## NDSU NORTH DAKOTA STATE UNIVERSITY

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#### Advancing Sunflower Breeding for Resistance to Sclerotinia sclerotiorum and Diaporthe/Phomopsis

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Presented by Dr. Denis Colombo

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#### Our work

 Genome-Wide Association Studies in Sunflower: Towards Sclerotinia sclerotiorum and Diaporthe/Phomopsis Resistance Breeding

•Main Objective: Investigate the genetic basis of resistance to two major necrotrophic fungi in sunflower.

This work contributes to breeding programs by identifying and characterizing sources of disease resistance for SC and DP, as well as genetic markers and candidate genes associated with resistance

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### Introduction

- Sunflower is one of the most important oilseed crops globally.
- Top Producers: Russia (31%), Ukraine(28%), European Union (18%) and Argentina (7%) are the leading producers of sunflowers. United States (2%) (USDA 2024).



Source: U.S. Department of Agriculture, National Agricultural Statistics Service



#### Introduction

- Diseases are, and have historically been, the major limiting factors for sunflower production.
- Resistance breeding is essential due to limited chemical control effectiveness and lack of full genetic resistance.
- Diseases caused by Sclerotinia sclerotiorum and the Diaporthe/Phomopsis complex severely impact sunflower production.

•Goal: Perform a genome-wide association study (GWAS) to identify resistance markers and candidate genes in the association mapping population (AMP) of INTA.

#### **Methodology: Phenotyping**

# Plant Material: 135 inbred sunflower lines from AMP of INTA

Sclerotinia sclerotiorum:

• Field Trials: Conducted in a randomized complete block design (RCBD) at the INTA Balcarce Experimental Station in 2011, 2013, and 2014.

 Inoculation: Plants were inoculated with the pathogen at the R5 growth stage (De Labrouhe and Vear 1984).

• Evaluations: Performed at different days postinoculation to assess disease incidence (DI), disease severity (DS), and other parameters.



#### **Sclerotinia Head Rot**





S. sclerotiorum is a cosmopolitan pathogen, capable of infecting a wide range of species

It can attack sunflower in several ways, depending on the site and mechanism of infection.

The DS was visually quantified, by applying a diagrammatic scale developed for SHR by the Plant Pathology group of INTA Balcarce (ratio scale 0 to 100%, with 10% intervals).



Filippi, C.V., Zubrzycki, J.E., Di Rienzo, J.A., Quiroz, F., Fusari, C.M., Alvarez, D., Maringolo, C.A., Cordes, D., Escande, A., Hopp, H.E. and Heinz, R.A., 2017. Phenotyping sunflower genetic resources for sclerotinia head rot response: assessing variability for disease resistance breeding. *Plant disease*, *101*(11), pp.1941-1948.

## **Methodology: Phenotyping**

#### Diaporthe/Phomopsis:

- Field Trials: Conducted in a randomized complete block design (RCBD) in 2017 and 2018 in General Pico.
- Field Conditions: Naturally infested fields with additional inoculum from infected crop residue.
- Evaluations: Conducted at the R7 and R8 stages to assess DI and DS for Phomopsis stem canker (PSC) and Phomopsis head rot (PHR).



#### **Phomopsis Stem Canker**



The Diaporthe/Phomopsis complex comprises multiple species involved in disease development in sunflower, with Diaporthe helianthi being the most widespread and the first to be reported (Muntañola-Cvetković et al. 1981)

Pictures at the R7-R8 sunflower stage.

PSC was scored using a scale:

- 0, asymptomatic;
- 1, length smaller than 10 cm;
- 2, length greater than 10 cm;
- 3, girdling on the stem;
- 4, wilted or broken stems

#### **Phomopsis Head Rot**



Colombo, D. N., Figueruelo, A., Paniego, N. B., Comerio, R. M., & Corró Molas, A. (2024). Phomopsis Head Rot caused by Diaporthe helianthi: A New Disease on Sunflower in Argentina. *Journal of Phytopathology*, *172*(5), e13416. <u>https://doi.org/10.1111/jph.13416</u>



### **Methodology: Genotyping**

- ddRADseq sequencing data for the AMP were analyzed to assign SNP genomic coordinates to the latest version of the sunflower genome (Han\_XRQ V2.0).
- Genotypic data comprised a panel of 4269 single nucleotide polymorphisms (SNP).
- The association between SNPs and phenotypes was evaluated using statgenGWAS v1.0.9.
- A univariate GWAS for each phenotypic trait was conducted.



#### **Results: Marker-Trait Associations**

## •Sclerotinia Head Rot (SHR):

- Identified 24 unique marker-trait associations.
- Chromosomes CR01, CHR05 and CHR10 had the highest number of associated markers.



(disease incidence, DI; disease severity, DS; area under the disease progress curve for DI, AUDPCI, and DS, AUDPCS; and incubation period, IP).

#### **Results: Marker-Trait Associations**

### •Diaporthe/Phomopsis Diseases:

- 19 unique marker-trait associations.
- Different markers were found for PSC and PHR. No common markers were found between *S. sclerotiorum* and *Diaporthe/Phomopsis* responses, suggesting different resistance mechanisms.





#### **Candidate Genes**

#### Gene Discovery:

 The exploration of regions physically close to the associated markers resulted in 364 genes, of which 19 were predicted as putative disease resistance genes, most of which are receptor-like kinases (RLK).



#### **Conclusion and Future Directions**

Summary:

This study provides key insights into the genetic basis of resistance to *S. sclerotiorum* and *Diaporthe/Phomopsis* in sunflower.

Identified inbred lines, markers and candidate genes can be used in breeding programs to develop resistant sunflower varieties.

Future Work:

Develop efficient inoculation methods.

Expand the study to understand pathogen variability and improve field trial consistency.



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