



GCIRC Rapeseed/Mustard Technical Meeting
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New Delhi, India



Structure of **genetic diversity** and elaboration of **core collections** for the three related *Brassica* species: *B. napus*, *B. oleracea*, *B. rapa*

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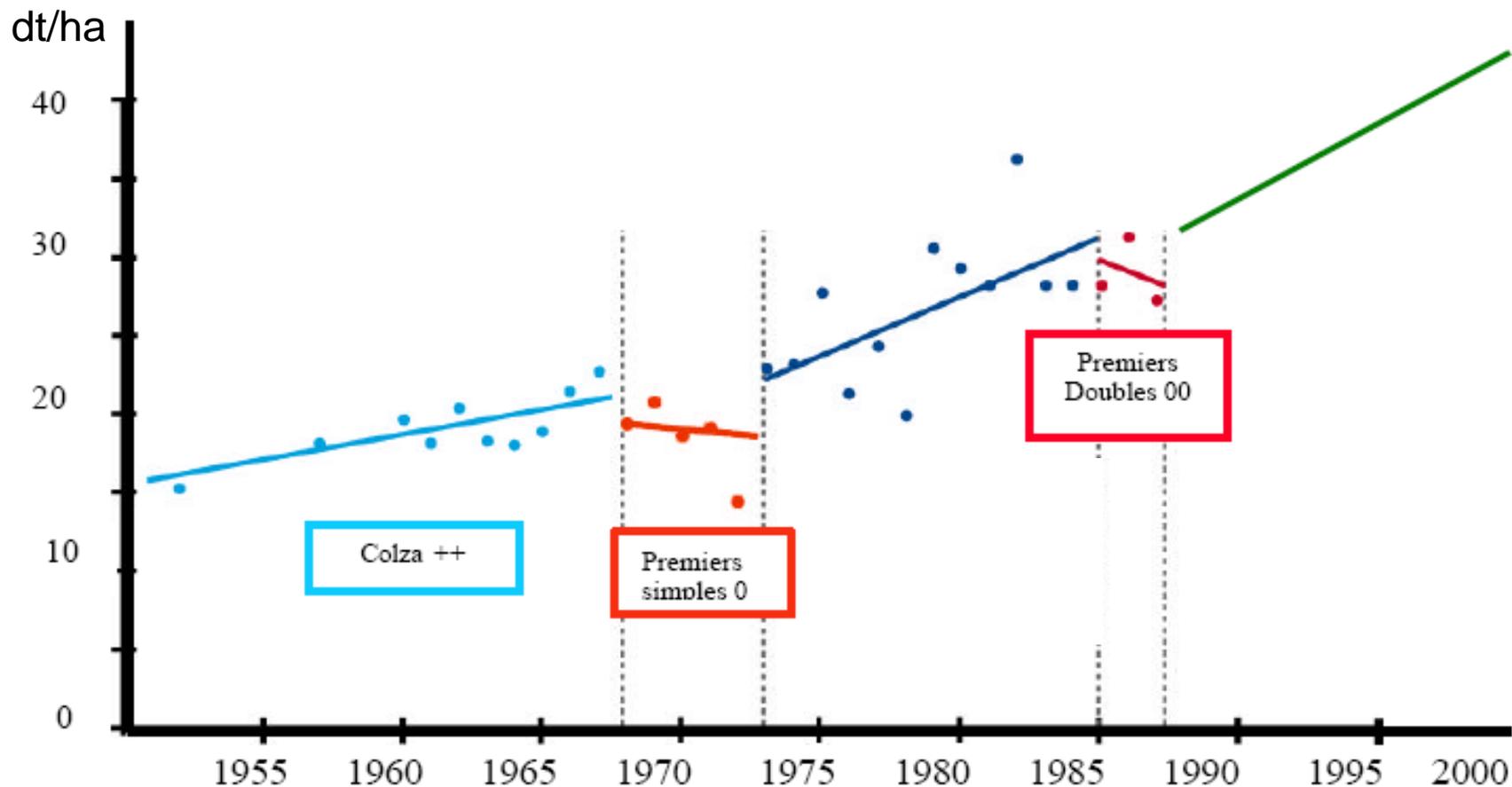


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Towards a reduction of exploited *B. napus* diversity



=> Need to broaden *B. napus* genetic diversity by exploiting its progenitors

Source CETIOM

Rationales

- How is Brassica genetic diversity organized?
- How to answer to new breeding challenges ?
 - Exploiting *Brassica* genetic diversity

⇒ A real need for defining core collections

Objectives

Study the **genetic diversity** of

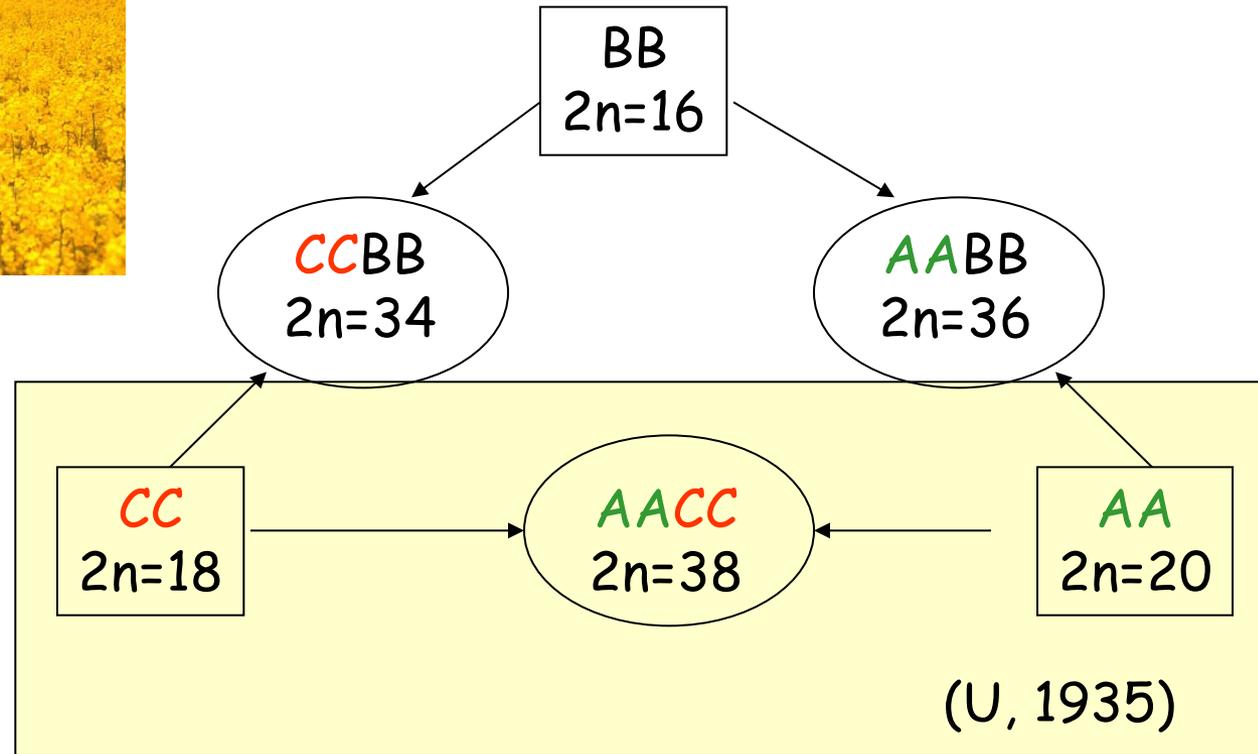
- a semi-autogamous species *Brassica napus*
- two allogamous species : *Brassica oleracea*,
Brassica rapa

Connect the diversity of *Brassica napus*, *rapa* and *oleracea*

Deliver public core collections to the scientific community

Which available genetic diversity for *Brassica napus* ?

Which diversity ? Relationships between Brassicae



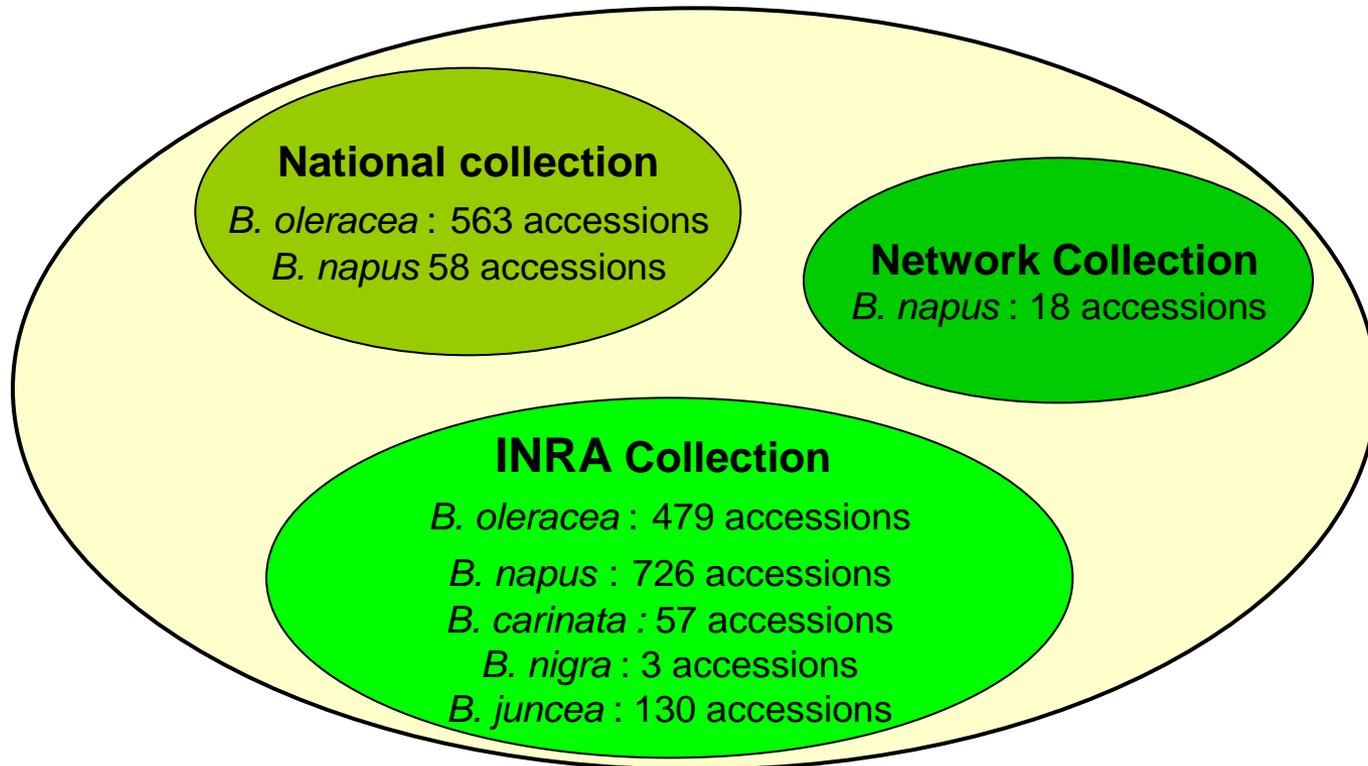
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Which available genetic diversity for the scientific community ?

Gene banks

Panels, diversity sets and core
collections

French Brassica Genetic Resources Center (BGRC)



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International organisation of *Brassica* diversity study

- RESGEN Project
 - *Brassica* core collections



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EU project RESGEN CT99 109-112

**"*Brassica* Collections for Broadening Agricultural Use" including
"Characterising and utilising genetic variation in *Brassica carinata* for its
exploitation as an oilseed crop"**

The RESGEN CT99 109-112 project on the genetic resources of *Brassica* was carried out in the framework of the European Community Programme on the Conservation, Characterisation, Collection and Utilisation of Genetic Resources in Agriculture. The project was funded by The European Commission and started January 1st 2000.

Core collections of the four *Brassica* species

Each of the four subgroups of the project developed their own core collection. The size of the four core collections is as follows:

- *B. oleracea*: 395 accessions
- *B. rapa*: 100 accessions
- *B. napus*: 150 accessions
- *B. carinata*: 80 accessions

<http://documents.plant.wur.nl/cgn/pgr/brasedb/brasresgen.htm>

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International organisation of *Brassica* diversity study

- RESGEN Project
 - *Brassica* core collections (Institute of Crop Science and Plant Breeding Giessen, Germany)
- BnDFFs «Diversity Fixed Foundation Sets» (OREGIN (www.oregin.info))

A Diversity Fixed Foundation Set (DFFS): is defined as
"an informative set of genetically fixed lines representing a structured sampling of diversity across a genepool"

Species	Set	Number of lines	Founder line seed available	Fixed line seed available	Founder DNA available	Fixed line DNA available	detail	MTA	Project	Contact
<i>B. napus</i>	BnaDFFS	188	152	56	152	53	 Oct 08	-		Graham Teakle (WHRI)
<i>B. oleracea</i>	BolDFFS	376	-	-	-	-	 Jan 09	-		Graham Teakle (WHRI)
<i>B. rapa</i>	BraDFFS	-	-	-	-	-	-	-	-	Guusje Bonnema (MUR)
<i>B. C genome</i>	BCgDFFS	88 (tbc)	-	-	-	-	-	-		Paul Hand (WHRI)



A web based User Interface has been developed to query the population Area of CropStore, to view data summaries and download Excel workbooks containing detailed data - [Available Here \(CropStore :: Populations\)](#)

www.oregin.info

International organisation of *Brassica* diversity study

- RESGEN Project
 - *Brassica* core collections
- BnDFFs «Diversity Fixed Foundation Sets» (OREGIN (www.oregin.info))
- *rapa* collection: China – Wageningen (G. Bonnema)
- Collections of Vavilov Research Institute of Plant Industry (*napus*, *rapa* and *oleracea*)

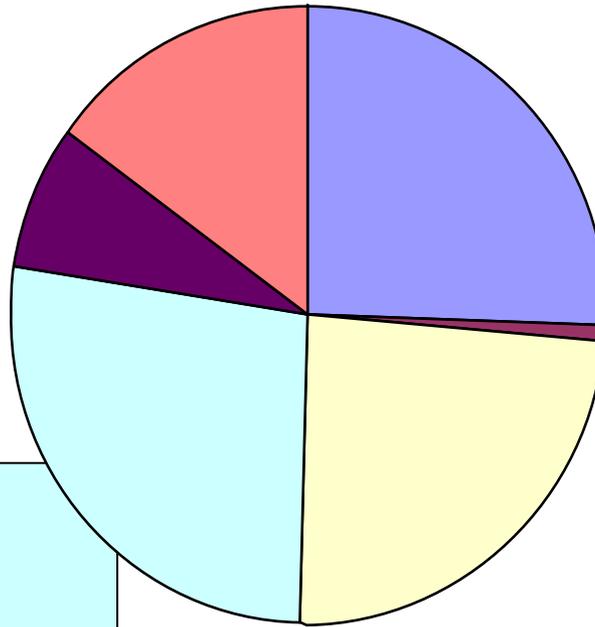
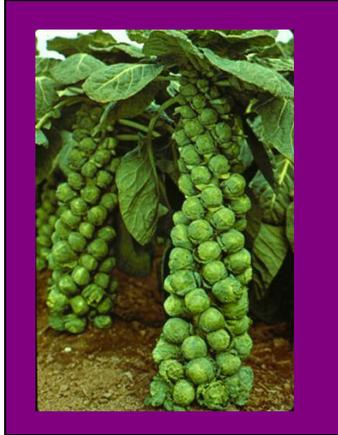
The first target:

Brassica oleracea

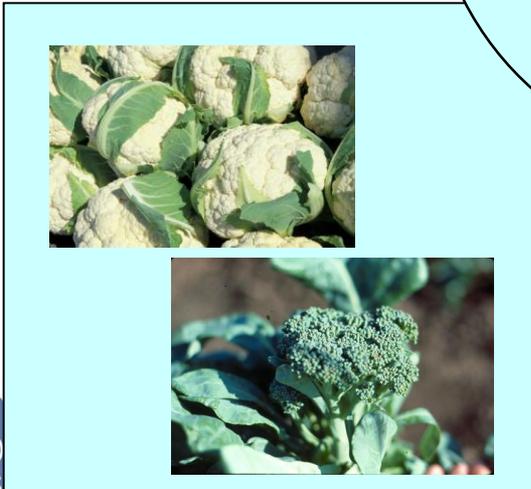
Plant material

Brassica oleracea collection

384 accessions



- acephala
- alboglabra
- capitata
- botrytis
- oleracea
- non défini



Definition of SSR marker sets

SSR pool

Public markers

582 SSR derived from EST Génoplante

40 SSR Australia (bo)

113 SSR Japan (br)

103 SSR USA (bo)

Quality indice

Position on genetic map

DnxY

1st SSR choice

- Quality

- distribution on maps

80 SSR Agriculture Canada

BBSRC England

Celera

2nd SSR Choice depending on pilote project

12 napus

6 oleracea

6 rapa

Private markers

130 SSR Trait Genetics

Position on
Traits Genetics
map

Set 76 SSR rapa



Set 76 SSR napus



Set 76 SSR oleracea

Data mining

Definition of an analysis strategy based on *Brassica oleracea* data

Current results

Study of 384 *B. oleracea* accessions using 22 SSR

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General strategy

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The ECPGR *Brassica* Database

[Centre for Genetic Resources, The Netherlands \(CGN\)](#)

Database managers:
[F. Menting](#) and [drs. N. Bas](#)



<http://documents.plant.wur.nl/cgn/pgr/brasedb/default.htm>



A large core collection of 384 accessions (RESGEN cc) defined according to cultigroups and origins of accessions



1. Acquisition of molecular data based on public SSR markers

2. Study of the genetic diversity structure

3. Sample and validate a core collection

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Methods: Definition of core collection

2. Study of genetic diversity structure

Bayesian approach
Software structure 2.2

Group definition and affiliation of accessions to groups

3. Sampling core collection

Maximisation (M)
(MSTRAT software)

Random (R)

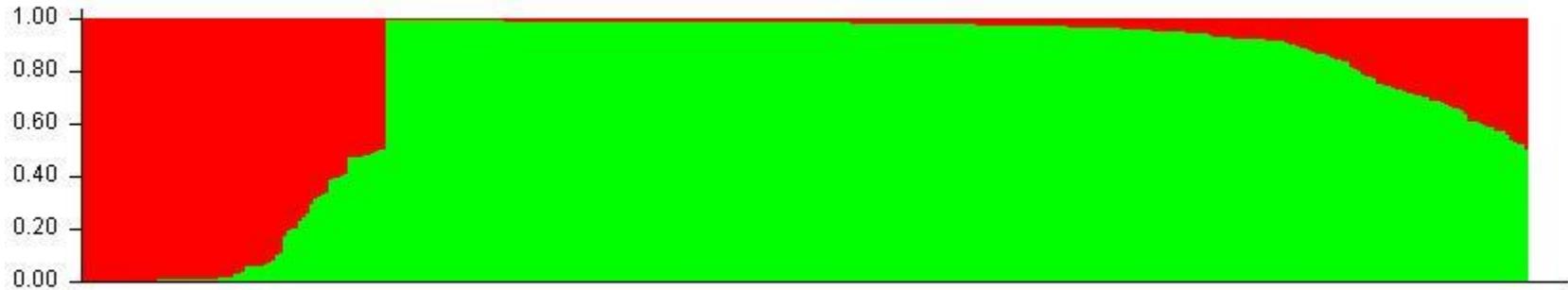
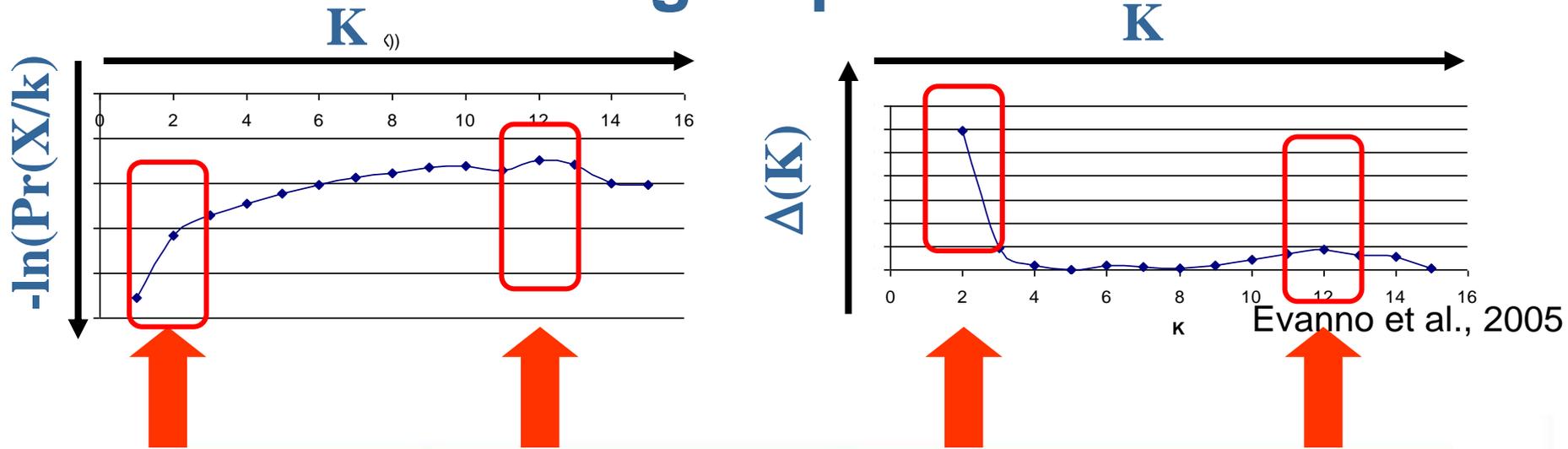
Methods based on
diversity structure results

Constant (C)

Logarithmic (L)

Proportional (P)

2 - Structure of the collection revealed by a bayesian approach: from 2 to 15 groups



Cauliflowers and Broccoli

Broccoli and others cultigroups

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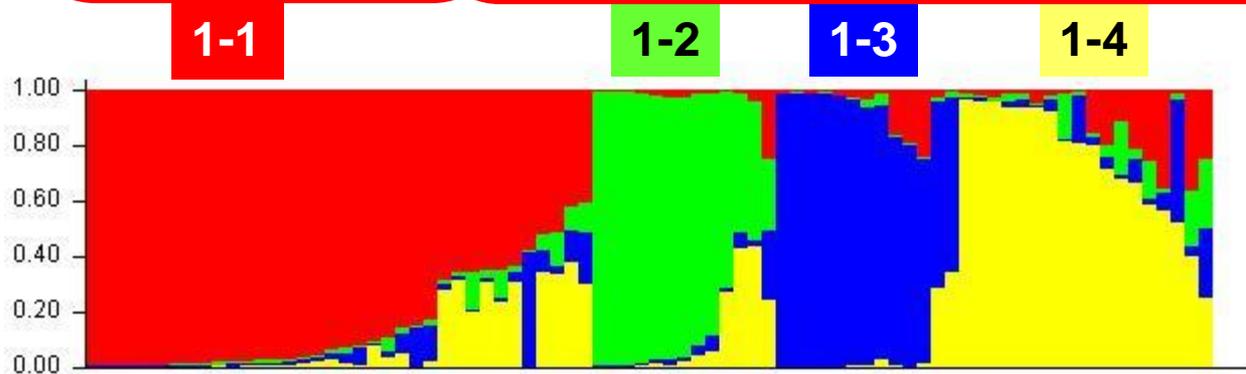
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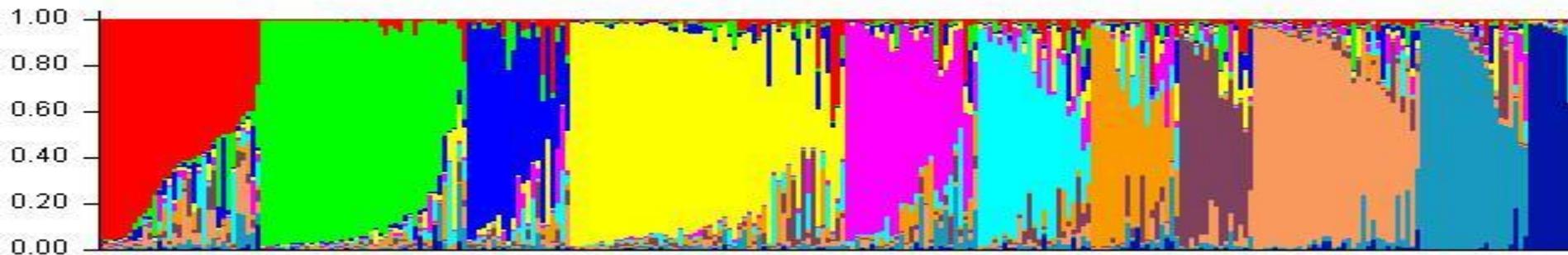
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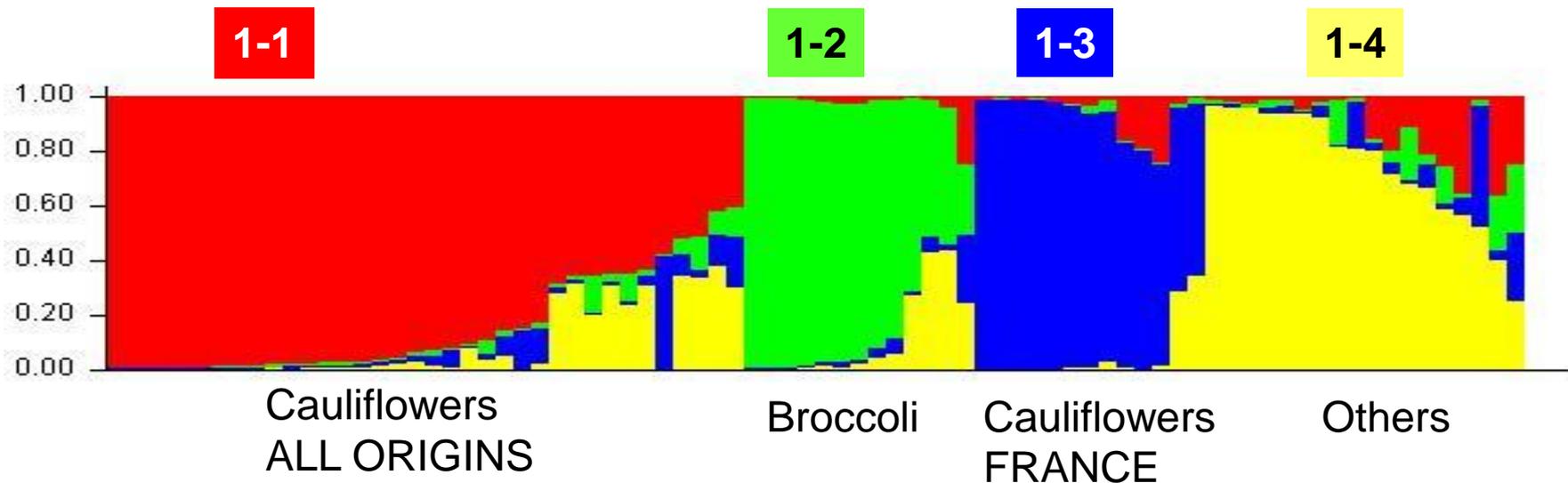
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80 accessions





Cultigroup
good indic

B. o. acephala
acephala medullosa
marrow-stem kale

2-1

B. Oleracea gemmifera
Brussels sprouts

B.o. acpehala sabellica curly kale

geographic origin are
structure

B.o. capitata
cabbage

2-4

B.o. botrytis italica (broccoli)
B.o. acephala gongylodes - Kohlrabi
(chou-rave) (ITALY)

2-5

B.o. hilarionis, campestris,

2-6

All cultigroups
EGYPT, TURKEY SYRIA

2-8

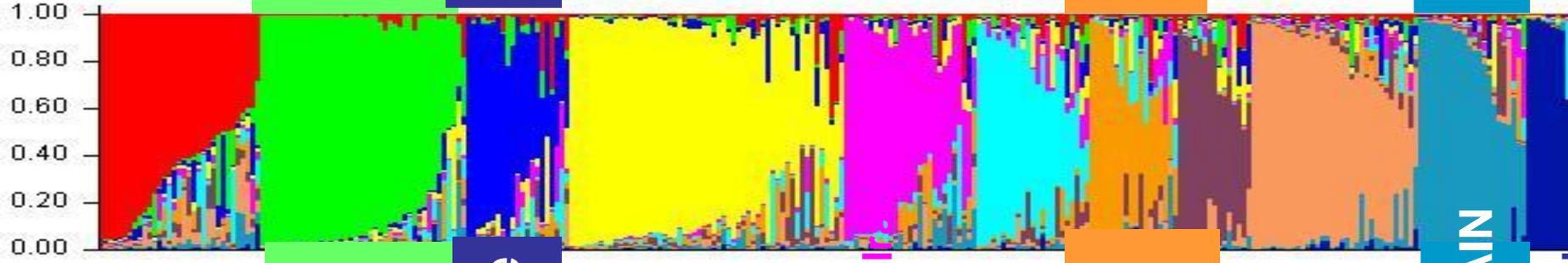
B.o. capitata costata, acephala
Cabbgae, tronchuda cabbage, kale
PORTUGAL SPAIN

2-9

B.o. capitata alba white cabbage SPAIN

B.o. acephala alboglabra – chinese kale

2-11



300 access

3 - Estimation of core collection size

Constant (C) Proportional (P) Logarithmic (L) Maximisation (M) Random (R)

Collection structure

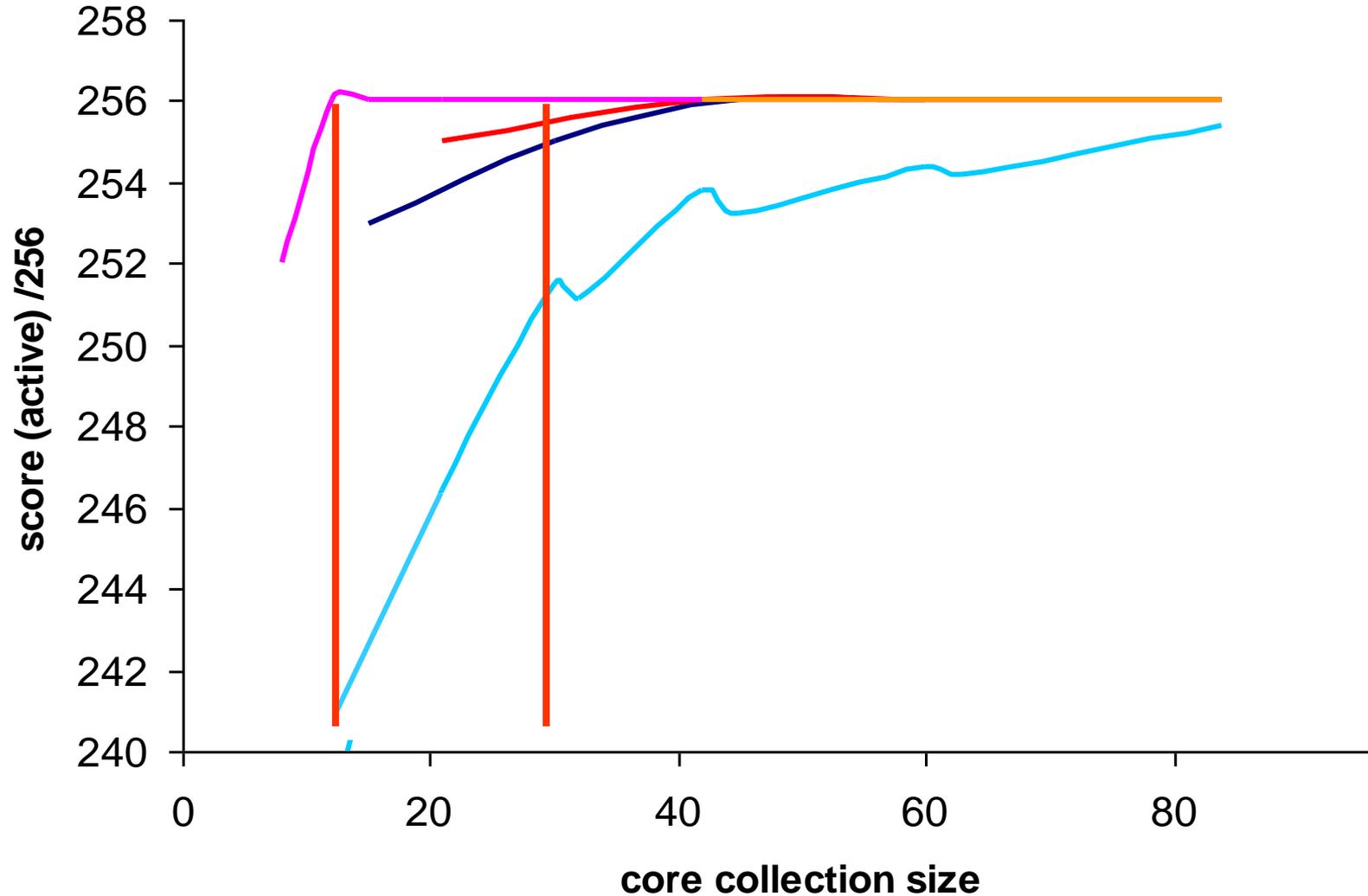
group	size
1-1	16
1-2	13
1-3	13
1-4	18
2-1	33
2-2	42
2-3	21
2-4	56
2-5	27
2-6	23
2-7	18
2-8	15
2-9	34
2-10	22
2-11	9

cc sizes tested



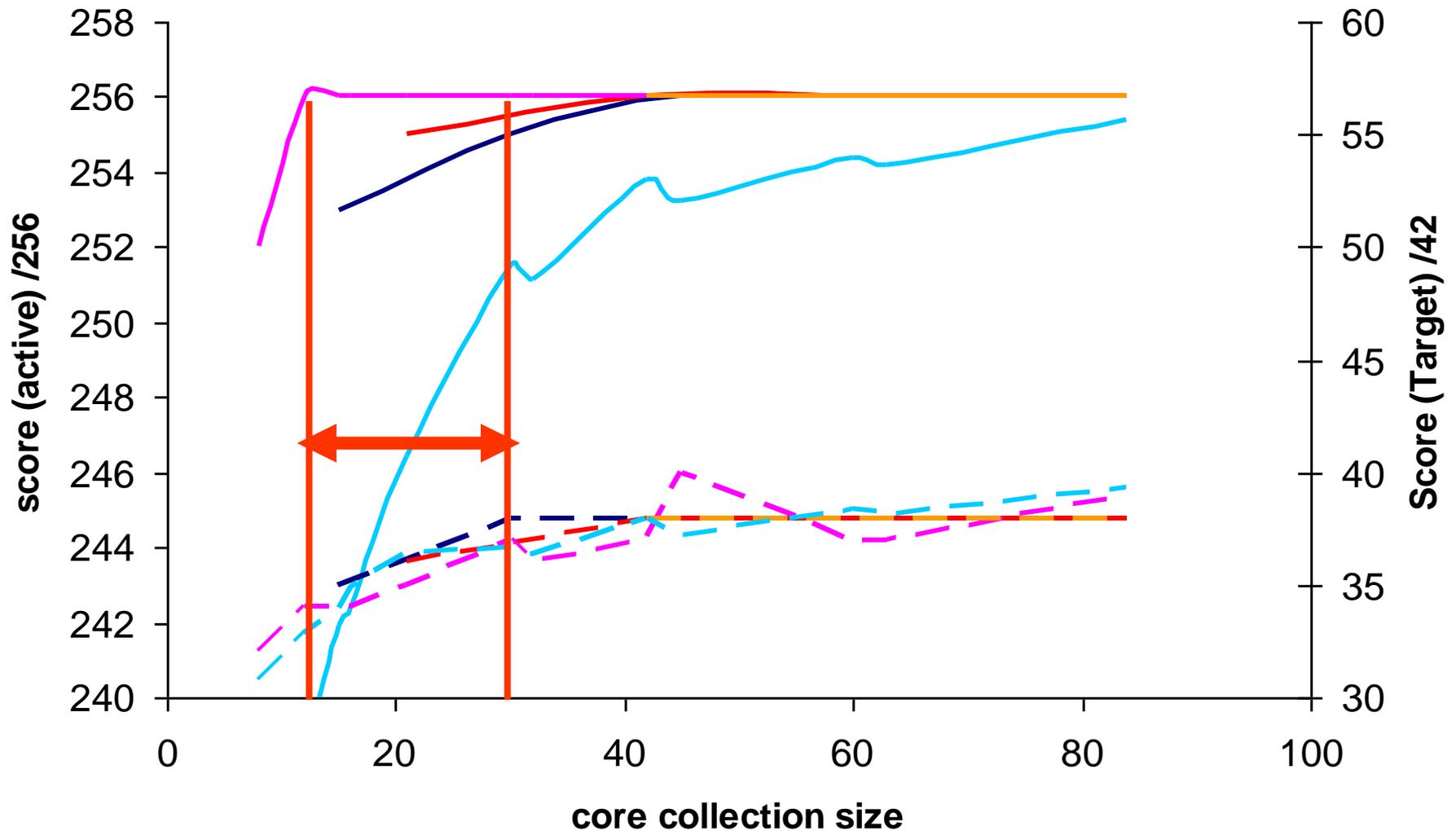
	C	P	L	M	R
8				X	X
15	X			X	X
16				X	X
21			X	X	X
30	X			X	X
32				X	X
42		X	X	X	X
45	X			X	X
60	X			X	X
63			X	X	X
84		X	X	X	X

Allele capture with the different strategies



— C_active — L_active — M_active — P_active — R_active

Towards nested core collections



Perspectives

- ▶ The presented results are preliminary
 - Completed with more SSR
 - Completed with targeted markers such as SNP defined in QTL regions.

- ▶ *B. napus* core collection in 2009

collaborations

- Thanks to genbank curators who provided the seeds
- platform INRA Clermont-Ferrand / GAP Division
- WUR
- Vavilov Plant Institute
- Open to other collaborations



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