



## Partner 17

# GenXPro

Genes never seen before...

Frankfurt am Main, Germany

Peter Winter, CEO

**Transcriptome :**

- SuperSAGE/ST-DGE or MACE (quantitative information)
- Normalization of cDNA libraries (qualitative information)
- RNAseq
- small RNAs/microRNA
- other non-coding RNAs
- qPCR service

**Genome:**

- Digital karyotyping (ST-DK), RCS, CNVs
- Methylation-specific DK (ST-MSDK)
- Genetic Markers
- Target Enrichment
- Whole-genome Sequencing

**Metagenomics:**

- COXI, 16s rRNA, others...

**Bioinformatics:**

- NGS Data Handling, Assembly, Quantification, BLAST
- Expression Data Interpretation: Functional analysis



### ROCHE 454



### Illumina Highseq 2000



### ABI Solid 3



Reads	1 Mio	80 Mio	50 Mio
Length	350-1000 bp	50-100 bp	50 bp
Subunits:	8	8	8



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## Objective

**To assess the**

**Genetic variability in potential resistance genes in 48 chickpea accessions from 4 South-East European countries and Turkey.**



## Sub-Project Status:

- **Not yet started**
- **Material from collections required**

## Overview of GenXPro Contribution:

<b>Total budget</b>	<b>14.228 €</b>
<b>EU-Contribution:</b>	<b>10.956 €</b>
<b>Funding:</b>	<b>77 %</b>

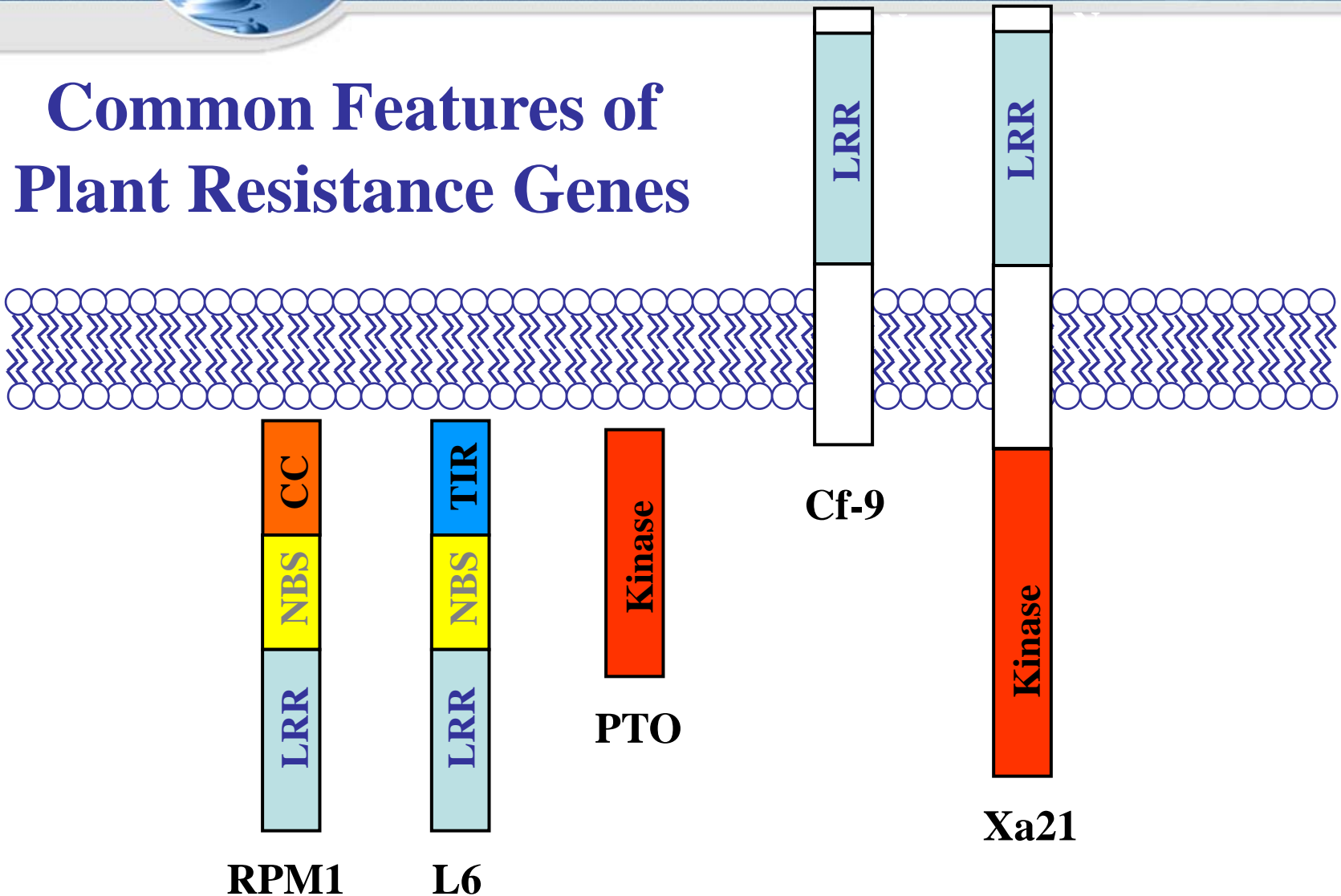


## **Plant Resistance (R) Genes:**

- **Among fastest evolving sequences in the genome.**
- **Genetic diversity reflects the co-evolution of plant host and pathogens**
- **Variability enables to estimate the pathogen pressure in their habitat**
- **Enables to stratify chickpea collections according to relevant molecular factors**
- **Most R-genes are receptor-like protein kinases with highly conserved domains**

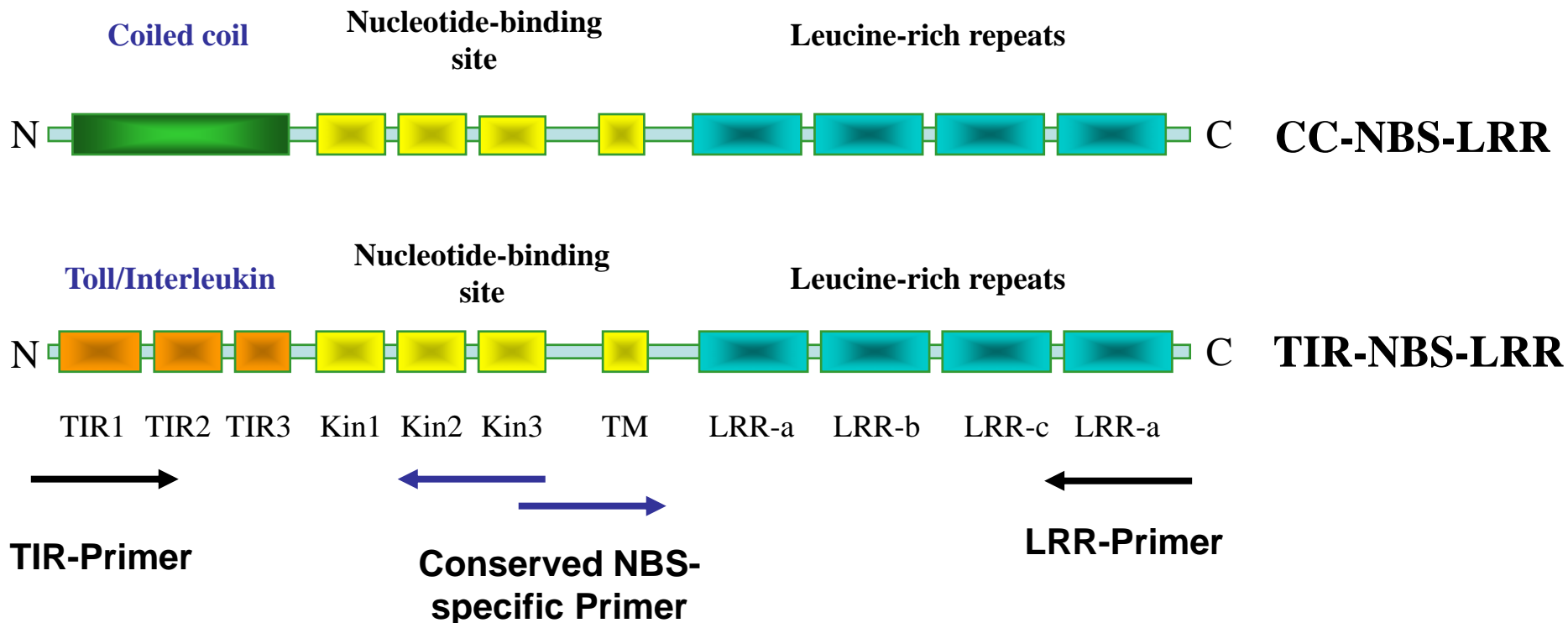


# Common Features of Plant Resistance Genes





# Conserved Features in the NBS-type R Proteins





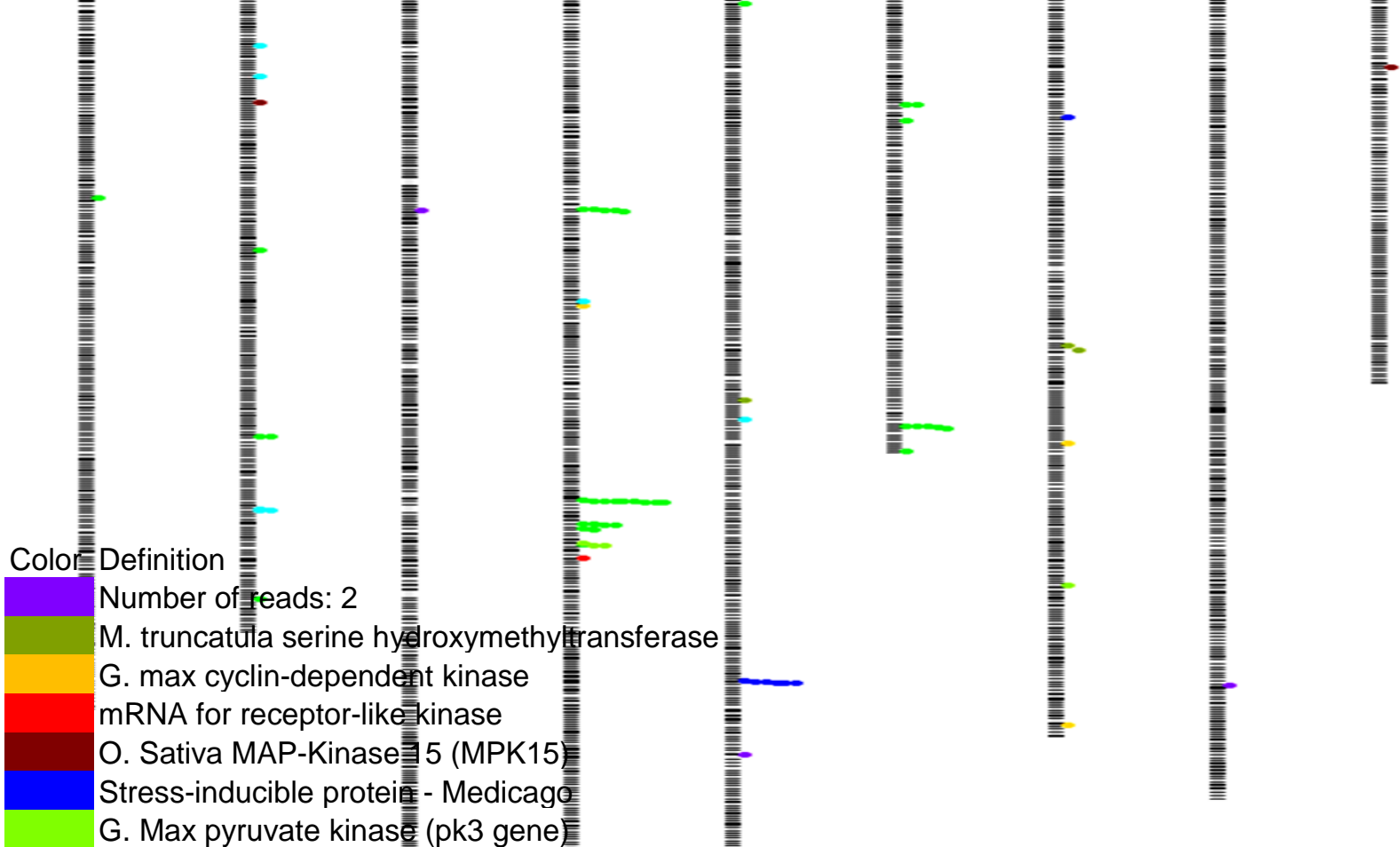


# BLAST of Lathyrus spp. NBS-containing contigues to the Medicago genome pseudomolecule

GENome-wide  
eXpression PROfiling

## hits on Medicago Genome

HtChr1 HtChr2 HtChr3 HtChr4 HtChr5 HtChr6 HtChr7 HtChr8 HtChr9



Query name	Color	Definition
contig00142	Purple	Number of reads: 2
contig00203	Olive	M. truncatula serine hydroxymethyltransferase
contig00139	Yellow	G. max cyclin-dependent kinase
contig00062	Red	mRNA for receptor-like kinase
contig00281	Brown	O. Sativa MAP-Kinase 15 (MPK15)
contig00125	Blue	Stress-inducible protein - Medicago
contig00252	Light Green	G. Max pyruvate kinase (pk3 gene)
contig00119	Bright Green	<b>S. arundinaceum NBS-LRR type R</b>
contig00156	Cyan	P. pyrifolia LRR-RLPK mRNA



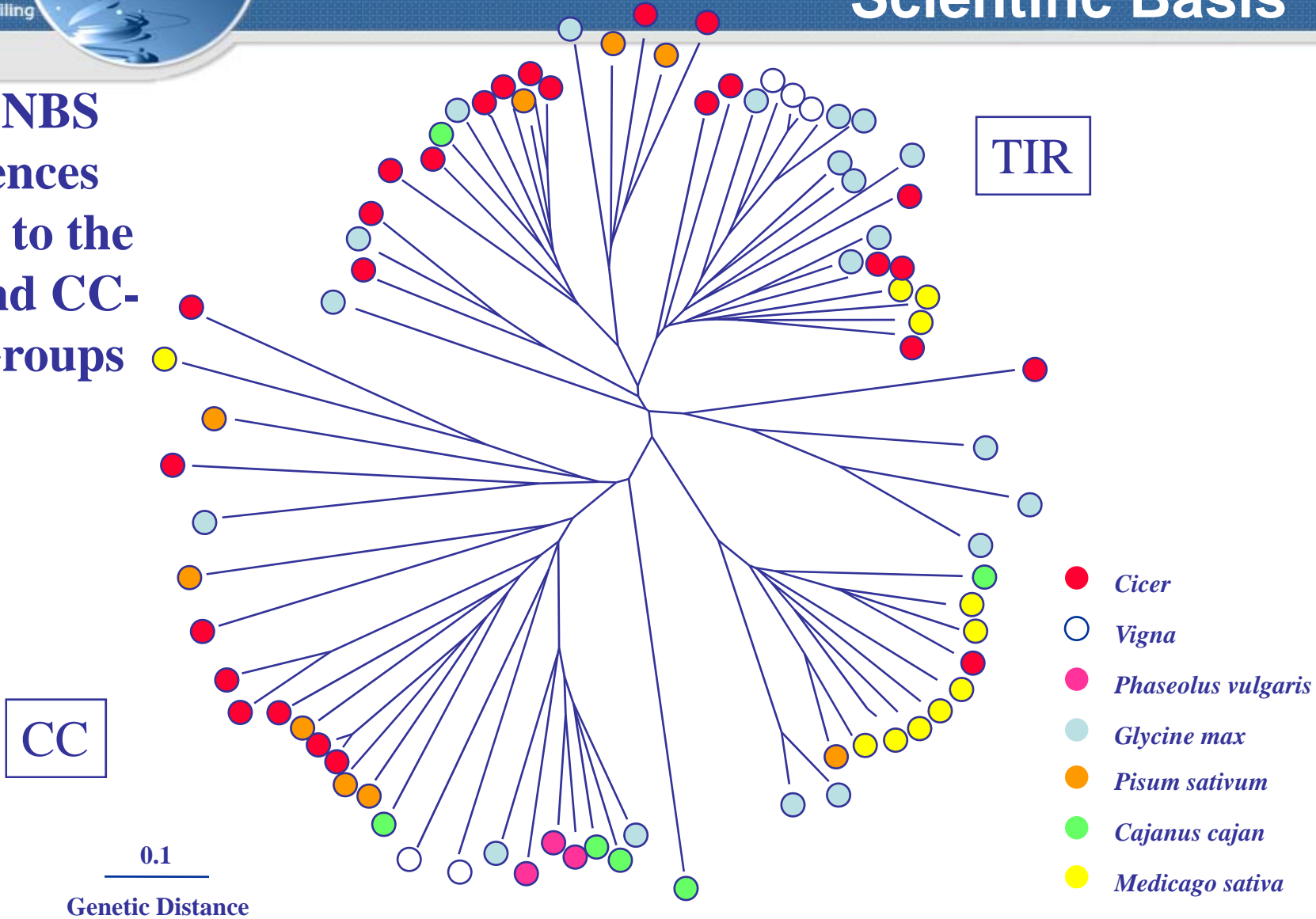
## Cloned Chickpea Candidate R Genes

Class	Total	cDNA
PTO-like STKs	11	n.d.
RLK-like STKs	3	3
CC-NBS type	7	3
TIR-NBS type	16	7
LRR	2	n.d.
MLO-like	3	2
	42	15

B. Huettel, D. Santra, F. Muehlbauer und G. Kahl (2002) Resistance gene analogues of chickpea (*Cicer arietinum* L.): isolation, genetic mapping and association with a *Fusarium* resistance gene cluster. TAG Theoretical and Applied Genetics 105: 479-490

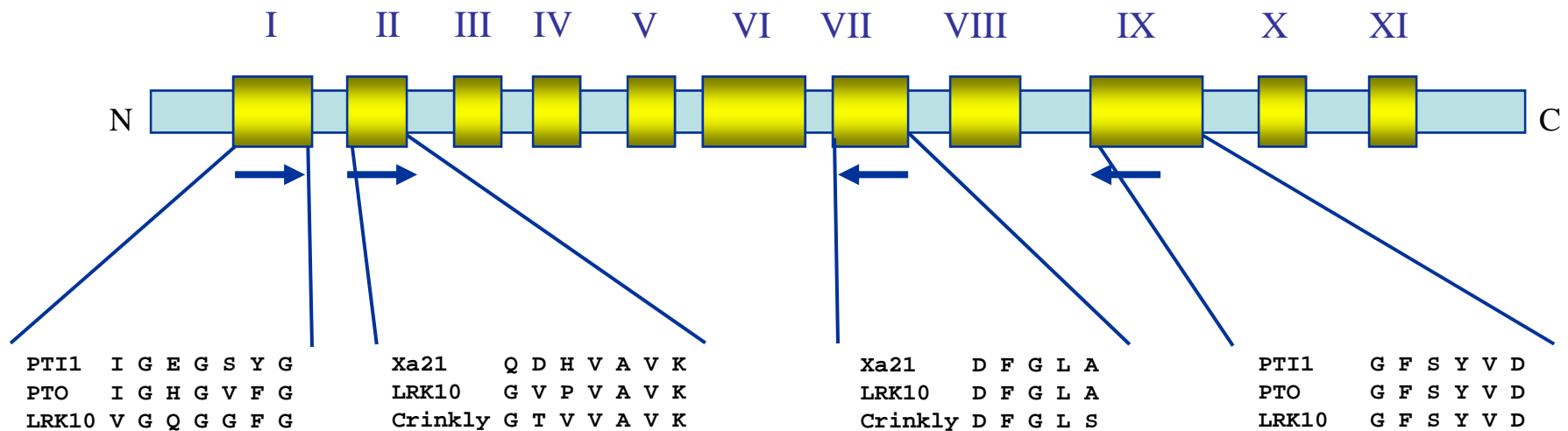


*Cicer* NBS  
Sequences  
belong to the  
TIR- and CC-  
NBS Groups



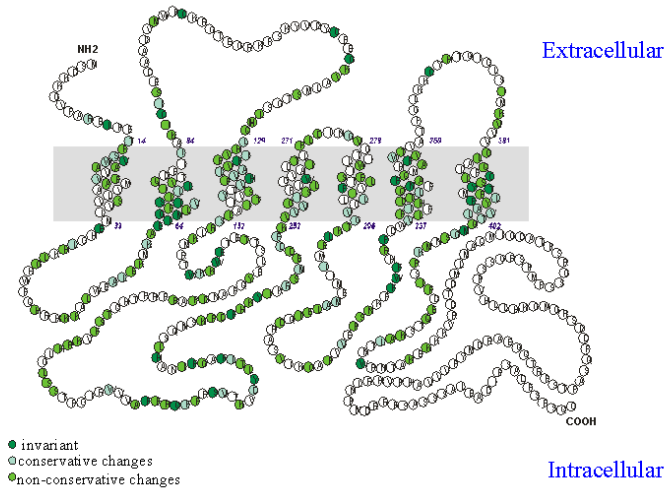


## Isolation of Resistance Gene Analogs: Exploiting conserved features of catalytic domains of Serine/Threonine Kinases

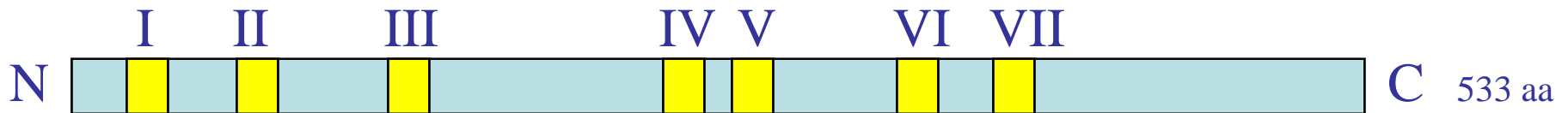




## Conserved sites for isolation of homologues of *mlo*: a cell death controlling factor



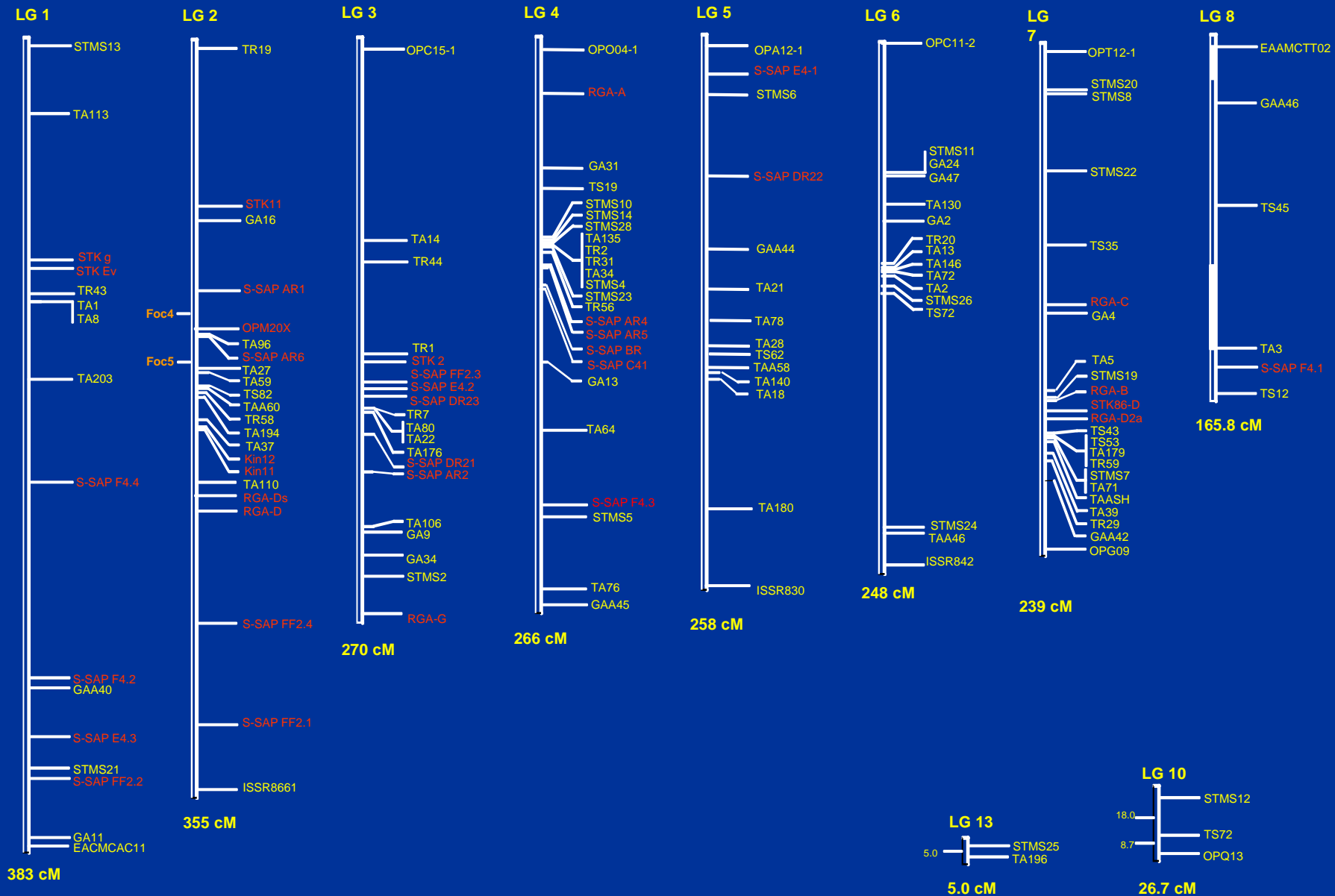
[http://www.mpiz-koeln.mpg.de/schlef/pic/psl\\_fig5b.gif](http://www.mpiz-koeln.mpg.de/schlef/pic/psl_fig5b.gif)



mlo (Barley) MEDDFK  
 Rice homologue LEDDFK  
 Flax homologue LEDDFK  
*Arabidopsis* homologue LEDDFK

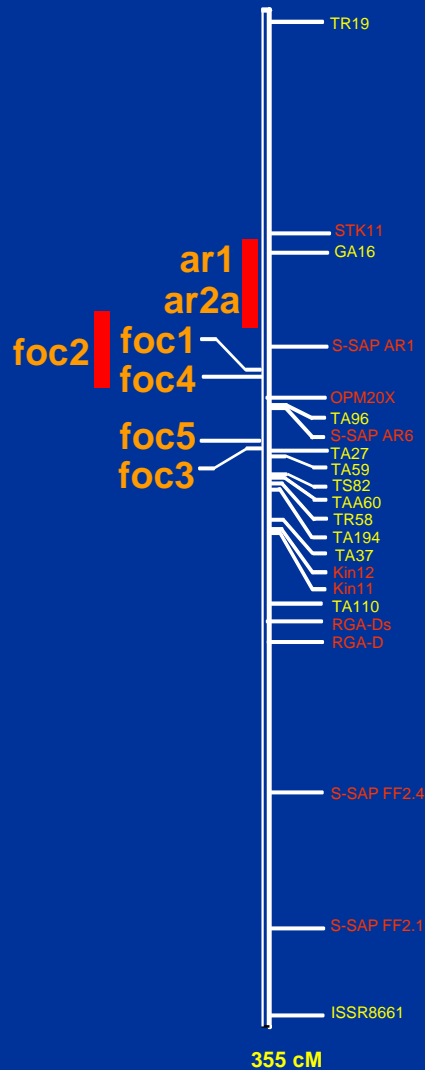
FWFHRP mlo (Barley)  
 FWFGRP Rice homologue  
 FWFNRP Flax homologue  
 FWFGRP *Arabidopsis* homologue

# Microsatellite Markers are often associated with Resistance-Gene Analogs

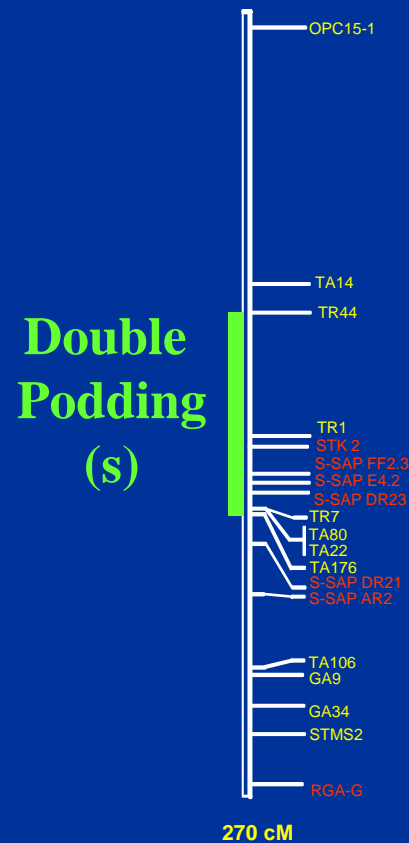


# STMS, Resistance-Gene Analogs, proven Resistance Loci and Loci of Agr. Importance

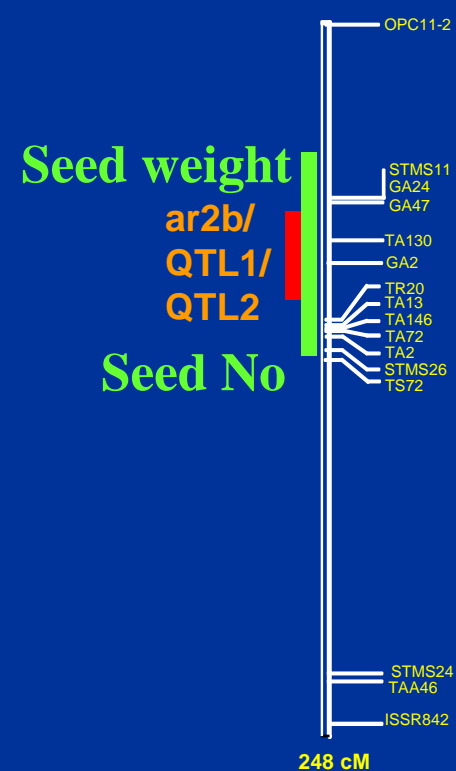
## LG 2



## LG 3



## LG 6





**Thank You for Your Patience!**

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