

Sorghum

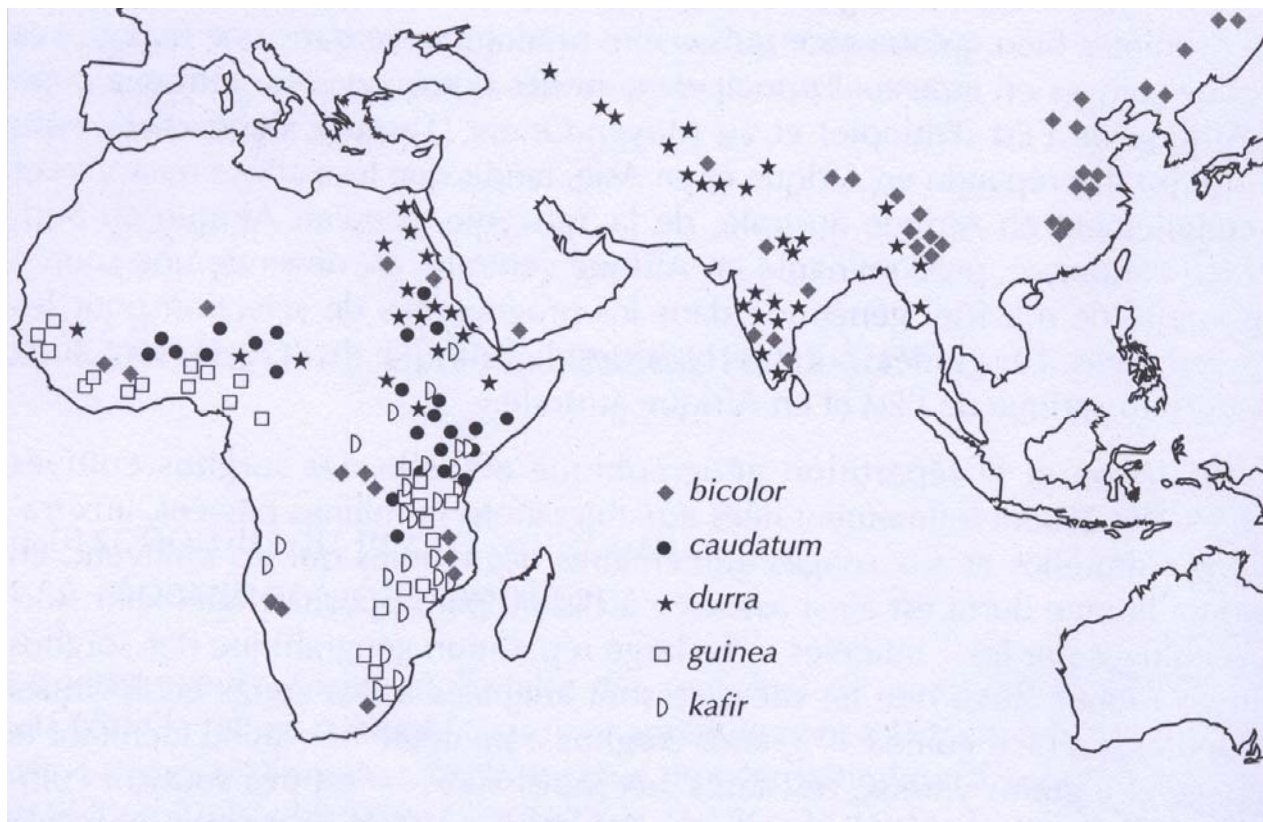
1st year PI: C. Billot (CIRAD)

2nd year PI: T. Hash (ICRISAT)

Collaborators: CAAS (Yu LI)

Presentation of Sorghum

- 5th cereal in the world (43 M ha, 62 M T)
- Major staple food and fodder crop
- Tropical and semi-tropical Africa and Asia



Classification

Family : Poaceae

Subfamily: panicoïdeae

Tribe: andropogoneae (like sugarcane, maize....)

Genus: *Sorghum*

5 sections including *Sorghum*

3 crossing species

- *S. halepense* (tetraploide)

- *S. propinquum* (diploïd)

- *S. bicolor* (diploïd)

ssp. *drumondii*

ssp. *arundinaceum*

ssp. *bicolor*

]

Wild, perennial

Cultivated, annual

$2n=2x=20$

750 Mb

Highly self pollinated

5 races : bicolor

caudatum

durra

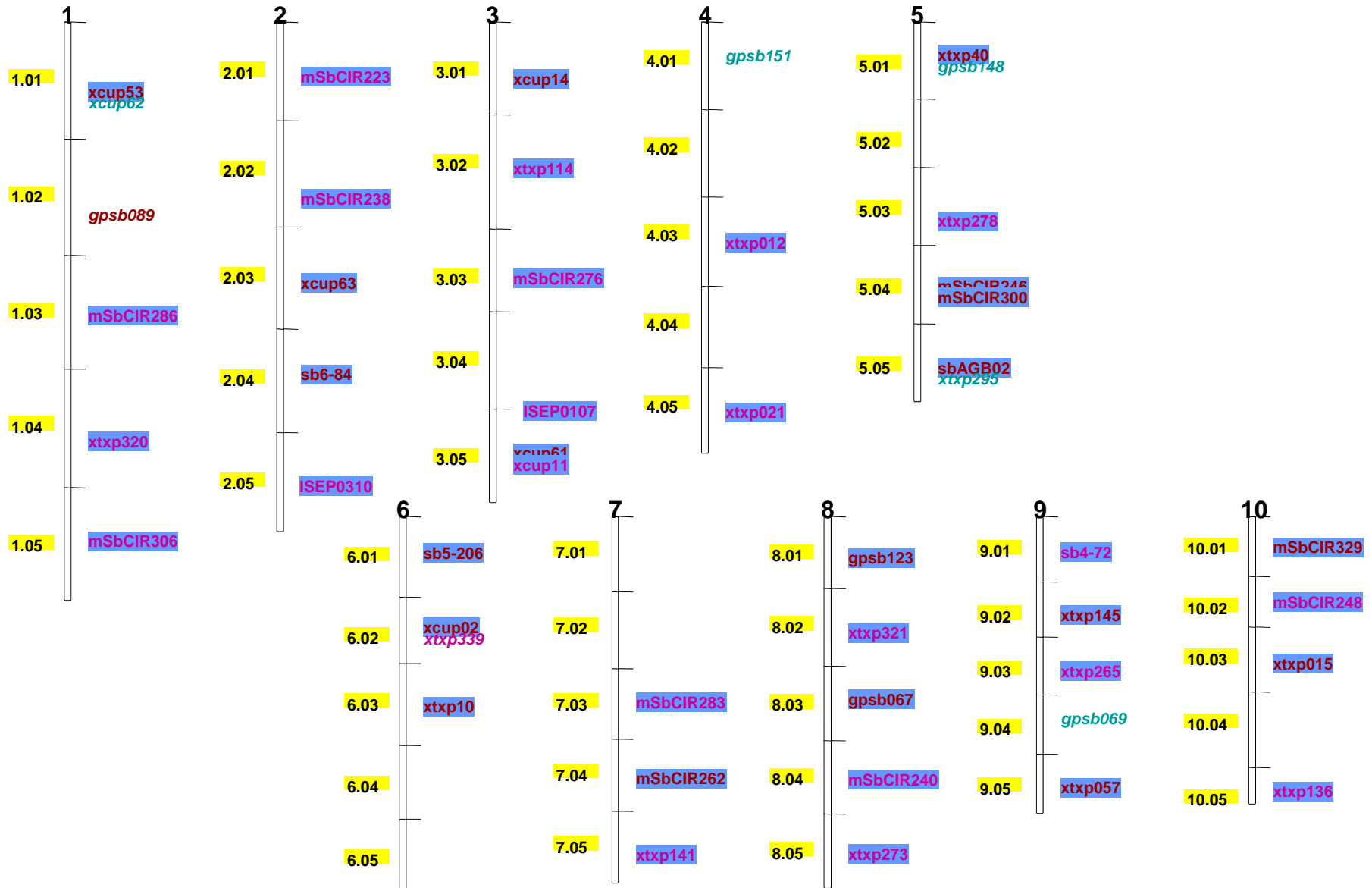
guinea

kaffir

10 intermediates



Selection of markers



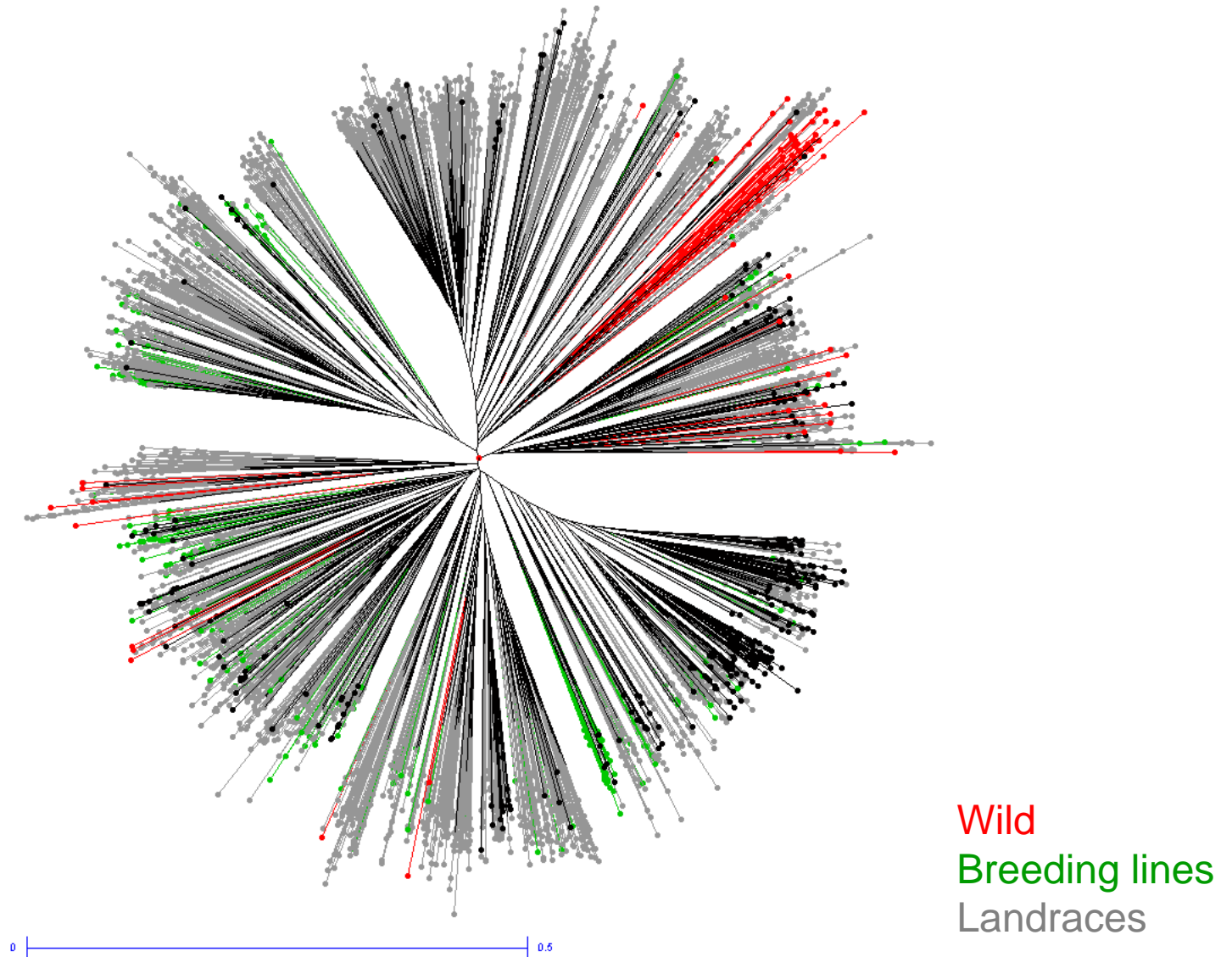
Selection of accessions

- 3393 accessions (including 10 “duplicates”, ie same germplasm number)
- x 43 SSR (provided by CIRAD and Icrisat, grouped into an access database) representing 145899 DP (diploid samples) scored, with 9307 missing data (6.4 %, thus 135592 DP)
- Due to some high level of missing data, **3365 accessions x 41 SSR** markers analysed (92 %)
 - Including
 - 8.6% breeding lines or advanced cultivars
 - 89.4 % landraces
 - 2 % wild samples
 - 5 major races (B, C, D, G, K) and 10 intermediates
 - 13 sub-continents

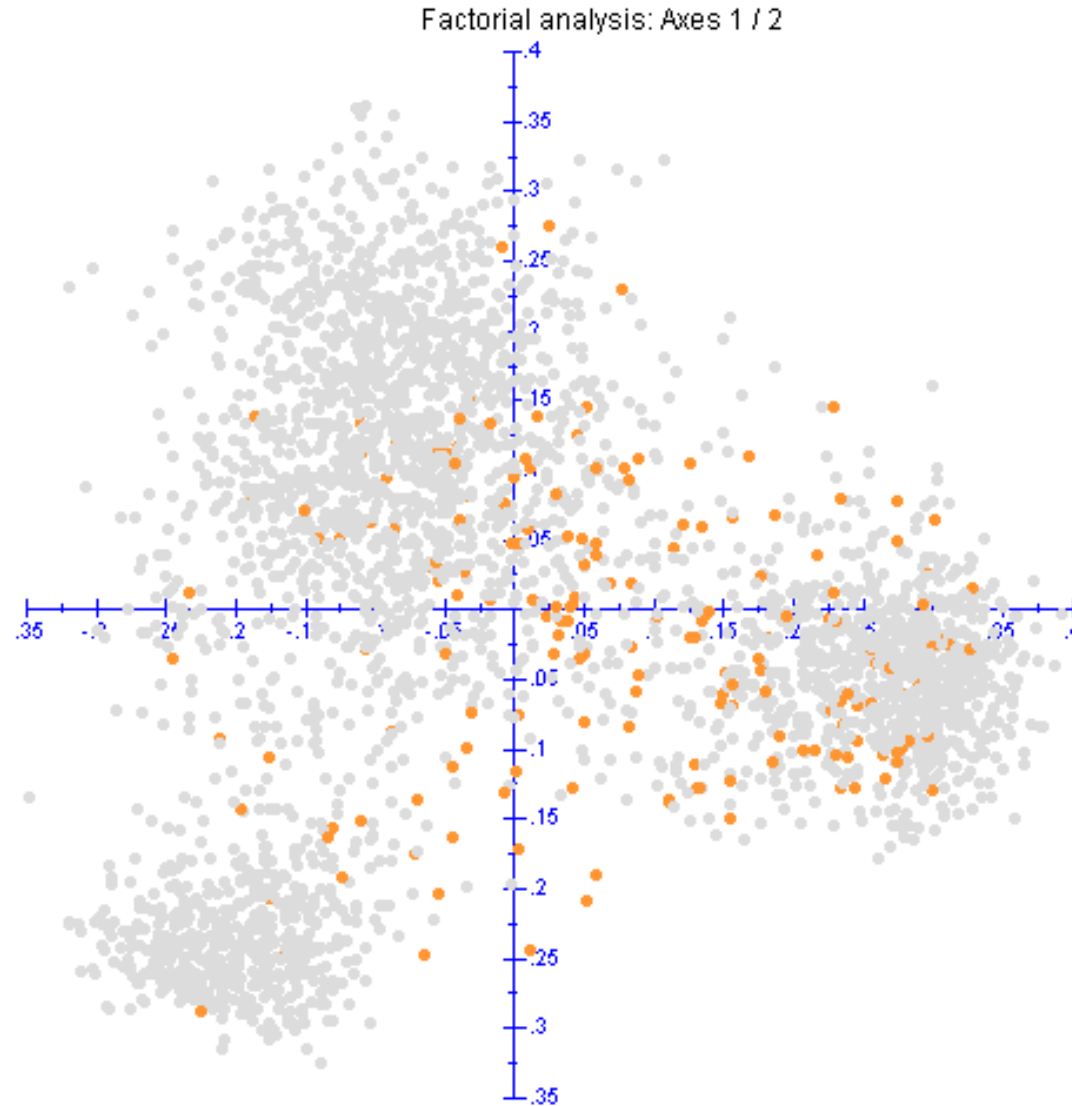
Diversity Analysis

- 788 alleles
 - Mean # alleles / Locus = 19.2 (range 2-39)
 - Very high number of rare alleles
 - 620 alleles below 5%
 - 428 alleles below 1%
- Simple matching dissimilarity index (Darwin)
 - NJ analysis
 - Factorial analysis

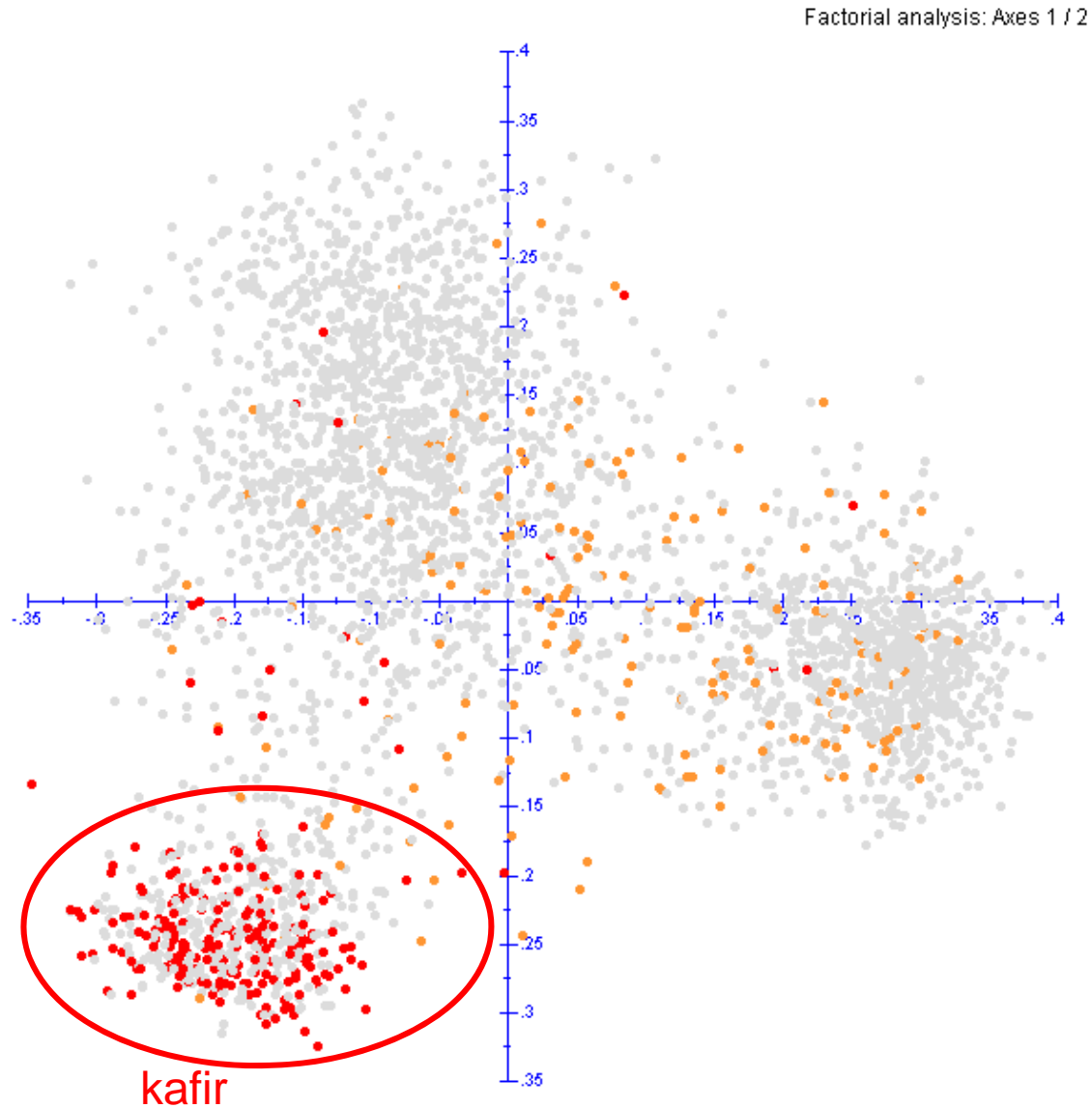
Global analysis



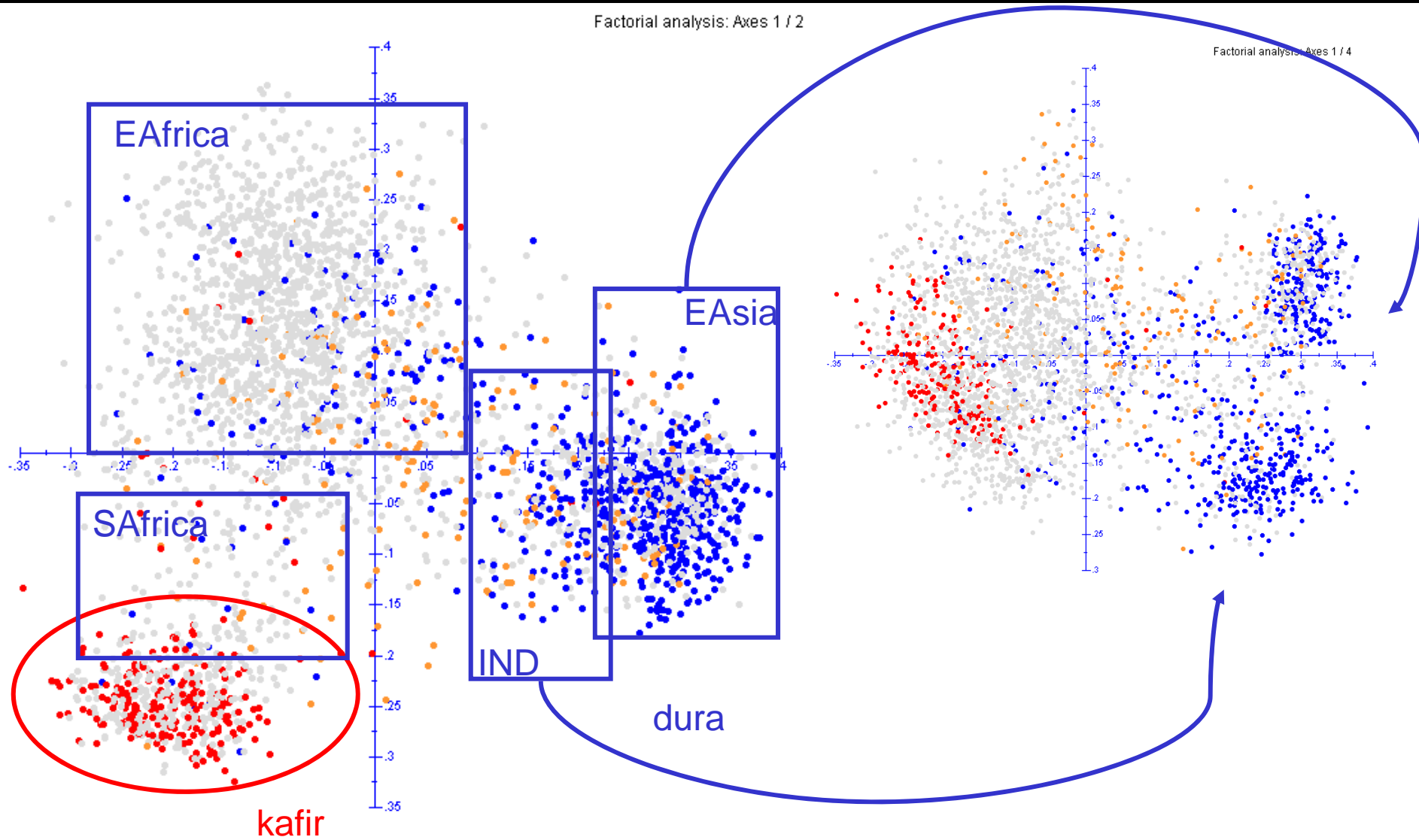
“Bicolor” are not structured



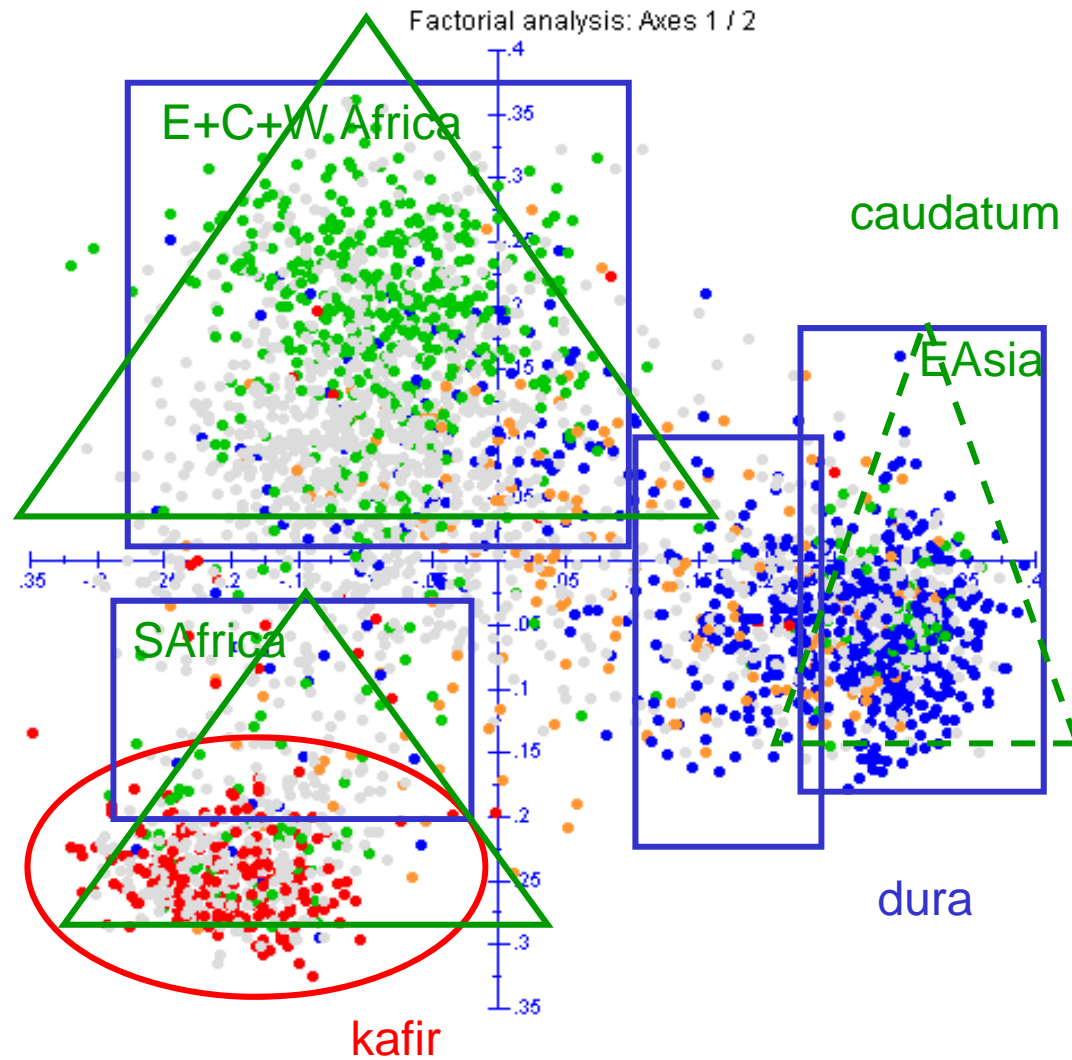
“Kafir” forms one group



“Dura” / 4 groups

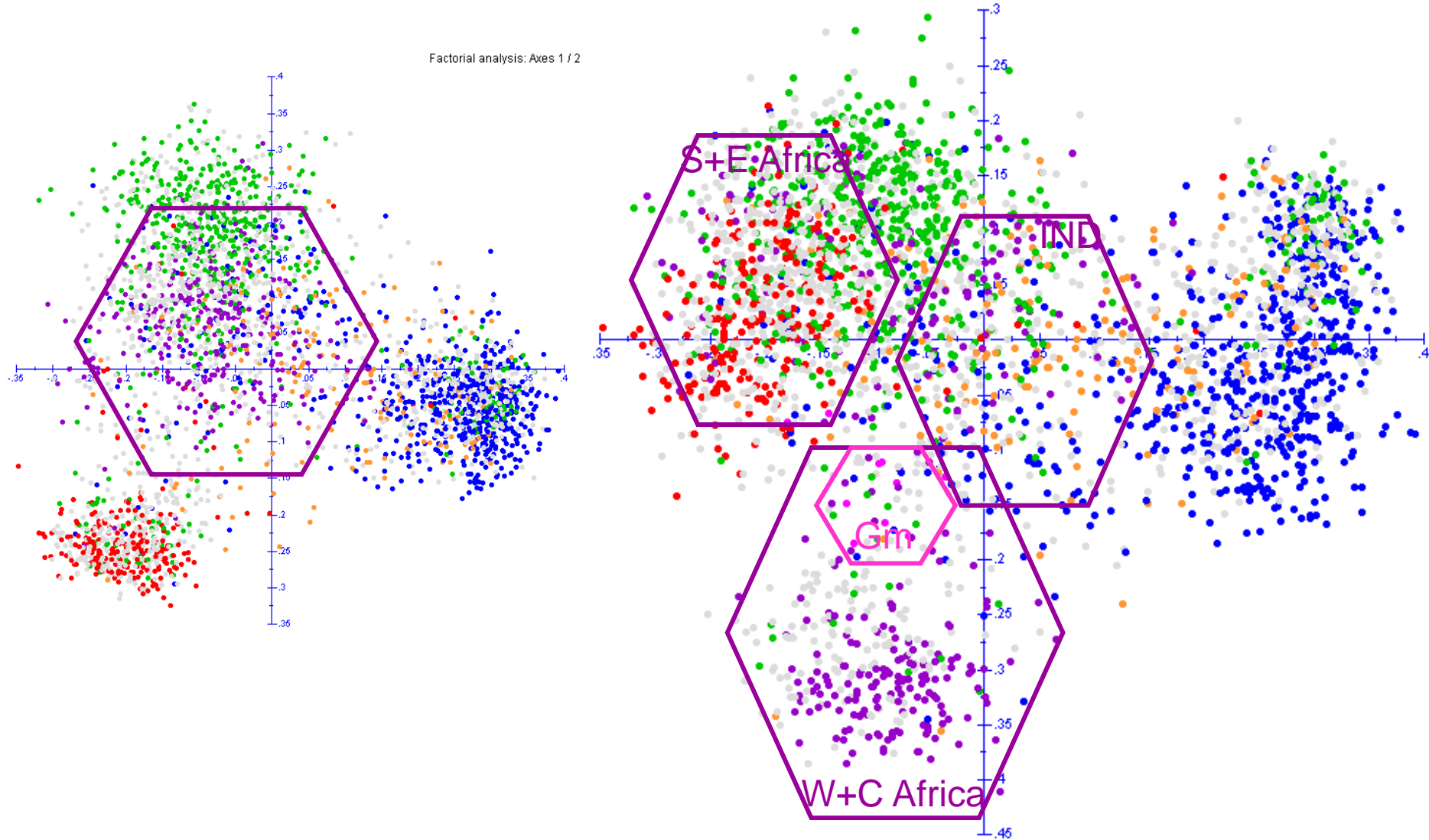


.... congruent with "caudatum"

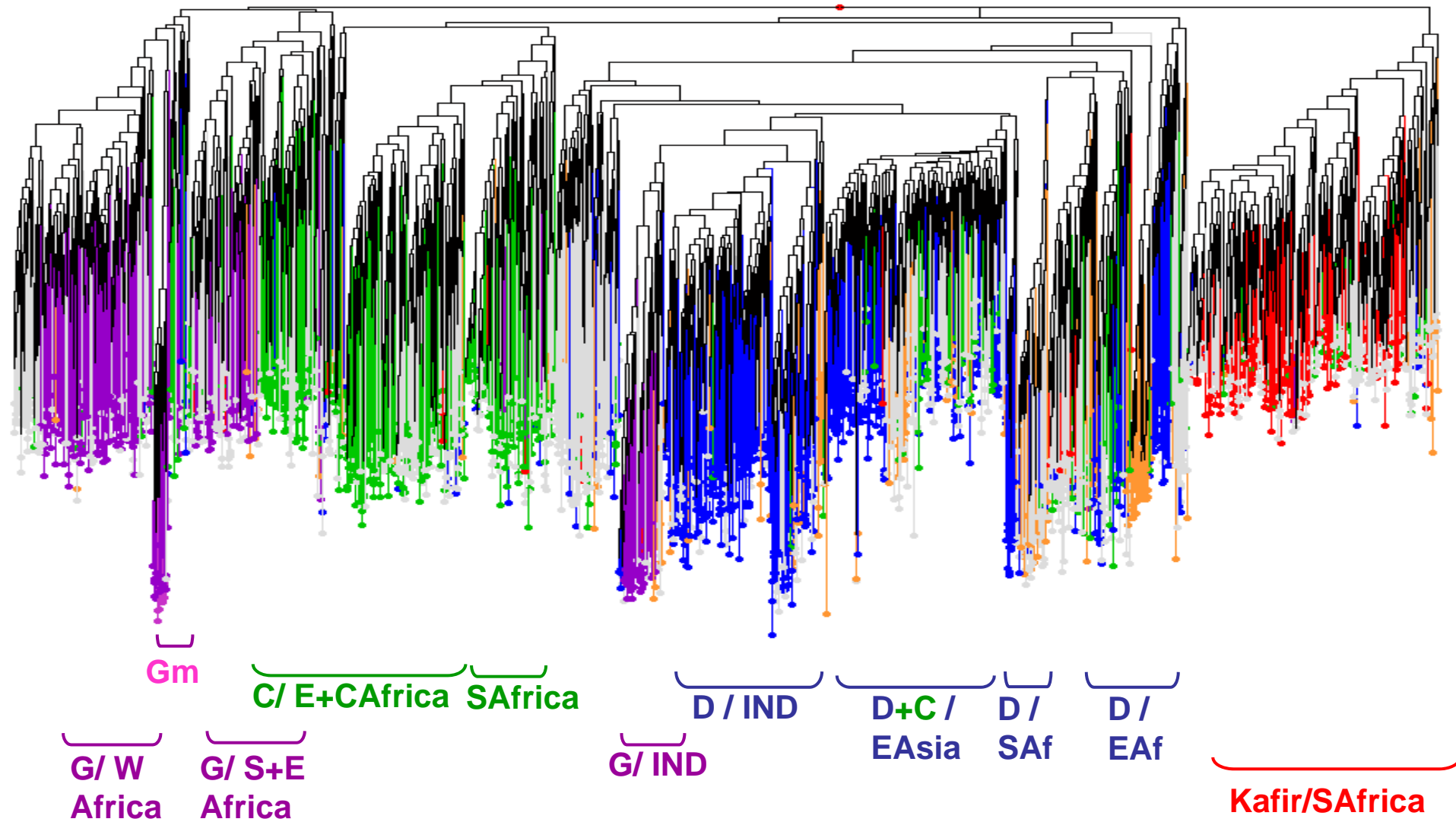


“Guinea” are structured in 4 groups

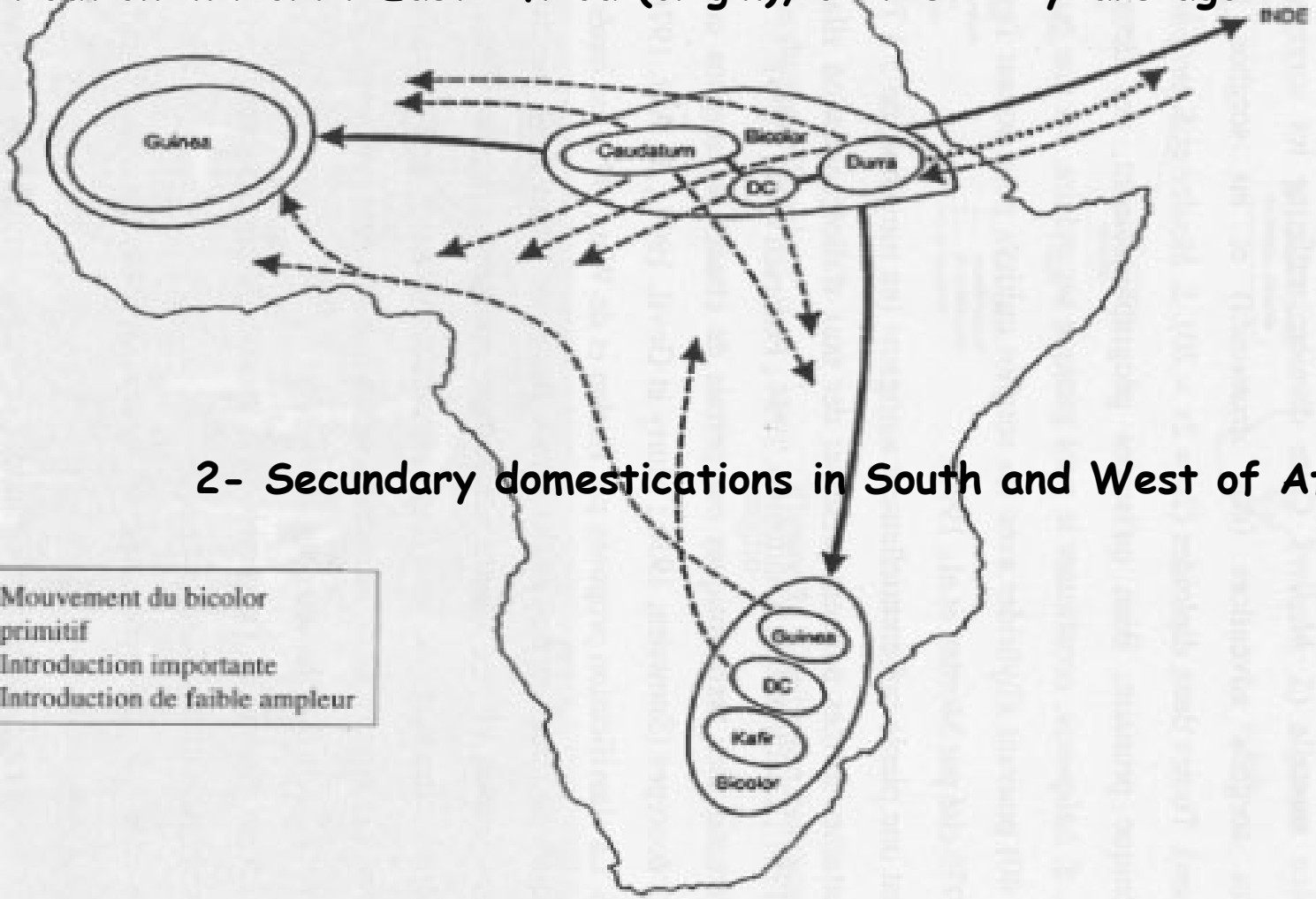
Factorial analysis: Axes 1 / 3



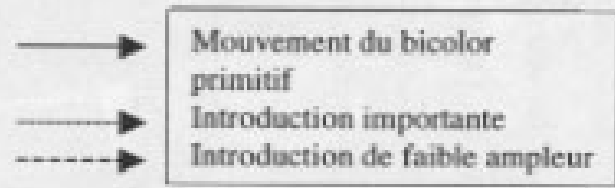
Landraces/"pure" races



1- Domestication in North-East Africa (origin), over 5000 years ago

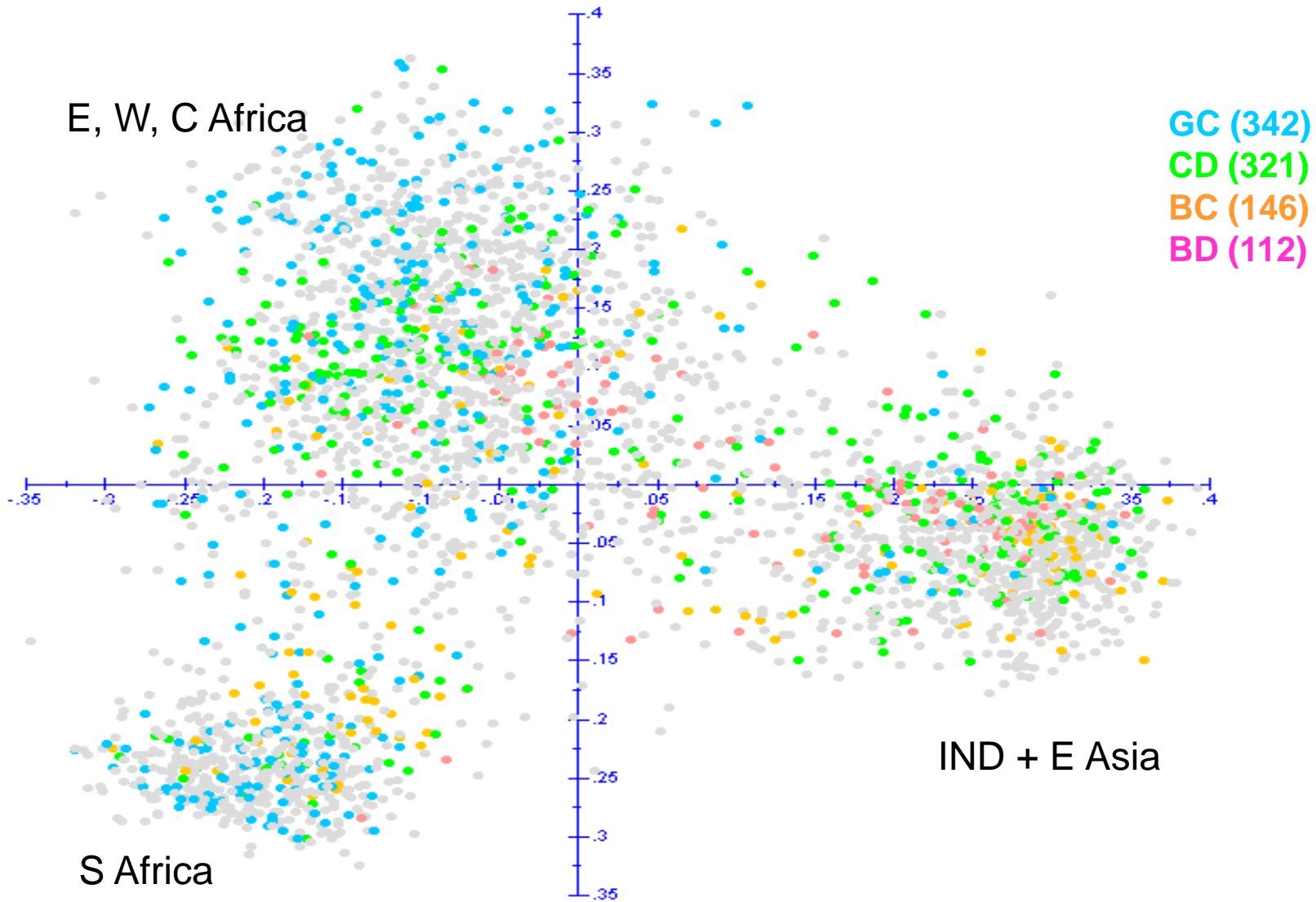


2- Secondary domestications in South and West of Africa

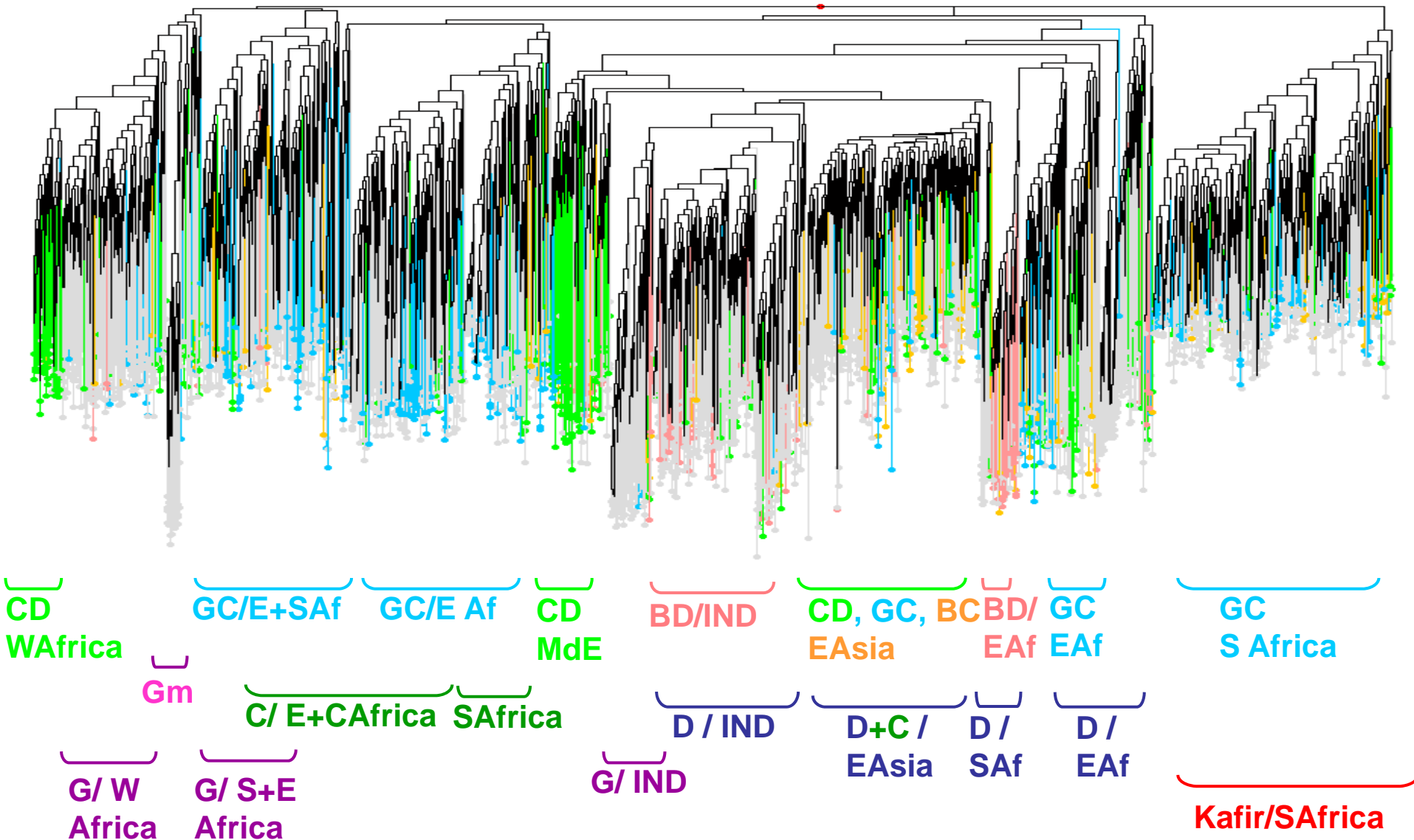


Landraces/"intermediates"

Factorial analysis: Axes 1 / 2



Landraces/"intermediates"



“Core-collection” ?

- Criteria ?
 - Genetic diversity
 - Representation of all clusters
 - Representation of intermediates (putative associations of alleles related to cluster structure)
 - Representation of wild accessions (domestication event)
 - Structure ? (spurious associations vs association to specific groups, multivariate)
 - Representation of breeding lines ?
 - Geographic origin
 - Adaptation to different E
 - Different uses
 - Suitable for different traits
 - Comon kernel (=microcore) + satellite collections
 - Previous phenotyping knowledge ?
- N ? Compatibility with phenotyping experiments ?
- Only public accessions....
- Choice among 3100 accessions

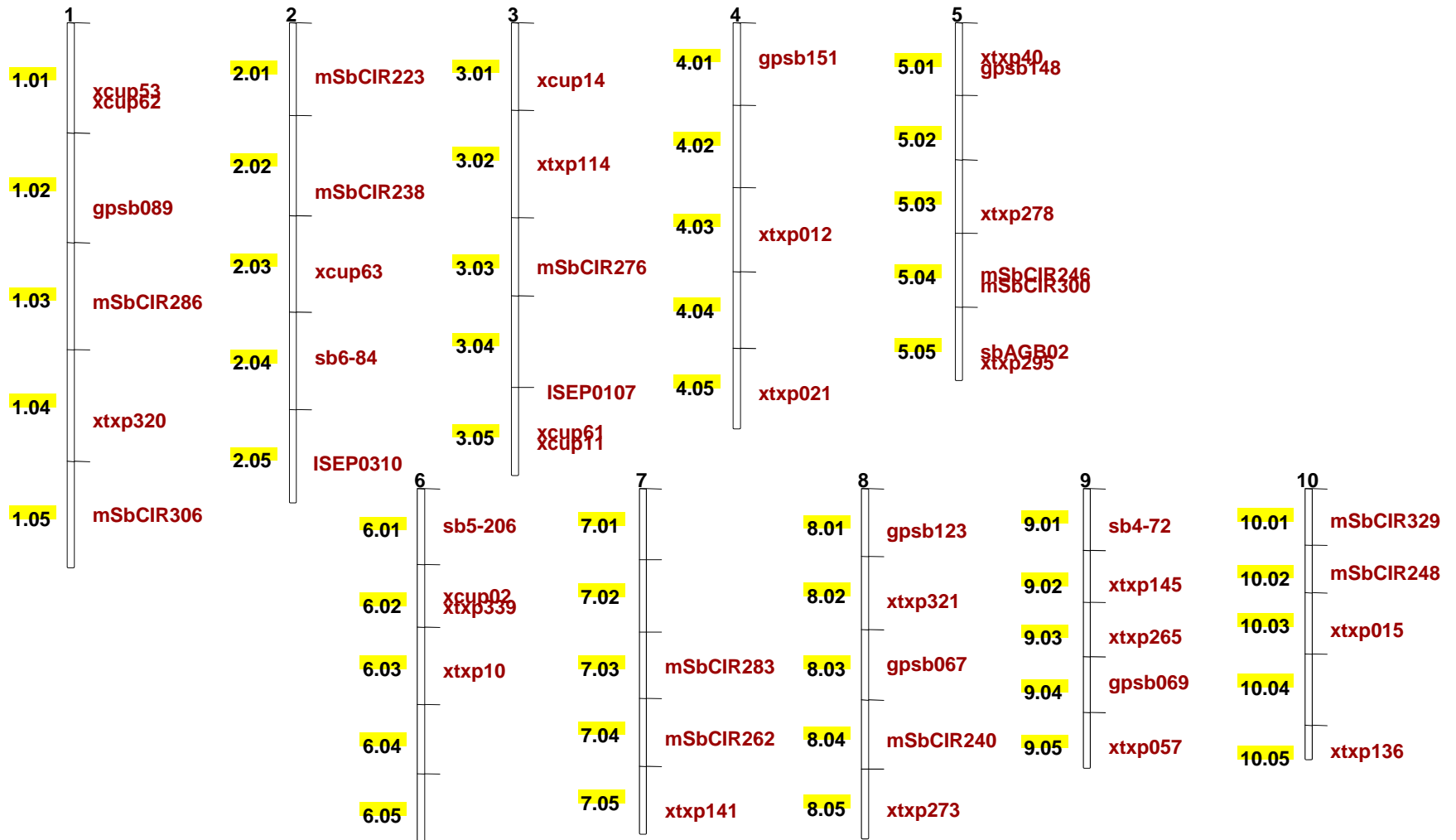
Genetic Diversity SSR Kit

- Allow to compare new genetic diversity assessments (enrich the large collection)
- Occasion to develop good laboratory practices
- Developed at Cirad (SP5 fellowship)
 - Easy to use
 - Easy to transfer (ie publicly available accessions)
 - Very robust across labs and accessions
 - Accurate sizes of the alleles (sequencing) and verification of repeat pattern

Choice of markers

- 10 chromosomes
- Divided into 5 bins each (no concern on the physical size)
- Choice of 105 markers, tests
- Addition of new markers
- Experiments (sequencing of the alleles, easiness to score)
- 48 markers

Choice of markers

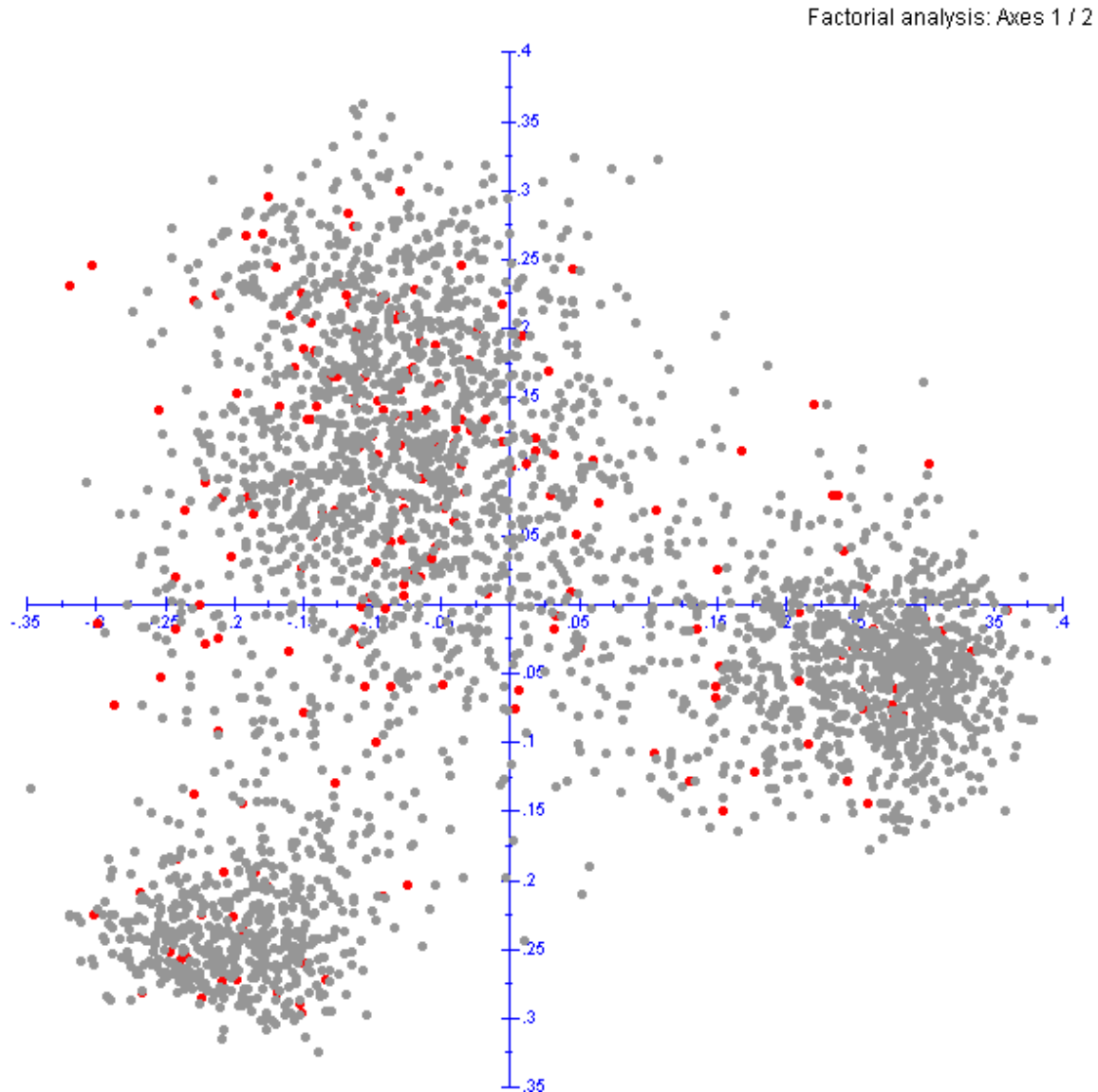


Choice of accessions

- Based on a first core-collection of 205 accessions
- Choice of 48 accessions that represent the best the genetic diversity of the core-collection
- Choice of 10 accessions = controls

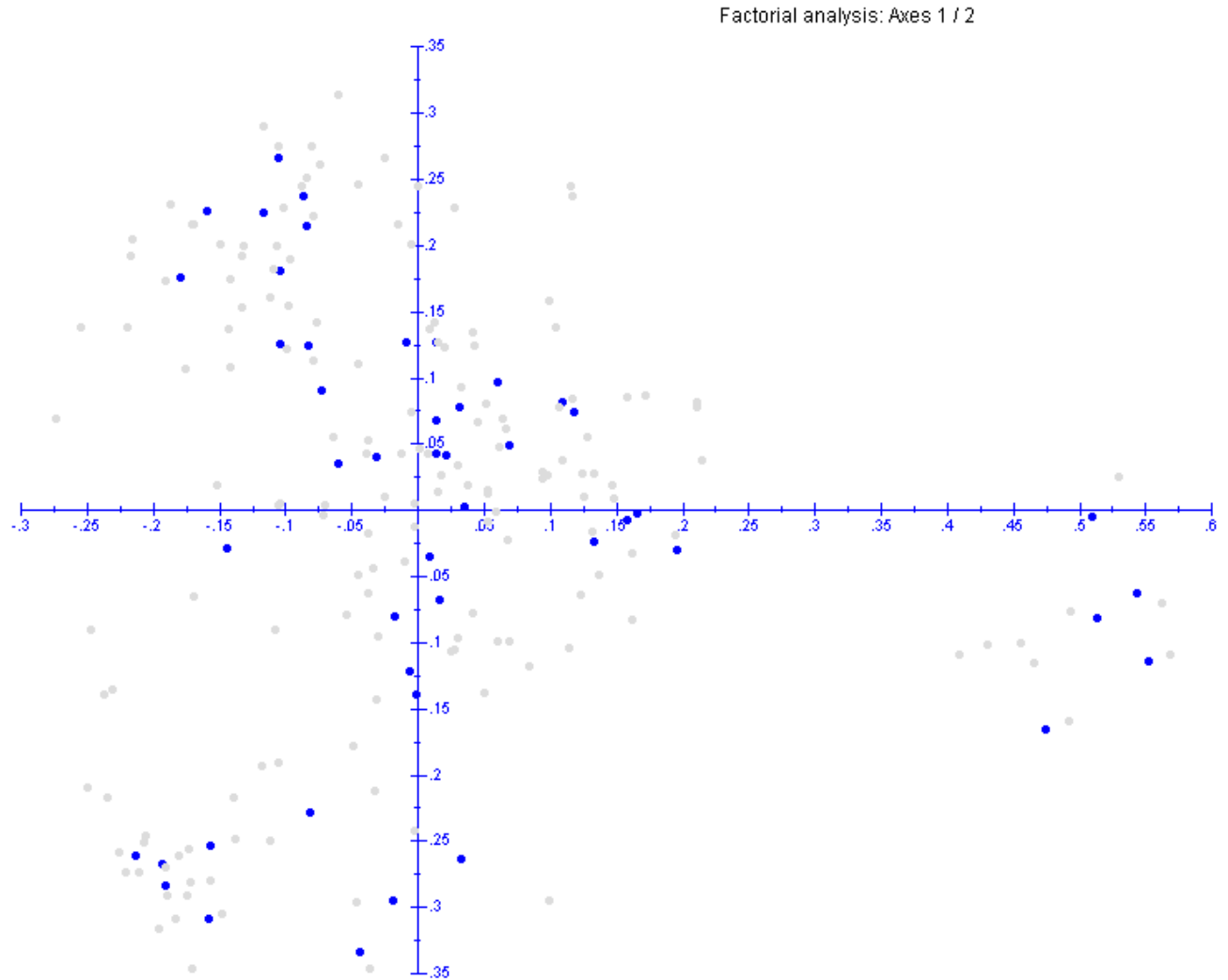
Choice of accessions

205 accessions
among the 3365
accessions



Choice of accessions

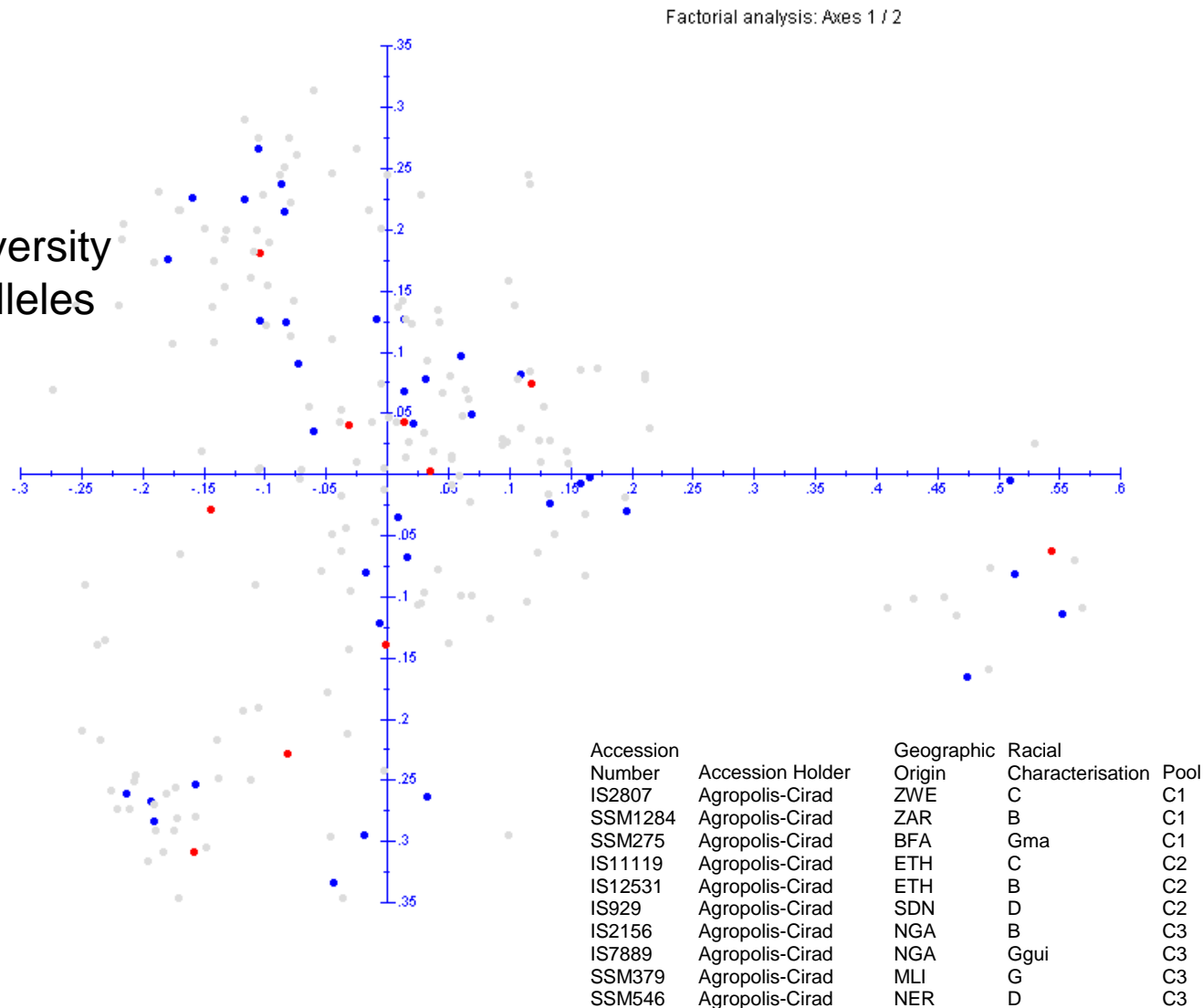
48 accessions
among the 205
accessions



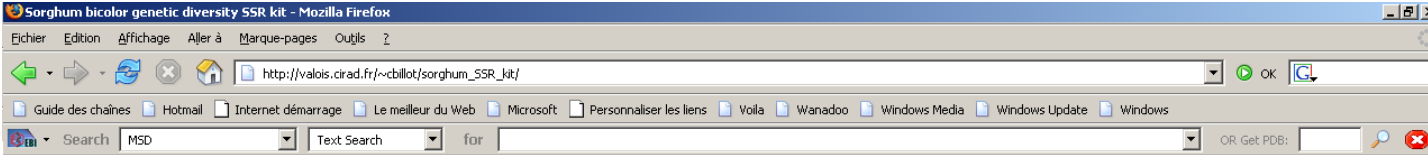
Choice of accessions

10 accessions
among the 48
Accessions

- large genetic diversity
- large range of alleles possibly largest



Output




Sorghum bicolor genetic diversity SSR kit - Mozilla Firefox

Eichier Edition Affichage Aller à Marque-pages Outils ?


http://valois.cirad.fr/~cbillot/sorghum_SSR_kit/

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SSR Kit to study Sorghum genetic diversity



This SSR kit has been elaborated in the frame of a large genotyping project (3000 sorghum accessions x 48 SSR loci) supported by the [Generation Challenge Program](#), Sub-Programs 1 and 5 (grants dedicated to Daniel Fonceka and MBaye NDoye Sall, formerly working at the Ceraas, Senegal). It is composed of the allelic sizes of 3 controls for each of the 48 SSR locus.

The 3 controls are composed of a mix of 10 DNA samples. They were chosen from 48 Sorghum samples presenting a fair picture of the overall genetic diversity, in order to represent a large range of allelic diversity, both in term of allele number and allele sizes. Each control is amplified for each marker, and allelic sizes are used as control sizes.

Loci are located regularly throughout the genome, so that there are roughly 5 markers per chromosome.

Composition of the controls
includes the accession number (as provided by ICRISAT), in the genotyping order, and there belonging to the controls.

Characteristics of the 48 markers
includes, for each locus, its name, the microsatellite motive, forward and reverse primers, the number of alleles observed among the controls and their range, its linkage group according to Kim et al. 2005.

You can also have a look at the [loci](#) which shows the locus image (obtained with Licor IR2), allelic content of each sample and allelic content of the controls.

All experiments related to this kit were performed on the [Languedoc Roussillon Genotyping Platform](#), hosted by the [CIRAD](#), under the supervision of Claire Billot and with the collaboration of Ronan Rivallan, Jean-François Rami and Monique Deu.

Terminé

Output

Mozilla Firefox
 http://valois.cirad.fr/~cbillot/sorghum_SSR_Kit/loci.html

Guide des chaînes Hotmail Internet démarrage Le meilleur du Web Microsoft Personnaliser les liens Voila Wanadoo Windows Media Windows Update Windows

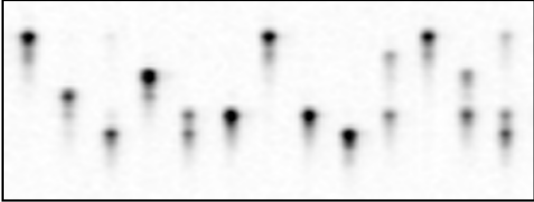
Search MSD Text Search for OR Get PDB:

List of SSR Loci

gpsb067	ISEP0107	mSbCIR248	mSbCIR306	xcup02	xcup63	xtxp057	xtxp273
gpsb069	ISEP0310	mSbCIR262	mSbCIR329	xcup11	xtxp010	xtxp114	xtxp278
gpsb089	mSbCIR223	mSbCIR276	sb4-72	xcup14	xtxp012	xtxp136	xtxp295
gpsb123	mSbCIR238	mSbCIR283	sb5-206	xcup53	xtxp015	xtxp141	xtxp320
gpsb148	mSbCIR240	mSbCIR286	sb6-84	xcup61	xtxp021	xtxp145	xtxp321
gpsb151	mSbCIR246	mSbCIR300	sbAG-B02	xcup62	xtxp040	xtxp265	xtxp339

gpsb067

Locus Image



T1, T2, T3, T4, T5, T6, T7, T8, T9, T10, C1, C2, C3
 Note: not all alleles are amplified in the controls

Allelic content
in the samples

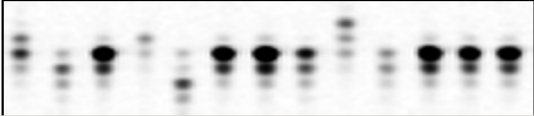
DNA_Sample	Control	Allele_Size
T1	C1	180
T2	C1	174
T3	C1	170
T4	C2	176
T5	C2	172
T6	C2	172
T7	C3	180
T8	C3	172
T9	C3	170
T10	C3	172
T10	C3	178

Allelic content
in the controls

Control	Allele_Size
C1	170,174,180
C2	172,176
C3	170,172,180

gpsb069

Locus Image



Allelic content
in the samples

DNA_Sample	Control	Allele_Size
T1	C1	195
T2	C1	191

Allelic content
in the controls

Control	Allele_Size
C1	191,193,195
C2	189,193,195


Terminé

Output

Mozilla Firefox
http://valois.cirad.fr/~cbillot/sorghum_SSR_kit/loci.html

gpsb151

Locus Image



T1, T2, T3, T4, T5, T6, T7, T8, T9, T10, C1, C2, C3

Allelic content in the samples

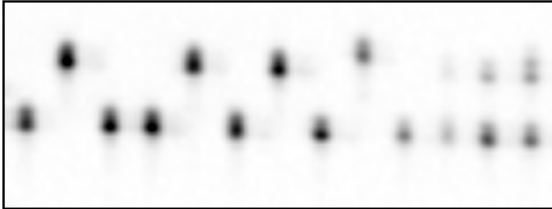
DNA_Sample	Control	Allele_Size
T1	C1	128
T2	C1	108
T3	C1	106
T4	C2	128
T5	C2	114
T6	C2	108
T7	C3	126
T8	C3	108
T9	C3	126
T10	C3	110

Allelic content in the controls

Control	Allele_Size
C1	106,108,128
C2	108,114,126,128
C3	108,110,126

ISEP0107

Locus Image



T1, T2, T3, T4, T5, T6, T7, T8, T9, T10, C1, C2, C3

Allelic content in the samples

DNA_Sample	Control	Allele_Size
T1	C1	199
T2	C1	204
T3	C1	199
T4	C2	199
T5	C2	204
T6	C2	199
T7	C3	204
T8	C3	199
T9	C3	205
T10	C3	199

Allelic content in the controls

Control	Allele_Size
C1	199,204
C2	199,204
C3	199,204,205

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