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Identification of a genetic factor determining the durability of a plant major resistance gene and quantitative resistance to virus accumulation

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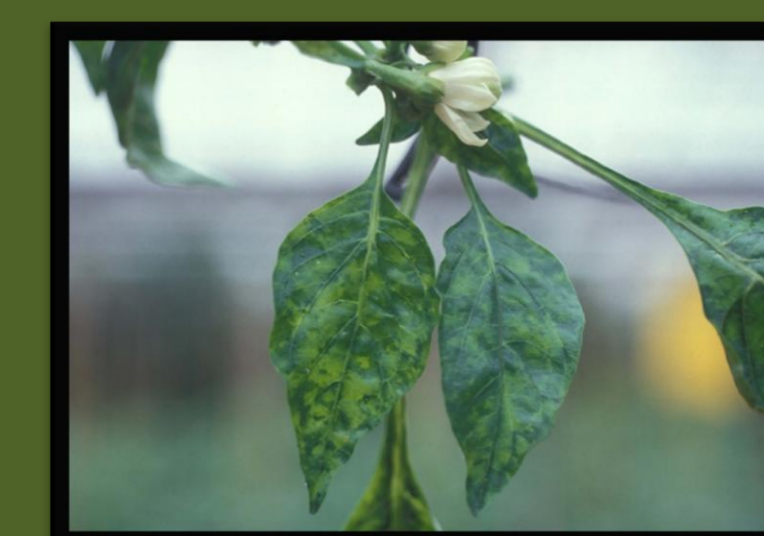
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Introduction

Genetic resistance provides efficient control of crop diseases but is **limited** by **pathogen evolution** capacities which often result in **resistance breakdown**.

The pepper resistance gene *pvr2³*, coding for a eIF4E (eukaryotic initiation factor 4E), confers a **recessive resistance** to Potato virus Y (PVY). This resistance is broken down by single amino acid substitutions in the VPg of PVY.

The **breakdown frequency** of *pvr2³* is highly dependent on the **genetic background** indicating that plant genetic factors directly **affect the durability** of the resistance.

Research question : Are the plant genetic factors involved in the durability of a major resistance gene and those controlling the quantitative resistance the same?

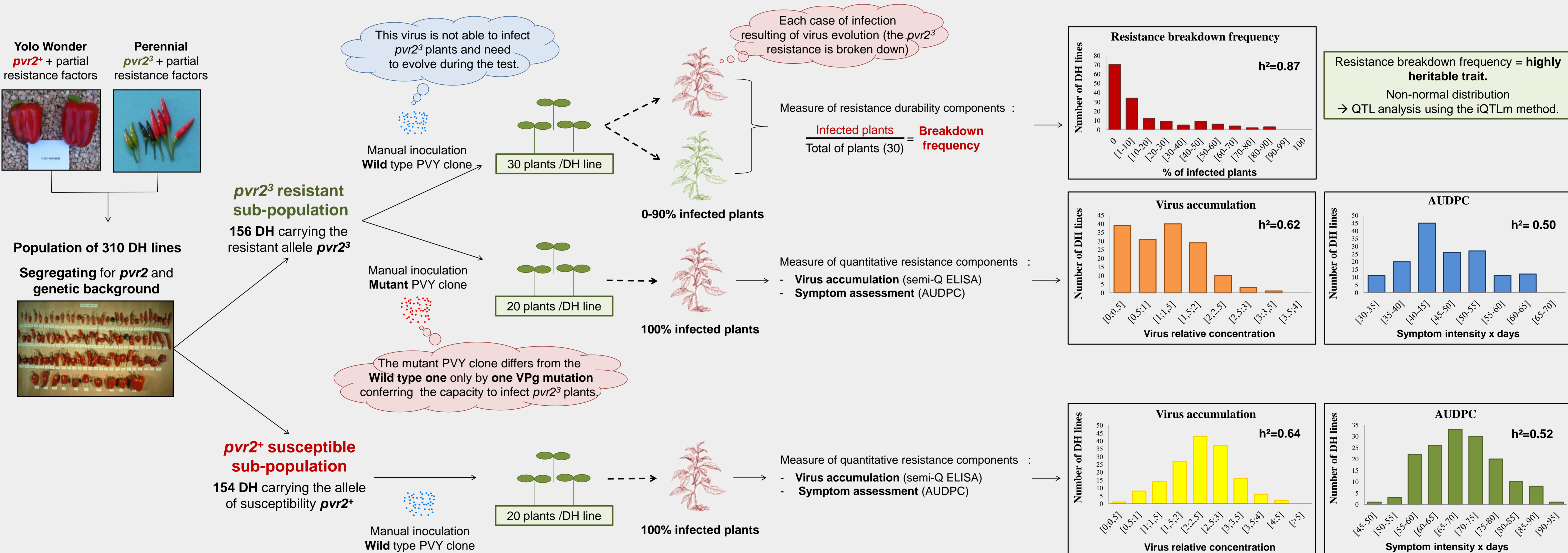
Objective

- Research and comparison of plant genetic factors involved in:
 - the durability of the *pvr2³* resistance gene.
 - the **quantitative resistance** to PVY.

Strategy

- Construction of a **doubled haploid (DH) progeny segregating** for the *pvr2* gene (*pvr2⁺* susceptibility allele or *pvr2³* resistance allele) and the **genetic background**.
- Phenotyping the DH progeny for :
 - **Breakdown frequency** of *pvr2³* → **component of resistance durability**.
 - **Virus accumulation** and **symptom intensity** (area under the disease progress curve (AUDPC)) → **component of quantitative resistance**.
- Genetic mapping** of the quantitative trait loci (QTLs) controlling each phenotyped trait.

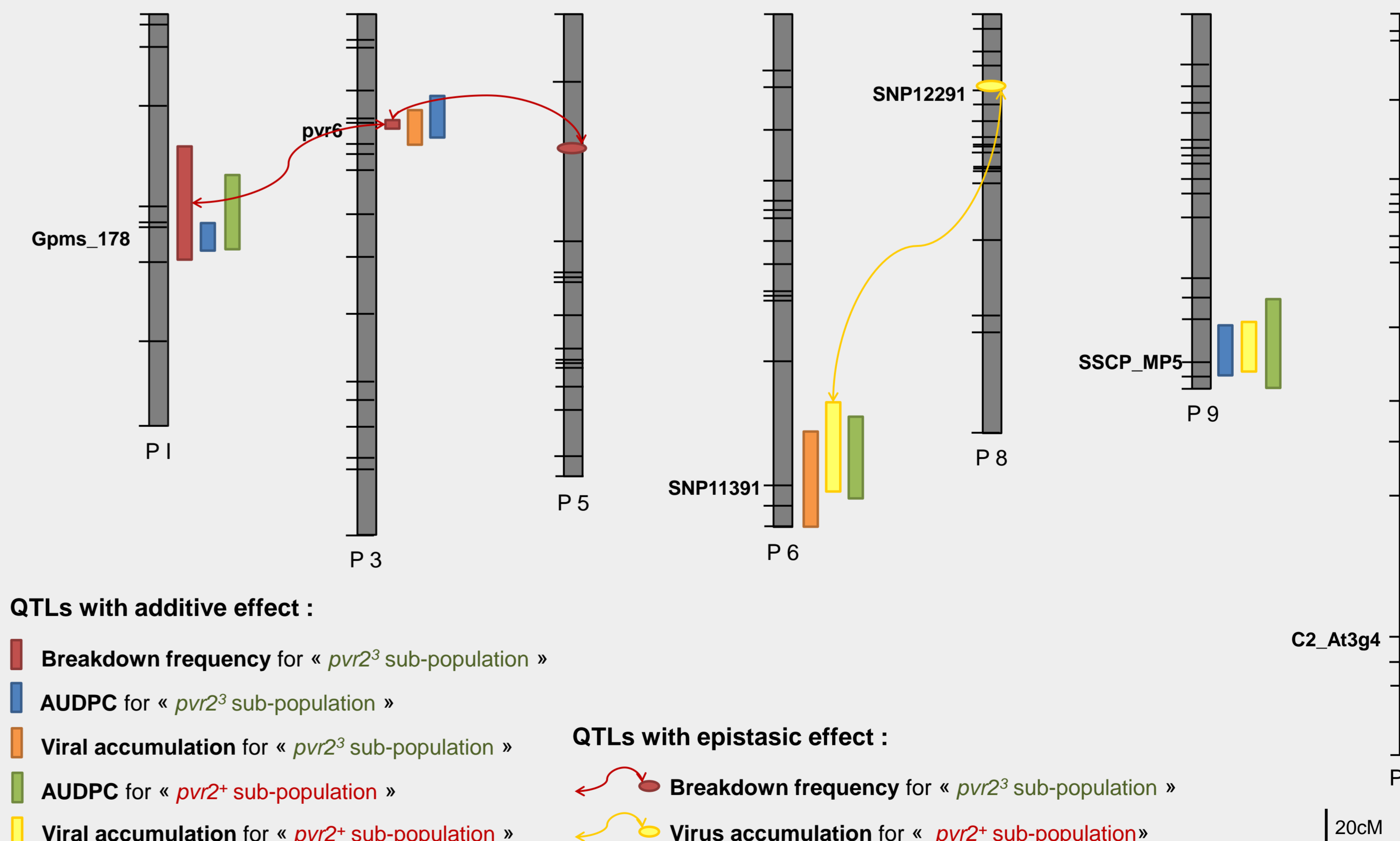
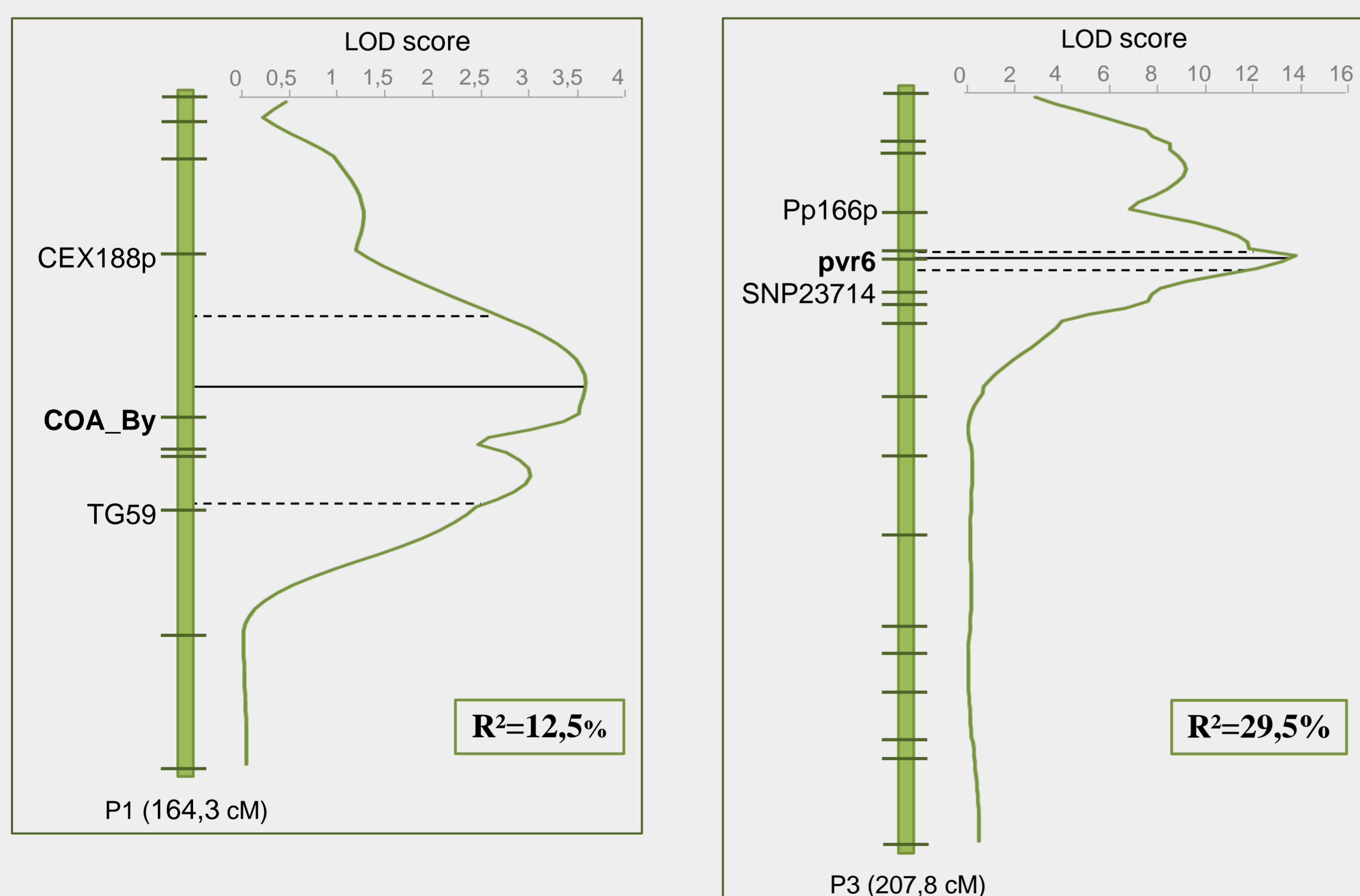
Phenotyping durability of *pvr2³* resistance gene and level of quantitative resistance.



Genetic factors control *pvr2³* resistance gene durability and quantitative resistance

1 **Detection of two "QTLs for durability"** : QTLs affecting the breakdown frequency of the major gene *pvr2³* were **successfully detected**.

2 **Comparative mapping** : the two significant QTLs for **Breakdown frequency** of *pvr2³* allele are **also involved in quantitative resistance**.



3 Descriptive table of QTL results

Allele at <i>pvr2</i> locus	Virus	Trait	Total R ² (%)	Additive QTLs			Epistatic QTLs				
				Location	LOD	R ² (%)	Yw allele effect	Location	LOD	R ² (%)	Yw - YW allele effect
<i>pvr2³</i>	Wild type PVY clone	Resistance breakdown (iQTLm)	54	1@70,6	4	10	+	1@91 - 3@43,1	5	13	-
				3@43,1	13	29	-	3@43,1 - 5@53,1	5	13	-
	Mutant PVY clone	Virus accumulation (iQTLm & MQM)	40	3@48	11	24	-				
				6@192,3	5	10	+				
		AUDPC (iQTLm & MQM)	33	1@87	5	12	+				
				3@40,8	5	11	-				
<i>pvr2⁺</i>	Wild type PVY clone	Virus accumulation (iQTLm & MQM)	38	2@191	3	7	-	8@28,1 - 9@134	4	11	+
				3@54,8	3	6	-				
	AUDPC (iQTLm & MQM)	50	6@188,3	5	11	+					
			9@139	4	9	+					
			1@76,8	5	8	+					
			6@188,3	6	11	+					
9@139	6	9	-								
11@258,8	5	9	+								

Conclusion

QTLs conditioning *pvr2³* resistance gene durability were successfully detected. Direct selection for alleles increasing the durability of virus resistance is consequently possible and opens new ways for durable resistance breeding.

Genetic factors affecting quantitative resistance and breakdown frequency colocalize in the genome suggesting pleiotropy for the two traits.

When direct selection for resistance durability is not possible (phenotyping test not available), indirect selection for quantitative resistance traits can be expected to improve the durability of a major resistance gene.

IS-MPMI 2012 XV International Congress

PROGRAM AND ABSTRACTS

July 29 (Sun.) – August 2 (Thu.), 2012 · Kyoto, Japan

