



OREGIN Plant Genetic Resources

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THE UNIVERSITY OF
WARWICK



Background

Defra promoting sustainable agriculture

- Disease R
- Reducing inputs - N, water ...
- Climate change
- Product diversification

The performance of a crop is a combination of several factors:

- Agronomy
- Interaction with environment
- Variety - **GENETICS** - manipulated by breeders

Oilseed rape has a relatively narrow genetic base - **allelic canalisation**

But more diversity available within the wider *B. napus* genepool

- Generate diversity collection for *B. napus*
- Adopt *B. napus* mapping population
- Assess allelic diversity with mapped SSR markers



Genomics

Graphical
genotypes

Genetic
markers

Genetic
maps

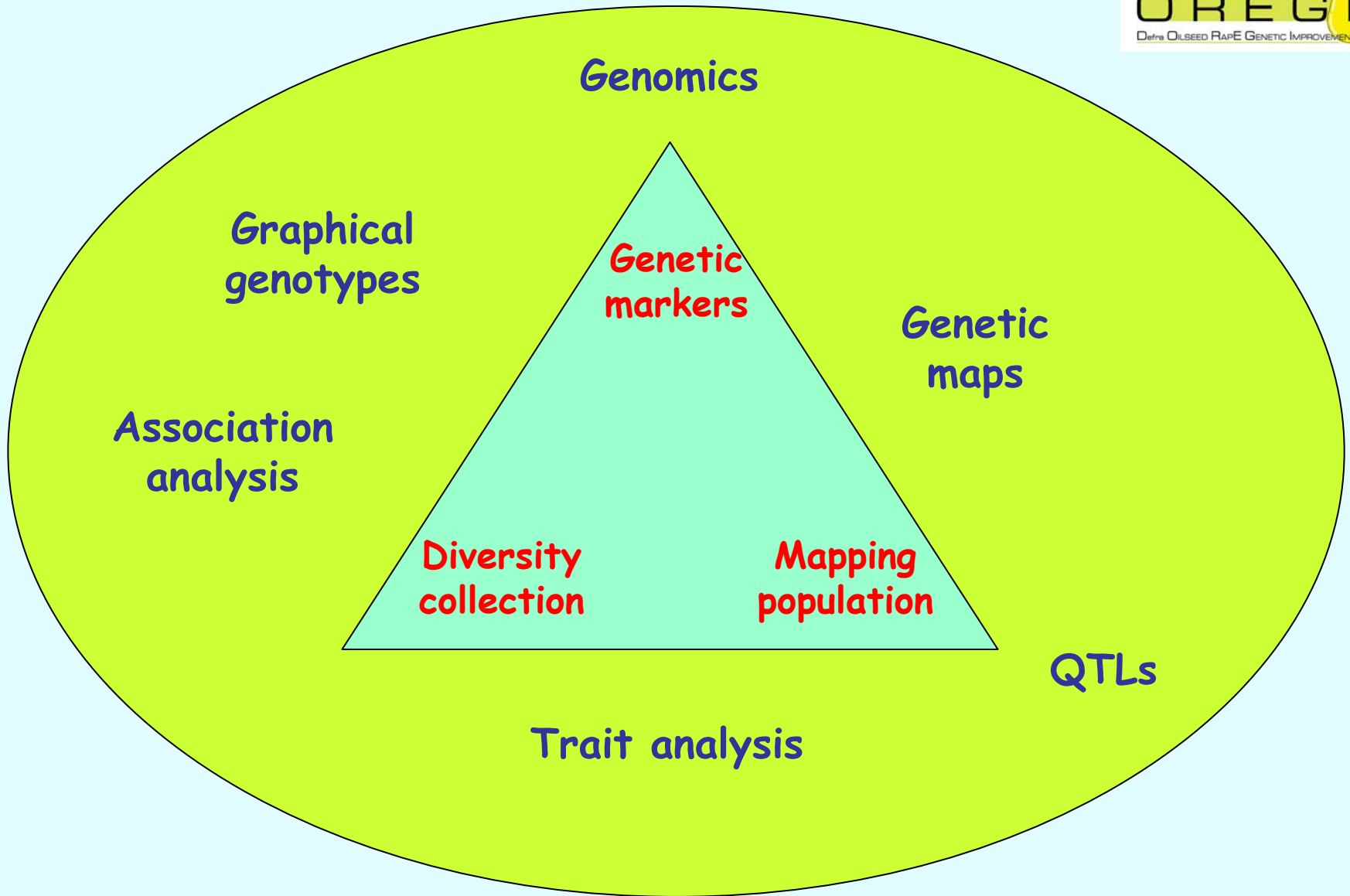
Association
analysis

Diversity
collection

Mapping
population

QTLs

Trait analysis



Rationalising the assessment and use of Biodiversity

Genebanks

Warwick HRI Genetics Resources Unit > 6000 *Brassica* accessions



Core collections

Reference sample representing diversity in *ex situ* collections
However, genetic heterozygosity/heterogeneity within accessions



Diversity Fixed Foundation Sets (DFFS)

Reference sample representing diversity in *ex situ* collections
Genetically homozygous (fixed) immortal lines
High throughput compatible
Public domain

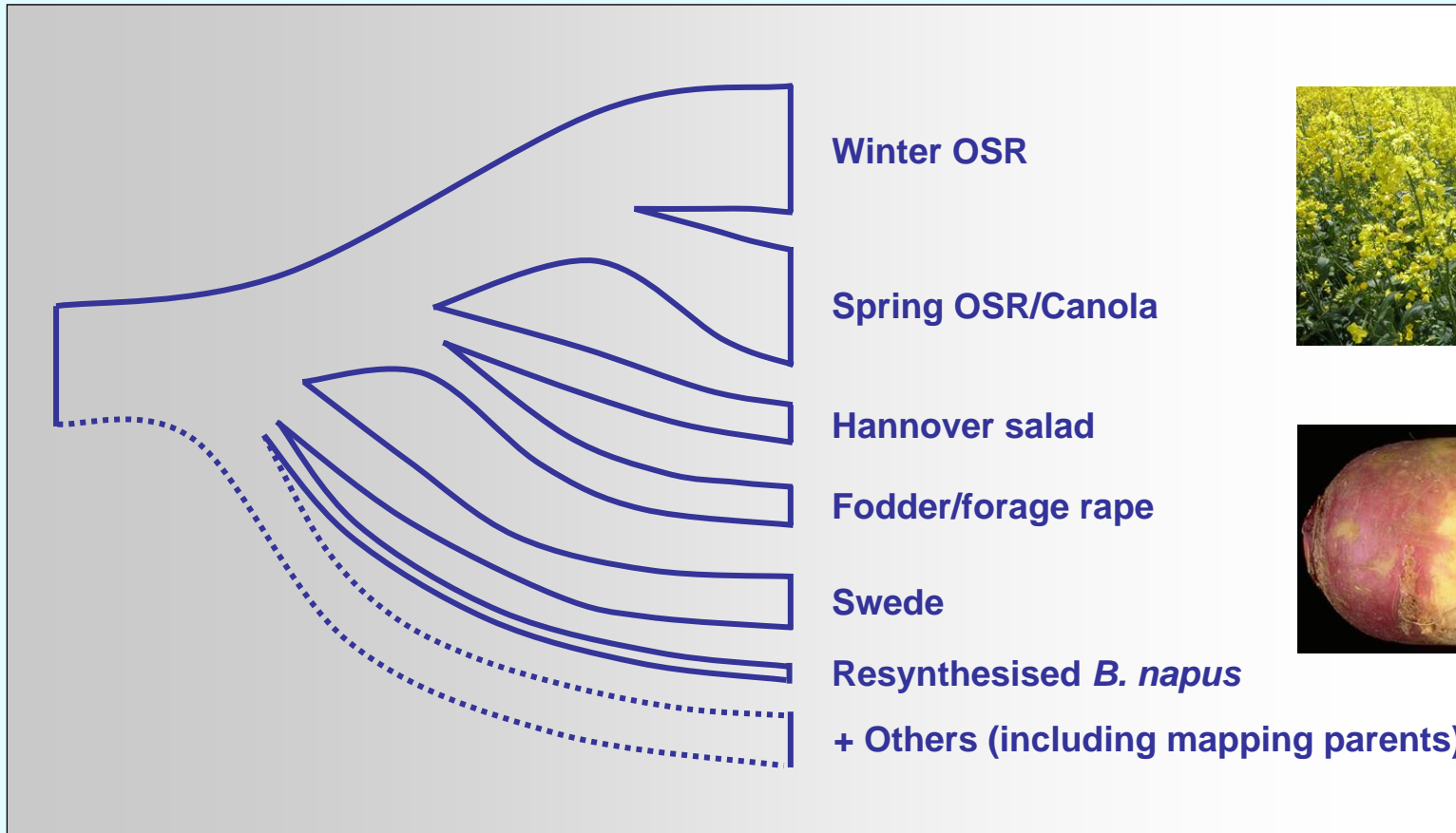
DFFS

A structured set of genetically fixed lines representing a snapshot of diversity across a genepool

- Standard reference sets for diversity analysis
- Organised into representative subsets of 94 lines
- Imortal lines
- Replicated trait testing
- Homozygous alleles in marker assays - allelic surveys
- Seed aliquots archived to ensure long term security



Schematic representation of the diversity available in *B. napus*



BnDFFS progress

- Based on EU **GENRES** collection
- Content review last year
- 38 fixed lines donated, including:
 - Mapping population parents
- Bulking up seed of founder plants
- GenomiPhi™ amplified DNA aliquots available for founder lines
- Ploidy testing being performed on some founder lines
- Microspore culture in progress

Diversity Fixed Foundation Sets

Genetic resource accessions (1000s)



Representative subsets (2x 94 = 188)



Founder plants



Archive:
DNA
seed



Fix (DH, single seed descent to S6) = **BnDFFS**



Archive:
DNA
seed

Multiply seed, DNA and distribute

***** PUBLIC DOMAIN *****

MTA

- Fixed lines are in the public domain
- Seed for research use only
- Lines can be used for crosses in commercial breeding programmes, subject to the international treaty
- Provided on a cost-recovery basis

DFFSs being generated

B. napus is a recent allotetraploid - likely exhibit less diversity than the older diploid *Brassica* species.



<i>B. napus</i>	188 lines	Defra/OREGIN Graham Teakle, Graham King, Dave Astley, Dave Pink	
<i>B. oleracea</i>	376 lines	Defra/core breeding Graham King, Dave Astley, Dave Pink, Graham Teakle	PUE, Water, Oil content
<i>Brassica C-genome</i> species	94 lines	Defra/core breeding Dave Pink	
<i>B. rapa</i>	???	Wageningen, Wuhan, WHRI Guusje Bonnema	

Mapping

Genetic map → QTL → Genome → Candidate genes

DH Mapping populations

Common name	Cross	Description	Source	Availability
TN	Tapidor x Ningyou 7	Winter x Semi-winter	Meng, China	202 public lines
DY	Darmor- <i>bzh</i> x Yudal	Winter x Spring	Delourme/Renard, INRA Rennes	120 public lines
SD	Stellar x Drakkar	Spring x Spring	Delourme/Renard, INRA Rennes	
DS	Darmor x Samourai	Winter x Winter	Delourme/Renard, INRA Rennes	
N-o-72-8	N-o-1 x N-o-9	Spring x Winter	Lydiate, Canada	
SG	(DH12075 (Westar x Cresor)) x (PSA12 (PS270 x A12DHd))	Spring x Resynth.	Lydiate, Canada	
MS	Major x Stellar	Winter x Spring	Osborn, USA	
	Mansholt x Samourai	Winter x Winter	Ecke, Germany	
	Sollux x Gaoyou		Ecke/Becker, Germany	

TN Mapping Population - EU IMSORB

Jinling Meng, China
Ian Bancroft, JIC



Tapidor

- Winter
- OO
- France
- TAC/BAC libraries

X

Ningyou-7

- Semi-winter
- ++
- China



201 DH lines

188 lines selected - seed + DNA
50 informative lines - bulk seed
IMSORB map near completion
QTL data accumulating

***** PUBLIC DOMAIN *****

Full details at:
<http://brassica.bbsrc.ac.uk/IMSORB/>



SSR markers



Simple Sequence Repeats (microsatellites) e.g. TATATATATATATA

- Highly polymorphic
- Sequence tagged - relate to genomic sequence
- Select SSRs distributed over the genome and in public domain

Map in TN population

- Alignment of TN map with other maps (e.g. DY)

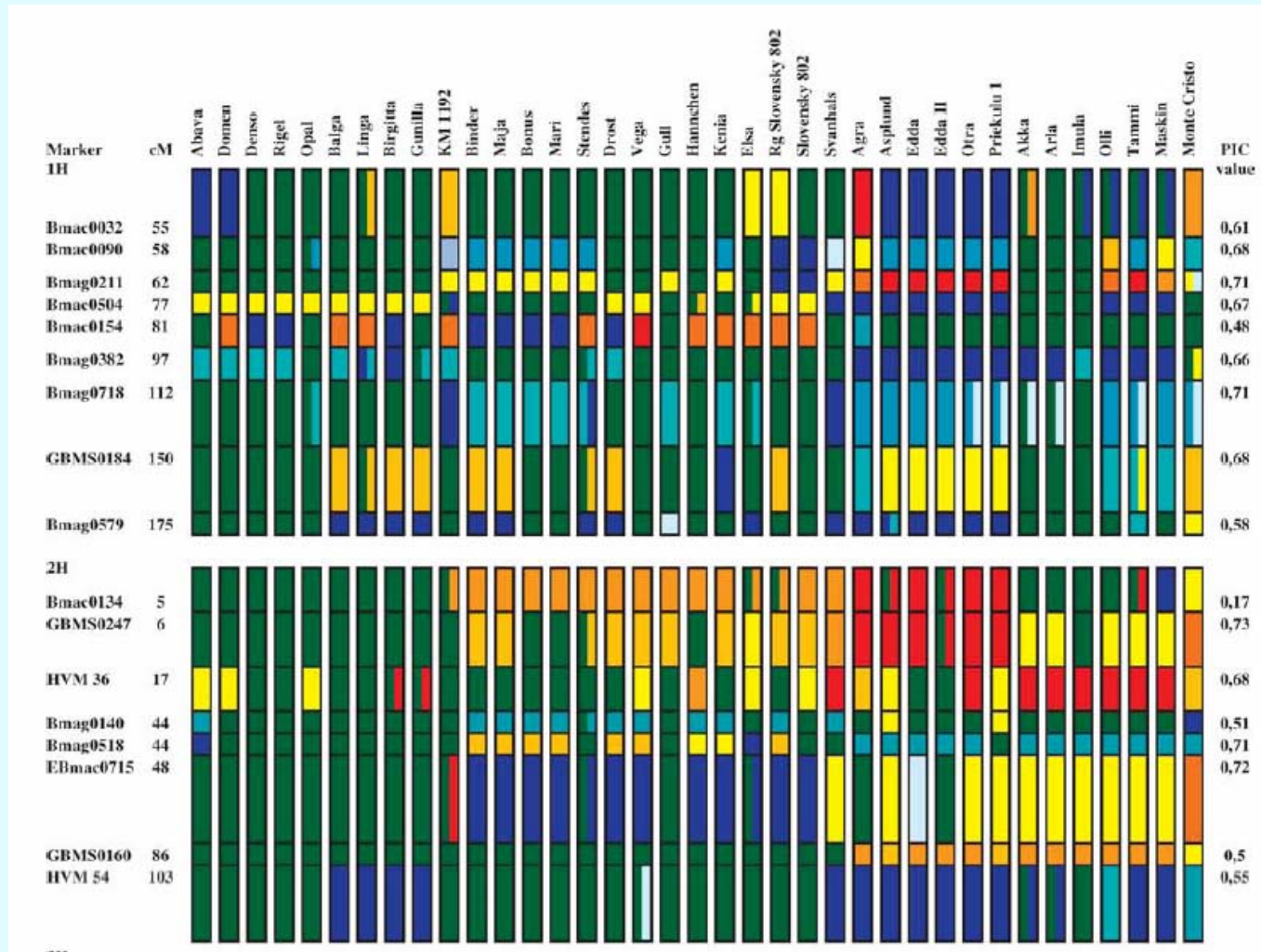
Diversity analysis

- Diversity estimates
- Graphical genotypes
- Association analysis ...

Quality control

	B napus			B. rapa		B. oleracea		Total markers
Markers	TN	DY	N-fo-69	CK	Suwabe	AG	NG	
Mapped	70	43	137	44	21	28	6	168 + TN markers

Example of Graphical Genotypes - Barley



From: T. G. Sjakste, I. Rashal, M. S. Roder (2003) Inheritance of microsatellite alleles in pedigrees of Latvian barley varieties and related European ancestors, TAG 106:539-549



	sORA26	OI12F02	OI10F09	Na12A07	Ra2E12	Na12F12	Na12A02	Na10G10	Na10A08
ApexRICP	3	3	2		2			2	2
ArianaCGN	2	3	2		1			4	3
AsahiRICP	2	5	2		3			2	5
BienvenuCGN	2	2	2		2			1	2
BristolCGN	2	2	2		2			1	2
BronowskiBAZ	3	3	2		2			2	3
CapitolRICP	3	2	2		1			2	2
CapricornCGN	2	2	1		2				2
CeresCGN	2	5	2		2			1	3
CobraCGN	3	3	2		1			1	
CometNGB	3	3	2					4	
DarmorBAZ	2	2	1					1	2
ElenaBAZ	2		2	4	1		4	2	3
EnvolRICP	2		2	4	2		3	7	3
FalconCGN	1			4	2		3	4	3
GazelleNGB	1		2	4	2		3	3	3
GlobalCGN	2		2	3	1		2	2	3
GulleBAZ	2		2	3	2		3	1	2
GulzowerBAZ	3		2	4	3		4	2	5
HannaCGN	2		1	3	1		2	3	2
HectorBAZ	3		2	4	3		2	2	4
HermesBAZ	2		2	4	2		2	1	3
JadeBAZ	2		2	4	1		2	2	3
KajsaiPK	2		2	3	1		3	3	2
KaratBAZ				5	1	3	2	3	3
LedosBAZ				5	1	3	2	2	2
LembkesRICP				4	2	3	3	2	5
LenoraBAZ				3	1	3	3		2
LibravoCGN				4	1	3	5	2	3
LictorBAZ				5	2	3	2	2	3
LictorIPK				5	2	3	3	2	4
LiholPK				4	2	3	3	3	2
LindoraBAZ				5	1	3	2	2	2
MajorBAZ				4	3	3	3	1	4
MarinkaNGB				5	1	3	2	2	3
MatadorBAZ				4	1	3	3	2	4
MikadoRICP		2		3	1	3	2	1	2
NavajoRICP		3		5	1	3	2		3
NiklasBAZ		4		4	1	3	2	4	3
NuggetBAZ		2		3	2	5	2	2	2
OroBAZ		2		3	1	3	2	3	2
PrimorBAZ		3		3	2				
QuintaBAZ		3		4	1	3	3		3
RafalBAZ		2		2	1	1	2	1	2
RapoIBAZ		3		3	2	3		2	3
RaporaRICP		4		4	2	3	3	3	3
ReginalPK		4		5	2	3	3	5	5
SamouraiCGN		2		5	2	3	2	1	2

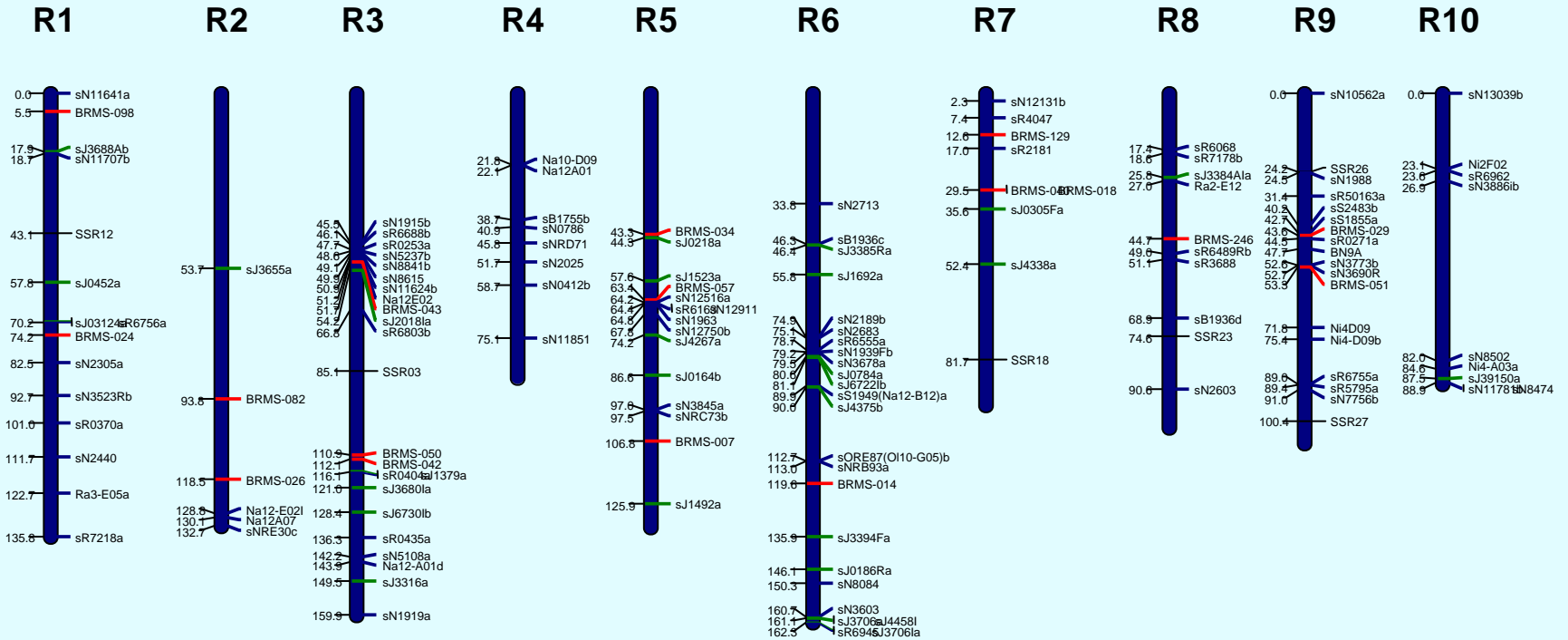
Within line variation in
48 *B. napus* accessions

8 plants per accession
genotyped

By Charlotte Allender,
WHRI

 All lines the same

SSR markers on the *B. rapa* CK map



Blue markers link to *B. napus* map

Green markers link to *B. juncea* map

Red markers link to the *B. rapa* map of Suwabe et al (2002)¹

Seed Requirement Survey

Distributed to OREGIN mailing list

		BnDFFS set 1	BnDFFS set 2	TN-50	TN-188	Comments
Neal Evans	RRES	15-20 g	15-20 g	15-20 g		
Renhu Liu	RRES				10 seed starter	
Colin Morgan	JIC	10 seed	10 seed			
Judith Irwin	JIC	10 seed	10 seed			
Matthew Hills	JIC	10 seed		10 seed		
Joanna Vicnete	WHRI	1 g	1 g			Dependent on funding
Tony Larson/Ian Graham	York	1 g	1 g		1 g	
Peter Berry	ADAS	20-30 g	20-30 g		20-30 g	Dependent on funding
Matthew Nelson	Univ. Western Australia	y	y		y	
Xiao-Ming Wu	Wuhan, China	y	y			
Joel Piquemal	Euralis Semences				y	

Also replies from Richard Jennaway and Jo Bowman – they would most likely use collections as part of collaboration
Collaborators would most likely request the seed