

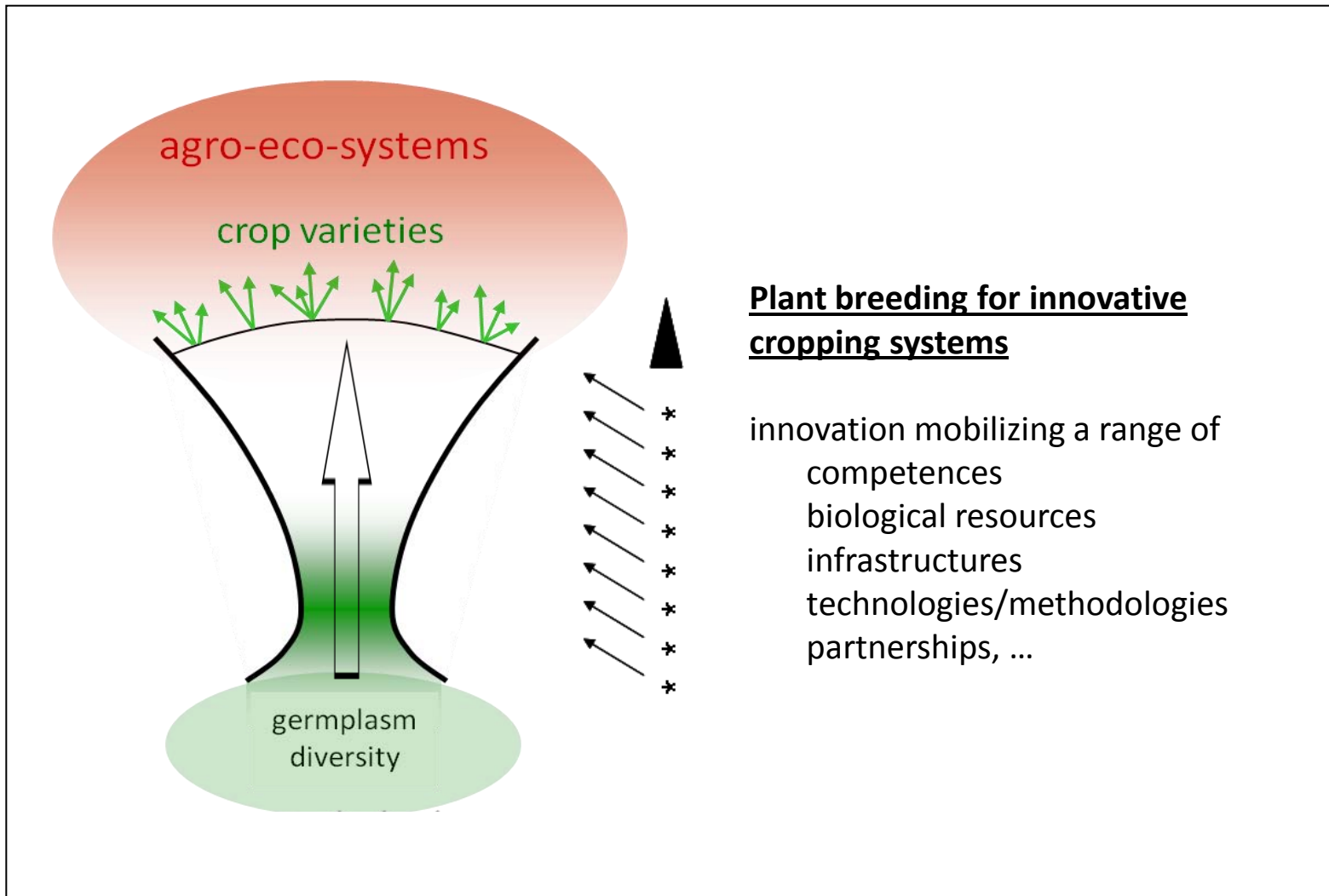
Making use of germplasm diversity for crop improvement in a range of tropical crops

Jean Christophe Glaszmann
Montpellier



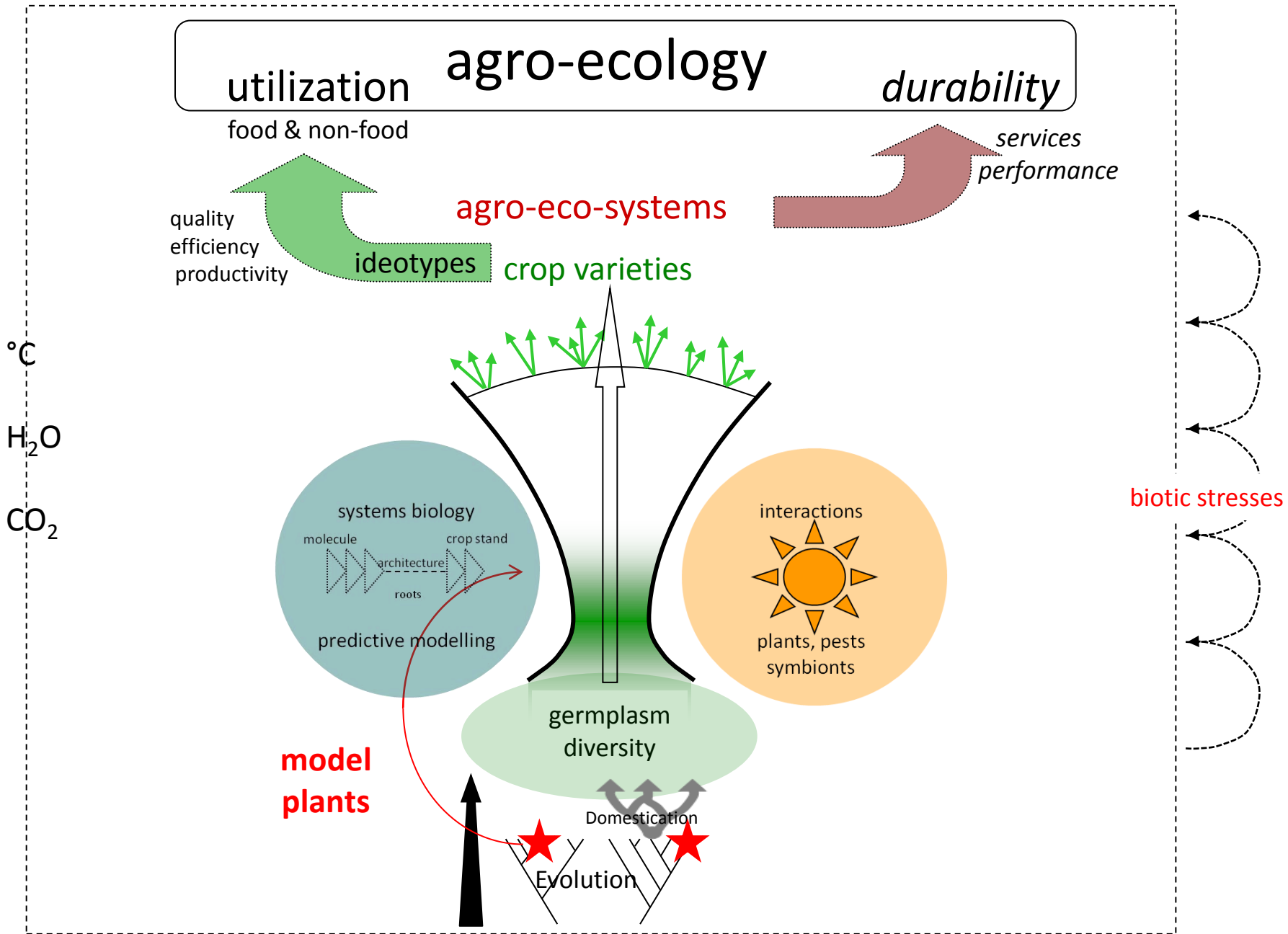
amélioration génétique et adaptation
des plantes méditerranéennes et tropicales

A representation of plant breeding

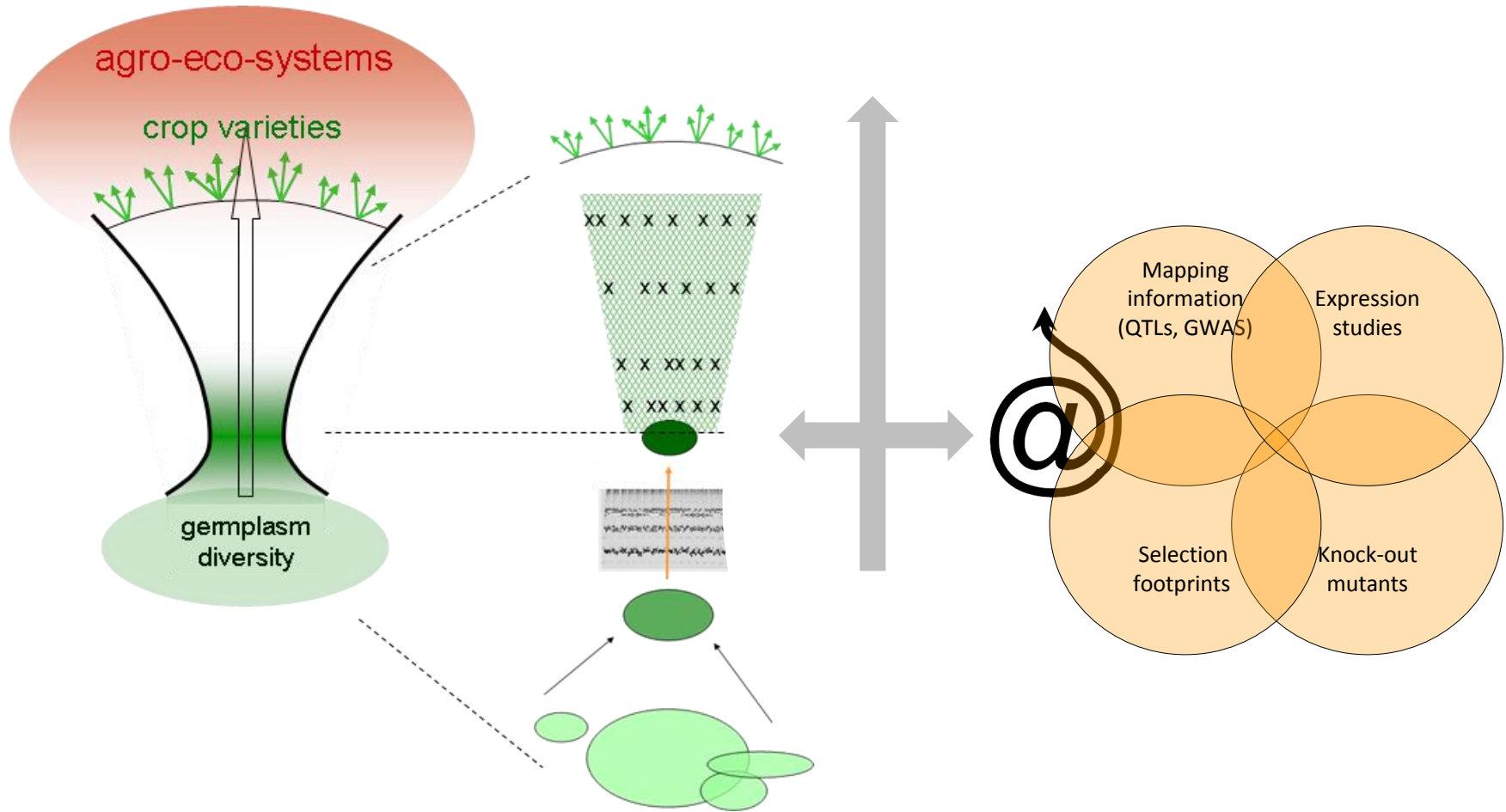


Plant breeding

Transforming genetic diversity into adaptation to agriculture(s)



Plant breeding, genetic resources and modern biology



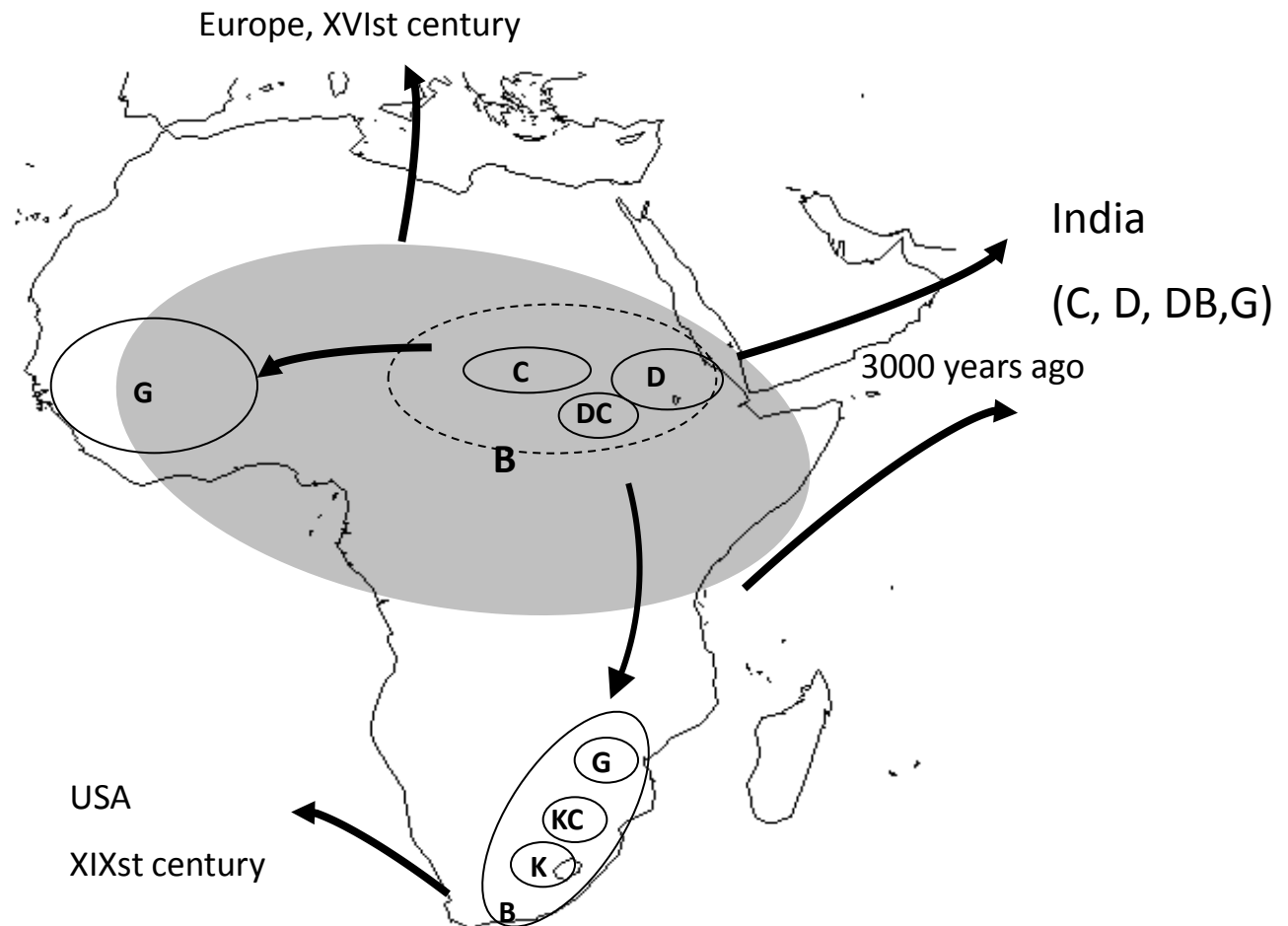
Sampling diversity

(using sorghum and cacao as examples)

- A representation of the collection
- Genes and populations
- Genomic correlations



Sorghum domestication



- B : bicolor
- G : guinea
- C : caudatum
- D : durra
- K : kafir

Clusters = combination of race and geographical origin

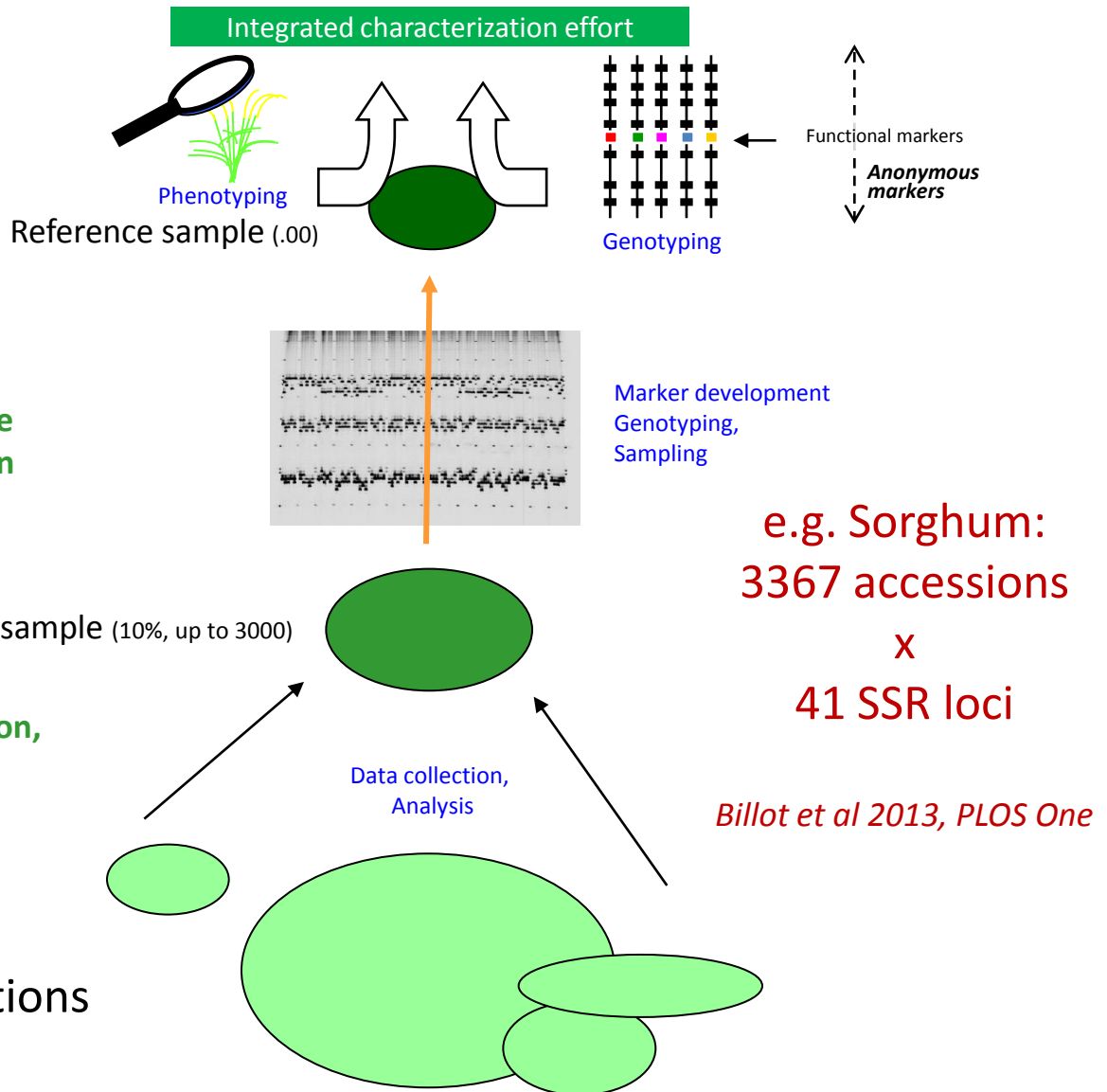
According to Ollitrault, 1987 (thesis)

Sampling global germplasm

Step 2: from molecular data sampling the core sample to produce a reference sample for integrated characterisation and evaluation efforts

Step 1: from passport information, sampling global resources to produce a core sample

Various collections





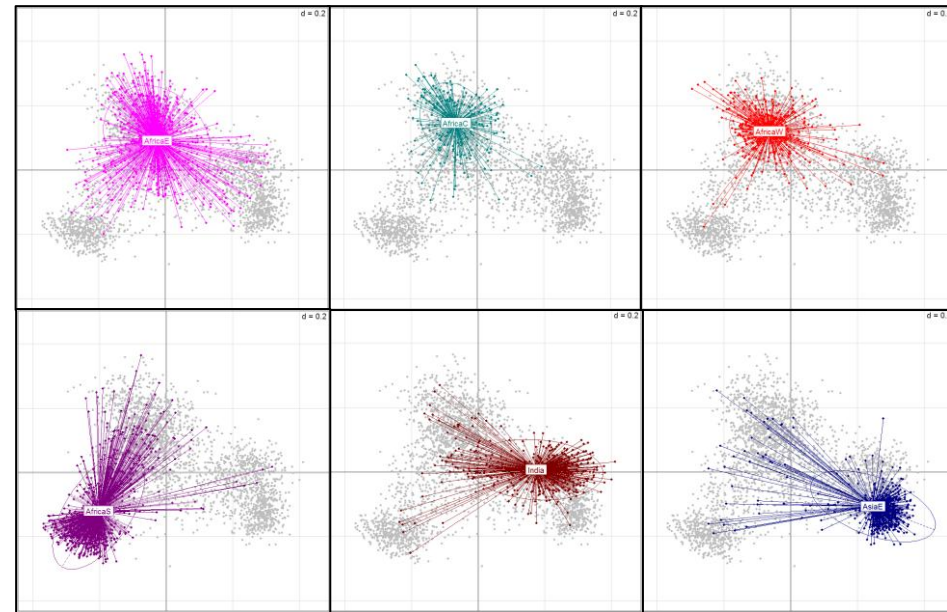
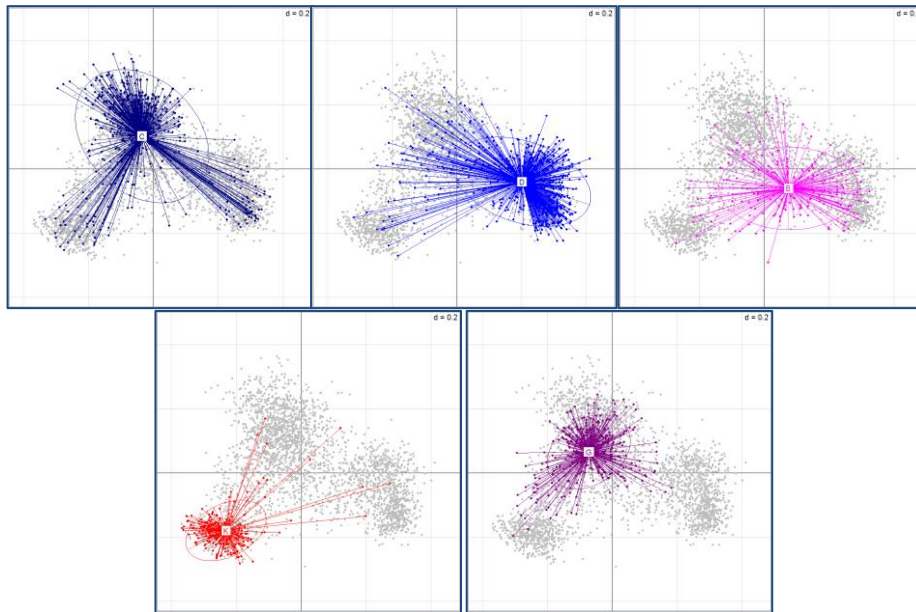
An international genotyping initiative

3365 accessions x 41 SSR markers

Races

Macro-Regions

Axis 1: 13%
Axis 2: 8%
Axis 3: 5%



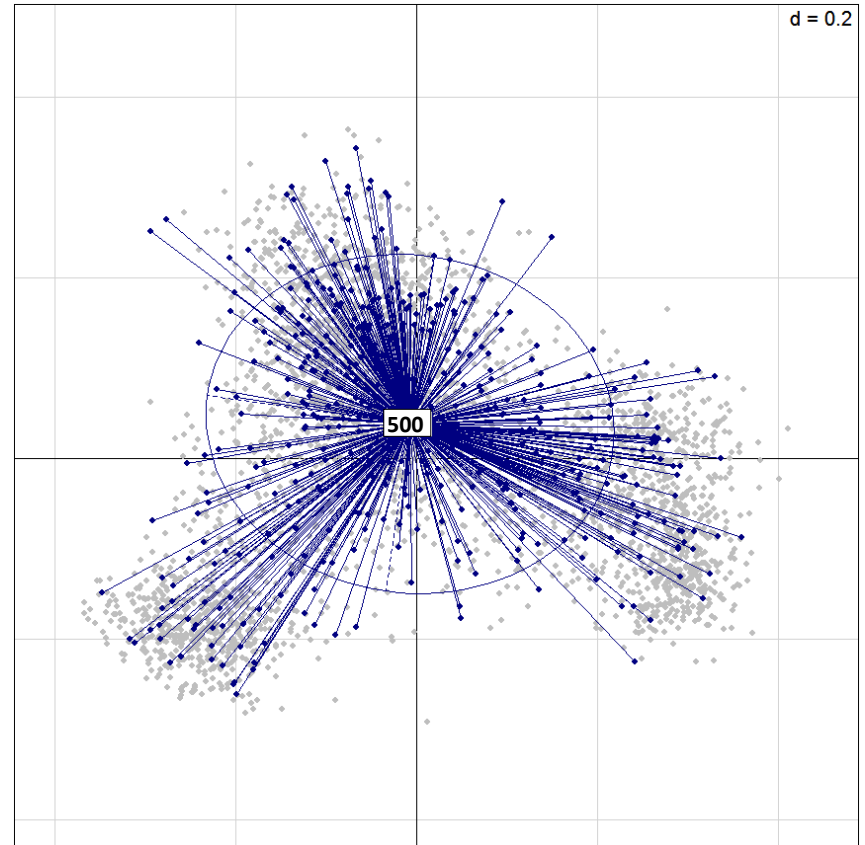
Geographic origin then race (morphotype)



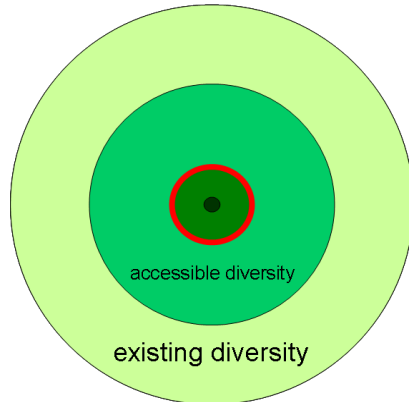
The core reference sample

Axis 1: 13%
Axis 2: 8%
Axis 3: 5%

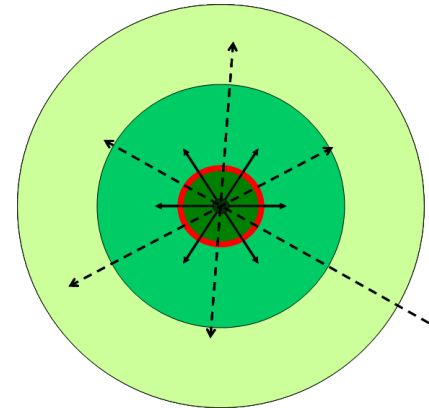
- A representation of diversity
- With minimized genetic structure
- To search for trait donors
- To foster characterization, genotypic and phenotypic
- To enter the whole collection
- To sub-sample on specific sub-compartments
- To assess associations
- Available for distribution



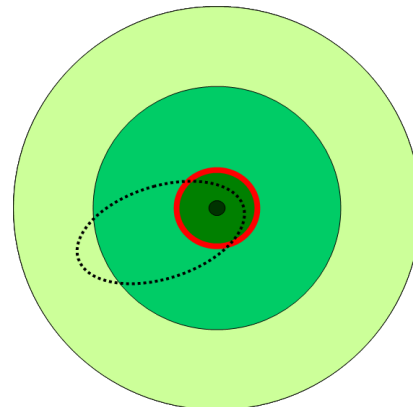
Value and uses of core reference sets of crop germplasm: **READ** germplasm



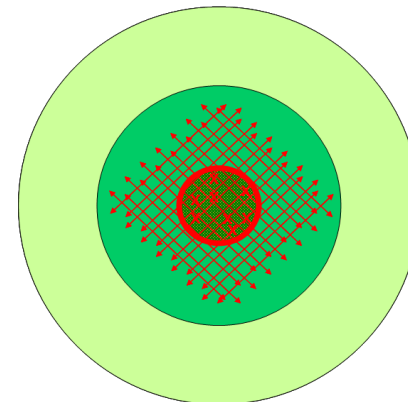
*Represent
existing diversity*



*Enter the
whole collection*



*Assess
trait variation*



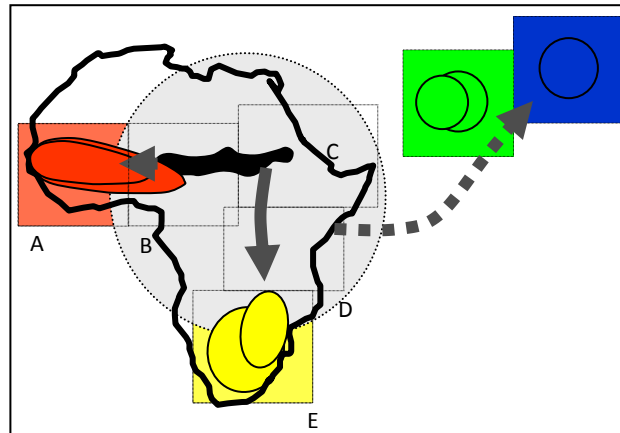
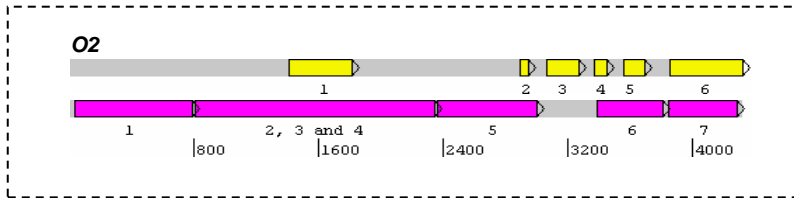
Dissect trait control

Genes and populations

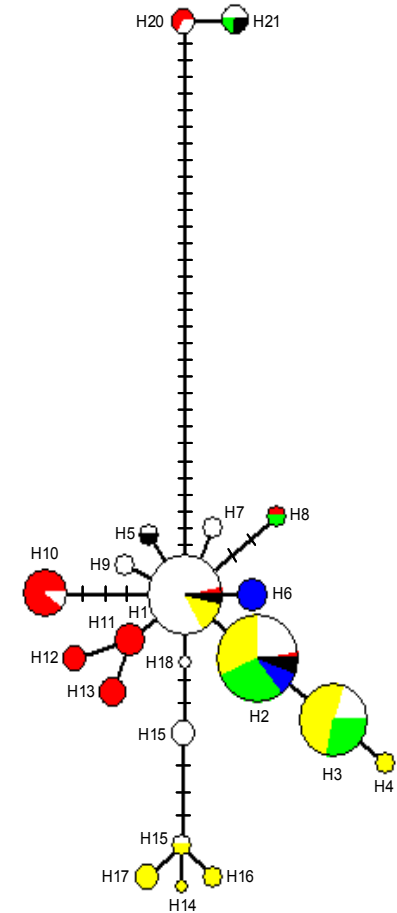


Gene diversity along crop migration/diversification

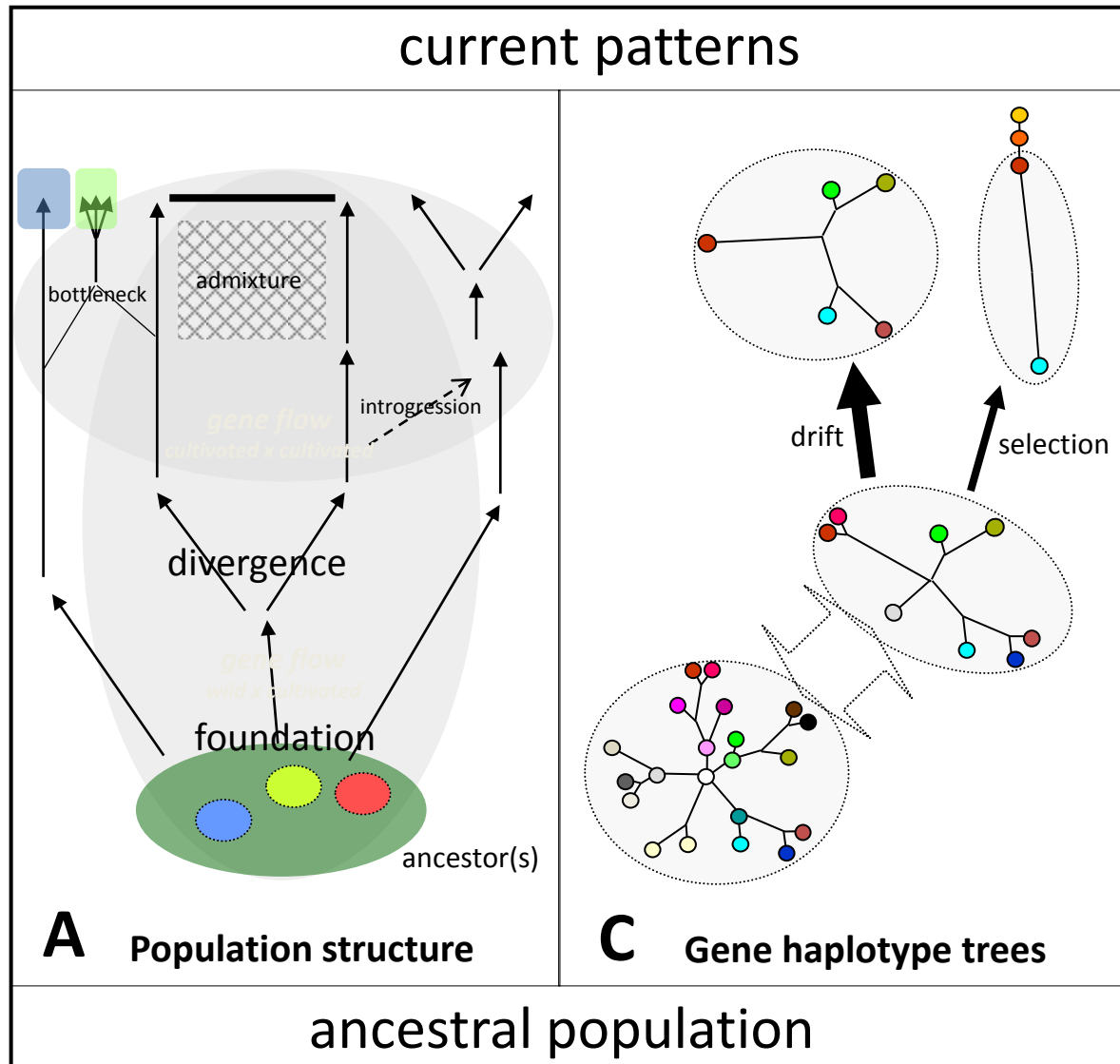
Opaque-2 gene, involved in regulation of grain protein content



Opaque2 (O2)



Global structure versus gene polymorphism → selection footprints

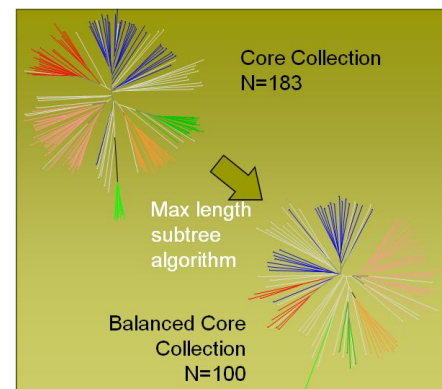
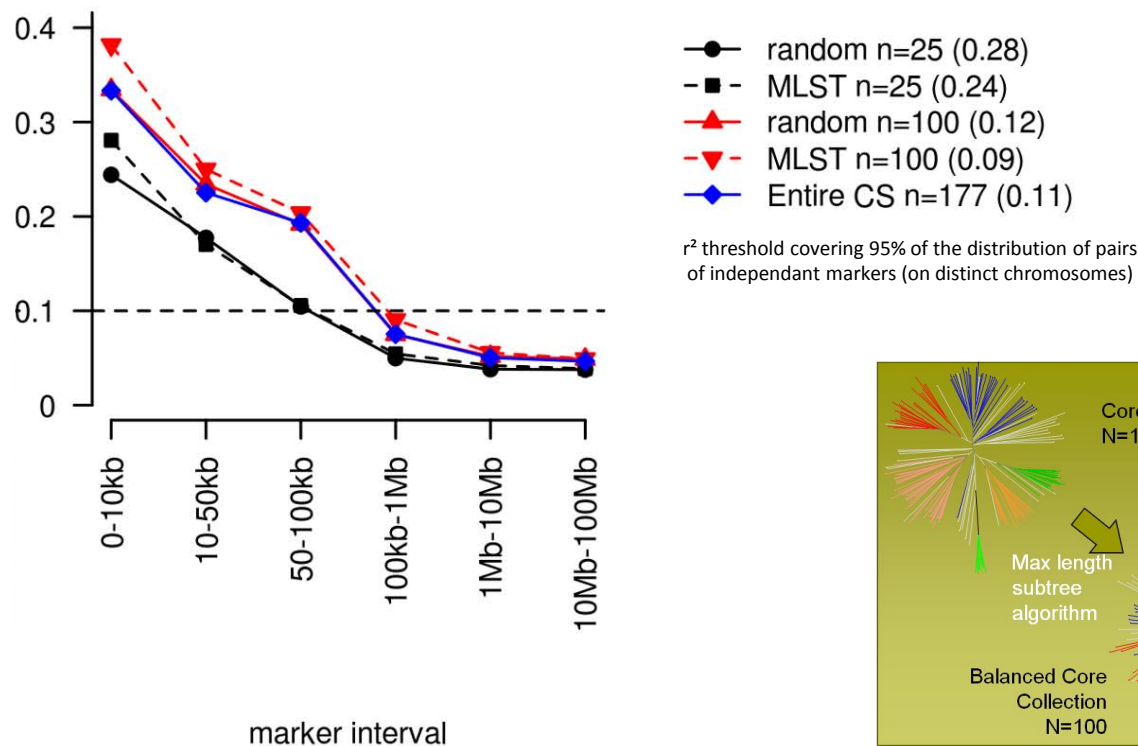
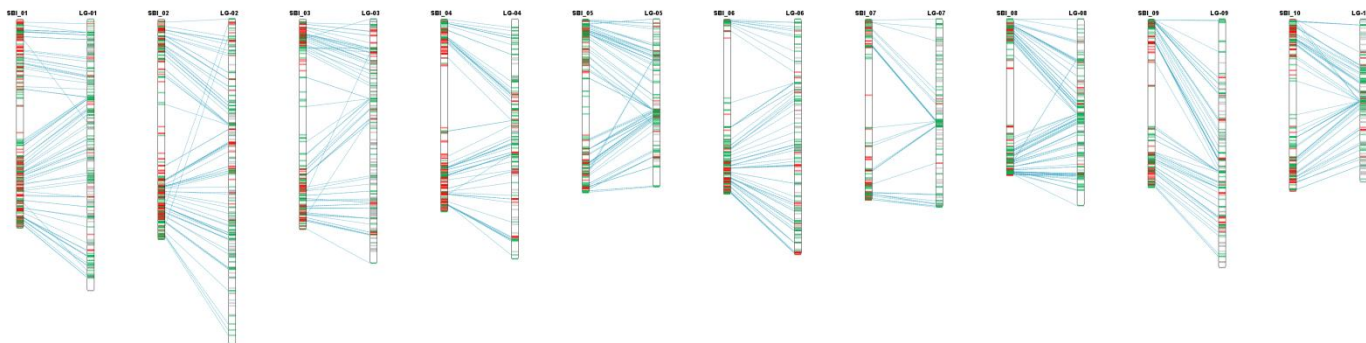


Genomic correlations



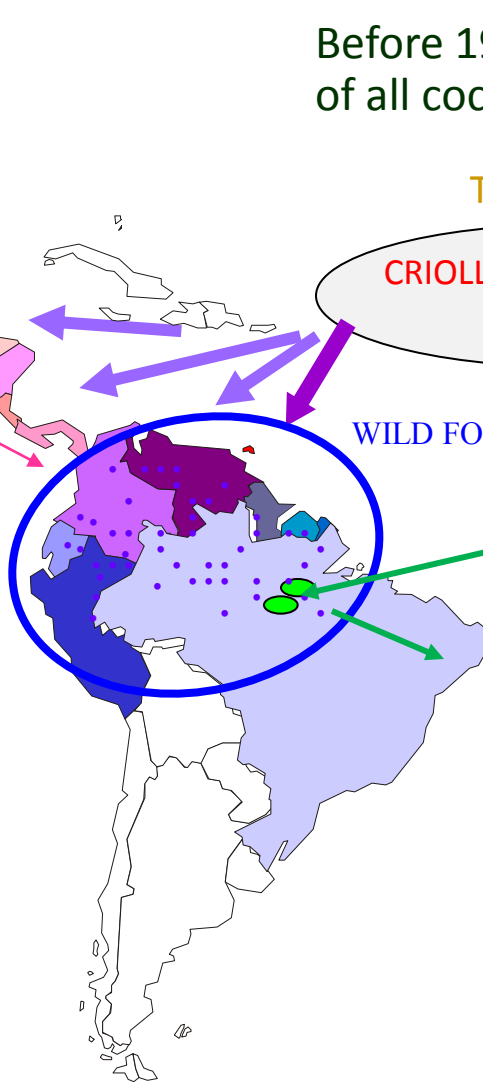
A whole-genome LD survey with DArT markers

Bouchet et al 2012 PLOS One



42% of marker pairs $r^2 >$ threshold when $d < 10^4$ pb

Adding value to *T. cacao* germplasm collections combining GWAS and genome sequence analysis



Before 1950, a few main types at the origin of all cocoa cultivated all around the world

TRINITARIO

CRIOLLO x FORASTERO
(250 years)

WILD FORASTERO POPULATIONS

L.A. FORASTERO

domesticated for 250 years(1750)

CRIOLLO

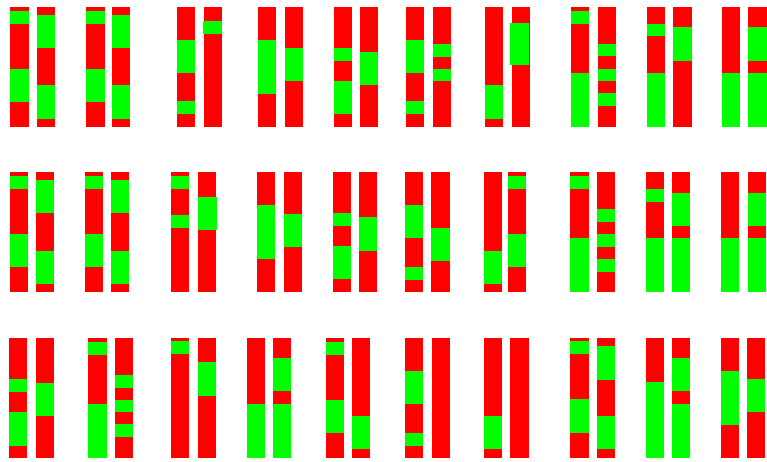
NACIONAL

NACIONAL x TRINITARIO
(100 years)

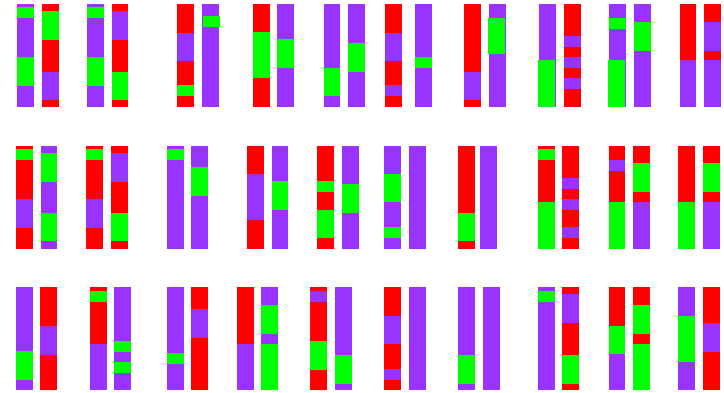


The modern cultivated Nacional pool

modern Criollo/Trinitario



modern Nacional

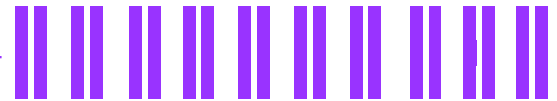


2 or 3 generations

TRINITARIO

x

NACIONAL

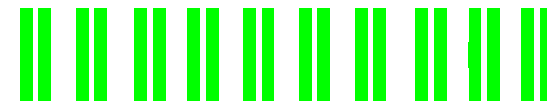


6 to 7 generations

CRIOLLO

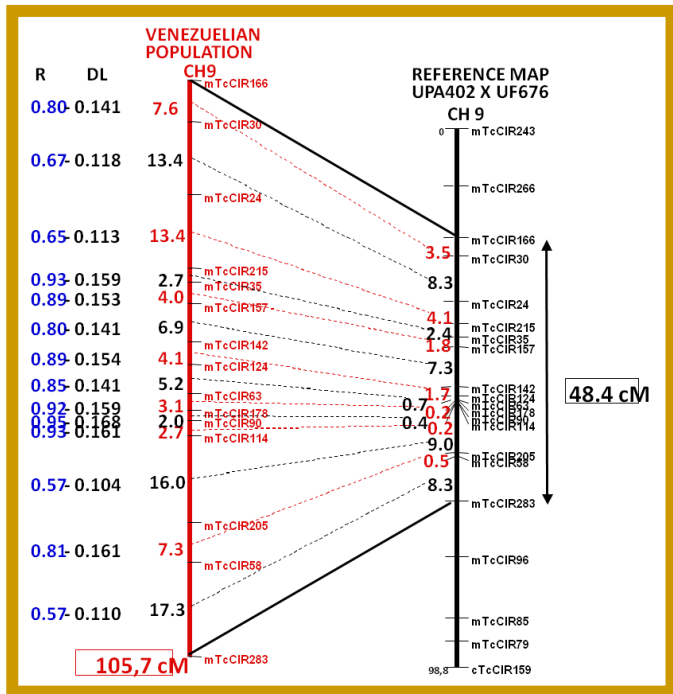
x

Lower Amazon FORASTERO



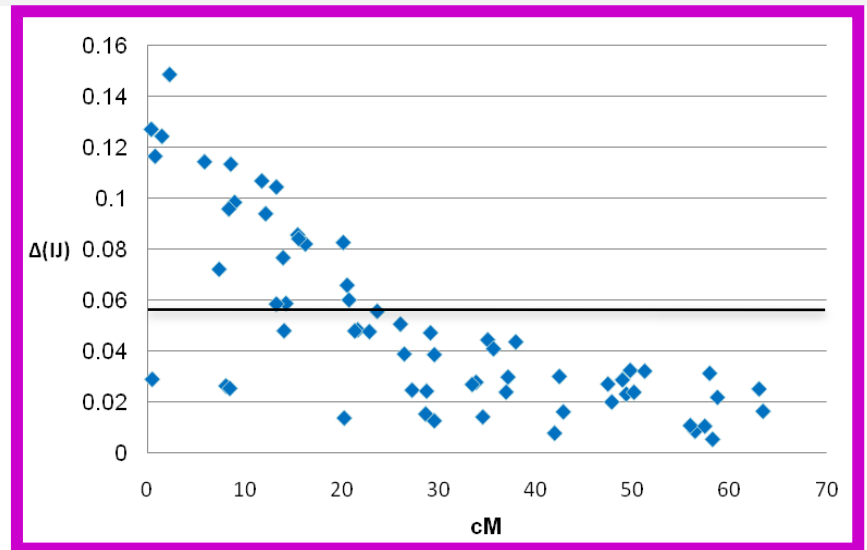
Three main ancestors

Diversity and linkage disequilibrium within Venezuelan germplasm and Ecuadorian “Nacional” germplasm




Apparent recombination rate in Criollo-Trinitario germplasm in Venezuela genotyped with 180 SSR markers

LD variation with genetic distance among 200 individuals from the INIAP germplasm collections genotyped with 180 SSR markers



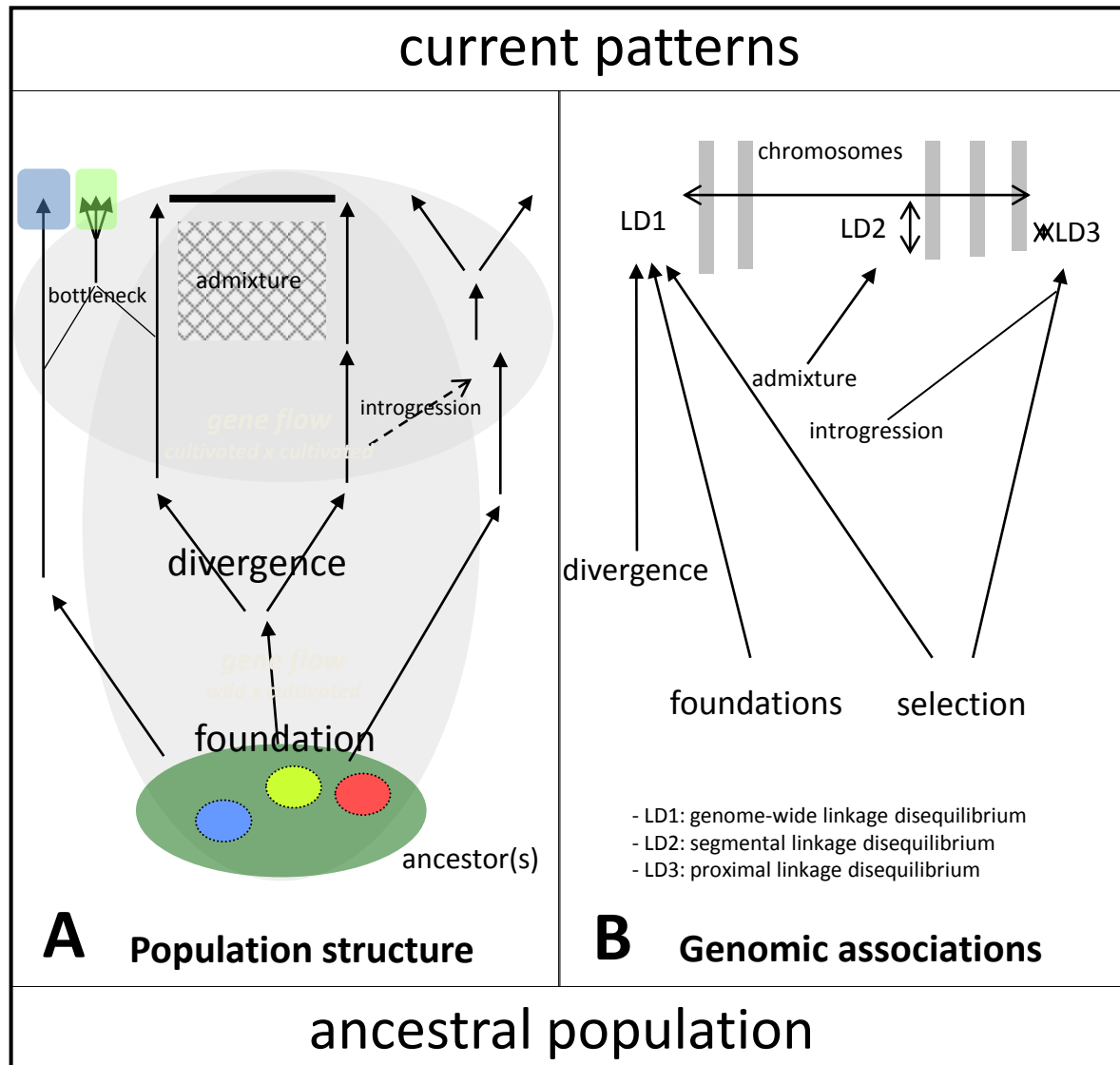
Germplasm collections established in all producing countries

- Local collections established in each producing countries
- International collections
 - CRU, Trinidad and Tobago (2300 accessions)
 - CATIE, Costa Rica (1150 accessions)

- 
- Phenotypic characterisation already carried out for many cocoa useful traits
 - Data could be exploited to conduct GWAS

Examples of associations for fruit and seed traits identified in the CATIE collection (*Marcano et al., TAG 2007, 2008*)

Understanding domestication to derive properties of genetic diversity in germplasm



Socializing diversity

- From the past
- From the present

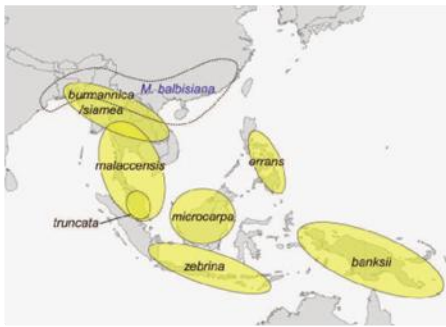
Socializing diversity: banana

The integration of archaeology, genetics, and linguistics provides robust insights into the history of banana domestication

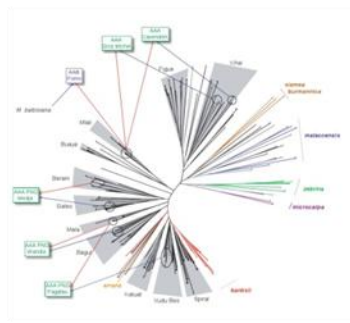
Multidisciplinary perspectives on banana (*Musa* spp.) domestication

Xavier Perrier^a, Edmond De Langhe^b, Mark Donohue^c, Carol Lentfer^d, Luc Vrydaghs^e, Frédéric Bakry^a, Françoise Carreel^f, Isabelle Hippolyte^a, Jean-Pierre Horry^a, Christophe Jenny^g, Vincent Lebot^h, Ange-Marie Risterucci^a, Kodjo Tomekpe^a, Hugues Doutrelepont^e, Terry Ballⁱ, Jason Manwaring^j, Pierre de Maret^k, and Tim Denham^{k,1}

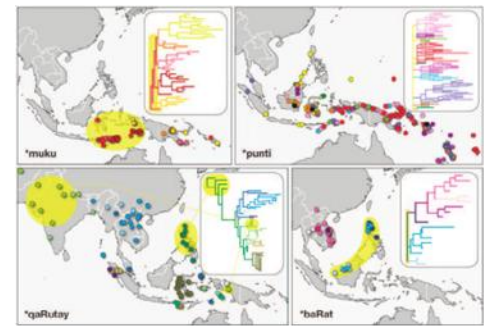
^aCentre de Coopération Internationale en Recherche Agronomique pour le Développement, Unité Mixte de Recherche Amélioration Génétique et Adaptation des Plantes, F-34398 Montpellier, France; ^bLaboratory of Tropical Crop Improvement, Katholieke Universiteit, 3001 Leuven, Belgium; ^cDepartment of Linguistics, Australian National University, Canberra 0200, Australia; ^dSchool of Social Science, University of Queensland, St. Lucia 4072, Australia; ^eResearch Team in Archaeo- and Palaeosciences, 1160 Brussels, Belgium; ^fCentre de Coopération Internationale en Recherche Agronomique pour le Développement, Unité Mixte de Recherche Biologie et Génétique des Interactions Plantes-Parasites, F-34398 Montpellier, France; ^gCentre de Coopération Internationale en Recherche Agronomique pour le Développement, Unité Mixte de Recherche Amélioration Génétique et Adaptation des Plantes, F-97130 Capesterre-Belle-Eau, Guadeloupe, France; ^hCentre de Coopération Internationale en Recherche Agronomique pour le Développement, Unité Mixte de Recherche Amélioration Génétique et Adaptation des Plantes, Department of Agriculture, Centre Agronomique de Recherche et de Formation du Vanuatu, 946 Port Vila, Vanuatu; ⁱDepartment of Ancient Scripture, Brigham Young University, Provo, UT 84602; ^jSecrétariat, Centre d'Anthropologie Culturelle, Université Libre de Bruxelles, 1000 Brussels, Belgium; and ^kSchool of Geography and Environmental Science, Monash University, Victoria 3800, Australia; ¹Corresponding author: tim.denham@monash.edu



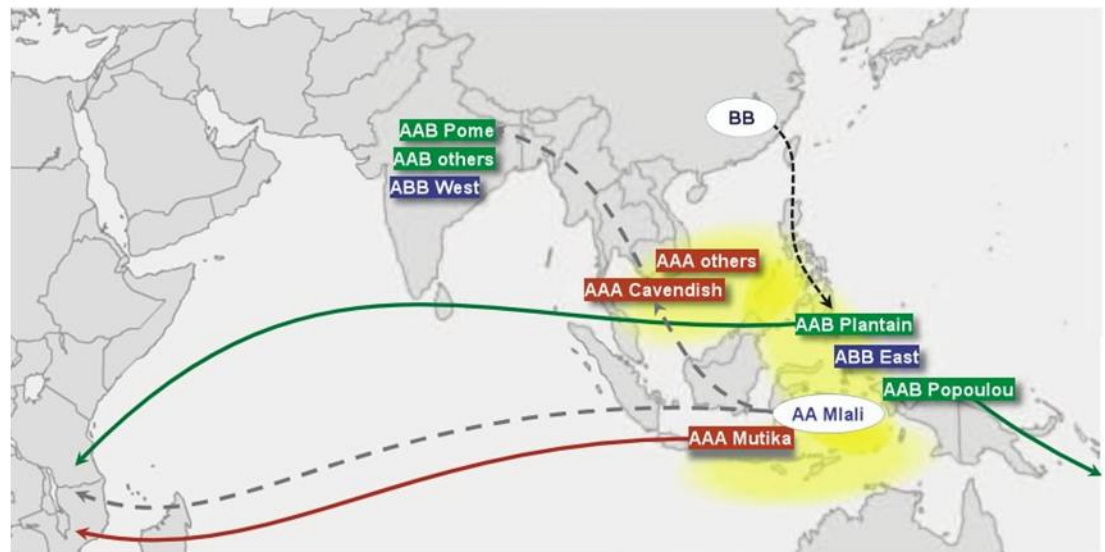
Spatial data



Crop genetic data



Linguistic data

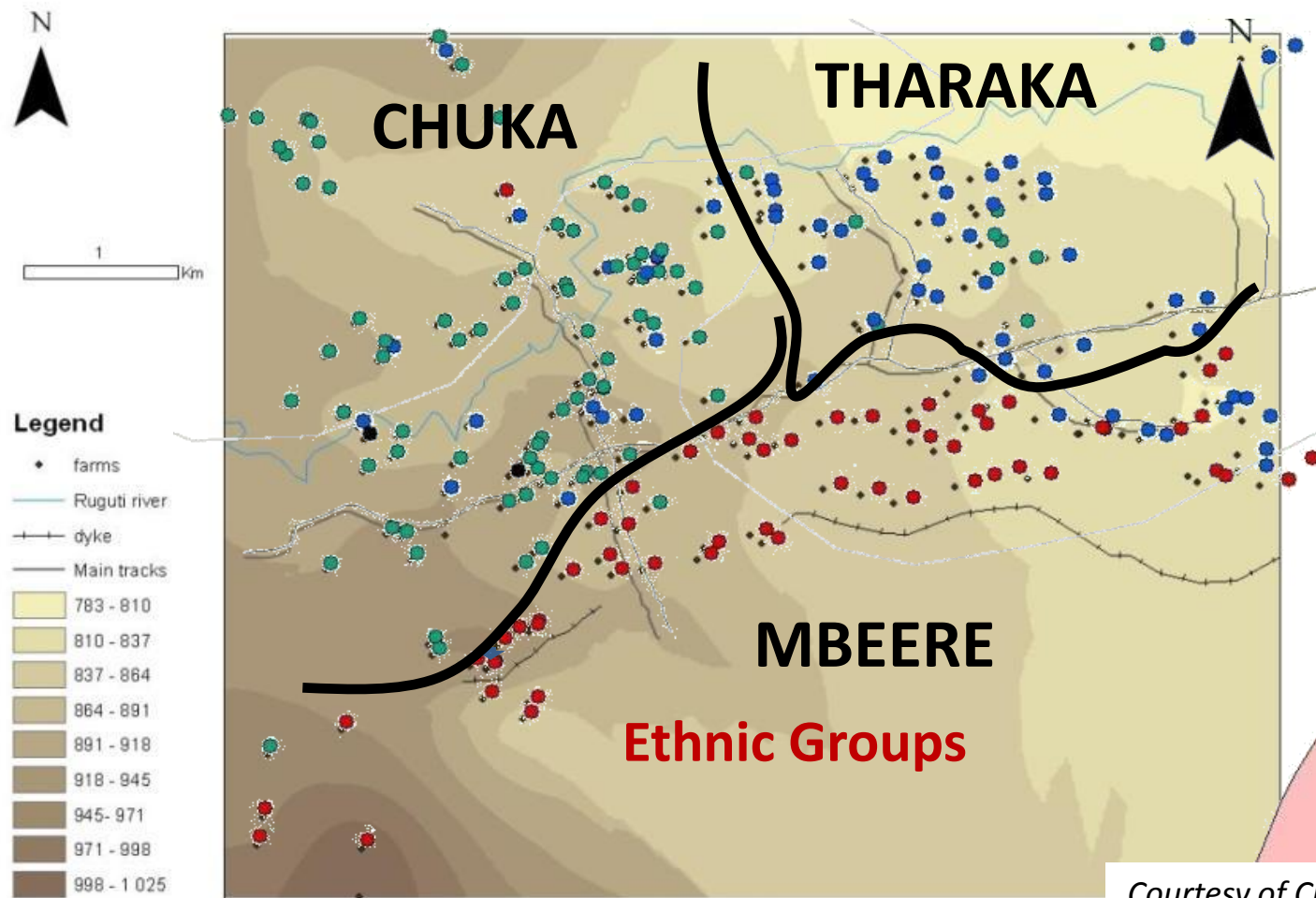


A geographical reading of the linguistic paths illustrates the movements of banana genotypes



Socializing diversity: sorghum

Is there a relation between Farmer social organisation and the Crop Genetic diversity?



Courtesy of Christian Leclerc

Socializing diversity: sorghum

The spatial distribution of landrace names and the overall genetic spatial patterns were significantly correlated with ethnolinguistic partition in Kenya.

Seed exchange is oriented more within than between linguistic communities.

The usual GxE interaction was decomposed in a three ways interaction model, GxExS, where S stands for the social factors

OPEN ACCESS Freely available online

PLOS ONE

Influence of Ethnolinguistic Diversity on the Sorghum Genetic Patterns in Subsistence Farming Systems in Eastern Kenya

Vanesse Labeyrie^{1*}, Monique Deu¹, Adeline Barnaud³, Caroline Calatayud¹, Marylène Buiron¹, Peterson Wambugu², Stéphanie Manel^{4,5}, Jean-Christophe Glaszmann¹, Christian Leclerc¹

1 UMR AGAP CIRAD, Montpellier, France, 2 National Genebank of Kenya, KARI, Nairobi, Kenya, 3 UMR DIADE, IRD, Montpellier, France, 4 UMR LPEd, Université Aix-Marseille/IRD Marseille, France, 5 UMR AMAP, CIRAD Montpellier, France

Diversity 2012, 4, 1-32; doi:10.3390/d4010001

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diversity

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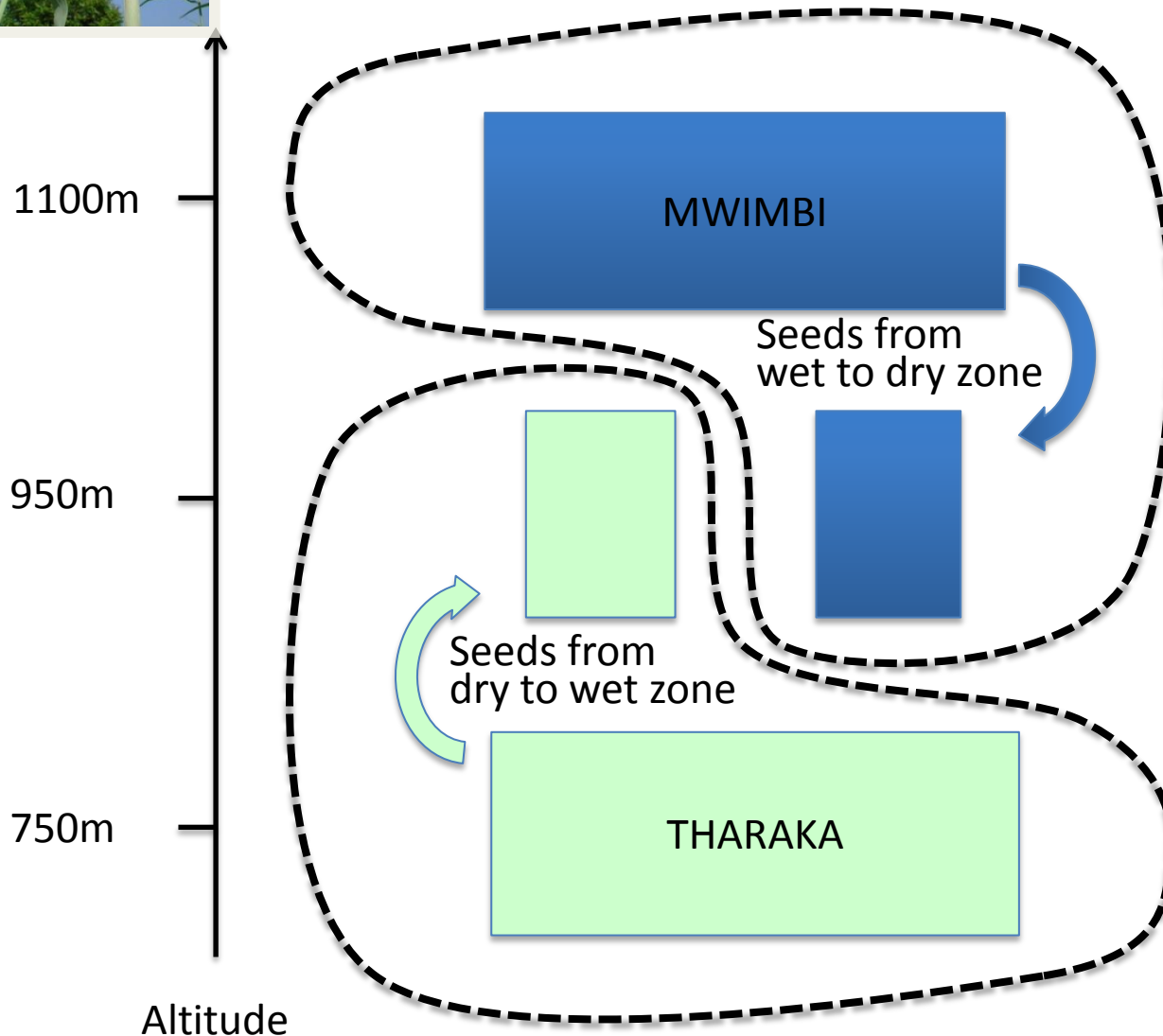
Article

Social Organization of Crop Genetic Diversity. The G × E × S Interaction Model

Christian Leclerc^{1*} and Geo Coppens d'Eeckenbrugge²



Context



MWIMBI live at 1100 m and part of the community moved down at 950 m

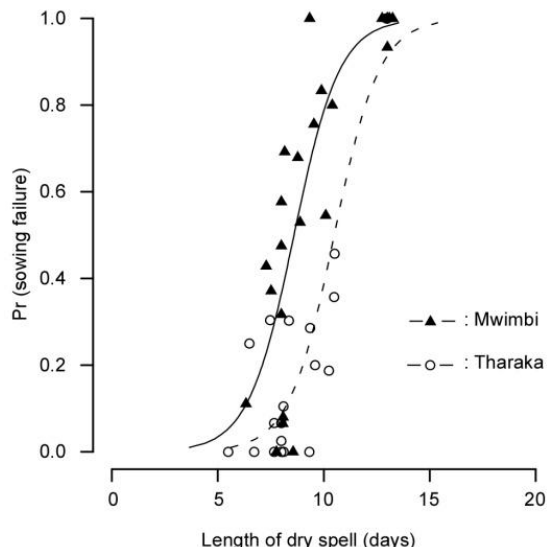
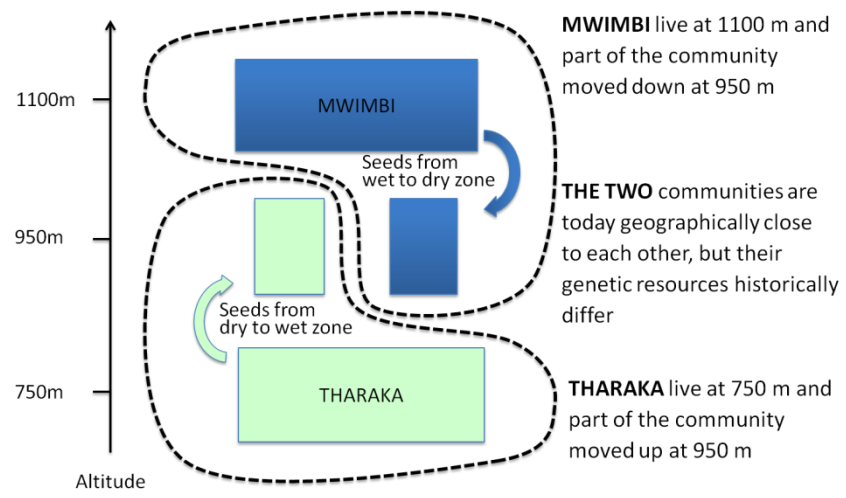
THE TWO communities are today geographically close to each other, but their genetic resources historically differ

THARAKA live at 750 m and part of the community moved up at 950 m

Social Process of Adaptation to Environmental Changes: How Eastern African Societies Intervene between Crops and Climate

Caroline Mwangera *Montpellier SupAgro, UMR AGAP, Montpellier, France*
 Joseph Boyard-Micheau *CRC, Biogéosciences, UMR 6282 CNRS/ Université de Bourgogne, Dijon, France*
 Christian Baron *CIRAD, UMR TETIS, Montpellier, France*
 Christian Leclerc* *CIRAD, UMR AGAP, Montpellier, France*

Context



extracted from
Nature Climate Change May 2014

research highlights

ADAPTATION
Adapting sowing in east Africa
Weath. Clim. Soc. <http://dx.doi.org/10.1038/ncc181> (2014)

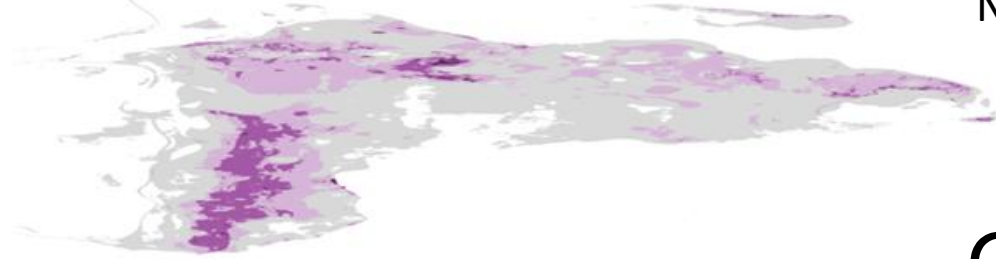


Climate variability increases farmers' risk of sowing failure by challenging their ability to anticipate rainfall and synchronize sowing accordingly. Observing changes in the practices of farming communities is crucial to better understand adaptation to future climate change, but requires costly long-term studies.

Caroline Mwangera, of AGAP Joint Research Unit, France, and colleagues used a space-and-time substitution approach to observe adaptation to climatic change. They compared two communities that migrated along the slope of Mount Kenya, Africa: the Tharaka community moved from the lowlands (750 m) to the midlands (950 m) and the Mwimbi went from upland (1100 m) to the midlands. Here, changes in location corresponded to changes in time, as induced by environmental alteration. The researchers

Potential adaptive traits from
Network interaction analysis GxExS

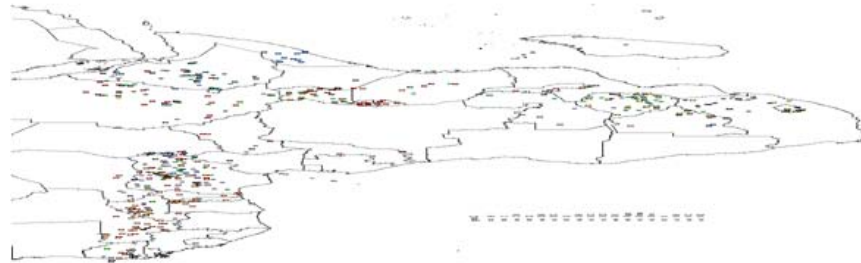
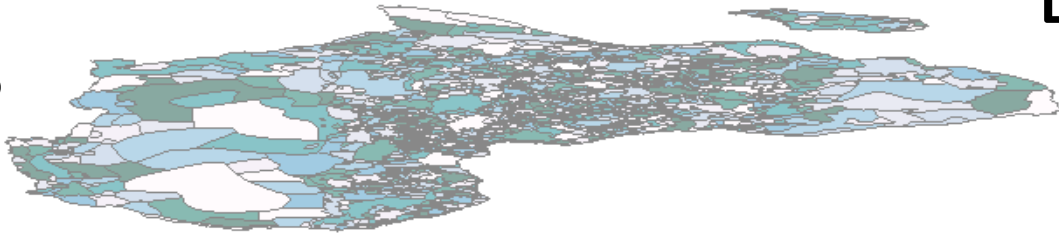
G



E



S



GxE

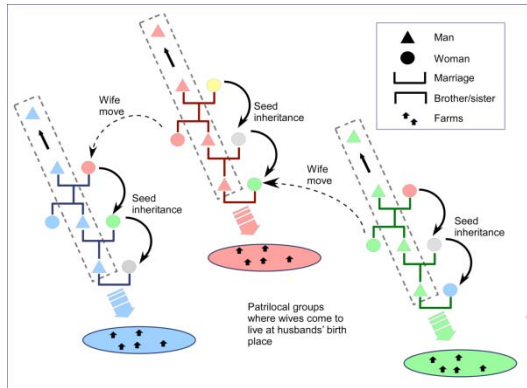
GxS

ExS

Geolocalization
of resources

Courtesy of Claire Billot

A new vision of germplasm diversity



Social Dynamics

Diversity 2012, 4, 1-32, doi:10.3390/d4010001

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 diversity
 ISSN 1424-2918
 www.mdpi.com/journal/diversity

Article
Social Organization of Crop Genetic Diversity. The $G \times E \times S$ Interaction Model
 Christian Leclerc ^{1,*} and Geo Coppens d'Eeckenbrugge ²

PNAS PERSPECTIVE

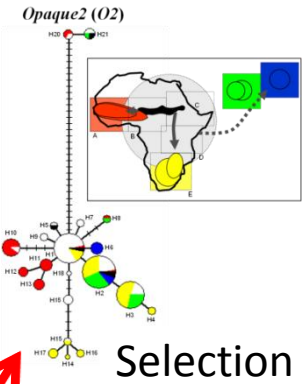
Multidisciplinary perspectives on banana (*Musa* spp.) domestication

Françoise Carreel¹, Kodjo Tomekpe²,
 Serge Amelioration
 Sobolev Universitet, 2007
 Social Science, University
 Centre de Coopération

Linguistic extension for terms
 "maku (1), "qafutay (2), "bafat(3) and their derivatives

Archeology and linguistics shed light on the historical roles of people in the movement and cultivation of banana in West Africa during the Holocene. The historical reconstruction of domestication processes is essential to diversify and improve banana cvs for the future.

Breeding



Mutation

Recombination

History
Linguistics

Foundation/
Selection

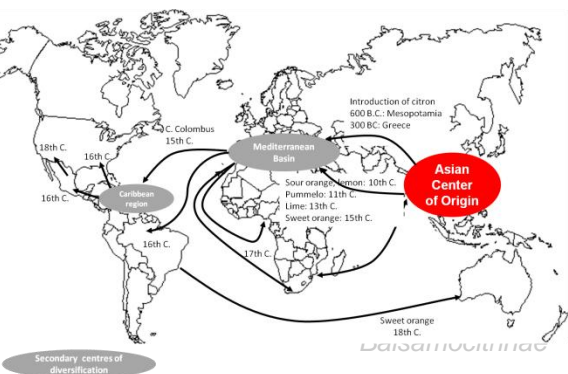
Mobilizing genetic diversity

- Brodening the genetic base
 - Citrus
 - Sugarcane
- Developing « progressive populations »
 - Groundnut
 - Sorghum

Citrus Botanical Classification

Family Rutaceae
Subfamily Aurantioideae

Tribe	Subtribe	Genus		
Clauseneae	Micromelinae	Micromelium		
		Glycosmis		
	Clauseneae		Clausena	
			Murraya	
	Merrillinae		Merrillia	
Citreae	Triphasalinae	Wenzelia		
		Monanthocitrus		
		Oxanthera		
		Merope		
		Tripashia		
		Pamburus		
		Luvunga		
		Paramingnya		
		Wenzelia		
		Citrinae	Primitive citrus	Severinia
				Pleiospermium
				Burkillanthus
				Limnocitrus
				Hesperethusa
			Near citrus	Citropsis
		Atalantia		
	True citrus	Fortunella		
		Eremocitrus		
		Poncirus		
		Clymenia		
		Microcitrus		
		Citrus		
		Swinglea		
		Aegle		
		Afraegle		
		Aeglopsis		
		Balsamocitrus		
		Feronia		
		Feroniella		



Fortunella



Eremocitrus



Poncirus



Clymenia



Microcitrus



Citrus



Limes

(*C. aurantifolia*)



Lemons
(*C. limon*)



Sour oranges
(*C. aurantium*)



Sweet oranges
(*C. sinensis*)



Grapefruits
(*C. paradisi*)

C. reticulata ***C. maxima***



C. medica

Papeda



New genomic-derived insight and tools

International Citrus Genome Consortium Haploid Clementine sequence

7 diploid accessions resequenced
Wu et al. Nature Biotech. 2014

Spanish consortium

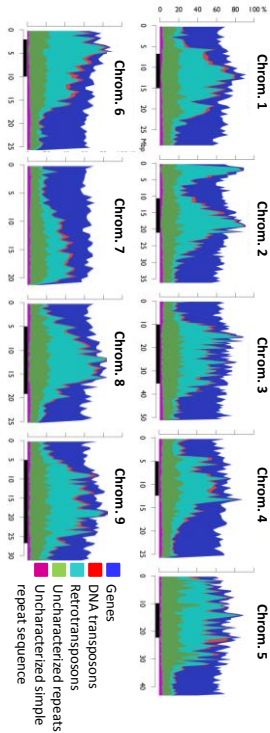
More than 100 accession resequenced (Illumina pair end)
Talon et al. ISC congress 2012

Sweet orange Haploid reference sequence 454

Resequencing: 5 diploid accessions
Xu et al. 2013. Nature Genetics 45, 59–66

Clementine & sweet orange genetic maps

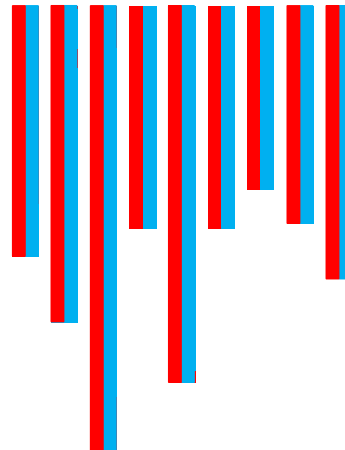
Ollitrault et al. BMC Genomics 2012



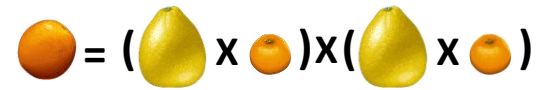
F1 Interspecific hybrids



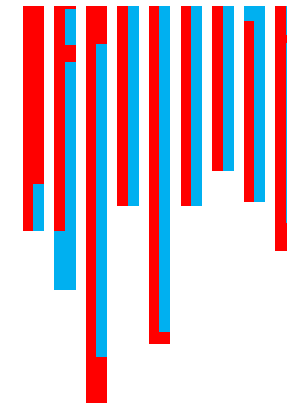
Sour orange like rootstock



F2-like and Backcross –like hybrids



Sweet orange like varieties



 Pummelo
 Mandarin

New approaches to optimize the mobilization of citrus biodiversity for breeding

Rootstock ploidy manipulation for a better adaptation; breeding strategies

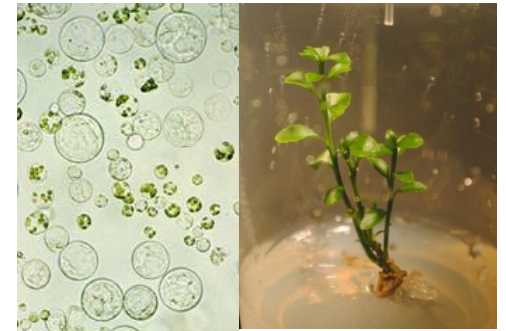
Doubled diploid AB → AABB

Obtention: spontaneous chromosome stock doubling in nucellar cells (Aleza et al., 2011)
Most traditional citrus rootstock are currently available as doubled diploid



Somatic hybrids AB + CD → ABCD

Obtention: protoplast fusion
(Grosser et al., 2010; Dambier et al., 2011)



Tetrazyg: AABB x CCDD; ABCD x EFGH

Obtention: sexual hybridization at tetraploid level
(Grosser et al. 2010)



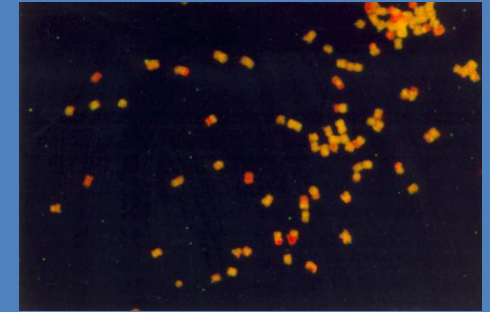
Sweet orange grafted on
FLHORAG1 somatic hybrid (CIRAD)
Calcareous soils Morocco

Sugarcane

modern sugarcane varieties



100 -130 chromosomes



S. spontaneum
 $2n = 40 - 128$
 $X = 8$

S. officinarum
 $2n = 80$
 $X = 10$



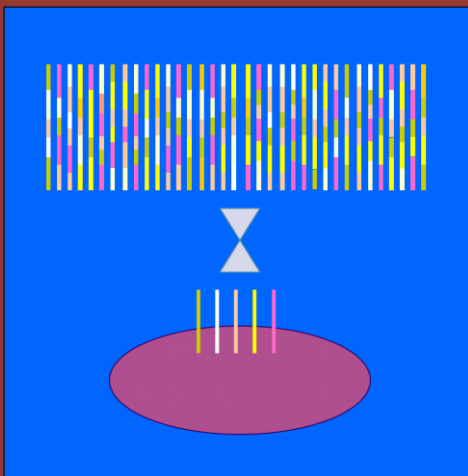
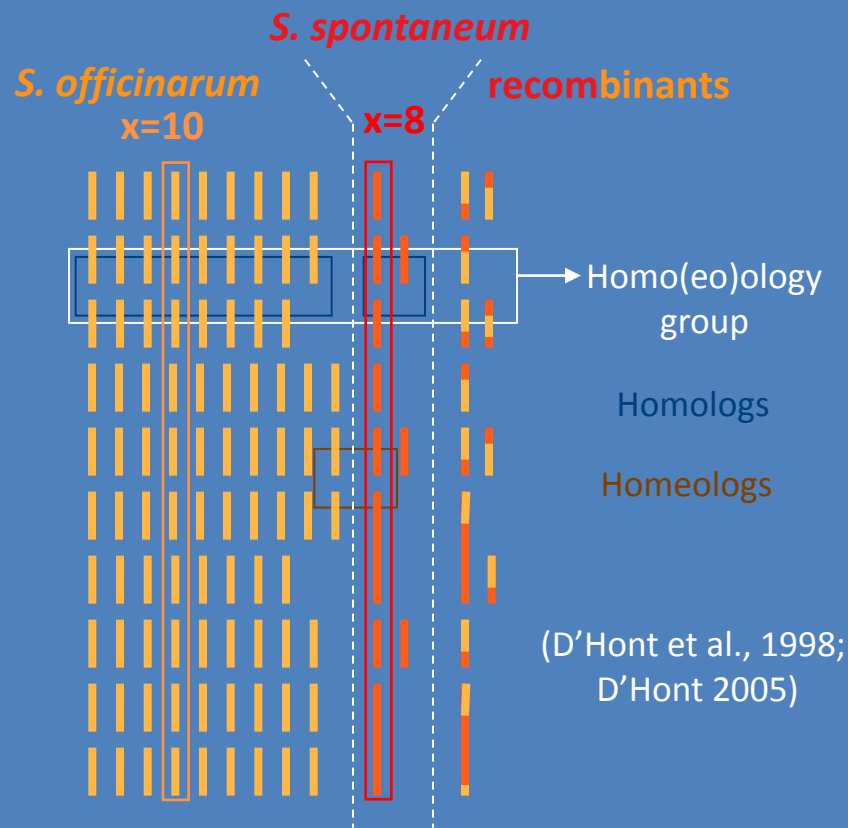


Global genome organization

R570, $2n=ca\ 115$
80 % *S. officinarum*
10% *S. spontaneum*
10% recombinants
 (D'Hont et al., 1996 Mol. Gen. Genet.)

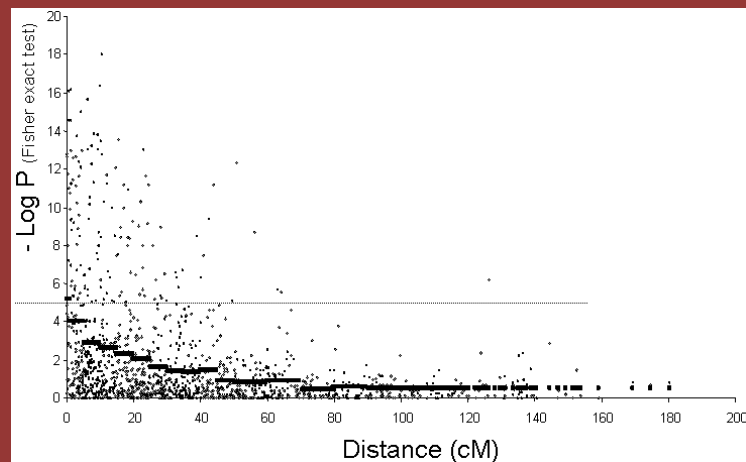
Chromosome pairing :

- mainly bivalents
- polysomy with some preferential pairing
 (Grivet et al, 1996 ; Jannoo et al, 2004)

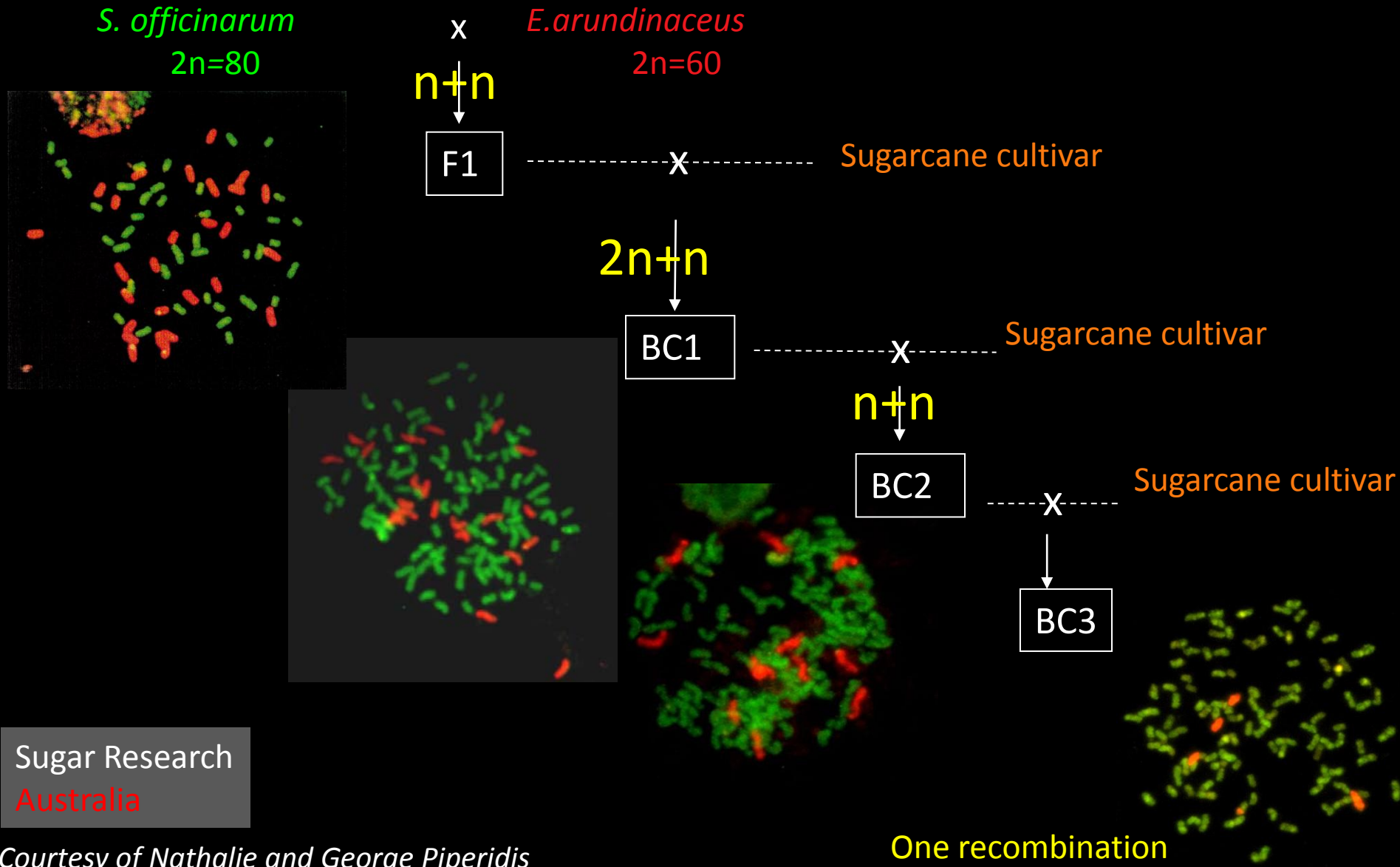


Linkage disequilibrium

among sugarcane cultivars
 (Jannoo et al 1999;
 Raboin et al 2008)

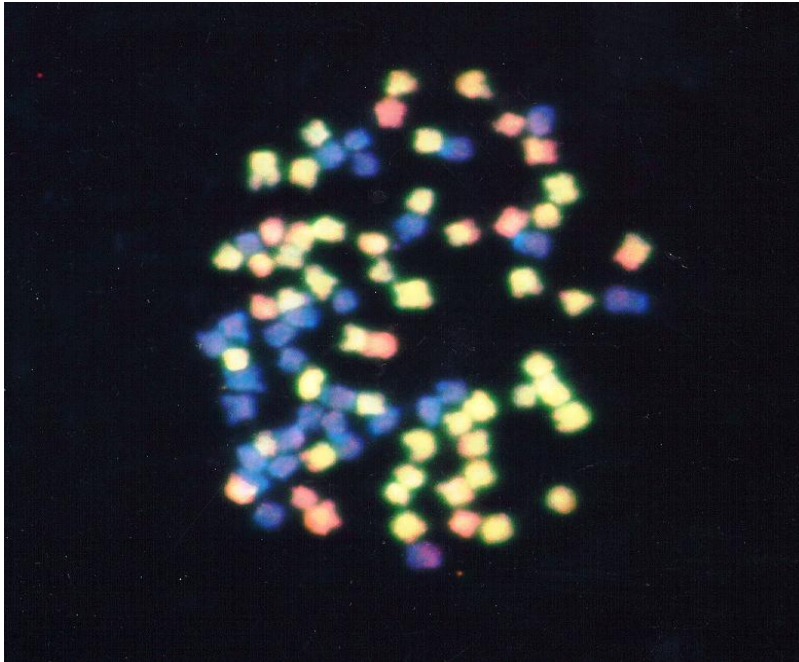


GISH to monitor chromosome transmission in Erianthus hybrids



Sugarcane cultivar X Erianthus

Possibility to detect three genomes



Blue: Erianthus chromosomes
orange: spontaneum chromosomes
Yellow: officinarum chromosomes



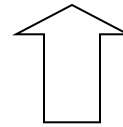
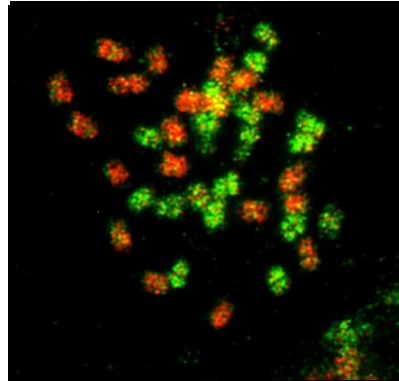
Interspecific introgression and trait dissection in Groundnut

Sequencing
ongoing

Arachis hypogaea **AABB**

Seijo et al. 2007

$2n = 4x = 40$

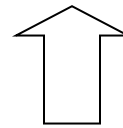


Spontaneous duplication

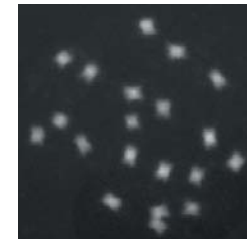
Sterile hybrid **AB** $2n = 20$



A. duranensis (AA)



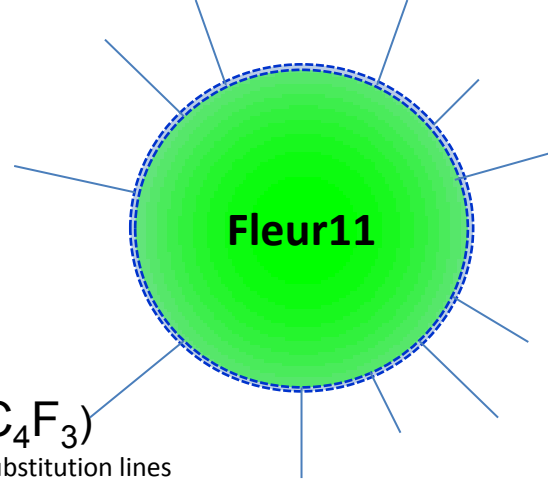
$n=10 \times n=10$



A. ipaensis (BB)



Foncéca et al. Plos ONE 2012



CSSLs (BC_4F_3)

chromosome segment substitution lines
122 lignées CSSL
92% genome coverage
40 cM segments on average



BC_4F_2

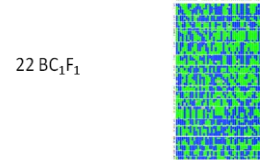
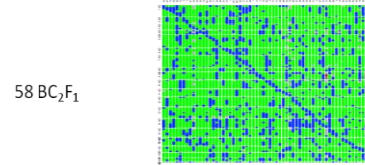
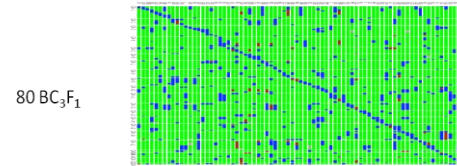
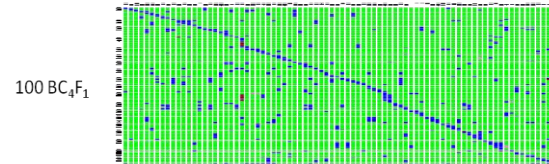
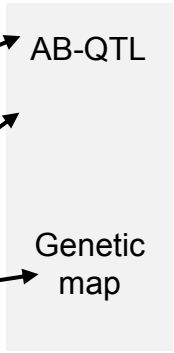
BC_4

BC_3

BC_2

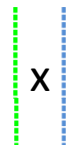
BC_1

F_1



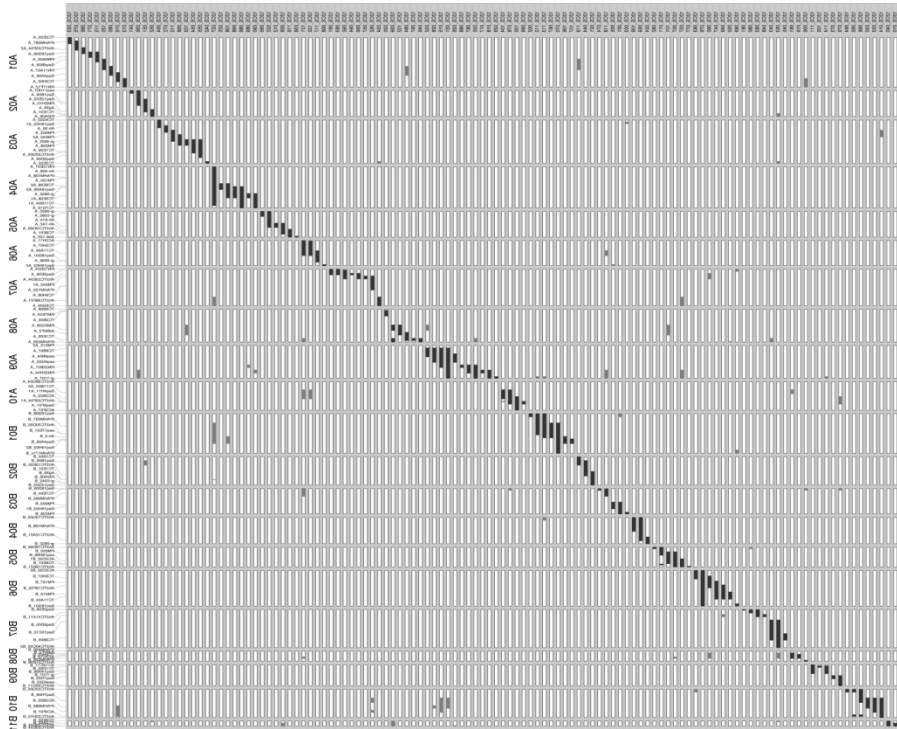
Fleur11

Fleur11(AABB) x **AiAd (AABB)**



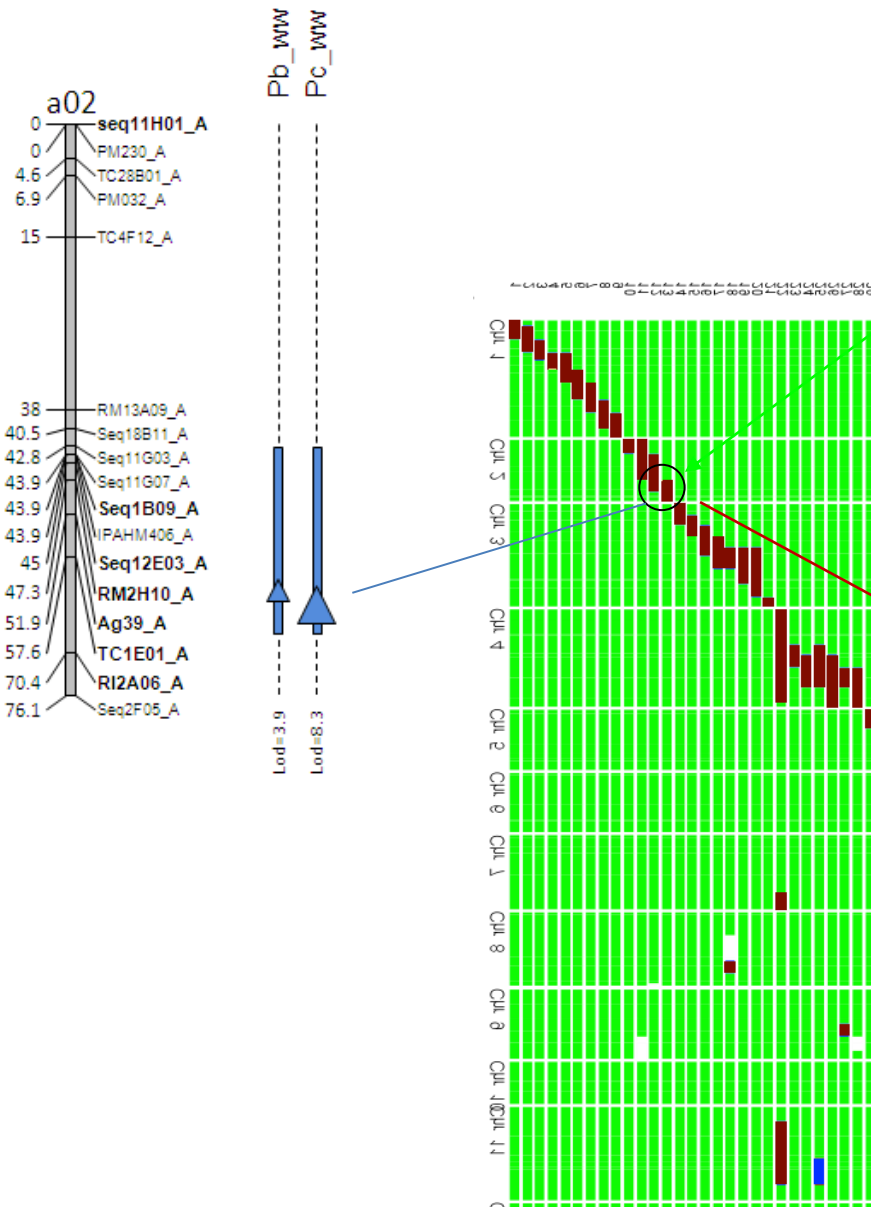
Exploring functional variation on a focussed genetic basis

AB_QTLs vs CSSL analysis

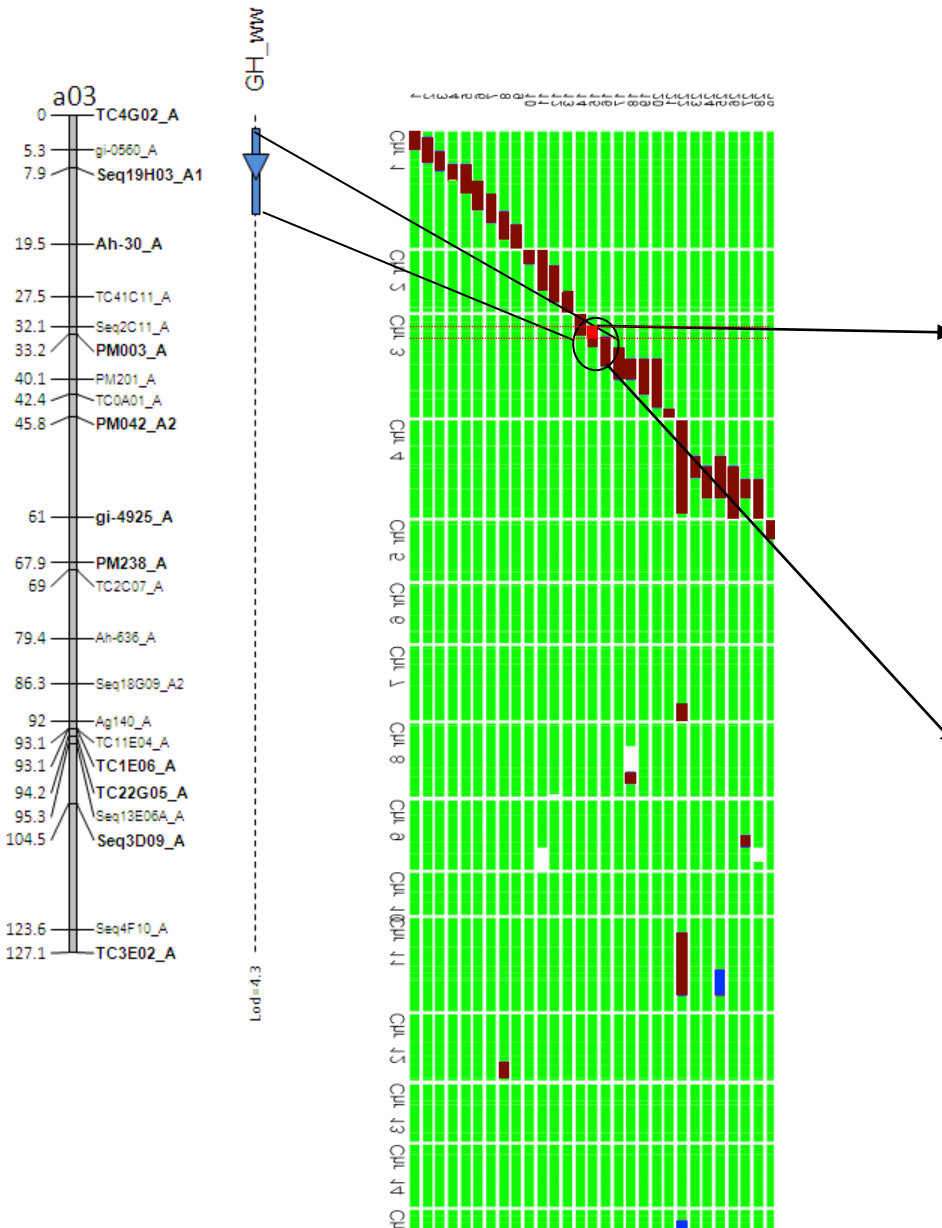


C	AB-QTLs	CSSLs	Common
GH	6	14	5
PH	5	15	3

AB-QTL and CSSLs: QTL Validation - Constriction



AB-QTL and CSSLs: Refining QTLs Position - GH





*Fonceka et al 2009, 2012a, 2012b
BMC Plant Biol, BMC Plant Biol, PLOS One*





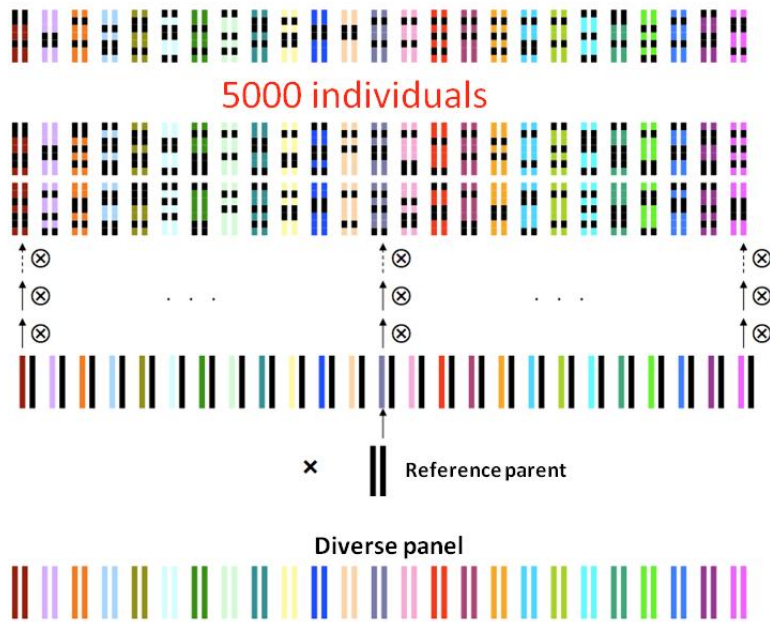
Sequenced
In 2008

Enhancing sorghum grain yield and quality for the sudano-sahelian zone of West Africa using the

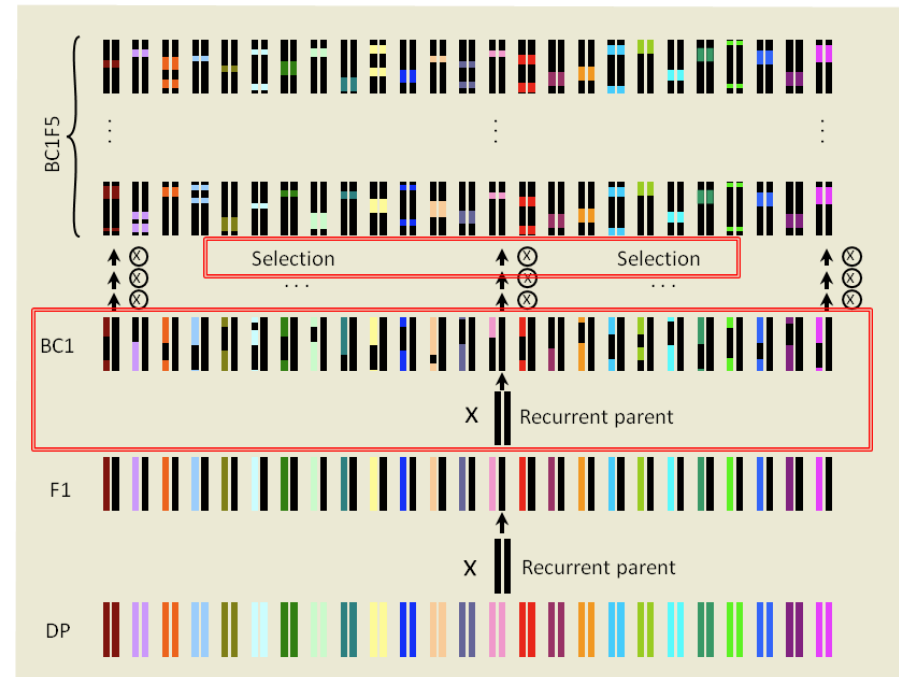


backcross nested association mapping (BC-NAM) approach

The maize NAM design



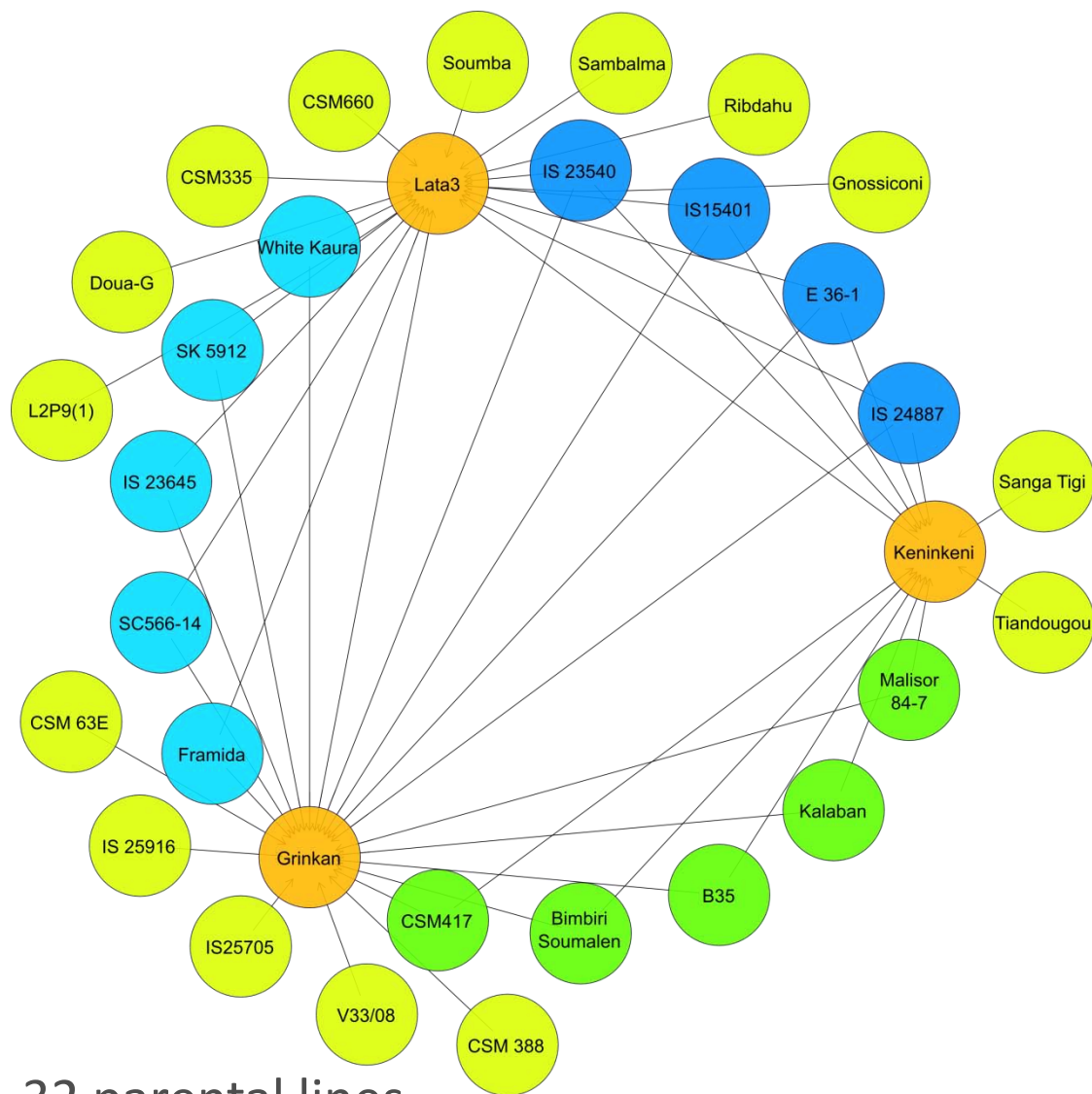
The Sorghum BC NAM design



Yu et al., 2008. Genetics 178: 539–55



BC-NAM populations

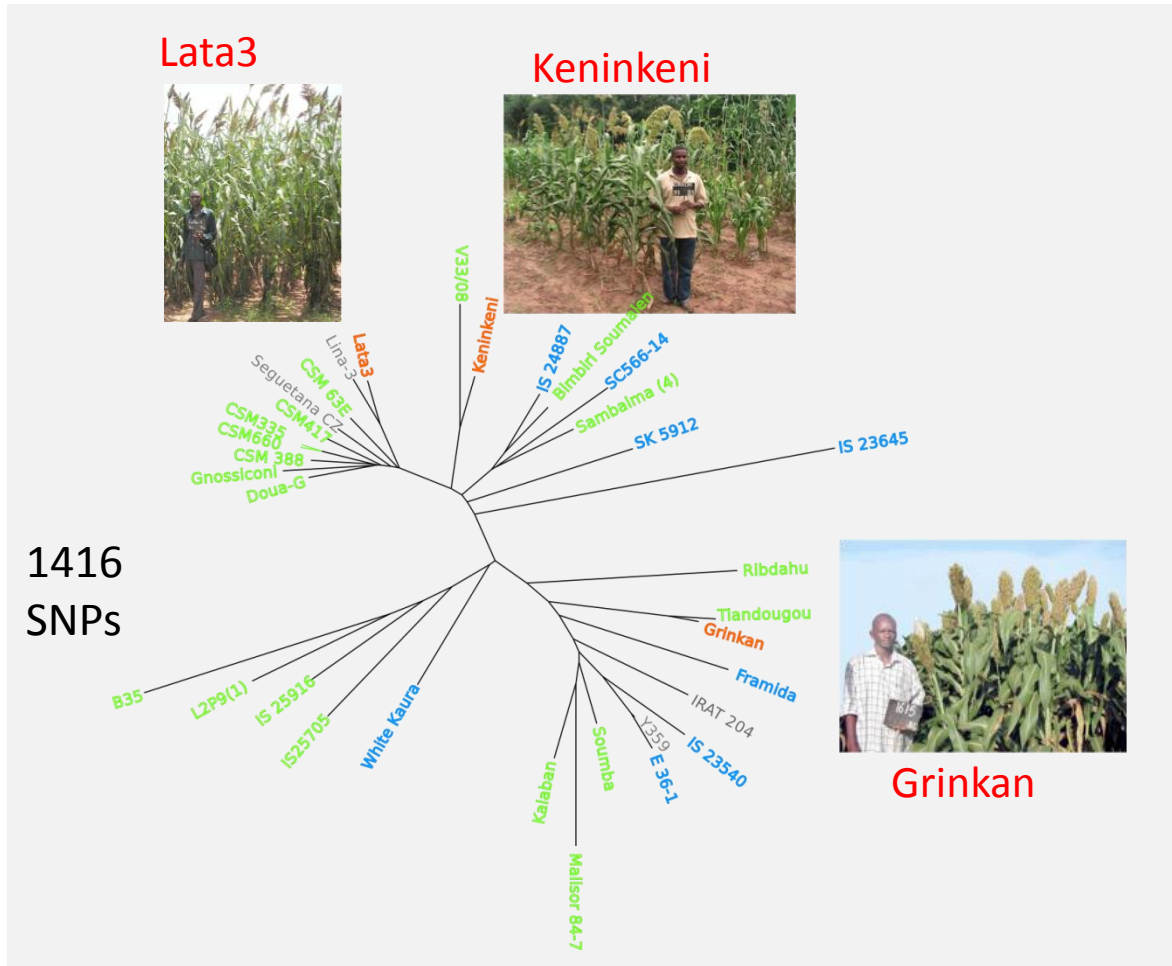


	Name	Race and origin	Origin	Specific advantages
Recurrent	Lata3	Guinea	Mali	Productivity, grain quality
	Grinkan	Caud./Guinea	Mali	Productivity
	Keninkeni	Guinea/Caud	Mali	Stable grain yield, grain quality
Common donors	E 36-1	Caudatum	Ethiopia	Drought resistance
	Framida		Burkina Faso	Striga tolerance
	IS15401	Guinea	Cameroon	Grain quality
	IS 23540		Ethiopia	Sweet stem
	SC566-14	Caudatum	Nigeria	Aluminium tolerance
	IS 24887	Guinea	Nigeria	Diversity
	IS 23645	Guinea	Gambia	Diversity
	SK 5912	Caudatum	Nigeria	Diversity
	White Kaura	"Kaura"	Nigeria	
Specific donors (ICR)	Gnossiconi	Guinea	Burkina Faso	Well adapted, high yielding
	Ribdahu	Guinea	Niger	Good sudanian Zone
	Sambalma (4)			Good for Sudanian zone
	Soumba	Caudatum		Early, good yielding
	CSM660	Guinea		High grain yield
	CSM335	Guinea		High stable grain yield, very good grain quality
	Doua-G	Guinea		High Grain Yield
	L2P9(1)	Caudatum	Eritrea	Striga resistant line
Specific donors (IER)	CSM 63E	Guinea	Mali	Precocity
	CSM417	Guinea	Mali	Grain quality, adaptation
	IS 25916	Durra	Mali	Grain weight
	IS25705	Durra	Mali	Grain weight
	V33/08	Caud./Guinea	Mali	Productivity
	Malisor 84-7	Caudatum	Mali	Head bug resistance
	Kalaban	Caudatum	Mali	Productivity
	B35	Durra	Ethiopia	Stay-Green
	Bimbiri Soumalen			
	CSM 388	Guinea	Mali	
	Tiandougou	Caud./Guinea	Mali	Productivity
Sanga Tigi	Guinée	Mali	Grain quality	

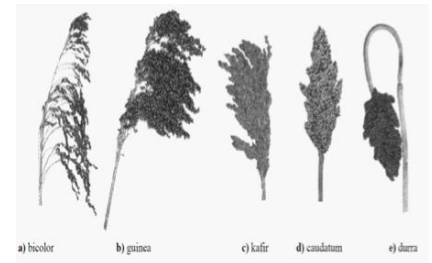
32 parental lines
50 populations BC₁F₄

Courtesy of Jean-François Rami

BC-NAM parents



Donor parents are diverse in height and botanical types.



BC-NAM: population development

	#BC1F4 Families			
	Recurrent parent	Grinkan	Lata3	Keninkeni
Common Donors	Grinkan		133	
	Keninkeni		152	
	Lata3	78		
	E 36-1	152	117	170
	Framida	149	112	
	IS 23540	120	143	116
	IS 23645	148	68	
	IS 24887	136		162
	IS15401	159	109	158
	IS24887		124	
	SC566-14	145	126	
	SK 5912	82	130	
	White Kaura	145	64	
	IFR Spec. donors	B35	132	
Bimbiri Soumalen		151		190
CSM 388		181		
CSM 63E		78		
CSM417		169		98
IS 25916		144		
IS25705		150		
Kalaban		150		148
Malisor 84-7		109		148
Sanga Tigi				141
Tiandougou				148
ICR Spec. donors	V33/08	97		
	CSM335		146	
	CSM660		128	
	Doua-G		120	
	Gnossiconi		71	
	L2P9(1)		26	
	Ribdahu		85	
Sambalma (4)		102		
Soumba		99		
Grand Total	2675	2055	1592	
		6322		

- MABC ms3 conversion of recurrent parents (Grinkan, Keninkeni)
- Generation advance during off-season



BC-NAM: phenotyping

- Phenotyping in 2012 rainy season on BC₁F₄ families

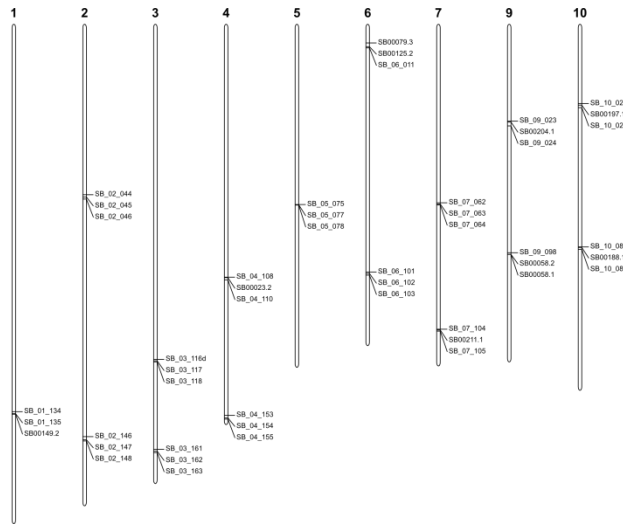


- IER: 21 BC₁F₄ populations in two locations (Sotuba and Cinzana) and two sowing dates.
- ICRISAT: 10 BC₁F₄ populations in Samanko in two locations with normal and low-P conditions.
- Selfing pursued and BC₁F₆ populations released at the end of the project

BC-NAM: genotyping

Phase 1 (2012): Conformity check

- 50 Kaspar SNPs (clustered)
- 32 IER populations (4330 BC₁F₃ ind)



Overall good conformity

- 1 wrong pop.: Kk x Tian > Kk x B35
- 1 donor parent (CSM417) very heterogeneous
- Few lines off-types
- 1 pop (IEG14) with altered version of recurrent parent used at BC₁.

Phase 2 (2013):

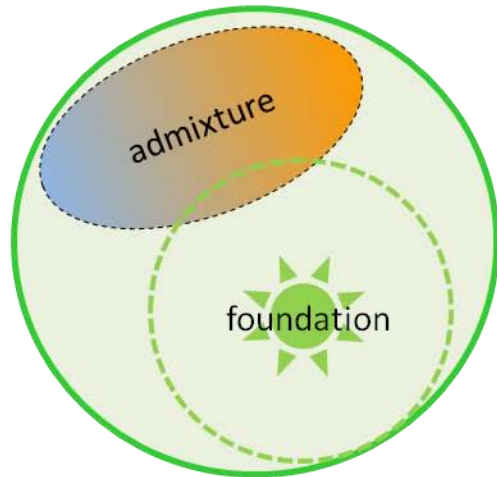
- BC₁F₃
- QTL density (Kaspar SNPs)
- Polym. assayed

Phase 3 (?):

- Parents reseq.
- BC₁F₆ > GBS

Cross	Rec.	DP	# Pol SNP
IEG08	Grinkan	IS 24887	411
IEG03	Grinkan	E 36-1	276
IEG05	Grinkan	IS15401	-
IEG02	Grinkan	Lata3	374
IEG16	Grinkan	V33/08	331
IEG06	Grinkan	IS 23540	249
IEG19	Grinkan	Kalaban	251
IEG18	Grinkan	Malisor 84-7	337
		Bimbiri	
IEG21	Grinkan	Soumalen	388
IEG20	Grinkan	B35	446
IEG09	Grinkan	IS 23645	444
IEG14	Grinkan	IS25705	346
IEG07	Grinkan	SC566-14	395
IEG04	Grinkan	Framida	277
IEG12	Grinkan	CSM417	361
IEG11	Grinkan	CSM 63E	373
IEG23	Grinkan	CSM 388	379
IEG13	Grinkan	IS 25916	366
IEG24	Grinkan	White Kaura	328
IEG10	Grinkan	SK5912	376
IEK06	Keninkeni	IS 24887	357
IEK07	Keninkeni	Tiandougou	366
IEK03	Keninkeni	E 36-1	470
IEK04	Keninkeni	IS15401	-
IEK08	Keninkeni	Sanga Tigi	-
IEK05	Keninkeni	IS 23540	457
IEK10	Keninkeni	Kalaban	426
IEK09	Keninkeni	Malisor 84-7	522
		Bimbiri	
IEK12	Keninkeni	Soumalen	324
IEK11	Keninkeni	B35	535
IEK14	Keninkeni	CSM417	-
ICL03	Lata3	E 36-1	469
ICL04	Lata3	Framida	460
ICL01	Lata3	Grinkan	374
ICL05	Lata3	IS15401	-
ICL06	Lata3	IS 23540	480
ICL09	Lata3	IS 23645	441
ICL02	Lata3	Keninkeni	309
ICL07	Lata3	SC566-14	381
ICL10	Lata3	SK 5912	348
ICL18	Lata3	CSM335	209
ICL17	Lata3	CSM660	209
ICL19	Lata3	Doua-G	231
ICL11	Lata3	Gnossiconi	221
ICL20	Lata3	L2P9(1)	470
ICL08	Lata3	IS24887	349
ICL12	Lata3	Ribdahu	421
ICL14	Lata3	Sambalma (4)	313
ICL16	Lata3	Soumba	447
ICL13	Lata3	White Kaura	402

Altogether, (pre)breeding populations allowing genetic analysis, genetic gain and broad cooperation



Historical populations, with significant LD,
bearing **diversity** and **agronomic value**

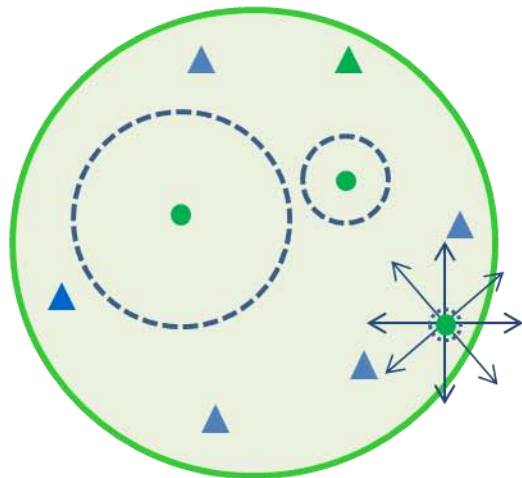
Perennials
...

Coordinate genotyping

Exchange data

Integrate
haplotype analysis

Multiple environments



NAM, BCNAM, CSSL centered,
bearing **diversity** around **elite material**

Annuals
...

Exchange materials

Exchange data

Compile information

Multiple environments

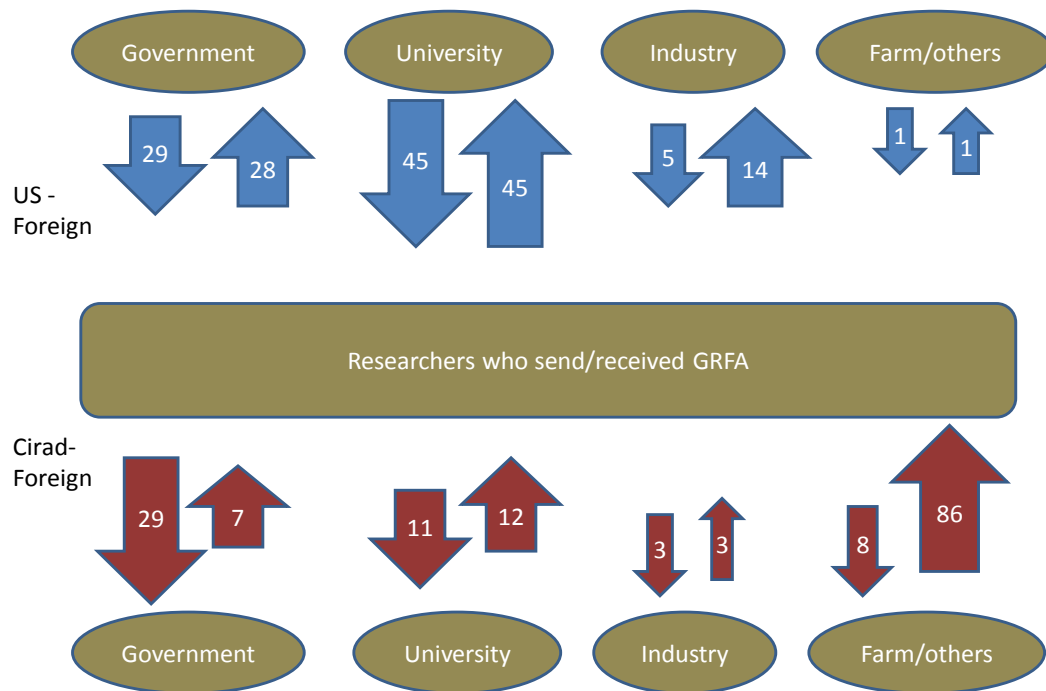
Mobilization of genetic diversity – *a social science perspective*

We are interested in the interplay between institutions, structures and behaviors in relation to the nature of the material and information exchanged.

Social, Biophysical, and Institutional Determinants of the Stoppage of Exchange

- What predicts whether or not exchange of GRFA stops?
 - Dependent variables: Have you ever refused to provide genetic resources to others who request them? Have you ever been refused genetic resources when you have asked for them?
- Reciprocity – social exchange theory – independent variables
 - Regulatory context of exchange** *National and International Regulatory Barriers*
 - Social context of exchange:** *Relational Closeness, Collegiality, Connections ; Compensation*
 - Individual characteristics :** *Open science attitude*
 - Resource context of exchange:** *Biophysical Value of the material*

Welch, E. and S. Louafi, 2014, Contested Inputs for Scientific Research: Why Access to Biological Materials Is Blocked, In : [72th Midwest political science association \(MPSA\) Conference](#) Chicago, USA, 3-5 April 2014



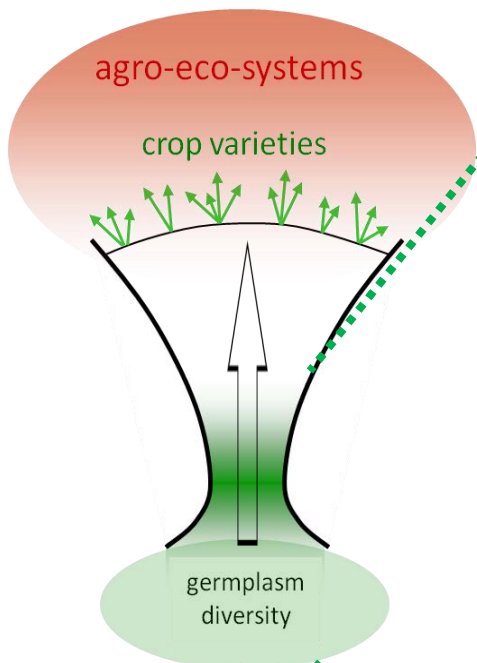
Conserving and cultivating agricultural genetic diversity : transcending established divides?

- Increased constraints & increased opportunities
 - Inadequacy of the linear ‘patrimonial’ model : collection=> storage=> characterization=> evaluation=> exchange
 - Need to come up with new models of conservation that better account for:
 - The dynamic nature of the continuum between in situ and ex situ,
 - The social nature of GR (the GxExS model) : GRs cannot not be considered only as material resources, i.e. without considering the historical and socio-cultural dimensions, notably, the users’ knowledge and practices
 - The distributed capacities of the various actors (beyond the curators) interested in testing/using GR
 - The equity dimension in relation to redistribution aspects

Louafi S., Bazile D., Noyer J.L. 2013. Conserving and cultivating agricultural genetic diversity : transcending established divides. In : Hainzelin Etienne (ed.). Cultivating biodiversity to transform agriculture. Heidelberg : Springer , p. 181-230..

Concluding remarks

- The linear model of innovation
- Towards more diverse situations
- Important times



Mobilize

NAM
BC NAM
CSSL
MAGIC
Wide crosses

Integrate breeding work & germplasm science

Access

Rules
Roles

Scientists' roles & responsibilities

Sample

Reference
Core
Specialized

Coordinate, exchange & integrate

Analyse

Historical
Genomic correlations

Exchange information (haplotypes)

Document

Environment
Actors
Uses

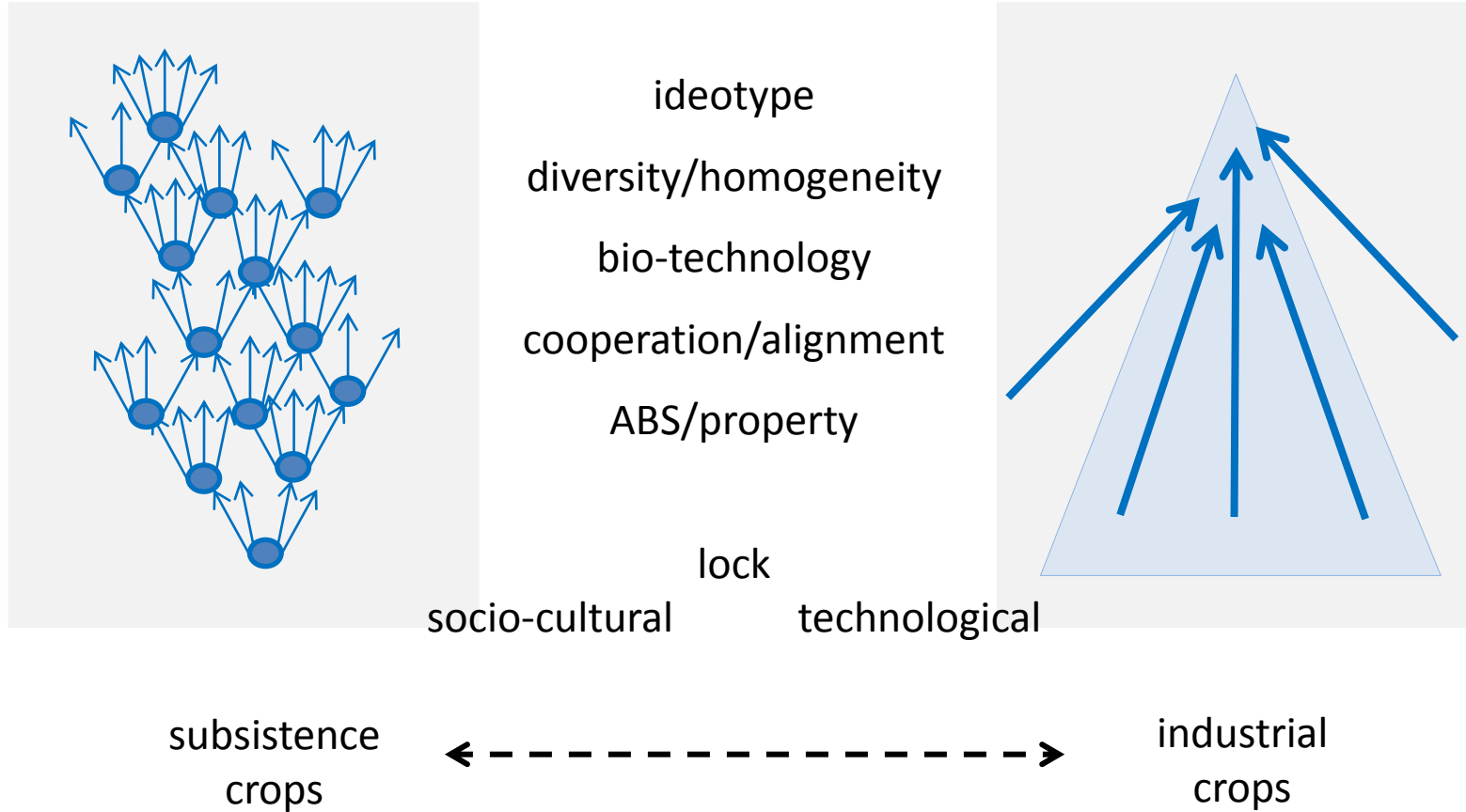
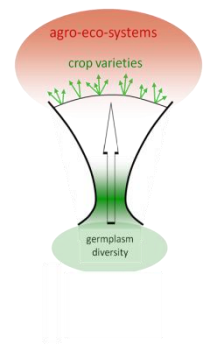
Integrate

Conserve

CRB
GCDT

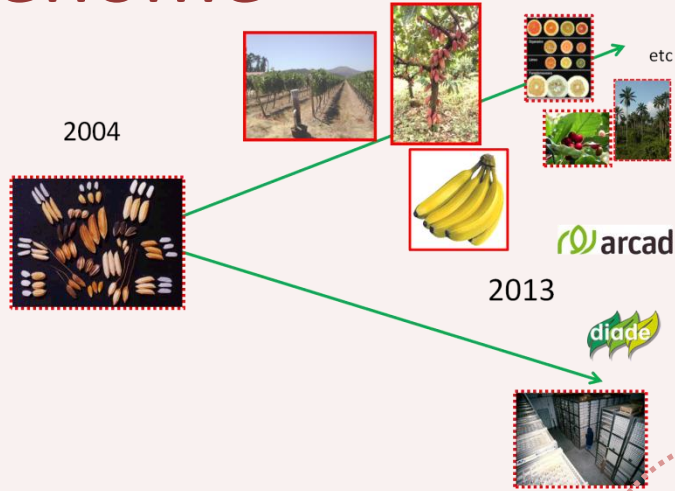
Genetic stocks

Pertinence of the linear model?

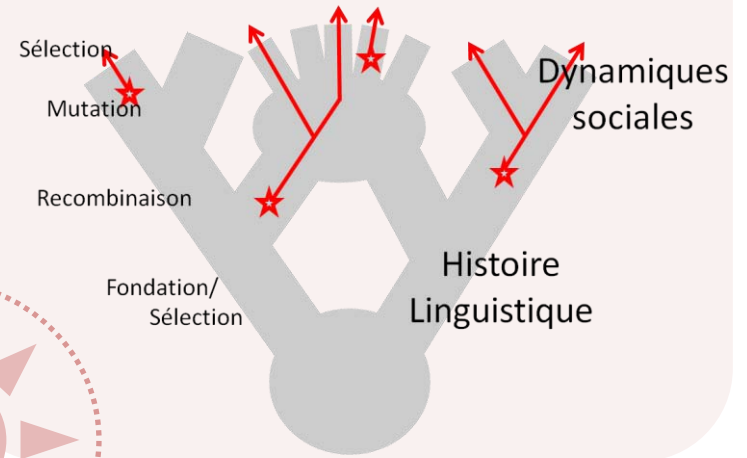


Confluences!

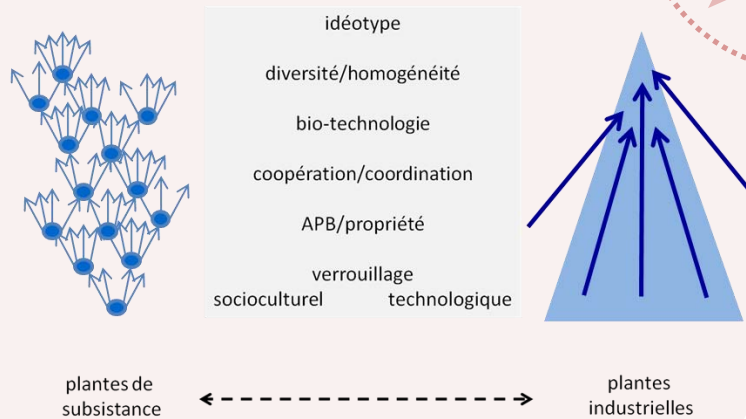
• Genome



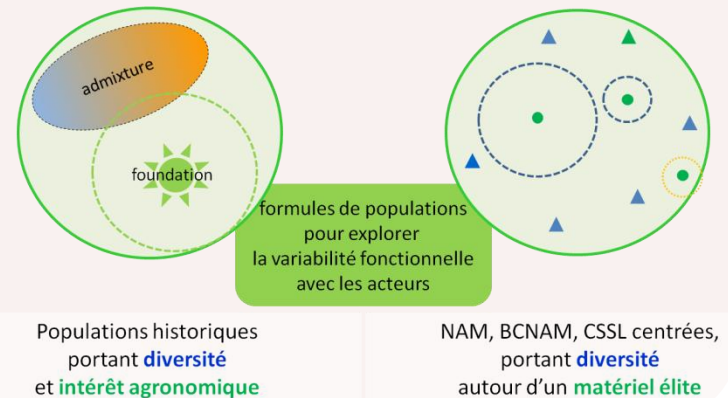
• Diversity



• Actors



• Populations





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Xavier Perrier

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Claire Billot

Christian Leclerc

Selim Louafi

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