

High-resolution genetic map of the *R10* gene for resistance to late blight in tetraploid potato

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Outline

- **Background**
- **Inheritance of the resistance in MaR10**
- **Fine mapping for the *R10* gene**



Outline

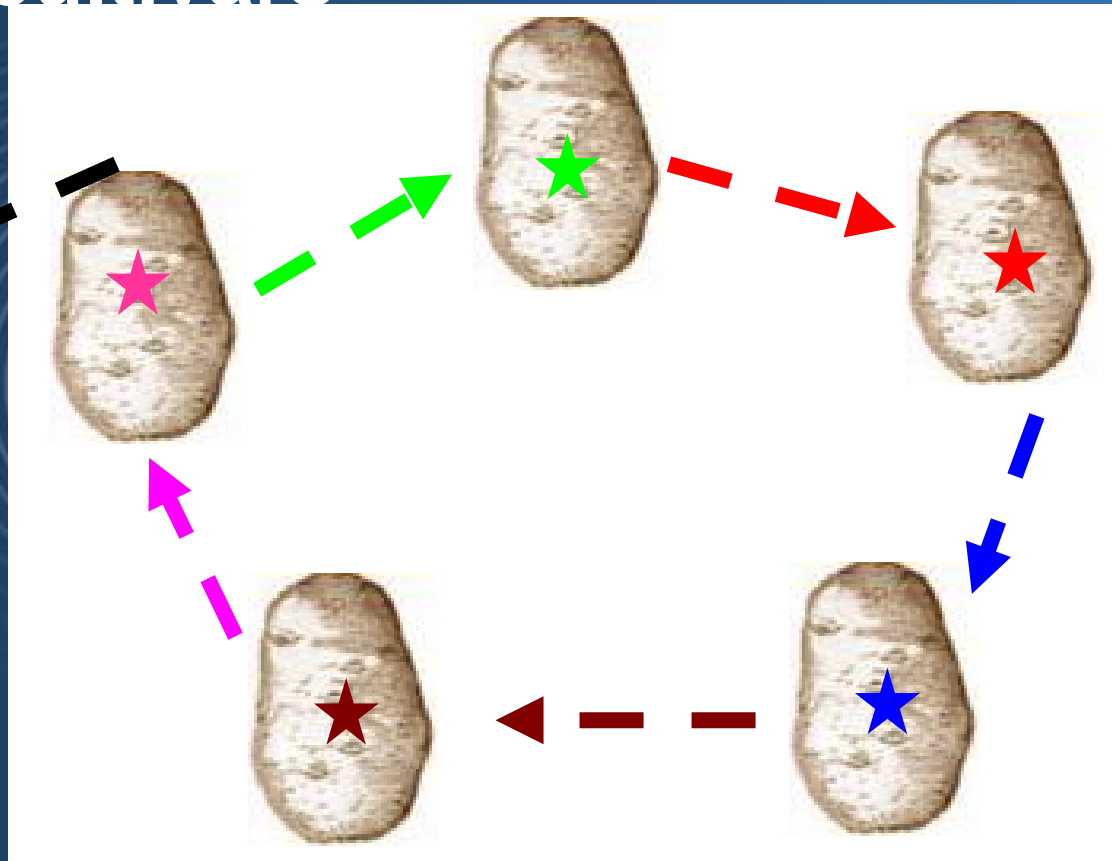
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Background

- “boom-bust” cycles of *R* genes in commercial cultivars

R genes pyramiding?
R genes polyculture?
Quantitative resistance?



--Pink D et al. 1999
Trends Plant Sci



Background

- ***R10* : weak but good field resistance**

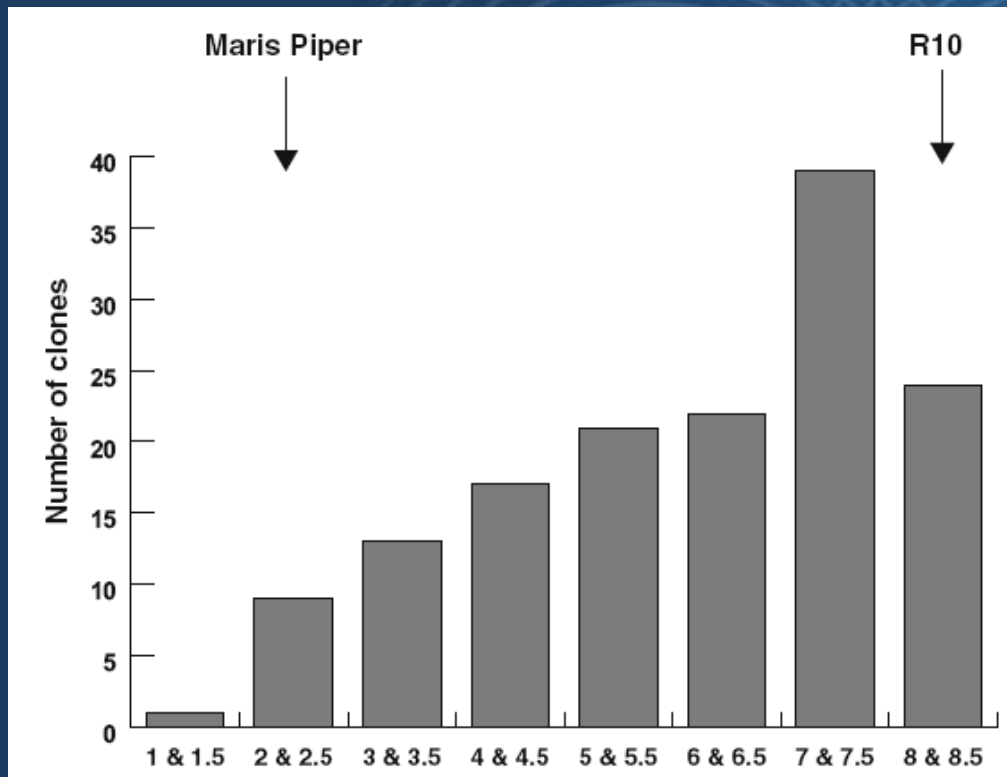
**Unlike resistance of other *R* genes:
black or white**

--Stewart HE, Bradshaw JE 2001
Potato Research



Background

The blight scores for the *R10* population displayed a continuous distribution.



Isolate 99/23 inoculated
race 1,2,3,4,6,7

--Bradshaw JE et al.2006
Theor Appl Genet



Questions to answer in this study

- Is *R10* gene a quantitative trait locus?
- What is the *R10* gene location on chr11?



Outline

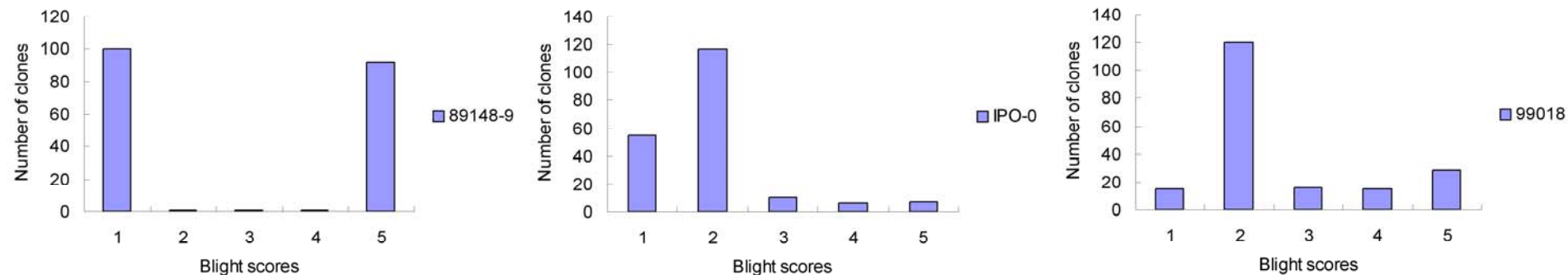
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Inoculation for *R10* population

Population of MaR10 × Katahdin: 195 clones

Isolates: 89148-9(race 0), IPO-0(race 3b), 99018(race 1,4)

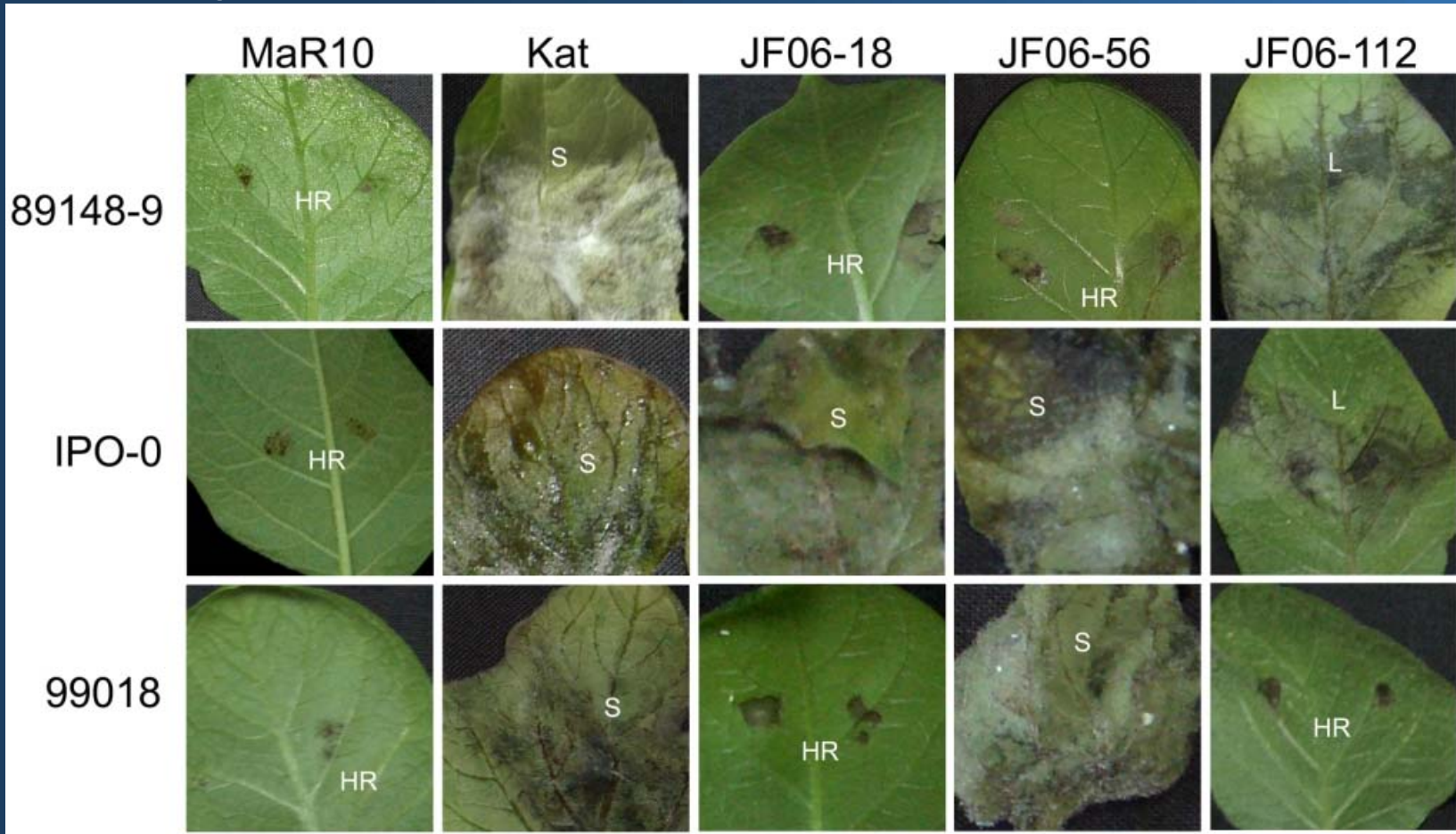


The resistance to isolate 89148-9 is inherited as a single dominant *R* gene in simplex (*Rrrr*). This gene was regarded as *R10*.



Paradox for “gene for gene”

These three isolates all have *Avr10*,
but they show different response to some clone.



u-test of blight scores on resistance to the isolate IPO-0 or 99018

a) Isolate IPO-0

Source	Number of clones	Mean score	Variance (s^2)	U value
<i>R10</i> clones	93	2.16	1.07	2.44*
Non- <i>R10</i> clones	101	1.60	0.24	

b) Isolate 99018

Source	Number of clones	Mean score	Variance (s^2)	U value
<i>R10</i> clones	93	3.25	1.75	8.53**
Non- <i>R10</i> clones	101	1.97	0.29	

*, ** significant at $P < 0.05$ and 0.01 , respectively.

Some resistance QTLs was linked to the *R10* gene



summary - inheritance of the resistance in MaR10

- The *R10* gene is a major resistance gene
- Some resistance QTLs were associated with the *R10* gene

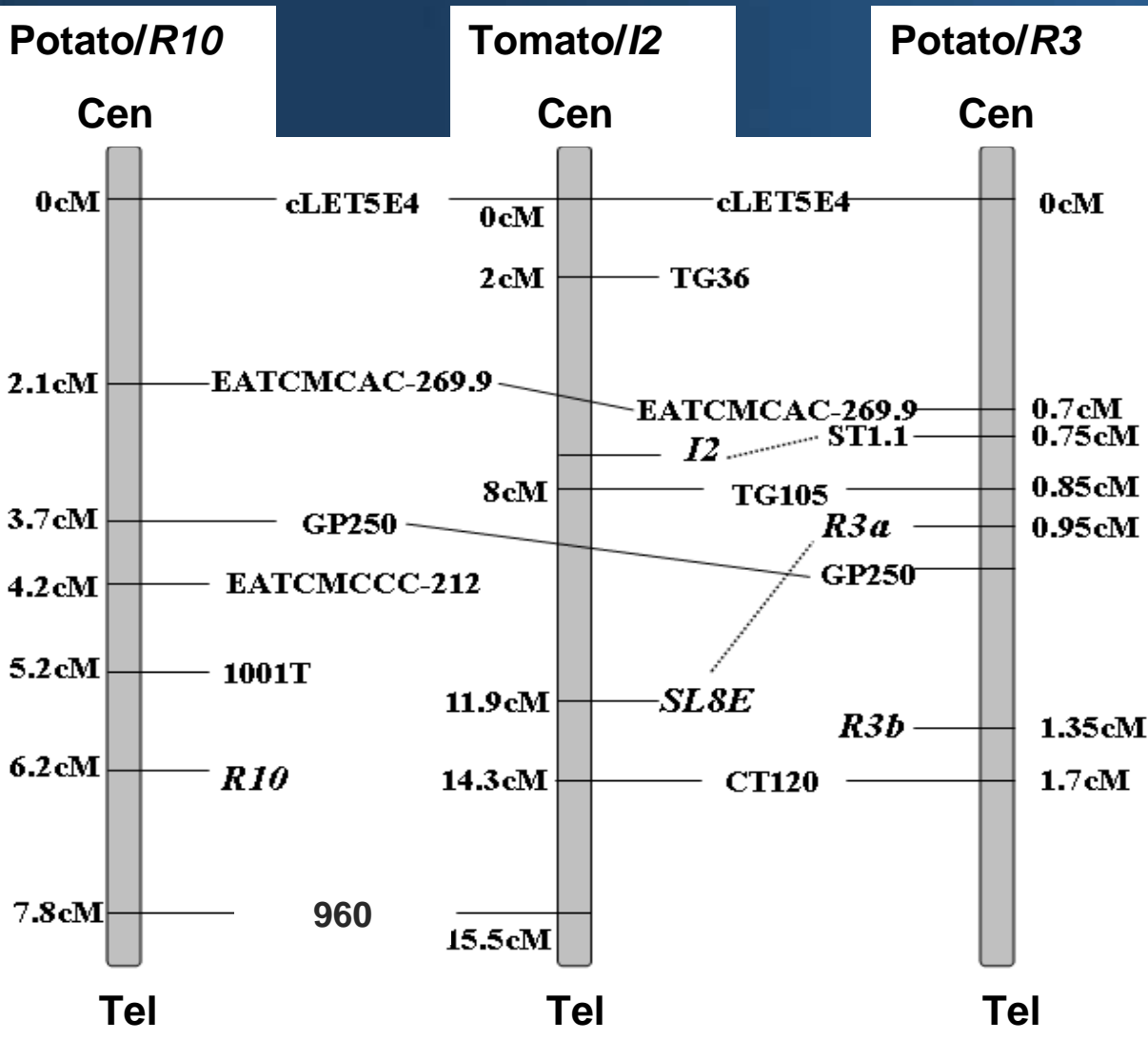


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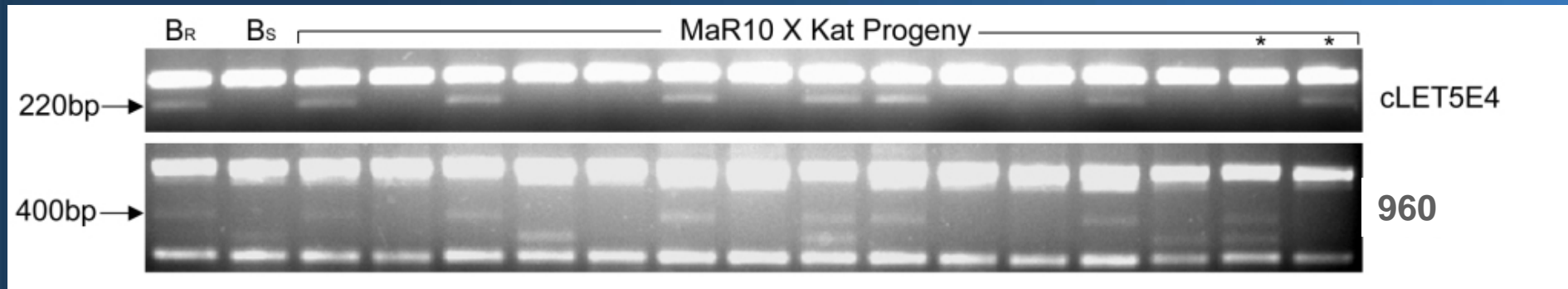
R10 location on chr11



Flanking markers for recombinants:
cLET5E4 and 960



Identification of recombination events

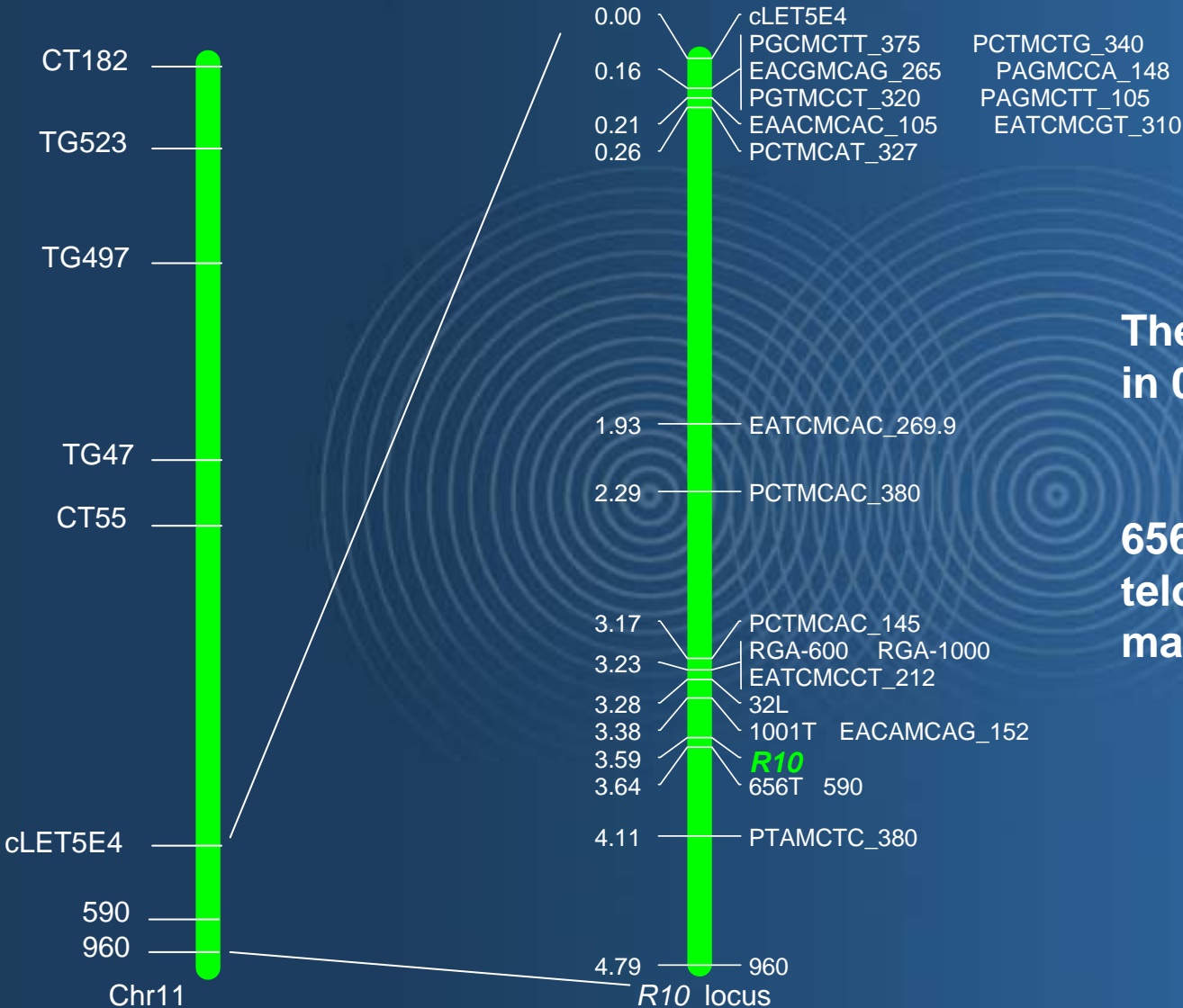


cLET5E4	960	plants
aa	aa	994
ab	ab	839
aa	ab	54
ab	aa	55
Total		1942
Recombination ratio		0.05098

99 recombinants in 1942 progeny



High- resolution map at the *R10* locus



The *R10* gene was located in 0.26cM interval.

656T /1001T is the closest telomeric/centromeric marker.



Acknowledgment

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Thanks!

Happy time in Beijing!



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