

Development of Clubroot Resistant Canola *Brassica napus* Germplasm



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Clubroot Resistance

Brassica napus
Brassica rapa
Brassica oleracea
Other Brassica sp.



Available
resistance,
and
search for
new
resistance



Introgression
of resistance
into canola
Brassica napus

Understand the genetic control of resistance



Identification of molecular
markers

Clubroot Resistance

- Resistance from *B. napus*
- Resistance from its parental species
 - Resynthesis of *B. napus*

Resistance from winter canola *B. napus*

Crosses and Screening for resistance in F₂

Cross #	Cross	HT type	# flowering plants*	# Resistant	# Susceptible	% Resistant
C590	Mendel x A02-22525	C	95	18	77	18.9
C591	Mendel x A02-22707	C	170	27	143	15.9
C591	Total	C	265	45	220	17.0

Clubroot resistance, agronomic and seed quality properties of the 77 F₅ families field tested in 2008

Clubroot resistance and agronomic characters:

Cross no. ¹	No. fam.	No. non-segr. R	% non-segr. R	Clubroot resistance ²			Days to flower			Days to maturity		
				No. fam	Range	Mean ± S.E.	No. fam	Range	Mean ± S.E.	No. fam	Range	Mean ± S.E.
C590	35	24	68.6	35	0.0 - 3.0	0.43 ± 0.15	35	44 - 52	47.1 ± 0.4	35	88 - 99	91.7 ± 0.4
C591	42	36	85.7	42	0.0 - 3.0	0.40 ± 0.15	42	43 - 51	46.0 ± 0.3	42	89 - 100	92.6 ± 0.4
Q2	5	0	0.0	5	2.5 - 3.0	2.90 ± 0.10	5	44 - 45	44.2 ± 0.2	5	88 - 89	88.8 ± 0.2
46A65	4	0	0.0	4	3.0 - 3.0	3.00 ± 0.00	4	44 - 45	44.5 ± 0.3	4	88 - 89	88.8 ± 0.3
C590	41	33	80.5	41	0.0 - 3.0	0.33 ± 0.12	31	45 - 53	50.7 ± 0.4			
C591	55	43	78.2	55	0.0 - 3.0	0.29 ± 0.09	44	43 - 53	49.3 ± 0.4			
Q2	9	0	0.0	9	0.0 - 3.0	1.40 ± 0.44	9	42 - 49	46.7 ± 0.9			
46A65	9	0	0.0	9	0.0 - 3.1	0.53 ± 0.37	9	41 - 46	44.4 ± 0.6			

Clubroot resistance, agronomic and seed quality properties of the F₅ families field tested in 2008

Seed quality characters:

Cross no.	No. fam seed	% Oil (whole seed, dry)			% Protein (whole seed, dry)			GLS (whole seed, 8.5% H ₂ O)			Saturated fatty acid (% of total fatty acids)		
		No. fam	Range	Mean ± S.E.	No. fam	Range	Mean ± S.E.	No. fam	Range	Mean ± S.E.	No. fam	Range	Mean ± S.E.
C590	35	30	45.0 - 52.7	48.9 ± 0.4	30	20.2 - 26.9	23.1 ± 0.3	30	7.3 - 15.8	11.6 ± 0.4	26	6.6 - 8.0	7.26 ± 0.07
C591	42	37	45.9 - 55.8	51.7 ± 0.4	37	18.2 - 26.0	21.4 ± 0.3	37	8.1 - 16.2	11.7 ± 0.3	29	6.2 - 7.4	6.85 ± 0.05
Q2	5	5	50.3 - 52.1	51.2 ± 0.4	5	20.3 - 23.2	21.6 ± 0.6	5	8.4 - 13.0	10.6 ± 0.8	5	7.2 - 7.3	7.20 ± 0.02
46A65	4	4	50.8 - 53.2	52.5 ± 0.6	4	21.2 - 24.8	22.4 ± 0.8	4	12.8 - 14.1	13.7 ± 0.3	4	6.8 - 7.0	6.90 ± 0.03
C590	41	28	43.0 - 55.9	48.3 ± 0.5	28	19.6 - 28.7	23.9 ± 0.4	28	11.1 - 22.1	16.7 ± 0.5	7	6.5 - 7.3	6.91 ± 0.10
C591	55	40	43.6 - 53.0	48.8 ± 0.4	40	18.2 - 28.5	23.1 ± 0.4	40	11.6 - 28.6	17.2 ± 0.6	12	6.1 - 7.1	6.40 ± 0.07
Q2	9	9	45.3 - 52.4	49.5 ± 0.7	9	20.1 - 26.4	22.6 ± 0.6	9	12.3 - 17.9	14.5 ± 0.6	2	6.8 - 6.9	6.84 ± 0.01
46A65	9	9	47.1 - 52.3	50.2 ± 0.6	9	21.8 - 26.0	23.8 ± 0.5	9	14.6 - 17.3	16.2 ± 0.3	2	6.6 - 6.7	6.65 ± 0.09

Evaluation of conventional F₆ families in greenhouse for clubroot resistance

Cross	No. selected F ₅ families	Total F ₆ families ¹	No. homozygous families	% Homo families	No. segregating families	% Segr. families
C590	4	14	13	92.9	1	7.1
C591	20	75	63	84.0	12	16.0
Total	24	89	76	85.4	13	14.6

¹From each family, 8 plants were tested for CR. Total plants tested = 89 x 8 = 712 plants

These families can be used in further breeding



Mapping the Mendel resistant gene(s)

Brassica

B. oleracea,
 $2n = 18$
Cabbage
Cauliflower
Broccoli
Kale
Kohlrabi
Brussels sprouts

CC

B. carinata,
 $2n = 34$
Abyssinian mustard

BBCC

B. napus,
 $2n = 38$
Rutabaga
Oil rape

AACC

B. nigra,
 $2n = 16$
Black mustard

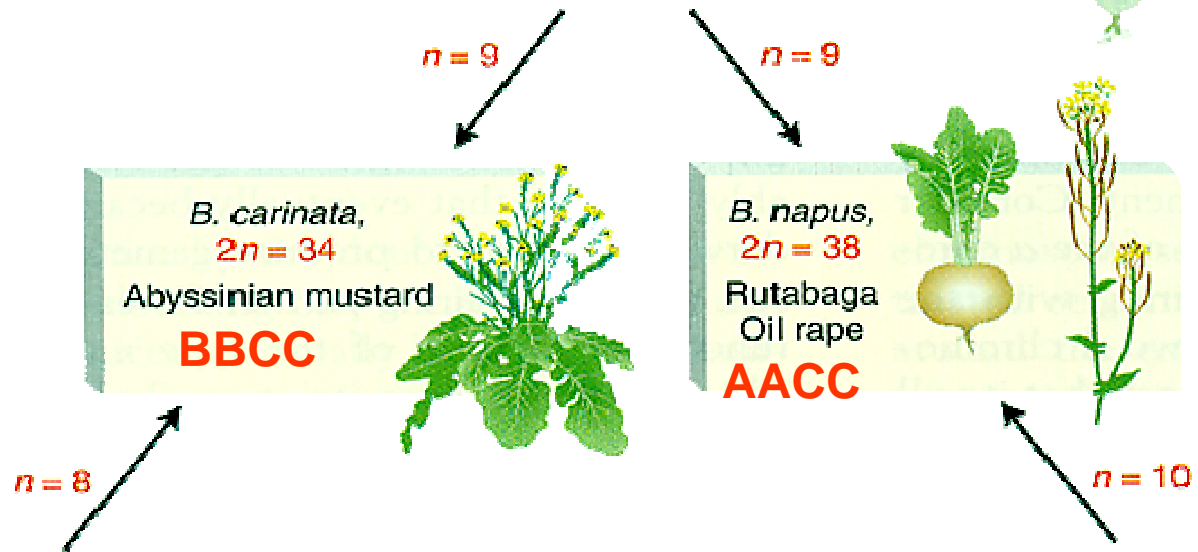
BB

B. juncea,
 $2n = 36$
Leaf mustard

AABB

B. rapa
 $2n = 20$
Chinese cabbage
Turnip
Turnip rape

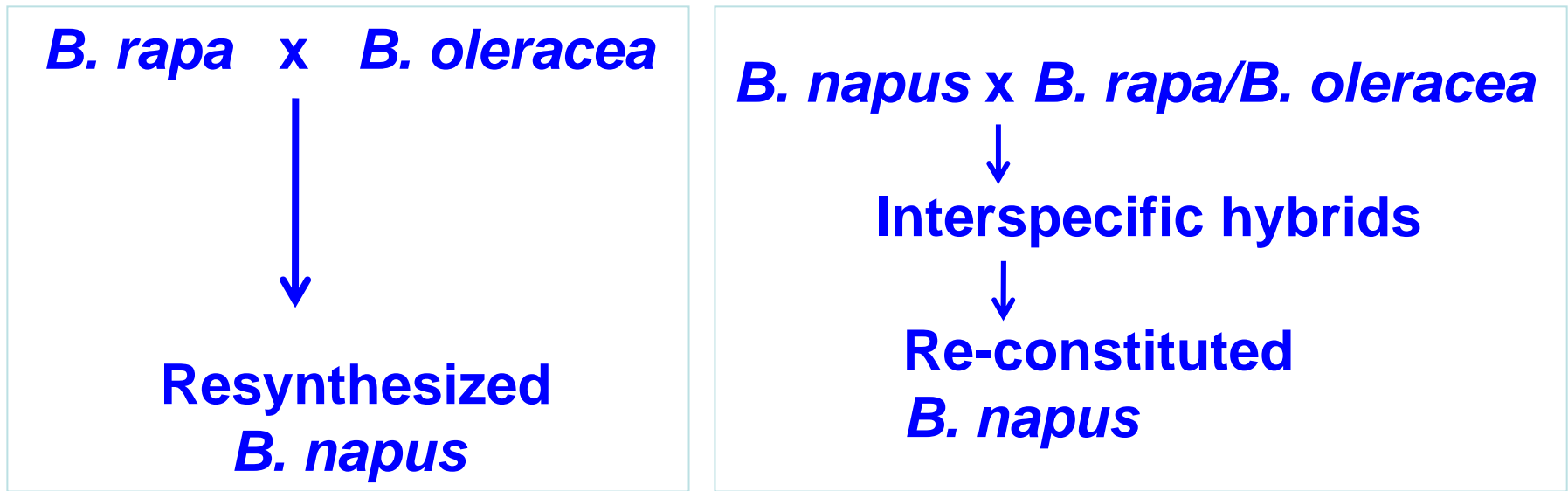
AA



Evaluation of germplasm for resistance to Clubroot

Name	# accession collected
<i>Brassica napus</i>	46
<i>Brassica juncea</i>	27
<i>Brassica carinata</i>	8
<i>Brassica villosa</i>	1
<i>Brassica oleracea</i>	100
<i>Brassica rapa</i>	59
<i>Raphanus sativus</i>	13
Total	254

Introgression of resistance from *B. rapa* and *B. oleracea* through resynthesis of *B. napus* and through interspecific hybridization



Agronomic and seed quality improvement

Mapping the resistant gene(s)

Screening for clubroot resistance



Susceptible

Moderate R

Resistant

Screening for clubroot resistance



Susceptible



Moderate R



Resistant

Screening for clubroot resistance



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