

Análisis comparativo del transcriptoma para el estudio de la resistencia a la raza 38 de *Colletotrichum lindemuthianum* localizada en el clúster Co-2 de judía común

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CONGRESO
NACIONAL
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GENÉTICA
de PLANTAS



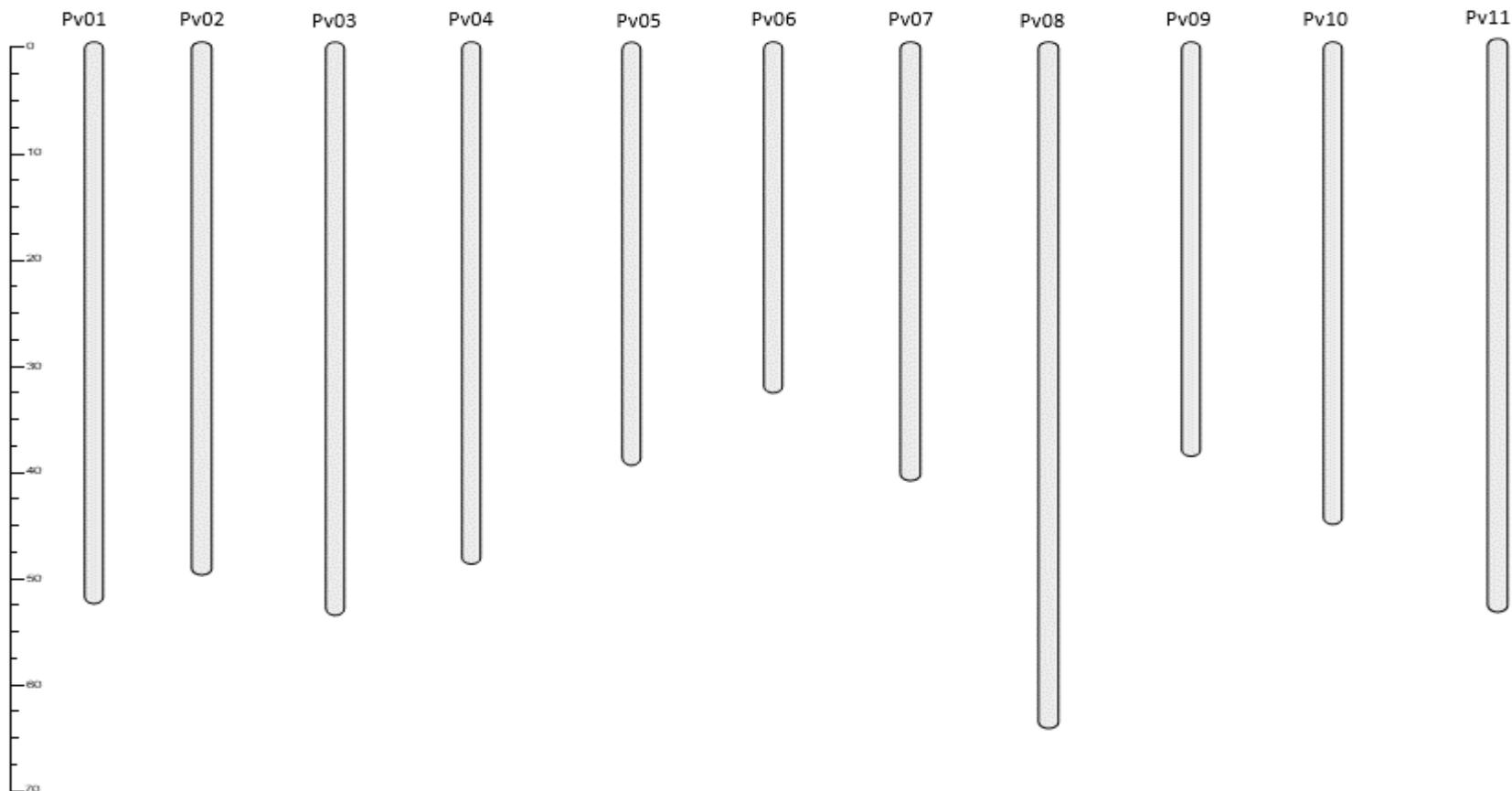
2022
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19 - 22 set | pazo da cultura

¿Qué es la antracnosis?



- Variabilidad patogénica
- Resistencia cualitativa, gen a gen, raza-específica
- Raza 38 → Co-2

¿Cómo es la resistencia a la antracnosis?



Pv11

Raza 38 → la más extendida en el norte de España

Clúster Co-2 : Resistencia a la raza 38 de *C.lindemuthianum* derivada de la variedad Cornell49242

Ampliamente introgresado en variedades comerciales



- ❖ Conocer a través de un análisis de expresión diferencial el gen/genes que controlan la resistencia a la raza 38 en el cluster Co-2
- ❖ Desarrollo de marcadores moleculares capaces de acelerar los programas de mejora

2 LÍNEAS ISOGÉNICAS
(NIL)



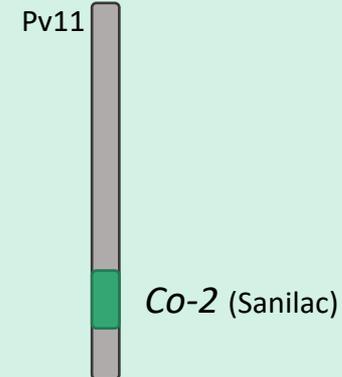
A25/Andecha

SUSCEPTIBLE a la raza 38 de
C.lindemuthianum



A4804

RESISTENTE a la raza 38 de
C.lindemuthianum



A25/Andecha

S 0 hpi

S 24 hpi

S 48 hpi

A4804

R 0 hpi

R 24 hpi

R 48 hpi

3 REPETICIONES/TEST DE INOCULACIÓN



Temperatura: 24°C
Humedad 90-95%
Fotoperiodo: 12 horas

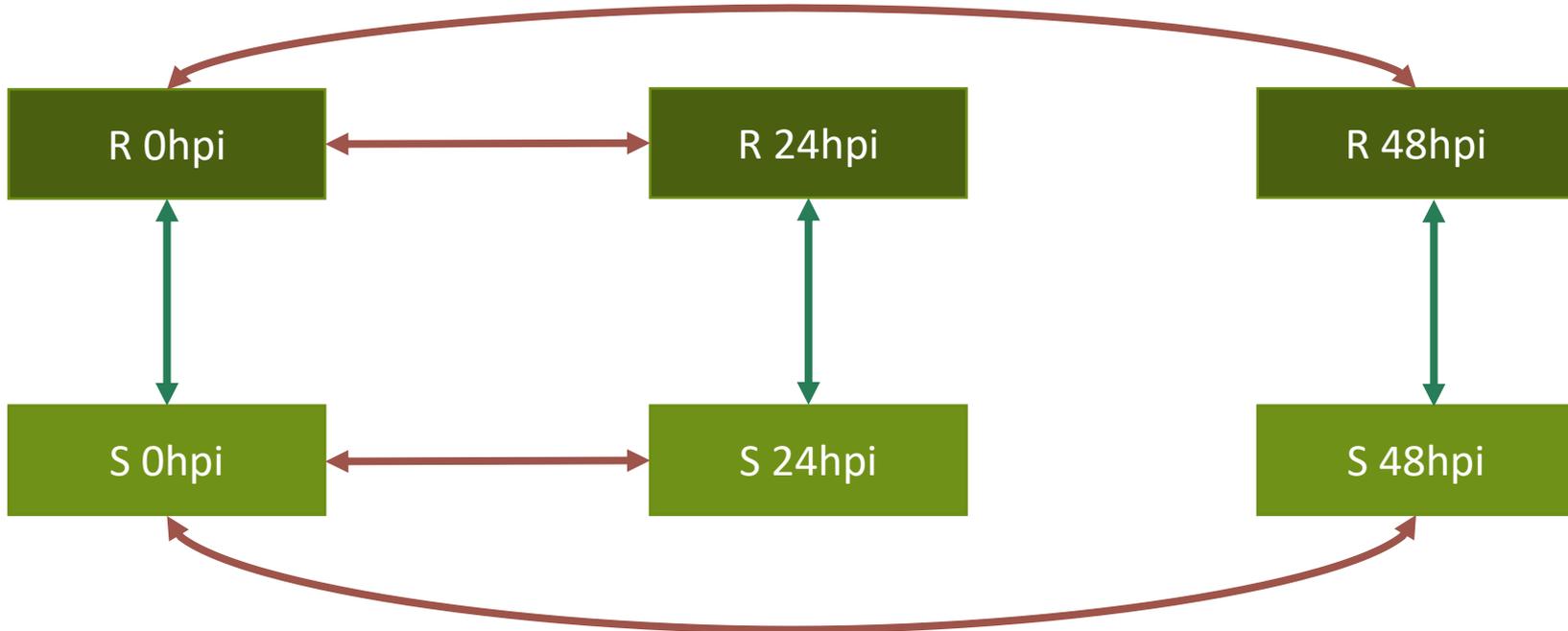


NOISeq: Differential Expression in RNA-seq

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NOISeq: Differential Expression in RNA-seq

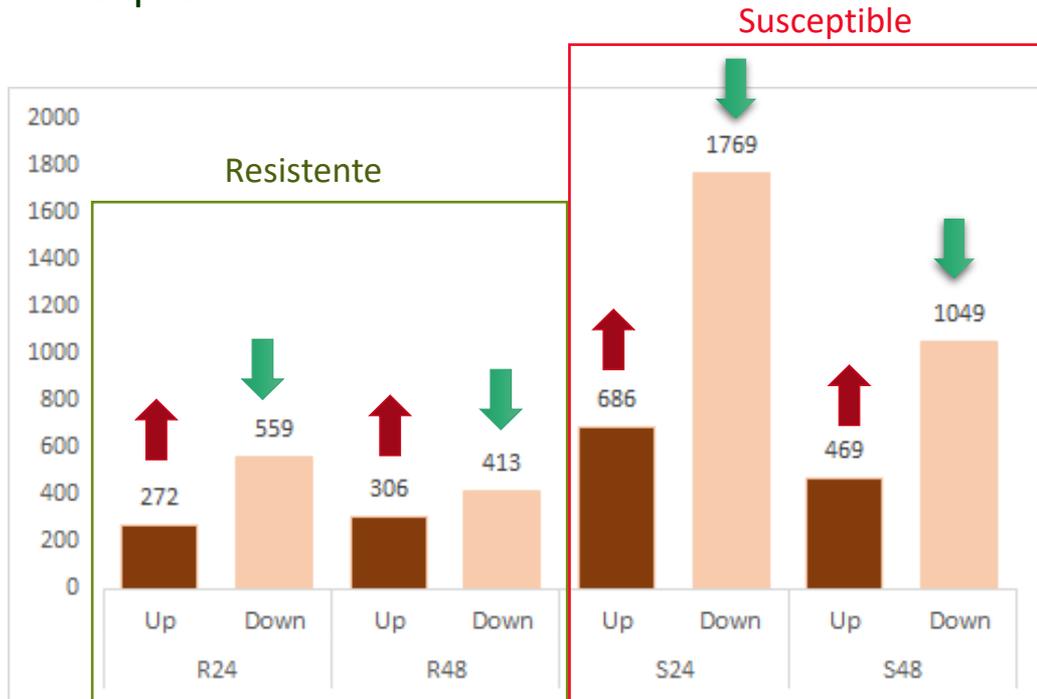
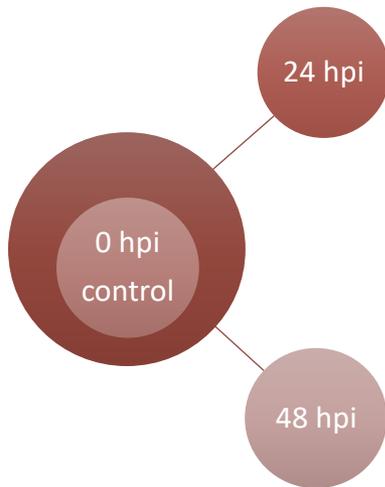


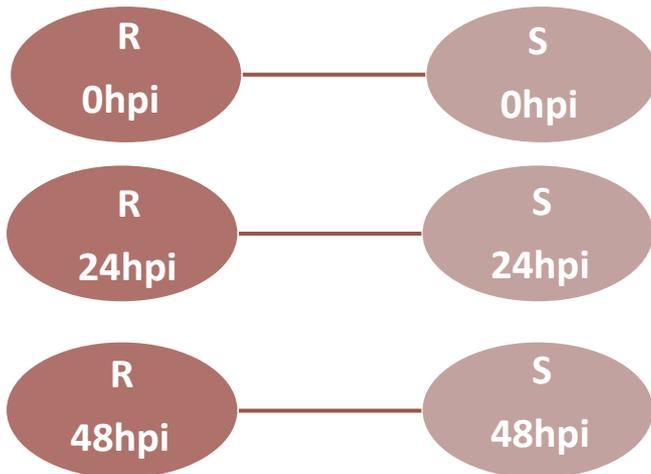
Comparaciones utilizadas para la detección de los genes expresados diferencialmente

5.740 GED → 2.850 GED

Genes diferencialmente expresados tras la inoculación con el hongo

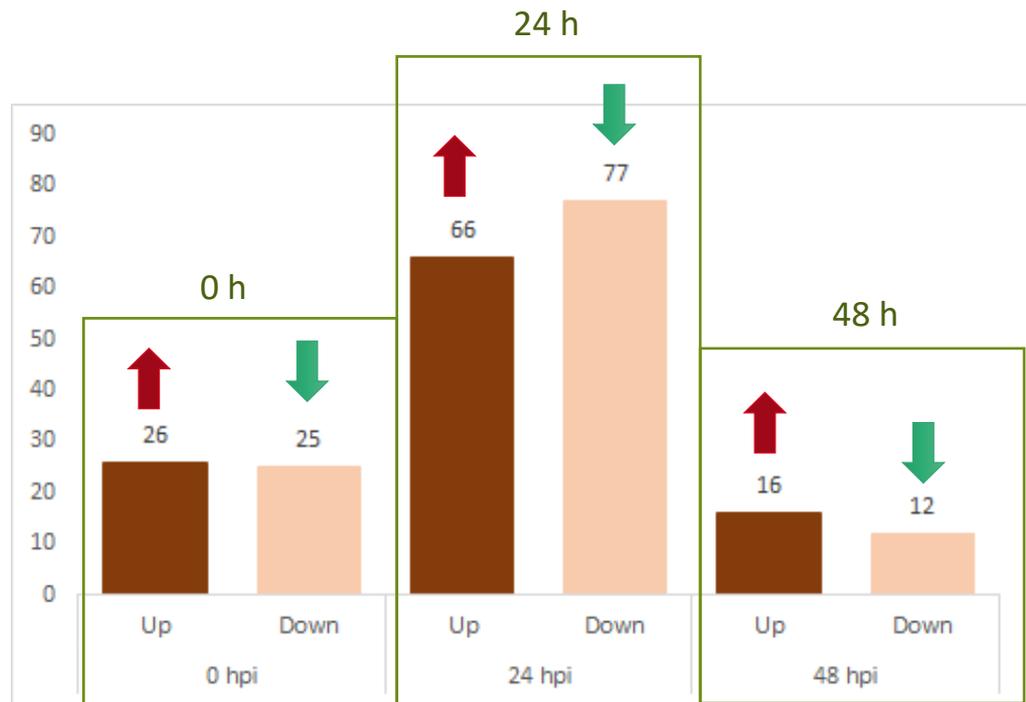
- Detectados principalmente en el genotipo susceptible.
- La mayoría decrecen su nivel de expresión.





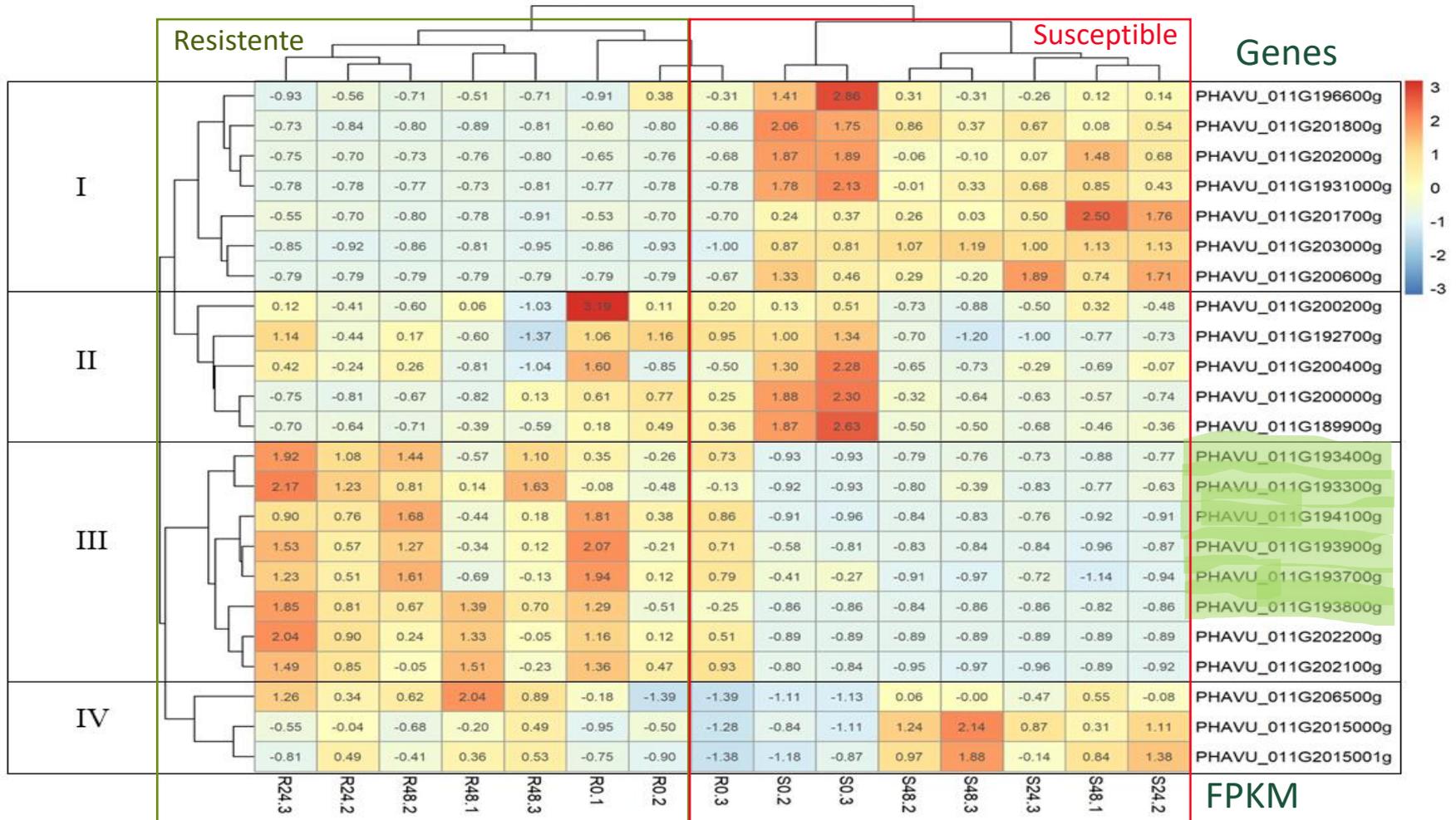
Genes diferencialmente expresados entre los genotipos a diferentes tiempos

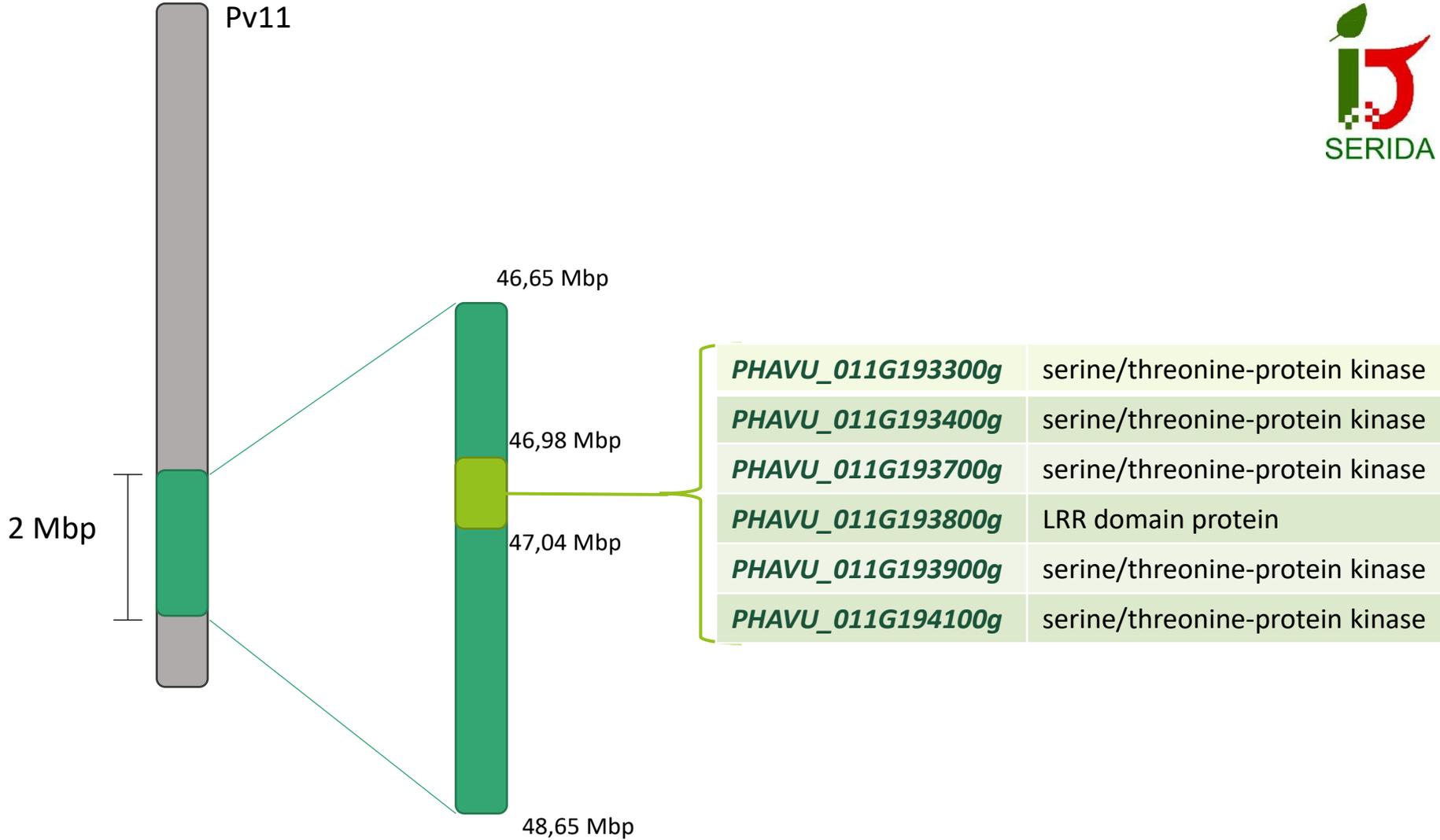
- Las mayores diferencias se encuentran a las 24 horas tras la inoculación.



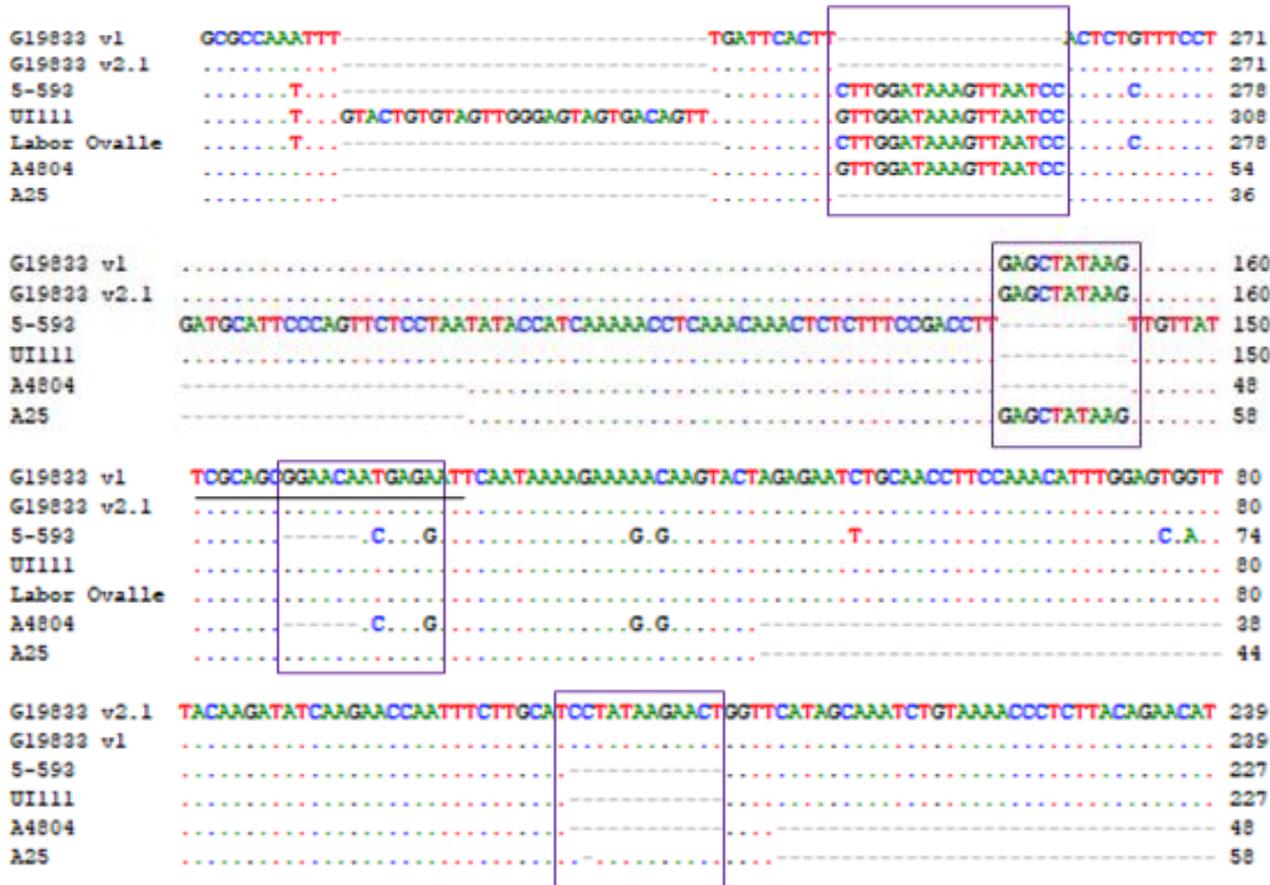
Región acotada Co-2: 46.65 – 48.65 Mbp Pv11

165 genes anotados -> 23 GED entre todas las comparaciones

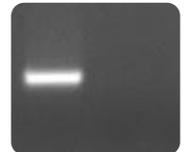
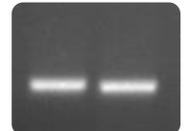




Polimorfismos encontrados entre el genotipo y susceptible y el resistente y otros genomas de judía para el desarrollo de marcadores moleculares



S R



- ❖ Combinar el posicionamiento físico de la región candidata y el estudio de los niveles de expresión de los genes permite una mayor aproximación a los genes responsables a controlar la resistencia.
- ❖ Este estudio permitió identificar 6 genes potencialmente candidatos a controlar la respuesta resistente frente a la raza 38 en el clúster Co-2 de judía común.
- ❖ Desarrollo de marcadores moleculares de fácil manejo para acelerar los programas de mejora.



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Differentially expressed genes against *Colletotrichum lindemuthianum* in a bean genotype carrying the Co-2 gene revealed by RNA-sequencing analysis

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Anthraxnose is responsible for large yield losses in common bean crops. RNA-sequencing was used to investigate the differentially expressed genes (DEGs) in response to race 38 of *Colletotrichum lindemuthianum* in two near-isogenic lines (A25 and A4804) that differ in the presence of a resistance gene located in the cluster Co-2. Their responses were analyzed at different hours after inoculation (0, 24, and 48) and within and between genotypes. In all, 2,850 DEGs were detected, with 2,373 assigned to at least one functional GO term. Enriched GO terms in the resistant genotype were mainly related to functions as a response to stimulus, hormone signaling, cellular component organization, phosphorylation activities, and transcriptional regulation. The region containing the Co-2 cluster was delimited at the end of chromosome Pv11 (46.65–48.65Mb) through a comparison with the SNP genotypes, obtained using ‘Genotyping by Sequencing,’ among seven resistant lines harboring the Co-2 gene and the susceptible line A25. The delimited region contained 23 DEGs, including 8 typical R genes, that showed higher expression levels in the resistant genotype and non-changes in the susceptible genotype after inoculation. Six R genes encoding protein kinases and an LRR domain formed a cluster in a core region between 46.98 and 47.04Mb. The alignment of the raw transcriptome reads in the core region revealed structural changes that were used to design four potential breeder-friendly DNA markers, and it revealed some alignments with the intergenic regions, suggesting the presence of genes in addition to those annotated in the reference genome.

KEYWORDS

resistance genes, candidate genes, gene ontology, InDel maker, anthracnose

[https://www.frontiersin.org/articles/10.3389/fpls.2022.981517/full?utm_source=Email_to_authors&utm_medium=Email&utm_content=T1_11.5e1_author&utm_campaign=Email_publication&field=&journalName=Frontiers in Plant Science&id=981517](https://www.frontiersin.org/articles/10.3389/fpls.2022.981517/full?utm_source=Email_to_authors&utm_medium=Email&utm_content=T1_11.5e1_author&utm_campaign=Email_publication&field=&journalName=Frontiers%20in%20Plant%20Science&id=981517)

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