EAPR 2022
21st Triennial Conference
Krakow, July 4-8, 2022

Organizers: eapr european association for potato research IHAR

EAPR Triennial, Kraków, Poland: 4-8 July 2022

- Originally scheduled for 2020, deferred three times
- Jadwiga Śliwka (IHAR), first woman President of the EAPR, welcomed over 200 delegates from 36 countries
- 10 Keynote lectures, 15 sessions covered topics including resistance breeding, bacterial & fungal diseases, viral diseases, late blight, disease control, storage
- I presented an update on AsiaBlight
- The conference dinner took place underground in the Wieliczka Salt Mine!

AsiaBlight

Potato late blight network for Asia

Update on AsiaBlight’s efforts to create a coarse-scale map of the *Phytophthora infestans* population in Asia

Louise Cooke, Christelle Lasserre, Alberto Maurer, Philip Kear,
Jorge Andrade-Piedra, David Cooke, Gregory Forbes

6th July 2022: **EAPR 2022**, 21st Triennial Conference, Krakow, Poland

EAPR Triennial, Kraków, Poland: 4-8 July 2022

Update on AsiaBlight

- Showed that we now have Regional Representatives covering 14 regions across Asia
- Showed examples of activities in selected countries: Bangladesh, India, Pakistan, China
- Described progress in genotyping and summarised results

Highlights of EAPR Triennial

Ian Barker’s keynote lecture

The potato program of the International Potato Center: successes, challenges and the way forward highlighted:

- The increasing importance of potatoes in Asia
- The role of increased potato production in reducing water usage
- CIP drought tolerant and disease resistant varieties help in achieving the UN Sustainable Development Goals
- 20% of the potato growing area in the global south is occupied by CIP varieties
- High bio-available iron in potatoes, particularly yellow-fleshed CIP varieties, could cover 50% of iron deficiency in women

Lowering the cost of seed production through seed production research (potato rooted apical cuttings)- driving adoption of late-blight resistant and heat-tolerant varieties

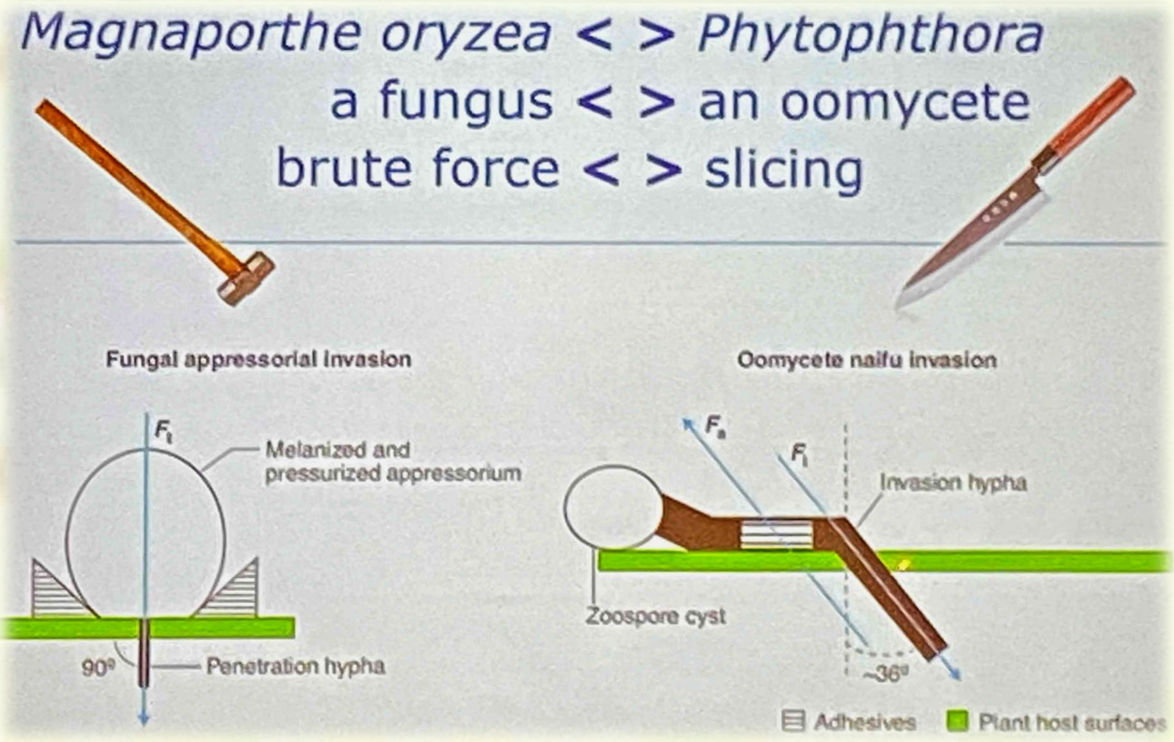
Cecinta Nduru, Decentralized potato seed producer, Meru, Kenya

Highlights of EAPR Triennial

Francine Govers keynote lecture

The mission of *Phytophthora*: explore, invade and manipulate brought to life how *Phytophthora* interacts with its host:

- Tracking zoospores: they explore their environment, swim, tumble and respond to attractants (glutamic acid) to locate their host
- The *Phytophthora* zoospore invades its host by slicing its way in with its sharp hyphal tip (very different from the approach of fungi whose appressoria use brute force to enter host cells)



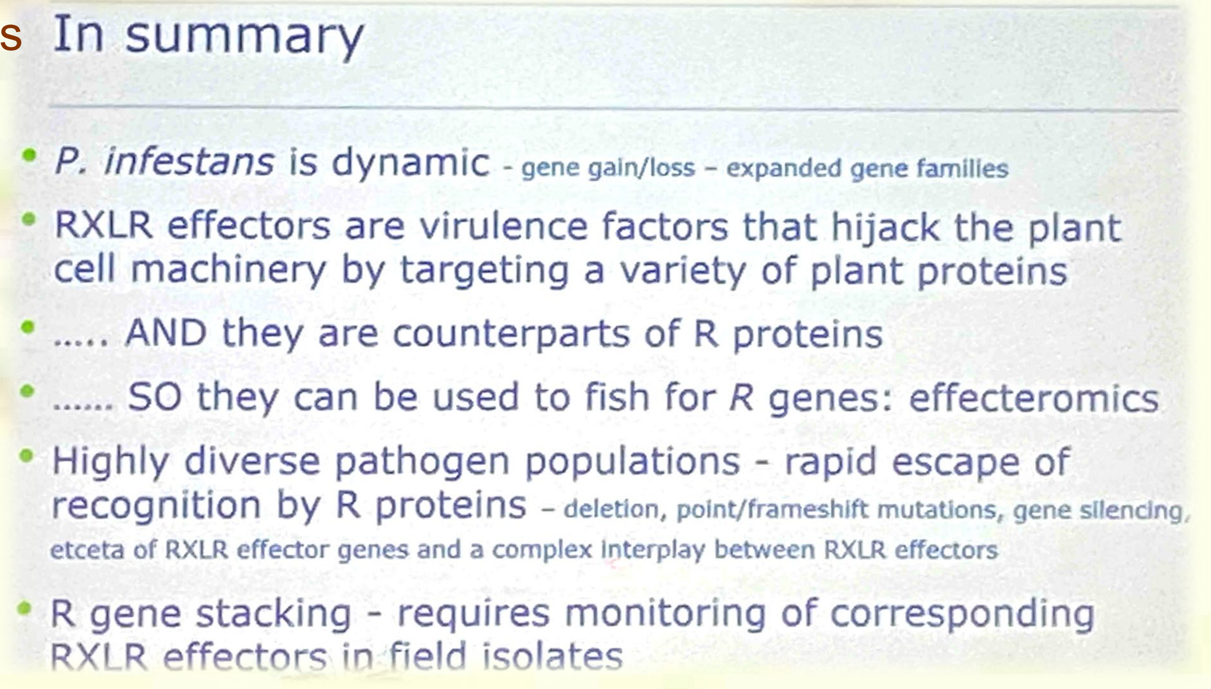
Magnaporthe oryzea < > Phytophthora
a fungus < > an oomycete
brute force < > slicing

Highlights of EAPR Triennial

Francine Govers keynote lecture

The mission of *Phytophthora*: explore, invade and manipulate brought to life how *Phytophthora* interacts with its host:

- Once in the host cell, *Phytophthora* haustoria deliver effectors which manipulate host defences: these are very dynamic, those recognised by the host can be deleted
- If R-gene stacking within potato cultivars for sustainable blight resistance then **monitoring the corresponding RXLR effectors in the field *P. infestans* population is essential**
- Francine has collaborators in China and provided contact details



In summary

- *P. infestans* is dynamic - gene gain/loss – expanded gene families
- RXLR effectors are virulence factors that hijack the plant cell machinery by targeting a variety of plant proteins
- ….. AND they are counterparts of R proteins
- …… SO they can be used to fish for *R* genes: effecteromics
- Highly diverse pathogen populations - rapid escape of recognition by R proteins – deletion, point/frameshift mutations, gene silencing, etceta of RXLR effector genes and a complex interplay between RXLR effectors
- R gene stacking - requires monitoring of corresponding RXLR effectors in field isolates

AsiaBlight
Potato late blight network for Asia

Highlights of EAPR Triennial

Poster from Ludwiczewska *et al*. (Jadwiga Śliwka's group)

Detection of genes for resistance to *Phytophthora infestans* in selected potato genotypes using PCR markers

- Gene sequencing being used in a co-operative project between Norway and Poland (DivGene) to diagnose the occurrence of resistance genes and analyse their diversity in potato cultivars
- Presented results of PCR detection of 12 *Rpi* genes in 223 potato genotypes
- The project will also analyse the diversity of genes encoding late blight effectors in *P. infestans* populations in Poland and Norway

Highlights of EAPR Triennial

Poster from Ludwiczewska *et al*. (Jadwiga Śliwka's group)

Detection of genes for resistance to *Phytophthora infestans* in selected potato genotypes using PCR markers

- Another output from this project is a review Paluchowska, Śliwka & Yin, 2022, *Planta* 255, article 127

Planta (2022) 255:127
https://doi.org/10.1007/s00425-022-03910-6

REVIEW

Late blight resistance genes in potato breeding

Paulina Paluchowska[1] · Jadwiga Śliwka[1] · Zhimin Yin[1]

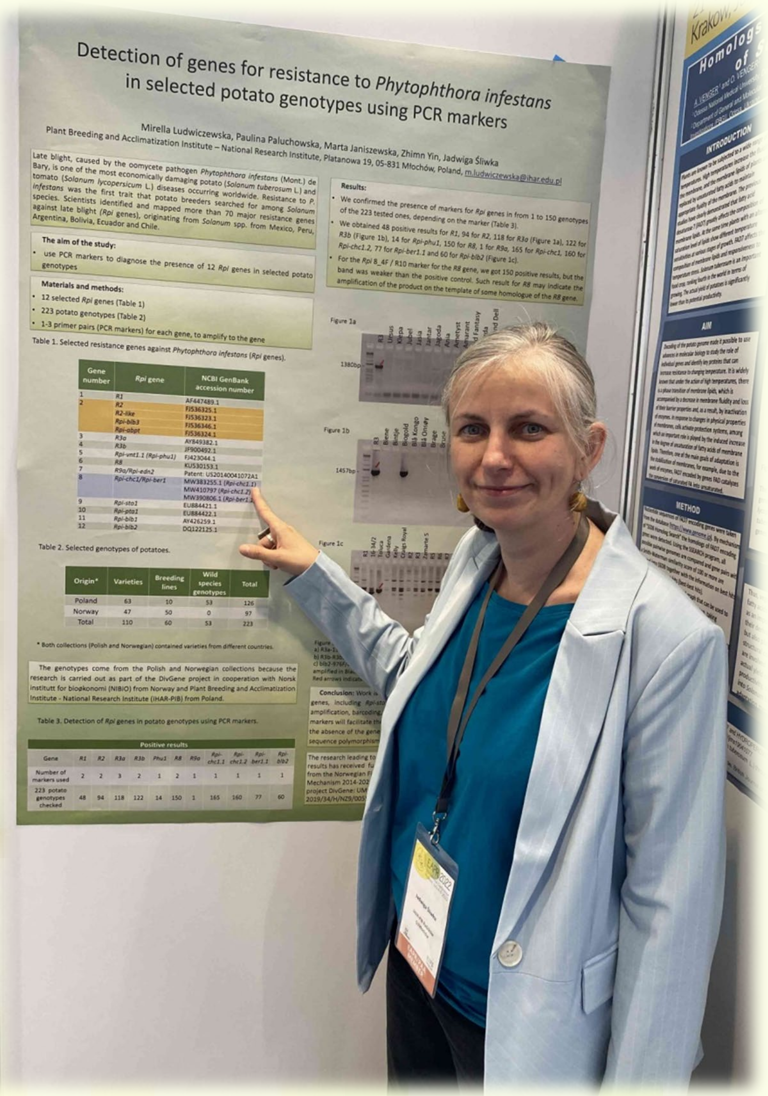
Received: 28 January 2022 / Accepted: 1 May 2022

Abstract

Main conclusion **Using late blight resistance genes targeting conservative effectors of *Phytophthora infestans* and the constructing gene pyramids may lead to durable, broad-spectrum resistance, which could be accelerated through genetic engineering.**

Abstract Potato (*Solanum tuberosum* L.) is one of the most important food crops worldwide. In 2020, potato production was estimated to be more than 359 million tons according to the Food and Agriculture Organization (FAO). Potato is affected by many pathogens, among which *Phytophthora infestans*, causing late blight, is of the most economic importance. Crop protection against late blight requires intensive use of fungicides, which has an impact on the environment and humans. Therefore, new potato cultivars have been bred using resistance genes against *P. infestans* (*Rpi* genes) that originate from wild relatives of potato. Such programmes were initiated 100 years ago, but the process is complex and long. The development of genetic engineering techniques has enabled the direct transfer of resistance genes from potato wild species to cultivars and easier pyramiding of multiple *Rpi* genes, which potentially increases the durability and spectrum of potato resistance to rapidly evolving *P. infestans* strains. In this review, we summarize the current knowledge concerning *Rpi* genes. We also discuss the use of *Rpi* genes in breeding as well as their detection in existing potato cultivars. Last, we review new sources of *Rpi* genes and new methods used to identify them and discuss interactions between *P. infestans* and host.

Keywords Cultivar · Effector · Genetic engineering · *Phytophthora infestans* · *Solanum tuberosum* · Wild crop relatives



Detection of genes for resistance to *Phytophthora infestans* in selected potato genotypes using PCR markers

Mirella Ludwiczewska, Paulina Paluchowska, Marta Janiszewska, Zhimn Yin, Jadwiga Śliwka
Plant Breeding and Acclimatization Institute – National Research Institute, Platanowa 19, 05-831 Młochów, Poland, m.ludwiczewska@ihar.edu.pl

Late blight, caused by the oomycete pathogen *Phytophthora infestans* (Mont.) de Bary, is one of the most economically damaging potato (*Solanum tuberosum* L.) and tomato (*Solanum lycopersicum* L.) diseases occurring worldwide. Resistance to *P. infestans* was the first trait that potato breeders searched for among *Solanum* species. Scientists identified and mapped more than 70 major resistance genes against late blight (*Rpi* genes), originating from *Solanum* spp. from Mexico, Peru, Argentina, Bolivia, Ecuador and Chile.

The aim of the study:

- use PCR markers to diagnose the presence of 12 *Rpi* genes in selected potato genotypes

Materials and methods:

- 12 selected *Rpi* genes (Table 1)
- 223 potato genotypes (Table 2)
- 1-3 primer pairs (PCR markers) for each gene, to amplify to the gene

Table 1. Selected resistance genes against *Phytophthora infestans* (*Rpi* genes).

Gene number	*Rpi* gene	NCBI GenBank accession number
1	*R1*	AF447489.1
2	*R2* *R2-like* *Rpi-blb3* *Rpi-abpt*	FJ536325.1 FJ536323.1 FJ536346.1 FJ536324.1
3	*R3a*	AY849382.1
4	*R3b*	JF900492.1
5	*Rpi-vnt1.1 (Rpi-phu1)*	FJ423044.1
6	*R8*	KU530153.1
7	*R9a/Rpi-edn2*	Patent: US20140041072A1
8	*Rpi-chc1/Rpi-ber1*	MW383255.1 (*Rpi-chc1.1*) MW410797 (*Rpi-chc1.2*) MW390806.1 (*Rpi-ber1.1*)
9	*Rpi-sto1*	EU884421.1
10	*Rpi-pta1*	EU884422.1
11	*Rpi-blb1*	AY426259.1
12	*Rpi-blb2*	DQ122125.1

Table 2. Selected genotypes of potatoes.

Origin*	Varieties	Breeding lines	Wild species genotypes	Total
Poland	63	10	53	126
Norway	47	50	0	97
Total	110	60	53	223

* Both collections (Polish and Norwegian) contained varieties from different countries.

The genotypes come from the Polish and Norwegian collections because the research is carried out as part of the DivGene project in cooperation with Norsk institutt for bioøkonomi (NIBIO) from Norway and Plant Breeding and Acclimatization Institute - National Research Institute (IHAR-PIB) from Poland.

Table 3. Detection of *Rpi* genes in potato genotypes using PCR markers.

	Positive results										
Gene	*R1*	*R2*	*R3a*	*R3b*	*Phu1*	*R8*	*R9a*	*Rpi-chc1.1*	*Rpi-chc1.2*	*Rpi-ber1.1*	*Rpi-blb2*
Number of markers used	2	2	3	2	1	2	1	1	1	1	1
223 potato genotypes checked	48	94	118	122	14	150	1	165	160	77	60

Results:

- We confirmed the presence of markers for *Rpi* genes in from 1 to 150 genotypes of the 223 tested ones, depending on the marker (Table 3).
- We obtained 48 positive results for *R1*, 94 for *R2*, 118 for *R3a* (Figure 1a), 122 for *R3b* (Figure 1b), 14 for *Rpi-phu1*, 150 for *R8*, 1 for *R9a*, 165 for *Rpi-chc1*, 160 for *Rpi-chc1.2*, 77 for *Rpi-ber1.1* and 60 for *Rpi-blb2* (Figure 1c).
- For the *Rpi* 8_4F / R10 marker for the *R8* gene, we got 150 positive results, but the band was weaker than the positive control. Such result for *R8* may indicate the amplification of the product on the template of some homologue of the *R8* gene.

Highlights of EAPR Triennial

Presentation from Ingo Hein, James Hutton Institute

Targeted mining of potato germplasm collections for novel disease resistance genes

- Ingo has shared his presentation and CIP (including Philip Kear) is part of this project

University of Dundee

TARGETED MINING FOR DISEASE RESISTANCE GENES

The James Hutton Institute

Yuhan Wang
Lynn Hunter Brown
Yuk Woon Cheung
Amanpreet Kaur
Brian Harrower
Miles Armstrong
Micha Bayer
Tom Adams

Ingo Hein
Ingo.Hein@hutton.ac.uk
EAPR meeting; July 6th 2022

Highlights of EAPR Triennial

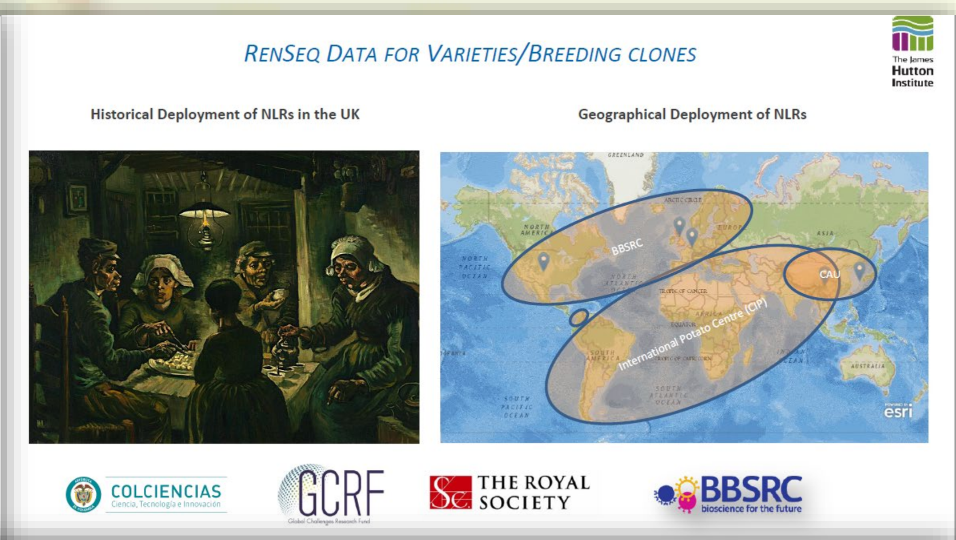
Presentation from Ingo Hein, James Hutton Institute

Targeted mining of potato germplasm collections for novel disease resistance genes

MAIN TARGETS OF OUR DISEASE RESISTANCE RESEARCH AND BREEDING EFFORTS

Late Blight	PCN	Viruses	Wart disease
Phytophthora infestans	*Globodera rostochiensis* *Globodera pallida*	*Potato virus Y* *PLRV*	*Synchytrium endobioticum*

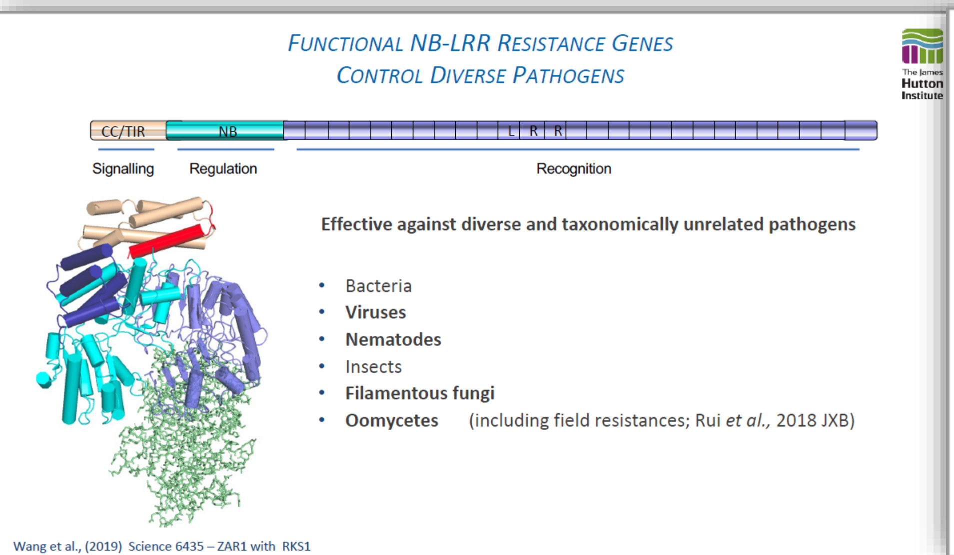
Photo by Ulrich Zunke; University of Hamburg;



RENSEQ DATA FOR VARIETIES/BREEDING CLONES

Historical Deployment of NLRs in the UK

Geographical Deployment of NLRs



FUNCTIONAL NB-LRR RESISTANCE GENES CONTROL DIVERSE PATHOGENS

Effective against diverse and taxonomically unrelated pathogens

- Bacteria
- **Viruses**
- **Nematodes**
- Insects
- **Filamentous fungi**
- **Oomycetes** (including field resistances; Rui *et al.*, 2018 JXB)

Wang et al., (2019) Science 6435 – ZAR1 with RKS1

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JHL
Drummond Todd
Vanessa Young
Matthew McDonald

CAAS Beijing
Jin Liping

Wageningen
Jack Vossen
Aska Govers

University of Dundee
Miles Armstrong
Paul Birch
Lynn Hunter Brown
Yuhan Wang
Yuk Woon Cheung

China Agricultural University
Xiaodan Wang
Li Jie
Daolong Dou

Yunnan Academy of Agricultural Sciences
Zhechao Pan

SASA
Triona Davey
Heather Campbell

CIP
Hannele Lindqvist-Kreuze
Philip Kear

The next EAPR Triennial

will take place in Oslo, Norway, 7-12 July 2024
under the Presidency of Arne Hermansen

AsiaBlight
Potato late blight network for Asia

I thank the British Society of Plant Pathology for a travel grant which assisted in funding my attendance