Resistance to turnip yellows virus (TuYV) in vegetable brassicas

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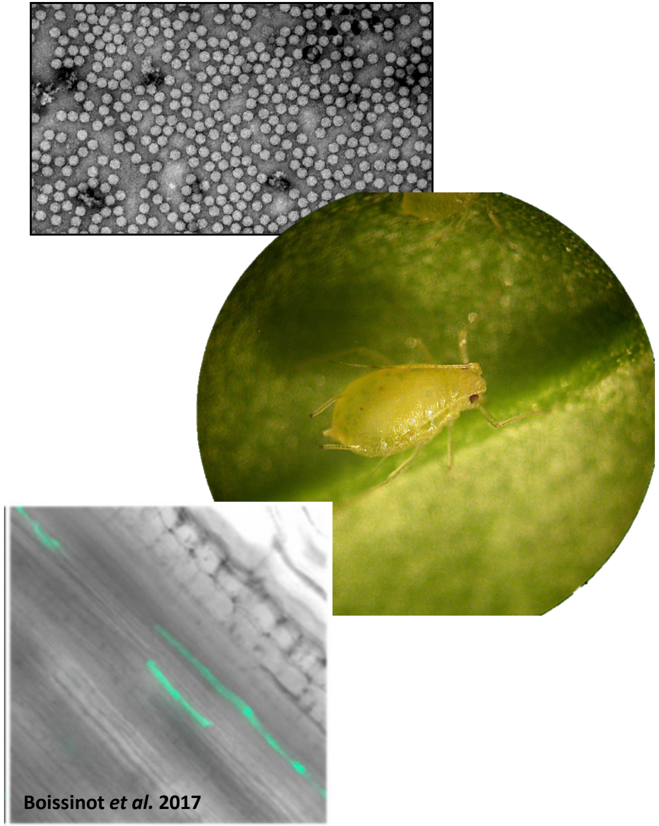
1 Dec 2021 / VeGIN Stakeholders Webinar

Turnip yellows virus (TuYV)

- Turnip yellows virus (TuYV) was previously known as beet western yellows virus (BWYV)
- RNA virus
- It has ‘spherical’ particles
- Transmitted from plant to plant by aphids, peach-potato aphid *Myzus persicae* is the major vector Europe
- Phloem limited



Boissinot *et al.* 2017

Symptoms of TuYV infection

- Most of the time it causes few distinct, or no noticeable symptoms

- TuYV is common in oilseed rape
  - Up to 100% detection in field
  - Overwintering reservoir

- Reduction of 16-22% harvestable yield in cabbage
  - Causes tipburn

- Reduction of up to 65% harvestable yield in Brussel sprouts

Incidence of TuYV

- High incidence of TuYV throughout UK, *e.g.*, 100% in 2009
- Maximum incidence of 100% in Germany and Poland

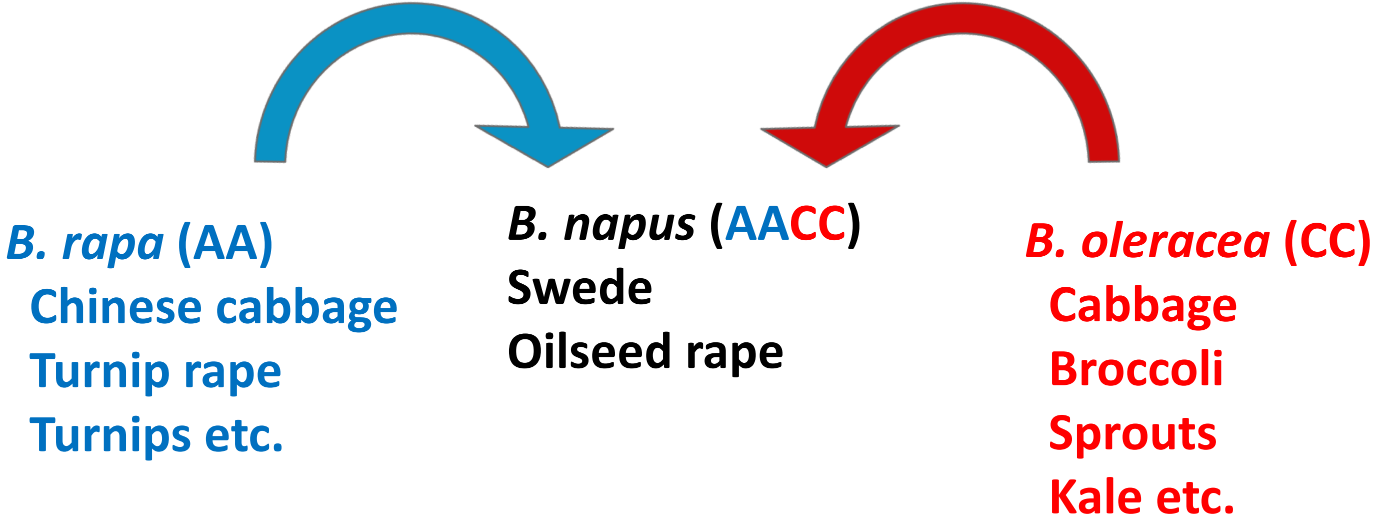
Incidence of TuYV within UK

Year	Maximum incidence
2007	89%
2008	24%
2009	100%
2012	76%
2013	92%
2014	32%
2015	74%

Incidence of TuYV within 6 European countries

Country	Maximum incidence
France	93%
Belgium	66%
Germany	100%
Denmark	77%
Ukraine	30%
Poland	100%

Strategy for utilization of TuYV-resistance sources



B. rapa (AA)
Chinese cabbage
Turnip rape
Turnips etc.

B. napus (AACC)
Swede
Oilseed rape

B. oleracea (CC)
Cabbage
Broccoli
Sprouts
Kale etc.

Sources of resistance to TuYV in *Brassica rapa*

Forest and Kim Starr

thebittenword.com

Screening *Brassica rapa* subspecies for resistance to TuYV

Brassica rapa subspecies	**Susceptible**	**Resistant**	**Marginal**	**Total**	**TuYV isolate**
ARB4 1-10	8	0	1	9	Clade 1
ARB4 11-20	9	0	0	9	Clade 1
ARB4 21-30	7	0	2	9	Clade 1
ARB4 31-40	7	0	1	8	Clade 1
ARB4 41-50	9	0	0	9	Clade 1
ARB4 51-60	5	0	2	7	Clade 1
ARB4 61-70	7	0	2	9	Clade 1
ARB4 71-80	9	0	0	9	Clade 1
ARB4 81-90	0	8	1	9	Clade 1
ARB4 91-100	1	5	3	9	Clade 1
ARB4 101-110	7	0	1	8	Clade 1
ARB4 111-120	9	0	0	9	Clade 1
ARB4 121-130	9	0	0	9	Clade 1
ARB4 131-140	4	0	0	4	Clade 1
R-o-18	9	0	0	9	Clade 1
ARB4 151-160	4	0	4	8	Clade 1
ARB4 91-100	0	7	0	7	Clade 2
ARB4 81-90	0	6	1	7	Clade 2

B. rapa mapping population pedigree

B. rapa trilocularis; Susceptible to TuYV

R-o-18 X TuYV resistant ARB4 81-90

F_1

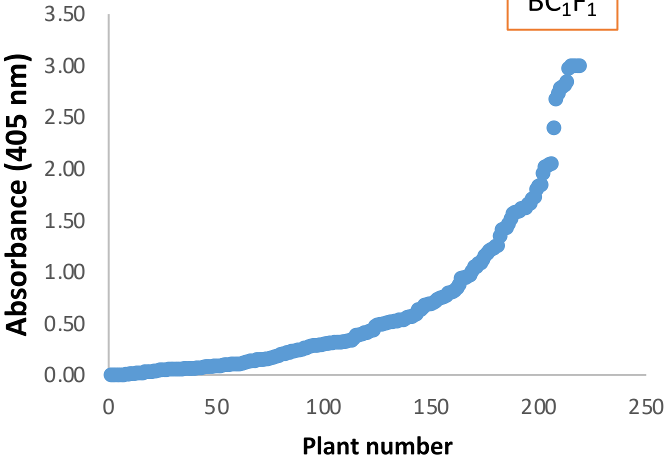
All F_1 plants tested were resistant; R is dominant

R-o-18 X F_1

BC_1F_1

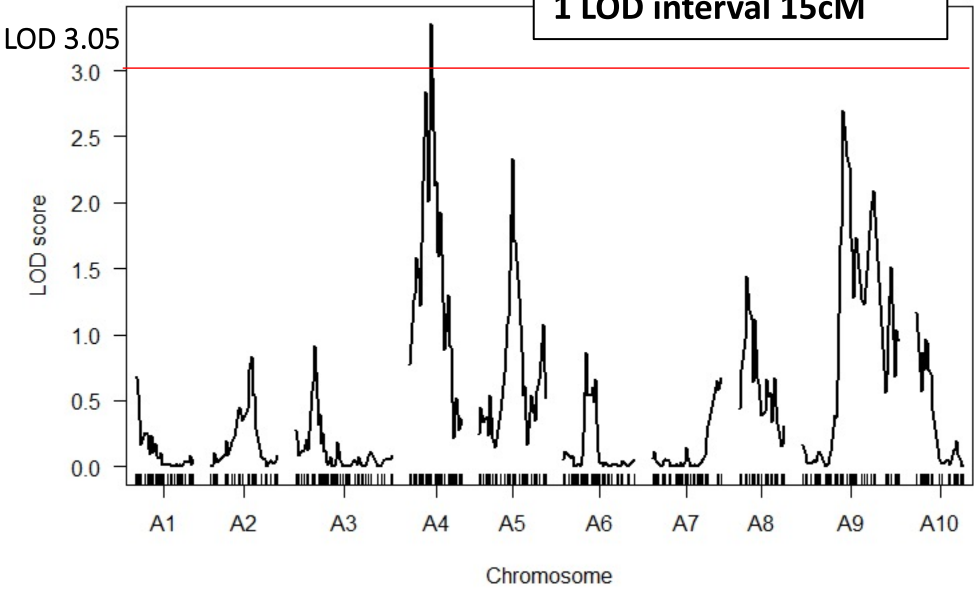
Mapping population; 200 plants phenotyped for TuYV resistance; 48 plants genotyped

- Genotyping conducted on the Illumina Infinium 60k array
- Generated 23,004 raw markers
- Rigorous filtering – 2431 markers remained
- Minimal number of 352 markers used in final QTL map

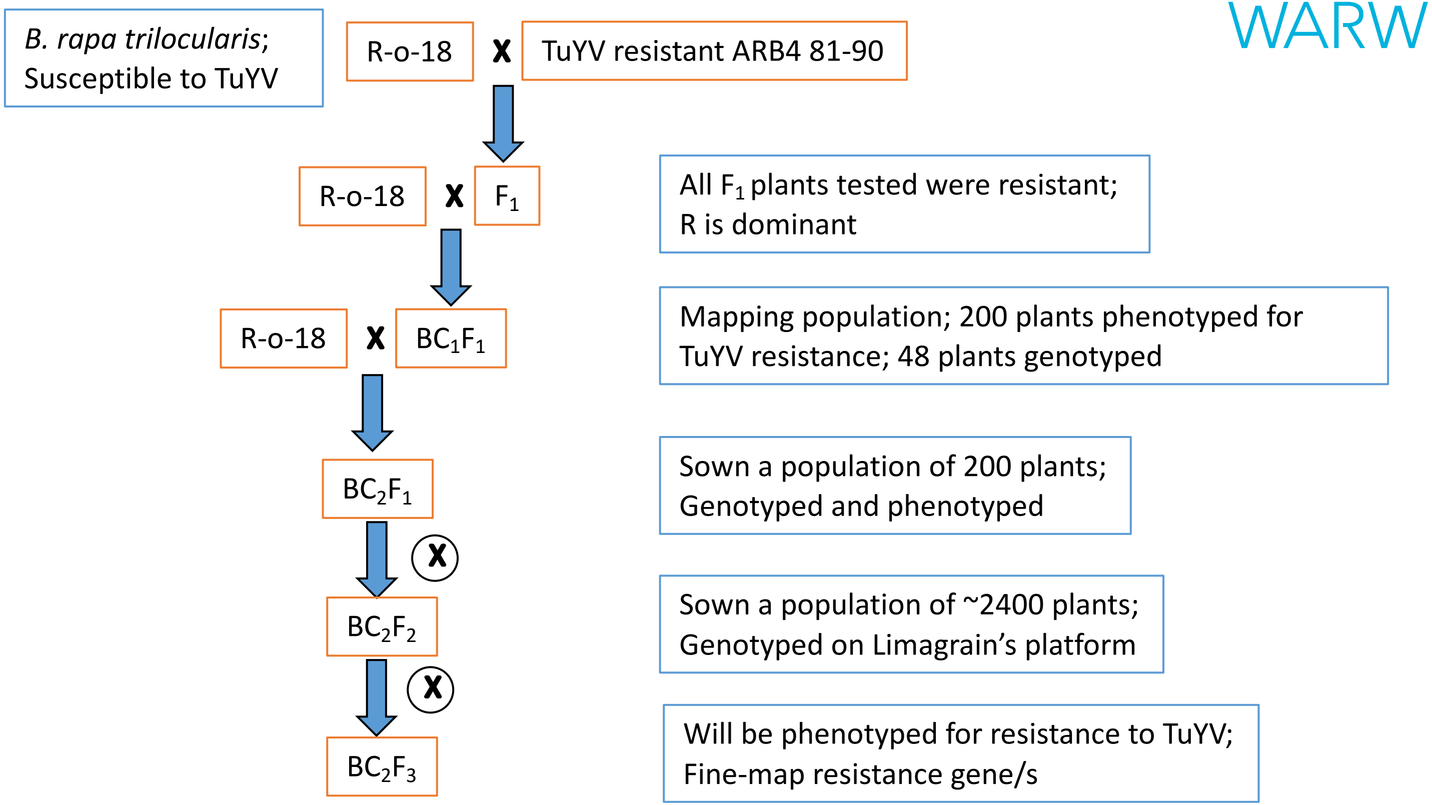


Major QTL found on A04 in *B. rapa* mapping population

Chromosome A04
22% variation explained
1 LOD interval 15cM



B. rapa mapping population pedigree



B. rapa trilocularis; Susceptible to TuYV

R-o-18 X TuYV resistant ARB4 81-90

R-o-18 X F_1

All F_1 plants tested were resistant; R is dominant

R-o-18 X BC_1F_1

Mapping population; 200 plants phenotyped for TuYV resistance; 48 plants genotyped

BC_2F_1

Sown a population of 200 plants; Genotyped and phenotyped

Ⓧ

BC_2F_2

Sown a population of ~2400 plants; Genotyped on Limagrain’s platform

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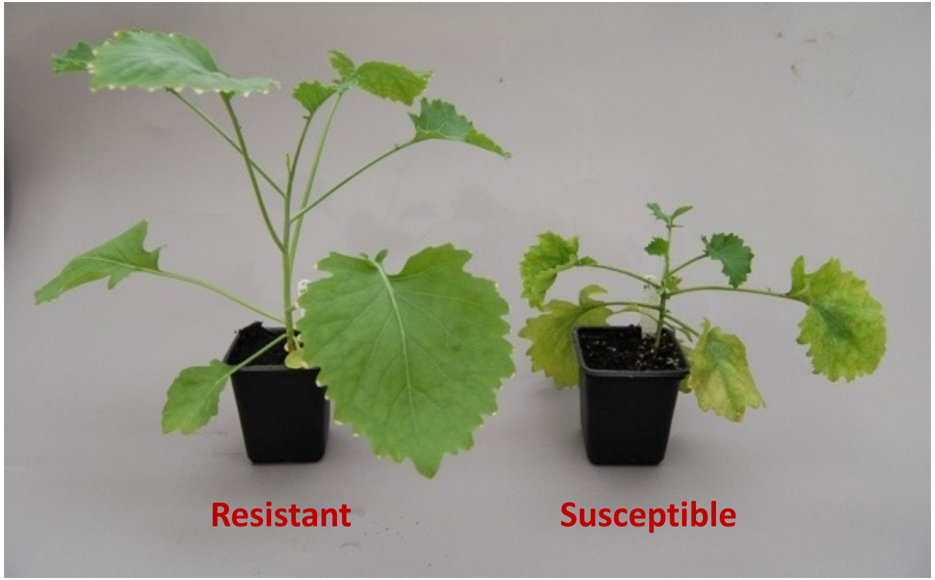
BC_2F_3

Will be phenotyped for resistance to TuYV; Fine-map resistance gene/s

Sources of resistance to TuYV in *Brassica oleracea*



B. oleracea following challenge with TuYV

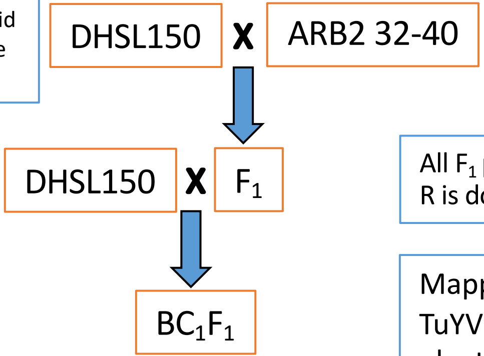
Myzus persicae feeding on resistant *B. oleracea*

Screening wild *B. oleracea* lines for TuYV resistance

Line	Susceptible	Resistant	Marginal	Total	TuYV isolate
DHSL150	7	0	1	8	Clade 2
ARB2 32-40	0	9	0	9	Clade 2
ARB2 42-50	0	9	0	9	Clade 2
ARB2 52-60	0	8	0	8	Clade 2
TO1000	10	0	0	10	Clade 1
JWBo1	6	3	0	10	Clade 1
JWBo2	10	0	0	10	Clade 1
JWBo3	10	0	0	10	Clade 1
JWBo4	10	0	0	10	Clade 1
JWBo5	9	1	0	10	Clade 1
JWBo6	0	8	0	8	Clade 1
JWBo7	6	4	0	10	Clade 1
JWBo8	10	0	0	10	Clade 1
JWBo9	7	3	0	10	Clade 1
JWBo10	3	6	0	10	Clade 1
JWBo11	6	4	0	10	Clade 1
JWBo12	6	4	0	10	Clade 1
JWBo13	2	8	0	10	Clade 1
JWBo14	10	0	0	10	Clade 1

B. oleracea ARB2 mapping population pedigree

DH line from 'Green Duke' crossed with rapid cycling line; Susceptible to TuYV

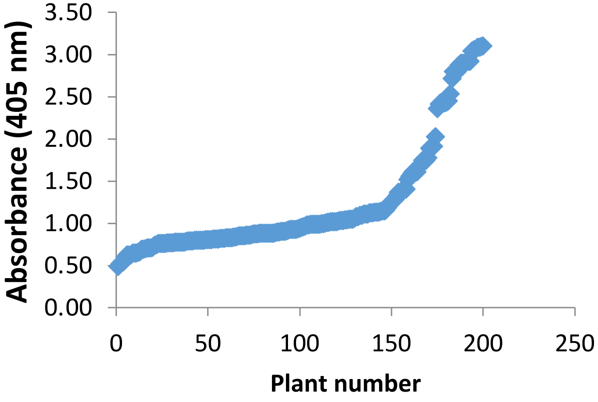

DHSL150 X ARB2 32-40

DHSL150 X F_1

BC_1F_1

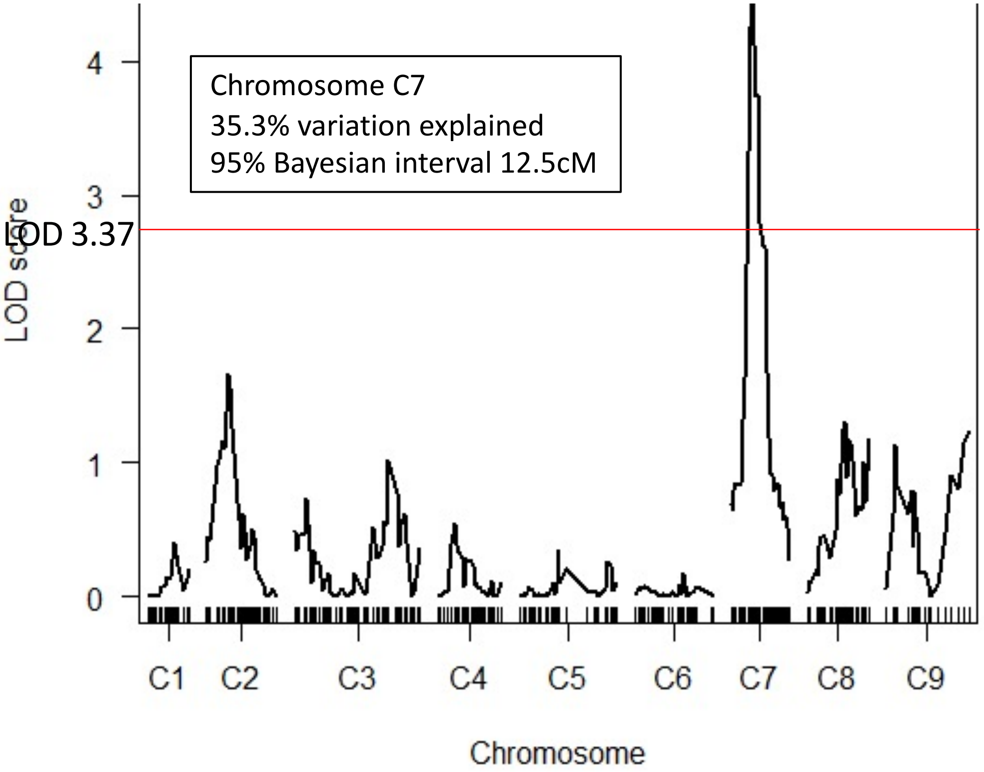
All F_1 plants tested were resistant; R is dominant

Mapping population; 200 plants phenotyped for TuYV resistance; 40 plants genotyped; 200 BC_1 plants genotyped with 30 KASP spread across C2, C7 and C8



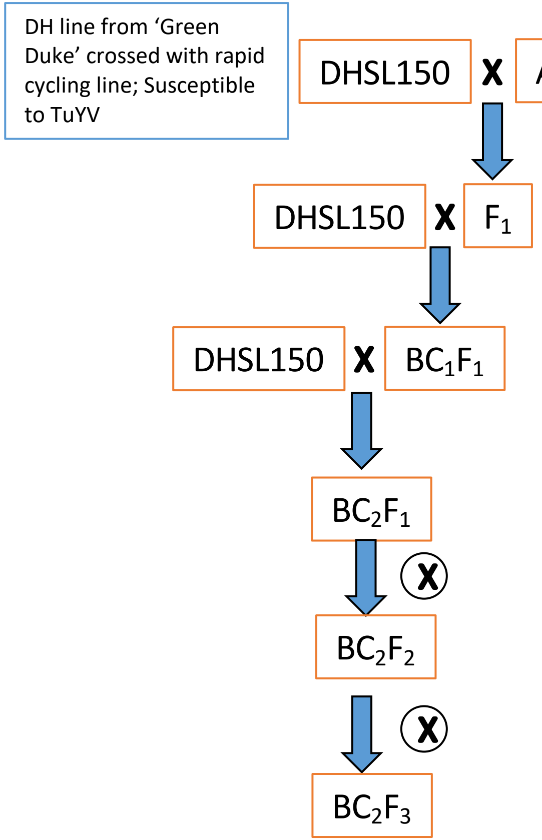
- Genotyping conducted on the Illumina Infinium 60k array
- Generated 24,775 raw markers
- 6956 markers were polymorphic between parents
- Minimal number of 253 markers used in final QTL map

Major QTL found on C07 in *B. oleracea* ARB2



Chromosome C7
35.3% variation explained
95% Bayesian interval 12.5cM

B. oleracea ARB2 mapping population pedigree



DH line from ‘Green Duke’ crossed with rapid cycling line; Susceptible to TuYV

27 F_1 plants tested; all resistant;
R is dominant

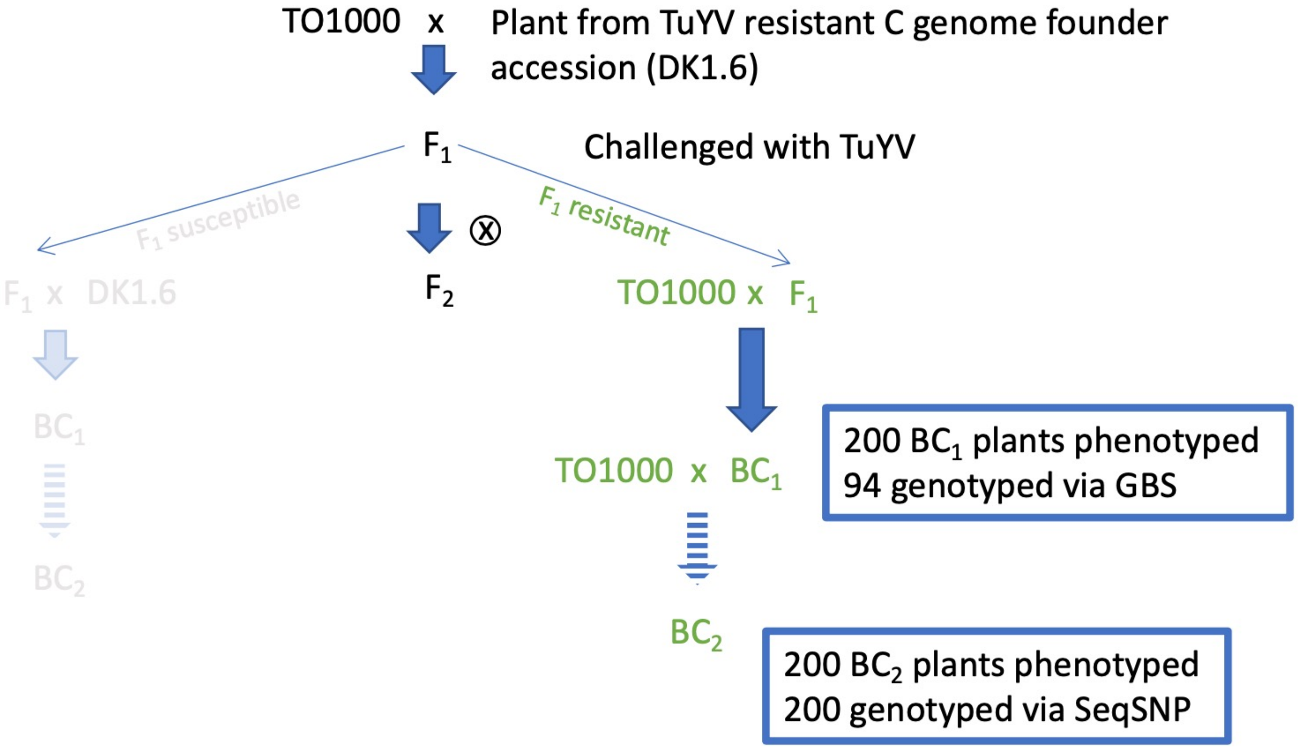
Mapping population; 200 plants tested v’s TuYV; 40 plants genotyped – Infinium 60k; 200 plants genotyped with 30 KASP

Sown a population of 200 plants;
Genotyped and phenotyped

Sown a population of ~4000 plants;
Genotyped using Syngenta’s platform

Will be phenotyped for resistance to TuYV;
Fine-map resistance gene/s

B. oleracea JWBo1 mapping population pedigree



TO1000 x Plant from TuYV resistant C genome founder accession (DK1.6)

F_1 Challenged with TuYV

F_1 susceptible

F_1 x DK1.6

BC_1

BC_2

⊗

F_2

F_1 resistant

TO1000 x F_1

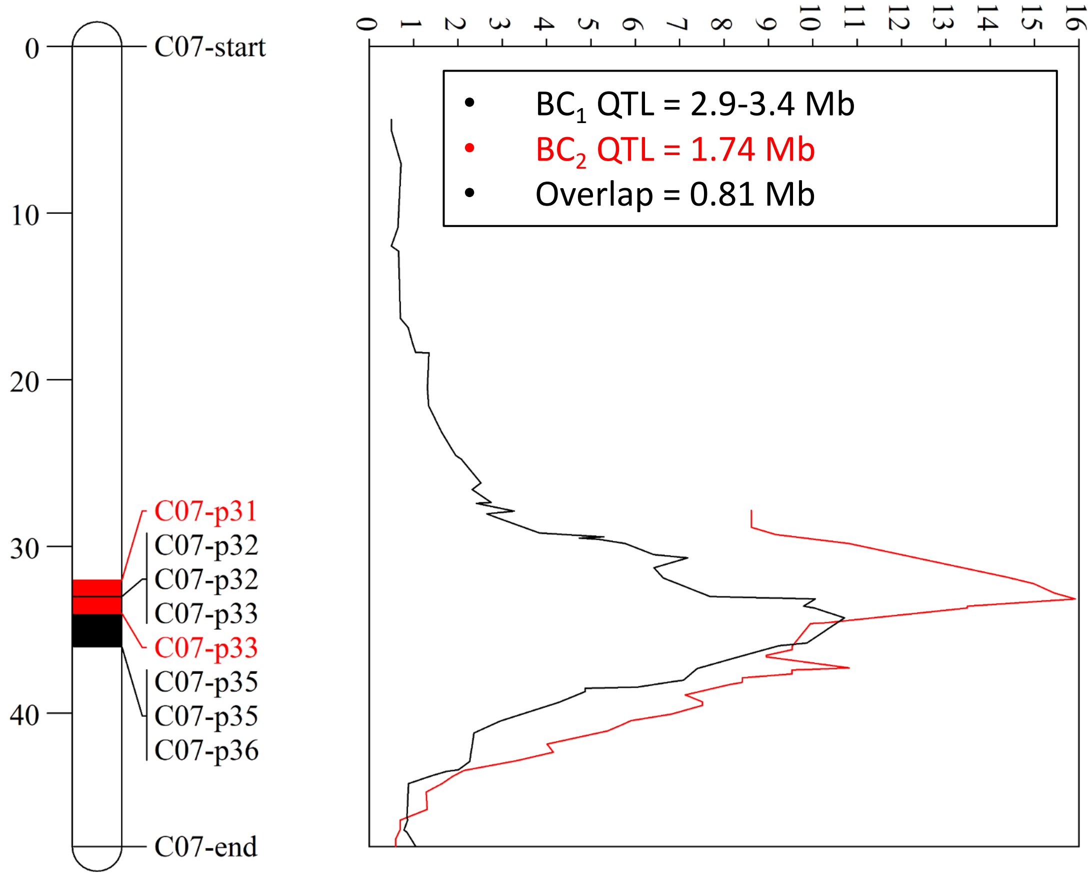
TO1000 x BC_1

200 BC_1 plants phenotyped
94 genotyped via GBS

BC_2

200 BC_2 plants phenotyped
200 genotyped via SeqSNP

Major QTL found on C07 in *B. oleracea* JWBo1



- BC_1 QTL = 2.9-3.4 Mb
- BC_2 QTL = 1.74 Mb
- Overlap = 0.81 Mb

Summary

- **TuYV resistance has been identified in *B. rapa* and *B. oleracea***
  - Mapping has identified a significant QTL in each species/source
  - Resistance sources seem to provide broad resistance against two TuYV phylogenetic groups
  - Further work is underway to refine QTL regions
  - Identify gene/s involved in TuYV resistance in both species
  - Resistant plant lines and markers will be given to breeders to use in breeding programs

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