

Decoding antioxidant dynamics and genetic mechanisms in early *Brassica napus* - *Verticillium longisporum* interactions



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INTRODUCTION

- Canola (*Brassica napus*) is a valuable crop with high global demand, particularly for human consumption and livestock production.
- As its cultivation expands, there has been a parallel rise in pathogen invasions, threatening yields. Verticillium stripe disease (VSD) is one of the major diseases caused by a soil-borne fungal pathogen *Verticillium longisporum* (VL), which significantly reduces canola productivity¹.
- Current disease management strategies, including fungicidal treatments, crop rotation, and cultural practices, are often costly and inconsistently effective, failing to provide reliable control².
- The lack of resistant cultivars against VL further intensifies the challenge of disease management, underscoring the urgent need for more effective and sustainable solutions.

OBJECTIVES

- Identify differentially expressed genes in response against *V. longisporum* infection by comparative transcriptome analysis.
- Study the variations of the antioxidant enzyme activity and gene expression related to the plant signaling hormones.

MATERIALS AND METHOD

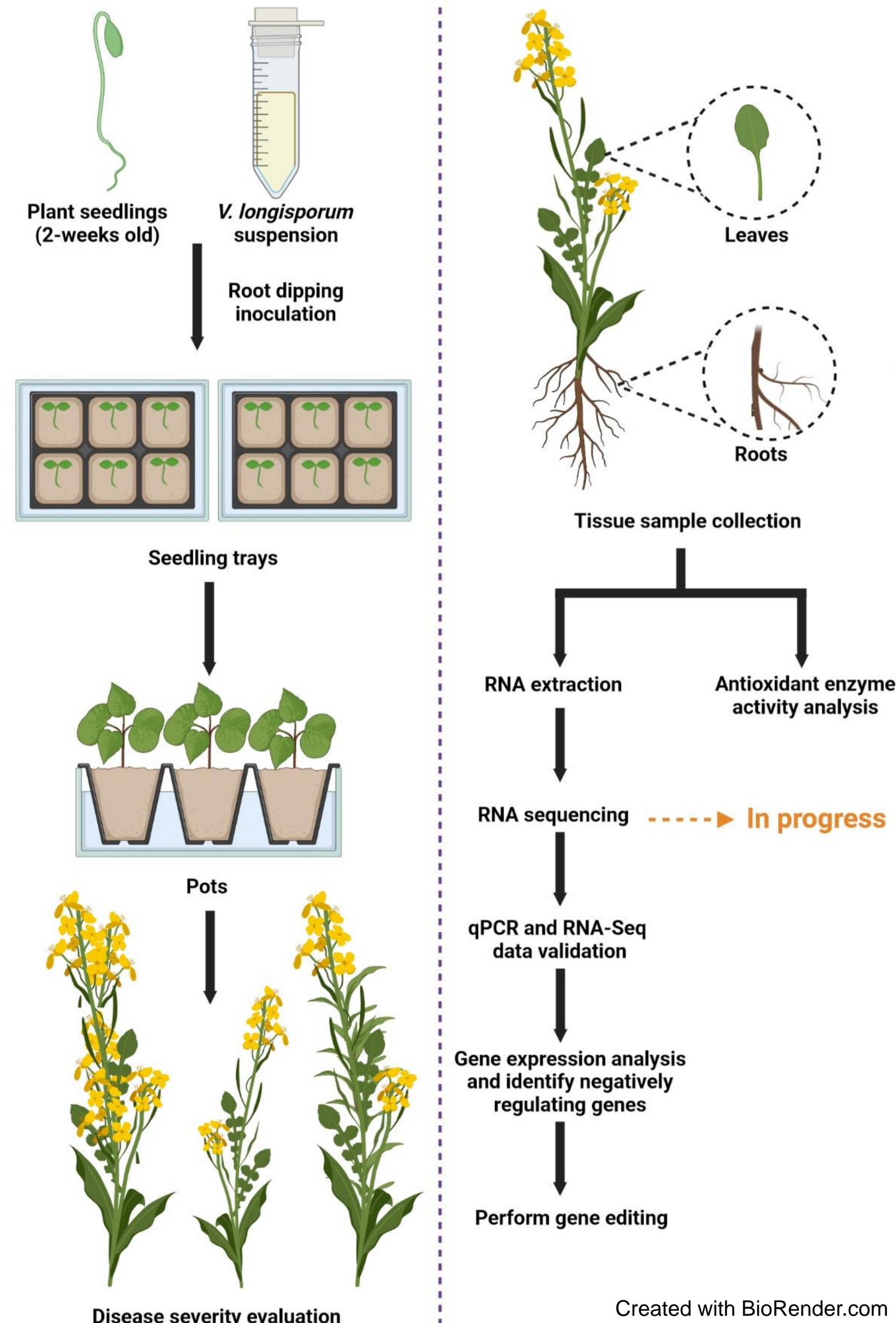


Figure 1: Workflow of the project.

- VL isolate A1D1 was used to prepare the conidial suspension and then for inoculation. The roots of 2-week-old seedlings of Quinta and Westar were wounded and dipped in the conidial suspensions (1×10^7 spores mL^{-1}) for 45 min prior to transferring them to the seedling trays³.
- Disease severity was assessed at 7 and 105 dpi (days post-inoculation) stages using 0 to 6 and 0 to 4 disease rating scales respectively⁴.
- The variation of the antioxidant enzyme activity was assessed.
- The disease progression inside the plant will be determined by the fungal DNA extraction from the roots, hypocotyl, cotyledons and first true leaves (at 7 and 14 dpi).
- The differentially expressed genes responsible for plant signaling hormones activity will be identified using RNA-Seq.

RESULTS AND CONCLUSION

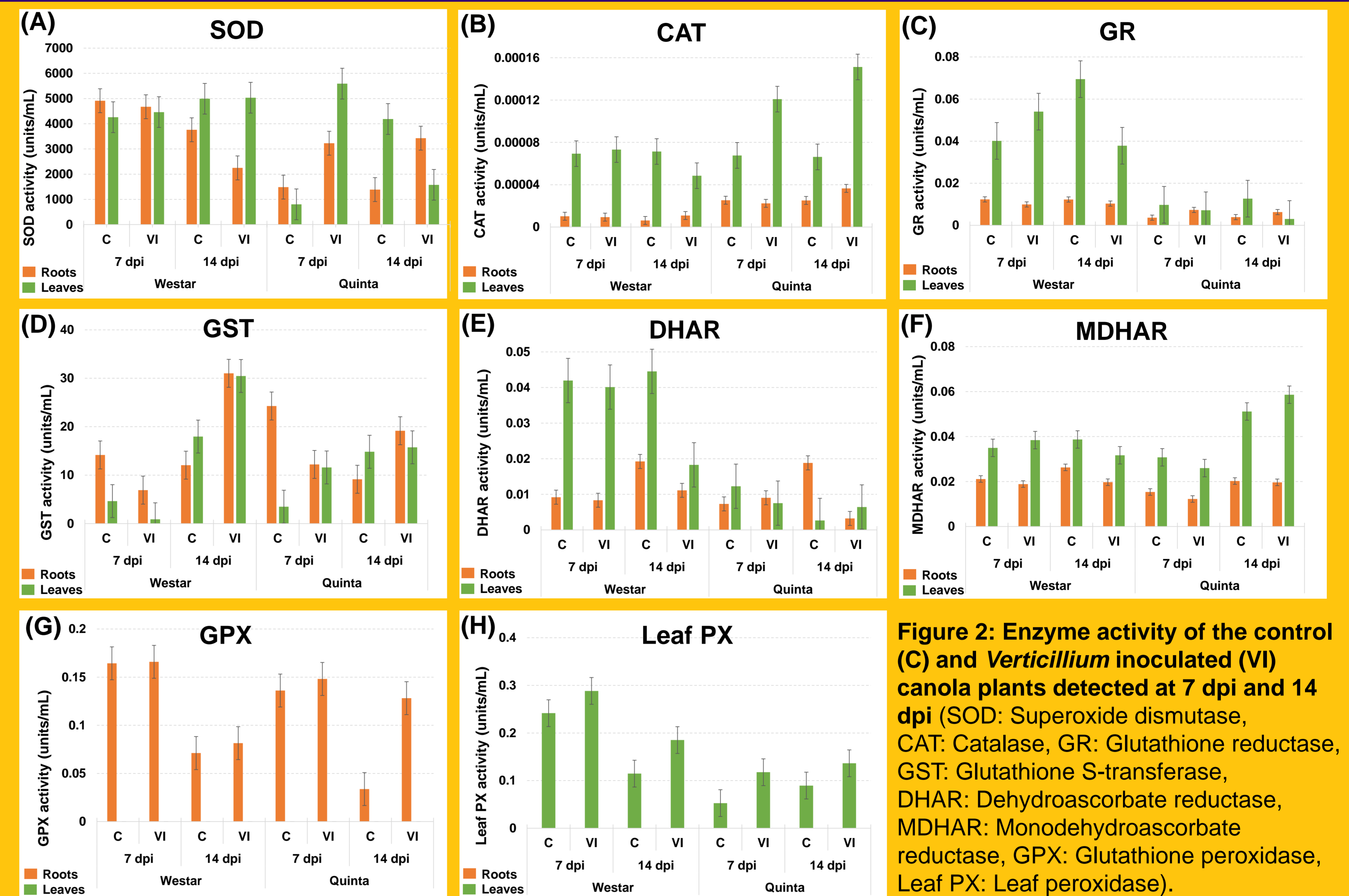


Figure 2: Enzyme activity of the control (C) and *Verticillium* inoculated (VI) canola plants detected at 7 dpi and 14 dpi (SOD: Superoxide dismutase, CAT: Catalase, GR: Glutathione reductase, GST: Glutathione S-transferase, DHAR: Dehydroascorbate reductase, MDHAR: Monodehydroascorbate reductase, GPX: Glutathione peroxidase, Leaf PX: Leaf peroxidase).

- The activities of SOD and CAT were predominantly detected in leaves compared to roots, regardless of the treatment (Figure 2).
- Inoculated Quinta plants showed relatively high SOD activity at the early stage (7 dpi), which then decreased significantly at 14 dpi in the leaves.
- In Westar, the activities of GR and DHAR were relatively high, suggesting that these enzymes are produced in greater quantities during a pathogenic attack, especially in leaves.
- GPX activity was not detected in leaves and its activity in roots decreased at 14 dpi compared to 7 dpi in both varieties.
- Leaf peroxidase activity was notably higher in Westar, indicating that more ROS were produced in Westar compared to Quinta.
- In the disease severity evaluation, at the young seedling stage, most VI Westar plants displayed partial necrosis of cotyledons, whereas nearly all Quinta plants showed complete cotyledon death. This confirms the effectiveness of the root-dipping inoculation method for canola plants (Figures 1, 3 & 4).
- Disease severity data at the adult stage of Quinta will be collected at 105 dpi and will be used to determine the most resistant variety between the two.

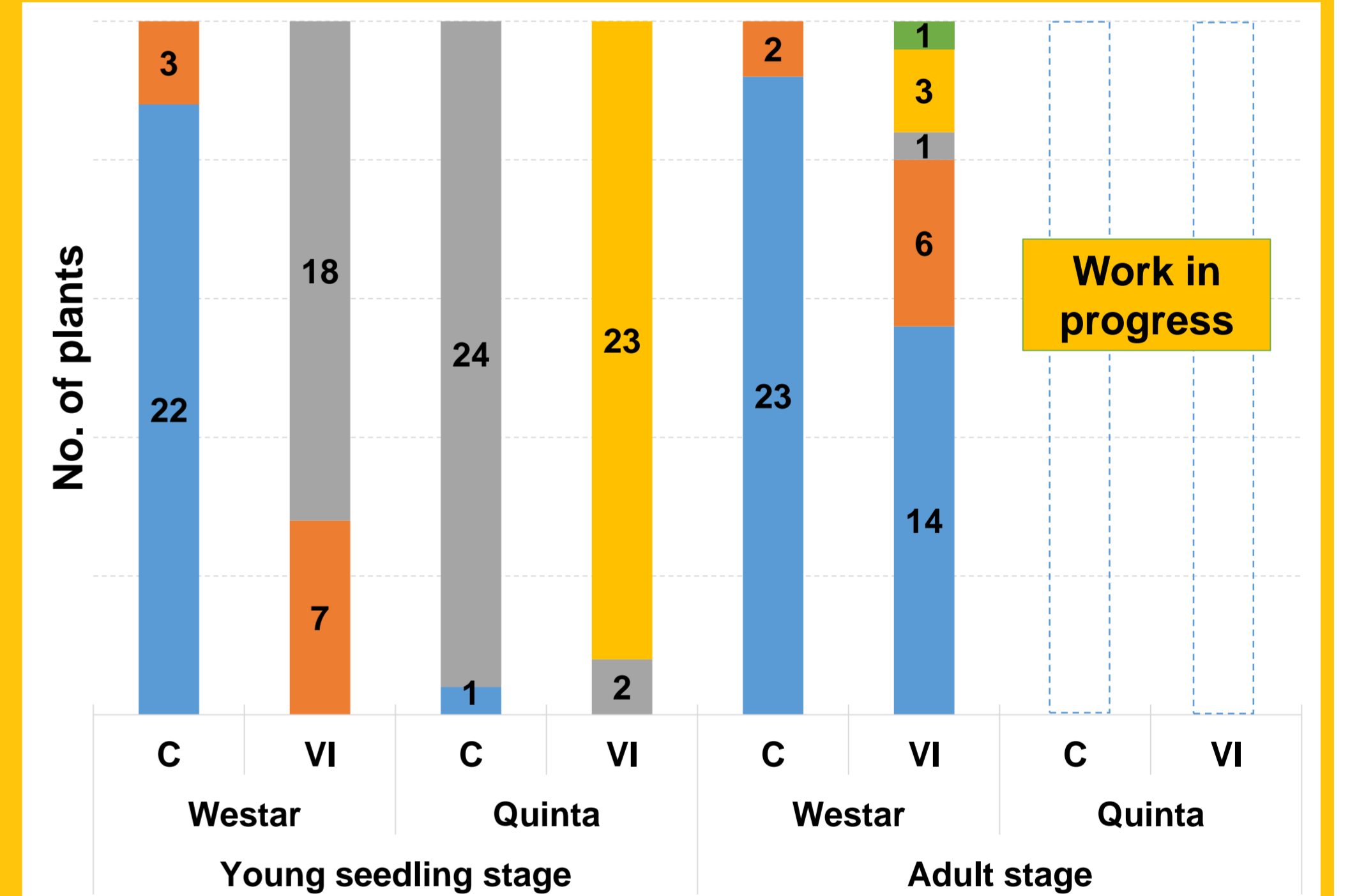


Figure 3: Disease severity evaluation of young and adult canola plants (25 plants were subjected to the evaluation).

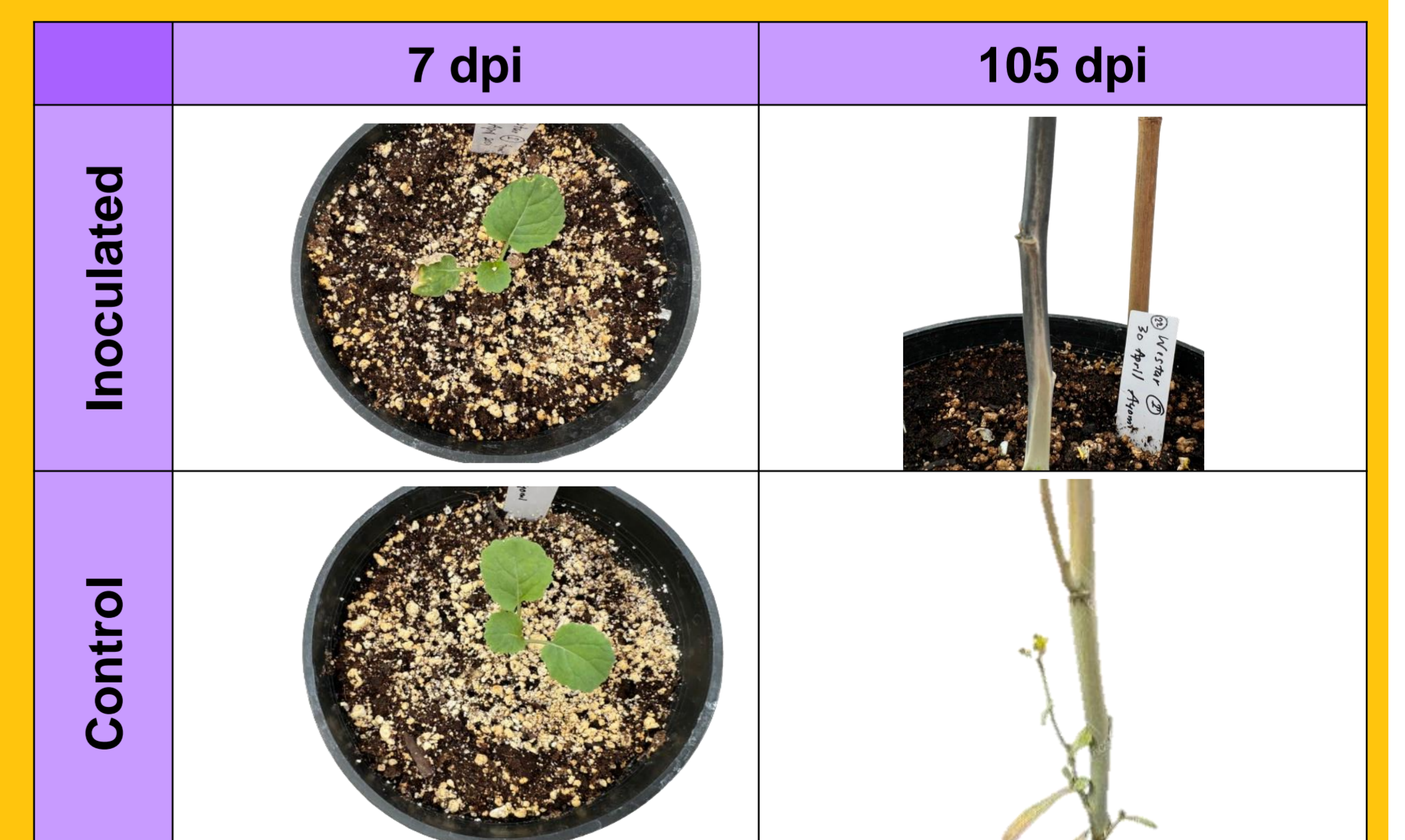


Figure 4: Phenotypic differences of inoculated and control Westar plants at young and adult stages (7 dpi and 105 dpi).

- Overall, the results suggest that certain enzymes are more active in Westar, while others show higher activity in Quinta. These variations may be due to differences in gene regulation mechanisms and the complex interactions between the host plant and the pathogen.

REFERENCES

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