

An ICM approach to combat Phytophthora

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Variety choice:

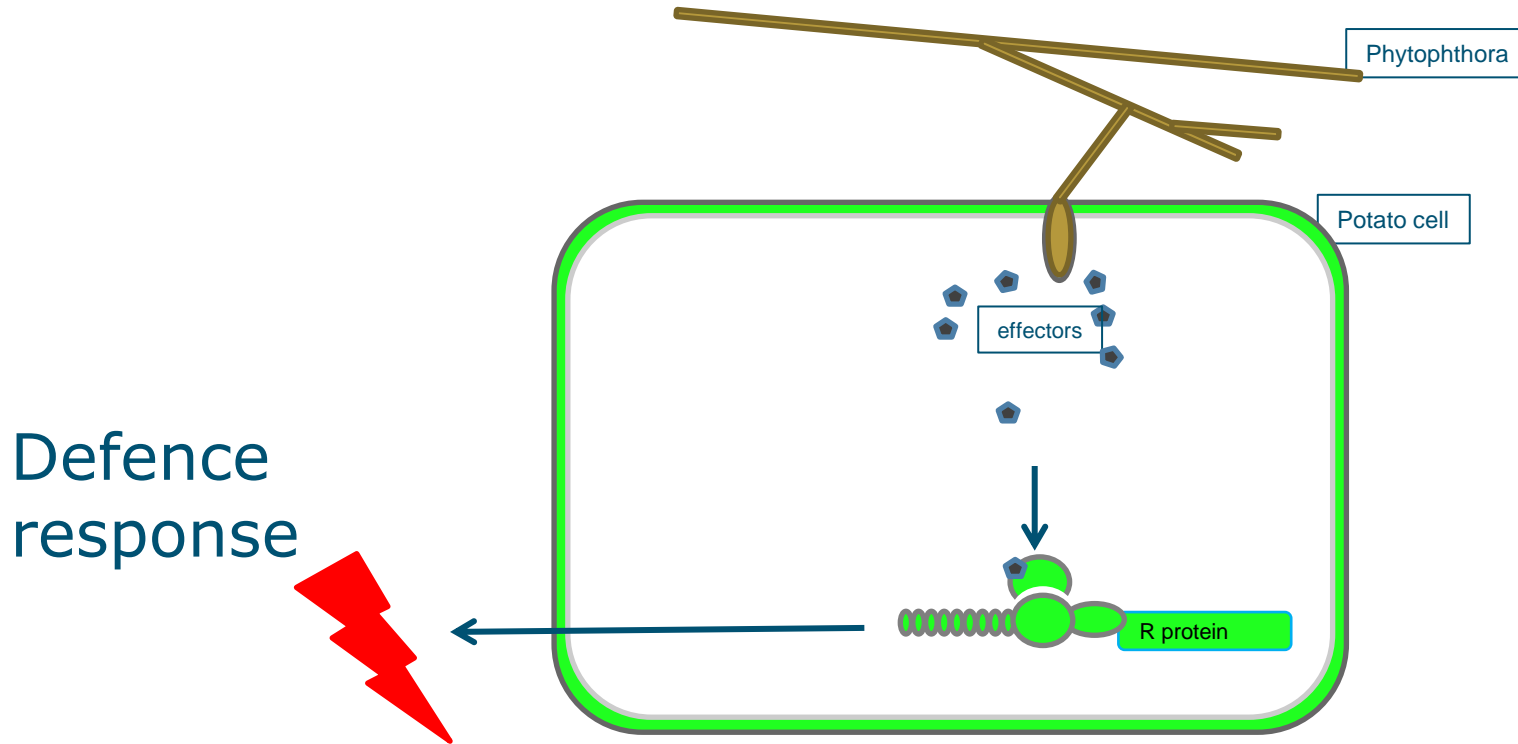
improved varieties
through breeding



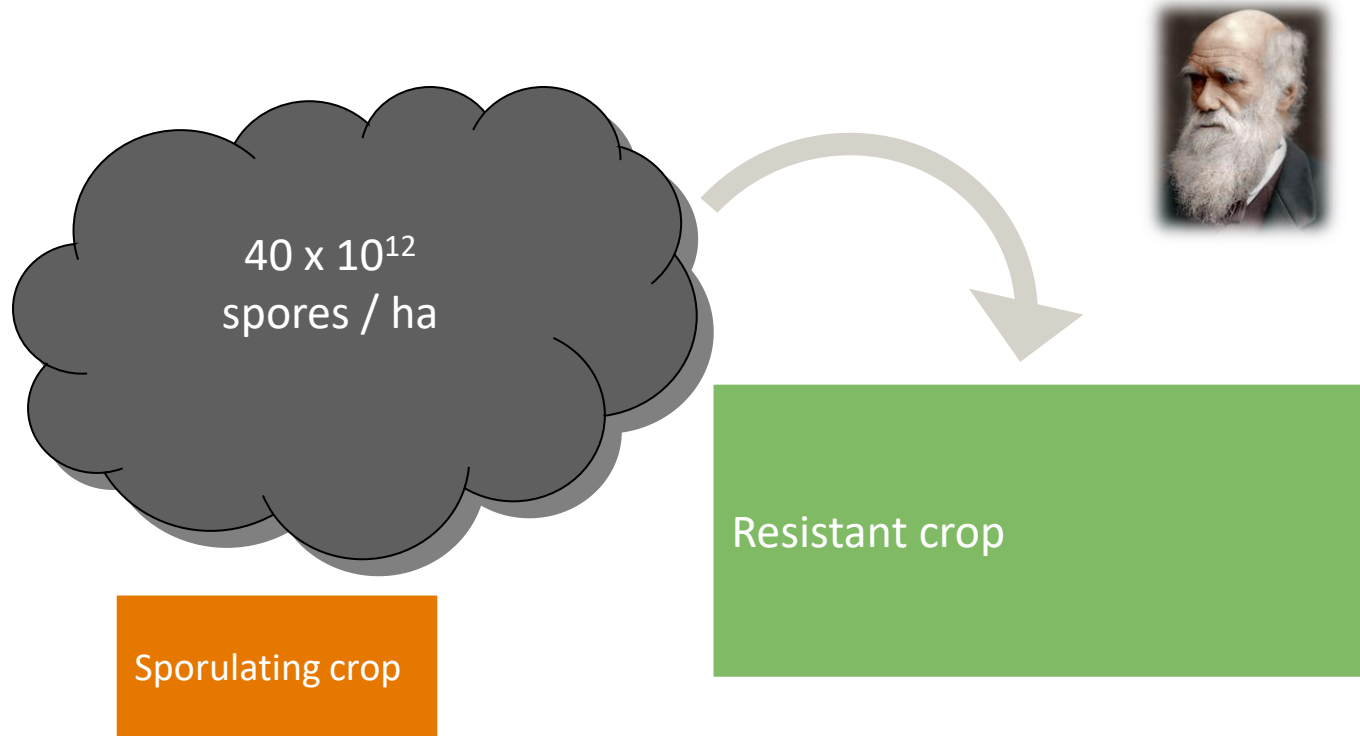
Phytophthora resistance in “Robust” varieties



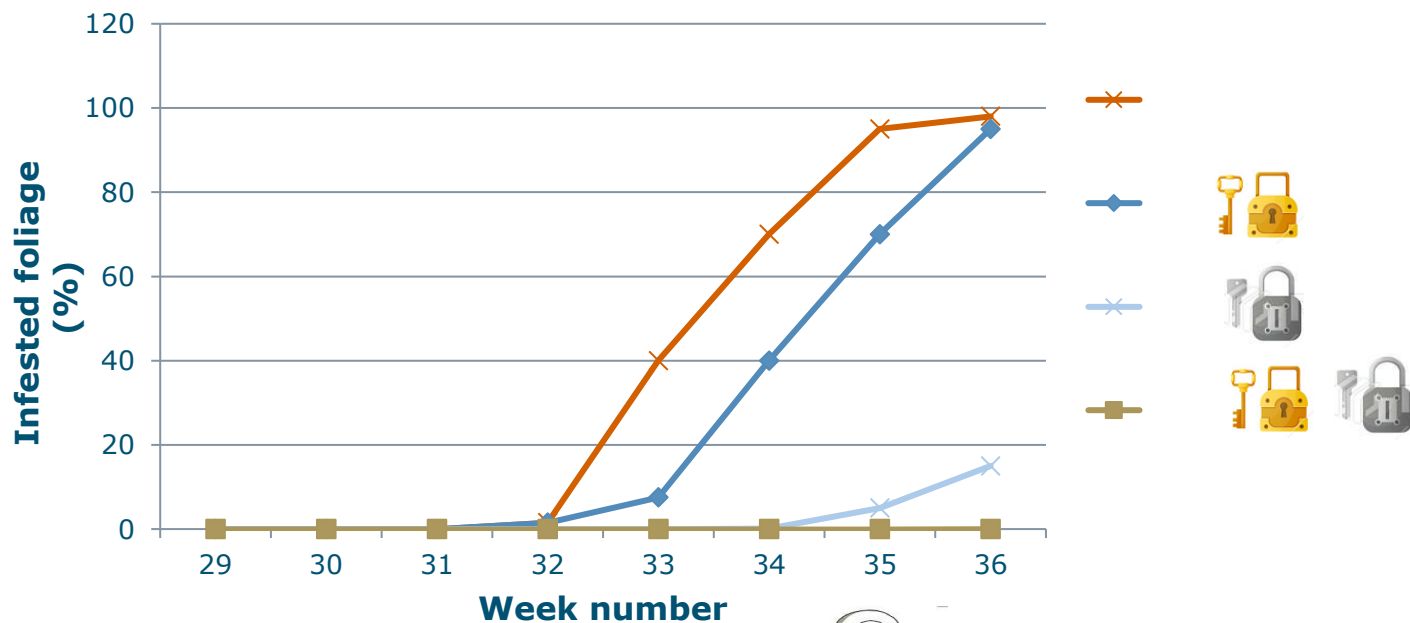
R proteins recognize Phytophthora effectors



Adaptation ability of *P. infestans*: Mutation & Selection



Single vs stacked resistance

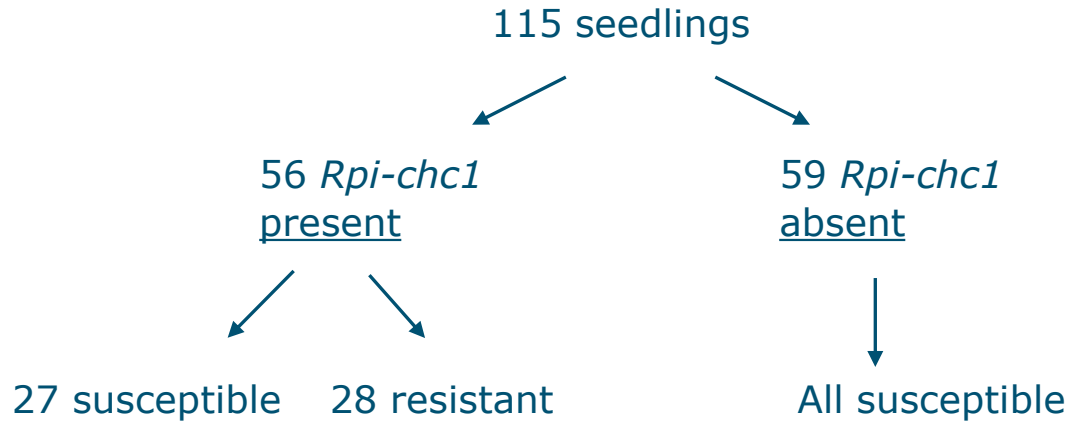


Background dependency of *R* genes

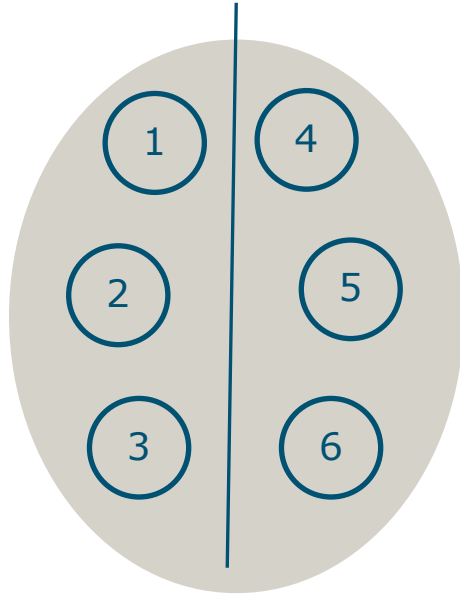
	Desiree	Premiere	Aveka	Atlantic	Bintje	Russet Burb.
edn2	95	10	100	50		5
blb3	90	80	80	90		85
vnt1	95	95	90	95	80	90
chc1	40	5	45	50		5
tar1	35					0
ber	60					20
sto1	70	80	80	85	70	
R8	90					75

Segregation of background dependency from Premiere

RasX+*Rpi-chc1* (resistant)*Premiere (susceptible)



Effector response assay for *R* gene activity in stacks



1. Avr2
2. Avrvnt1
3. Avr3a

4. Avr3b
5. - control
6. Avrb1b1

Conclusions Variety choice



- Varieties with single resistance are vulnerable
- Varieties with stacked resistance are still scarce
- Resistance can be dependent on the genetic background
- Breeders need tools to select for varieties with functional stacks

Monitoring en evaluation

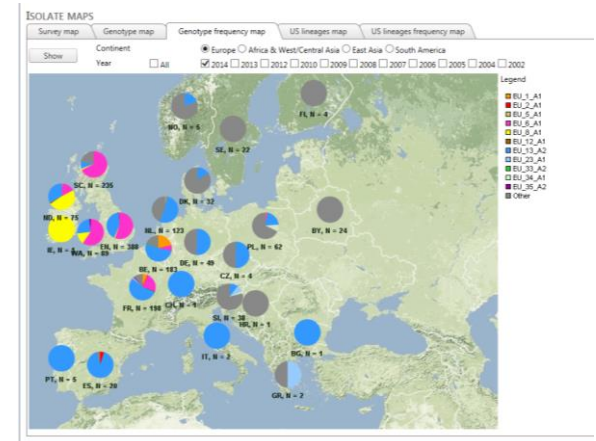
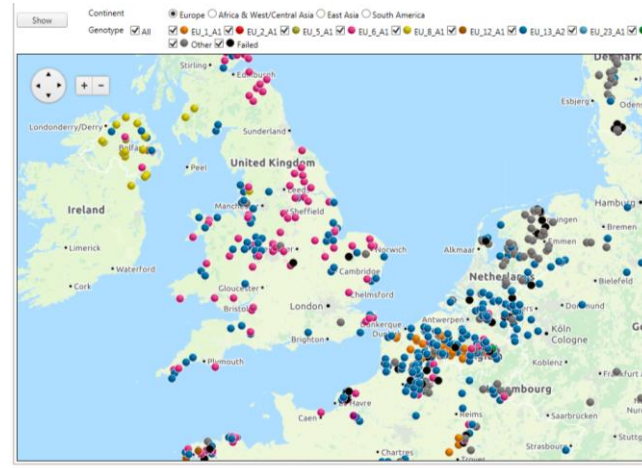


SSR typing of *Phytophthora* populations

Sample collection:

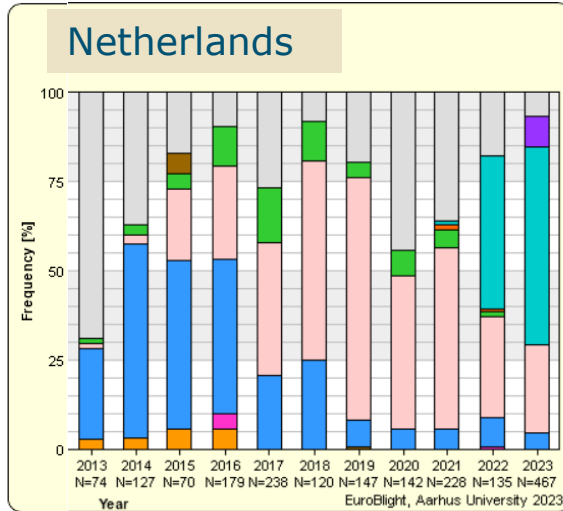


Genotype distribution
(2014):



Web site provided by Aarhus University, Faculty of Science and Technology, Department of Agroecology. Report technical problems to webmaster: Eoul.Laessle. Optimized for screen size 1280x800

Virulence profiles of EU groups



	R3a	R3b	R2	blb2	vnt1	ber1	R8	cap1
EU13	v	v	v	a	a	a	a	a
EU36	v	v	a	a	a	a	a	a
EU43	v	v	a	a	a	a	a	a
EU46	?	v	a	a	a	a	a	a
other	?	?	?	?	?	?	?	?

Virulence build-up in major EU groups

Group	acquired virulence	2020	2021	2022	2023
EU36	ber1	-	Fl	NH	NH, Fl, Fr
EU43	R2	-	NB	NB	NB, Fl, Fr
EU43	R2, blb2	-	-	-	NB
Other	R8, R9a	Fr, Fl	Fr, Fl	Fr, Fl	Fr, Fl

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

Conclusion Monitoring en evaluation



- The current P infestans genotyping system does not detect virulence
- Isolate analysis (after the growth season) shows the build up of virulence
- A quick, in-season, virulence monitoring system is needed

Targeted intervention



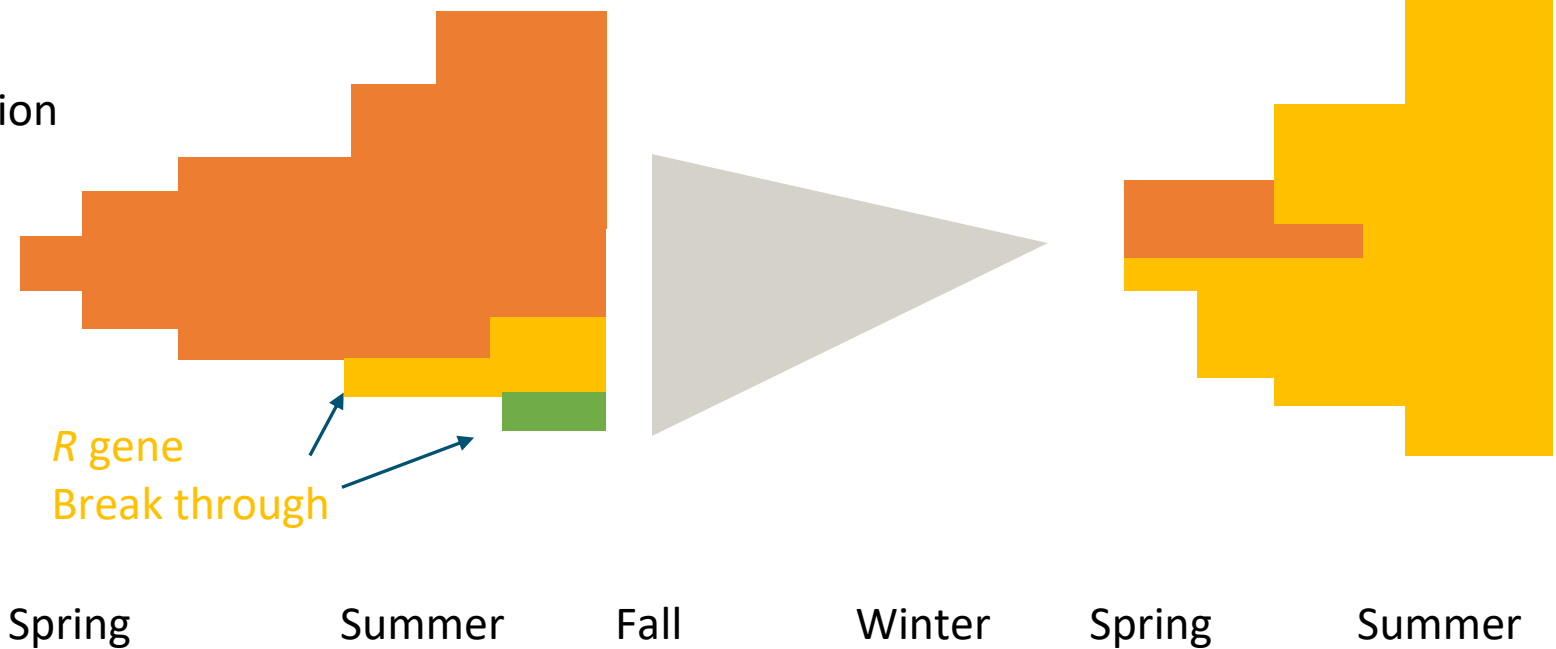
Variety choice
(*R* gene stacking)

Seed tuber selection

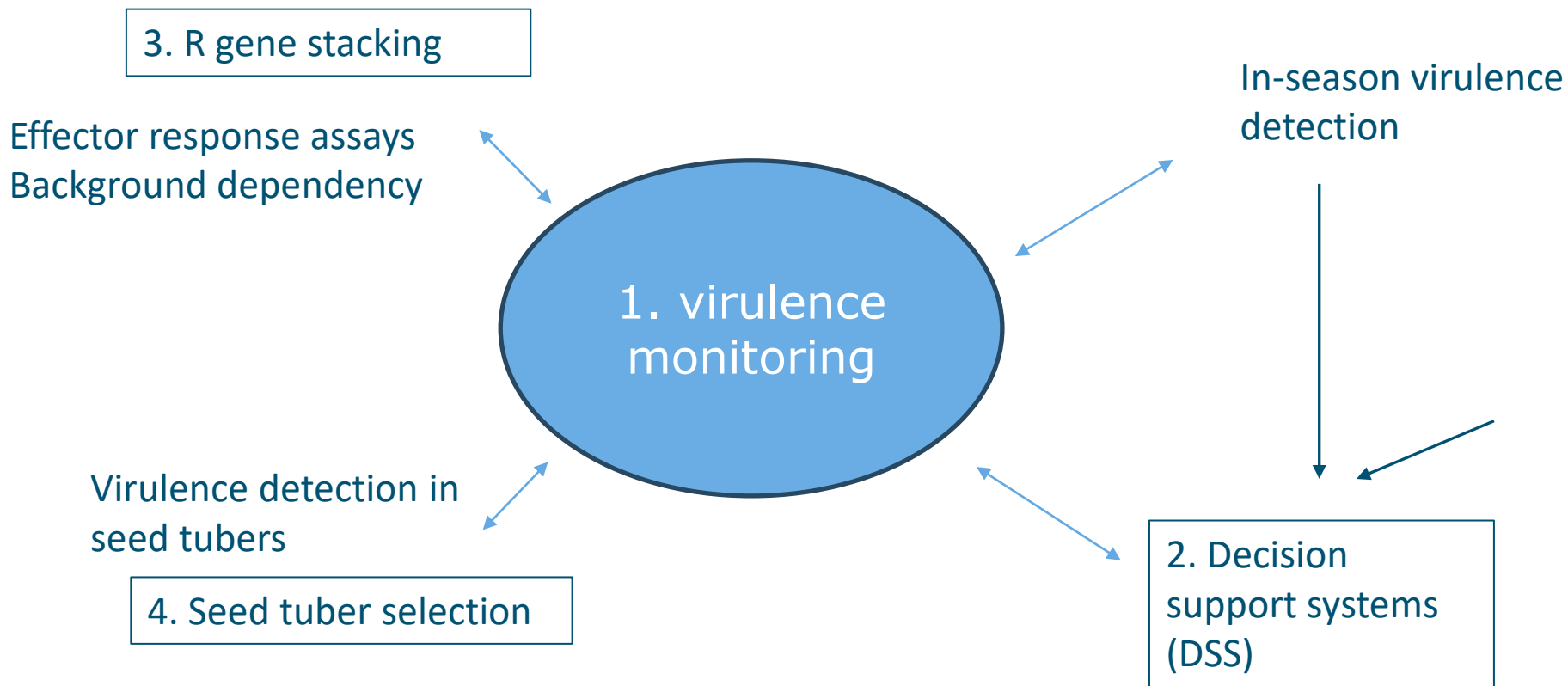
Decision support systems

Volunteer control

Pi population



Themes in this project



Workpackage 1: Virulence monitoring

■ Questions

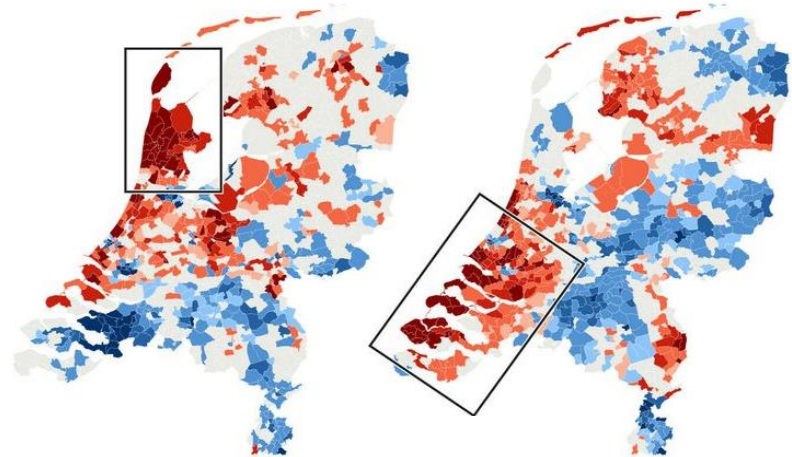
- How does *Phytophthora* evade recognition by *R* genes (R2, R8, R9a, vnt1, blb2, ber1, cap1)

■ Approach (**Liveseq**)

- Capture and collect *Phytophthora* isolates from agr. practice
- Sequencing of all effectors
- Identify (expression) polymorphisms
- Functional validation of polymorphisms

Workpackage 2: Decision support systems

- Practical trials with **Liveseq** as input for DSS (year 3, 4)
 - Msample collection (regional, national)
 - Targetted spray advice
 - Evaluation of (cost-)effectiveness



Workpackage 3: Tools for *R* gene stacking

- Questions:
 - How can we detect *R* gene activity in stacks
 - Which genetic factors determine *R* gene background dependent activity
- Approach:
 - Test effector (variants) in multitude of varieties
 - Map background dependency/effector non-responsiveness

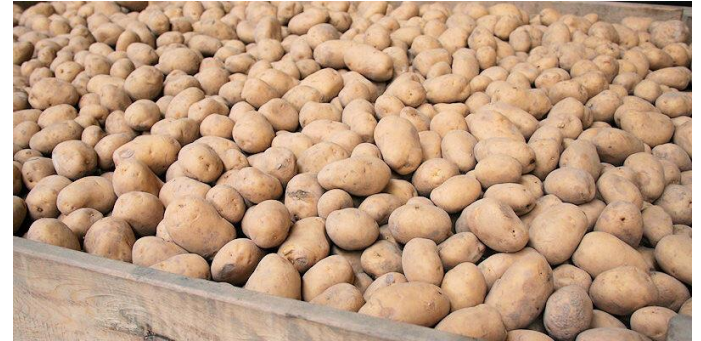
Workpackage 4: Role of seed tubers in virulence build-up

Question:

- Do virulent isolates pass to the next season through latent infection of seed tubers

Approach:

- Detect *P. infestans* in seed tuber DNA collection of NAK
- Detect virulent *P. infestans* using **Liveseq** in seed tuber lots



Budgets

	2025	2026	2027	2028
WP1, virulentie monitoring	150	95	40	40
WP2, DSS	15	25	130	130
WP3, breeding tools	70	100	80	80
WP4, Seed tuber testing	20	50	25	25
totaal	255	260	275	275

Private contributions per year:

In cash: 66, 6kE/y

In kind: 66, 6kE/y

Public funding (TKI): 133,1 kE/year

In kind contributions:

- *P infestans* samples from “robust” varieties
- Potato genotypes (varieties, populations)
- Marker development
- Field trails (2027-2028)

Output of this project

■ Knowledge

- Mechanism of virulence development
 - Effector variation
- Mechanism of background dependency of resistance

■ Tools

- **Liveseq**, rapid in-season virulence-typing system (<1 week)
 - DSS and seed tuber tests
- *R* gene stacking (breeding)
 - Effector response assays
 - Markers to eliminate background dependency

Dank voor uw
aandacht!

