The Quest for Durable Disease Resistance, a Case Study – Turnip mosaic virus Resistance in Brassicas

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## Outline

- I You shall have no other gods pathogens before me -Background
- II Love Know thine enemy Pathogen diversity
- III Thou shalt not kill Plant resistance to TuMV
- IV Do not work on Sundays Identity of the resistance genes
- V Thou shalt not worship graven images -Arabidopsis can confuse!
- VI You shall not commit adultery Be careful what you cross your plants to!

VII What next?



I. The importance of the *Potyviridae* and *Turnip mosaic virus* (TuMV) *Potyviridae* 

- Largest group of plant viruses
- Contains some of the most important and damaging plant viruses
- Turnip mosaic virus (TuMV) transmitted by many (89) aphid species nonpersistently
- It has a very wide host range and infects many different crops, including all brassicas, lettuce, peas, radish, watercress, horseradish, ornamental plants, many weeds and rhubarb

#### I. The importance of *Turnip mosaic virus* (TuMV)

Turnip mosaic virus

- Causes severe symptoms including internal symptoms in *B. oleracea* cabbage
- It also infects and causes severe symptoms in *B. rapa*
- TuMV infects oilseed rapa and swede (B. napus) and severly reduces seed yield in the former

# II. Know thine enemy - diversity of TuMV

- In order to identify broad-spectrum resistance to Turnip mosaic virus it is important to know about variation in the virus
- We studied:

biological serological geographical and genetic

diversity of TuMV

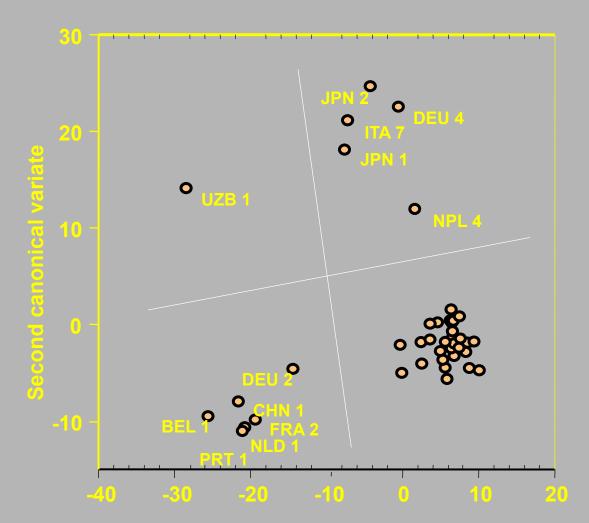
### Biological and geographical diversity

	Virus	Differential plant line				
	pathotype	Rape	Rape	Swede	Swede	
		S6	R4	165	S1	
	1	+	0	0	+	
	2	R	R	0	R	
Pathotypes	3	+	+ <sub>N</sub>	0	+	
of TuMV	4	+	+	+	+	
	5	+	+	0	+	
	6	+	+ <sub>N</sub>	0	R	
	7	+	0	0	R	
	8	+	+ <sub>N</sub>	R <sub>N</sub>	R	
	9	+	R <sub>N</sub>	0	R	
	10	+	+	0	0	
Jenner & Walsh, (1996). Plant	t 11	R	+	0	R	
Pathology 45, 848-856.	12	+	+	+ <sub>N</sub>	+	

### Biological and geographical diversity

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of TuMV	4	+	+	+	+	
	5	+	+	0	+	
	6	+	+ <sub>N</sub>	0	R	
	7	+	0	0	R	
	8	+	+ <sub>N</sub>	R <sub>N</sub>	R	
	9	+	R <sub>N</sub>	0	R	
	10	+	+	0	0	
Jenner & Walsh, (1996). Plan	11	R	+	0	R	
Pathology 45, 848-856.	12	+	+	+	+	

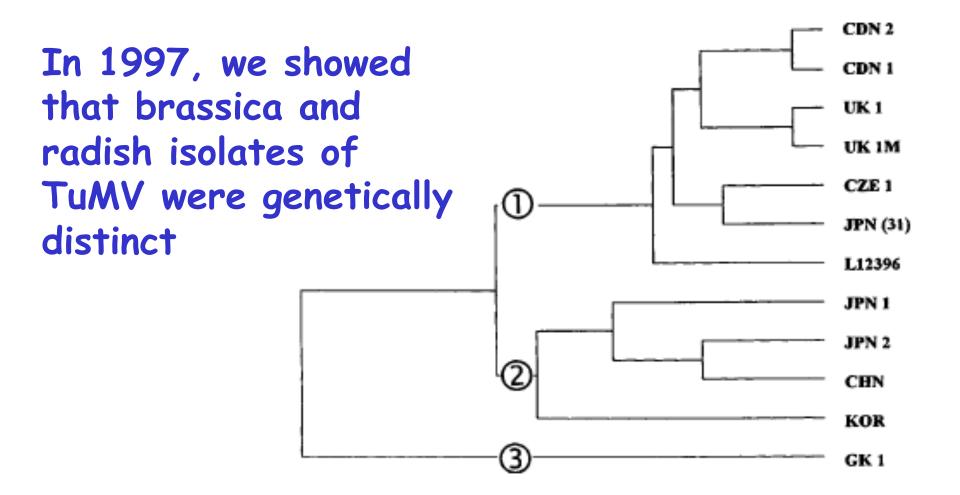
### Serological and geographical diversity



#### First canonical variate

Jenner, Keane, Jones & Walsh, (1999). Plant Pathology 48, 101-108.

#### Genetic variation

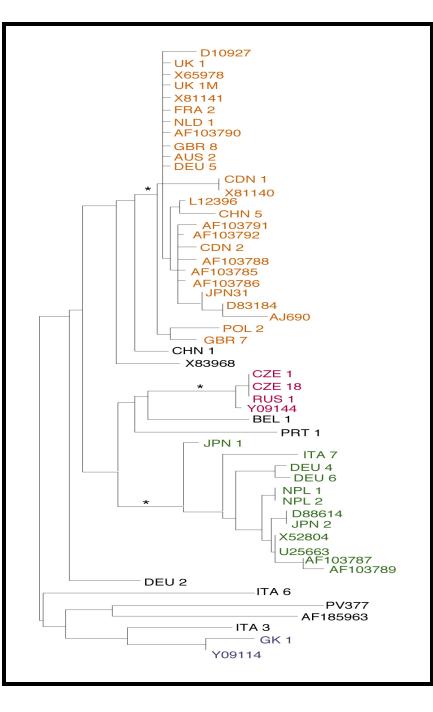


Lehmann, Petrzic, Jenner, Greenland, Spak, Kozubek & Walsh, (1997). Physiological and Molecular Plant Pathology 51, 195-208.

# Genetic variation

Further sequencing and whole genome sequencing confirmed these differences

Tomimura, Gibbs, Jenner, Walsh & Ohshima (2003). Molecular Ecology 12, 2099 - 2111.



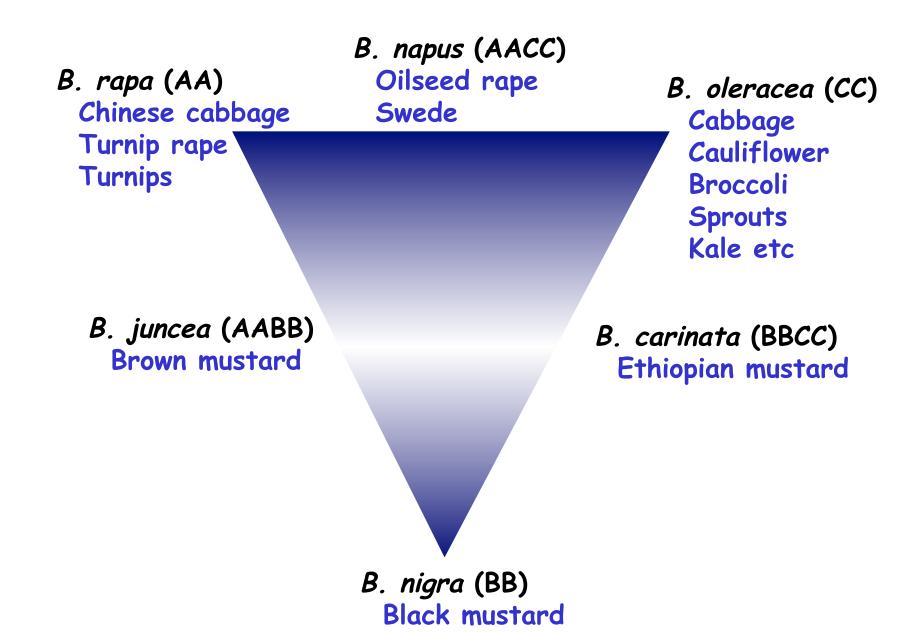
#### III. Thou shalt not kill - Plant resistance to TuMV

Having studied the variation in the pathogen - TuMV, we were then able to go about looking for resistance to TuMV in brassicas

We looked for resistance in:

The C genome of Brassica oleracea The A genome of Brassica rapa The A+C genome of Brassica napus

#### Sources of resistance: Triangle of U

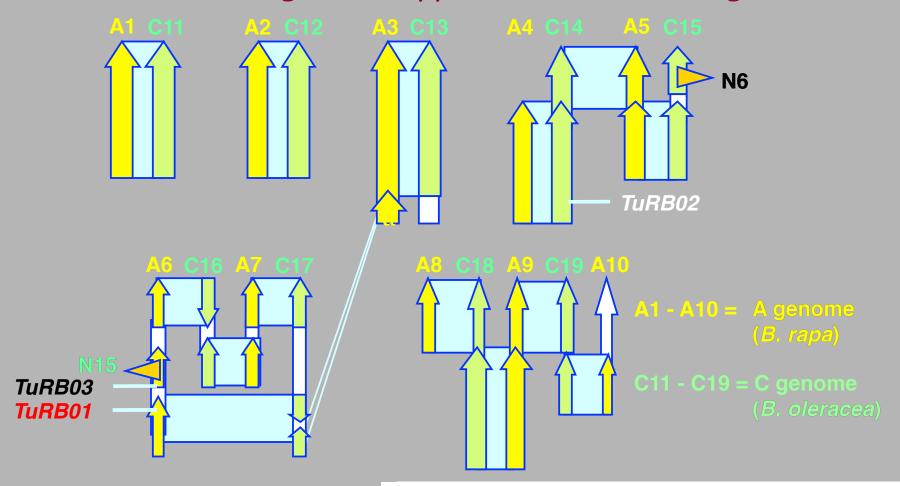


# Sources of resistance to TuMV in BrassicaPlant lineVirus isolate (pathotype)UK 1 (1)CZE 1 (3)CHN 5 (3)CDN 1 (4)

ι	JK 1 (1)	<i>C</i> ZE 1 (3)	CHN 5 (3)	CDN 1 (4)
N-o-1 ( <i>TuRBO1</i> )	0	<b>+</b> N	+N	+
No. 2	0	+	+	+
No. 22 ( <i>TuRBO3</i> )	) + <sub>N</sub>	+ <sub>N</sub>	+ <sub>N</sub>	0
Ap 1	+	+	R/+	+
M 1	0/R	R/+	+	+
G 1	0	R/+ <sub>N</sub>	<b>+</b> N	+
165	0	0	Ο	+
V 1	0	0/+	0/R	+
0-2'-5	0	0	R	0/R
No. 1	0	0	R	R
RLR22	R	R	R	R
BP-4	R/0	R/0	R	R/0

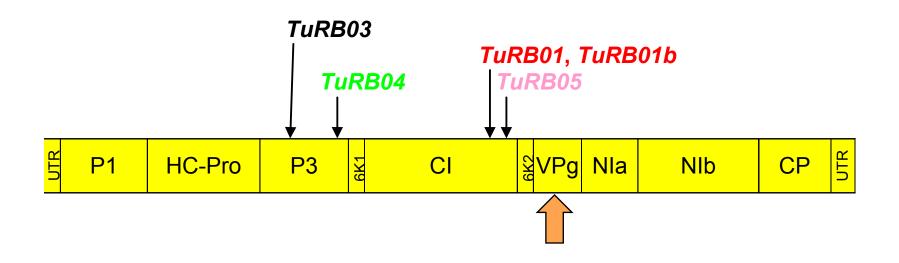
# 2. Past research - mapping TuMV resistance genes

TuMV resistance genes mapped in the Brassica genome



Hughes, Hunter, Sharpe, Kearsey, Lydiate & Walsh (2003). Theoretical and Applied Genetics 107, 1169 - 1173.

### Past research pathogenicity / avirulence factors



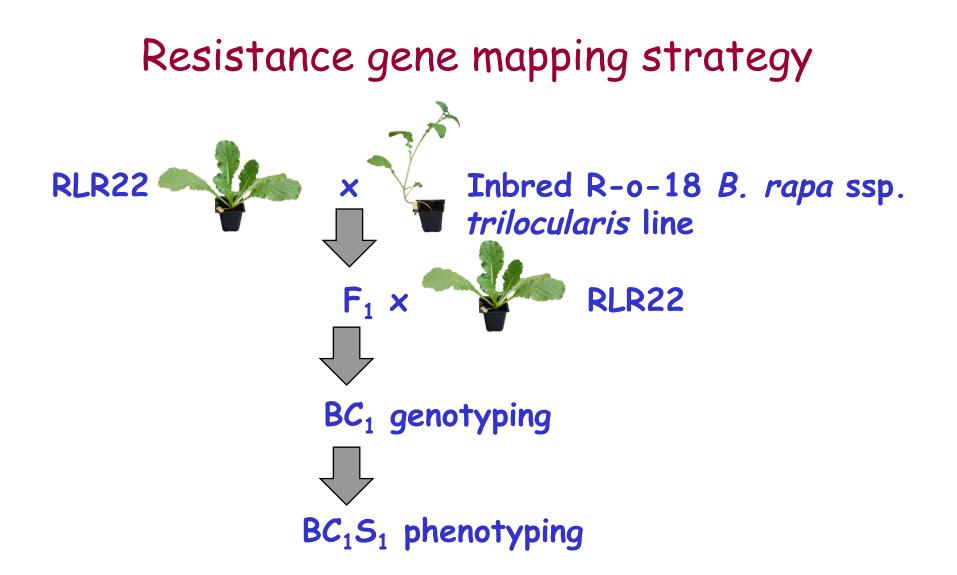
IV. <del>Do not</del> work on Sundays -Identity of plant resistance genes

Most recently focussed on *Brassica rapa* line RLR22 with broad-spectrum TuMV resistance

#### Parental phenotypes

	TuMV isolate (pathotype)							
	UK 1 (1)	CZE 1 (3)	CHN 5 (3)	CDN 1 (4)	JPN 1 (7)	DEU 7 (8)	GK 1 (9)	UK 4 (12)
RLR22	R	R	R	R	0	R	R	R
R-o-18	+	+	+	+	+	+	+	+

Walsh, J.A. et al. (2002). European Journal of Plant Pathology 108: 15-20.



Segregation ratios in  $F_1$ ,  $BC_1$  and  $BC_1S_1$  generations suggested the resistance was controlled by a recessive gene and a dominant gene.

#### Two gene model

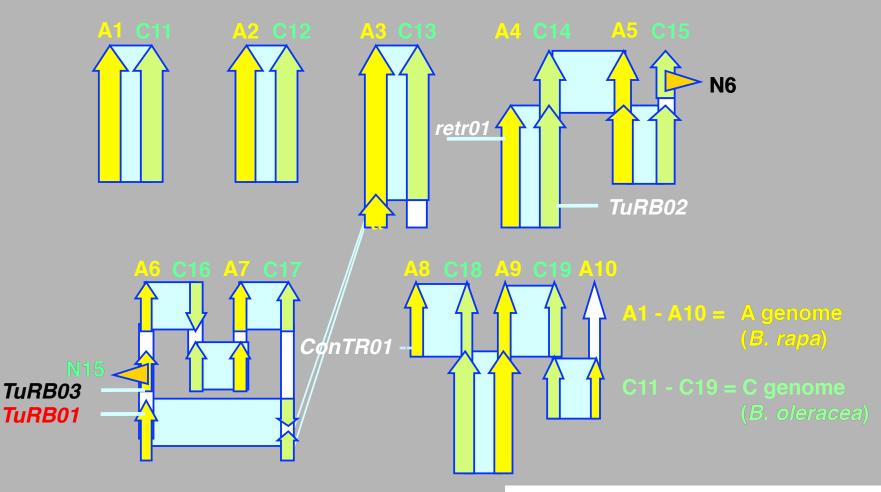
Recessive resistance gene:

<u>recessive TuMV resistance 01</u> retr01

Dominant resistance gene:

<u>Conditional TuMV resistance 01</u> ConTR01

### Mapping the TuMV resistance genes



Rusholme, Higgins, Walsh & Lydiate (1999). Journal of General Virology 88, 3177 - 3186.

# Identity of the resistance genes indicated from the R-o-18 cross

Recessive resistances have been discovered to some potyviruses

 More than half the resistance genes associated with potyviruses are recessive compared to only 20% against other plant viruses (Provvidenti and Hampton, 1992)

Recessive resistance was believed to be based on a passive mechanism Resistant plants are lacking in a specific host factor that is required for the virus to complete its life-cycle (Fraser, 1986)

 Many of these recessive resistances have been found to be based on eIF4E or eIF(iso)4E Potyviruses use the eukaryotic translation initiation complex to translate their positive sense RNA genome into protein

# Potyviruses use the eukaryotic translation initiation complex to translate their plus strand RNA into protein

Mutations in the plant *eIF4E* gene result in the potyviral VPg protein being unable to bind with the eIF4E protein

#### Identity of the resistance genes indicated from the R-o-18 cross

- Probes for members of the *eIF4E* and *eIF(iso)4E* gene families were used to locate these genes in the A genome.
- Probes for one of the copies of *eIF4E* and one of the copies of *eIF(iso)4E* were closely linked to the *ConTRO1* locus.
- A probe for one of the other copies of *eIF(iso)4E* was closely linked to the *retr01* locus.

Rusholme, R.L., Higgins, E.E., Walsh, J.A. & Lydiate, D.J. (2007). *Journal of General Virology* 88:3177-3186.

2002 Mutation and transposon knockout of *Arabidopsis eIF(iso)4E* demonstrated the requirement of this gene for TuMV susceptibility

Arabidopsis transposon knock-out line Col-O::dSpm eIF(iso)4E was found to be resistant to TuMV (Duprat et al., 2002) SO .....

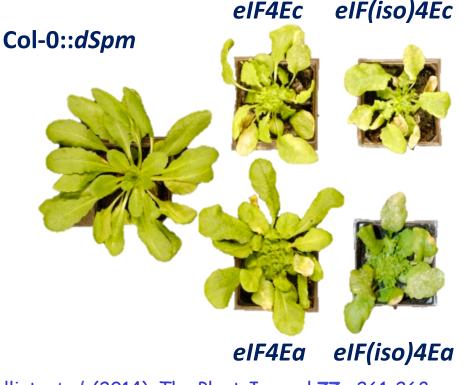
- We found that *Brassica rapa* has 3 copies of *eIF4E* one of which is a pseudogene
- We also found that *Brassica rapa* has 3 copies of *eIF(iso)4E*
- Copies of two *eIF4E* and two *eIF(iso)4E* genes were identified in a BAC library of the susceptible plant line R-o-18 and a fosmid library of the resistant plant line RLR22 and cloned
- The genes were transformed in to the *Arabidopsis* mutant line Col-O::*dSpm eIF(iso)4E* which is resistant to TuMV

 This showed that TuMV can use multiple copies of both genes from R-o-18 when ectopically expressed in Arabidopsis



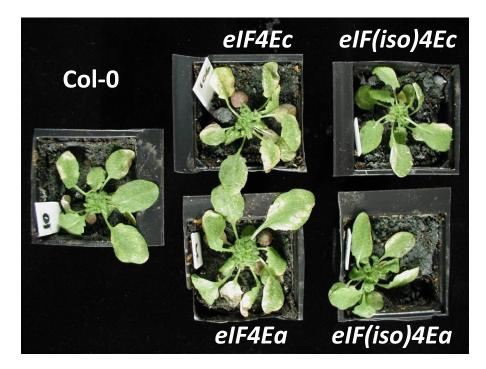
Jenner *et al.* (2010). Mol. Plant-Microbe Interactions **23**: 1498-1505.

• This also showed that TuMV can use multiple copies of both genes from RLR22 when ectopically expressed in *Arabidopsis* 

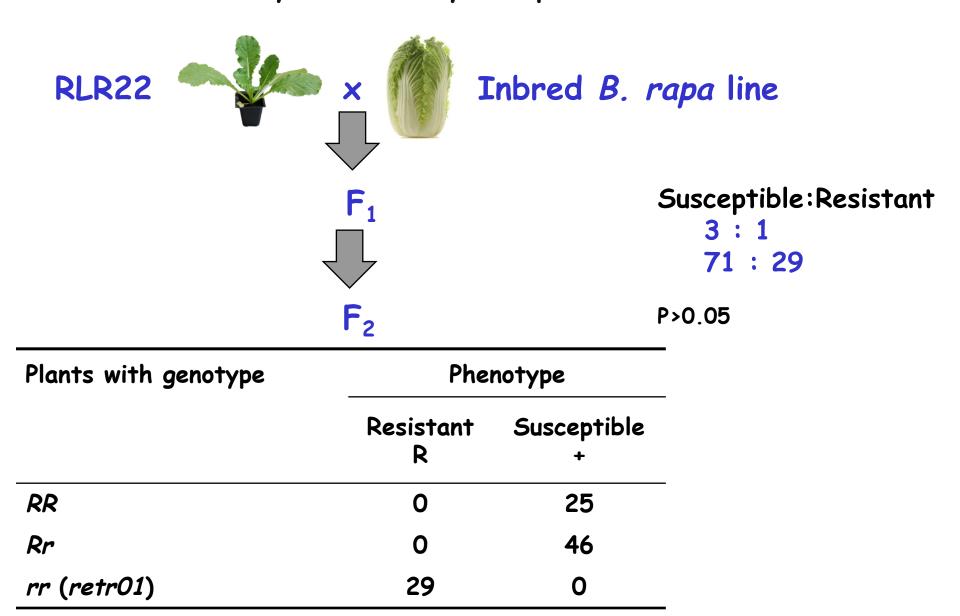


Nellist et al. (2014). The Plant Journal 77: 261-268.

Control transformations in Col-0



Jenner *et al.* (2010). Mol. Plant-Microbe Interactions **23**: 498-1505. VI. You shall not commit adultery – Be careful what you cross your plants to



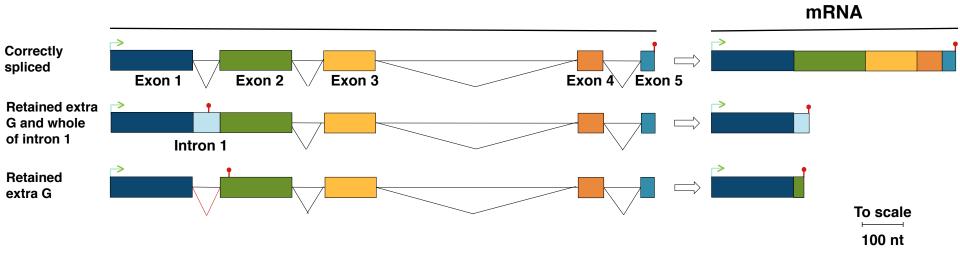
# Identity of the resistance gene indicated from the *B. rapa* cross

 gDNA sequencing of candidate eIF(iso)4E.a revealed an extra G at the exon 1 - intron 1 splice site in RLR22 compared to susceptible lines

 gDNA sequencing of two other lines with broad-spectrum resistance revealed they also possessed the extra G

Nellist et al. (2014). The Plant Journal 77: 261-268.

# The resistance mechanism - mis-splicing of *eIF(iso)4E.a*



Expression studies revealed the mis-splicing of eIF(iso)4E.a

retr01 was identified as eIF(iso)4E.a

Nellist et al. (2014). The Plant Journal 77: 261-268.

#### What next?

#### Alternative sources of broad-spectrum resistance to TuMV

Plant Line	Broad-spectrum Resistance	Indel at position 201 bp	Phenotype	Mis-spliced?
RR	$\checkmark$	No	0	No
СР	$\checkmark$	No	0	No
BR	$\checkmark$	No	0	No
BP	$\checkmark$	Yes	R	Yes
RLR22	$\checkmark$	Yes	R	Yes
JB	$\checkmark$	Yes	R / +	Yes / No
TD	X (TuRB01)	No	+	No
R-o-18	×	No	+	No

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#### Thank you for your attention