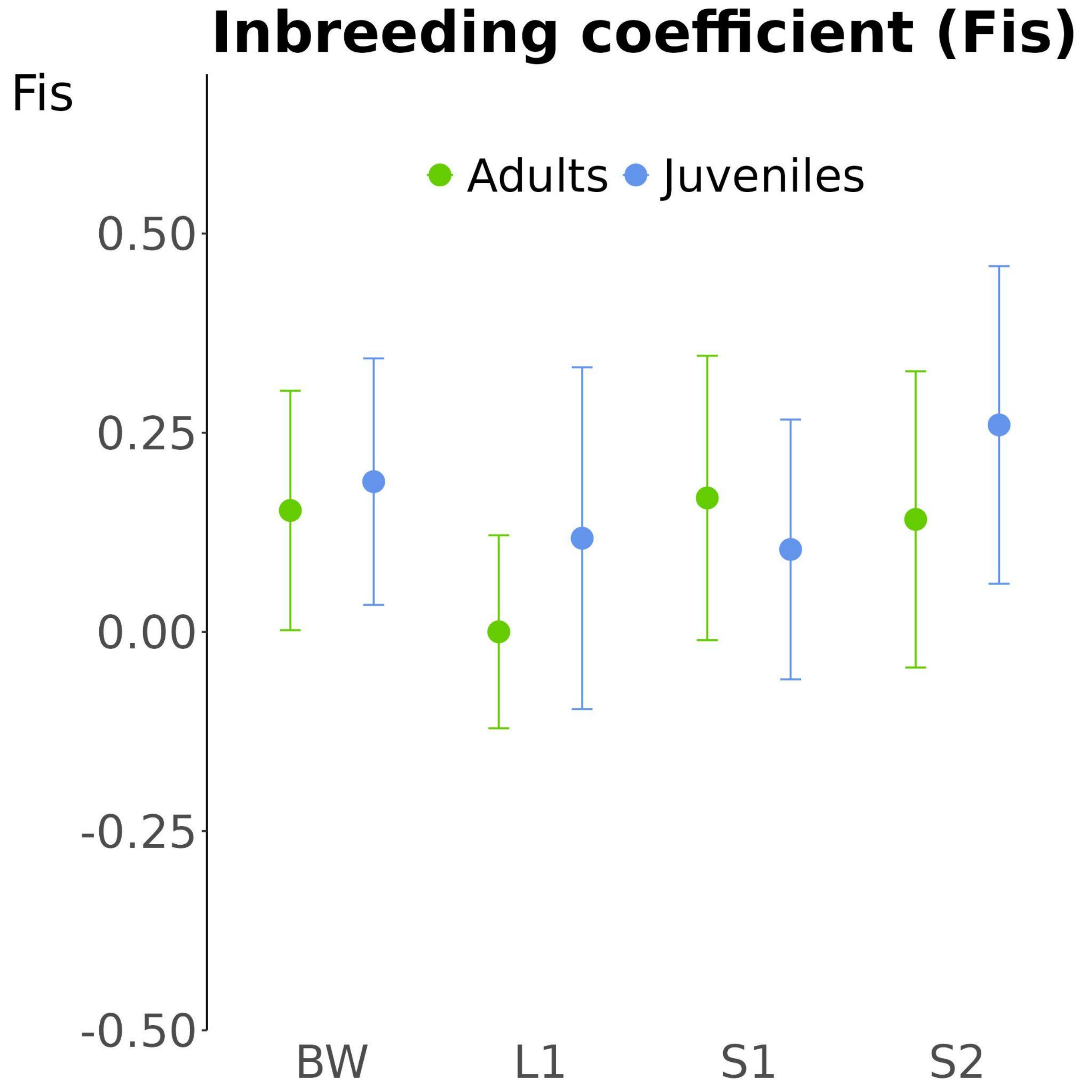
TP

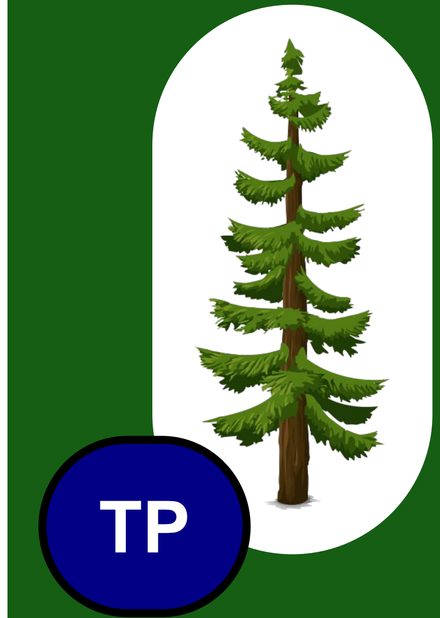
Assisted gene flow?

Genetic diversity indicators

Fis: is a measure of how much the heterozygosity in a population is different from what would be expected if the population was not inbred.

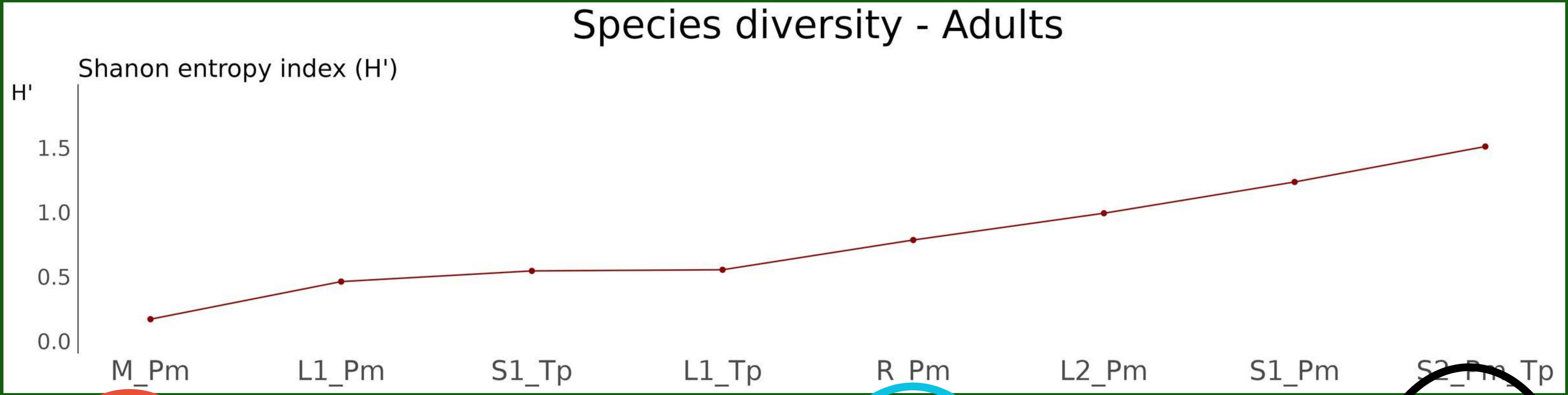


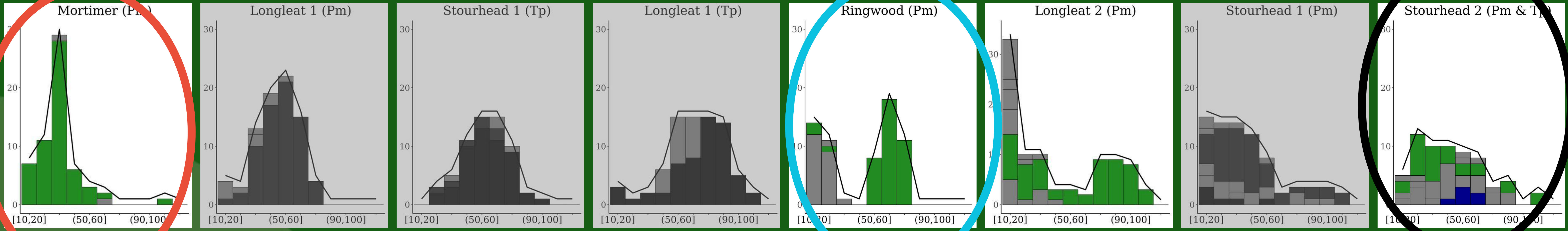




can be showing a trend to future generations

Species diversity - Adults





Min

Max

???

PM Ne<500
TP Ne<10

Although a plantation can be naturalised and increase in diversity of species and structure, we can't assume that it will behave as an adapted natural population just because it looks like it. Genomics and genetics studies are key to determine potential adaptation to climate change.

Ella Glover

Dr Heather Dun

Barley Rose Collier Harris

Will Hoare

George MacKay

Prof. John MacKay

Dr Gary Kerr

Forest Research

- Current and past ForesTree Biology Group members
- Patty Bowman and Sarah Rodgers
- Stourhead, Longleat, Bagley Woods landowners & Forest Research

Thank you!

the genetics society

John Oldacre Foundation

Department of BIOLOGY

UNIVERSITY OF OXFORD