



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

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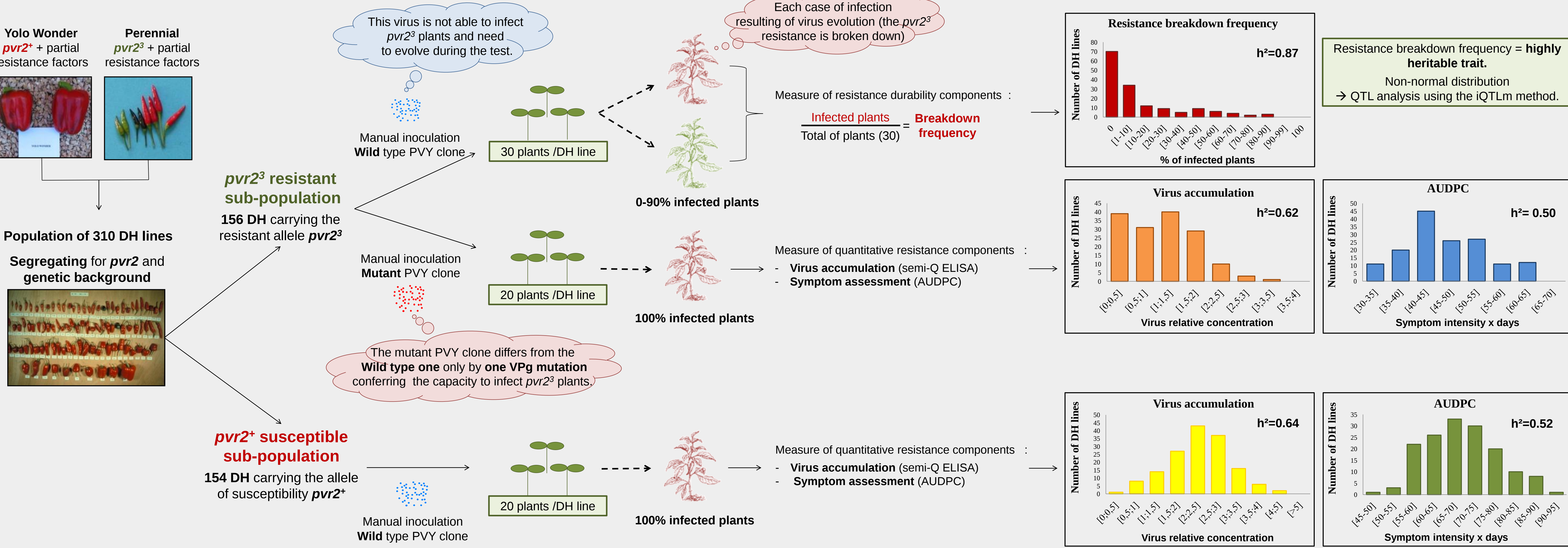
Introduction

- 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

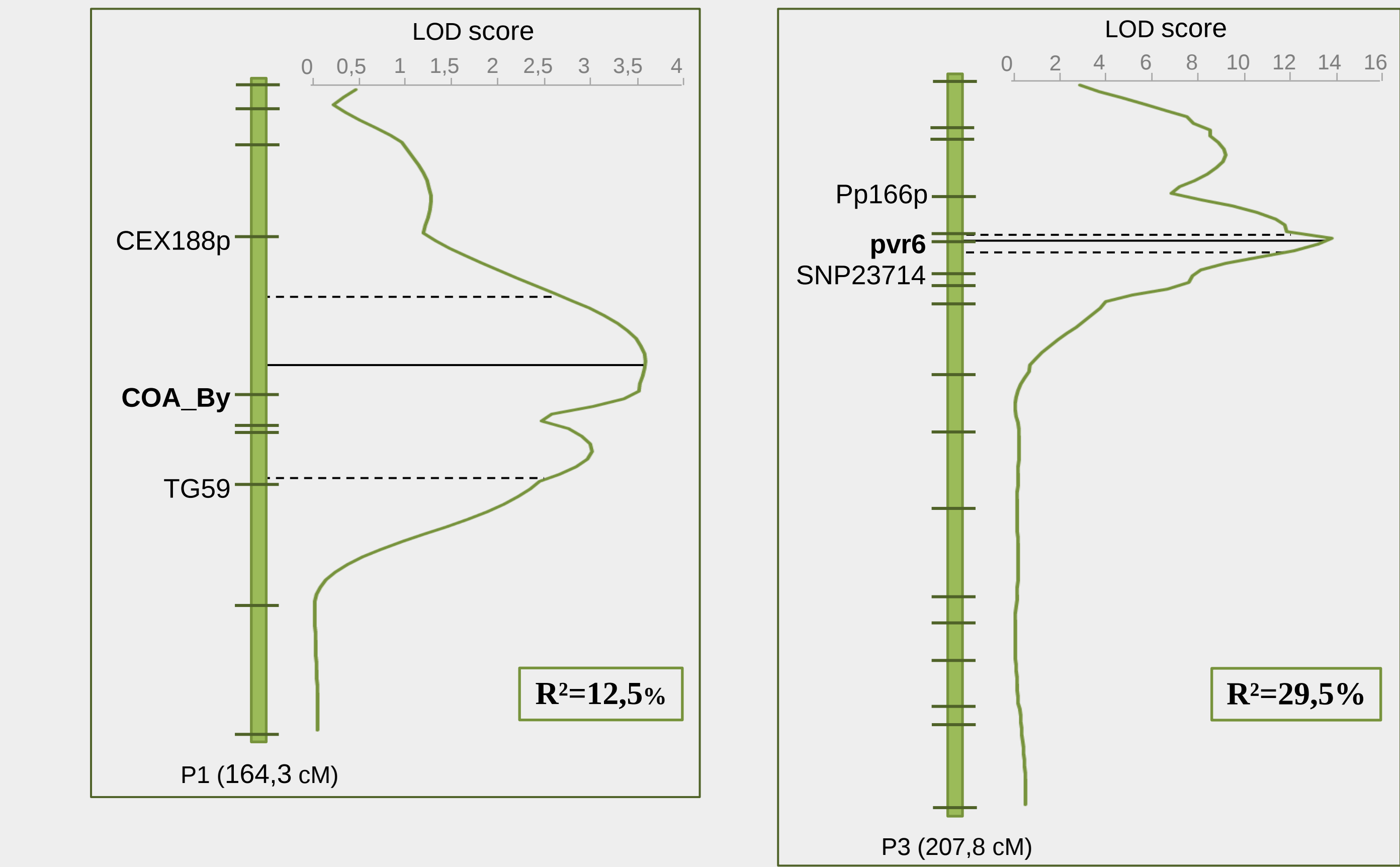
- Research** and **comparison** of plant genetic factors involved in:
 - the durability of the ***pvr2³*** resistance gene.
 - the **quantitative resistance** to PVY.
- Construction of a **doubled haploid (DH) progeny segregating** for the ***pvr2*** gene (*pvr2⁺* susceptibility allele or *pvr2³* resistance 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.



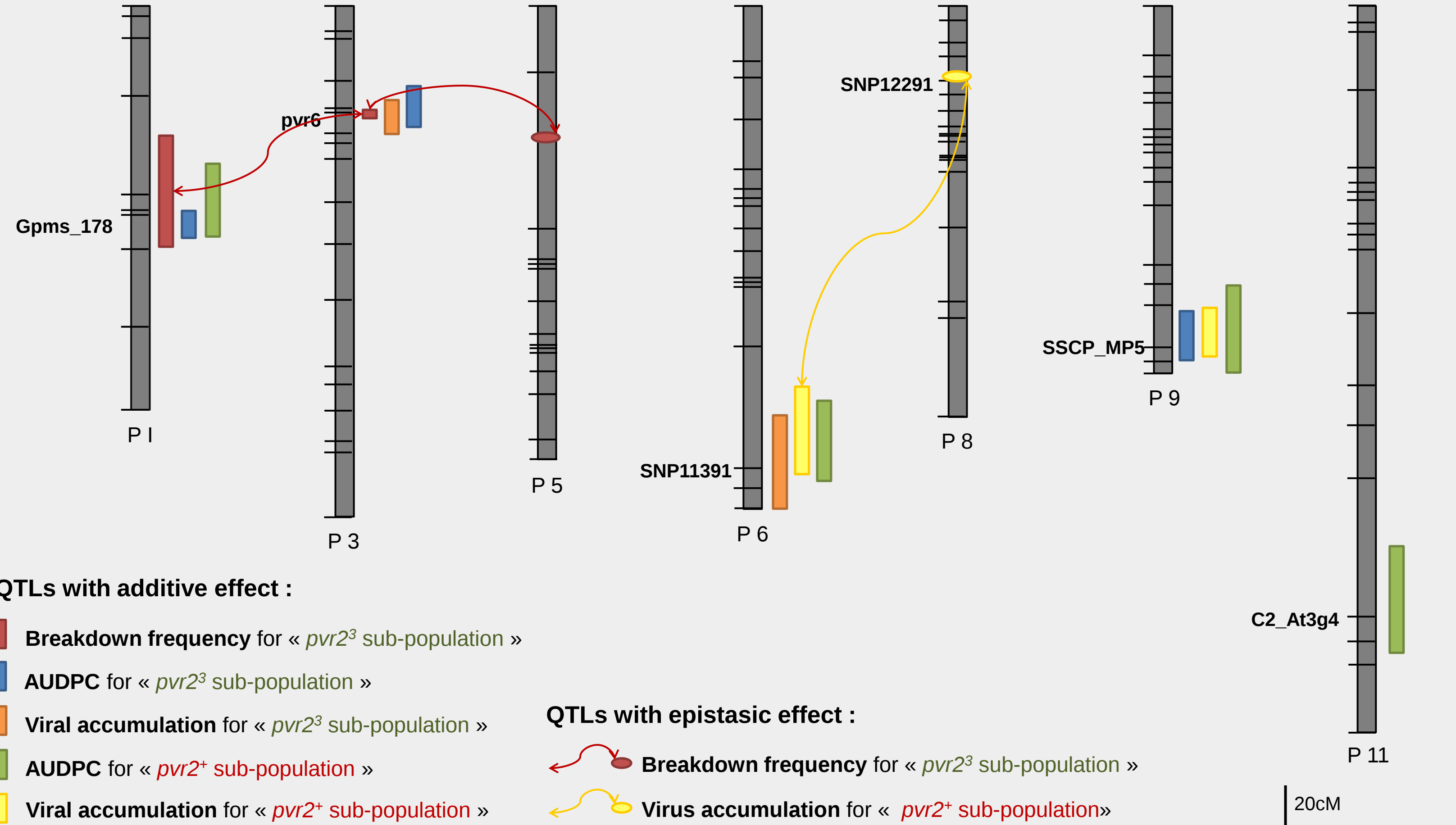
Genetic factors control *pvr2³* resistance gene durability and quantitative resistance

- Detection of two “QTLs for durability”** : QTLs affecting the breakdown frequency of the major gene *pvr2³* were **successfully detected**.
- Comparative mapping** : the two significant QTLs for **Breakdown frequency** of *pvr2³* allele are **also involved in quantitative resistance**.



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	-
				3@48	11	24	-				
				6@192,3	5	10	+				
				1@87	5	12	+				
	Mutant PVY clone	Virus accumulation (iQTLm & MQM)	40	3@40,8	5	11	-				
				9@138	5	11	-				
				2@191	3	7	-	8@28,1 - 9@134	4	11	+
				3@54,8	3	6	-				
				6@188,3	5	11	+				
	Mutant PVY clone	AUDPC (iQTLm & MQM)	33	9@139	4	9	+				
				1@76,8	5	8	+				
				6@188,3	6	11	+				
				9@139	6	9	-				
				11@258,8	5	9	+				
<i>pvr2⁺</i>	Wild type PVY clone	Virus accumulation (iQTLm & MQM)	38								
	Wild type PVY clone	AUDPC (iQTLm & MQM)	50								



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.

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PROGRAM AND ABSTRACTS

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