



New breeding opportunities for disease resistance

Ruth Bryant - RAGT - rbryant@ragt.fr

Rouergue, Auvergne, Gévaudan, Tarnais



Breeding programmes



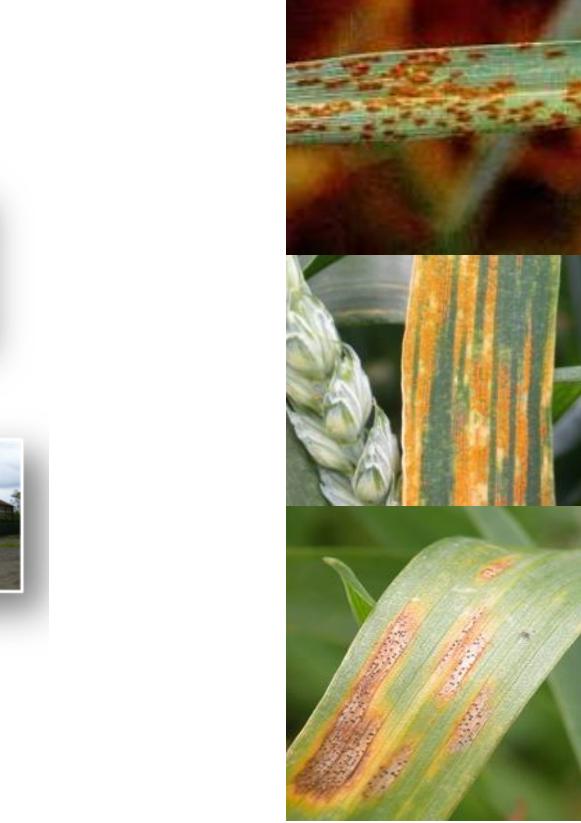
Premesques/la Chapelle



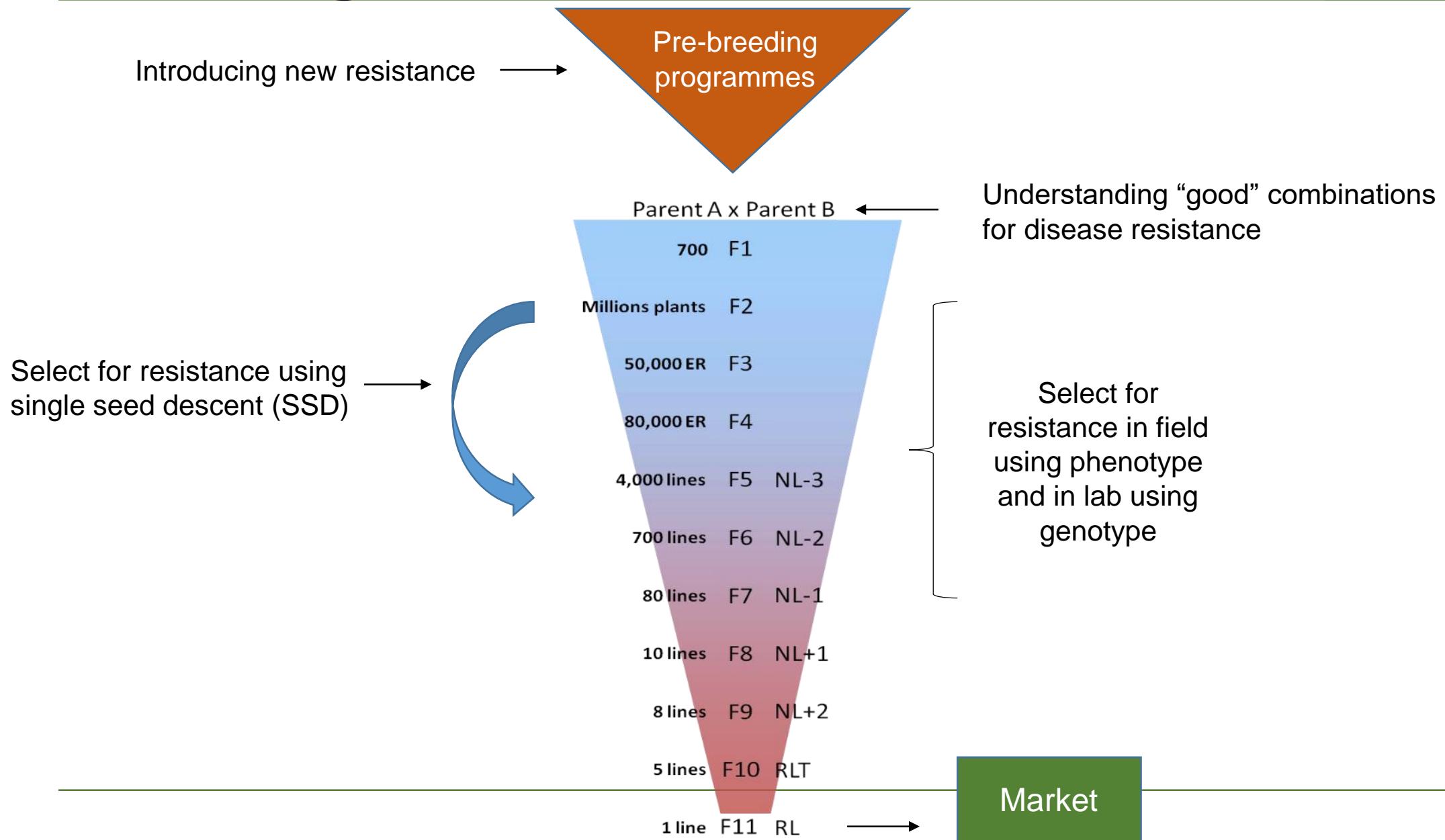
Louville-la-Chenard



Montbartier



Breeding for resistance



Working with elite material



- Already adapted
- Resistance to most diseases already present
- Genetics behind resistance still poorly understood

Resistance genes/QTL in elite material



Bi-parental populations

GWAS

Bulk segregate analysis

A

B

C

D

F

E

H

G

A + B

A + B

C + G

F

None

C + G + I

B



Variety 1



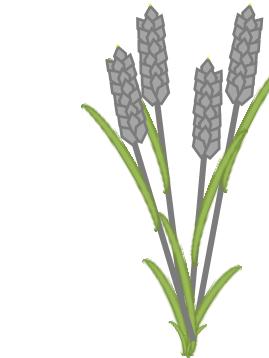
Variety 2



Variety 3



Variety 4



Variety 5



Variety 6

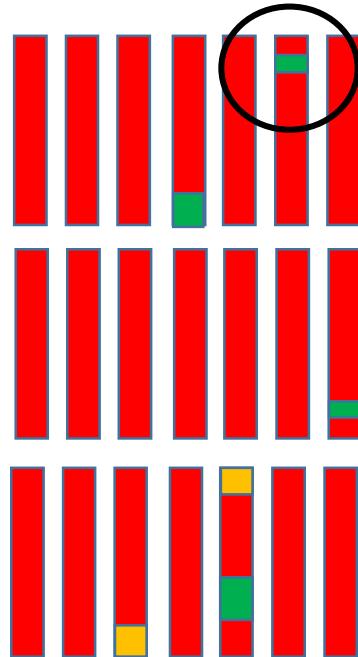


Variety 7

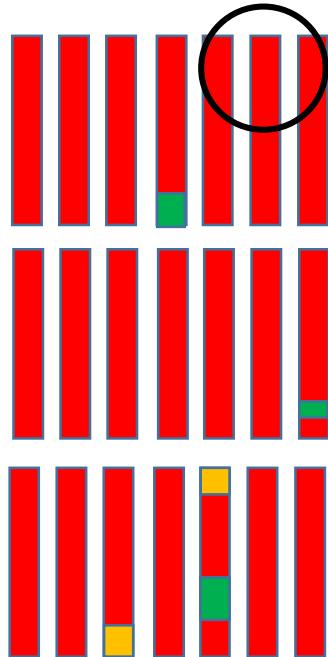
NILs for monitoring resistances



Resistant NIL

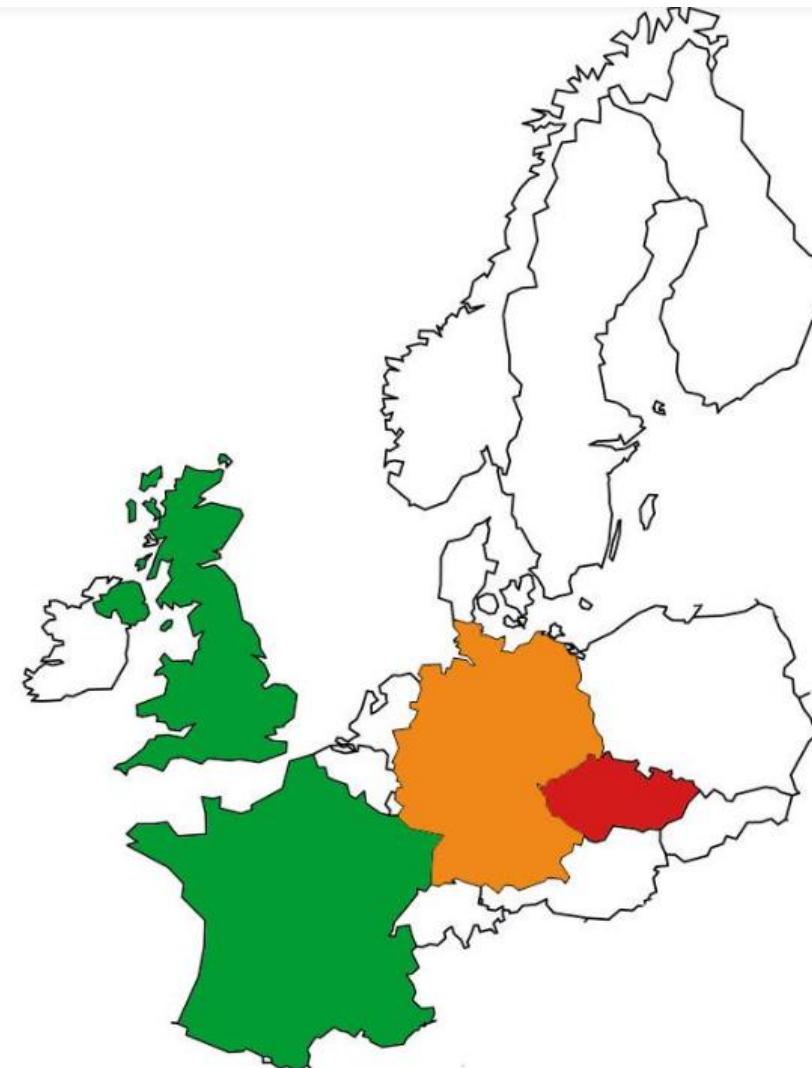


Susceptible NIL

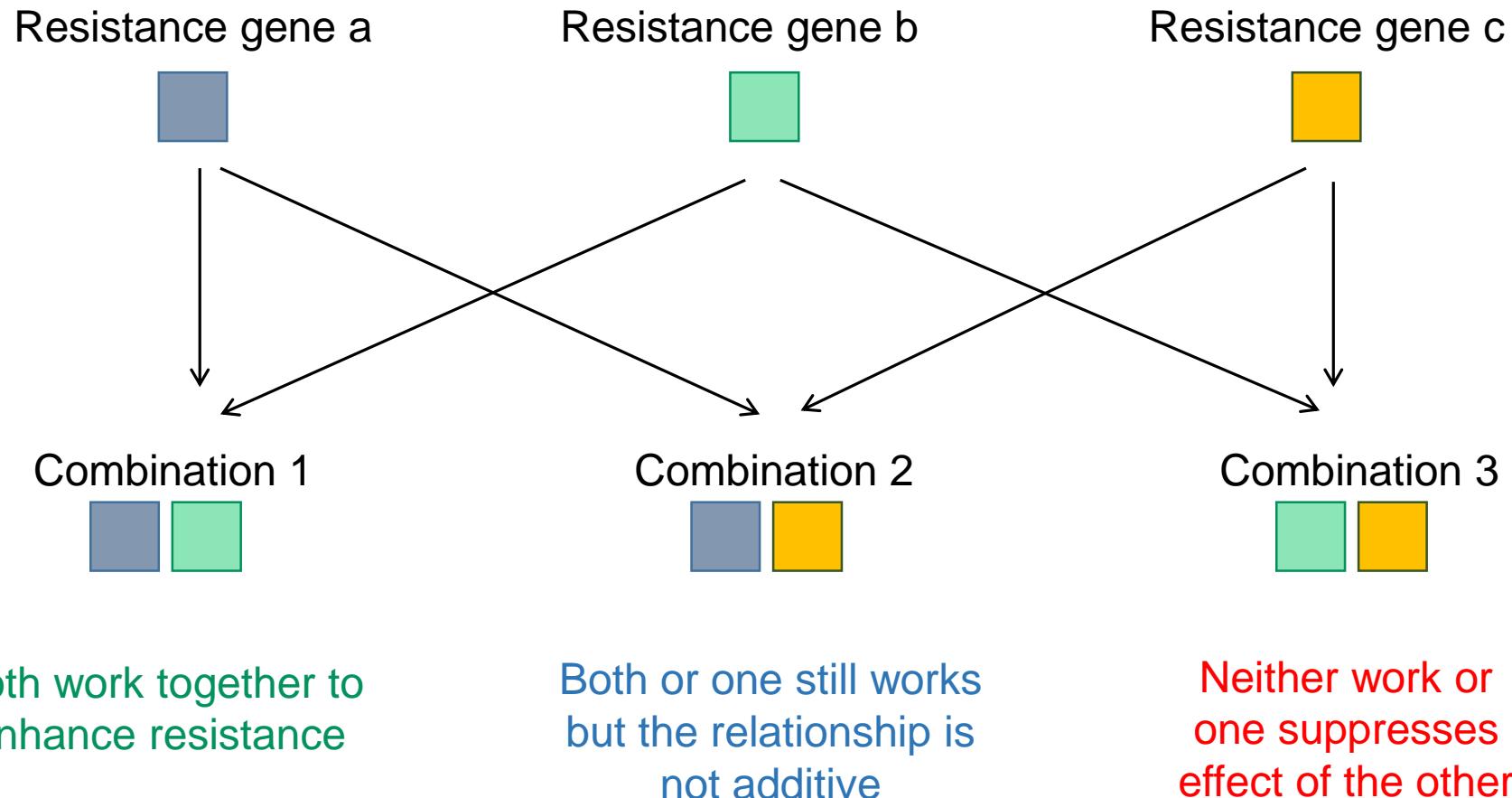


Resistant parent

Susceptible parent



Understanding gene/QTL interactions



Negative genes/QTL

Susceptibility factors

Examples:-

MLO



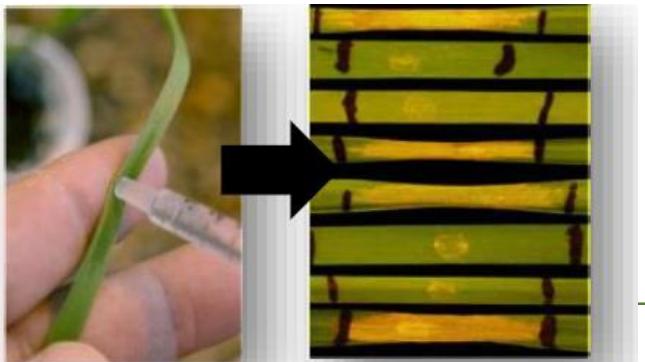
Letter | Published: 20 July 2014

Simultaneous editing of three homoeoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew

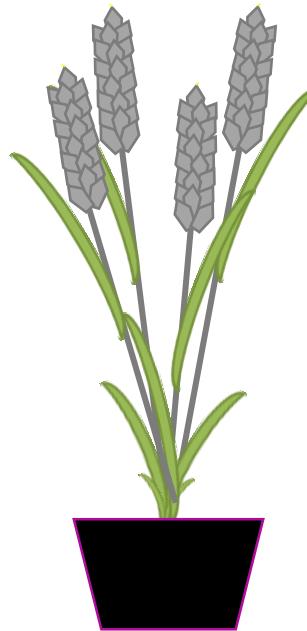
Yanpeng Wang, Xi Cheng, Qiwei Shan, Yi Zhang, Jinxing Liu, Caixia Gao & Jin-Long Qiu



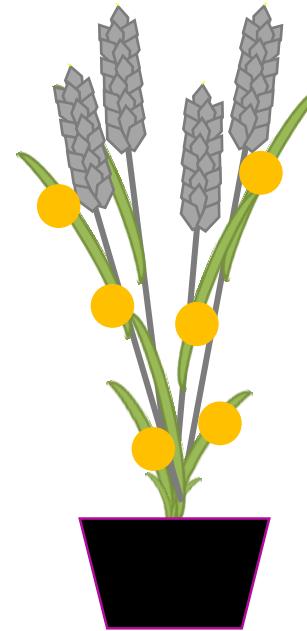
Tox-A – Tsn1



Suppressors



Resistant gene
No suppressor



Resistant gene
Suppressor

Genetic resources



Scientists sequence wheat genome in breakthrough once thought 'impossible'

Genome able to be used to produce hardier wheat varieties as greater food security needed



The
Guardian



the plant journal

S E B

SOCIETY FOR EXPERIMENTAL BIOLOGY

Technical Advance | Open Access | CC BY

Resistance gene enrichment sequencing (RenSeq) enables reannotation of the NB-LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations

Florian Jupe, Kamil Witek, Walter Verweij, Jadwiga Śliwka, Leighton Pritchard, Graham J. Etherington, Dan Maclean, Peter J. Cock, Richard M. Leggett, Glenn J. Bryan, Linda Cardle ... See all authors ▾

First published: 13 August 2013 | <https://doi.org/10.1111/tpj.12307> | Cited by: 127

 ProdINRA
The INRA Open Archive

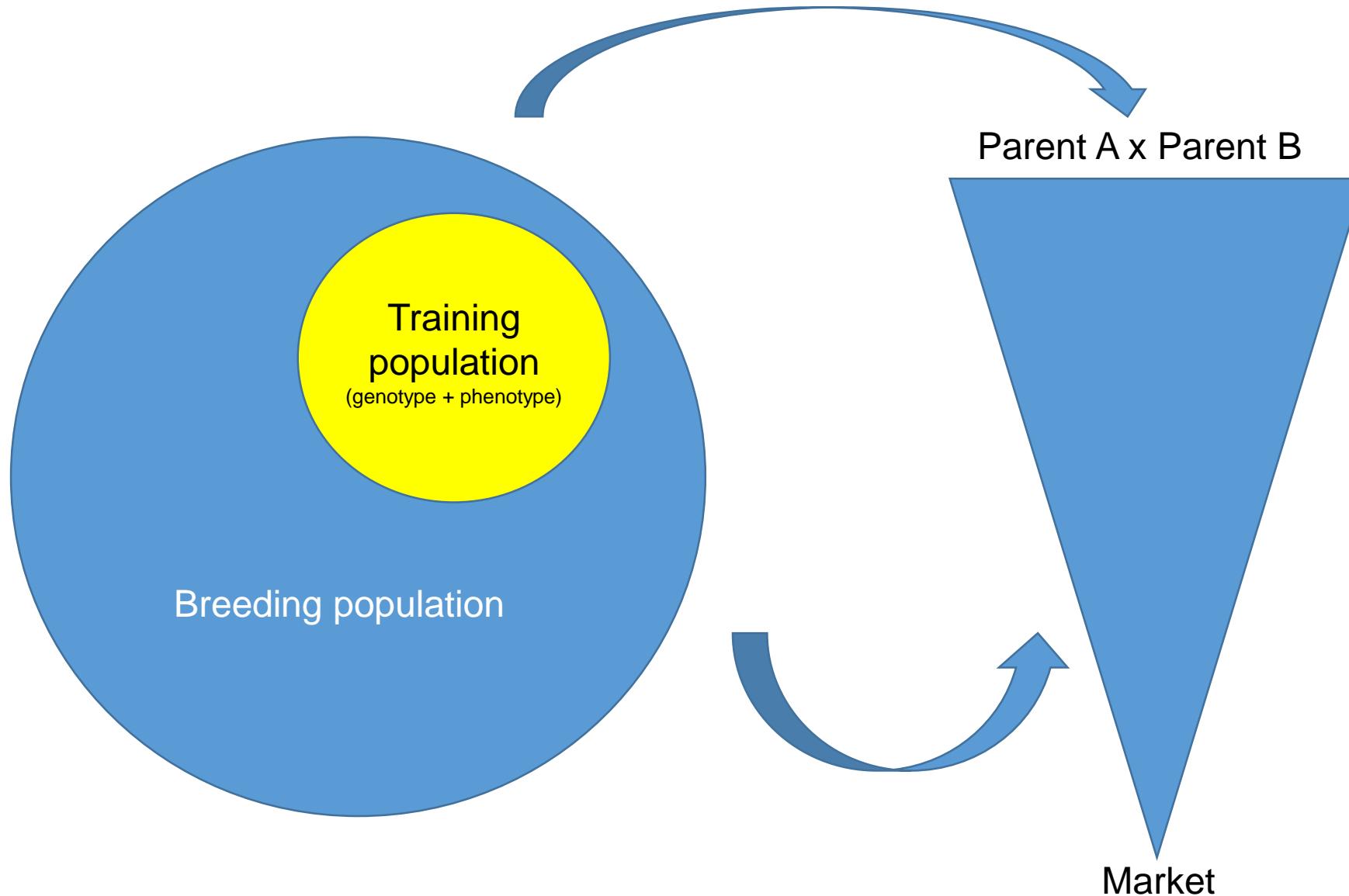
 ADVANCED SEARCH SEARCH HISTORY

Full record

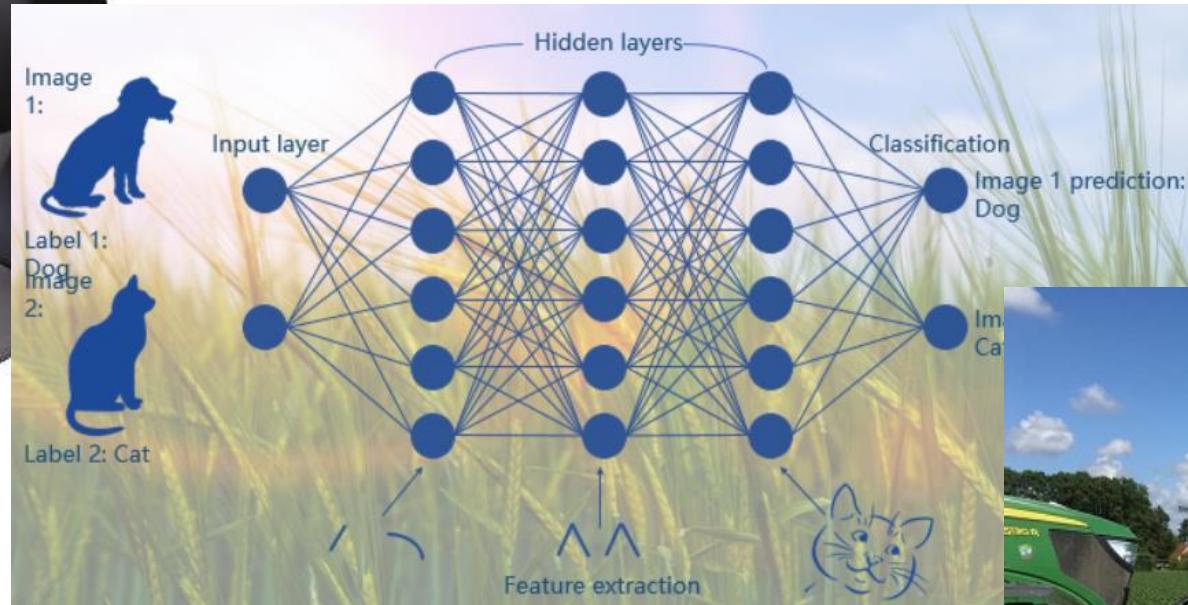
URL <https://prodinra.inra.fr/record/185046>

Title. Subtitle WAKomics : large-scale functional analysis of the WAK genes involved in the rice Magnaporthe grisea interaction

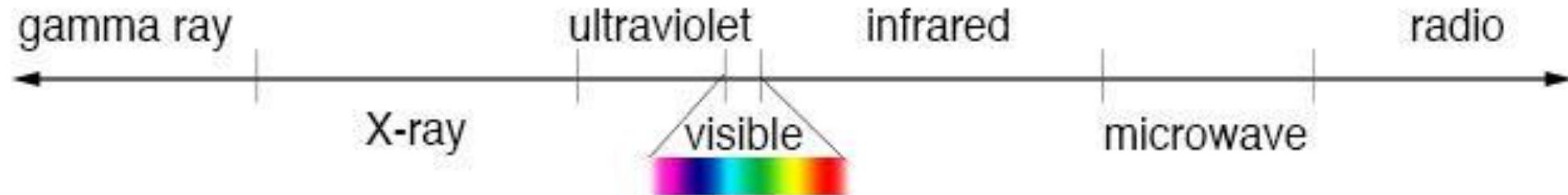
Genomic selection – the way forward?



New phenotyping opportunities



Multispectral imaging



UV-VIS-NIR
Multispectral imaging
analyser from Analytik Ltd

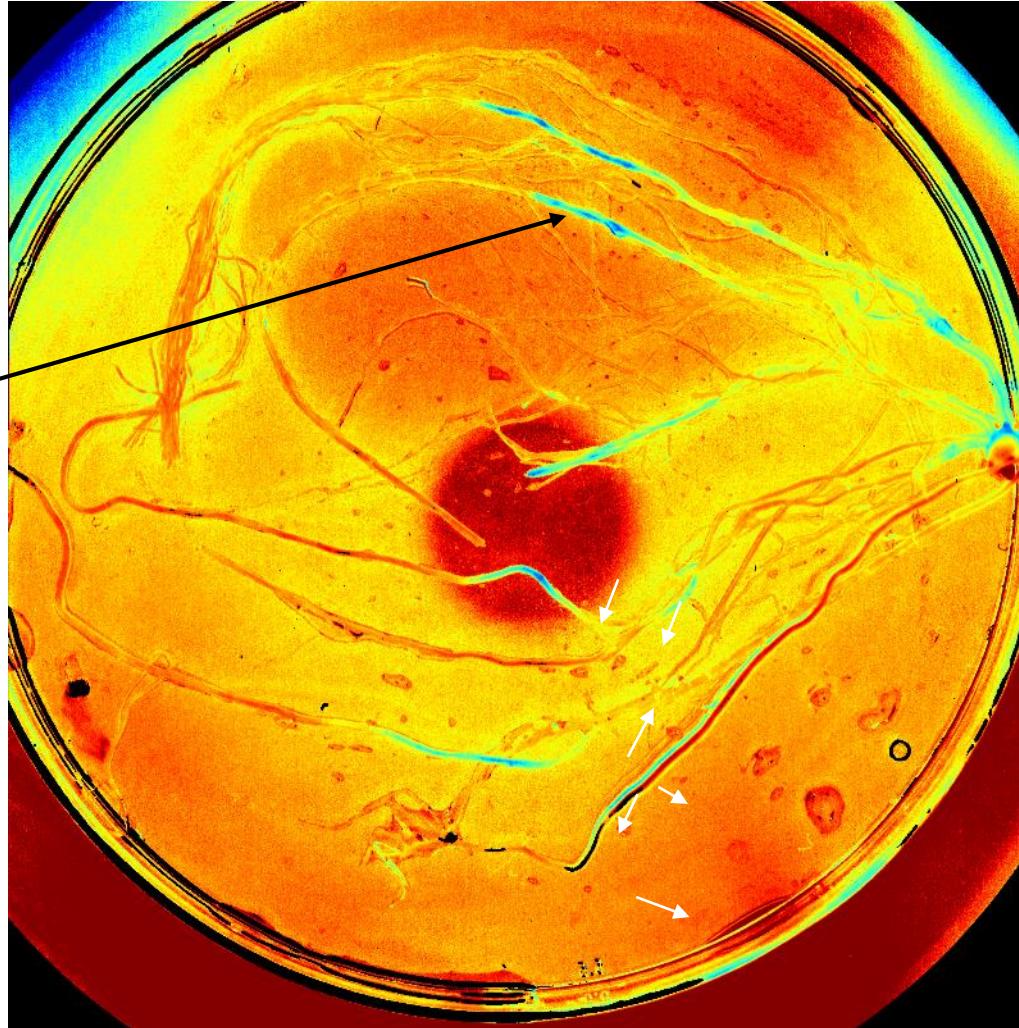
Multispectral imaging

Blue highlights indicate the take-all infections throughout the wheat root system

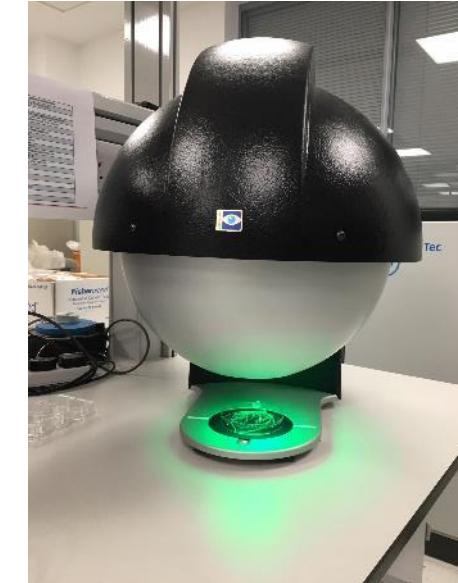


ROTHAMSTED
RESEARCH

Jess Spong (PhD student)
Gail Canning
Kim Hammond-Kosack

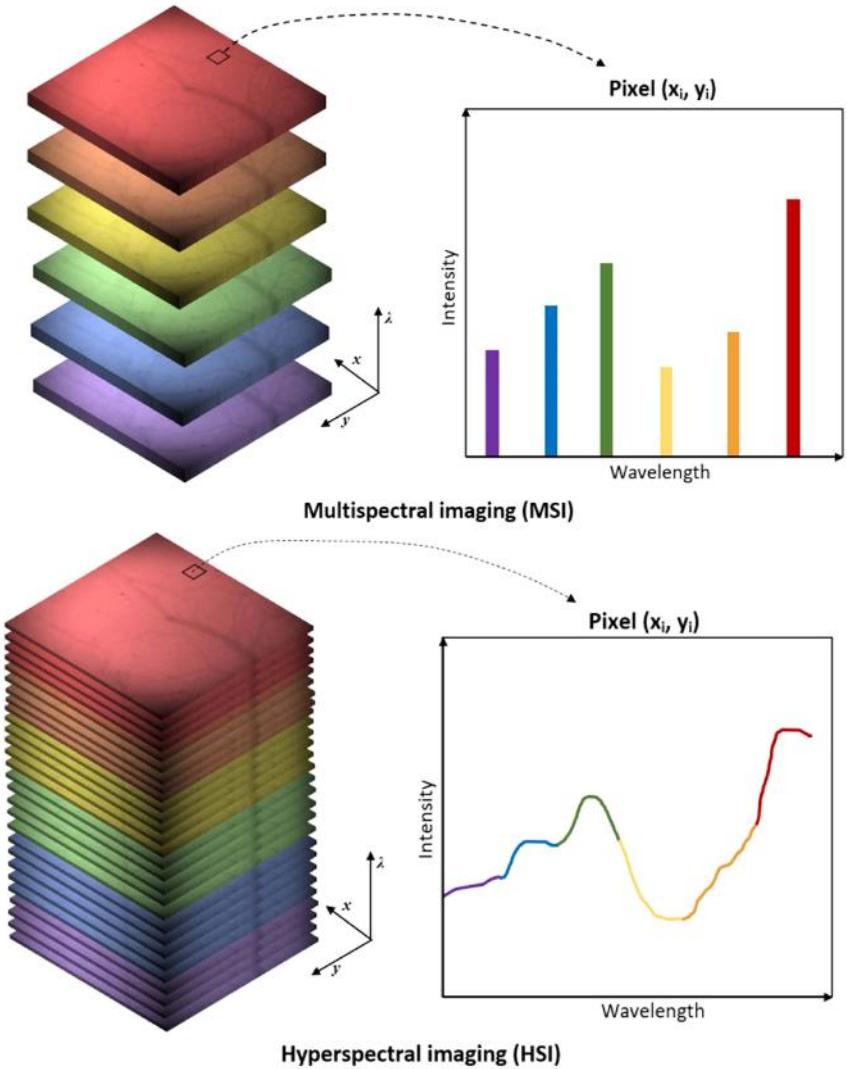


Root system in a 9 cm petri dish



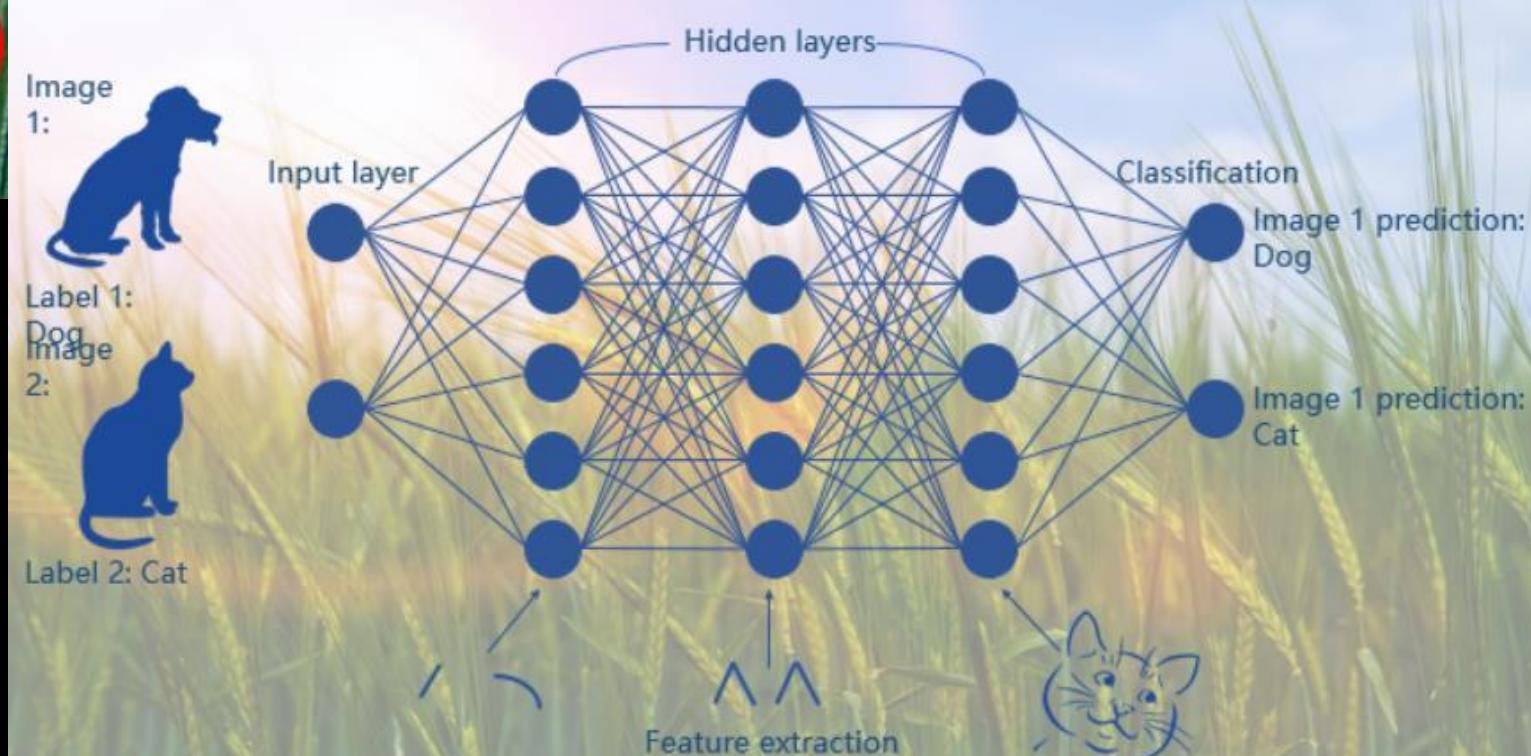
UV-VIS-NIR
Multispectral imaging
analyser from Analytik Ltd

Hyperspectral imaging



Polder Gerrit, Blok Pieter M., de Villiers Hendrik A. C., van der Wolf Jan M., Kamp Jan, '*Potato Virus Y Detection in Seed Potatoes Using Deep Learning on Hyperspectral Images*', 2019, **Frontiers in Plant Science**, Vol. 10.

AI and machine learning



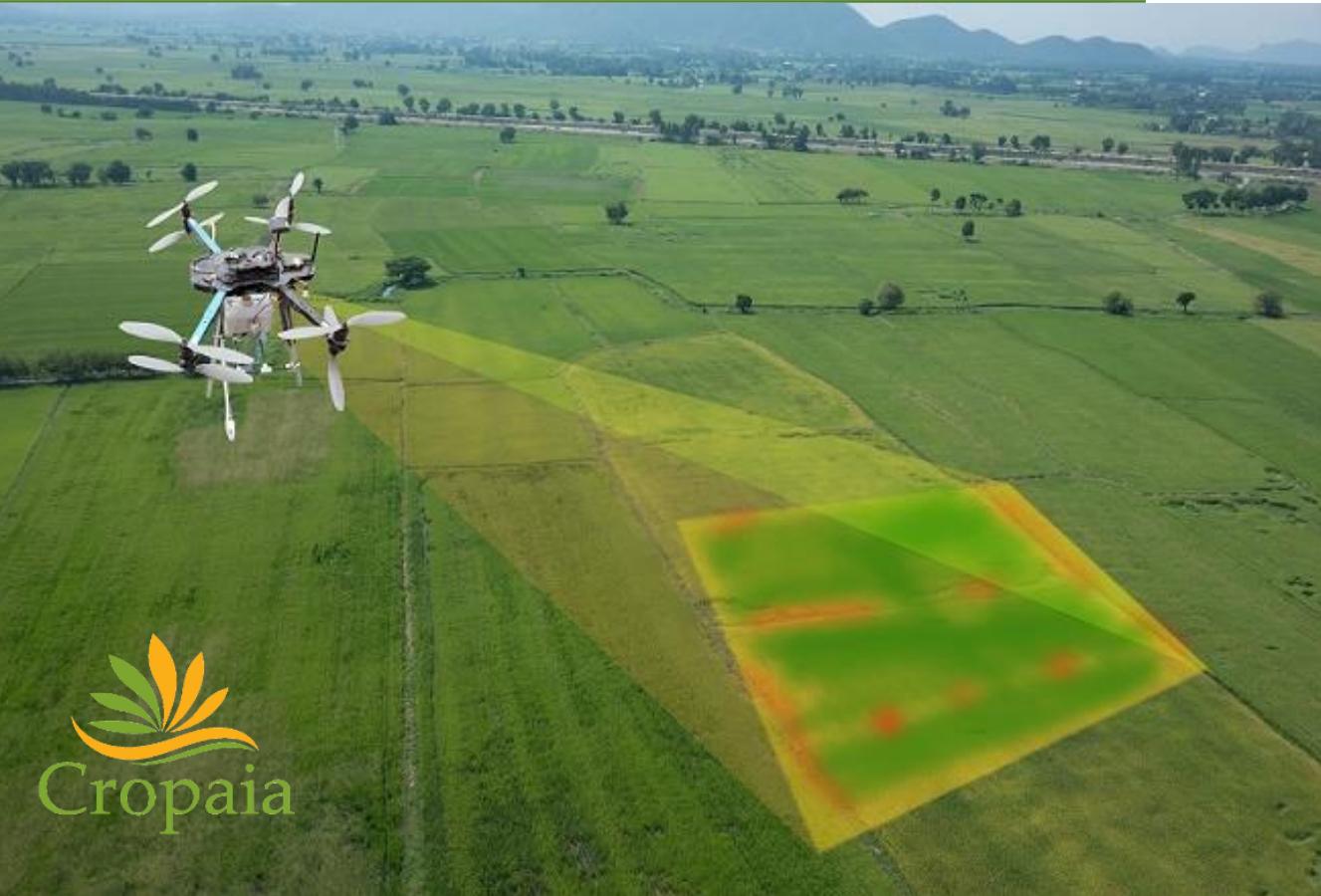
Megan Long
James Brown
Richard Morris



Precision agriculture

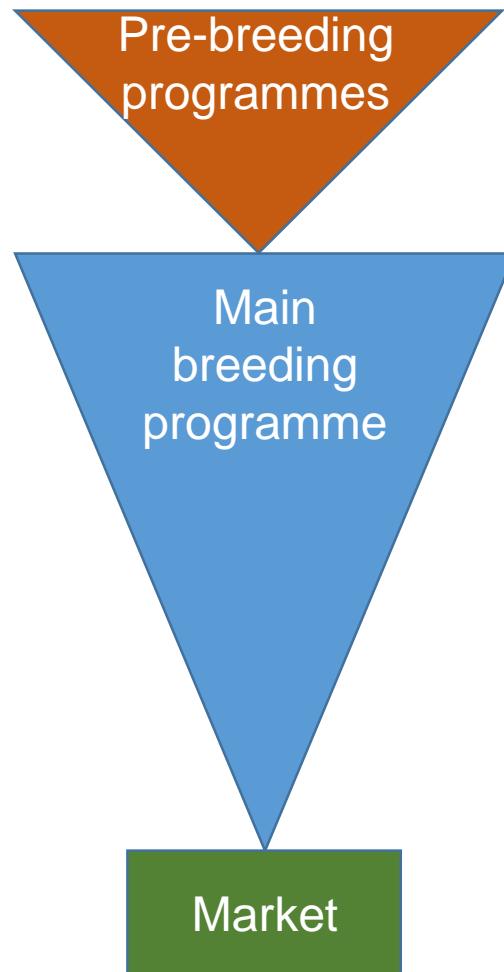


Phenospex – John Innes



Introducing new diversity

Introducing new diversity:-



Choosing the right novel traits



Choosing the right donors



Choosing the right elite parent to cross in the trait



Tracking the novel traits once in the elite programme

New sources of resistance



The image is a composite of two parts. The left side shows a world map with numerous blue location pins scattered across continents, indicating global distribution or collection sites. The right side is a photograph of a large-scale seed storage facility. Rows of tall, blue shelving units are filled with numerous glass jars, each labeled with a yellow tag containing a number like 267, 268, 269, 270, or 271. A person is visible in the background, standing between the shelves and looking at one of the jars.

- The Focused Identification of Germplasm Strategy (FIGS)
- Increased genotyping
- Increased phenotyping

Breeder's Observation Panel



BBSRC Designing Future Wheat

Watkins lines - JIC
Landraces from around the world



Wheat synthetics -
NIAB



Wheat wild relative
introgressions -
Nottingham



Breeder's Toolkit



BTK Selection Committee



Simon Griffiths
Chair



Julie Ellwood
DFW Project Manager



Simon Orford
GRU BTK Coordinator



Jacob Lage
KWS



Chris Burt
RAGT



David Schaefer
LSPB



Phil Tailby
LimaGrain



David Feuerhelm
Syngenta



Mike Kerns
Bayer



Matthew Kerton
DSV



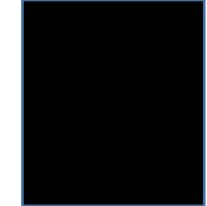
Stephen Smith
Elsoms



Malcolm Hawkesford
DFW WP1



Cristobal Uauy
DFW WP2



Delegated to
JK, AB, or IK
DFW WP3



Rob Davey
DFW WP4



Keith Edwards
Bristol



Alison Bentley
NIAB



Ian and Julie King
Nottingham



Cadenza TILLING population



PNAS

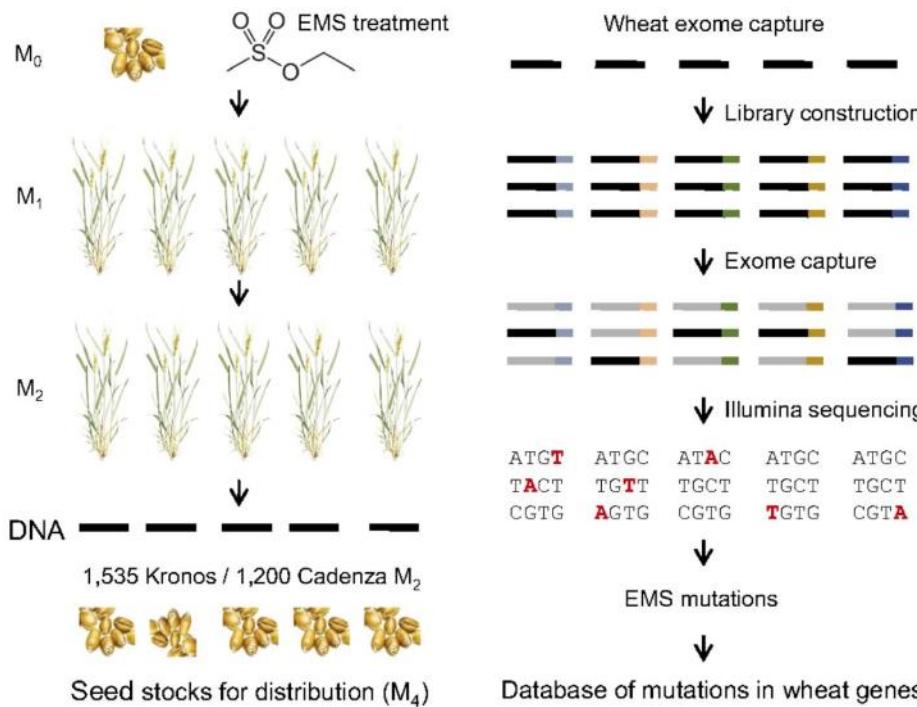
Uncovering hidden variation in polyploid wheat



Ksenia V. Krasileva, Hans A. Vasquez-Gross, Tyson Howell, Paul Bailey, Francine Paraiso, Leah Clissold, James Simmonds, Ricardo H. Ramirez-Gonzalez, Xiaodong Wang, Philippa Borrell, Christine Fosker, Sarah Ayling, Andrew L. Phillips, Cristobal Uauy, and Jorge Dubcovsky

PNAS February 7, 2017 114 (6) E913-E921; first published January 17, 2017 <https://doi.org/10.1073/pnas.1619268114>

Contributed by Jorge Dubcovsky, December 20, 2016 (sent for review November 22, 2016; reviewed by Beat Keller and Joachim Messing)



Forward genetics:-



Fiona Doohan
Thalia Christodoulou

Reverse genetics:-

Plant Biotechnology Journal



Research Article | Open Access | CC BY

mlo-based powdery mildew resistance in hexaploid bread wheat generated by a non-transgenic TILLING approach

Johanna Acevedo-Garcia, David Spencer, Hannah Thieron, Anja Reinstädler, Kim Hammond-Kosack, Andrew L. Phillips, Ralph Panstruga

Introgression tracking

CerealsDB

Tools for the analysis of the wheat genome.

Home Wheat Seq DArT Markers SNPs (KASP) SNPs (Axiom®) SNPs (iSelect) SNPs (TaqMan®) TGB

Search for Introgressed regions in elite wheat varieties

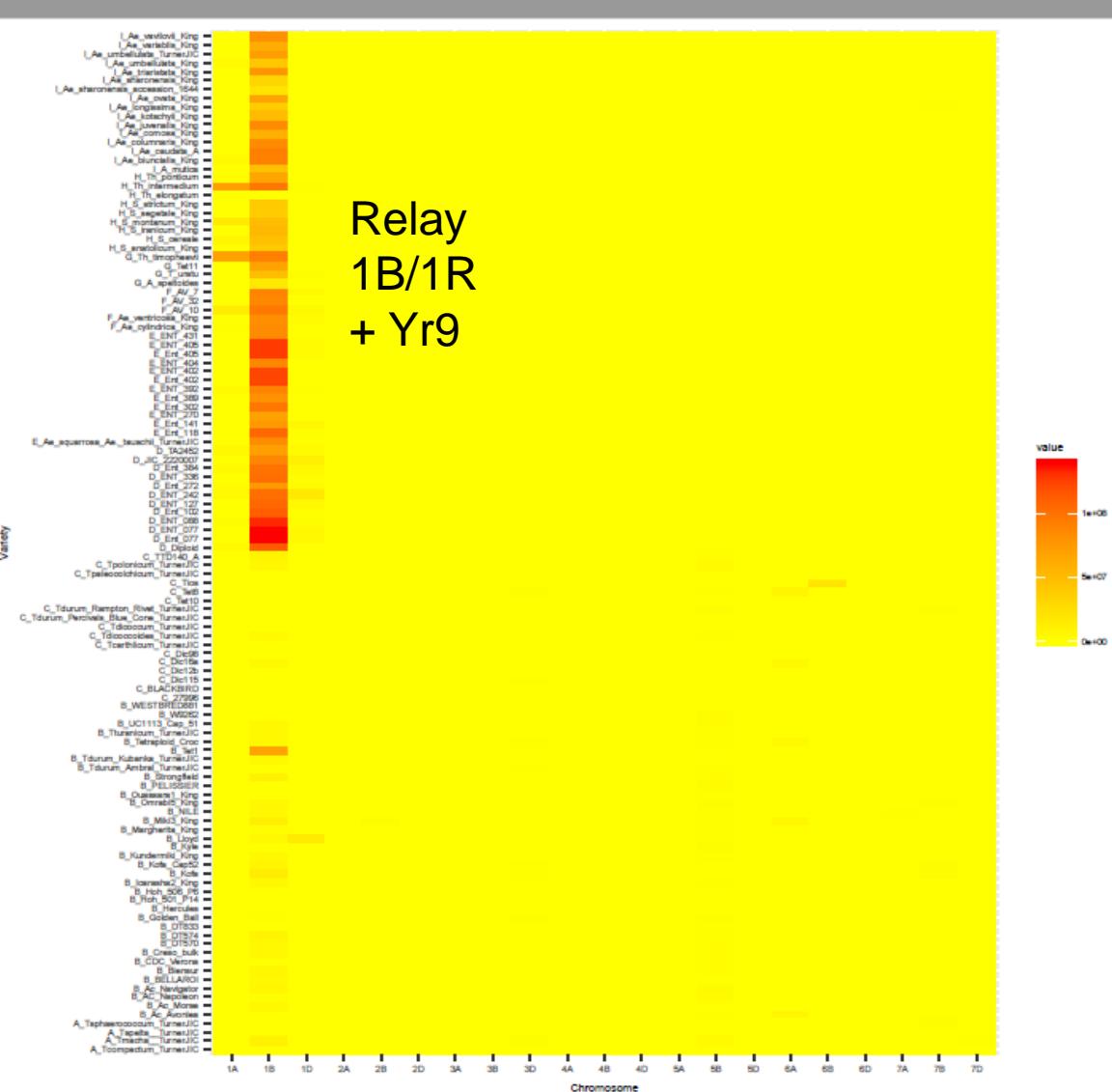
Using the form below, you can search for introgressions for a particular elite wheat variety that have come from over a hundred wheat relatives and progenitor species.

Enter the wheat variety into the field below and click the submit button.

Please enter a wheat elite variety in this field - begin typing and the field will auto complete.

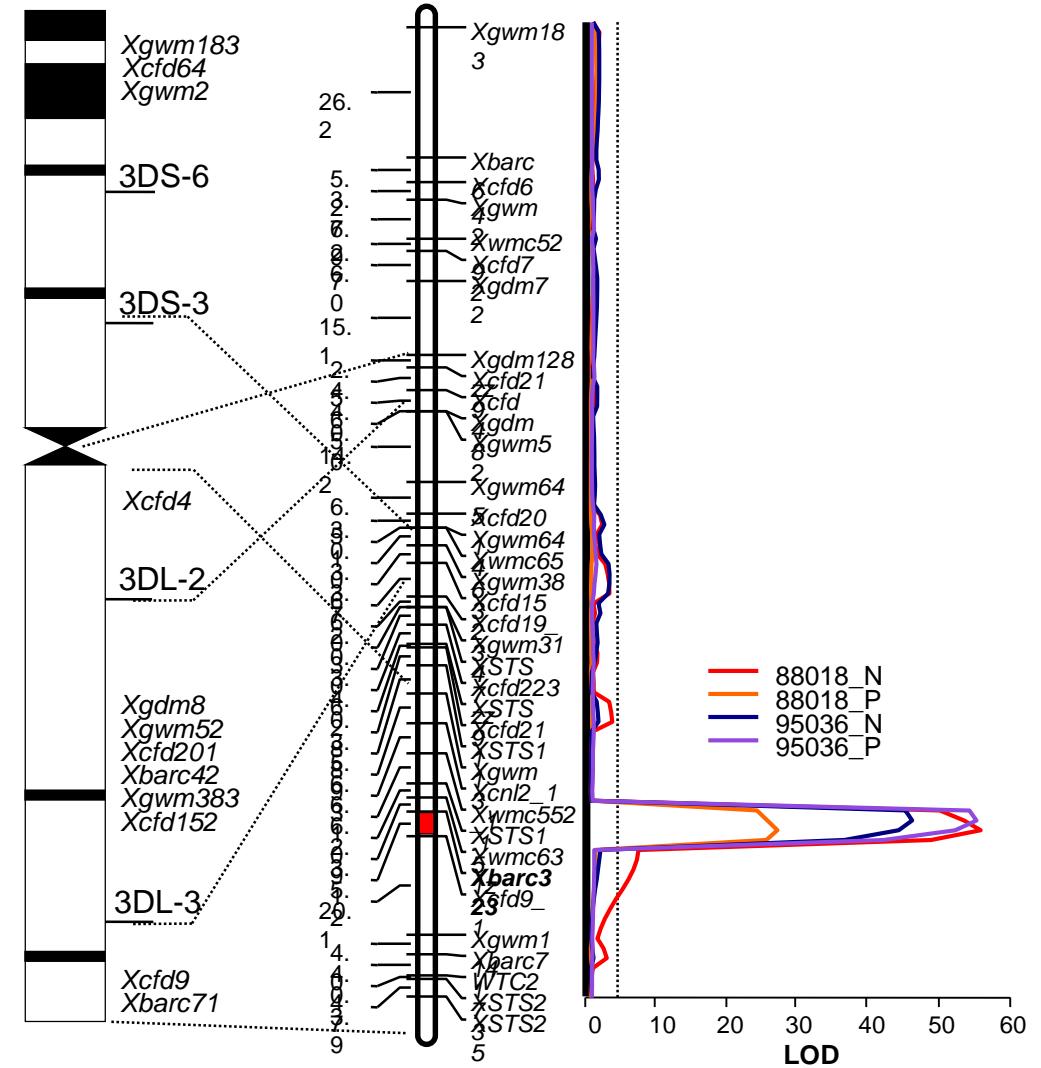
Percentage match cutoff: 40% This is the percentage of matching SNP scores to the wheat relative (Default = 40%).

Exclude small introgressions: Yes No



Durability

- Stb16 originated from a synthetic wheat
- Broad spectrum of resistance to multiple isolates
- Located on chromosome 3D
- The gene was introduced into some French elites
- Only recently made it to market
- Broke down last year



Acknowledgments



Chris Burt



Jess Spong
Gail Canning
Kim Hammond-Kosack



John Innes Centre

James Brown
Richard Morris
Megan Long



Fonds de soutien à l'Obtention Végétale

Cyrille Saintenac
(INRA)



Fiona Doohan
Thalia Christodoulou

CerealsDB

Tools for the analysis of the wheat genome.

