



# Exploring and exploiting resistance to *Globodera pallida* in potato

**Ulrike Gartner**

University of Idaho, 08 March 2019



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# Background

- ❖ 5.2 million tonnes of tuber production in UK in 2016 (44 tonnes/ha)
- ❖ 45% of land is used for the production of seed potatoes in Scotland



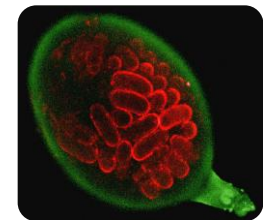
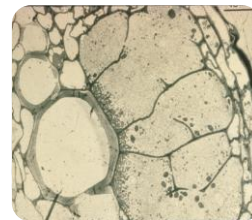
Healthy potato plants and plants affected with PCN



Tubers from various commercially available potato cultivars

# Potato Cyst Nematodes

- ❖ Two species, *G. rostochiensis* and *G. pallida*, have been described in the UK
- ❖ Feed and develop in the root system
- ❖ Cysts fall into the soil and can survive there for many years
- ❖ Listed as quarantine organism and therefore subject to monitoring

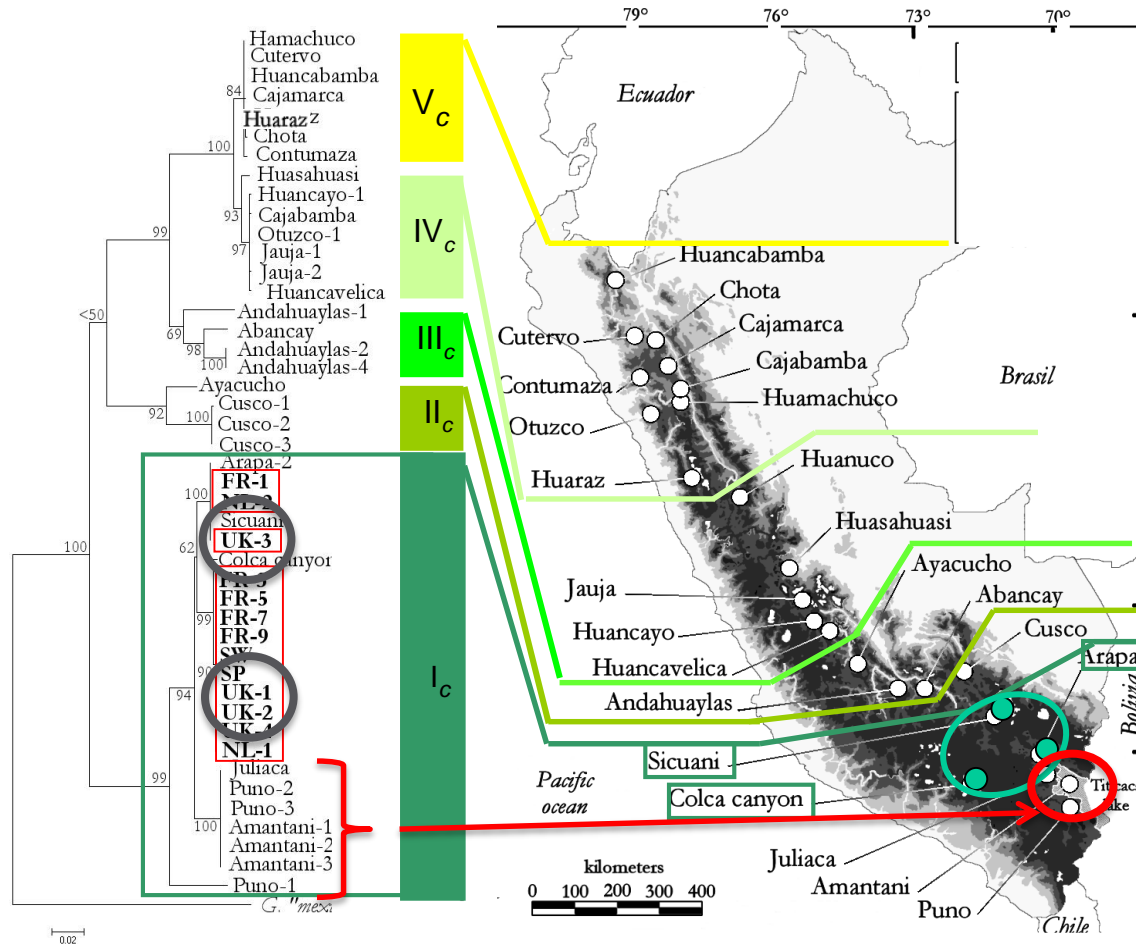




- 1. Characterisation of UK *G. pallida* populations and their distribution; finding markers to distinguish between pathotypes**
2. Wild potatoes species as source of new resistance to *G. pallida*



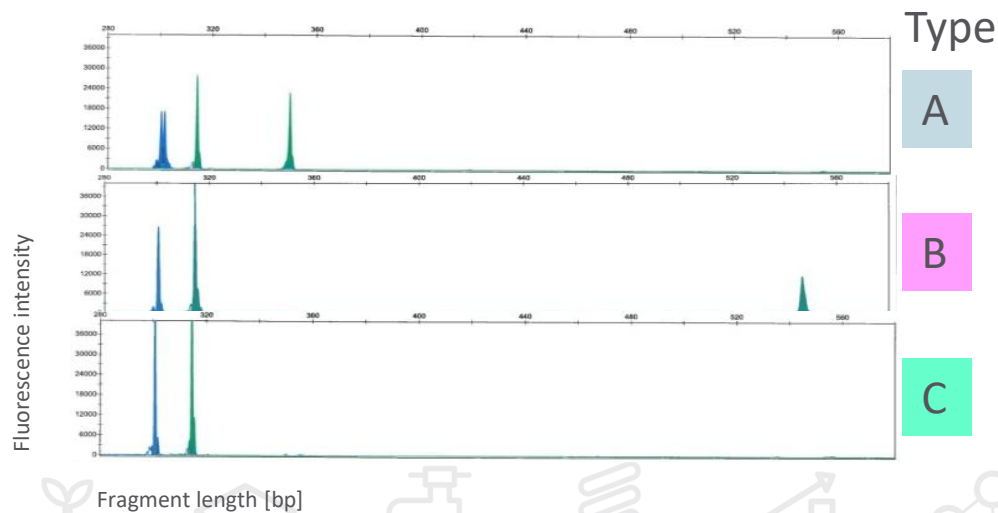
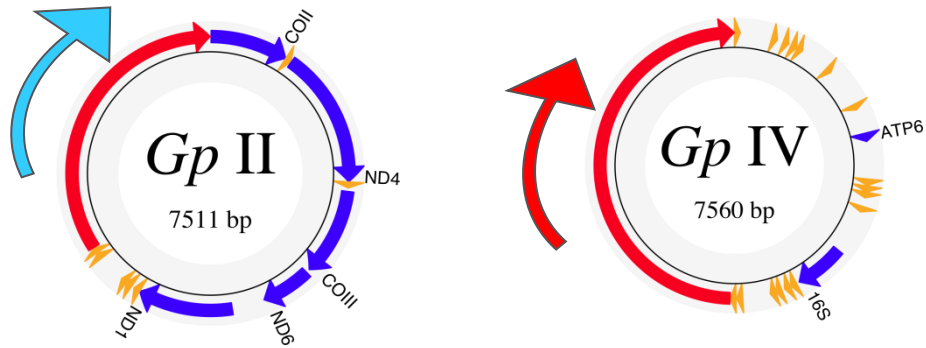
# *G. pallida* populations in the UK originate from South America based on microsatellites and Cytb



Plantard *et al* (2008),  
*Molecular Ecology*



# A mitochondrial marker can distinguish between the three introductions of *G. pallida*



PCR amplification of a non-coding region of mitochondrial circles II and IV with primers that are labelled with two different fluorophores, Taq1 digestion, electrophoresis and laser detection of fluorescent DNA fragments.



# Composition of *G. pallida* from the historical JHI collection

Samples	Population	Type A	Type B	Type C	No. cysts analysed
JHI collection	Lindley	25 (96%)	1 (4%)		26
	Luffness field 1	2 (6%)	33 (94%)		35
	Pa1	4 (19%)	2 (10%)	15 (71%)	21



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“Pa2 end of Pa2/3”  
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Can these markers be used as pathotype markers?



# Composition of *G. pallida* in historical and recent field samples

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Field	Luffness field 1		7 (39%)	9 (50%)	2 (11%)	18
	Luffness field 2				2 (100%)	2
	Luffness field 3		4 (100%)			4
	Luffness field 5		1 (33%)		2 (67%)	3

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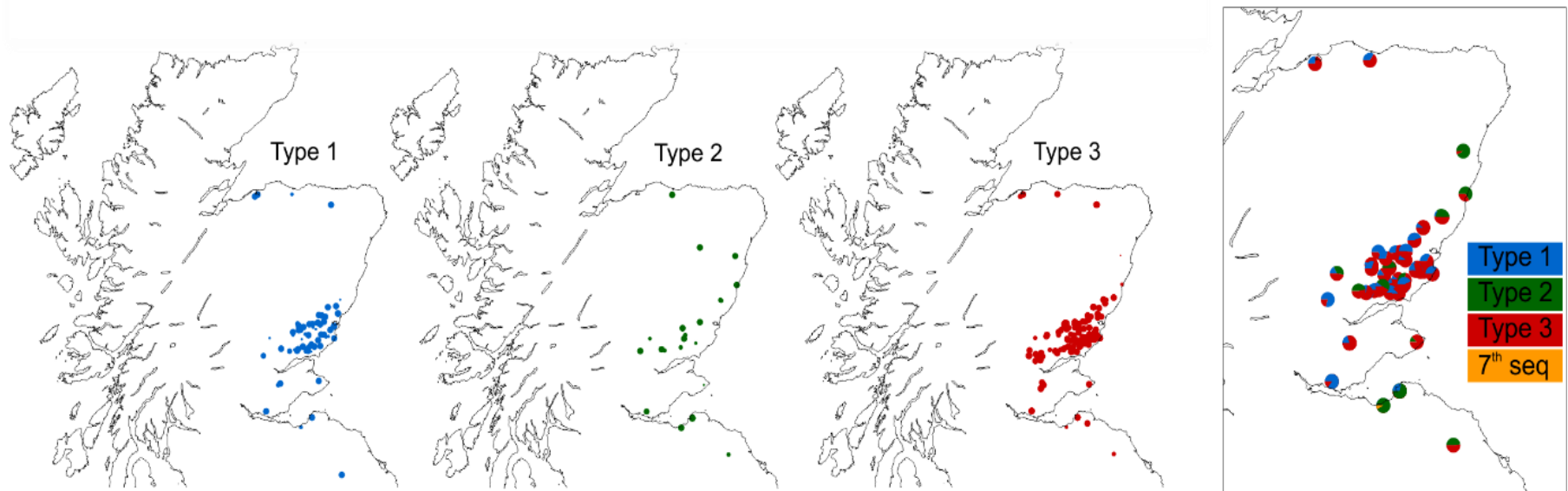
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## In Scotland the 3 *G. pallida* introductions are widespread



- All 3 types are widespread
- Most fields have 1 cytb type
- 1/5 fields contain mixtures
- <3% contain all three types
- 1 field has a 4<sup>th</sup> type



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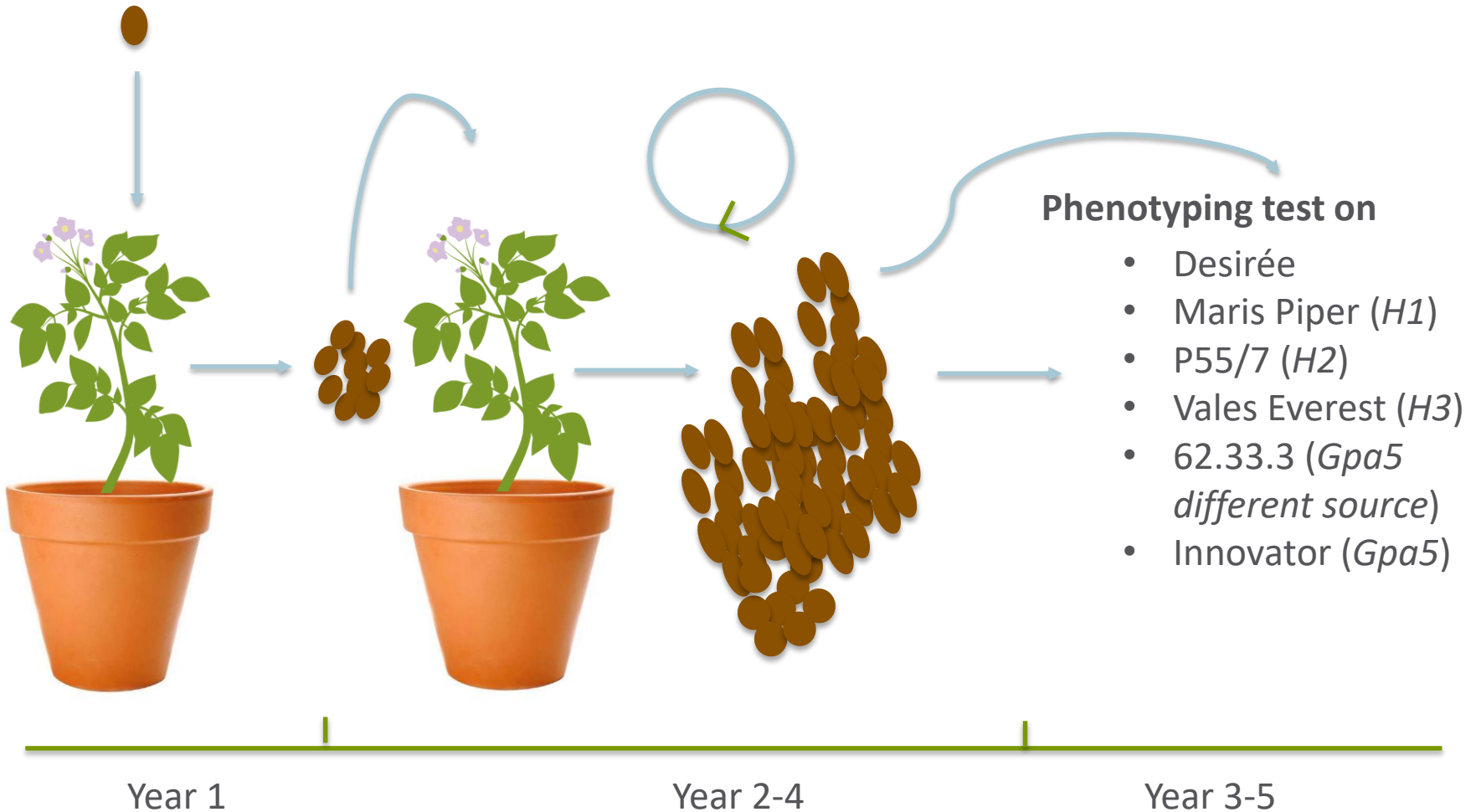
If UK fields contain multiple introductions of  
*G. pallida*, are they also mixtures of  
phenotypes?

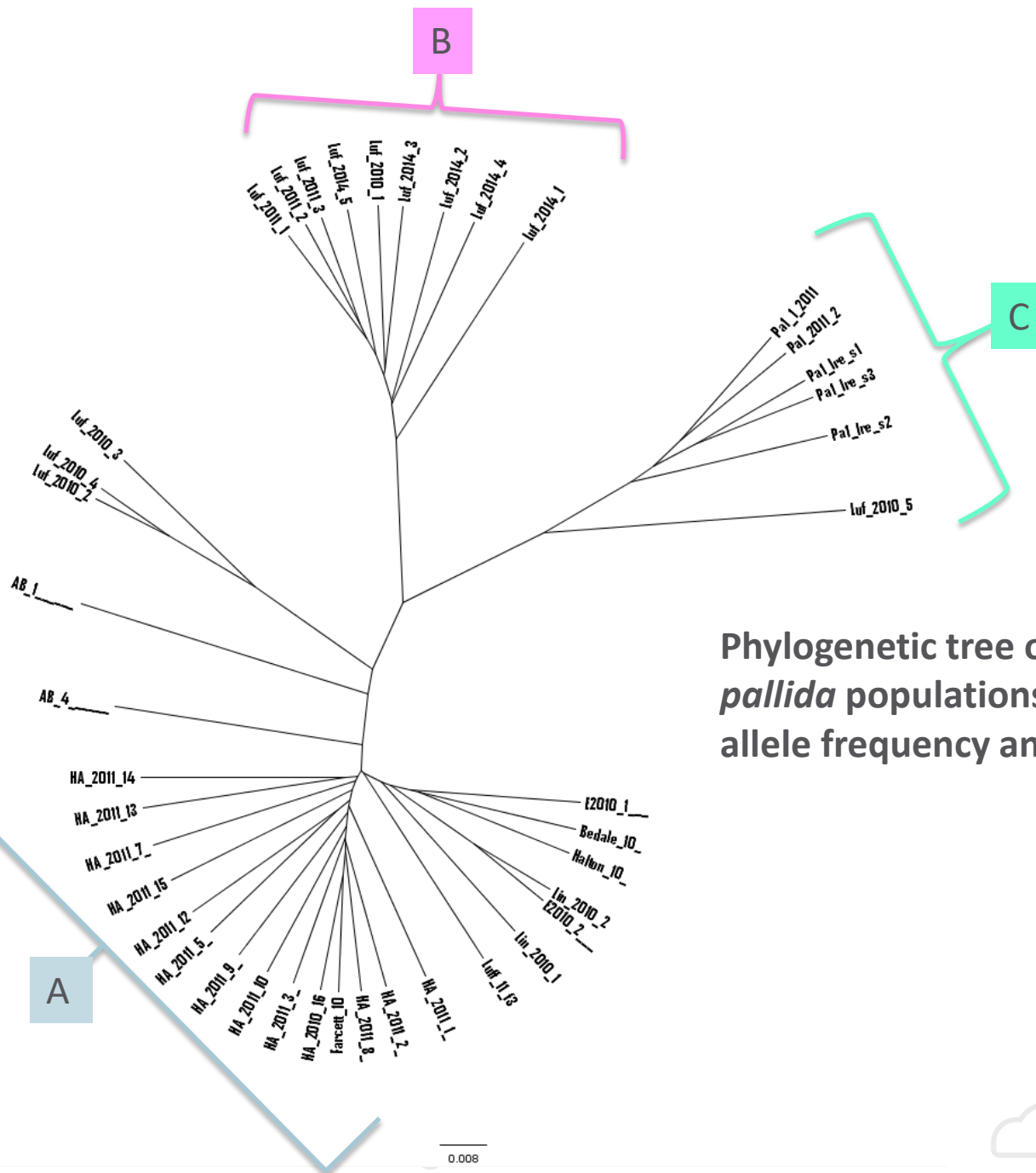


# Generation of single cyst lines



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Phylogenetic tree of different British *G. pallida* populations based on genome-wide allele frequency analysis of 1500 loci



# Results



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		Desirée	M. Piper	P55/7	VTN 62.33.3	V. Everest	Innovator
Lindley 2010 11	2016	Red	Red	Orange	Yellow	Yellow	Green
Lindley 2010 11	2017	Red	Red	Orange	Orange	Orange	Green
Lindley 2010 3	2017	Red	Red	Orange	Orange	Orange	Green
Lindley JHI pool	2016	Red	Red	Orange	Light Green	Green	Green
Lindley JHI pool	2017	Red	Red	Orange	Light Green	Orange	Green
Luff 2011 3-8	2017	Red	Red	Light Green	Green	Green	Green
Luff 2011 3-17(b)	2016	Red	Red	Orange	Green	Green	Green
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Luff 2011 3-18(a)	2016	Red	Red	Orange	Green	Green	Light Green
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Lindley 2010 11	2016							A	A
Lindley 2010 11	2017							A	A
Lindley 2010 3	2017							A	A
Lindley JHI pool	2016							A	
Lindley JHI pool	2017							A	
Luff 2011 3-8	2017							A	A
Luff 2011 3-17(b)	2016							A	A
Luff 2011 3-17(b)	2017							A	A
Luff 2011 3-18(a)	2016							A	A
Luff 2011 3-18(a)	2017							A	A
Luff 2011 1-12	2016							B	B
Luff 2011 1-12	2017							B	B
Luff 2014 1-4	2017							B	B
Luff 2014 1-19	2017							B	B
Luff 2014 1-30	2017							B	B
Lufness JHI pool	2016							B	B
Lufness JHI pool	2017							B	B
Pa 1 2011 3	2017							A	C
Pa 1 2011 12	2017							A	C
Pa1 2011 pool	2016							C	C
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AB A8-2	2016	Red	Red	Orange	Light Green	Light Green	Light Green
AB A8-2	2017	Red	Red	Orange	Light Green	Light Green	Green
AB Pb-3	2016	Red	Red	Orange	Light Green	Light Green	Light Green
AB Pb-3	2017	Red	Red	Orange	Light Green	Light Green	Light Green
AB Pb-12	2017	Red	Red	Red	Green	Light Green	Light Green
HA 2011 9	2016	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 9	2017	Red	Red	Orange	Light Green	Light Green	Green
HA 2011 32	2016	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 32	2017	Red	Red	Yellow	Yellow	Light Green	Light Green
HA 2011 12	2016	Red	Red	Orange	Orange	Yellow	Light Green
HA 2011 12	2017	Red	Red	Orange	Orange	Yellow	Light Green
HA 2011 27	2016	Red	Red	Orange	Orange	Orange	Light Green
HA 2011 27	2017	Red	Red	Orange	Yellow	Yellow	Light Green
HA 2011 34	2017	Red	Red	Orange	Yellow	Orange	Light Green
HA 2011 49	2017	Red	Orange	Orange	Yellow	Light Green	Light Green

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AB Pb-3	2017	Red	Red	Orange	Light Green	Light Green	Light Green
AB Pb-12	2017	Red	Red	Red	Light Green	Light Green	Light Green
HA 2011 9	2016	Red	Red	Orange	Light Green	Light Green	Light Green
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AB A8-2	2017	Red	Red	Orange	Light Green	Light Green	Light Green
AB Pb-3	2016	Red	Red	Orange	Light Green	Light Green	Light Green
AB Pb-3	2017	Red	Red	Orange	Light Green	Light Green	Light Green
AB Pb-12	2017	Red	Red	Red	Light Green	Light Green	Light Green
HA 2011 9	2016	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 9	2017	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 32	2016	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 32	2017	Red	Red	Yellow	Yellow	Light Green	Light Green
HA 2011 12	2016	Red	Red	Orange	Orange	Yellow	Light Green
HA 2011 12	2017	Red	Red	Orange	Orange	Yellow	Light Green
HA 2011 27	2016	Red	Red	Orange	Orange	Orange	Light Green
HA 2011 27	2017	Red	Red	Orange	Yellow	Yellow	Light Green
HA 2011 34	2017	Red	Red	Orange	Yellow	Orange	Light Green
HA 2011 49	2017	Red	Orange	Orange	Yellow	Light Green	Light Green

Level of Resistance

-



+



# Results



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Population ID	Year Tested	Potato Genotypes with Different Sources of Resistance					
		Desirée	M. Piper	P55/7	VTN 62.33.3	V. Everest	Innovator
AB A8-2	2016	Red	Red	Orange	Light Green	Light Green	Light Green
AB A8-2	2017	Red	Red	Orange	Light Green	Light Green	Light Green
AB Pb-3	2016	Red	Red	Orange	Light Green	Light Green	Light Green
AB Pb-3	2017	Red	Red	Orange	Light Green	Light Green	Light Green
AB Pb-12	2017	Red	Red	Red	Light Green	Light Green	Light Green
HA 2011 9	2016	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 9	2017	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 32	2016	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 32	2017	Red	Red	Yellow	Light Green	Light Green	Light Green
HA 2011 12	2016	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 12	2017	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 27	2016	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 27	2017	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 27	2017	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 34	2017	Red	Red	Orange	Light Green	Light Green	Light Green
HA 2011 49	2017	Red	Red	Orange	Light Green	Light Green	Light Green

Level of Resistance

-



+



# Results



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Population ID	Year Tested	Potato Genotypes with Different Sources of Resistance						Mito-type	GBS Group
		Desirée	M. Piper	P55/7	VTN 62.33.3	V. Everest	Innovator		
AB A8-2	2016							A	
AB A8-2	2017							A	
AB Pb-3	2016							A	A
AB Pb-3	2017							A	A
AB Pb-12	2017							A	A
HA 2011 9	2016							A	A
HA 2011 9	2017							A	A
HA 2011 32	2016							A	A
HA 2011 32	2017							A	A
HA 2011 12	2016							B	A
HA 2011 12	2017							B	A
HA 2011 27	2016							B	A
HA 2011 27	2017							B	A
HA 2011 34	2017							B	A
HA 2011 49	2017							B	A

Level of Resistance



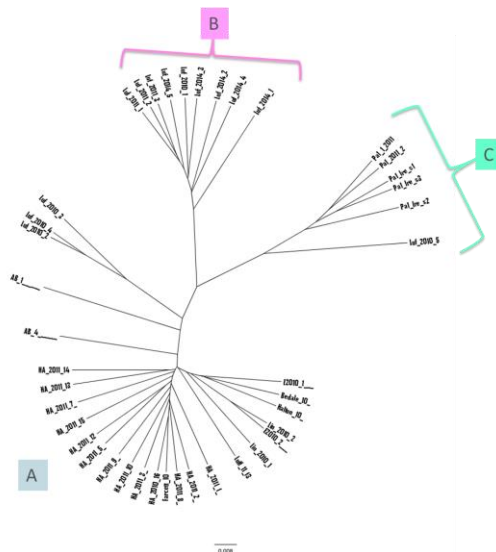
# Characterisation of UK *G. pallida* populations and their distribution summary

- ❖ Our data suggest that PCN populations became more complex over time.
- ❖ Current *G. pallida* field populations are likely to comprise mixtures of up to the three different historical introductions from South America.
- ❖ VTN62.33.3, P55/7 and Vales Everest show the greatest variability in nematode multiplication.
- ❖ Innovator consistently provides a good level of resistance for all *G. pallida* populations. There is evidence that this resistance will be overcome. We need more resistant varieties, pyramiding of different resistance genes.
- ❖ The mitochondrial markers for the different introductions are not suitable as pathotype markers



# Future Work: Development of molecular pathotype markers for *G. pallida*

Combining the SNP data obtained from the GBS analysis with the phenotypic data obtained for the single cyst lines and population pools provided SNP candidates in order to find robust molecular pathotype markers.



Single cyst line/population	Pheno type	Mito type	GBS group
HA 12	PA3	B	A
HA27	PA3	B	A
HA34	PA3	B	A
PB-12	PA2	A	A
Luff3-18	PA2	A	A
Luff 3-8	PA2	A	A
Luff1-12	PA3	B	B
Luff1-4	PA3	B	B
Luff1-30	PA3	B	B
Pa1-12	PA1	A	C
Pa1 pool	PA1	C	C
Pa1 ire 1	PA1	n/a	C





# Future work: Candidate SNPs for molecular pathogen markers for *G. pallida*

	Allele1/2	% allele 1 in populations			
		PA2	PA3	PA1	
1	A/T	0.0	0.0	100.0	some populations sequenced, mixture of sequences.
2	T/C	0.0	9.1	100.0	some populations sequenced, SNPs found in Pa1 compared to Pa2/3
3	G/A	100.0	100.0	16.7	some populations sequenced, no pathotype specific SNPs found
4	G/A	100.0	100.0	16.7	primers designed, not sequenced yet
5	G/A	100.0	100.0	16.7	primers designed, not sequenced yet
6	T/C	0.0	9.1	100.0	
7	G/C	87.5	81.8	16.7	
8	T/C	100.0	9.1	100.0	
9	T/C	25.0	81.8	0.0	
10	T/A	37.5	90.9	0.0	
11	T/C	50.0	81.8	0.0	
12	G/A	75.0	90.9	16.7	

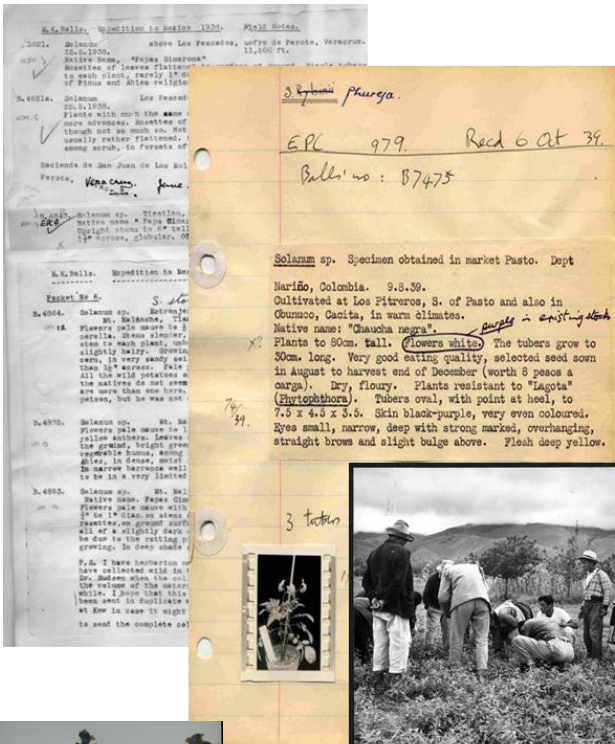




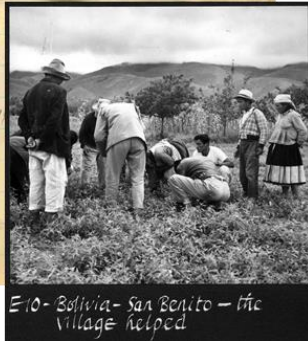
1. Characterisation of UK *G. pallida* populations and their distribution; finding markers to distinguish between pathotypes
2. **Wild potatoes species as source of new resistance to *G. pallida***



# History of the Commonwealth Potato Collection (CPC)



- Discovery of blight resistant spontaneous hybrid between cultivated potato and the Mexican species *Solanum demissum*.
- Collecting expeditions to South America 1938-1939.
- Jack Hawkes.
- Empire Collection created, now CPC.



# CPC today



- One of a network of international potato gene banks.
- Currently over 1500 accessions with over 80 different species.

- 2/3 wild tuber bearing species 1/3 primitive cultivated types.
- Collection held in true seed form.
- High health status.
- Working collection and base collection system.



# Identifying natural sources of resistance



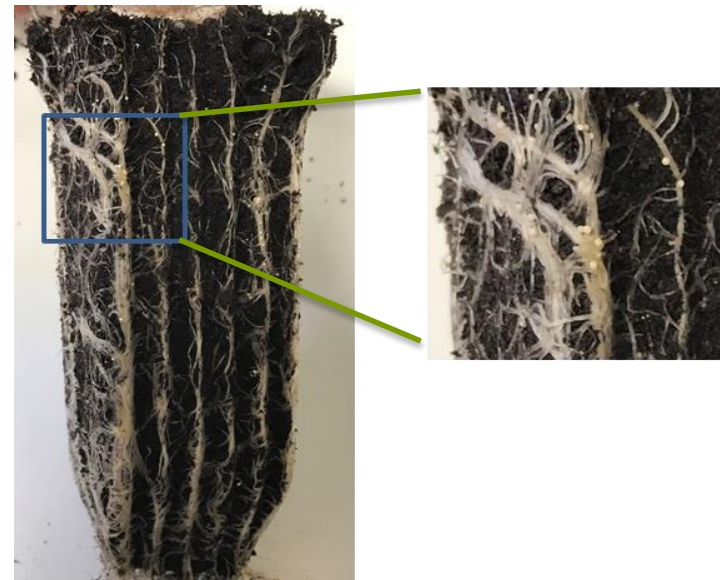
- *S. spegazzinii*, acc. 7195, shows natural resistance to *G. pallida*.
- Diploid wild potato species.
- 1966 collected in Argentina, la Riocha, Fatima 1950 m altitude

- 2003: *S. spegazzinii* 7195(10) x *S. tuberosum* group phureja DB337(37)
- Scoring for resistance against PCN in progeny, selection of one resistant plant 02.F1.3a (35) as parent for my screen.
- 2013 backcross 02.F1.3a (35) x *S. tuberosum* group phureja DB337(37) 13.A.02 ~1000 F1



# Identification of resistant and susceptible progeny

200 F1 plants from 13.A.02 and their parents were scored for *G. pallida* population Lindley resistance/susceptibility in 4 replicate by counting infection the number of females on the surface 8 weeks post infection.



# Mapping of genes conferring resistance to *G. pallida* in the wild potato species *S. spegazzinii*

Crossing 13A02	<i>S. tuberosum</i> phureja DB327(37) susceptible	
Resistant clone	r	r
03.F1.3.35a from crossing	R	Rr
<i>S. Spegazzinii</i> CPC7195	r	rr
x		
<i>S. tuberosum</i> phureja		

Backcrossing resistant parent with susceptible parent screening of F1 and parents for resistance/susceptibility to PCN

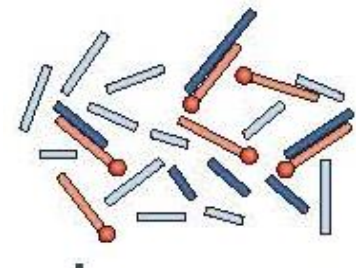
Bulking resistant and susceptible plants, preparation of genomic DNA



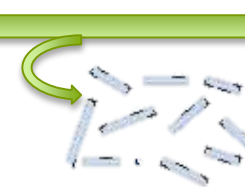
Construction of indexed library



Hybridisation with biotinylated RNA library baits,



Pulldown, wash  
Enrichment step



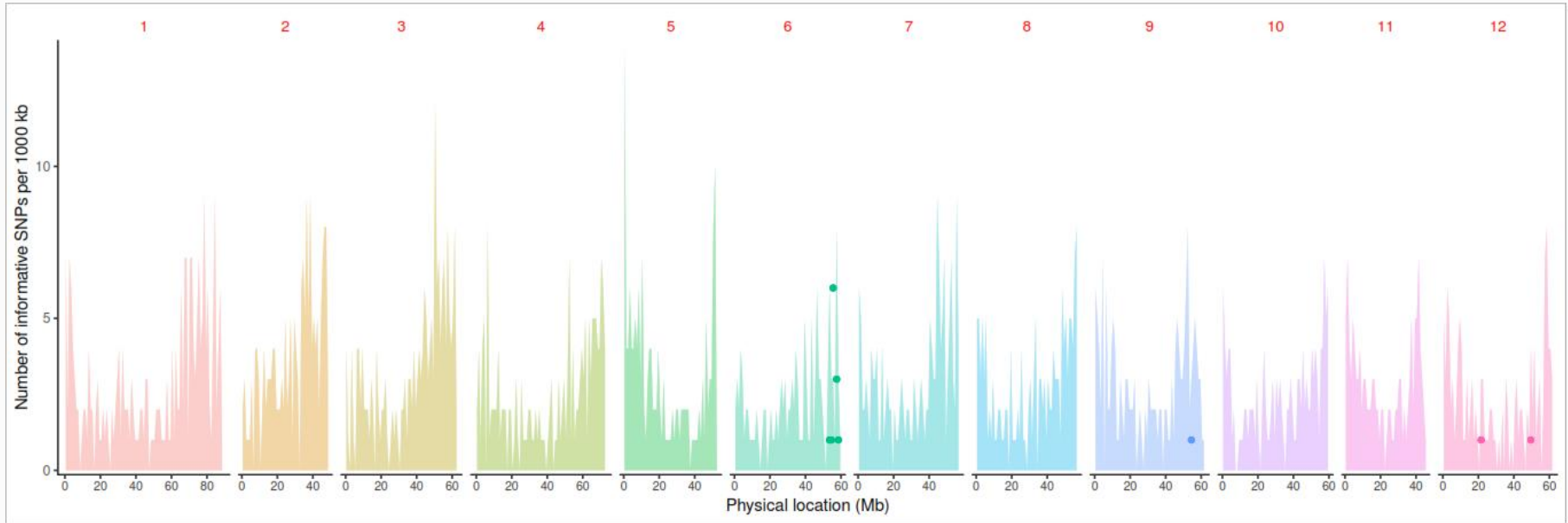
Next Generation Sequencing

Analysing data

AGGTCGTTACGTACGCTAC  
GACCTACATCAGTACATAG  
GCATGACAAAGCTAGCTGT

Mapping, alignment,  
variant calling

# Generic-mapping enrichment Sequencing (GenSeq)



Informative SNPs from GenSeq: enrichment of ~2000 single/low copy number genes: the background color on the y-axis show the areas covered by the enrichment, the dots indicate the number and location of informative SNPs, which are SNPs present in all resistant plants but not in any of the susceptible ones.





# Development of KASP (Kompetitive Allele Specific PCR) markers

Flanking sequences (50 bp each upstream and downstream) around the SNP positions were used to design KASP primers (KASP by Design Oligos, LGC Genomics limited).

Markers were validated by testing them on the parents.

Resistant Parent 

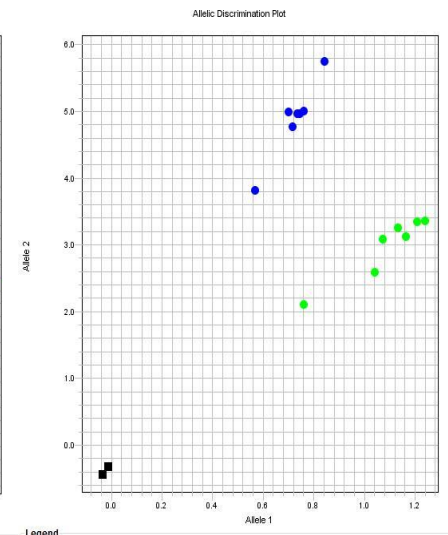
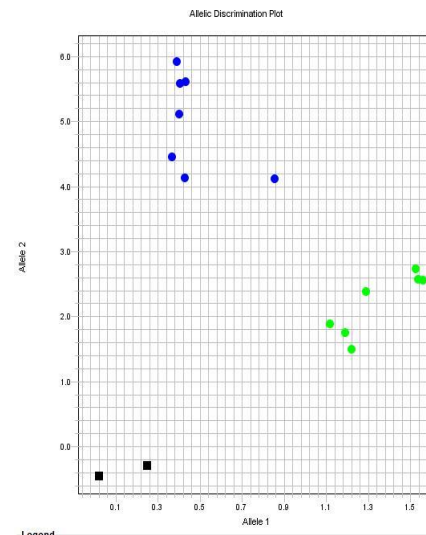
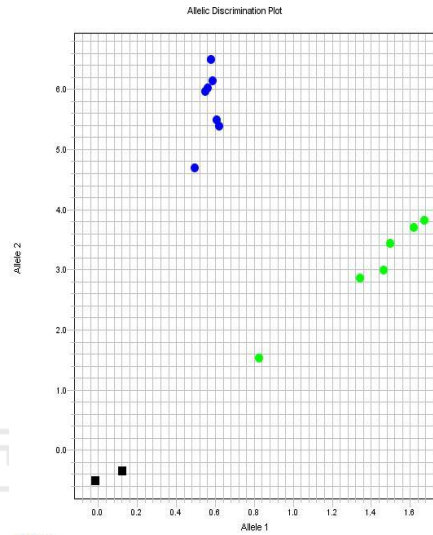
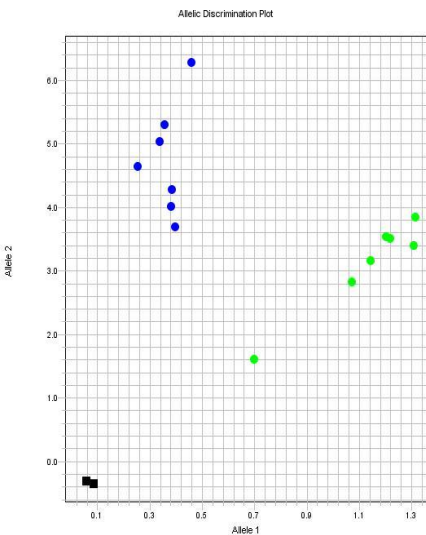
Susceptible Parent 

KASP 5

KASP 6

KASP 7

KASP 8



# Graphical Genotyping



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	SP	RP
K5	S	R
K6	S	R
K7	S	R
K8	S	R

K5 to K8 comprise 5.4 Mb

K5 to K7 comprise 3.4 Mb

	615	524	58	444	448	465	467	471	479	510	519	545	628	635	637	638	643	644	566
K5	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
K6	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
K7	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S
K8	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S	S

	A036	686	49	70	446	463	495	512	516	523	568	586	633	648	700	579	678	500
K5	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
K6	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
K7	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R
K8	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R

S	susceptible
R	resistant
	homozygot
	heterozygot



# Work in progress

- Screening of all 1000 progenies of the crossing with marker K5 and K7, looking for recombinants
- Recombinants are also screened with K6 and new markers to narrow down position
- Recombinants will be screened of resistance/susceptibility



# Introgressing the resistance to tetraploid cultivars and breeding clones.



- Diploid tetraploid crossing relies on unreduced gametes
- If successful, small berries with only a few seeds.
- Pyramiding of resistances
- Validating markers



# Summary

- The wild potato species *S. spegazzinii*, acc. 7195, shows natural resistance to *G. pallida*.
- With enrichment sequencing we have identified a region on chromosome VI which contains SNPs linked to the resistance.
- Kasp markers were developed and the locus for this new resistance locus for *G. pallida* in *S. spegazzinii* could be mapped to a region of 3.4 Mb.
- More markers have been designed and should provide more information about the locus.
- Evaluation if markers can be used more universally
- Introgression into tetraploid breeding clones to pyramid resistances.



# Acknowledgements



The James  
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## James Hutton Institute

Vivian Blok

Glenn Bryan

Ingo Hein

Miles Armstrong

Karen McLean

Brian Harrower

Katrin MacKenzie

Nematology lab

Potato-genetics lab

Glasshouse staff

## Agriculture and Agri-Food Canada

Benjamin Mimee

Pierre-Yves Veronneau

## SASA Edinburgh

Jon Pickup

Andrew Pitt

Nematology lab



Scottish Government  
Riaghaltas na h-Alba  
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