

Genetic database as a tool to provide proof of origin of autochthonous forest reproductive material

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NATURE AND FOREST



Importance of origin

- European Green Deal sparks interest in (re)forestation projects
- Origin of planted trees key for
 - Resilience
 - Resistance
 - Adaptation potential to future climate conditions



Flemish forest reproductive material (FRM)

- Flemish quality label 'Plant van Hier'
 - Autochthonous FRM
 - By Agency for Nature and Forests (ANB)
 - For certified tree nurseries and selling points



Guarantee of origin

- Routine controls on tree nurseries by 'Agency for agriculture and fisheries'
 - Plant counting based on seed harvest
- Genetic control system
 - Based on genetic fingerprints of parent-trees of autochthonous seed orchards (category 'source identified')

Species

Source: © Rasbak



Carpinus betulus

Source: © Sten Porse



Corylus avellana

Source: © Biopix JC Scou



Frangula alnus



Ulmus laevis

Source: © I. Hugo.arg



Populus tremula

Source: © Georgy Vinogradov iNaturalist



Sorbus aucuparia

Source: © camifex, iNaturalist



Tilia cordata



Tilia platyphyllos

Source: © felix_riegel, iNaturalist



Quercus robur

Molecular markers

- SSR makers (microsatellite markers)
- 12 – 24 markers per species
- New markers developed for
 - *Carpinus betulus*
 - *Ulmus laevis*

Source: © Rasbak



Source: © Biopix JC Scou



Genetic control system



Orchard

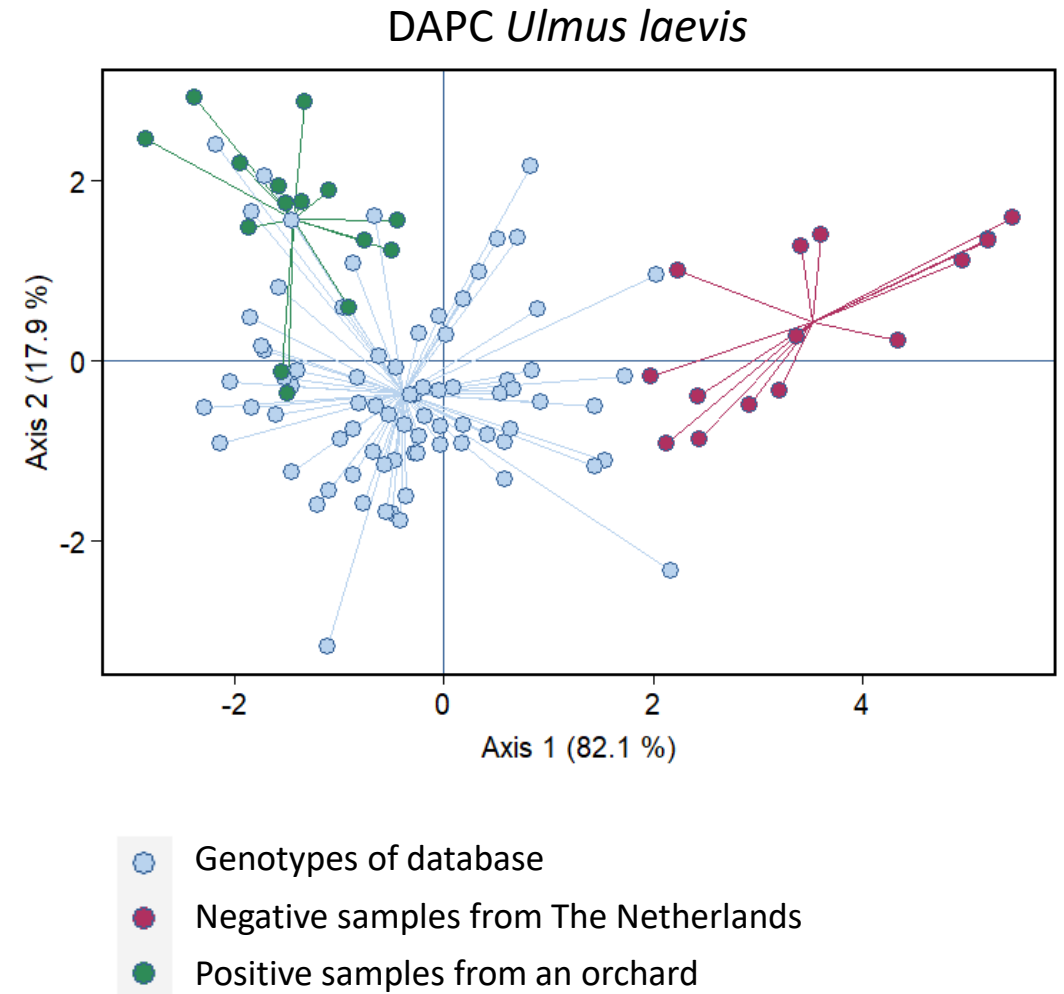


Database

Code boom	Populatio	ORPM_1	ORPM_2	ORPM_3	ORPM_4	WPMS_1	WPMS_2	ORPM_1	ORPM_2	WPMS_1	WPMS_2	PTK2_1	PTK2_2
P.TREM_4		196	208	200	200	223	229	181	181	207	213	211	217
P.TREM_1		184	196	204	204	229	229	181	181	207	228	211	211
Onkewand			MD	MD	MD	MD	MD	MD	MD	MD	MD	MD	MD
P.TREM_2		196	208	200	200	223	229	181	181	207	213	211	217
P.TREM_6		187	193	204	204	223	229	181	181	207	243	208	217
HAL1	HAL	184	184	204	204	217	229	181	181	228	228	211	220
DS4	DS	184	196	200	220	223	229	MD	MD	219	228	211	214
DS6	DS	184	193	204	204	229	229	181	181	213	228	211	211
P.TREM_6		187	193	204	204	223	229	181	181	207	243	208	217
KIA2	KIA	196	208	200	200	223	229	181	191	228	243	211	217
DS2	DS	184	184	204	204	229	229	181	193	210	213	211	211
P.TREM_4		196	208	200	200	223	229	181	181	207	213	211	217
DS2	DS	184	184	204	204	229	229	181	193	210	213	211	211
DS3	DS	184	184	200	200	223	223	181	181	228	228	208	217
MCE1 VZA	MCE	184	193	214	220	229	229	MD	MD	207	228	208	208
P.TREM_3		184	196	200	218	229	229	MD	MD	219	228	208	211
P.TREM_5		184	196	200	208	223	223	181	191	228	234	208	211
DS6	DS	184	193	204	204	229	229	181	181	213	228	211	211
WC1	WC	184	193	200	200	229	229	181	181	228	243	199	208
DS2	DS	184	184	204	204	229	229	181	193	210	213	211	211
P.TREM_6		187	193	204	204	223	229	181	181	207	243	208	217
KAP1 KEM	KAP	184	196	200	200	229	229	MD	MD	207	228	208	211
KAP1 KEM	KAP	184	196	200	200	229	229	MD	MD	207	228	208	211
SCH1 KEM	SCH	199	199	200	200	229	229	181	181	207	243	211	214
MEL1 VVG	MEL	196	196	200	200	223	229	181	181	219	228	208	211
P.TREM_4		196	208	200	200	223	229	181	181	207	213	211	217
TUR2 KEM	TUR	184	199	204	220	229	229	181	181	228	243	205	220

Genetic control system

- Positive control samples:
 - Seedlings raised from seeds of orchards
- Negative control samples:
 - Non-autochthonous seedlings
- DAPC-plot and parentage analyses (COLONY & CERVUS)



More than a database

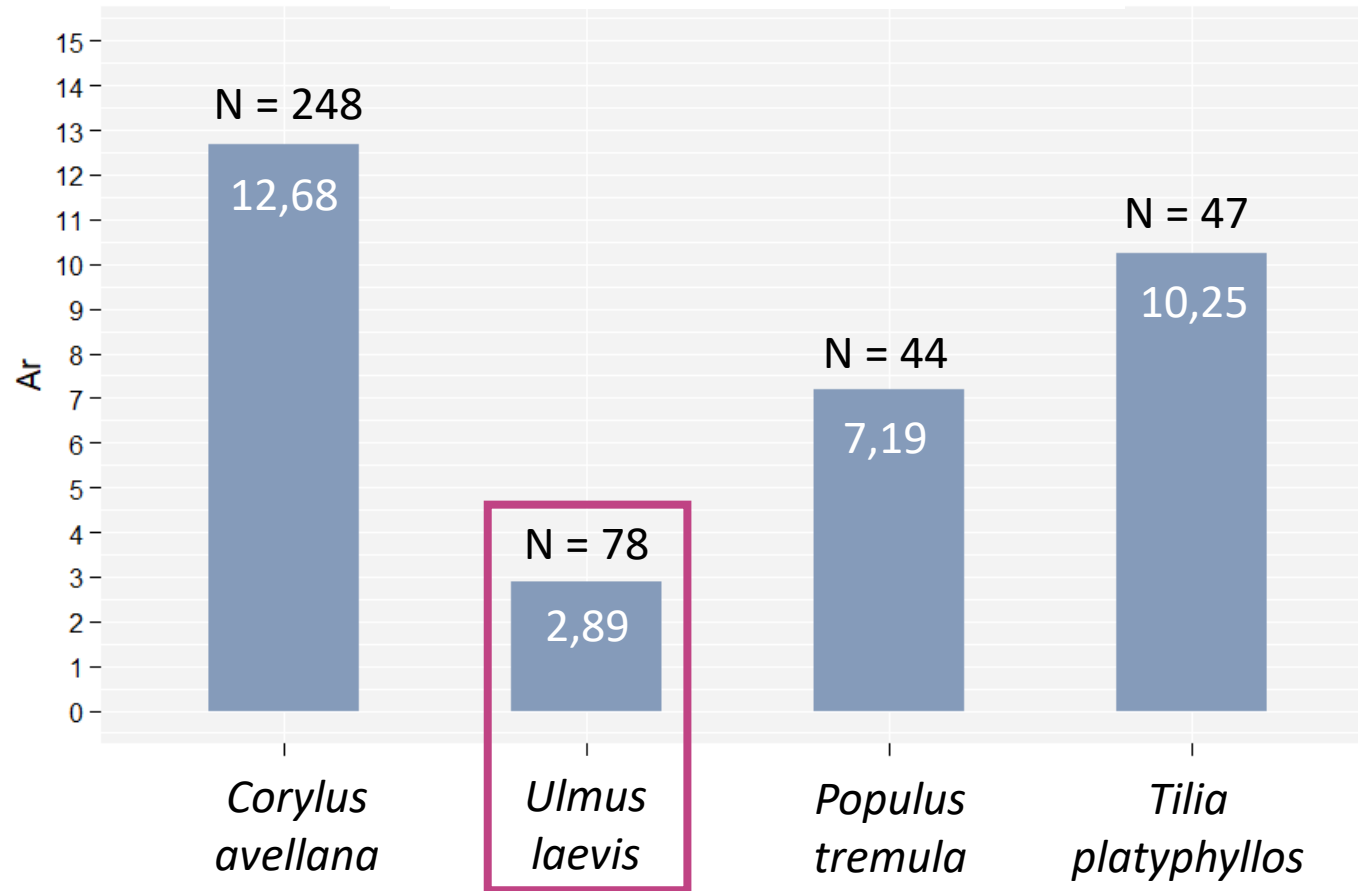
- Genetic fingerprints useful for future scientific research
- Genetic diversity within our seed orchards
- Detection of hybridisation and cultivars
- Information for new seed orchards

More than a database

Genetic diversity



Corrected allelic richness (Ar)



N = total number of genotypes

Comparison to natural European populations:

Location	Ar	Ho	He
BE - Flanders	2,89	0,29	0,38
PL	4,0	0,64	0,55
DK	2,75	0,54	0,55
NL	2,14	0,56	0,50

More than a database



Populus tremula



Populus alba

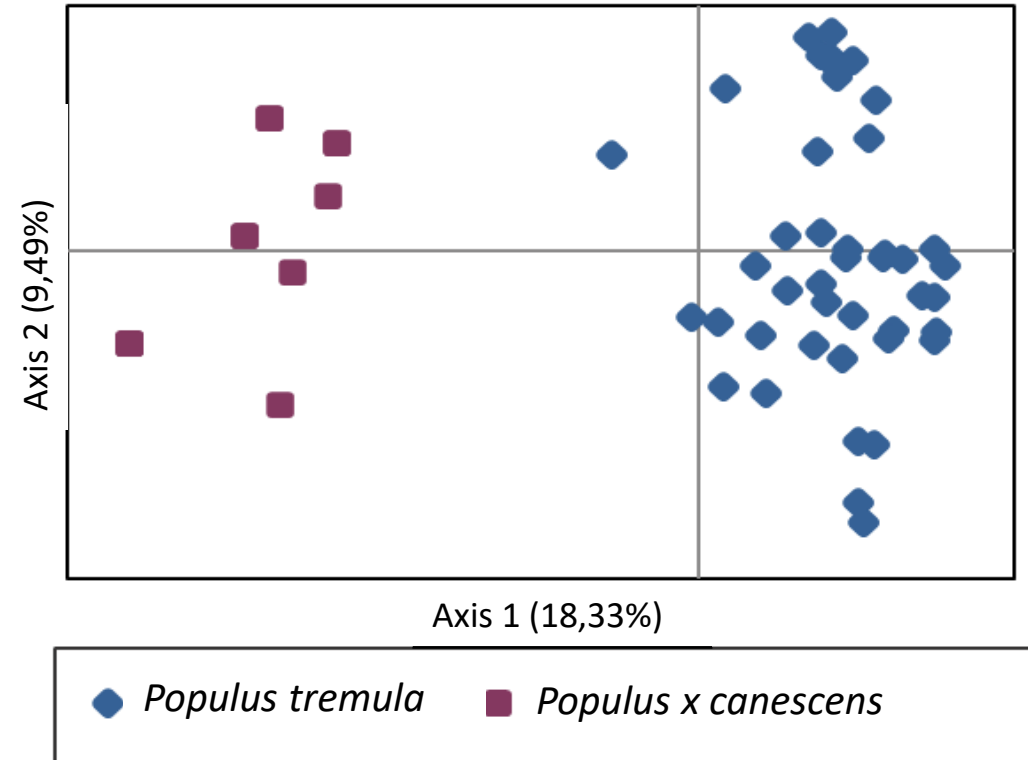
x



Populus x canescens

Natural hybridisation

Principal component Analyse: axis 1 vs axis 2



More than a database

Natural hybridisation



Populus tremula

x

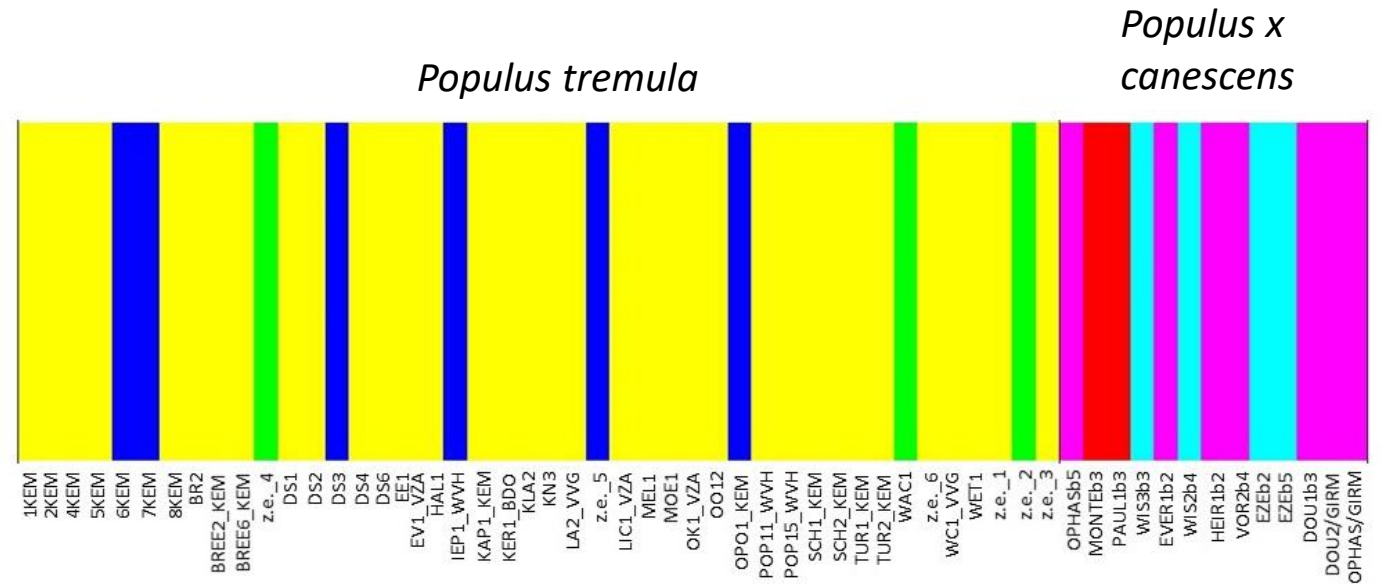


Populus alba



Populus x canescens

STRUCTURE-analysis



More than a database

Cultivar detection

Common hazelnut

- Comparison to Whole Hazelnut Germplasm Collection
 - Core collection of 181 cultivar genotypes
 - Characterized by Boccacci et al. 2021



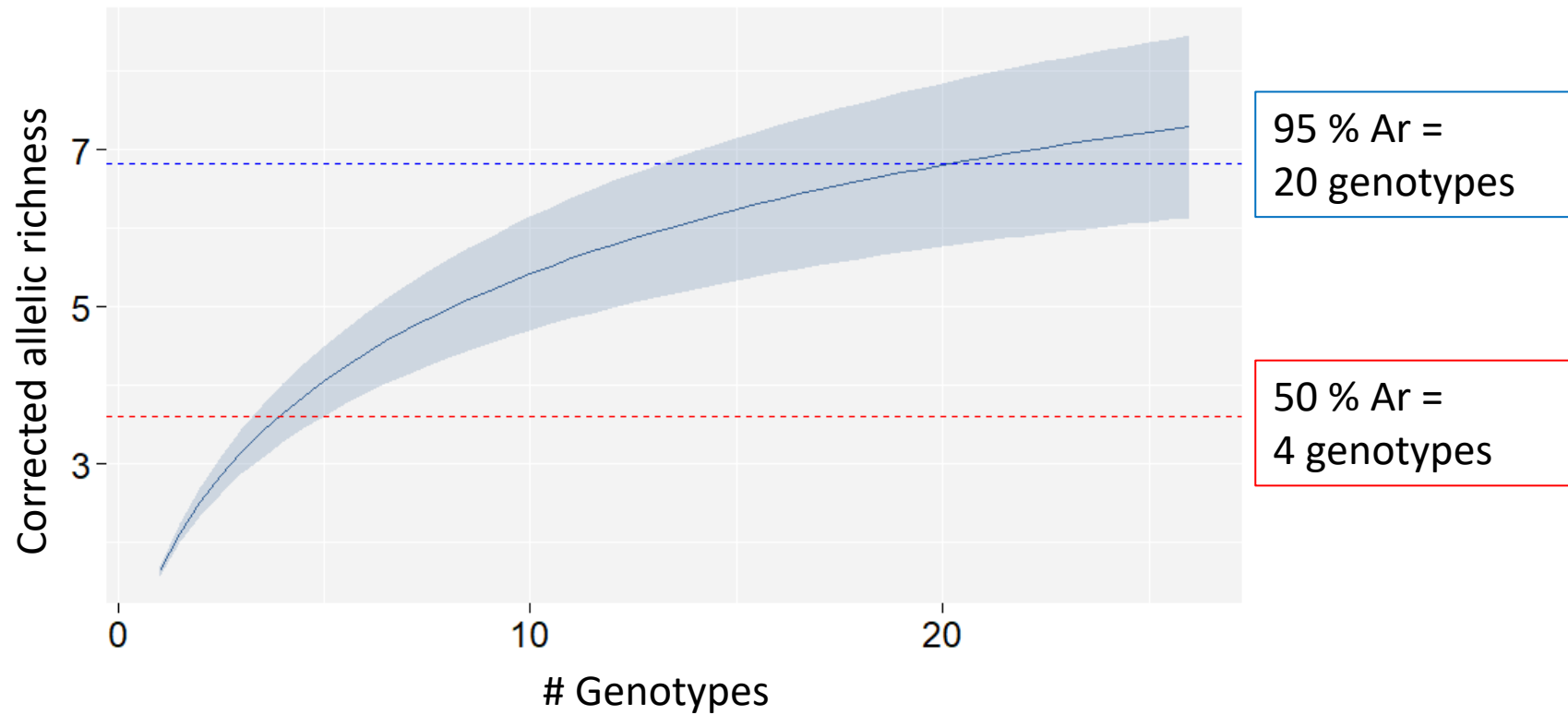
Comparison of selection methods for the establishment of a core collection using SSR markers for hazelnut (*Corylus avellana* L.) accessions from European germplasm repositories

Paolo Boccacci¹ · Maria Aramini² · Matthew Ordidge³ · Theo J. L. van Hintum⁴ · Daniela Torello Marinoni⁵ · Nadia Valentini⁵ · Jean-Paul Sarraquigne⁶ · Anita Solar⁷ · Mercè Rovira⁸ · Loretta Bacchetta² · Roberto Botta⁵

More than a database

New seed orchards

Populus tremula - Vloethemveld



Take-home message

Autochthonous FRM genetic database =

- Tool to prove the origin of Forest Reproductive Material
- Ex-situ conservation of genetic diversity
- Seed orchard management



Interreg - MigFoRest

Interreg



Co-funded by
the European Union

North-West Europe

MigFoRest

Assisted **M**igration to increase **F**orest **R**esilience in north-western Europe

Main genera: *Quercus sp.* – *Tilia sp.* – *Sorbus sp.* – *Abies sp.*

Goals:

- Develop common strategy for implementing Assisted Migration in NWE
- Identification of the best tree species and provenances
- Planting 100,000 trees on selected locations
- Creation of new seed orchards
 - Genetic screening



SRFB • KBBM



Forest Research
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Thank you for the attention!

Questions?

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