Réunion de la section 2 Forêts -filière bois

Récentes avancées en génomique des arbres forestiers

Microévolution et adaptation du chêne en réponse aux changements environnementaux

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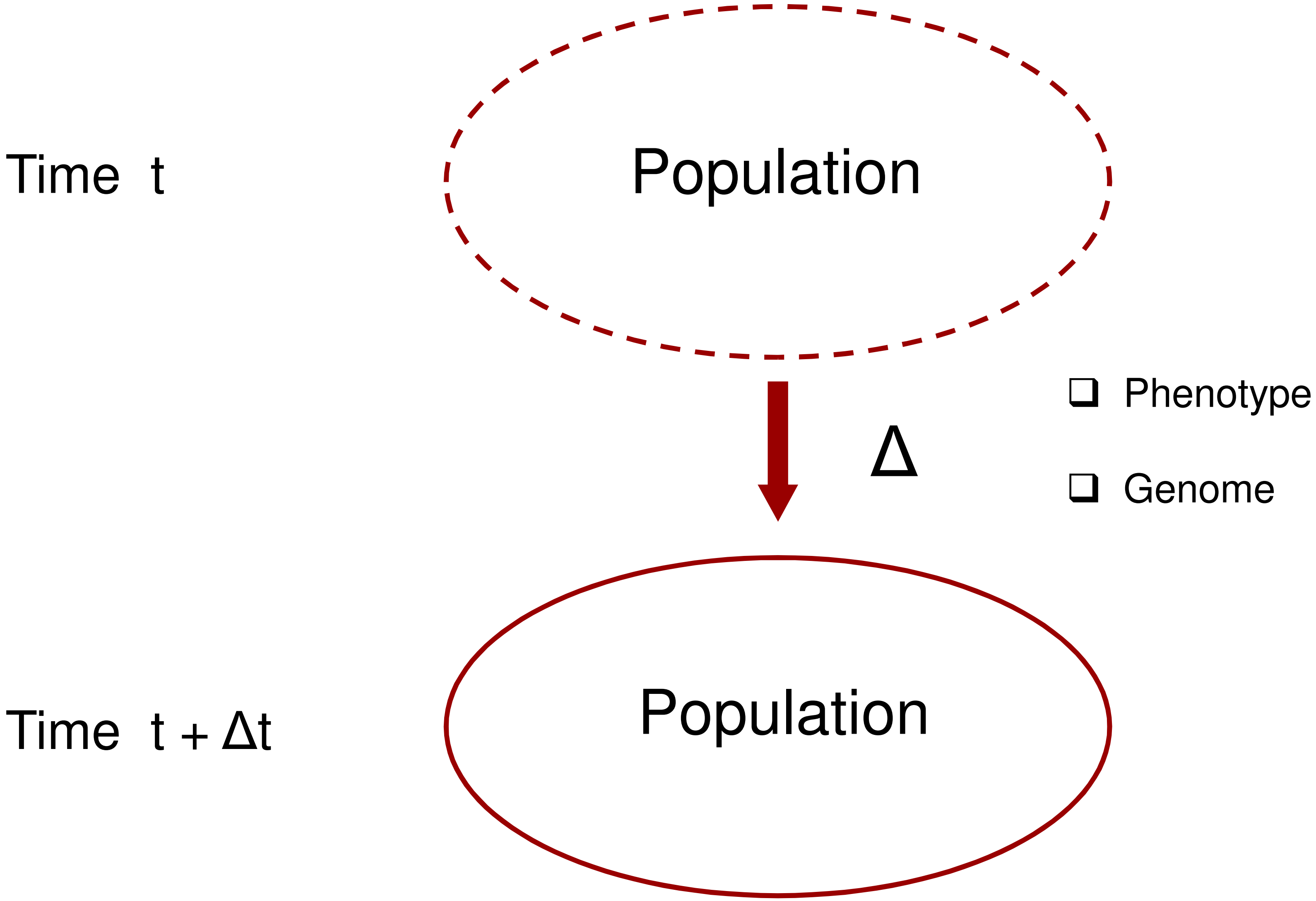
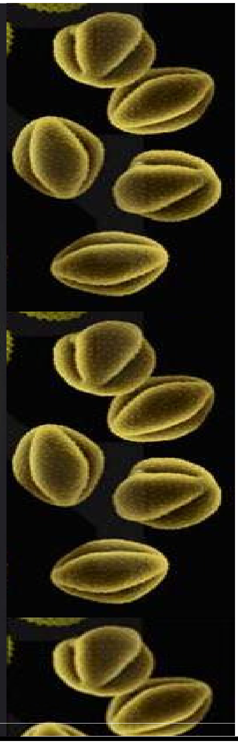
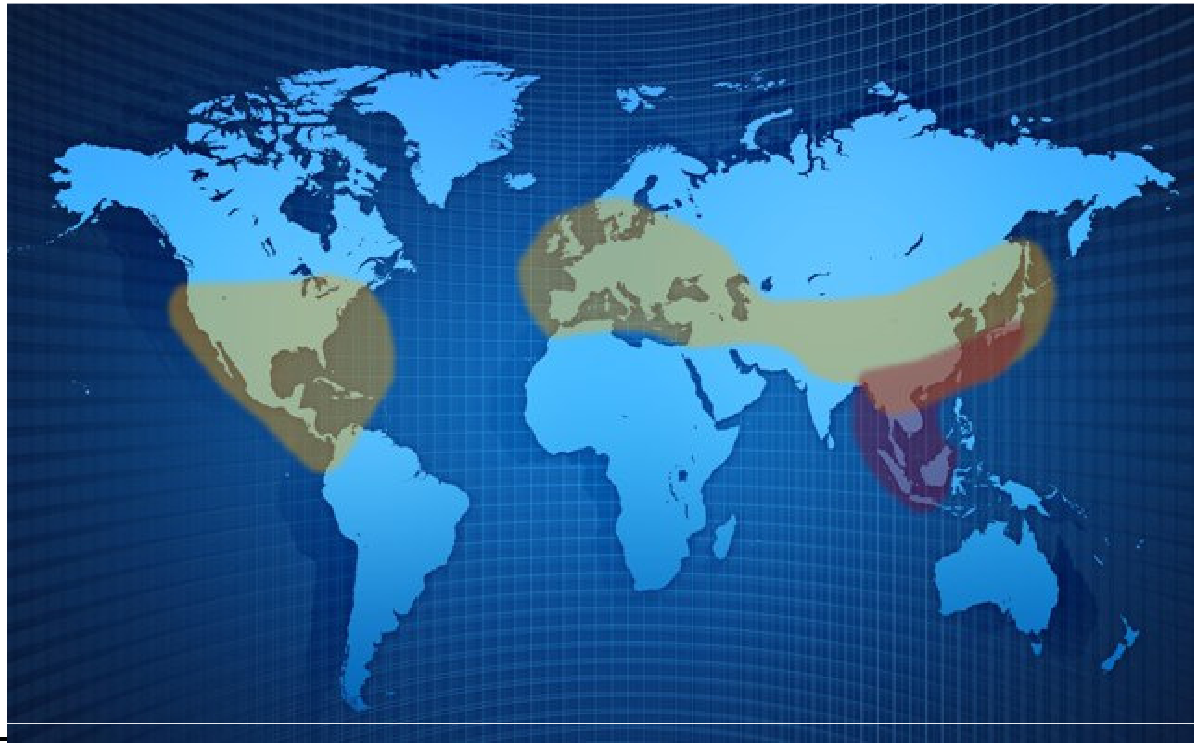
université de BORDEAUX

BioGeCo
Biodiversité, gènes & communautés

INRA
SCIENCE & IMPACT

MICROEVOLUTIONARY CHANGE

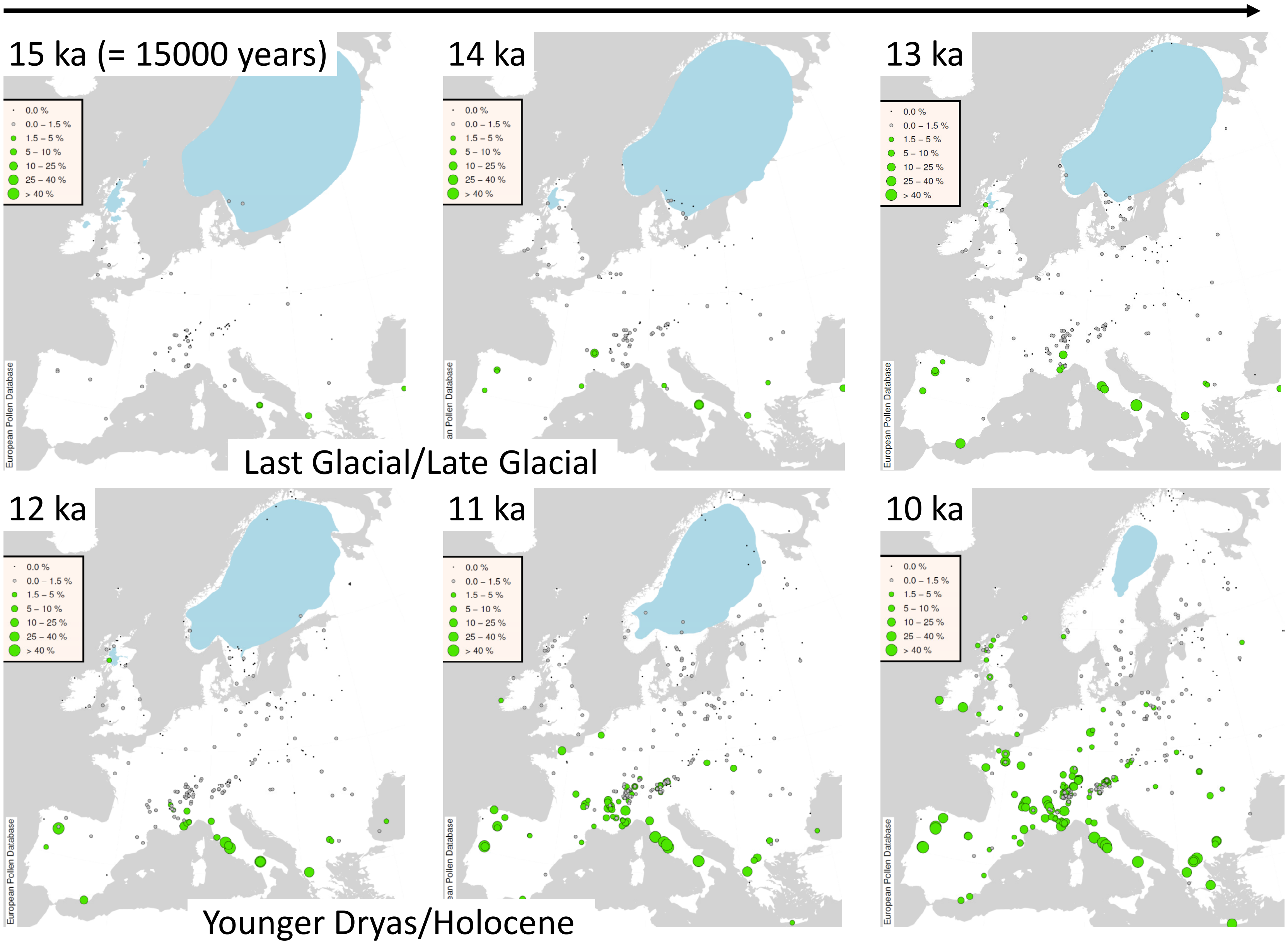


GENUS *QUERCUS*

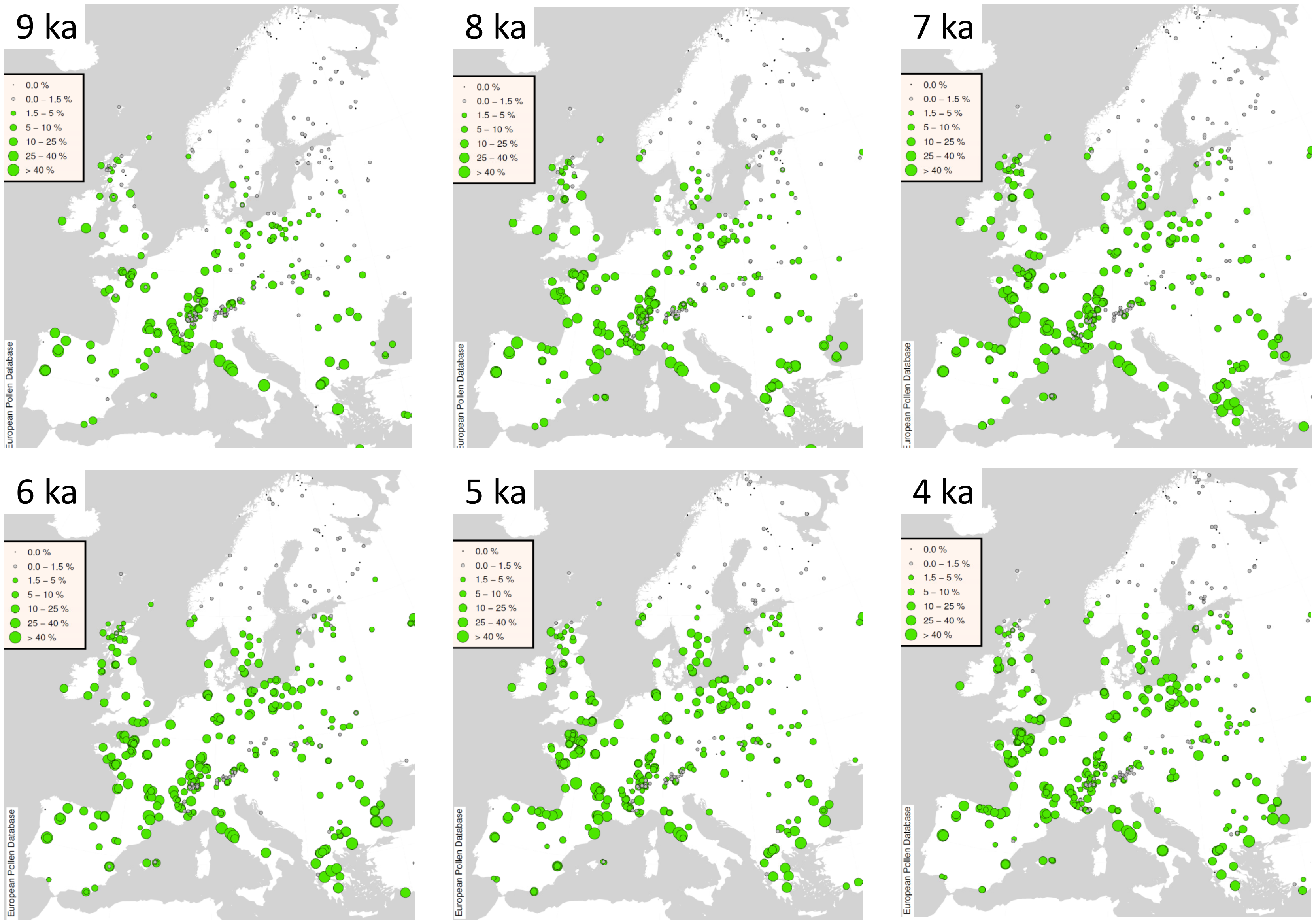



Postglacial oak recolonisation documented by pollen



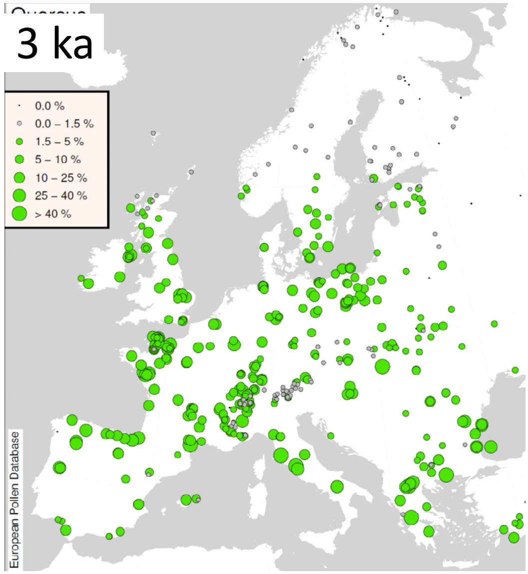
[Giesecke *et al.* submitted]

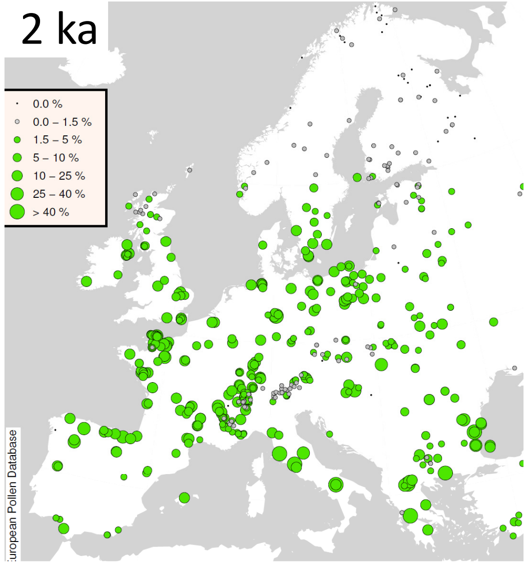
Postglacial oak recolonisation documented by pollen

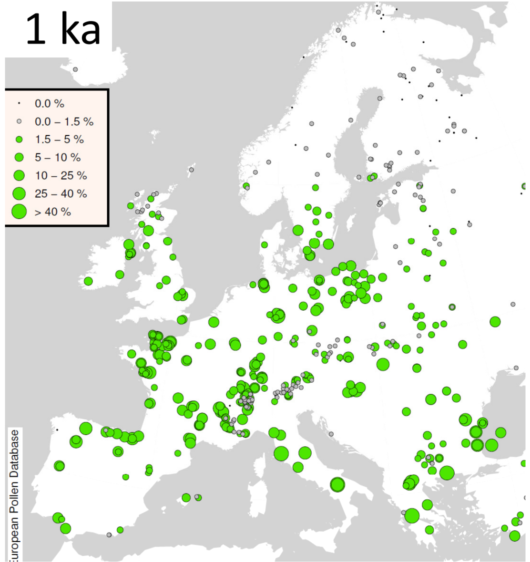


[Giesecke *et al.* submitted]

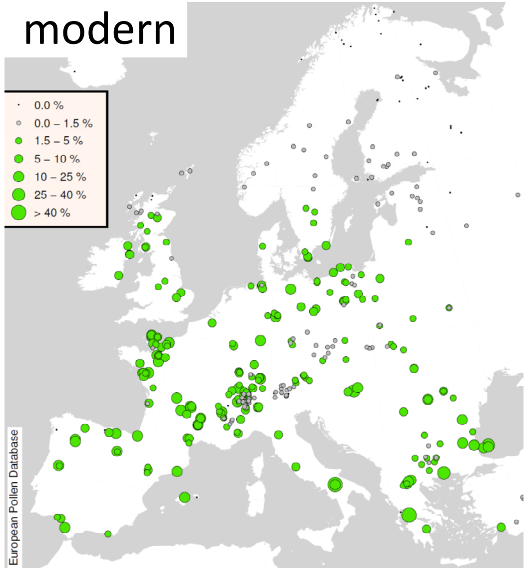
Postglacial oak recolonisation documented by pollen







[Giesecke *et al.* submitted]



- Highly precise chronological pollen data since 15 ka
- Complemented by macrofossils

Subfossil oak wood, c. 5200 years, dated by dendrochronology [W. Tegel]

INDIVIDUAL HETEROZYGOSITY IN HUMANS AND OAKS

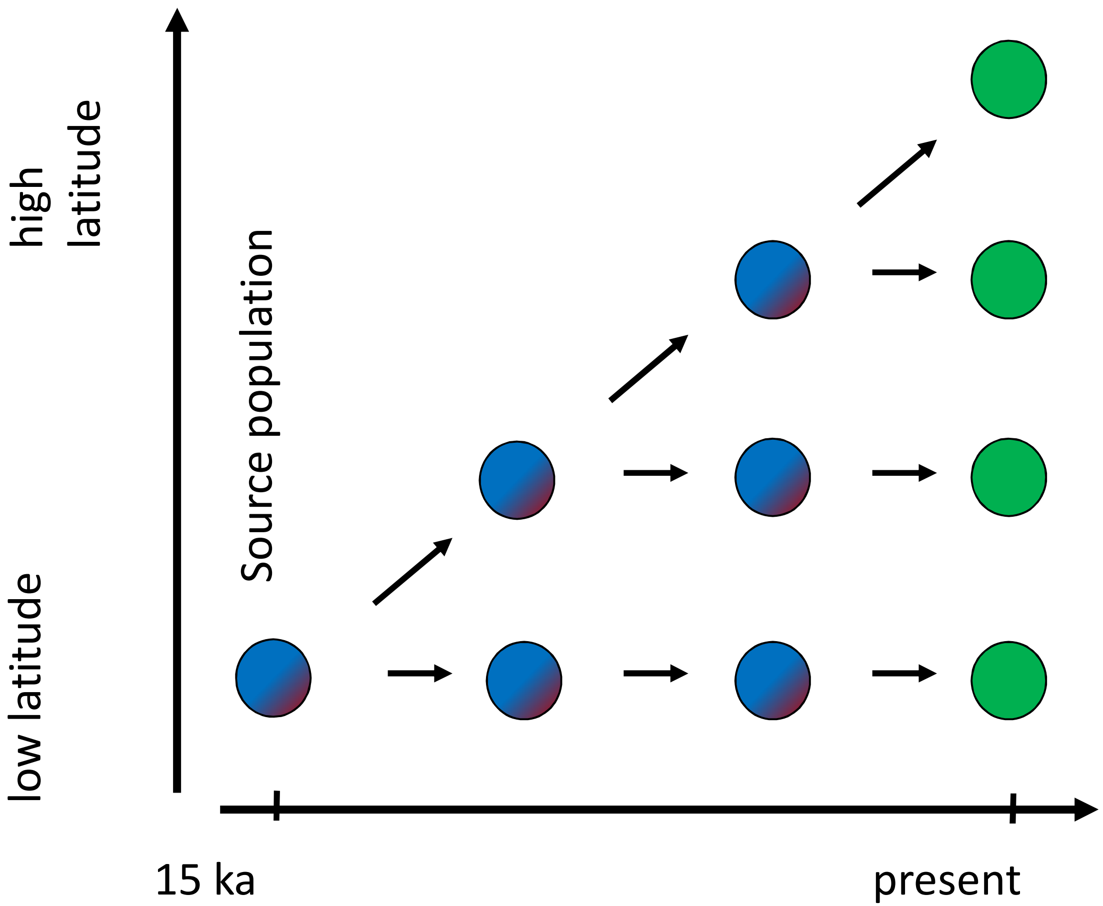
0.0012

McVean et al, 2012 Nature 491: 56-65 ; Plomion et al., 2015 Molecular Genetic Resources,

0.02

Trees tend to become hyperdiverse: they generate diversity as other species, but do not loose it.. They accumulate diversity, hence become hyperdiverse.

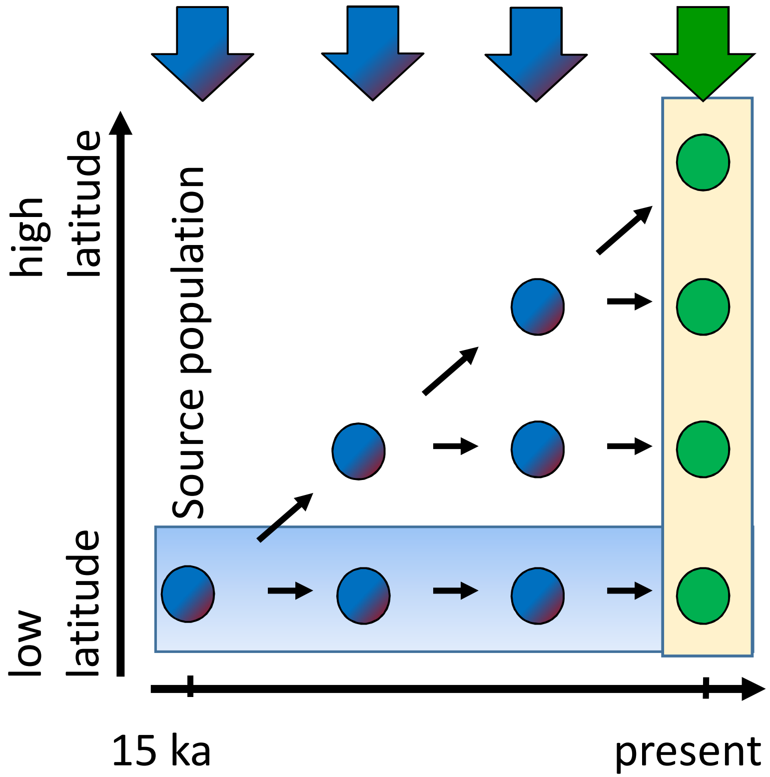
EVOLUTIONARY TRAJECTORIES



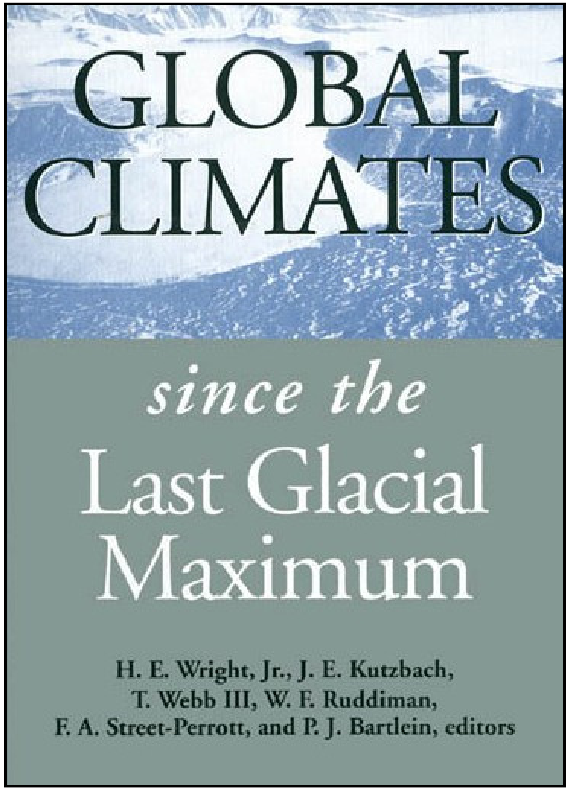
MICROEVOLUTION ALLOCHRONIC vs SYNCHONIC APPROACHES

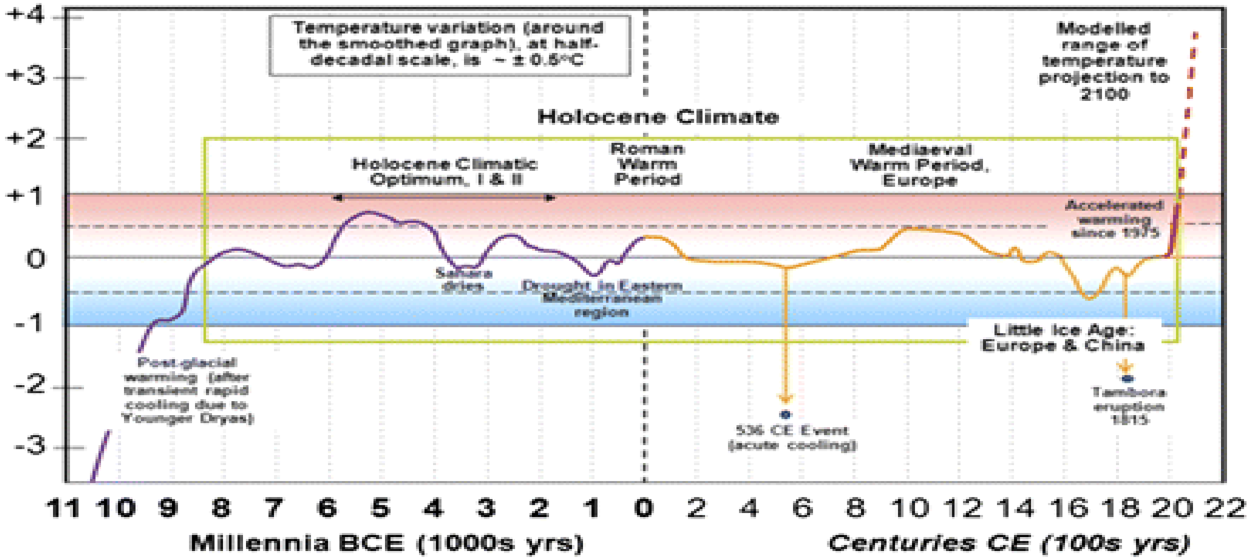
Paleoecology and Paleogenomics
- Ancient populations

Genetics & Genomics
- Extant Populations



EVOLUTIONARY CHANGE AFTER ***THE LAST GLACIAL MAXIMUM***





McMichael AJ PNAS 2012 109 4730-4737

Variations in northern hemisphere temperature, ℃ (relative to mean temperature during 1960–1980), averaged from multiple sources published since 2007.

ANCIENT WOOD SAMPLES FOR aDNA ANALYSIS

Fossil wood	**Archaeological remains**
Logs in gravel pits	Pile dwellings
Submerged forests	Water well
Buried logs	Fisheries
< 8000 BP	8000 BP to present

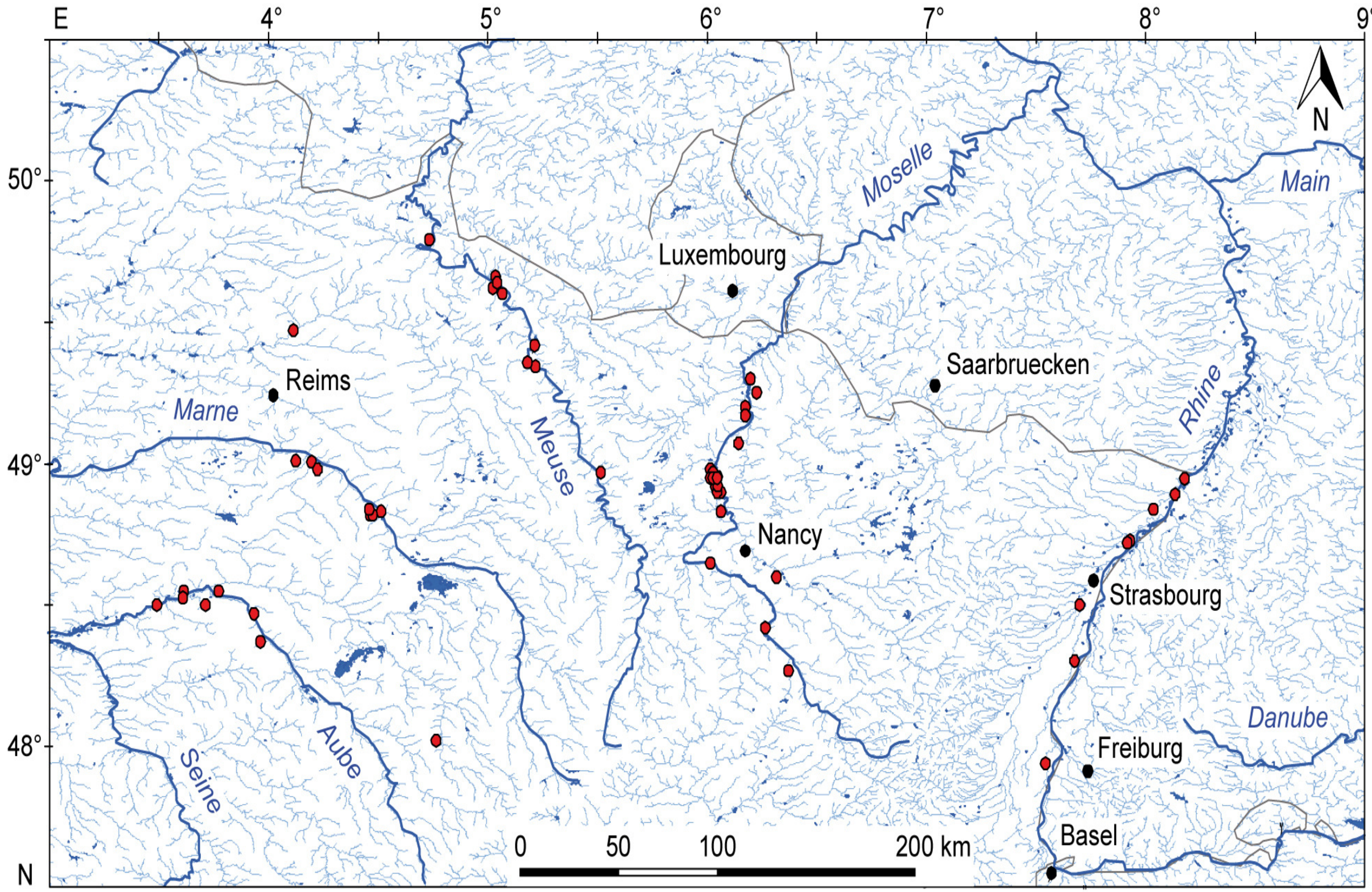
ANCIENT LOGS IN GRAVEL PITS

Albert-Ludwigs-Universität Freiburg
Institut für Geo- und Umweltnaturwissenschaften
79085 Freiburg
Benoit Sittler & Willy Tegel

Vallée du Rhin

Champey, vallée de la Moselle

DISTRIBUTION OF ANCIENT LOGS IN RIVERS OF NORTHEASTERN France (up to 10 000 BP)



Courtesy of Willi Tegel

SUBMERGED FORESTS

MORTA en BRIERE 7000 BP

ARCHAEOLOGIC AL REMAINS   PILE   DWELLINGS

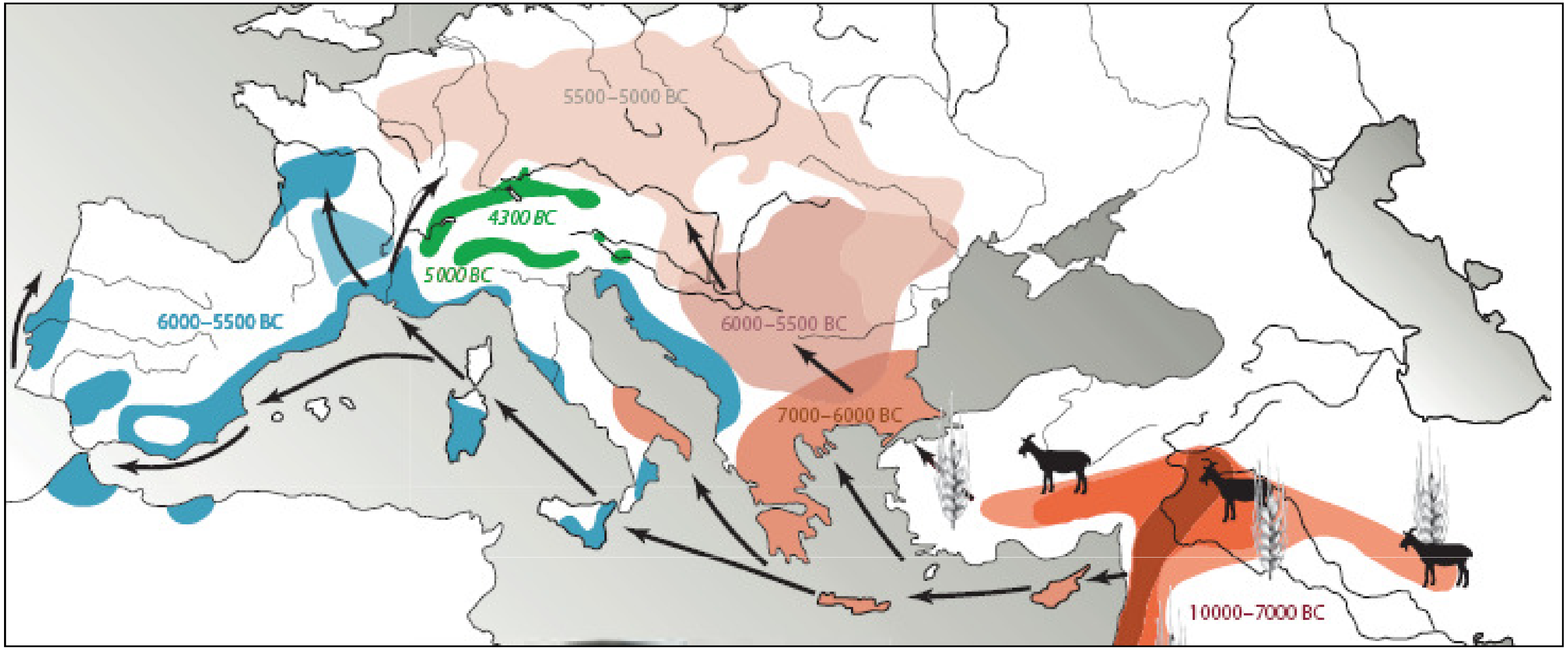
Dossiers de l'Archéologie, 2013, 355, 1: 96

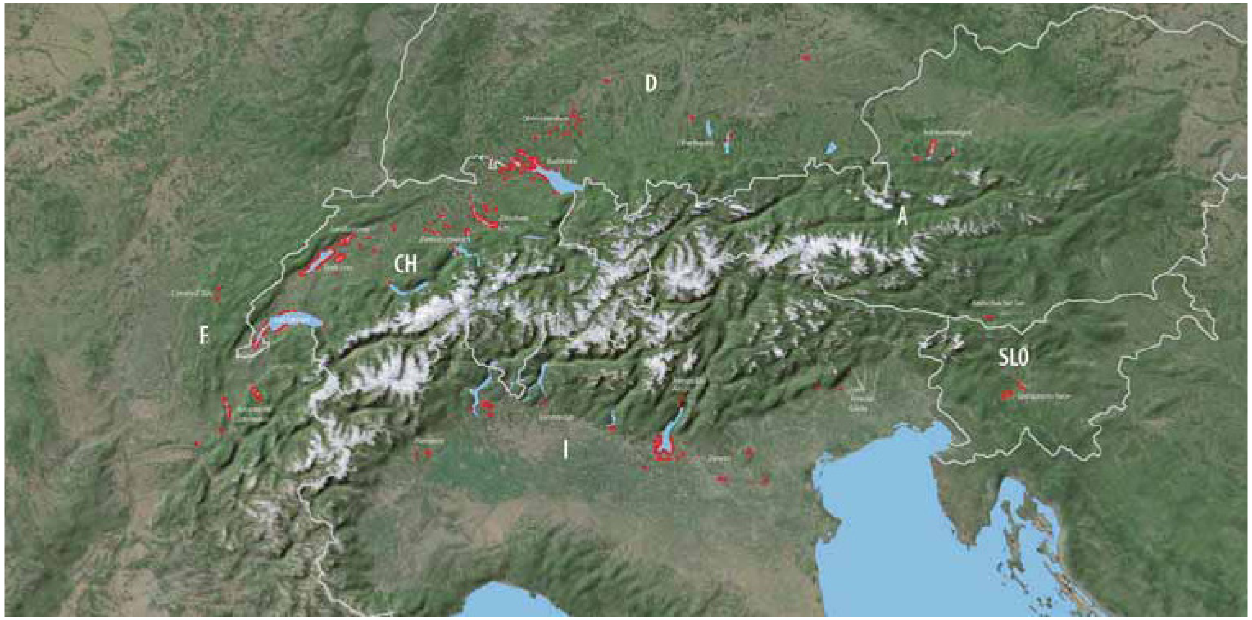
SITES PALAFITTIQUES PRÉHISTORIQUES AUTOUR DES ALPES

United Nations Educational, Scientific and Cultural Organization

Siti palafitticoli preistorici dell'arco alpino
iscritti nella Lista del Patrimonio Mondiale nel 2011

INTRODUCTION OF FARMING AND DWELLING SETTLEMENTS IN EUROPE

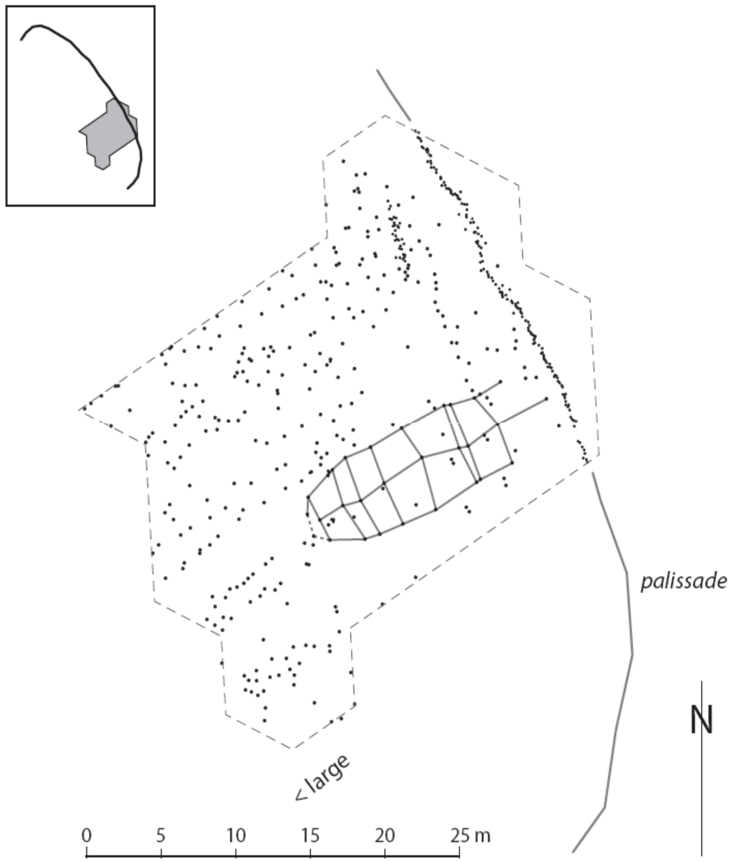




More than 1000 pile dwellings sites

http://sites.palafittes.org/

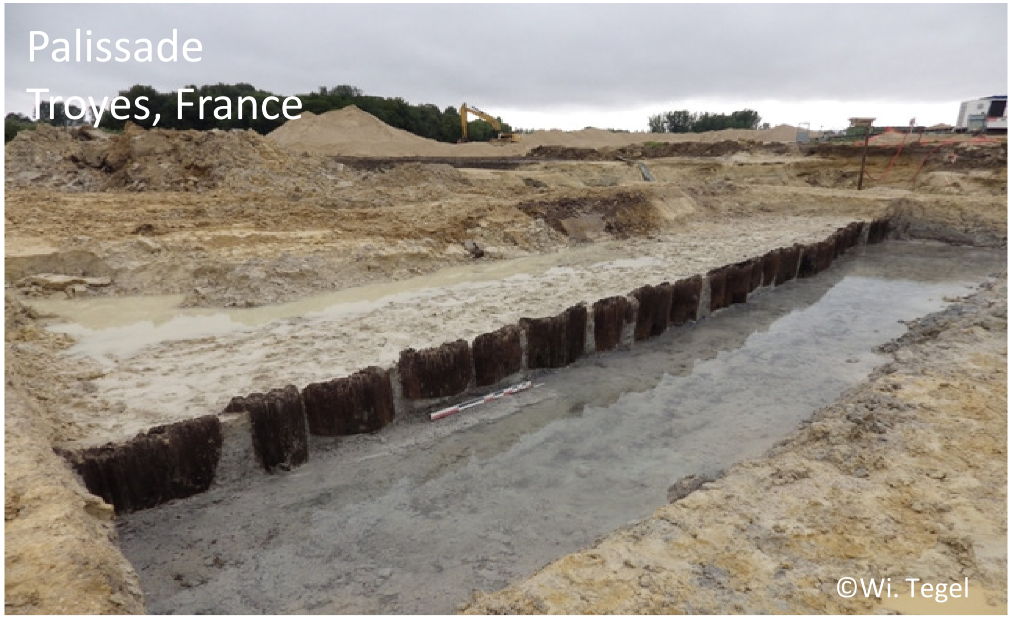
Pile dwellings (2900 BP)
Lac du Bourget



Billaud Y 2012, Cahiers Archéologie Romande 132: 345-361

Water Well Construction (3500 BP)
Erstein, France

Waterlogged piles (3000)
Etang de Thau

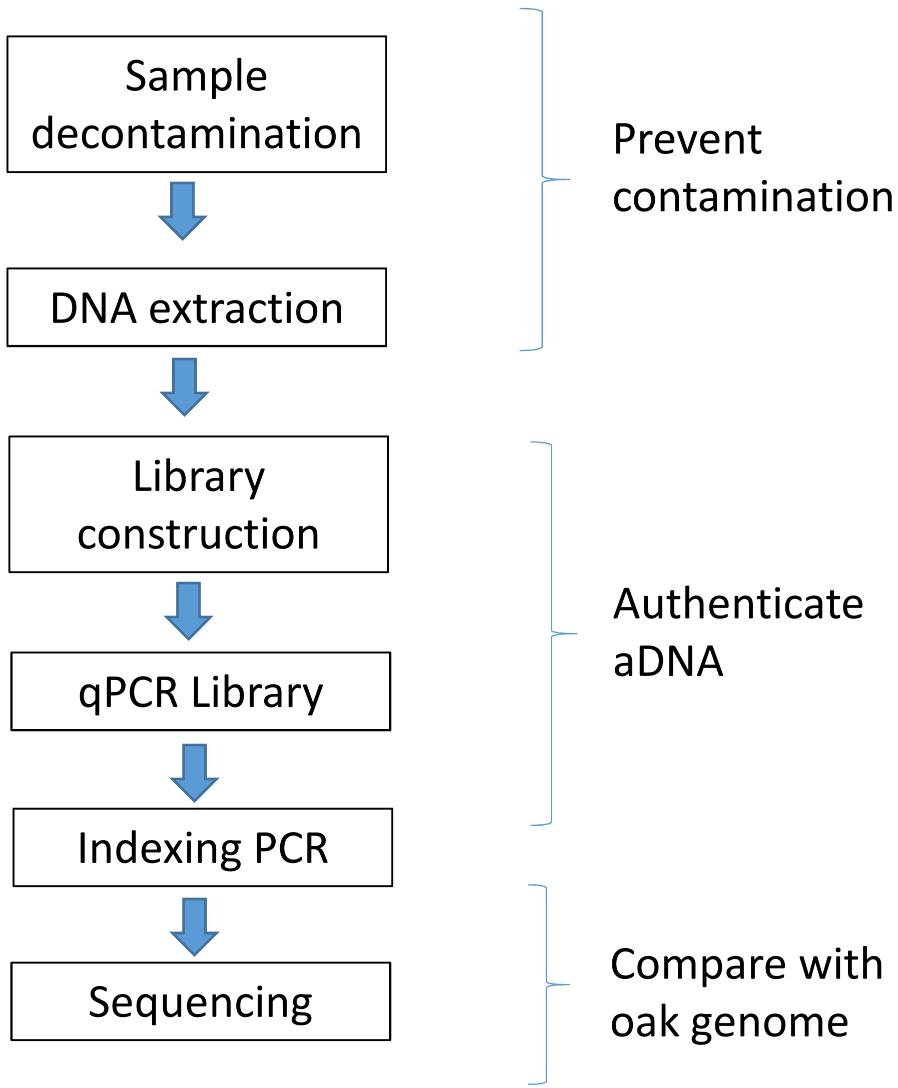


Palissade
Troyes, France

RETRIEVING & ANALYZING ANCIENT DNA OF OAKS

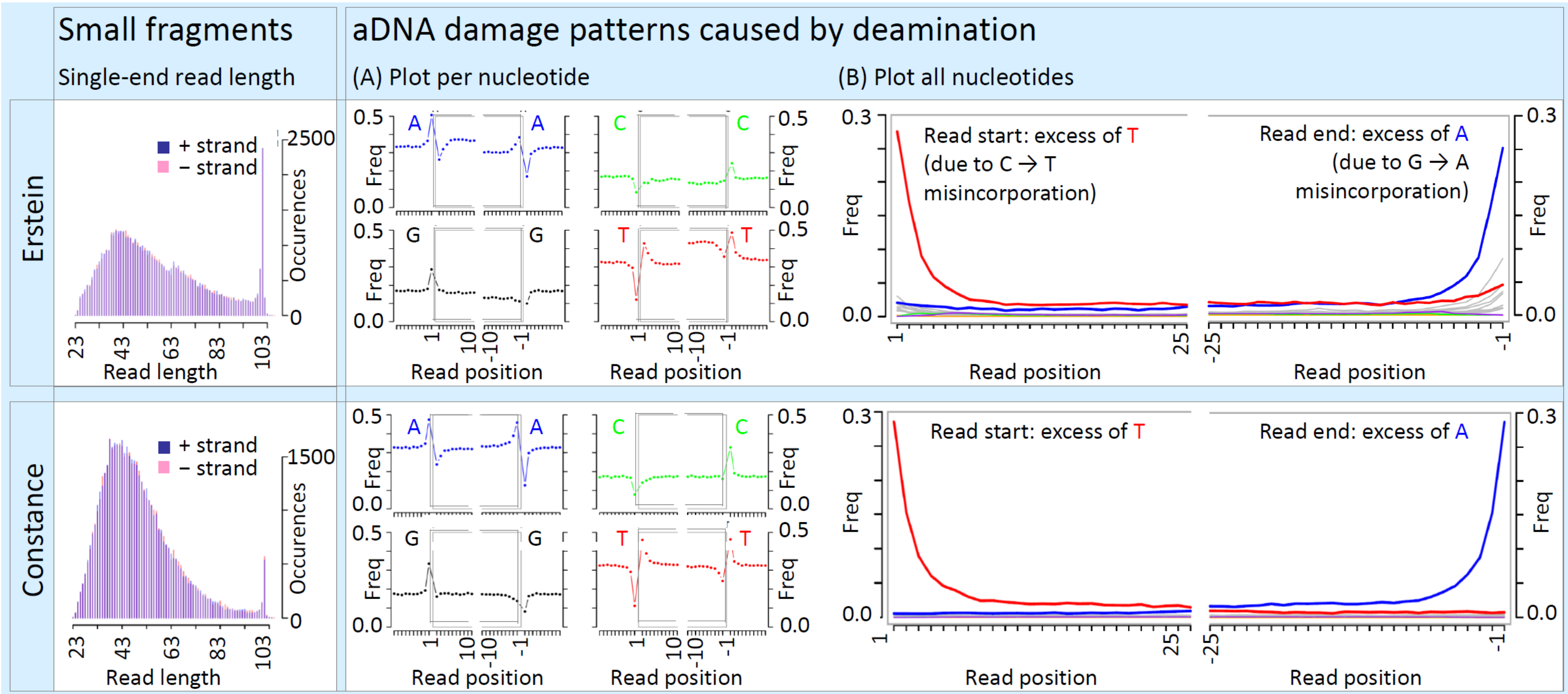
Ludovic Orlando *University of Copenhagen*

Stefanie Wagner *INRA Bordeaux*



Orlando et al. 2015. Reconstructing ancient genomes and epigenomes. Nature Reviews Genetics 16: 395-408

Screening authenticates aDNA ....

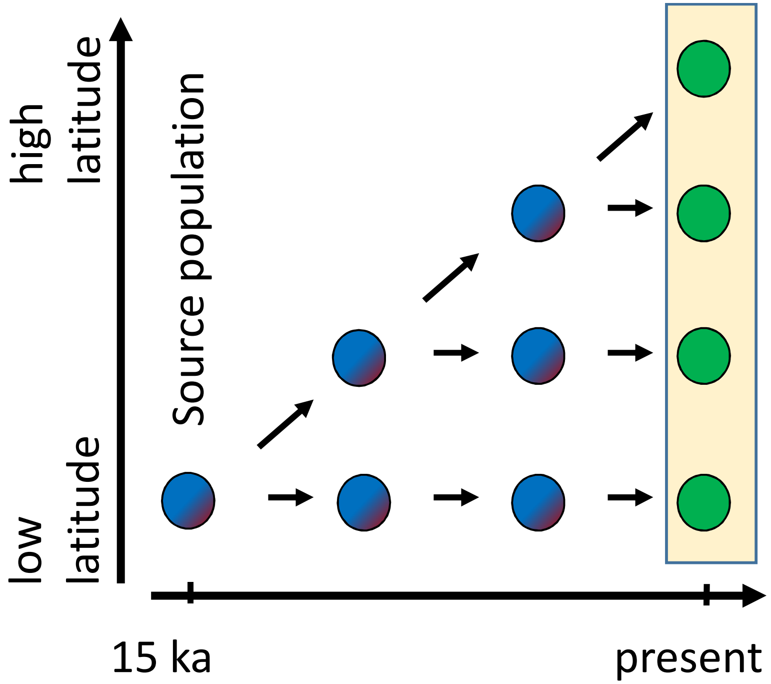


… and provides first ancient chloroplast genomes

Sequencing results and genome coverage		
	Erstein	**Constance**
Nb of retained reads	31,274,714	54,758,872
Nb of cp DNA hits	27,219	22,820
Estimated cp DNA coverage	**10.2**	**6.7**
Nb of nuclear DNA hits	100,718	241,415
Estimated nuclear DNA coverage	<1%	<1%

APPROCHE SYNCHRONIQUE

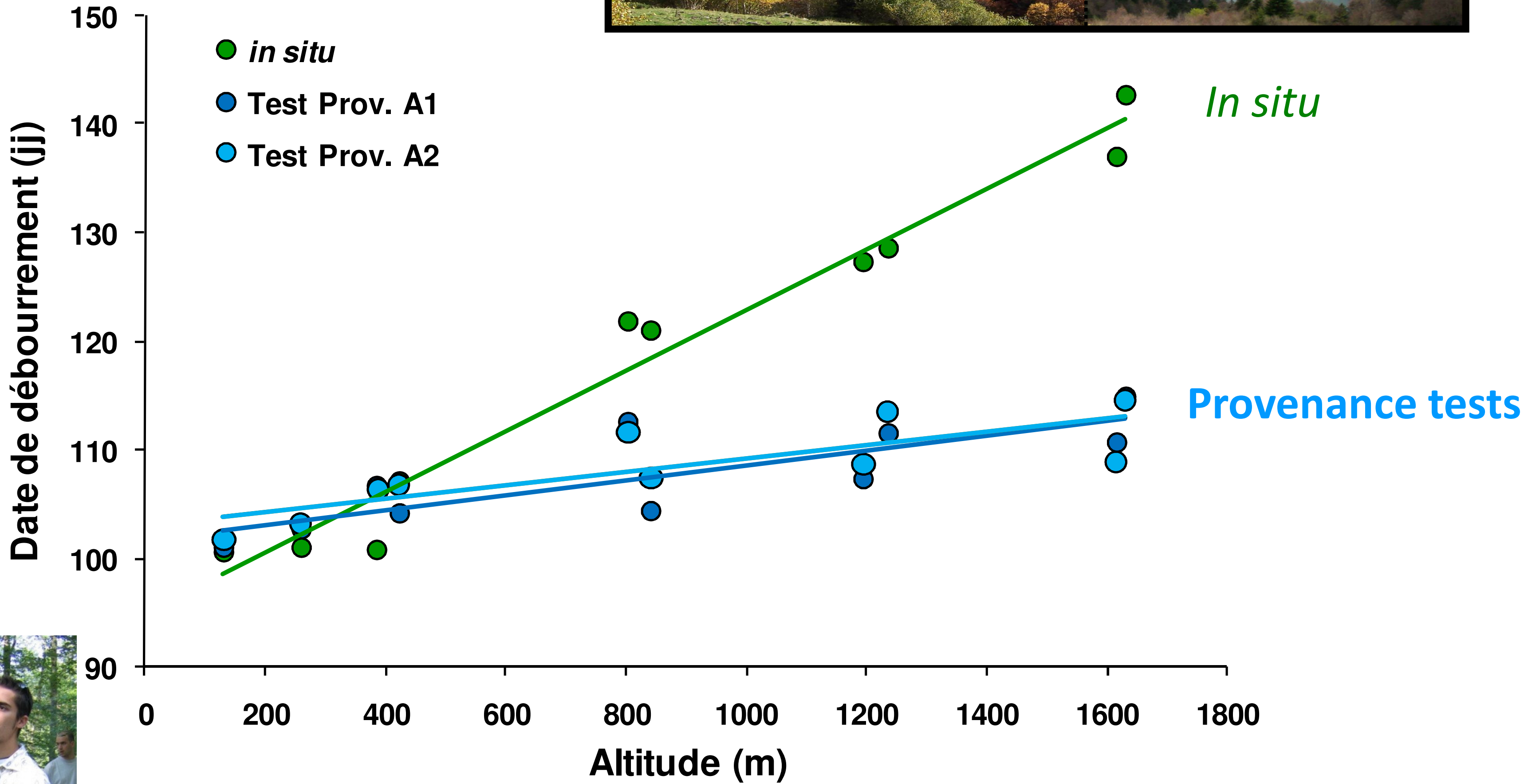
DIVERGENCE LE LONG DE GRADIENTS ENVIRONNEMENTAUX



GENETICS OF BUD BURST

Large within population variation ($h^2 > 0.5$)

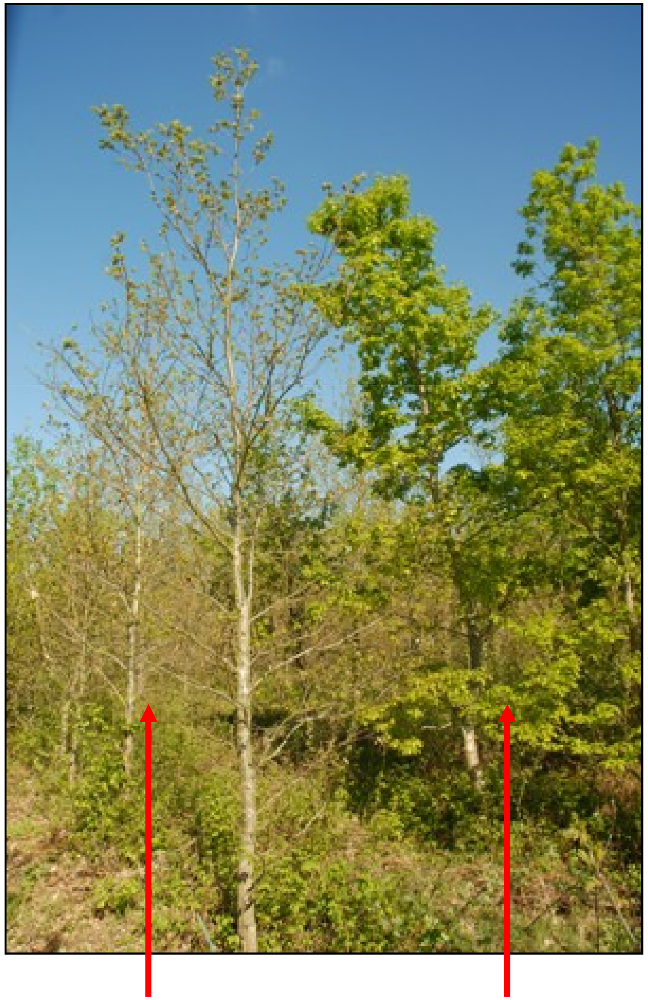
CLINAL VARIATION OF BUD BURST IN OAKS



Alberto et al. 2011, *Journal of Evolutionary Biology* **24**, 1442-1454

GENOMIC FOOTPRINTS OF ADAPTIVE DIVERGENCE

TARGETED APPROACH VERSUS BLIND APPROACH (GENOME WIDE) ??

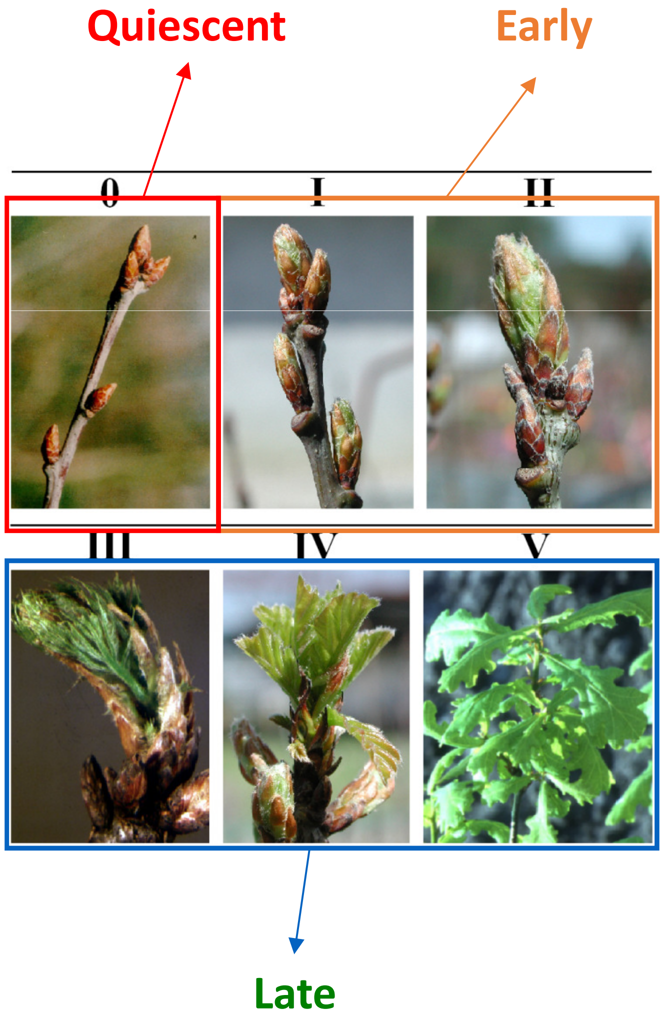


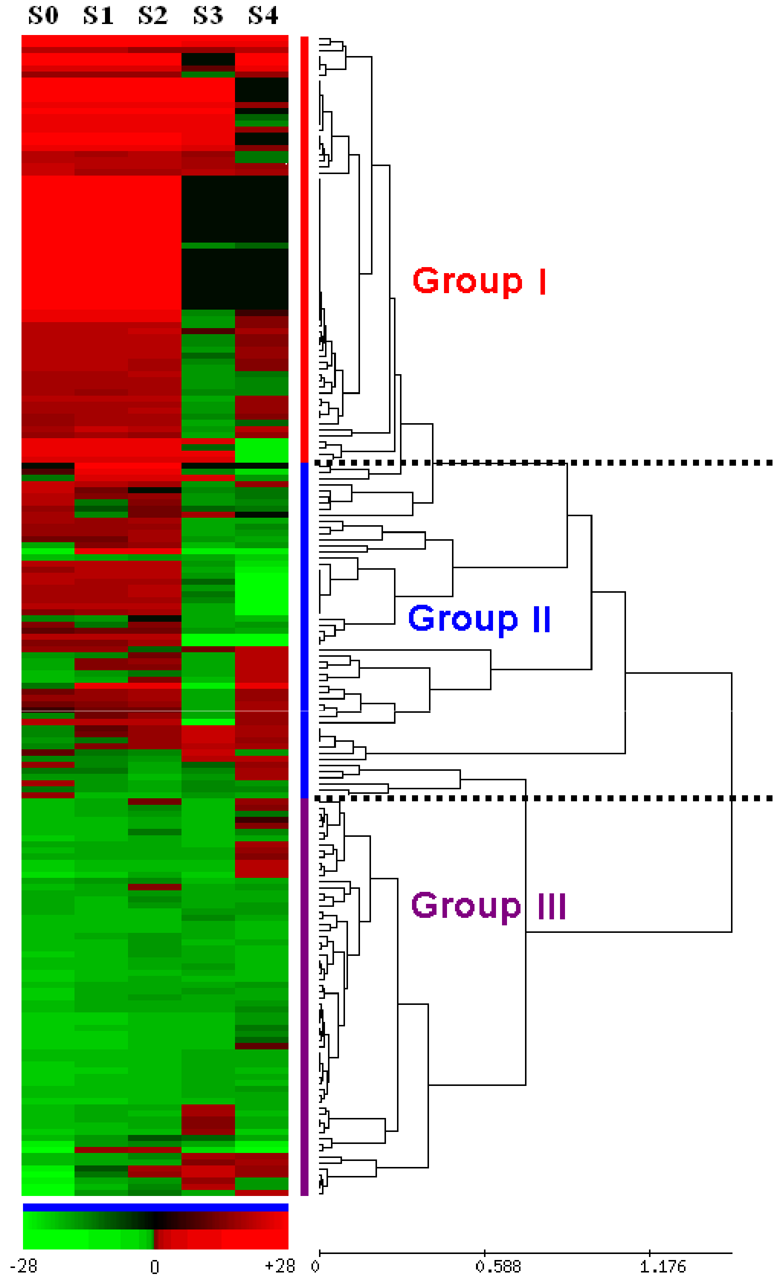
Bertranges Klostermarienberg

Nagybatony Fontainebleau

SEARCHING FOR CANDIDATE GENES

cDNA macroarrays experiments available for **801 ESTs** (233 unique transcripts) isolated from **SSH** libraries

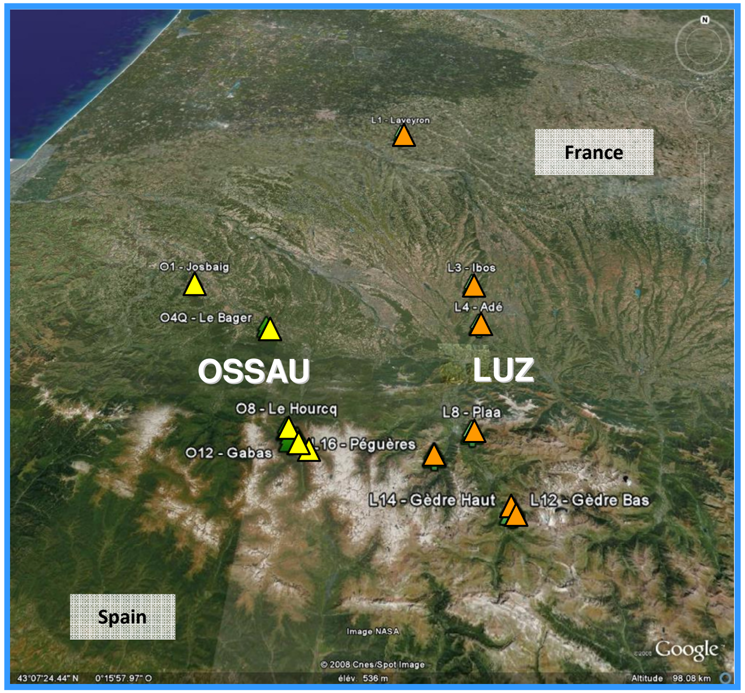




Derory et al., 2006 *New Phytologist* 170: 723–738

CLINES IN CASE STUDIES

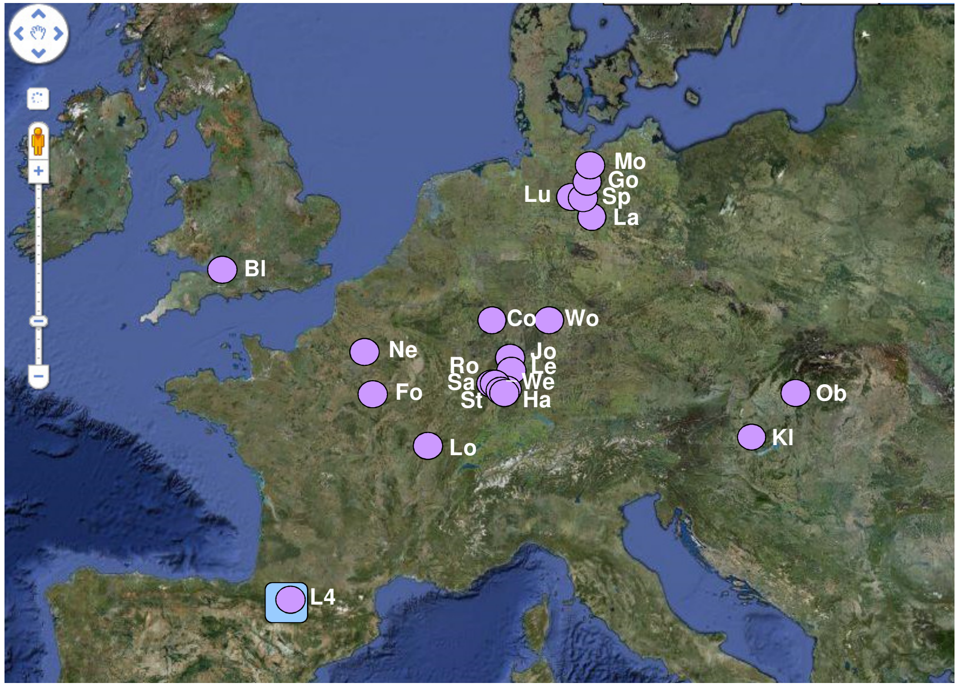
Altitudinal gradient



100 m → 1600 m

12 populations / 274 trees

Latitudinal gradient



43,1 °N → 53,6 °N

21 populations / 484 trees

Progeny / provenance test at low elevation and low latitude

Genotyping of 384 SNPs (105 genes) on populations of both clines

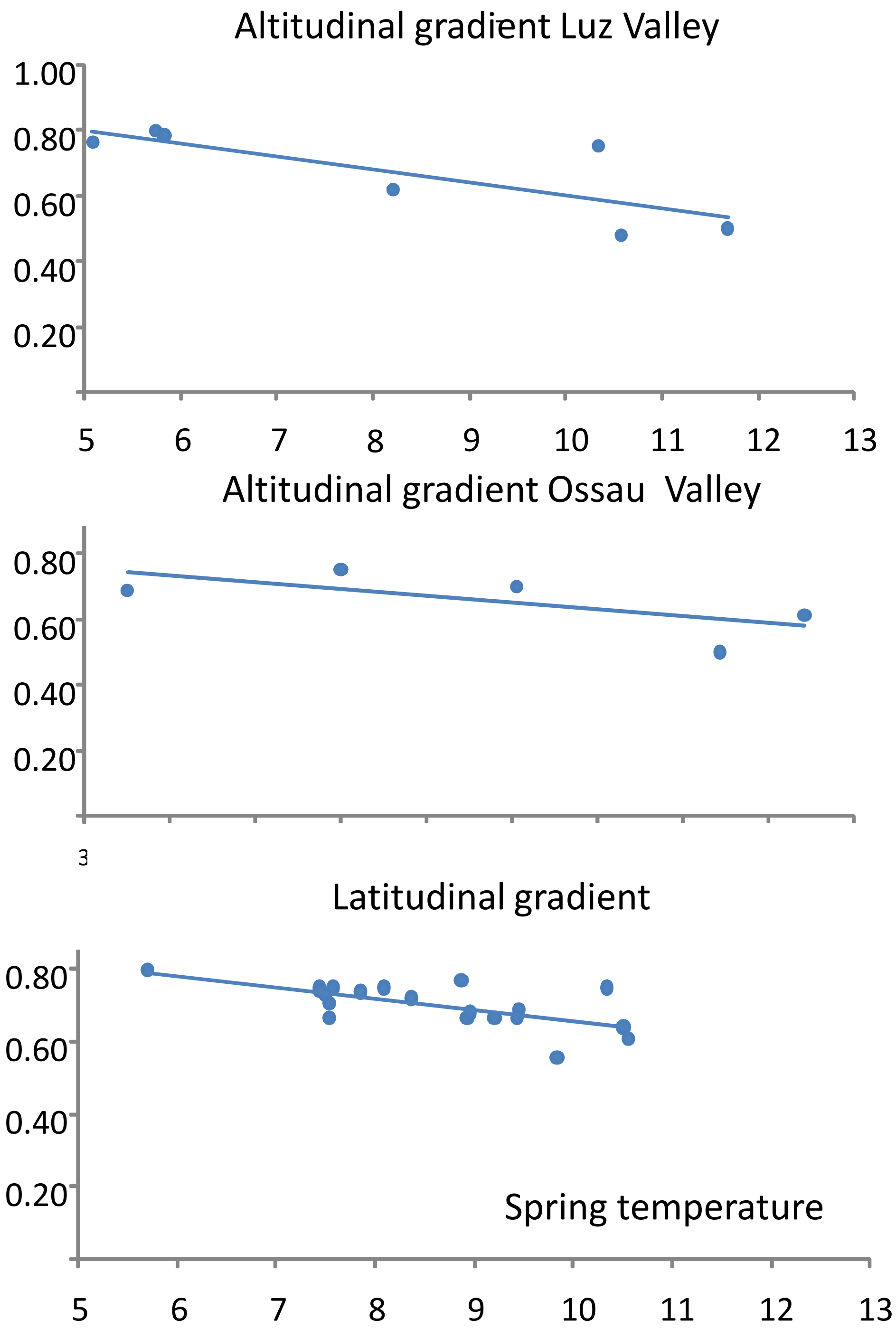
Bud burst in progeny/provenance tests

Detection method	**Altitudinal gradient**	**Latitudinal gradient**	Genes common to both gradients
Clinal patterns	5 genes	3 genes	*APS*

***F_{ST}* outliers**	9 genes	9 genes	*L18a, GI, PSII*
Association tests	9 genes	4 genes	*S11*

Common to the 3 methods		L18a	

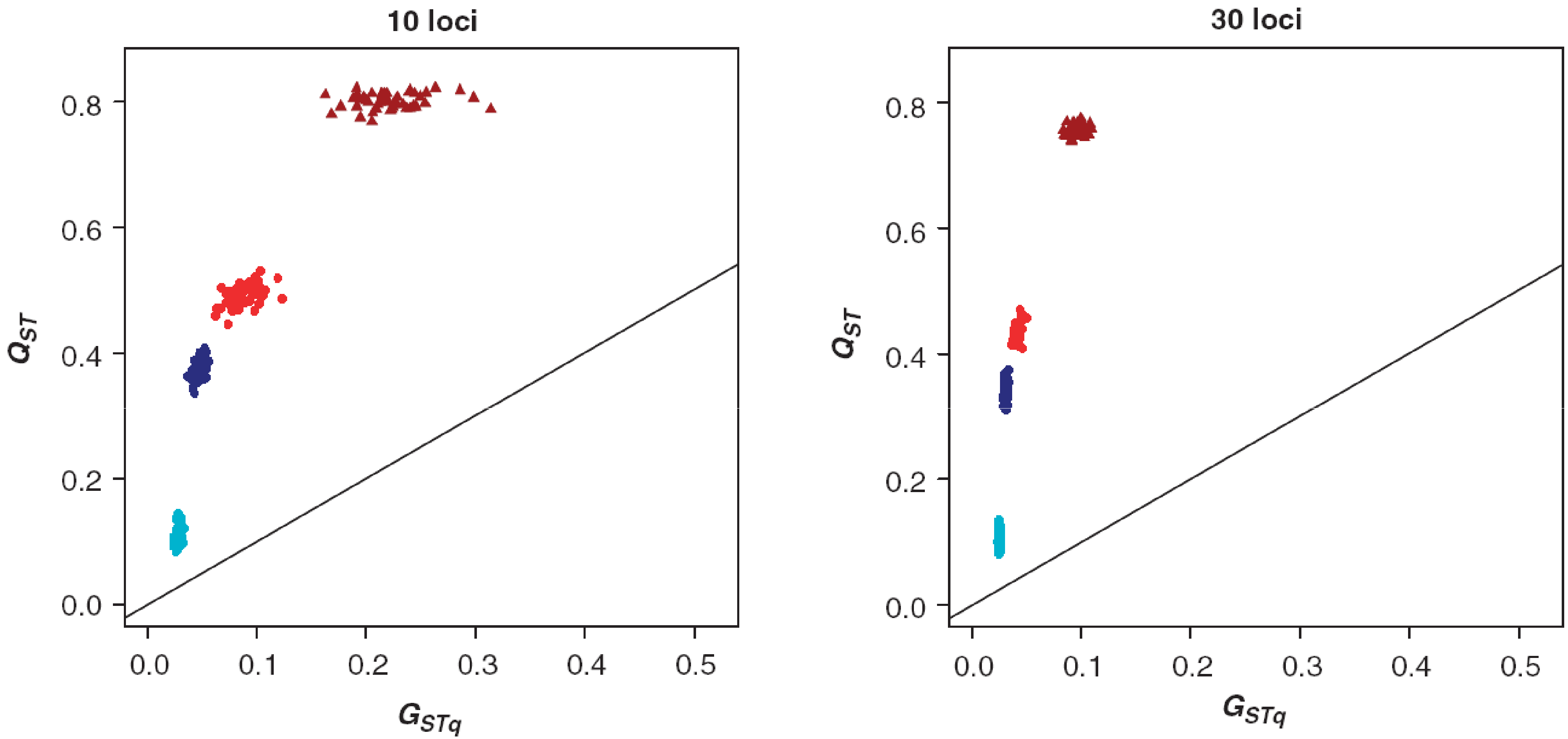
Alberto *et al.* 2013 Genetics 195, 495–512



Convergent clinal variation of APS in three biological replicates

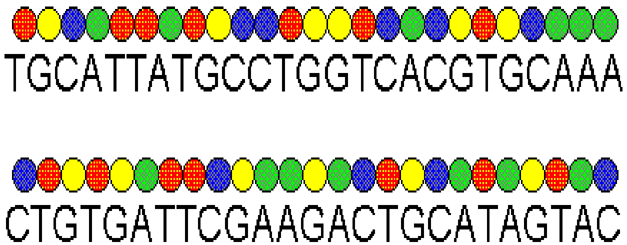
Alberto *et al.* 2013 Genetics 195, 495–512

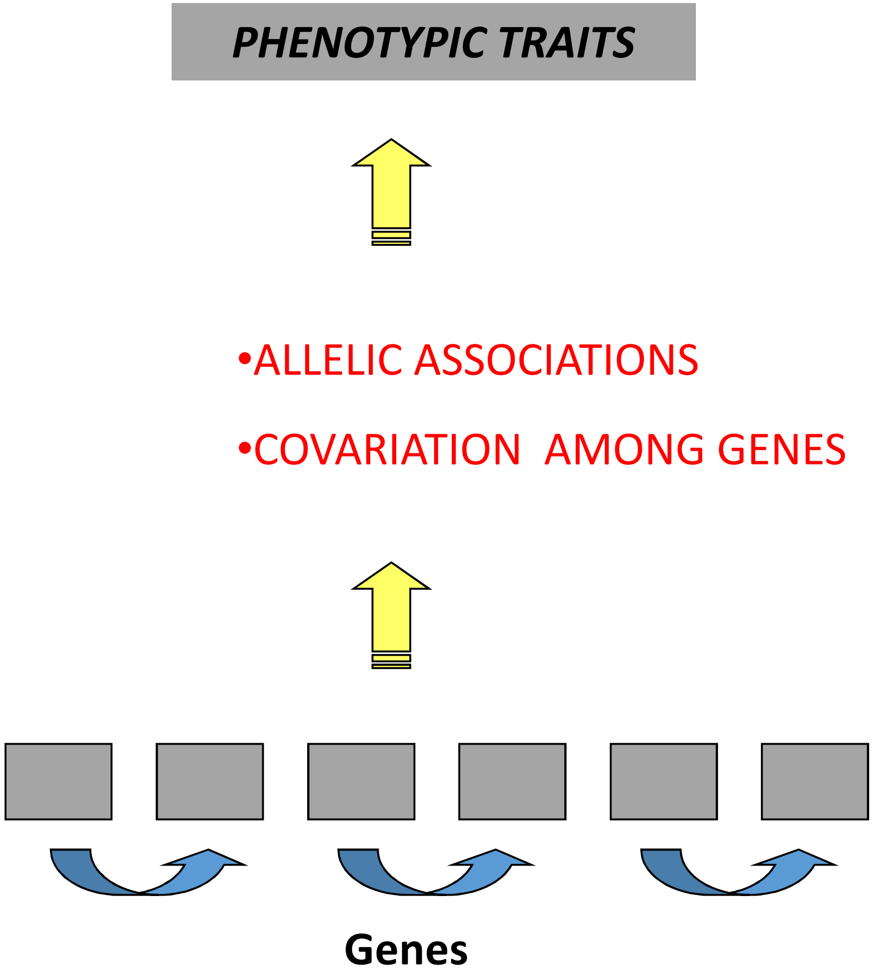
Single locus signature diluted under complex genetic architecture



Kremer A & Le Corre V 2012 *Heredity* **108** *:* 375-385

THE CASE OF MISSING POPULATION DIFFERENTIATION





NATURAL SELECTION CAPTURES FIRST ALLELIC ASSOCIATION AND COVARIATION THEN SINGLE FAVORABLE GENE EFFECTS

Kremer A, Le Corre V 2012 Decoupling of differentiation between traits and their underlying genes in response to divergent selection. *Heredity. 108, 375–385*

Estimation des changements microévolutifs au cours de l'holocène devient possible

Nouveaux défis pour estimer l'empreinte génomique de l'évolution. Nécessité des approches GWAS

Dilution de l'empreinte: covariation et « homoplasie » du signal.

Génomique comme outil pour affiner les prédictions des valeurs génétiques des individus in situ.