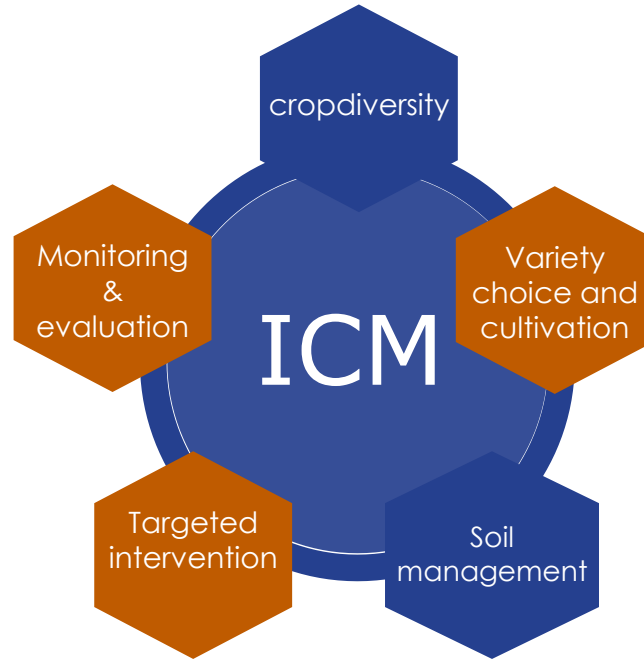


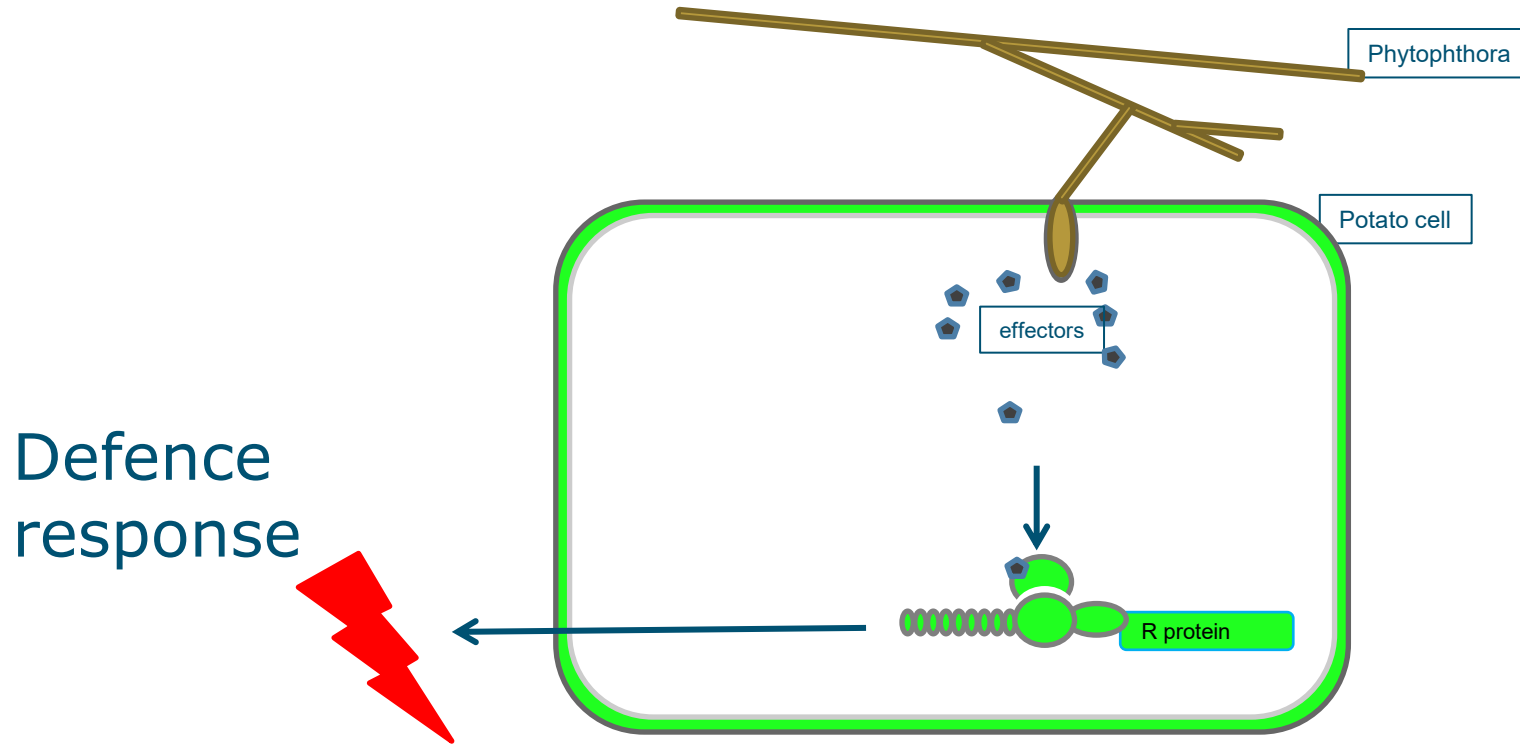
# Emergence and detection of virulence towards host encoded Late Blight resistance

Jack Vossen, Trudy van den Bosch, Brian Lavrijssen, Geert Kessel

Euroblight workshop, *Ourense*, May 19<sup>th</sup> 2026

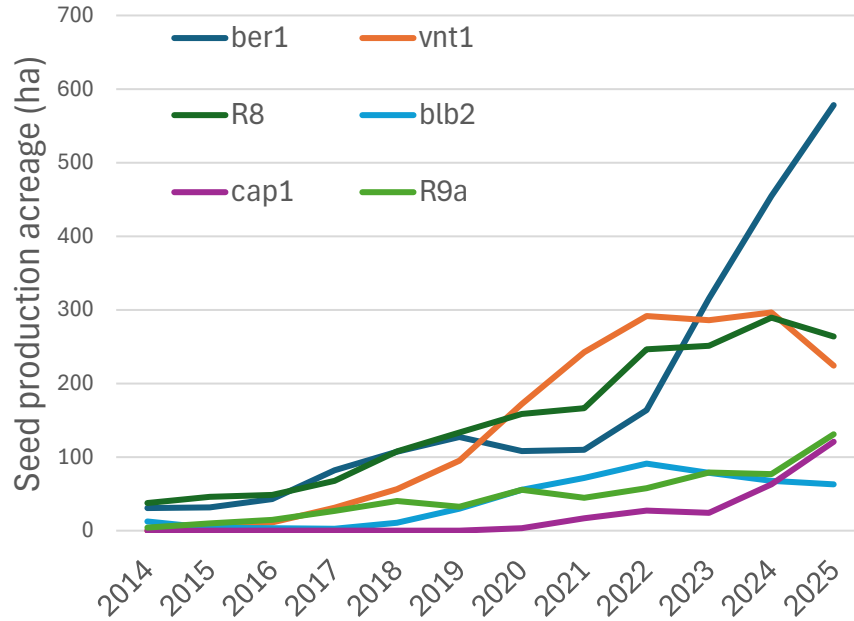


# R proteins recognize Phytophthora effectors





# Late blight *R* genes in varieties in NL



percentage of total seed  
tuber production in NL  
0.2% (2014)  
3.5% (2025)

# Yearly *Phytophthora* virulence evaluation



Day 0



Day 5

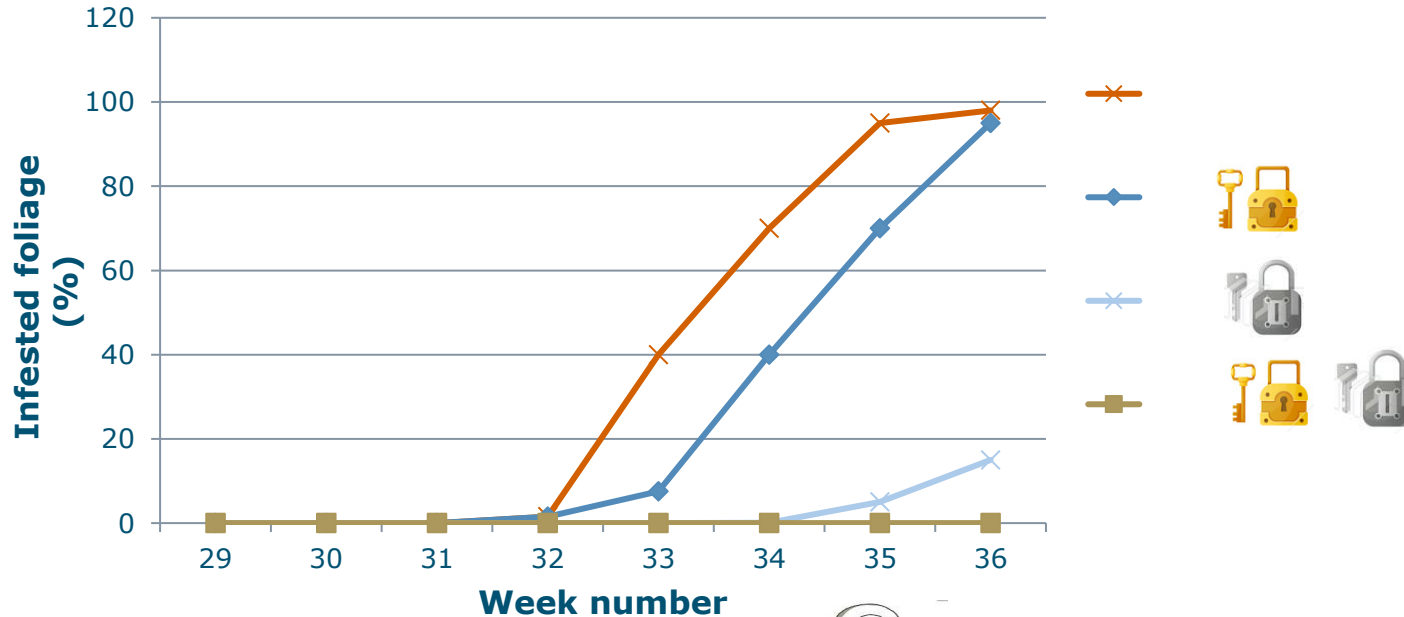


# Phytophthora virulence in relation to R gene deployment















Resistance gene	Introduction year	Percentage virulence 2010-2014*	Percentage virulence 2020-2023**
<b>R1</b>	<1970	100	Not tested
<b>R3a</b>	<1970	98	100
<b>R3b</b>	<1970	96	96
<b>R2</b>	<1990	47	28
<b>R8</b>	<2003	7	20
<b>R9a</b>	2013	2	20
<b>Rpi-blb2</b>	2006	8	15
<b>Rpi-chc1</b>	2012	9	25
<b>Rpi-vnt1</b>	2014	2	15
<b>Rpi-cap1</b>	2023	0	1

\* 64 isolates tested; \*\* 115 isolates tested

# Stacking of R genes is essential!!



# Virulence profiles of EU groups

 EU_1_A1	 EU_6_A1
 EU_12_A1	 EU_13_A2
 EU_33_A2	 EU_36_A2
 EU_37_A2	 EU_39_A1
 EU_41_A2	 EU_43_A1
 EU_45_A1	 EU_46_A1
 EU_47_A1	 Other

	R3a	R3b	R2	blb2	vnt1	ber1	R8	R9a	cap1
EU13	v	v	v	a	a	a	a	a	a
EU36	v	v	a	a	a	a	a	a	a
EU37	v	v	v	a	a	a	a	a	a
EU41	v	v	v	a	a	a	a	a	a
EU43	v	v	v	a	a	a	a	a	a
EU46	v	v	v	a	a	a	a	a	a
EU47	v	v	a	a	a	a	v	v	a
other	v	v	var	var	var	var	var	var	var

# Virulence build-up within EU36 in the Netherlands

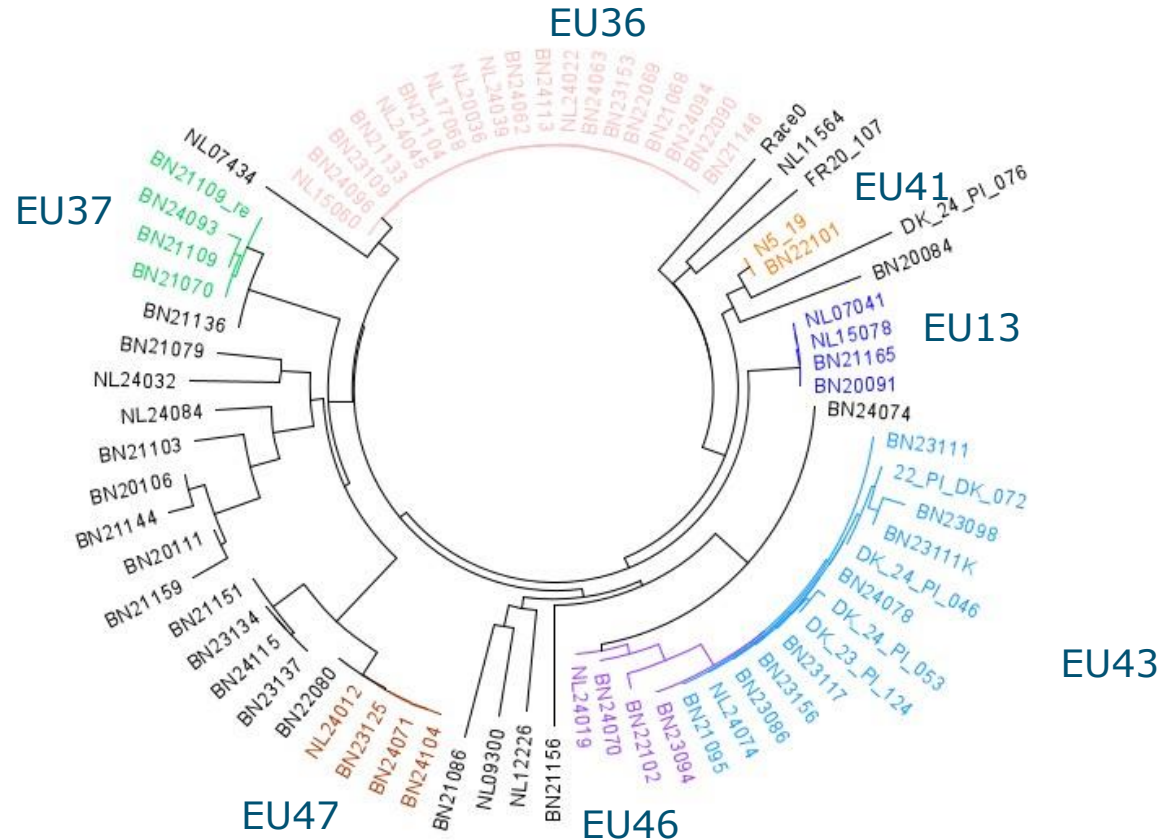
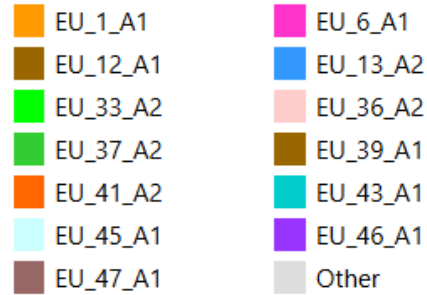
Group	acquired virulence	2020	2021	2022	2023	2024
EU36	ber1	-	Fl	NH	Fl, Fr	NB, Fl, Fr
EU36	ber1, cap1	-	-	-	-	Fr
EU36	ber1, blb2	-	-	-	-	Fr
EU36	ber1, R9a	-	-	-	-	NB
EU36	R2	-	-	-	-	NB
EU36	vnt1	Fl	Fr, Fl	Fr	-	Fr
EU36	R9a, blb2	-	-	-	-	Fl

NH: Noord Holland  
 Fr: Friesland  
 Fl: Flevoland  
 NB: Noord-Brabant  
 Ov: Overijssel

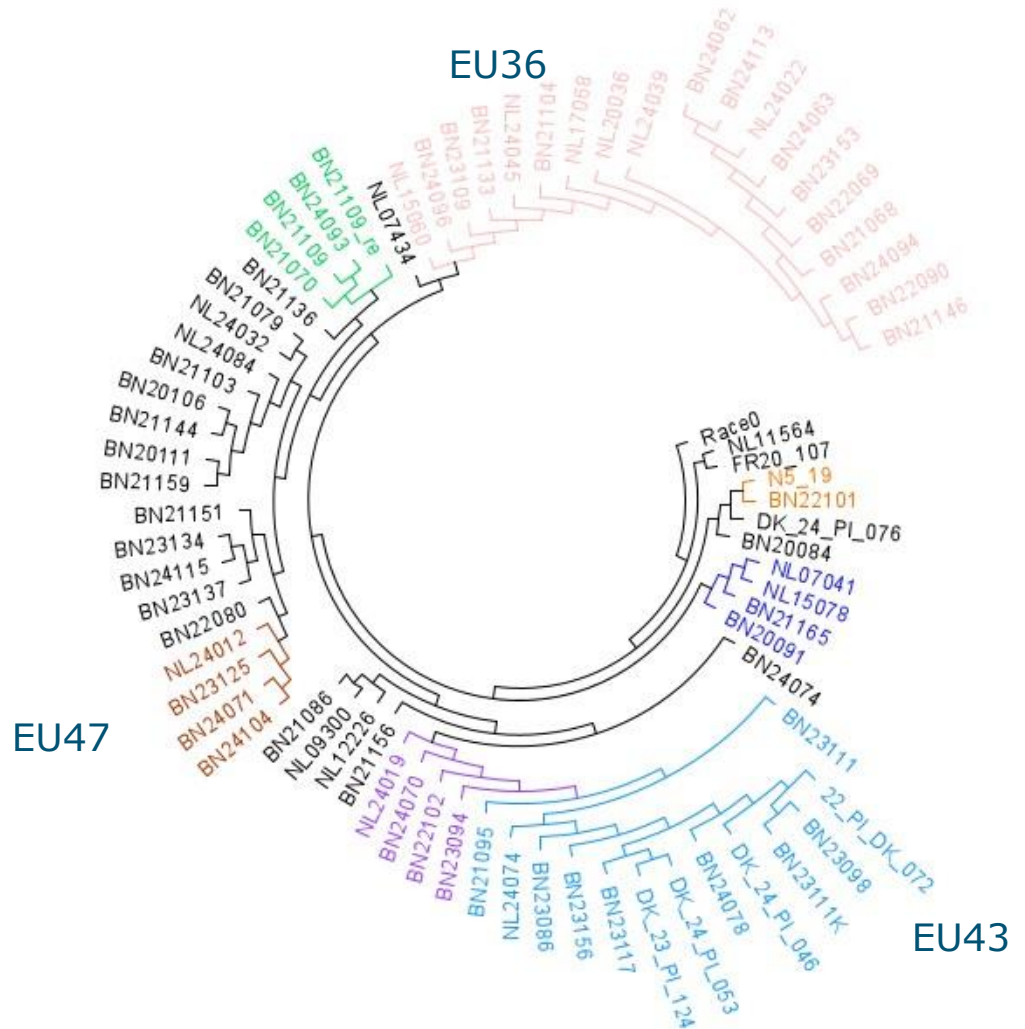
# Selection of isolate panel for Genome sequencing

virulence	Nr of isolates	Virulence (partially) lost	Virulence stable	Sequenced
R2	24	0	24	9
R3b	60	3	57	3
Rpi-ber1	11	3	9	8
Rpi-vnt1	6	2	4	4
R8, R9a	14	0	14	14
R9a	1	1	0	0
Rpi-blb2	4	0	4	4
Rpi-cap1	2	0	2	2
Combined virulence	18	5	13	13
Zero types	18		18	18

# Phylogeny of exon sequences reproduces SSR structure



# Enhanced resolution reveals variation within clonal groups



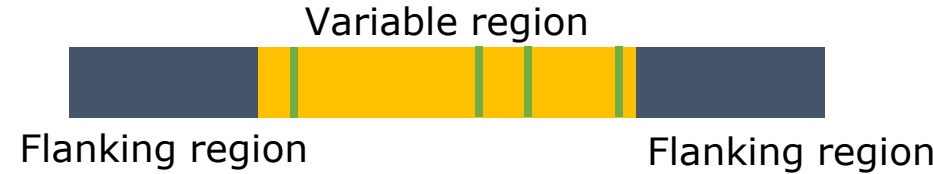
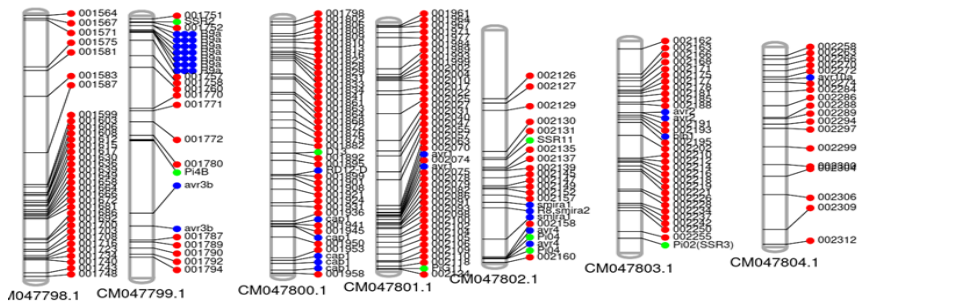
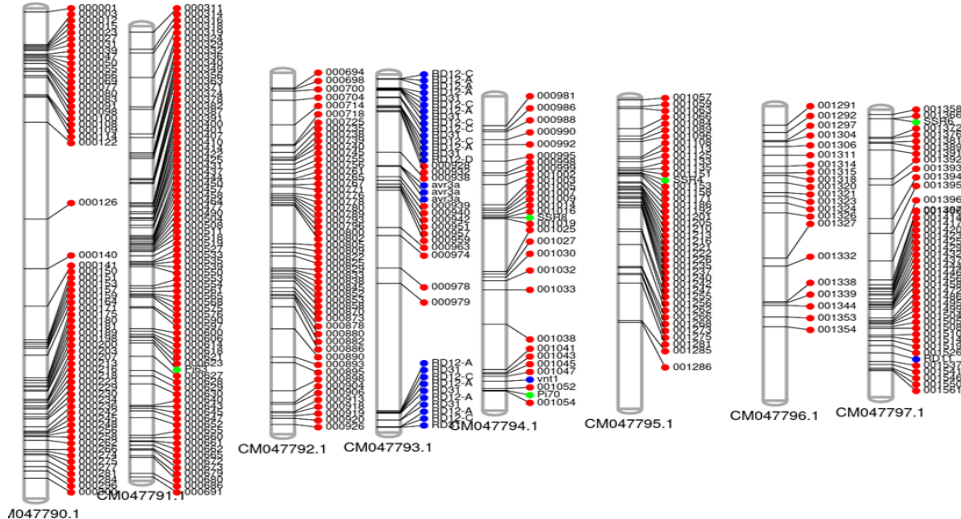


# Conclusions and perspective

- Build up of virulence since introduction of single *R* gene varieties
- (differentially) virulent isolate collection was build and sequenced.
- Markers for virulence will be deduced
- ICM systems require a fast, quantifiable virulence detection system



# Amplicon sequencing for *Phytophthora* (PhytoSeq)



- AVR
- SSR
- Phytoseq amplicons

# Liveseq

## Lineage and virulence emergence sequencing

- Amplicon sequencing
  - Neutral Phytoseq markers
  - Functional *virulence markers*
  - Active compound resistance markers
- Link to spore trap network

# Thank you for your attention!

