International workshop: on food security through potato production and human nutrition
Bogotá, 24 – 25 on June 2013

Towards potato precision breeding

Teresa Mosquera Vásquez

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Canadian International Development Agency | Agence canadienne de développement international

IDRC | CRDI
International Development Research Centre
Centre de recherches pour le développement international

What is precision breeding or SMART breeding?

SMART breeding

SMART = **S**election with **M**arkers and **A**dvanced **R**eproductive **T**echnologies

In smart breeding the gene or gene variant responsible for a specific trait can be accurately identified.

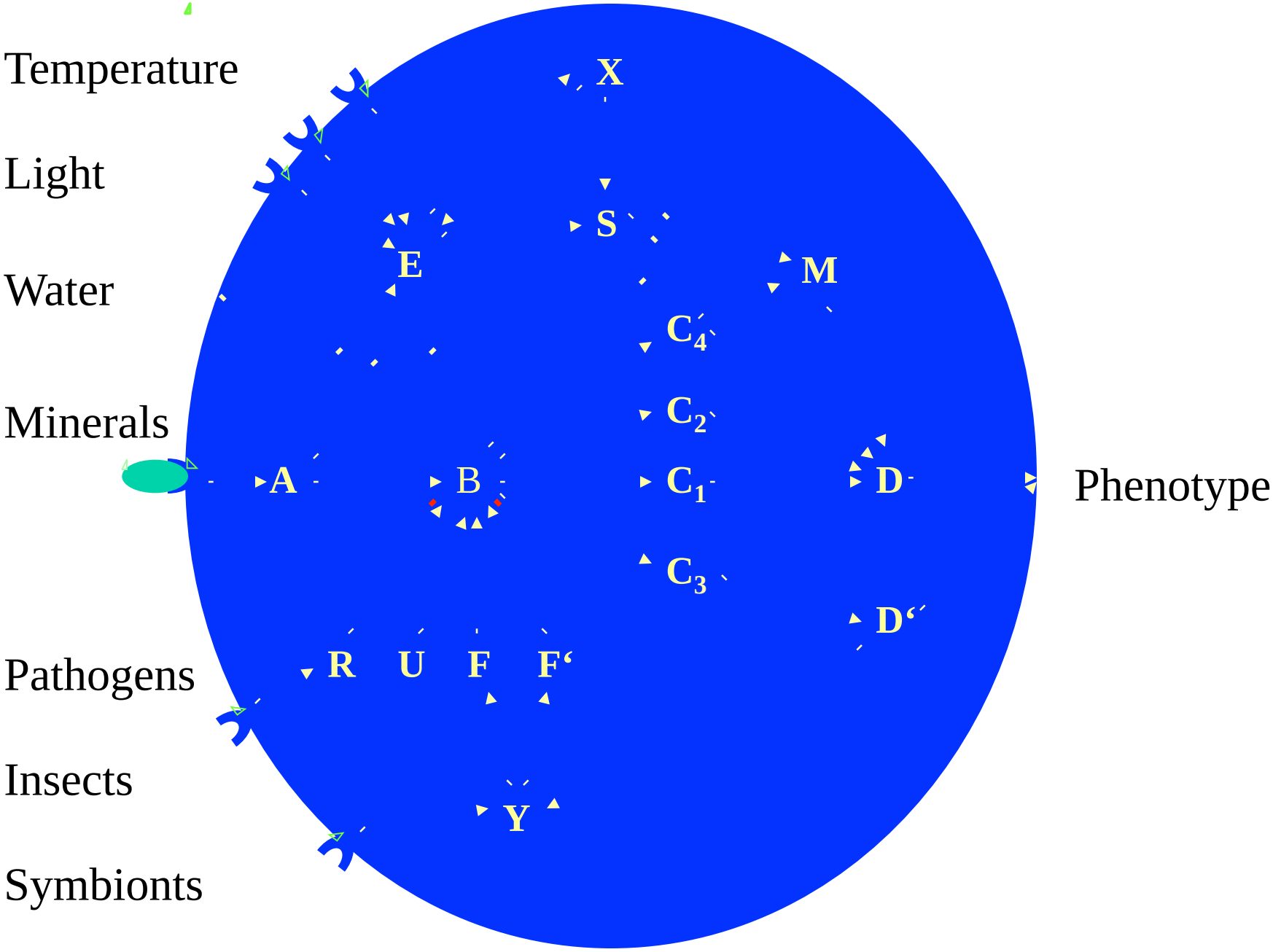
It is possible using molecular and biological procedures.

It is possible to test a population for the presence of the gene, even before the actual trait is expressed.

Precision breeding

Is it worth it?

Is it possible?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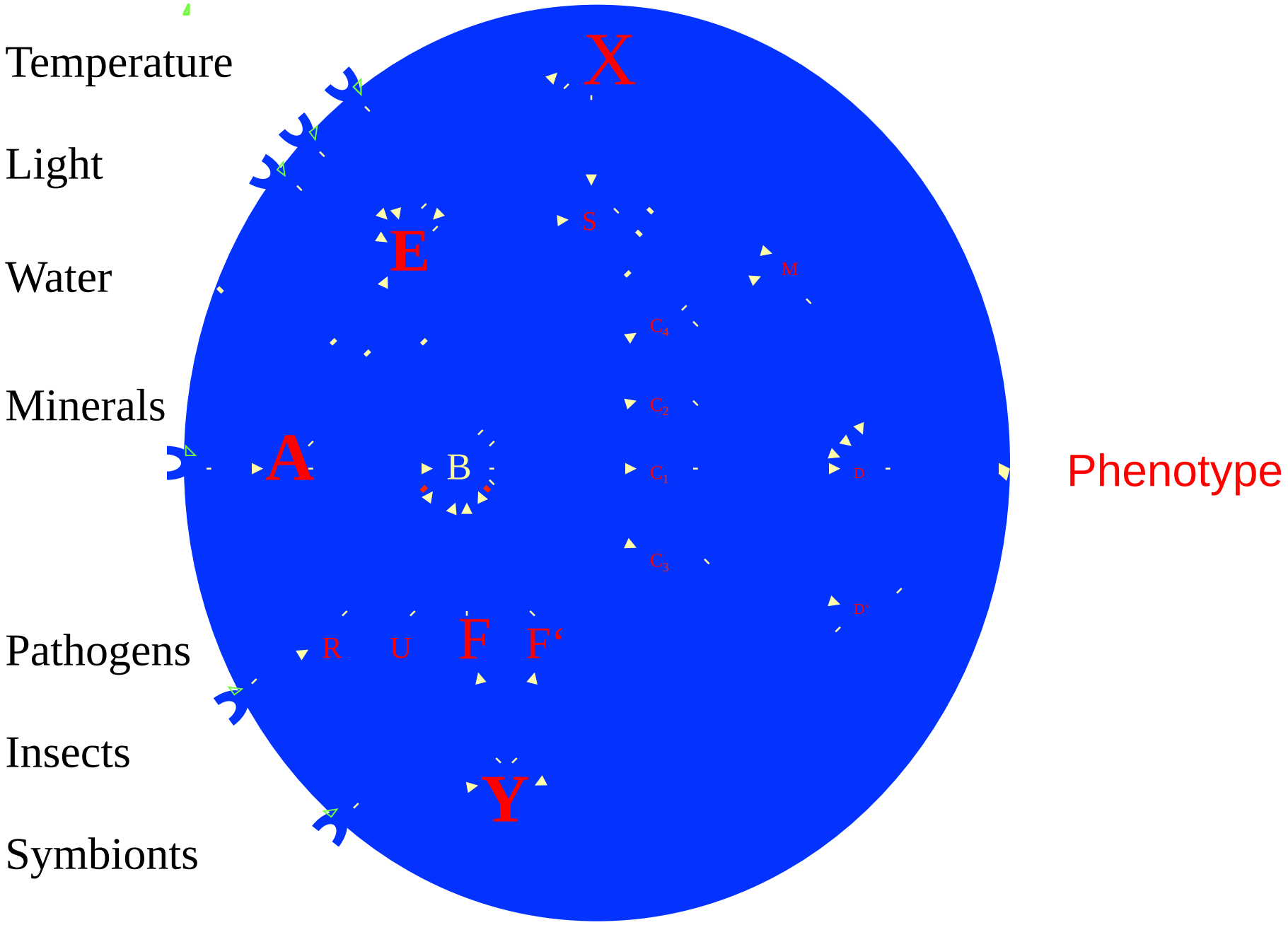
Phenotype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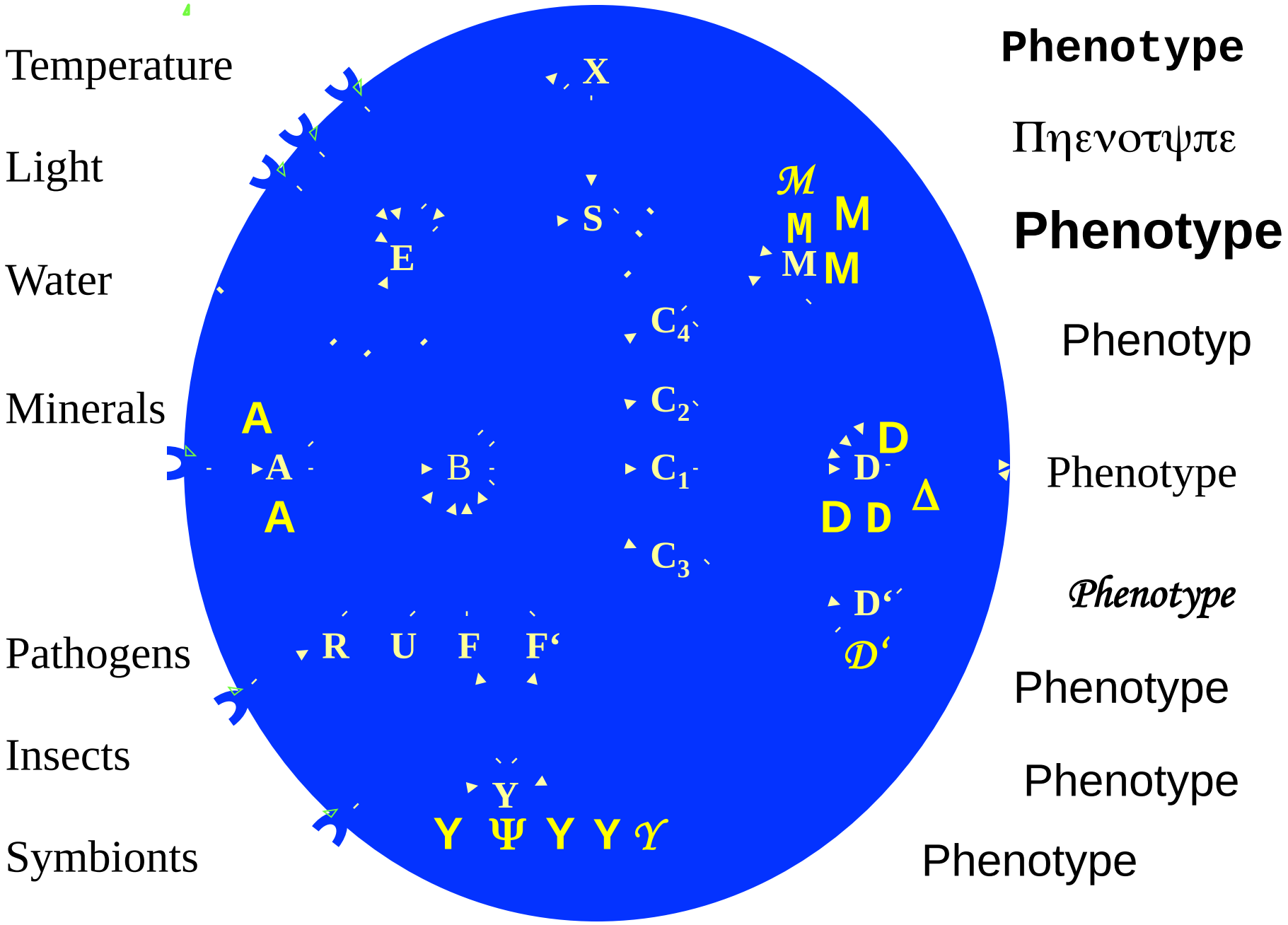
Phenotype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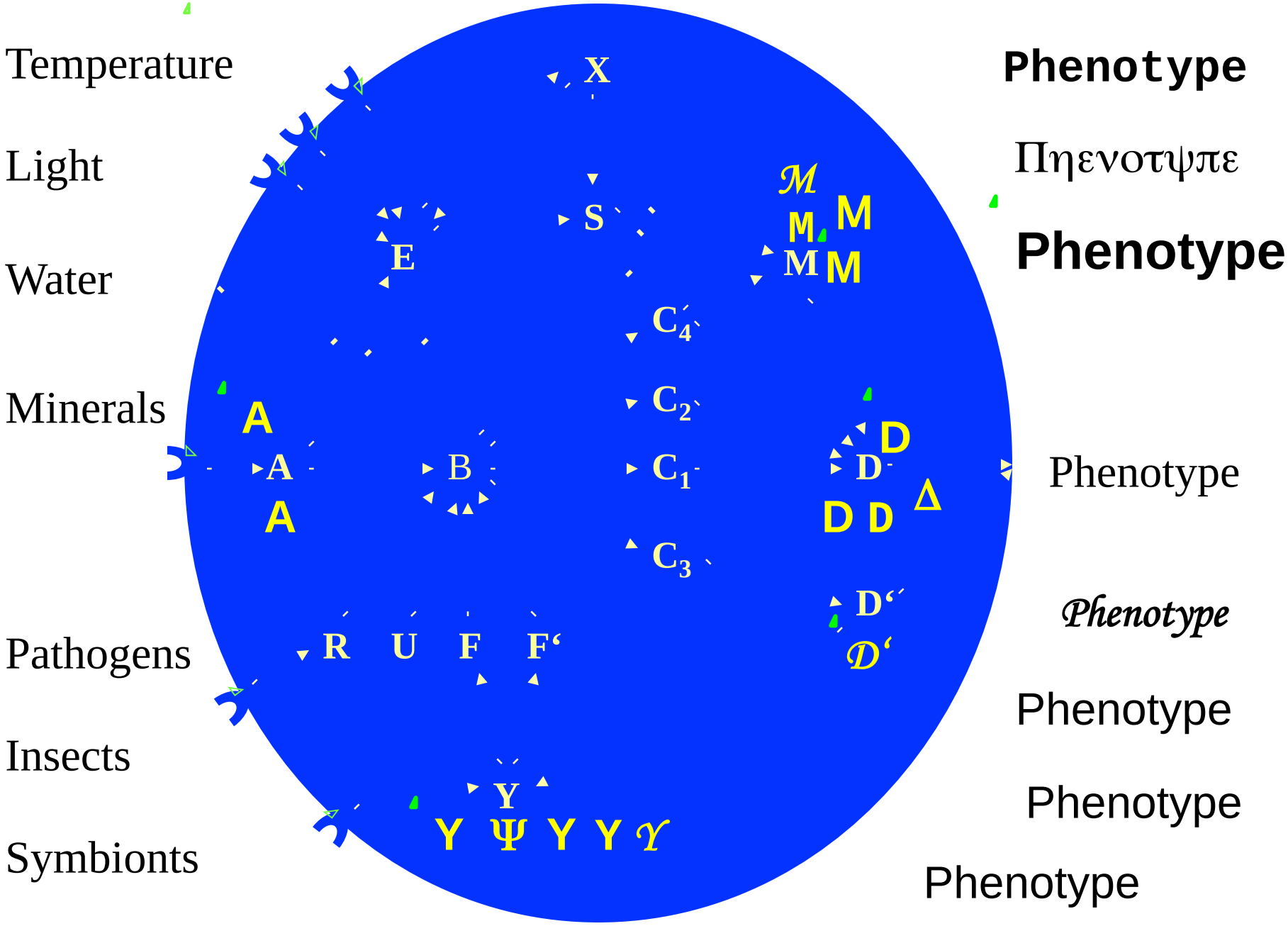
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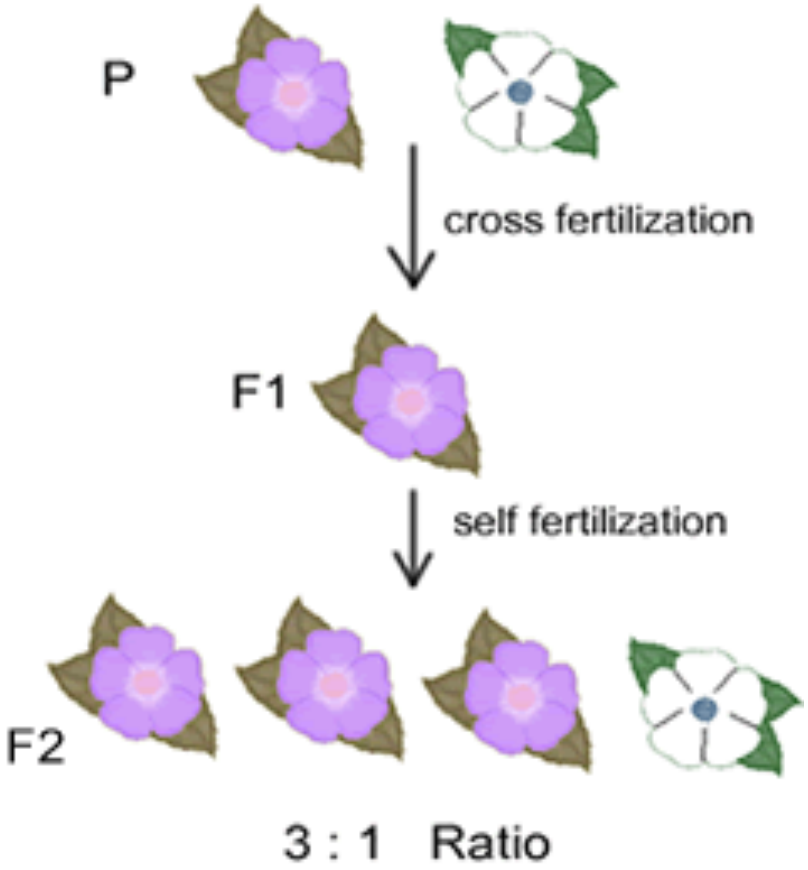
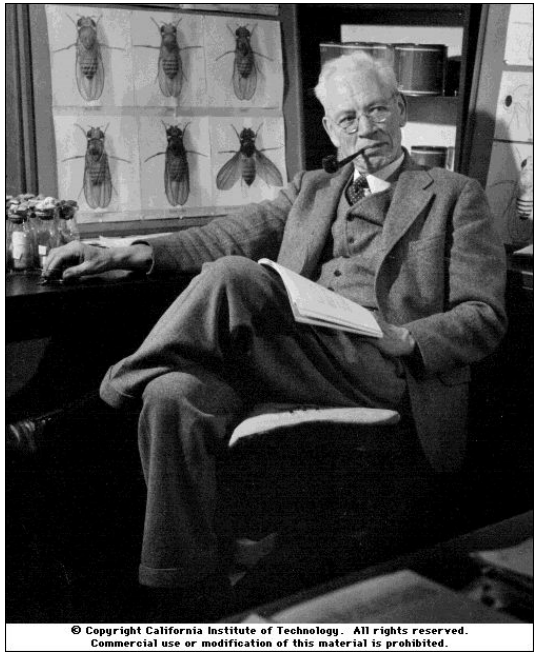
Gregor Mendel (1822 – 1884)

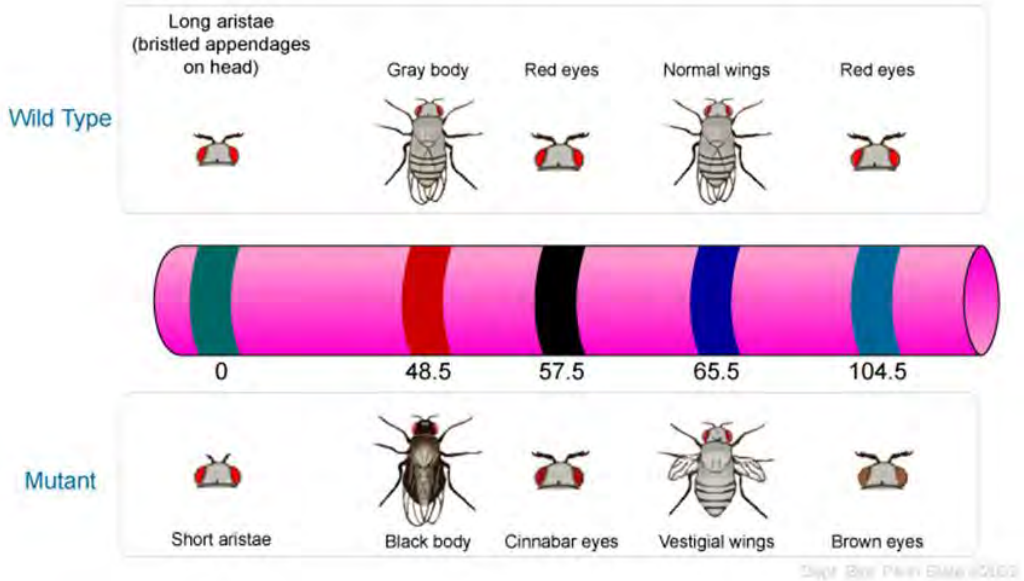


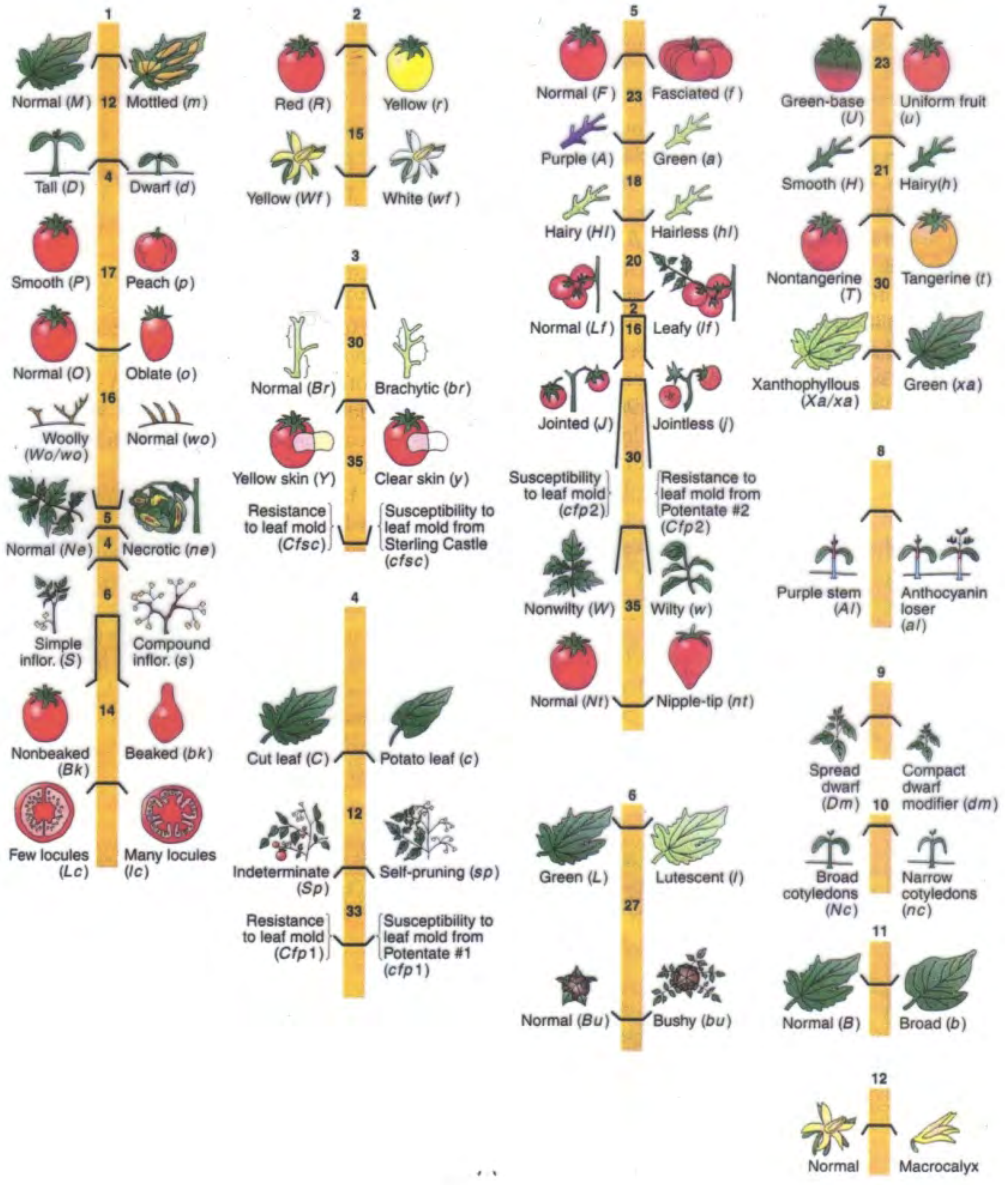
Fundamentals of genetics, inheritance bases, segregation

Thomas Hunt Morgan (1866-1945)

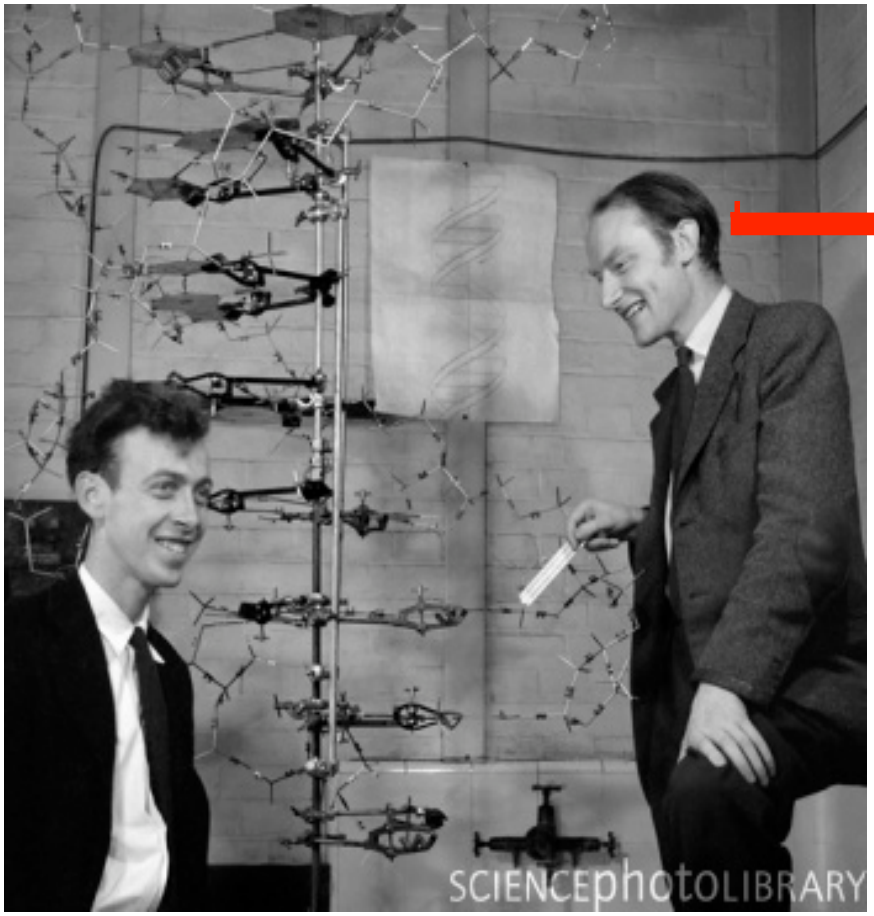


Alfred Sturtevant (1891-1970)

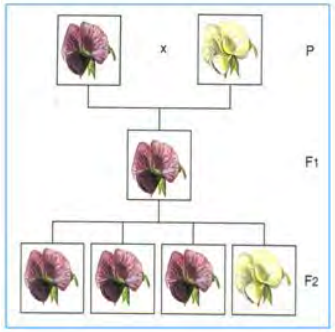




Tomato genetic linkage map using morphological traits

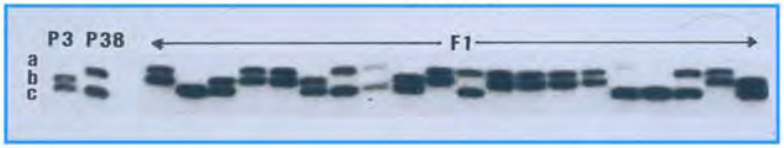


Watson and Crick took a crucial conceptual step, suggesting the DNA molecule was made of two chains of nucleotides.

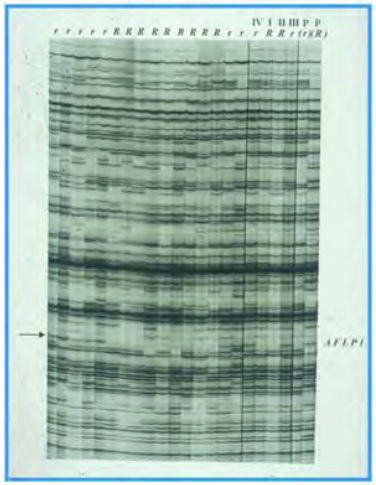


Old and new marker types

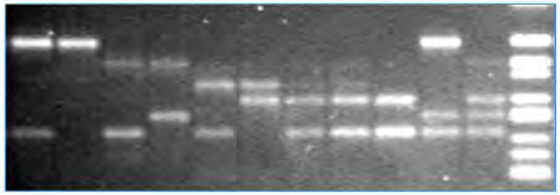
RFLP



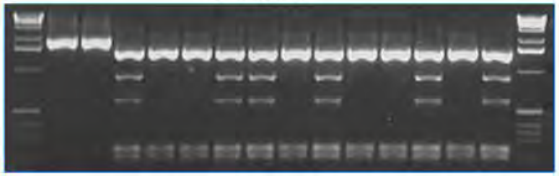
AFLP



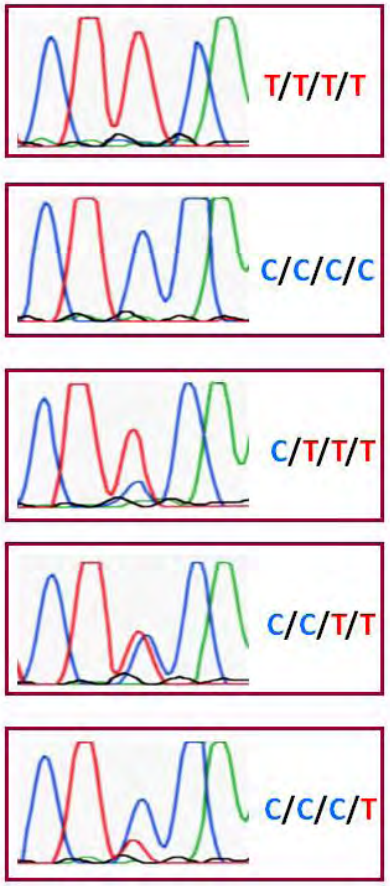
SSR



CAPS



SNP



Cordiality: Gebhardt C.

Kary Mullis

PCR reaction

Courtesy: Gebhardt C.

History of potato genetics

After Mendel: potato was one of the first species studied, because the fungi *Synchytrium endobioticum*

After 60 years only dominant characters were studied

Two important technical developments

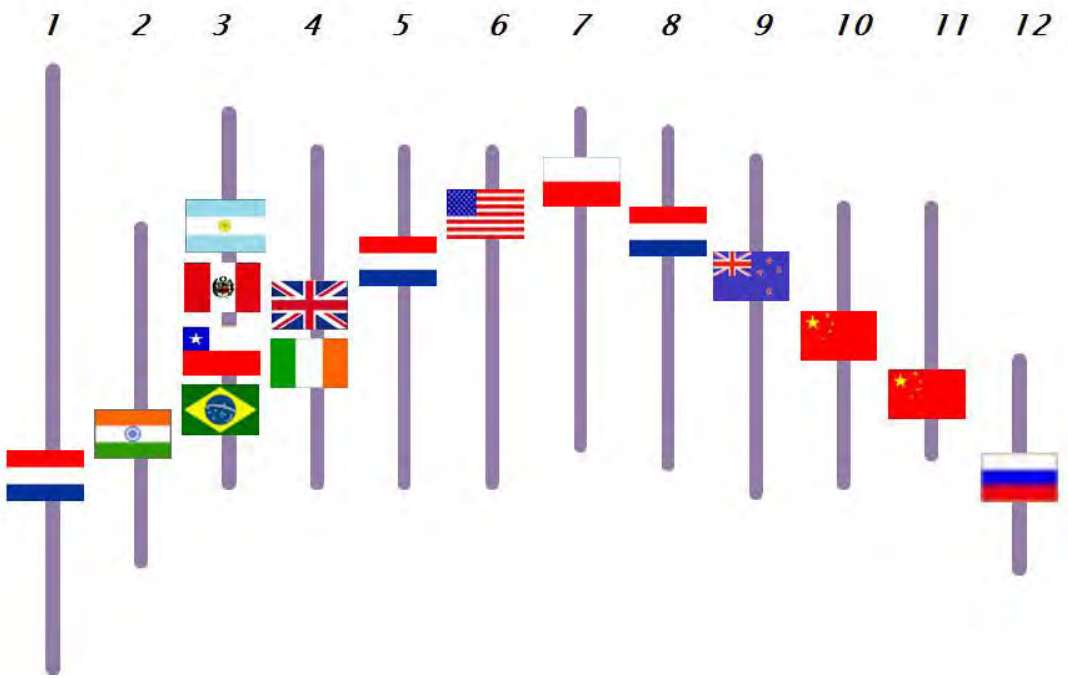
1. To reduce the ploidy level: tetraploid to diploid
2. Advent of molecular markers

Genetic maps

Bonierbale, M. 1988

Gebhardt, C. 1989

Potato genome sequence 2011

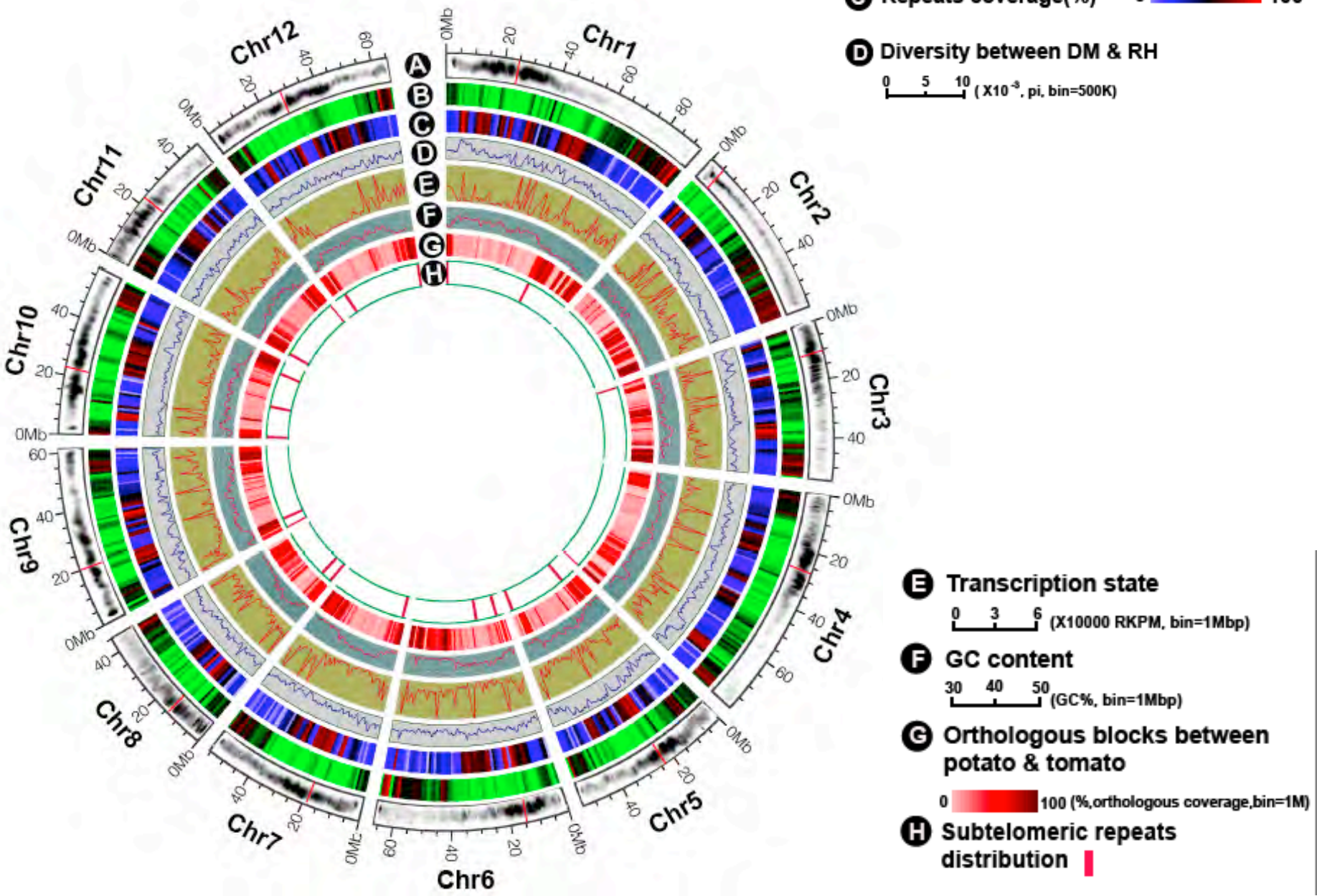


PGSC

New Zealand
China
India
Russia
Poland
Italy
The Netherlands
UK
Ireland
Brazil
Argentina
Chile
Peru
USA

Potato Genome Sequencing Consortium

Genome View of Potato

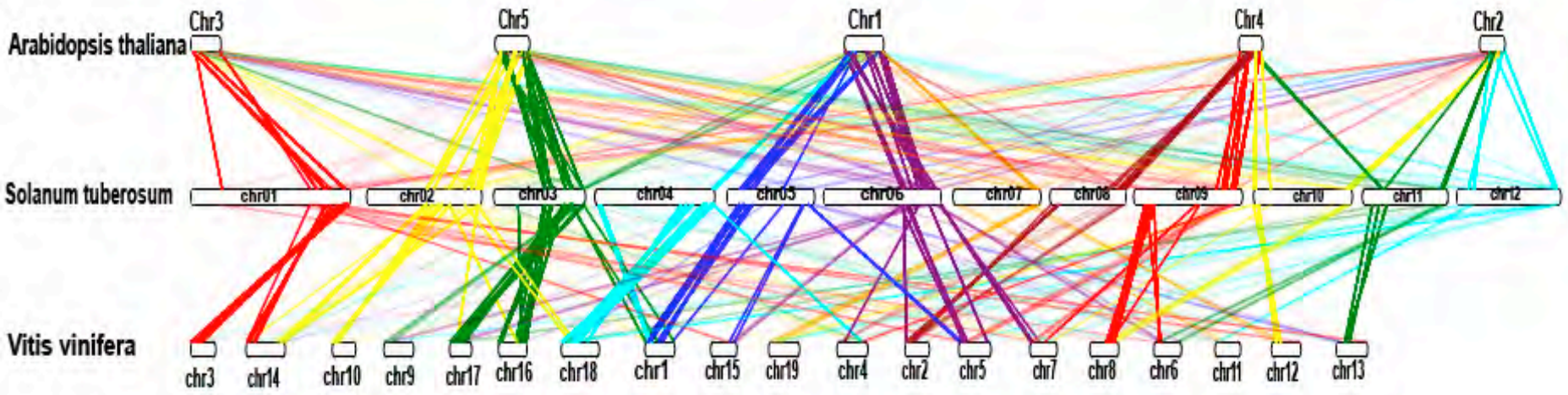


Comparative Genomics

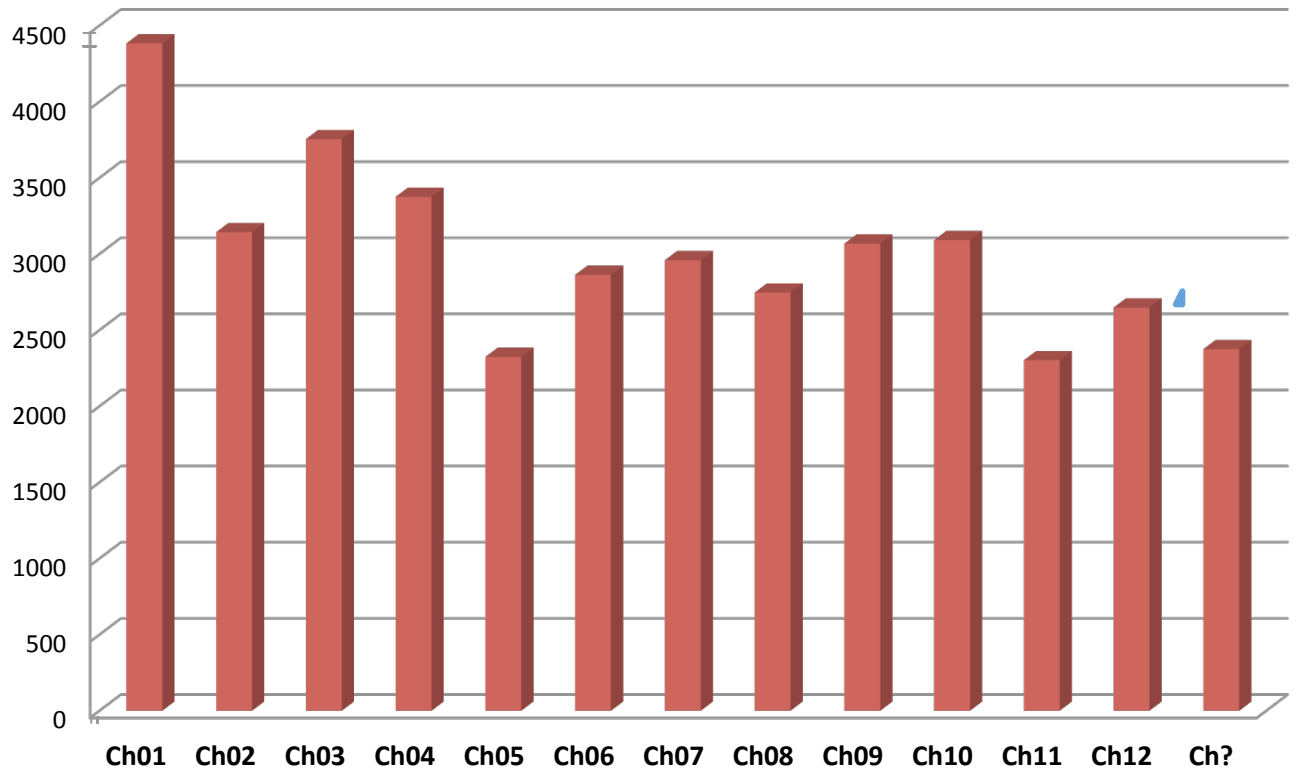
I apologize for this latest entry. I can´t find a chimp making a face as dumb as this rich one

http://www.google.com.co/imgres?imgurl=http://www.scobypoker.com/adcenter/bushmonkey811_465.jpg&imgrefurl=http://www.stormfront.org

Synteny between dicotyledonous



Gene numbers on the 12 potato chromosomes



Why invest so much time and money to decode the genetic blueprints of plants, animals and humans?

Once the location of all the genes in an organism is known, scientists can begin to systematically:

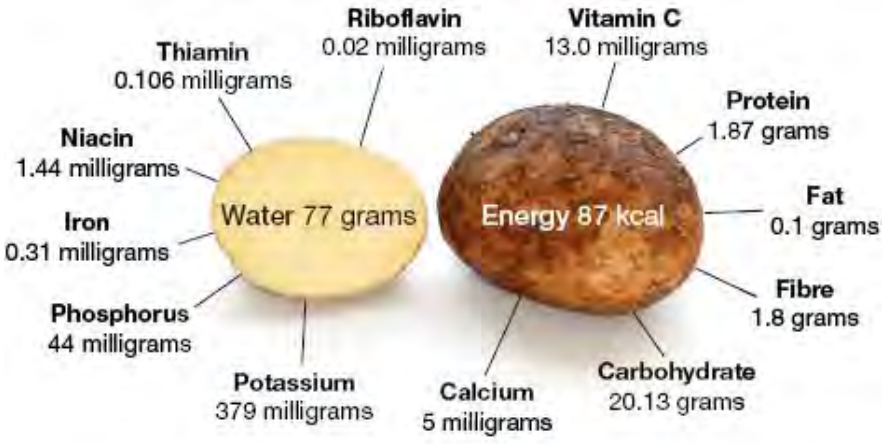
- ✓ Explore their various functions
- ✓ Transfer desired traits to other plants
- ✓ ‘Switch off’ undesirable properties

Traits under study

1. Resistance to late blight

2. Quality of potato tuber for industry process

3. Nutritional quality



Omics for interesting agronomical traits

Deissy Juyó

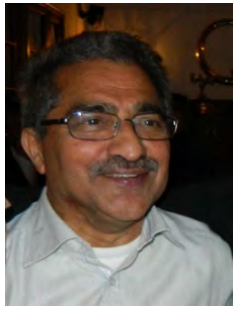
Fernanda Álvarez

Genomics approach

Max Planck Institute for Plant Breeding Research

- Genome Wide Association Study (GWAS)
- Candidate genes

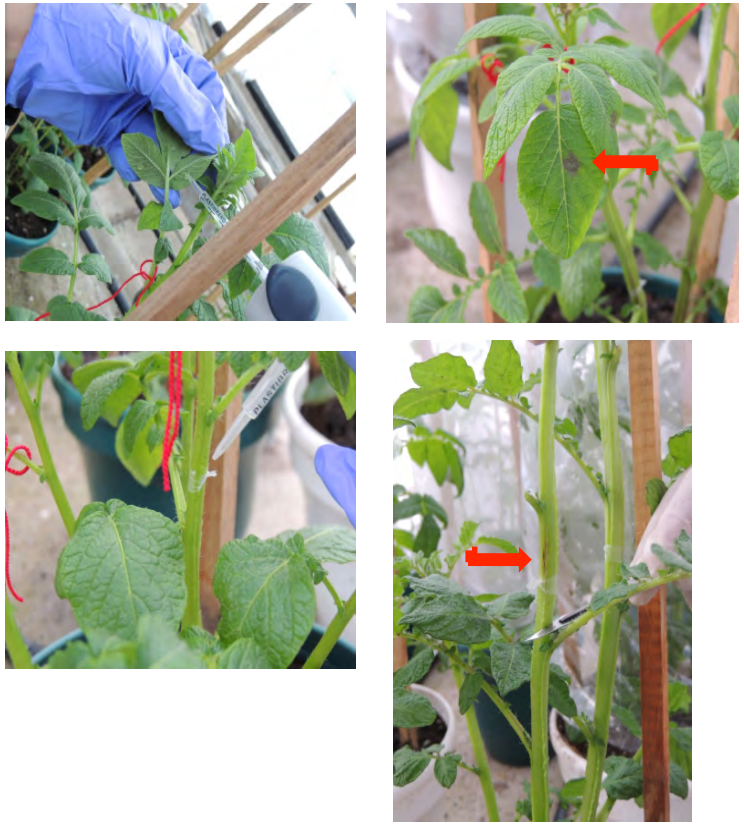
Metabolomics approach



McGill

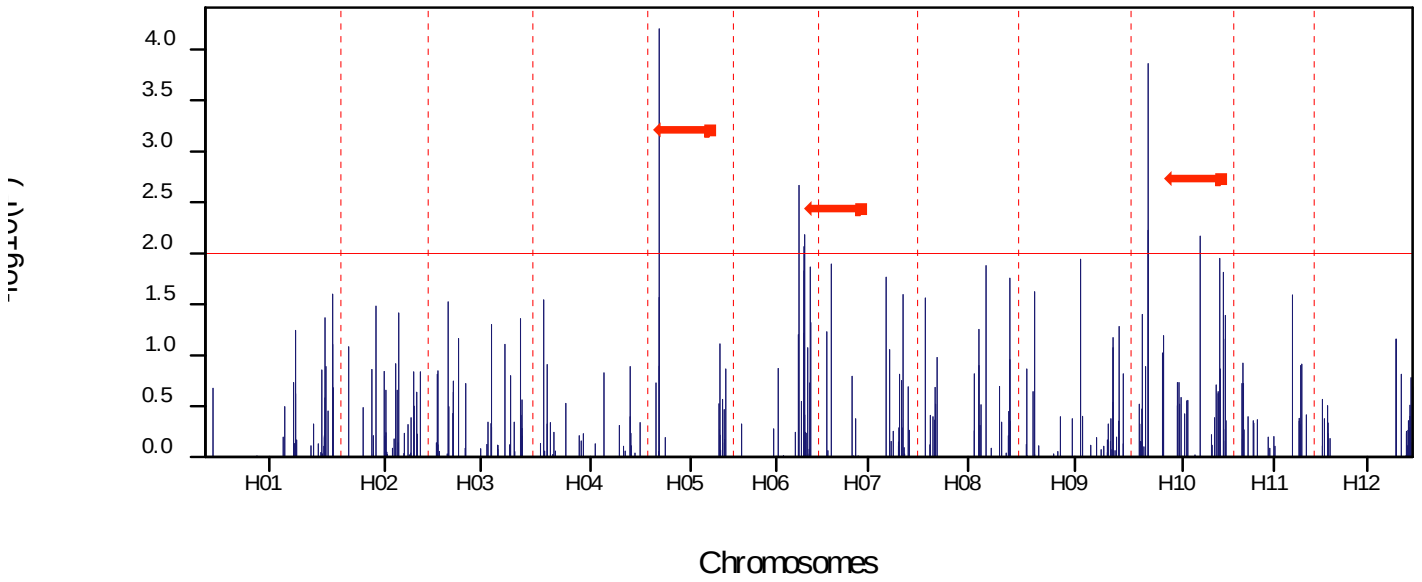
Looking for resistance to late blight

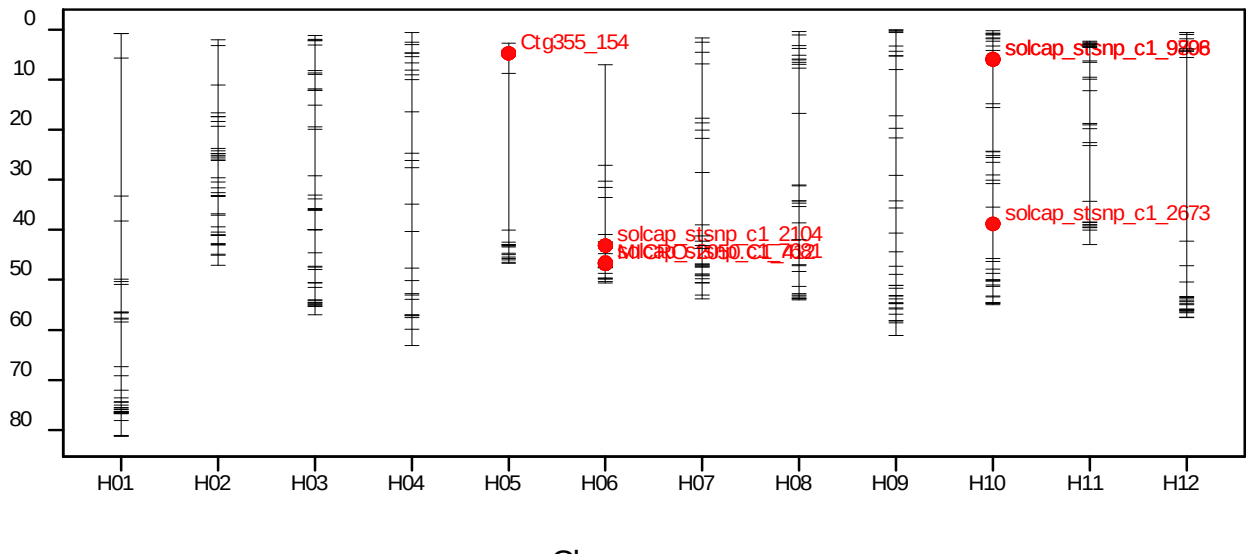
Late blight evaluation under field conditions



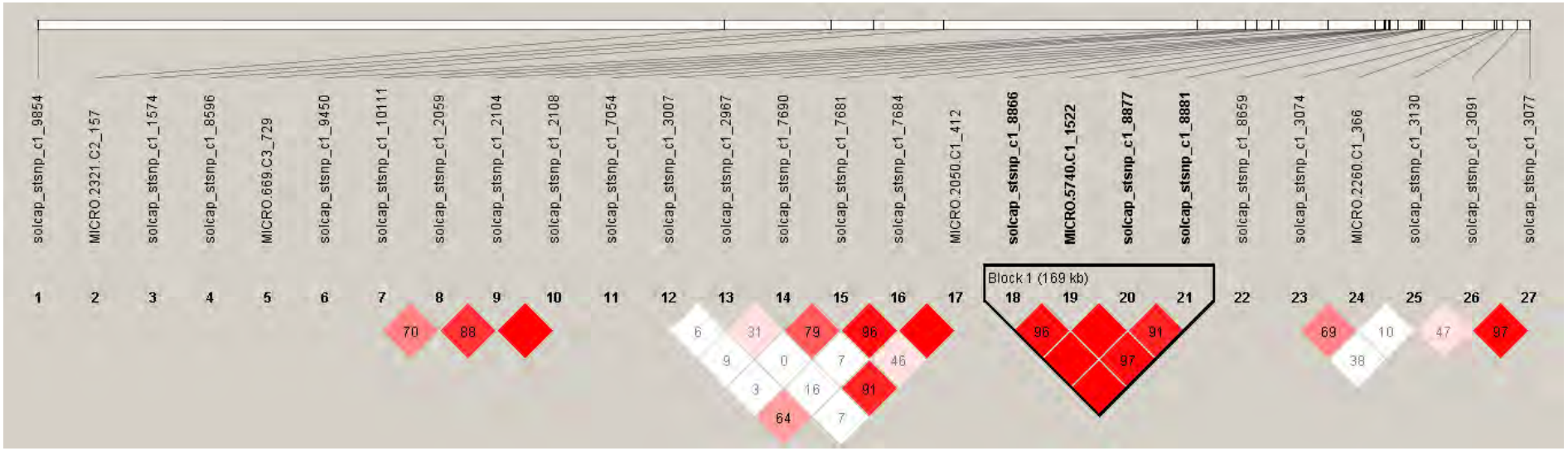
Late blight evaluation in greenhouse

Association mapping analysis: using GWAS approach





Heat Map Chromosome 6



Red: high LD
Pink: medium LD
White: low LD

- 27 Markers
- 1 Spine of LD 169 Kb

HaploView

Differential transcriptome experiment for candidate genes

Sampling: T0, T1, T2

- *P. infestans* races
  (contains isolates that overcome all 11 *R*-genes)

- **Transcriptomics GenXPro**

325,000 SNPs were identified

3,366 SNPs were significantly ($p<0.05$)
between the 8 quantitative more and 8 quantitative less resistant

1,920 candidate genes
contained at least 1 significant SNP were selected

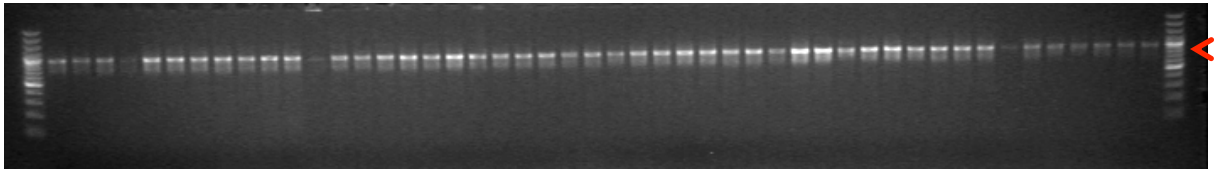
Courtesy Meki Shehabu - Max Planck Institute

Candidate genes analyzed in potato

No.	Chr.	Primer Name	Gene	Superscaffold	Function Described
1	chr01	TM10f	PGSC0003DMG400000204	PGSC0003DMB000000083	Thylakoid membrane phosphoprotein 14 kDa, chloroplastic
2	chr02	TM11f	PGSC0003DMG400029694	PGSC0003DMB000000083	Eukaryotic translation initiation factor 3 subunit
3	chr03	TM14f	PGSC0003DMG400016749	PGSC0003DMB000000059	TMV - induced protein I
4	chr03	TM15f	PGSC0003DMG400009178	PGSC0003DMB000000040	Pectinesterase
5	chr06	TM18f	PGSC0003DMG400034939	PGSC0003DMB000000180	Thylakoid lumenal 15 kDa protein 1, chloroplastic
6	chr04	TM20f	PGSC0003DMG400029517	PGSC0003DMB000000189	Desacetoxyvindoline 4-hydroxylase
7	chr07	TM25f	PGSC0003DMG400022241	PGSC0003DMB000000076	Photosystem II 10 kDa polypeptide, chloroplastic
8	chr08	TM27f	PGSC0003DMG400020809	PGSC0003DMB000000303	Cytochrome P450 71D11
9	chr10	TM29f	PGSC0003DMG400007205	PGSC0003DMB000000506	Calmodulin
10	chr10	TM30f	PGSC0003DMG400028151	PGSC0003DMB000000494	VAMP protein SEC22
11	chr12	TM31f	PGSC0003DMG400016959	PGSC0003DMB000000314	ATP synthase delta chain, chloroplastic

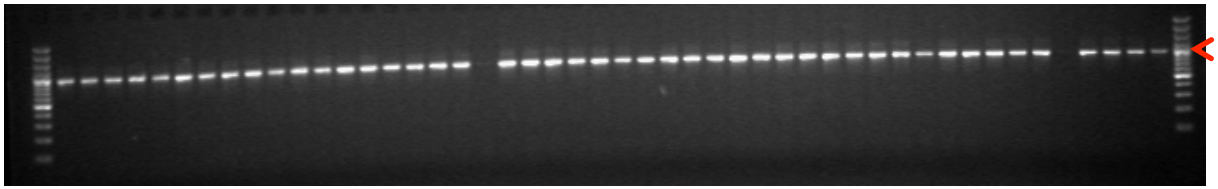
Chromosome 8: cytochrome P450 71D11 (Position: 34096306..34098612)
Primer - TM27

SAKA



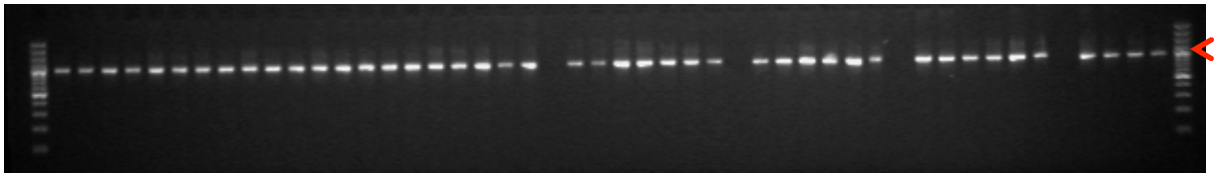
901 bp

BNA

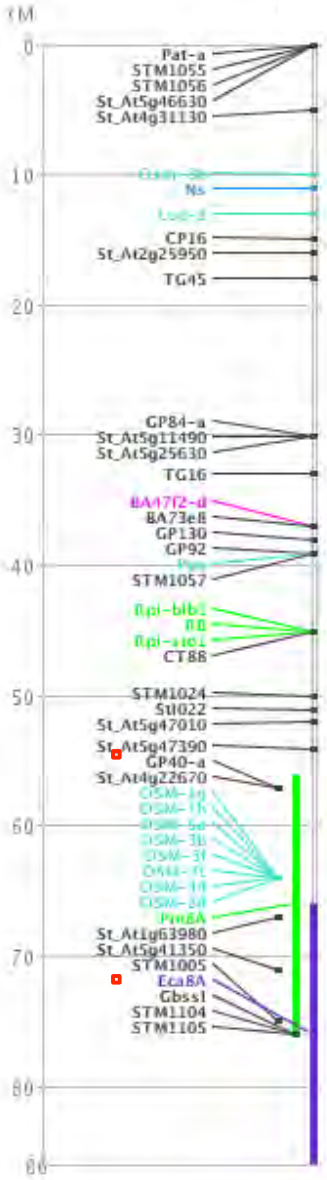


901bp

***Solanum phureja* (Colombian Central Collection)**



901bp



39000000bp

41000000bp

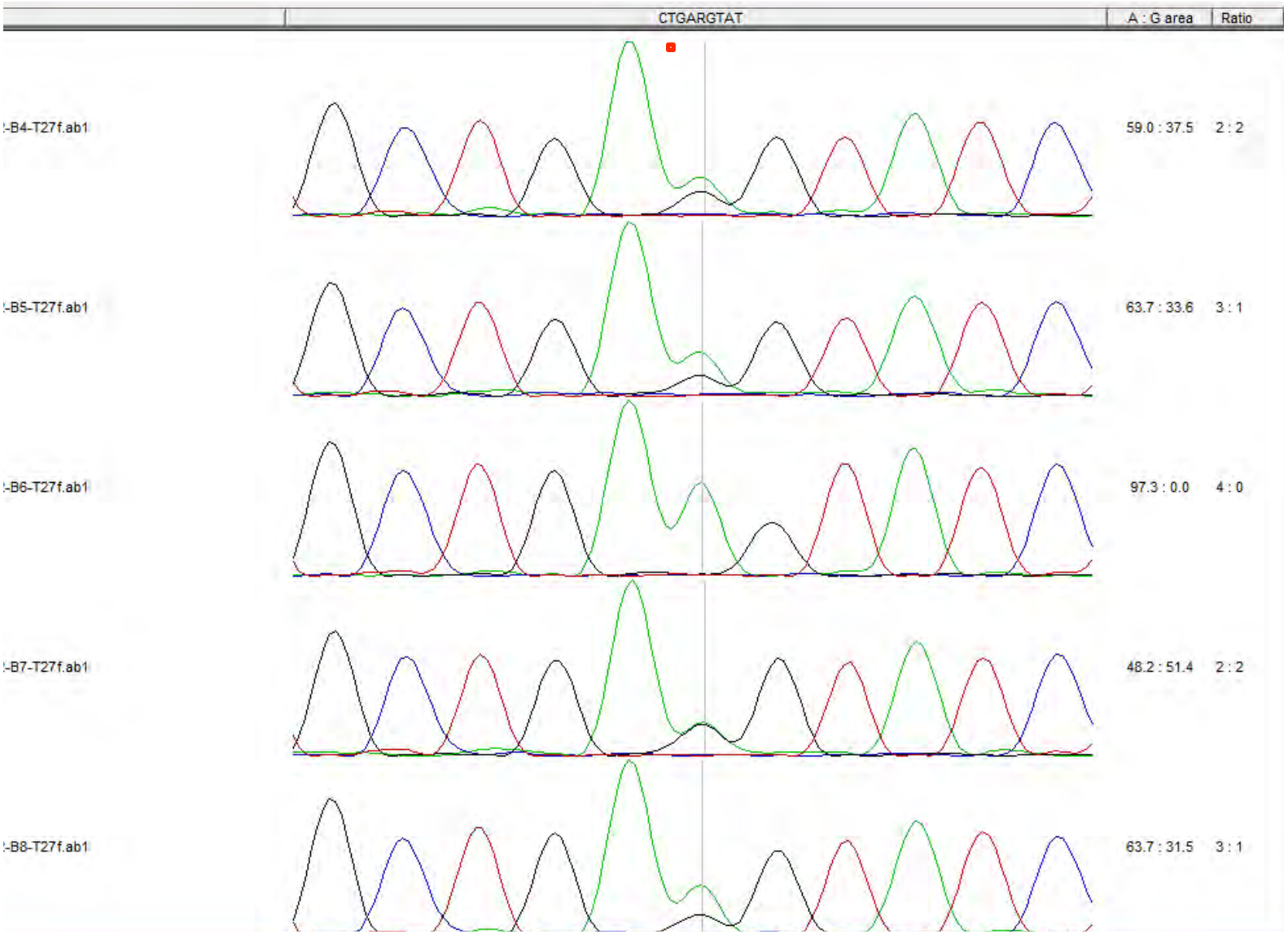
R genes and QTL for resistance to oomycetes

R genes and QTL for resistance to bacterial pathogens

Marker loci related by sequence similarity to defense response genes

TM27 BNA SNP p. 505 CTGA(A/G)GTAT

position on potato genome sequence 34097059



Univariate analysis variance

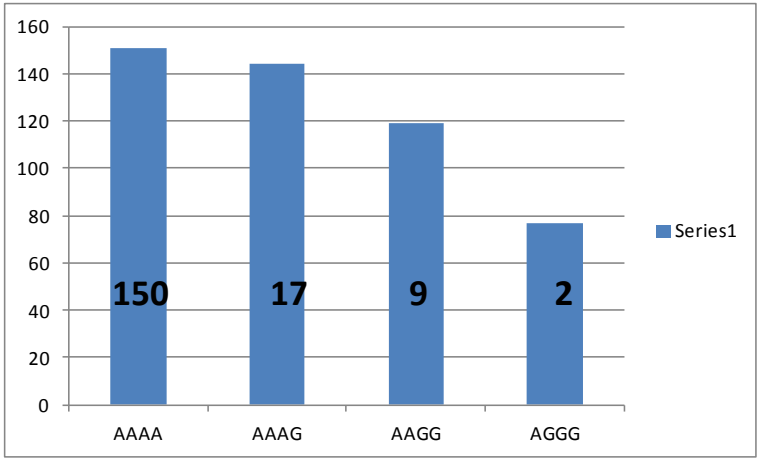
Chromosome 8: cytochrome P450 71D11

SNP	Position	AUDPC	rAUDPC	MCR	Maturity
AATG(G/A)TATA	40	.	.	.	0,01
CTGC(T/C)TTAA	181	.	.	.	0,001
TTAG(C/T)GTCT	340	.	.	.	.
CCTG(A/G)CTTC	425	.	.	.	.
TCTT(C/G)TTGT	432	.	.	.	.
AGAC(A/T)CTTG	451	0,033	0,037	0,051	.
ACAC(T/C)TGGG	453	.	.	.	0
TCCA(A/T)TCAA	484	.	.	.	.
CTGA(A/G)GTAT	505	0	0	0	0,469
CATC(G/A)TATG	547	.	.	.	.
ATCG(T/C)ATGA	548	.	.	.	.

Analysis of variance
SNP (505): CTGA(A/G)GTAT

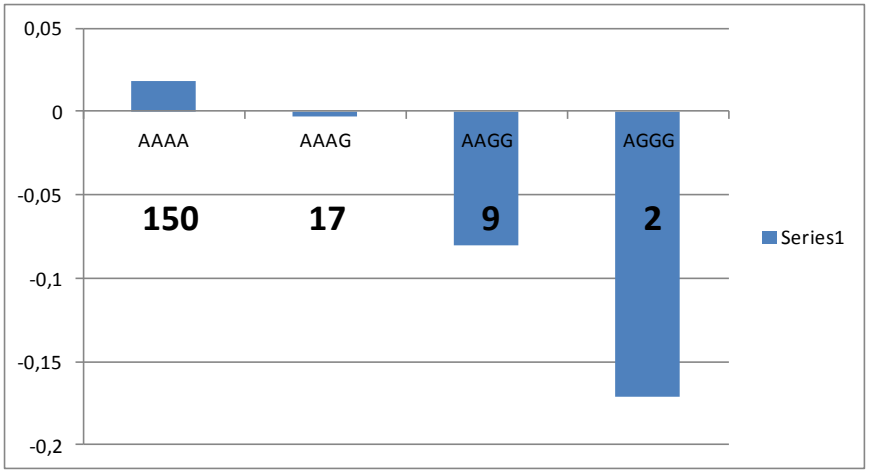
18.6% of phenotypic variance

Area under disease progress curve (AUDPC)



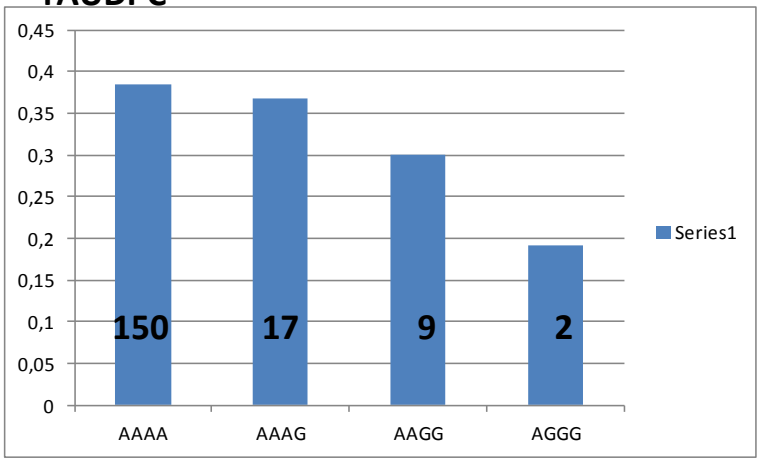
P-value **0,000346780**

Maturity corrected resistance (MCR)



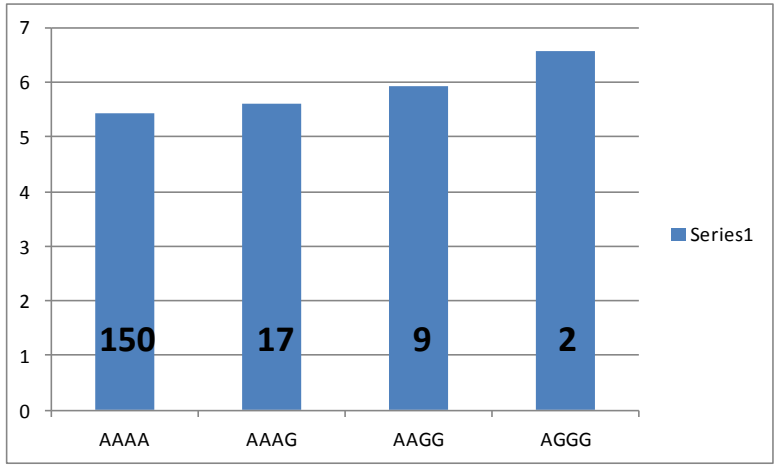
P-value **1,51113047873982E-060**

rAUDPC



P-value **0,00043539630**

Maturity



P-value **0,44971309**

Genes associated significantly with resistance to late blight

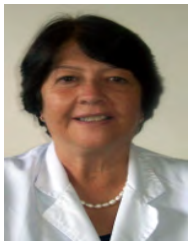
Chr.	Gene (ID)	Function described	Population	SNP (ID)	Significance	Primer Name
1	PGSC0003DMG400000204	Thylakoid membrane phosphoprotein 14kda, chloroplast	BNA/SAKA	257	*	TM10
3	PGSC0003DMG400009178	Pectinesterase	Phu	279	*	TM15
6	PGSC0003DMG400034939	Thylakoid lumenal 15 kDa protein 1, chloroplastic	BNA/SAKA	139 - 297	*	TM18
6	PGSC0003DMG400034939	Thylakoid lumenal 15 kDa protein 1, chloroplastic	Phu	66 - 88 - 108	**	TM18
7	PGSC0003DMG400022241	Photosystem II 10 kDa polypeptide, chloroplastic	BNA/SAKA	387 - 294	*	TM25
8	PGSC0003DMG400020809	Cytochrome P450 71D11	BNA/SAKA	505	**	TM27
10	PGSC0003DMG400007205	Calmodulin	BNA/SAKA	163	*	TM29

- Gene highly associated with quantitative resistance to late blight
- Same gene for SAKA, BNA and Phu

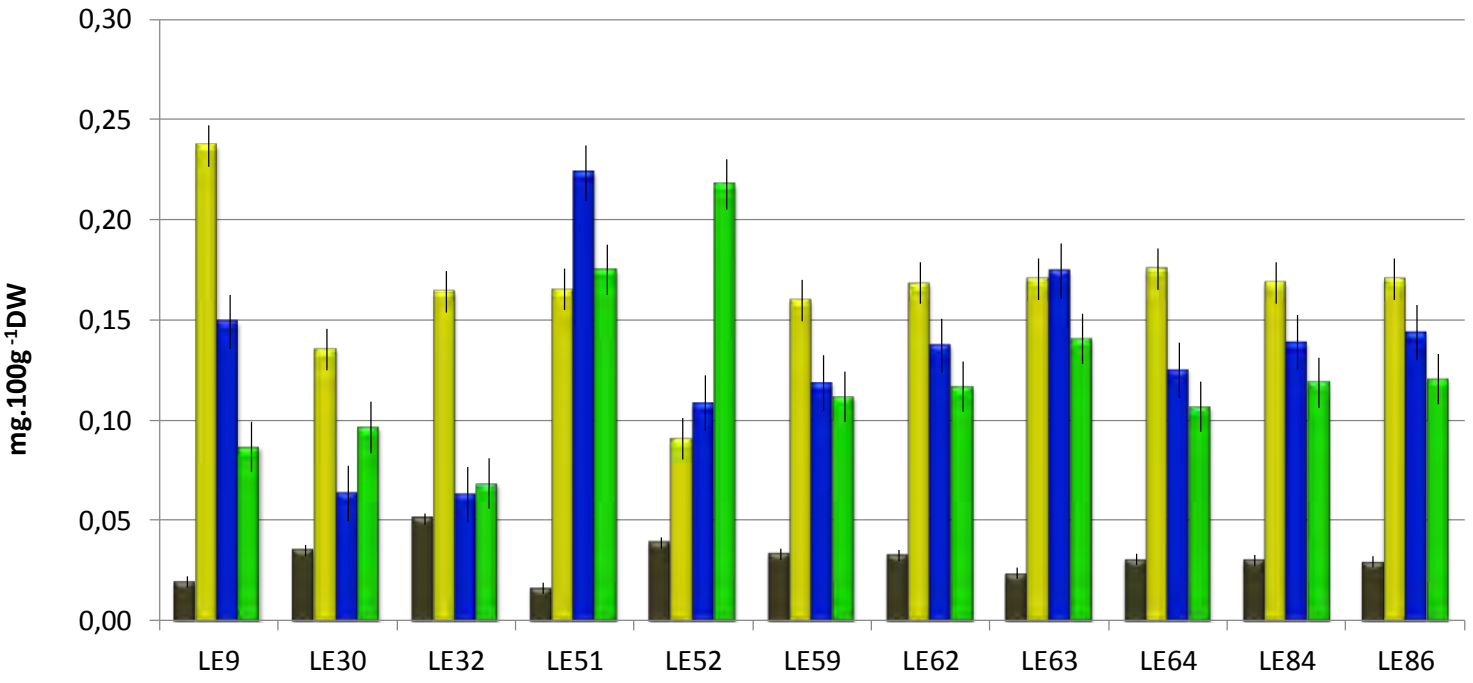
** Highly significant

* Significant

Introducing nutritional criteria in potato breeding



Content of phenols in 11 genotypes of *Solanum phureja*



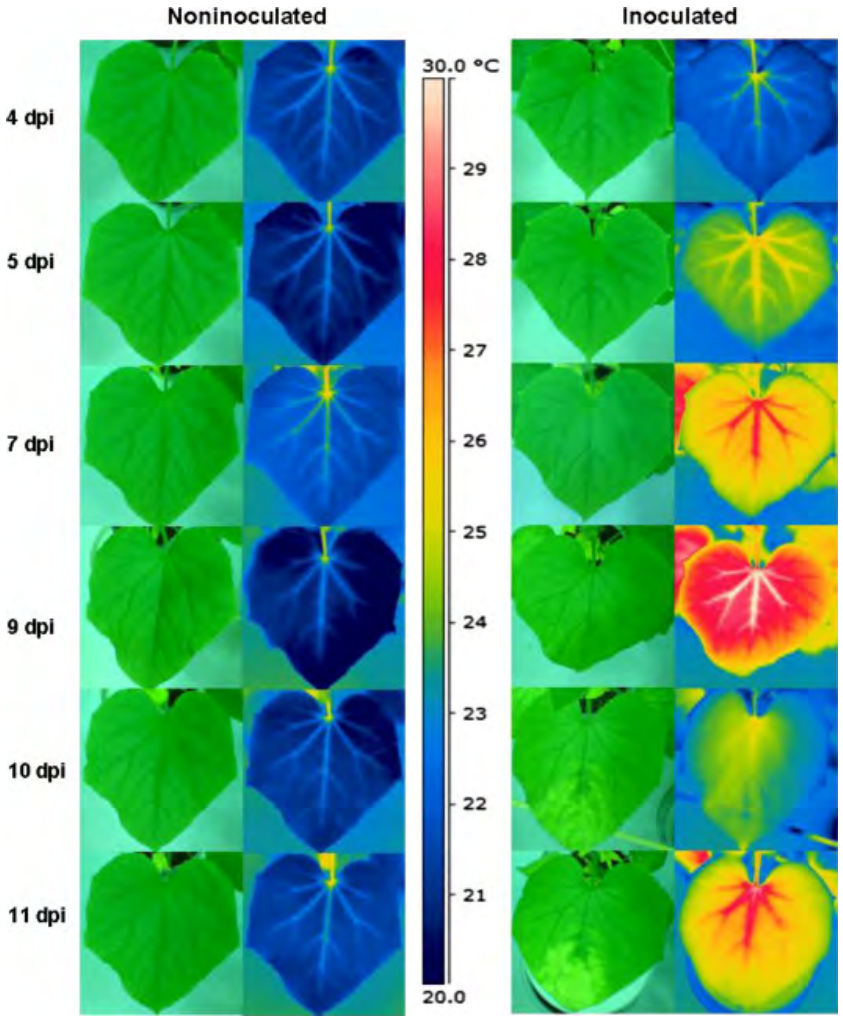
Challenge: to move the results from the laboratory bench and computer to the farm

?

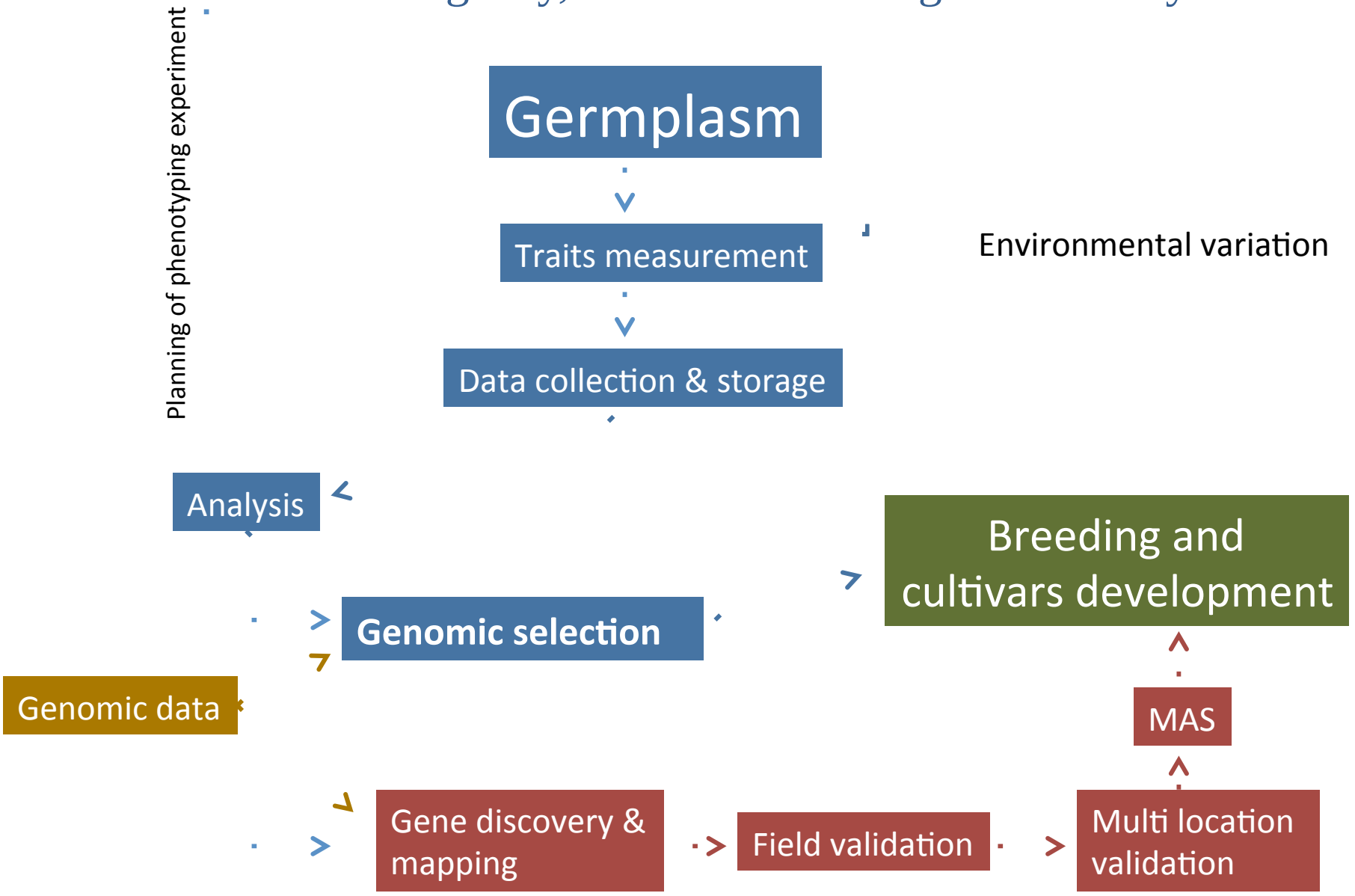
Plant systems biology:
the road from genotype to phenotype

To improve the assessment for the traits

Evaluation of resistance to late blight



It is a long way, but we have enough tools today



Proyecto SAN Nariño

UNIVERSIDAD NACIONAL DE COLOMBIA SEDE BOGOTÁ

Thanks for your attention

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