

# The Genetic Resource Support Service

## Justification:

- ◆ GCP time-bound
  - ◆ continued and sustainable use of products after its lifespan
  - ◆ secure support and commitment beyond “GCP’s Phase”
    - ◆ Product quality and attractive packaging
  
- ◆ Biological resources, including genetic stocks, generated during GCP’s lifespan a major legacy to the plant scientist community
  - ◆ a top priority to ensure these resources will not be lost when the Programme terminates

# Materials

per crop

today

* reference sets	50 – 1000	CG centers, + GCP
* collection of mutants	?	diverse
* introgression lines	100s	diverse
* mapping populations	1000s	diverse
* near isogenic lines	10s	diverse

for simulations:

1 major crop =

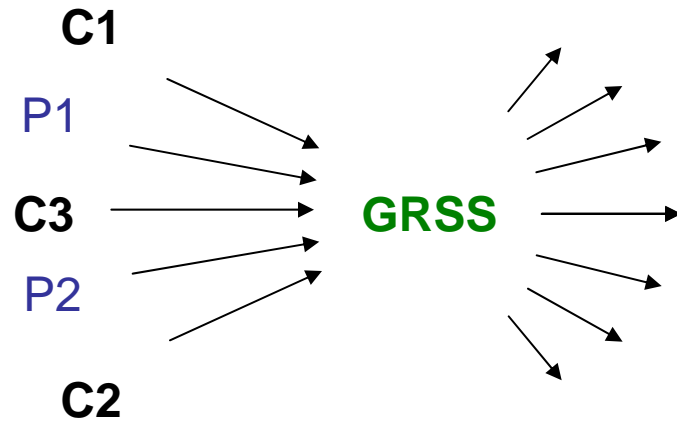
1 000 reference diverse genotypes  
5-10 000 segregating genotypes

1 minor crop =

500 reference diverse genotypes  
1 000 segregating genotypes

\* genomic resources: BAC libraries, cDNA libraries, markers, etc

# Several crops



Users

across  
crops  
Gene specialists

DNA

Trait specialists

Seed

Plant breeders

per crop

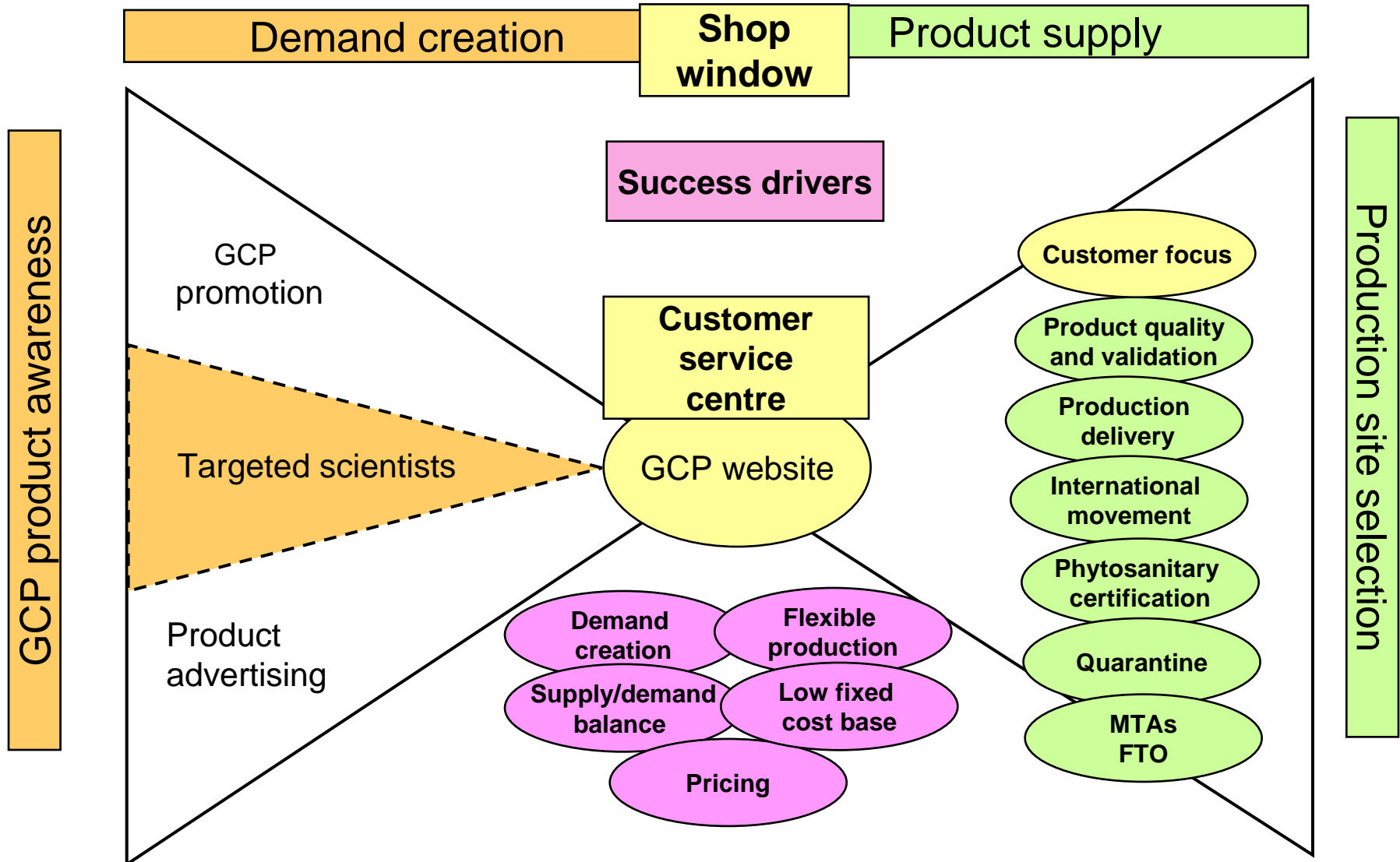
# GCP Genetic Resources (stocks) Supply

## Scoping project

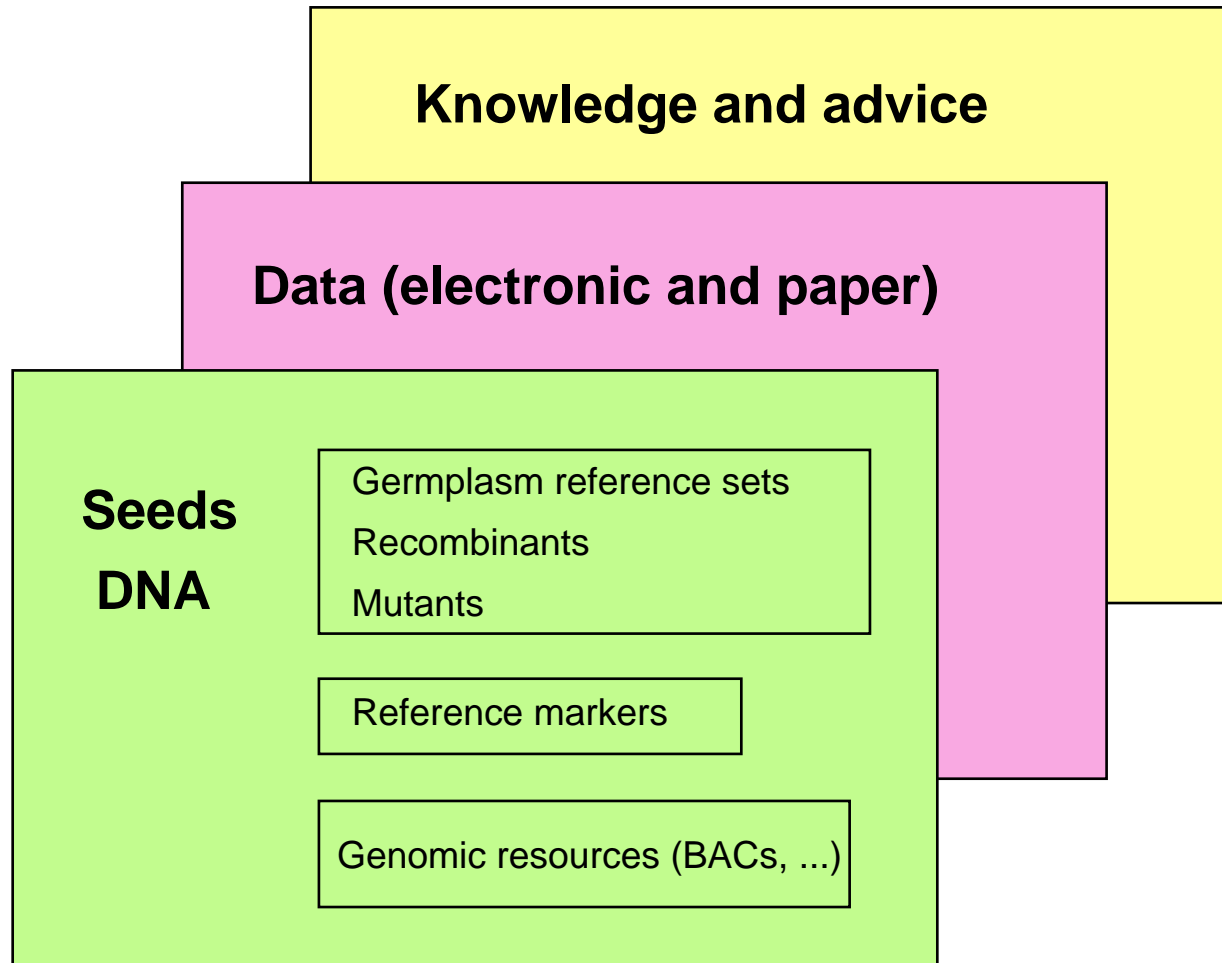
Viv Anthony, 2 May 2008

- GRSS project concept
- Products and current status of availability
- Priorities and phasing
- Product quality
- Customers and product demand
- Criteria and selection of production sites
- Technical and customer support models
- Pricing
- SWOT
- Key resources
- Project milestones and timetable
- Action plan

# GRSS project: concept and drivers



# GRSS products



# Feedback from the RAP

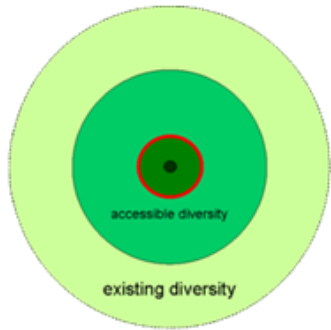
- “Special and immediate care should be taken by the management team as far as the availability of the actual vegetative/seed **reference germplasm collections** to the GCP research groups as well as outside interested parties”
- “Also special attention should be given to guaranteeing the **correct identity** of the germplasm supplied as well as the correct merging of the genotypic data with the phenotypic data for the reference collections”

## The EPMR Panel Recommends:

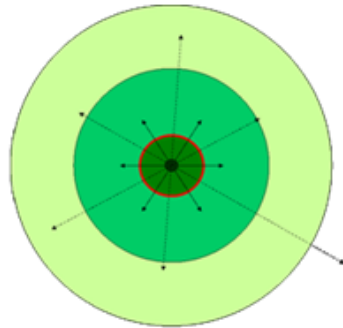
That GCP management in consultation of the curators of the source collections establish **the protocols by which each Core Collection will be maintained and distributed;**

and the means by which the current genotypic data and passport (catalogued) information on these Core Collections will be maintained and augmented by current GCP and future non-GCP discovery efforts.

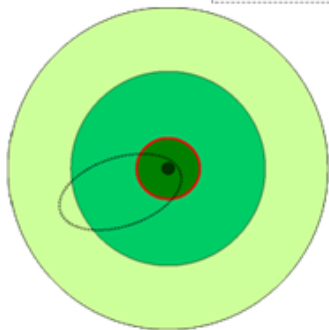
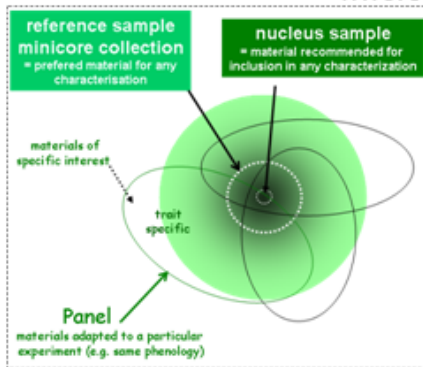
The Panel encourages that these protocols be developed and devolved **over the next 3-yrs years** to ensure orderly transfer of responsibilities and adequate support by GCP beyond the transfer of responsibilities (prior to the wind-down of GCP).



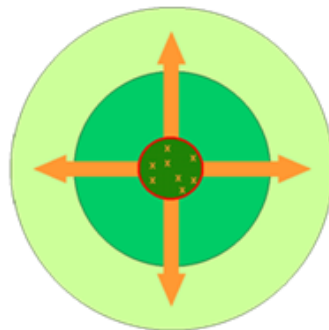
*Representation of existing diversity*



*Exploration of the whole collection*



*Association between traits and genes*



*Dissection through multi-parental progenies*

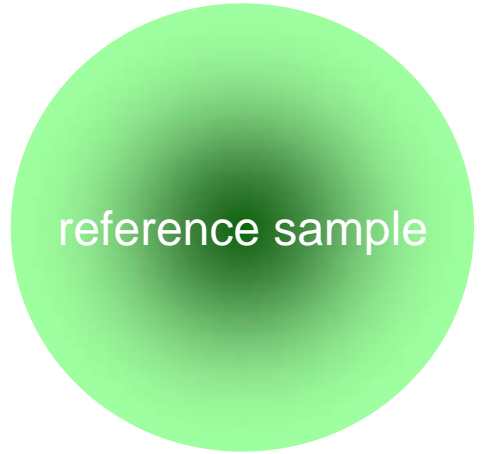
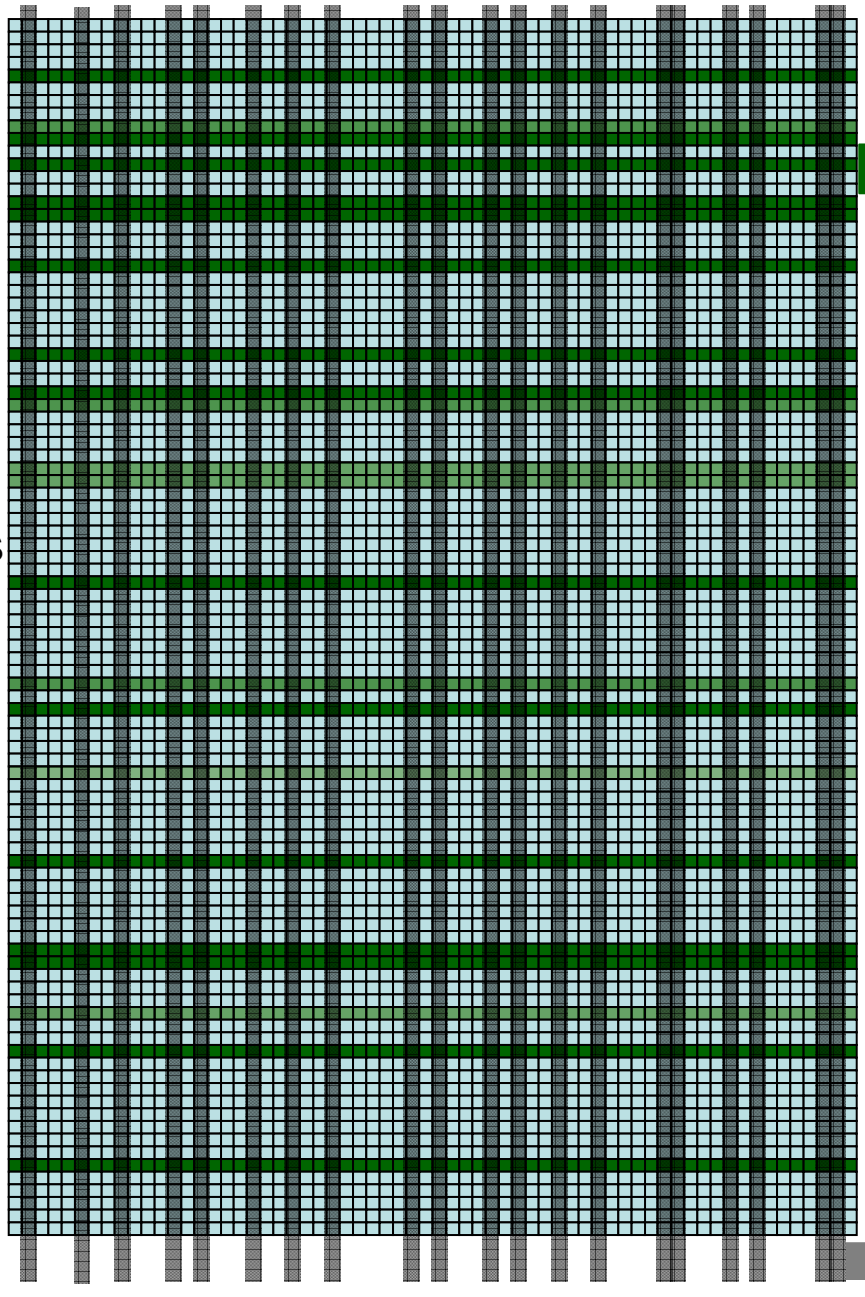
Figure 2. Concepts proposed for an organised access to genetic diversity based on **R.E.A.D.**ing germplasm

**R.E.A.D.:** Represent and Root –  
 Enter and Explore –  
 Assess and Associate –  
 Diversify and Dissect.

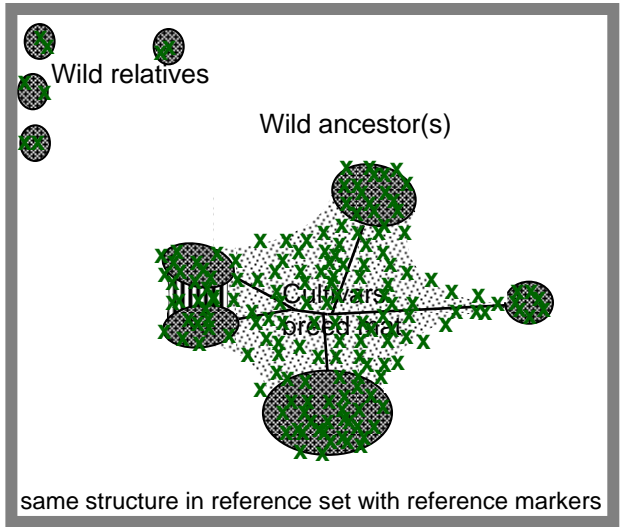
Existing diversity is distributed among numerous accessions (pale green) gathered in **base collections** that overpass the capacity of observation of the community. The **core collection** concept can be used to focus broad surveys using molecular markers, which then provide complementary information for identifying a smaller set of manageable size that represents the diversity thus described (dark green); currently the option adopted is in the 300-500 range. A molecular description helps identify lineages in the domestication process and root them in wild germplasm diversity. This material being used by the community, new information can regularly be compiled and analysed, and correlations with **passport data** can be used to further enter and explore the broad collection with specific objectives. This makes it a material of choice for contributing to **association panels** for assessing diverse phenotypes and relating traits to genes and alleles through association studies, as well as a valuable source for generating breeder-relevant germplasm as a new platform for dissecting trait-gene associations. The **reference set** is a flexible concept that invites updates and adjustments under monitoring by the community. It should be accompanied by a **nucleus sample** that any experiment addressing and characterizing diversity should be invited to incorporate

how?

Markers



Accessions



reference markers

# The GCP genotyping data validation project

hosted by SP1

- PI JF Rami, now helped by S McGrath
- collaborators are GCP genotyping labs + outsider (ADNid, Montpellier)
- repeat analysis for ref set (max 300) and best SSR loci (max 20)

Species	Original Genotyping	Reference set chosen	Size of Ref. set	Nb of markers	DNA delivered	Genotyping completed
Barley	Y	Y	300	15	Y	Y
Chickpea	Y	Y	300	20	Y	Y
Coconut	Y	Y	359	20	Y	Y
Finger Millet	Y	Y	300	20	Y	Y
Groundnut	Y	Y	300	20	Y	Y
Maize	Y	Y	234	20	Y	Y
Pigeon Pea	Y	Y	300	20	Y	Y
Sorghum	Y	Y	345	20	Y	Y
Wheat	Y	Y	372	20	Y	Y
Common Bean	Y	Y	192	20	Y	N
Cowpea	Y	Y	345	20	Y	N
Lentil	Y	Y	150	10	Y	N
Musa	Y	Y	96	20	Y	N
Yam	Y	Y	342	20	Y	N
Cassava	Y	Y	250	20	N	-
Foxtail Millet	Y	Y	200	20	N	-
Pearl Millet	Y	Y	300	20	N	-
Rice	Y	N	-	20	N	-
Sweet Potato	Y	N	-	20	N	-
Potato	Y	N	-	20	N	-
Fababean	Ongoing	N	-	20	N	-



# Chickpea

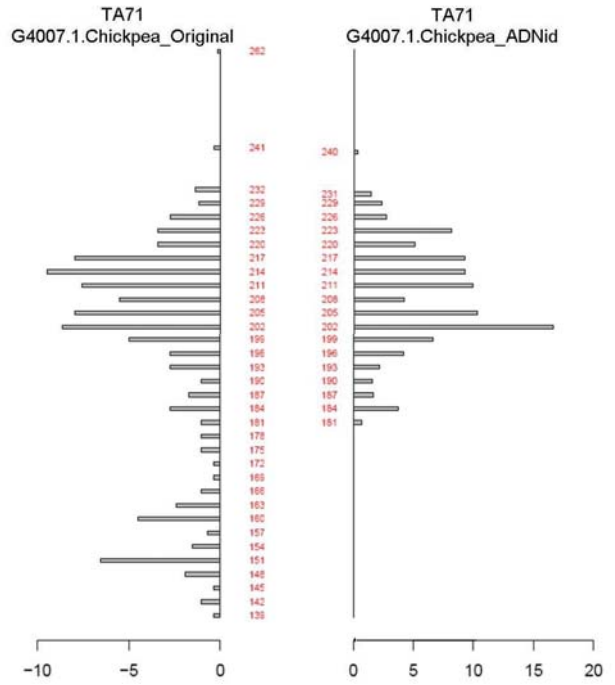
# Primary genotyping lab at ICRISAT

TA71

	181	184	187	190	193	196	199	202	205	208	211	214	217	220	223	226	229	231	240	
139	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.
142	.	.	.	.	1	.	.	1	1	.	.	.	.	.	.	.	.	.	.	.
145	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.
148	.	.	1	.	1	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.
151	.	2	.	1	.	.	1	3	3	.	2	2	.	.	3	.	.	.	1	.
154	.	.	.	.	.	.	.	2	.	.	.	.	.	.	2	.	.	.	.	.
157	.	.	.	.	.	.	1	.	.	1	.	.	.	.	.	.	.	.	.	.
160	.	.	.	1	.	.	1	1	1	.	1	2	1	1	2	.	.	.	.	.
163	.	.	.	.	.	.	.	3	.	.	1	.	.	.	2	.	.	.	.	.
166	.	.	.	.	.	.	.	1	.	1	.	.	.	.	1	.	.	.	.	.
169	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.
175	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	2	.	.	.	.
178	.	.	.	.	.	.	.	.	1	.	.	.	1	.	1	.	.	.	.	.
181	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
184	6	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
187	.	3	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	.
190	.	.	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
193	.	.	.	5	1	.	1	.	.	.	.	.	.	1	.	.	.	.	.	.
196	.	.	.	.	6	1	1	.	.	.	.	.	.	.	.	.	.	.	.	.
199	.	.	.	.	1	10	1	.	.	.	.	.	.	.	.	.	.	.	.	.
202	.	.	.	.	.	1	19	1	.	2	.	1	.	.	.	.	.	.	.	.
205	.	.	.	.	1	.	2	17	.	.	.	.	1	.	.	.	.	.	.	.
208	.	1	.	.	.	.	3	1	7	1	1	.	.	.	.	.	.	.	.	.
211	.	.	.	.	.	.	.	.	.	18	1	.	1	.	.	.	.	.	.	.
214	.	.	.	.	.	1	1	1	1	19	1	1	1	1	1	.	.	.	.	.
217	.	.	.	.	.	.	1	.	.	1	.	14	1	1	1	.	.	.	.	.
220	.	.	.	.	.	.	.	1	.	.	.	1	7	1	.	.	.	.	.	.
223	.	.	.	.	.	.	.	1	1	.	.	.	.	7	.	.	.	1	.	.
226	.	.	.	.	.	.	.	.	.	.	.	.	1	5	1	.	.	.	.	.
229	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	2	.	.
232	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	3	.

contamination at ADNid??  
duplicate loci??

not compatible from distributions

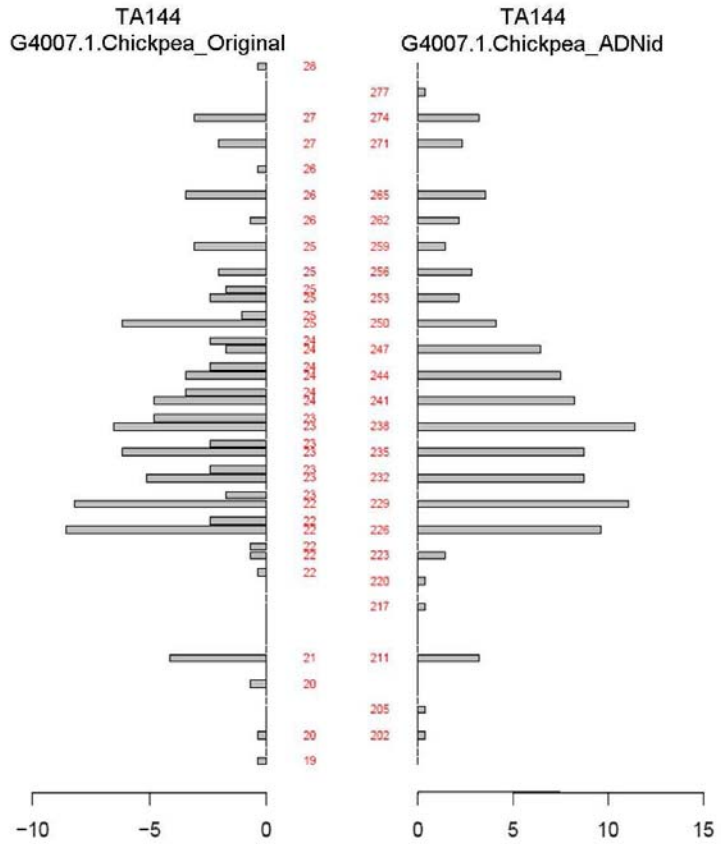


# Chickpea

# Primary genotyping lab at ICRISAT

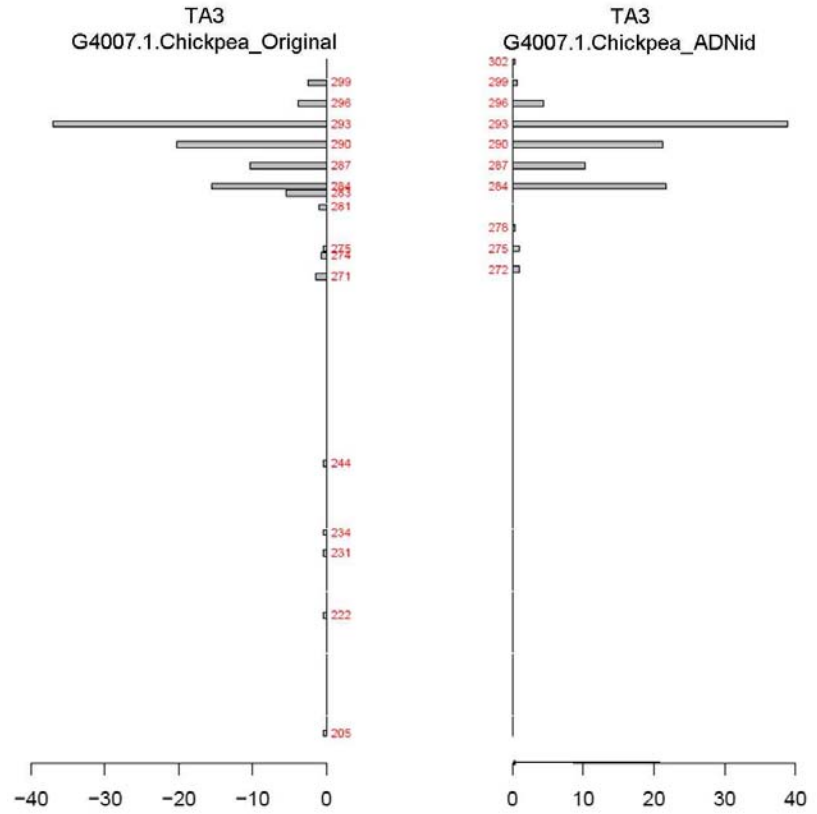
TA144

	202	205	211	217	220	223	226	229	232	235	238	241	244	247	250	253	256	259	262	265	271	274	277		
199	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	
202	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	1	.	.	
208	.	.	.	.	.	1	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	
211	.	.	.	.	.	1	3	2	1	1	1	.	.	1	.	.	.	.	.	2	.	.	.	.	
221	.	.	.	.	.	.	.	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	
223	.	.	.	.	.	2	.	1	.	.	1	.	.	.	.	.	.	.	.	.	.	.	.	.	
226	.	1	.	.	1	3	2	2	3	6	2	2	3	1	.	.	1	.	1	1	.	1	.	.	
229	1	.	.	.	.	4	3	3	1	5	1	2	2	1	.	.	1	1	1	1	.	.	.	.	
232	.	.	2	.	.	.	.	4	4	2	1	3	1	.	.	1	.	.	.	.	.	.	.	1	
235	.	1	.	.	.	3	2	.	3	3	.	2	.	.	2	1	.	1	.	1	.	3	2	.	
238	.	.	1	.	1	1	2	2	3	1	3	2	3	2	1	2	.	1	2	2	2	2	.	.	
241	.	.	2	1	.	1	1	4	.	2	2	1	2	2	2	1	.	.	.	.	.	.	.	.	
244	.	.	.	.	.	.	3	3	2	1	3	.	1	1	1	1	.	.	.	.	.	.	.	.	
247	.	.	.	.	1	.	1	.	2	1	.	1	1	1	1	.	.	.	.	1	.	2	.	.	
250	.	.	.	.	.	4	3	3	1	3	.	1	.	2	.	.	1	1	.	.	.	1	.	.	
253	.	.	1	.	.	1	2	.	2	1	2	3	.	.	.	.	.	.	.	.	.	.	.	.	
256	.	.	.	.	.	.	1	.	.	1	.	1	.	1	.	1	.	1	.	.	.	.	.	.	
259	.	.	.	.	.	1	2	.	.	2	3	.	.	.	.	1	.	.	.	.	.	.	.	.	
262	.	.	.	.	.	.	.	.	.	1	1	.	.	.	.	.	.	.	.	.	.	.	.	.	
265	.	.	1	.	.	1	1	.	.	1	.	.	3	.	.	.	1	.	1	.	.	.	.	.	
271	.	.	.	.	.	1	.	.	.	2	.	.	1	.	.	.	.	.	.	.	.	.	.	.	
274	.	.	1	.	.	.	2	.	.	1	1	1	.	.	.	.	.	.	1	2	.	.	.	.	
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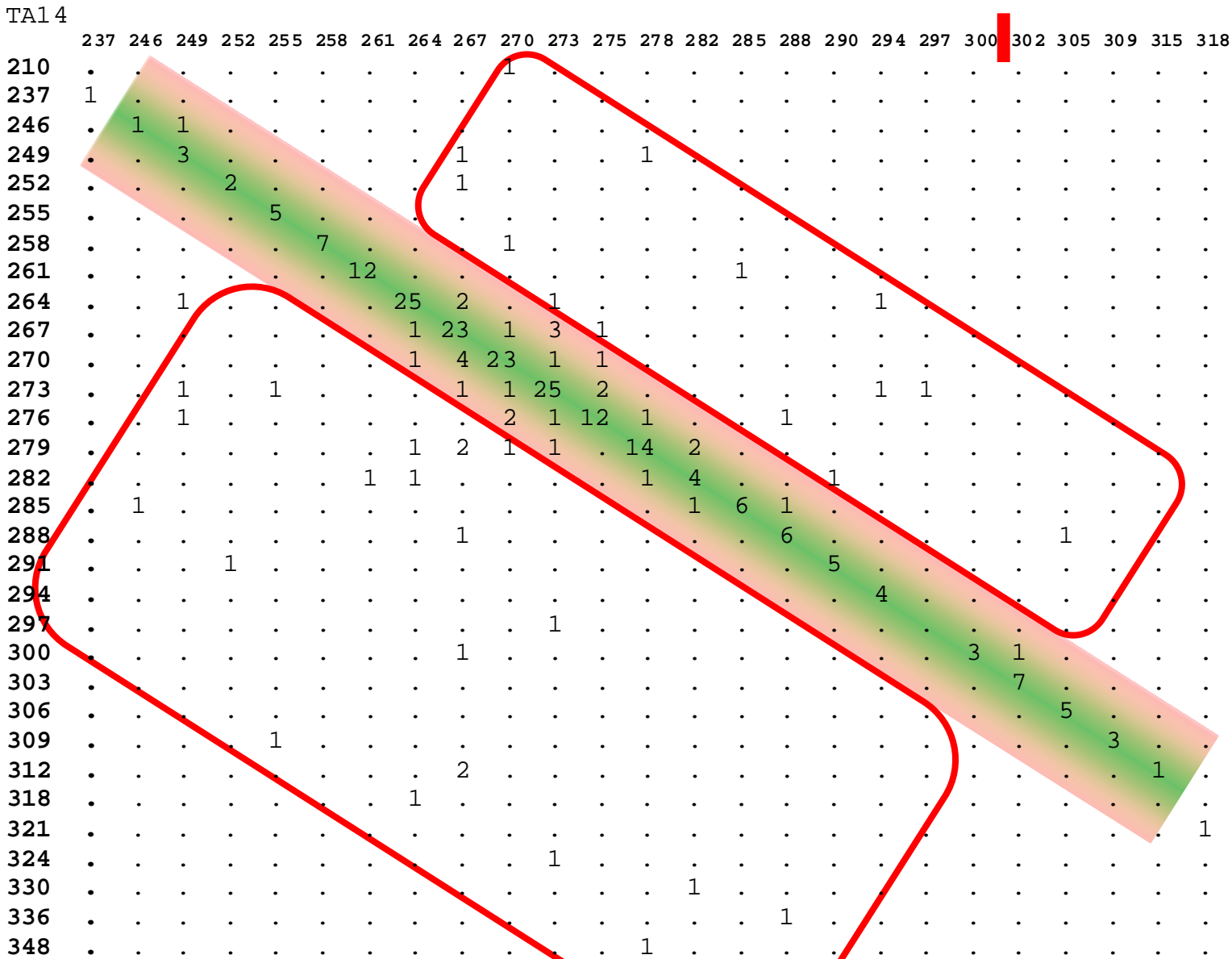
TA3

	272	275	278	284	287	290	293	296	299	302
205	.	.	.	1	.	.	.	.	.	.
222	.	.	.	1	.	.	.	.	.	.
231	.	.	.	.	1	.	.	.	.	.
234	.	1	.	.	.	.	.	.	.	.
244	.	.	.	.	.	.	1	.	.	.
271	.	.	.	.	.	.	2	1	.	1
275	.	.	.	.	.	.	3	.	.	.
281	.	.	.	1	.	1	.	.	1	.
284	.	.	.	17	5	15	20	1	.	.
287	1	.	.	5	2	12	8	2	.	.
290	.	.	1	11	10	9	22	3	.	.
293	2	1	.	19	8	19	48	4	1	.
296	.	.	.	3	2	1	2	1	.	.
299	.	1	.	2	.	1	3	.	.	.



# Chickpea

# Primary genotyping lab at ICRISAT



196:29:37

# Sorghum

## Primary genotyping labs at ICRISAT and CIRAD

Table 3: Diversity characteristics of the markers

Marker	MV	MAF	Ng	Na	GD	H	PIC	TRO
gpsb067	5.47	0.395	21	12	0.757	0.063	0.727	23
gpsb123	13.28	0.283	16	10	0.803	0.036	0.776	9
ISEP0310	2.08	0.727	17	11	0.460	0.026	0.447	39
mSbCIR223	1.82	0.392	14	10	0.737	0.013	0.697	1
mSbCIR238	3.13	0.19	34	27	0.909	0.021	0.903	36
mSbCIR240	2.86	0.45	39.00	27.00	0.76	0.04	0.75	15.00
mSbCIR246	1.82	0.792	14	9	0.362	0.031	0.347	38
mSbCIR248	1.56	0.42	17.00	8.00	0.70	0.24	0.65	26.00
mSbCIR262	5.99	0.436	20	12	0.735	0.060	0.703	22
mSbCIR276	3.39	0.495	12	8	0.644	0.026	0.586	4
mSbCIR283	2.34	0.313	29	23	0.835	0.023	0.819	2
mSbCIR286	1.04	0.362	23	14	0.808	0.029	0.789	5
mSbCIR300	0.78	0.35	17.00	10.00	0.73	0.03	0.68	33.00
mSbCIR306	0.78	0.44	9.00	6.00	0.66	0.02	0.60	37.00
mSbCIR329	3.65	0.350	16	10	0.782	0.026	0.752	3
Sb4-72	1.56	0.35	26.00	20.00	0.80	0.03	0.78	10.00
Sb5-206	4.69	0.12	50.00	32.00	0.95	0.05	0.95	20.00
Sb6-84	7.03	0.271	42	28	0.881	0.039	0.873	29
SbAG-B02	5.21	0.422	42	30	0.786	0.044	0.772	16
Xcup02	2.08	0.39	18.00	9.00	0.72	0.05	0.68	27.00
Xcup11	1.30	0.590	9	6	0.505	0.044	0.403	40
Xcup14	4.95	0.54	26.00	20.00	0.67	0.02	0.65	32.00
Xcup53	4.95	0.52	12.00	9.00	0.64	0.03	0.58	34.00
Xcup61	2.60	0.546	8	6	0.532	0.047	0.431	18
Xcup63	1.30	0.738	11	7	0.417	0.036	0.375	11
Xisep0107	4.17	0.546	8	5	0.592	0.031	0.525	7
Xtxp010	2.08	0.36	24.00	12.00	0.79	0.09	0.76	28.00
Xtxp012	9.11	0.103	36	25	0.936	0.029	0.932	6
Xtxp015	9.38	0.189	40	18	0.880	0.096	0.869	25
Xtxp021	0.78	0.46	31.00	22.00	0.76	0.04	0.75	12.00
Xtxp040	3.13	0.699	23	16	0.496	0.039	0.482	13
Xtxp057	4.69	0.30	40.00	24.00	0.86	0.06	0.85	31.00
Xtxp114	1.82	0.47	17.00	11.00	0.62	0.04	0.55	14.00
Xtxp136	0.52	0.639	4	3	0.465	0.044	0.362	41
Xtxp141	0.78	0.27	31.00	20.00	0.88	0.03	0.87	8.00
Xtxp145	1.82	0.22	42.00	25.00	0.91	0.05	0.91	19.00
Xtxp265	1.30	0.11	48.00	26.00	0.93	0.07	0.92	30.00
Xtxp273	1.82	0.41	25.00	19.00	0.78	0.02	0.76	35.00
Xtxp278	1.56	0.64	24.00	18.00	0.55	0.06	0.51	24.00
Xtxp320	5.73	0.230	34	17	0.873	0.057	0.861	21
Xtxp321	2.60	0.16	41.00	27.00	0.93	0.04	0.93	17.00
Mean	3.34	0.407	24.63	15.90	0.727	0.046	0.696	

MV: percentage of missing values, MAF: frequency of the major allele, Ng: number of genotypes, Na: number of alleles, GD: gene diversity (sensus Nei), H: Heterozygosity, PIC: Polymorphic Information Content, TRO: order to remove the most redundant markers



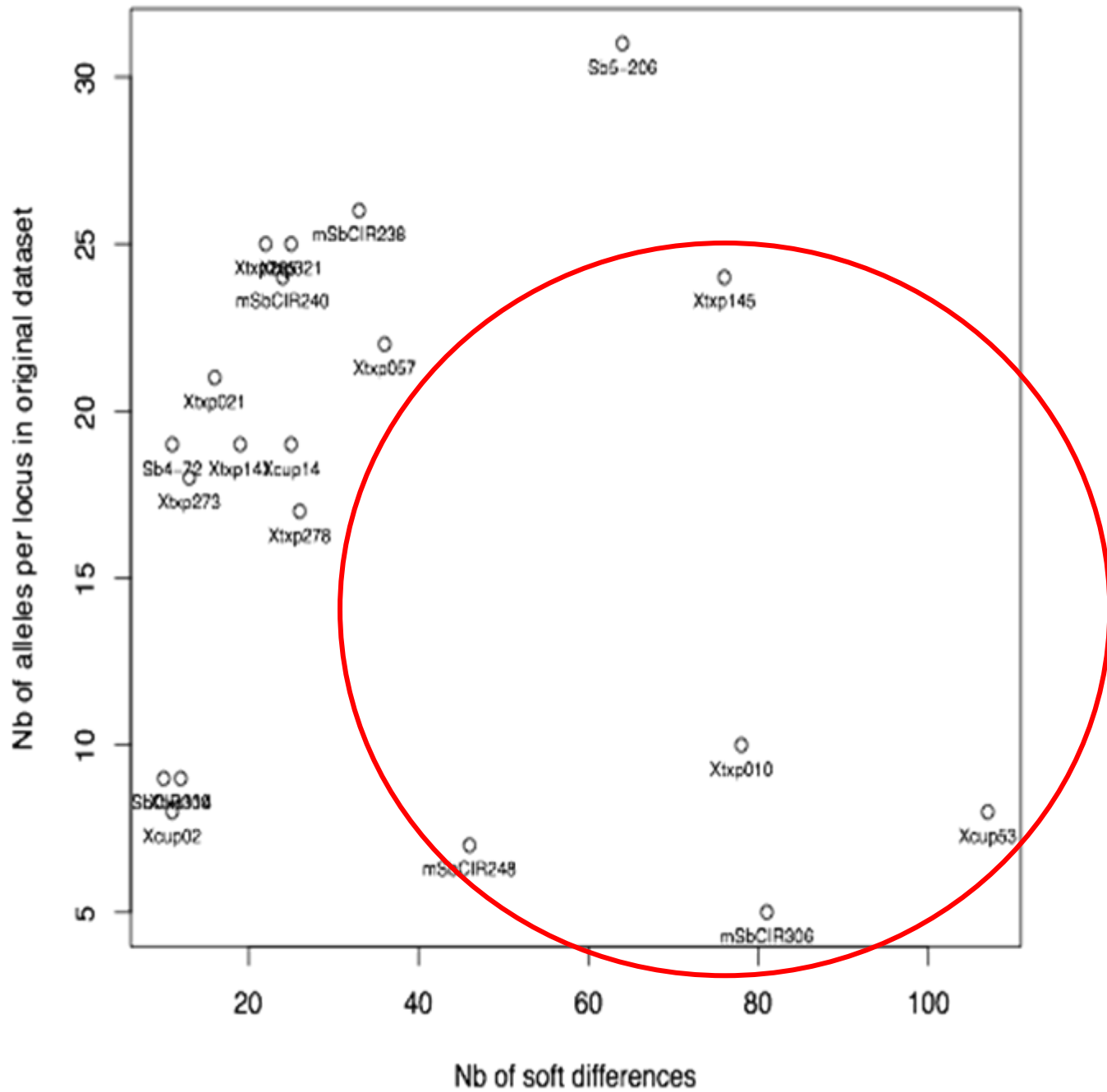
# Sorghum

Primary genotyping labs  
at ICRISAT and CIRAD

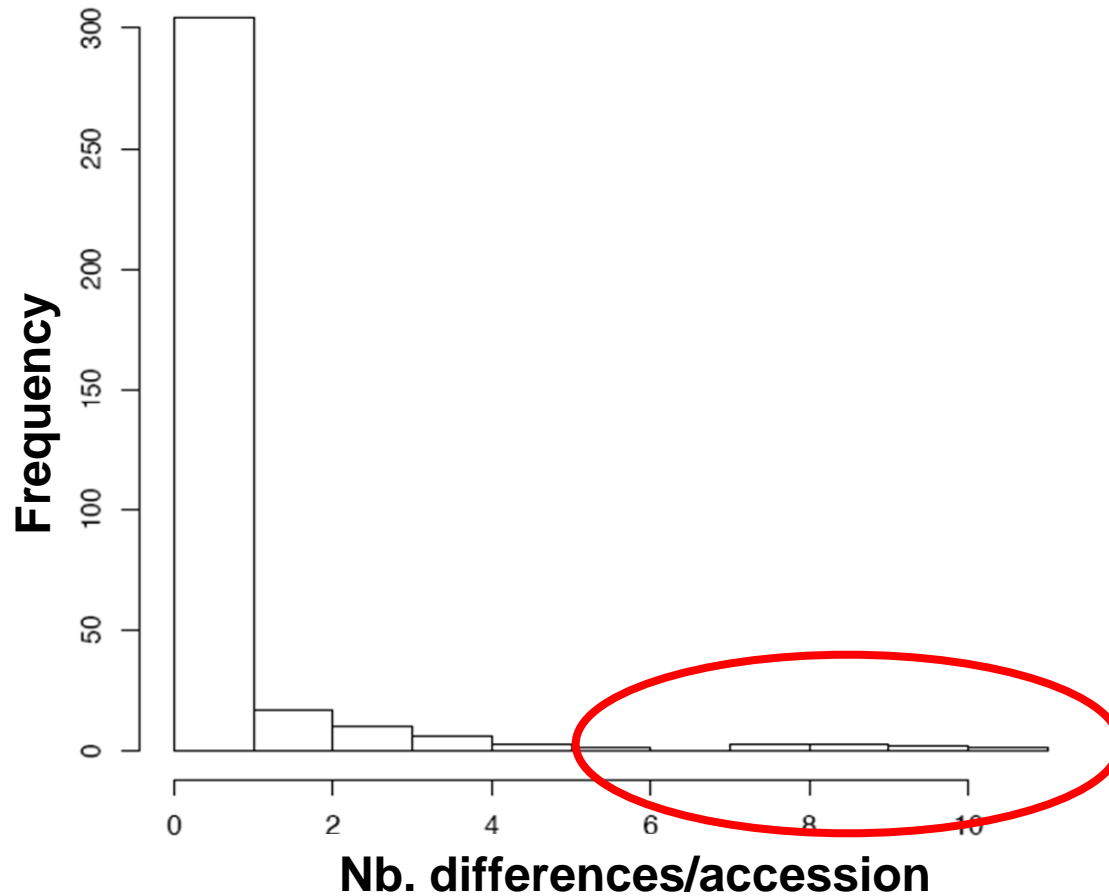
## Xtxp321

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188	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
190	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
192	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
194	0	0	0	0	23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
196	0	0	0	0	0	4	0	1	0	0	0	0	0	0	0	0	0	1	0	0
198	1	0	0	0	0	0	40	0	0	0	0	0	0	0	0	0	0	0	0	1
200	0	0	0	0	0	0	0	24	1	0	0	0	0	0	0	0	0	1	0	0
202	0	0	0	0	0	0	0	2	29	0	0	0	0	0	0	0	0	0	1	0
204	0	0	0	0	0	0	0	0	0	20	0	0	0	0	0	0	0	0	0	0
206	0	0	0	0	0	1	0	1	0	1	22	0	0	0	0	0	0	0	0	0
208	0	0	0	0	0	0	0	0	0	0	0	13	0	0	1	0	0	2	0	0
210	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0
212	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0
214	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0	0
216	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0	0	0	0
218	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	7	0	0	0
220	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0

233:19



## Distribution of nb of differences/accession



13 accessions showed 5 differences or more between data sets



**Chickpea reference set:** A reference set of 300 genetically most diverse accessions was formed, representing 78 % allelic diversity of the composite collection (2915 accessions with 48 SSR markers). The seed of single plant for each reference accessions (from which DNA was extracted) was regenerated in field and 50g seed of each reference accessions is available.

**Sorghum reference set:** A reference set of 384 genetically most diverse accessions was formed, representing 78 % allelic diversity of the composite collection (3365 accessions with 41 SSR markers). The self seed of single plant for each 375 reference accessions (from which DNA was extracted) was regenerated in field. The seed of remaining 9 reference accessions is not available at ICRISAT. 100g seed of each 342 sorghum reference accessions, designated with FAO is available.



# Reference sets of food crop germplasm for international collaboration GCP Workshop held in Montpellier, November 13-17, 2008



*Jean-Christophe Glaszmann<sup>1</sup>, Carmen de Vicente<sup>2</sup>*

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71 participants from 28 countries, specialized scientists involved (30%) or not (20%) in GCP projects, germplasm scientists and managers (25%) and breeders (25%)



# Main conclusions

The Generation Challenge Program approach was affirmed in exploring, evaluating and using germplasm diversity, in defining reference sets on the principles that all GCP products must be delivered to users.

The expectation extends also to related initiatives in the System-Wide Genetic Resources Program (SGRP) of the CGIAR, the Global Crop Diversity Trust and the Global Partnership Initiative for Plant Breeding Capacity Building (GIPB).

GCP-derived reference sets can play a prominent role provided that

- there is clarity on political availability of the resource and the attached data by placing them under the Multi-Lateral System
- research continues on their use as an entry to the broader collections.

Their description and access have a natural place in the web system being put in place by the SGRP and Bioversity, which can therefore be used for publicizing and ordering.

Information has been shared ... we have been made aware of the broad diversity of situations among crops and some limitations that need to be overcome, on

- representation and comprehensiveness of original composite collections,
- choice and justification of methodology to select reference sets,
- data quality of both collections, composite and reference,
- traceability of germplasm,
- availability of the minimum required information to be distributed with the material
- quality control (label, certification, ...) of the material to be distributed

## Next steps – Issues to be addressed (currently addressed) and action to be taken (currently taken)

**Governance:** Who will decide which sets are ready to get the GCP seal of quality and approval? How will this decision be made?

**Multiplication:** Who will do it? Who will finance it? Relationships between CG Centers and NARS, Development of the sets and ensuring their quality and their readiness should go together with the development of the information systems to support them (to be developed in conjunction with Bioversity, Compliance with Multilateral System (MLS), Availability of methodologies is a must

**Evaluation of the demand:** survey past and current demand for minicore/reference sets, Circulate questionnaire among curators and networks of crop researchers (questionnaire to be accompanied by a clear description), write simple document on concept, utility, methods, ... pertaining to the reference sets

**Upgrade situation on a crop by crop basis:** Collect/compile passport data and currently available information on composite set

**Have molecular data analysis validated** by outsider (see project G4007.01)

- Quality assessment with simple criteria: Inform original lab(s) of abnormalities found, Produce new (if necessary) GCP template data matrix (TDM): derived from labX and used as template by GCP for structure analysis, Gross structure analysis with standard methods and compared with reports and publications of lab X

- Have data compared between the GCP TDM and the results of the validation exercise (with reference markers): Analyze discrepancies between data; types, sources, distributions, Infer impact on global quality of gross structure

- Compare structure between GCP TDM and GCP reference data (reference set of materials characterized with reference markers; GCP reference data should reflect the structure obtained with GCC TDM)

**Identify expert committee per crop:** Establish expert committee with breeders and partners, Request expert advice for representativeness and complementation, Collect/compile/update information on status of seed production/availability

**Promote visibility** through SINGER-ALIS, SGRP, CDT, GIPB, Coordinate with Bioversity officer, Communicate, distribute, publish

# GCP Project Title: Establishing a Genetic Resource Support service (GRSS) for the plant breeding community

- Targeted Subprogram: SP1
- Principal Investigator and Lead Institution: JC Glaszmann, GCP and CIRAD
- Collaborating Scientists and Institutions: Hari Upadhyaya, ICRISAT (co-PI)  
E Arnaud, Bioversity International (co-PI)
- collaborating projects/programmes D Williams, Bioversity International, SGRP  
JF Rami, CIRAD- Agropolis
- **Project start and end dates:** 1 July 2009 through 30 June 2011 (2 years)

appointed in March 2009 as postdoc fellow

Sarah McGrath

# Objectives and selected outputs

**Objective 1: Monitor and upgrade the quality of the current genetic resources developed and used in the GCP in order to make them stable genetic stocks.**

*Outputs:*

- *a catalogue of labeled genetic stocks currently available for the GCP priority crops, setting the biological foundation for the GRSS*  
***in a five-year horizon, reference sets should be available for 15 CGIAR crops, recombinant panels for 10 crops, introgression panels for four crops and mutants collection for two crops***

**Objective 2: Elaborate a global policy and processes with other partners for the identification of the genetic resources, the maintenance of the genetic stocks and their distribution**

*Outputs:*

- *a steering mechanism for the GRSS with representation of the breeding community and the main international actors of crop germplasm conservation (CGIAR centres' and programmes' representatives, GCDT, ...)*
- *a high pertinence of the service in terms choice of materials and a clear positioning in a global community for germplasm conservation and use*
- *contracts established with the major partners for the GCP priority crops*

**Objective 3: Develop a service integrated in the global germplasm system ensuring maintenance and distribution of genetic stocks for the priority GCP crops.**

*Outputs:*

- *a pilot service implemented with ICRISAT for at least one cereal and one legume, including a GCP branded portal to GRSS using the CGIAR Center (here ICRISAT) web site and the SINGER web interface technology*  
***in a five-year horizon, it is expected that a service be implemented and be distributing genetic stocks for at least 10 GCP crops to at least 100 users.***

	Year 1												Year 2											
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
Activity 1				1																				
Activity 2							2					3						4						
Activity 3						5								6										
Activity 1									7															
Activity 2			8									9												
Activity 1			10											11										
Activity 2										12														
Activity 3																					13			
Activity 4			14									15								16				

1. a scientific communication on the reference sets  
2. an assessment of the quality of the data and composition for the first eight crops  
3. an assessment of the quality of the data and composition for the next five crops  
4. complete assessment of the data quality  
5. an assessment of the seed situation for the first eight crops  
6. an assessment of the seed situation for the next thirteen crops  
7. First meeting the Steering Committee  
8. A survey of past and current demand for minicore/reference sets  
9. crop-specific questionnaires circulated among networks of crop researchers (questionnaire including reference set and other resources)  
10. ICRISAT contracted for seed increase and phenology documentation  
11. Contract started with other PIs (tbd) for seed increase and phenology documentation for three crops  
12. Service started with two crops with ICRISAT  
13. Contracts signed with service providers for other priority crops  
14. Agreement with Bioversity/SGRP on the web integration of the GRSS  
15. Proper communication implemented  
16. Facilities implemented in SINGER for handling sets of materials and genotyping/phenotyping data

# Thanks for your kind attention

JC Glaszmann

JF Rami

C Billot

S McGrath

C de Vicente



## **Generation**

**Cultivating Plant Diversity for the Resource-Poor**