Advancements in Sunflower Multiparental Population Phenotyping for Verticillium Wilt Using UAV-based Multispectral Imagery

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INTRODUCTION

Here we present progress in phenotyping a sunflower Multiparent Advanced Generation Inter-Crosses (MAGIC) population for Verticillium wilt (VW), one of the most important sunflower diseases in Argentina. In addition, the implementation of high-throughput phenotyping (HTP) using unmanned aerial vehicles (UAV) is being explored to complement manual phenotyping and integrated it into breeding pipelines.

MATERIALS AND METHODS

A subset of 349 F2-MAGIC families was studied during the 2020/21 summer season in a VW-infested field in the EEA INTA Balcarce (37°50' 0" S, 58°15' 33" W, Argentina) (Figure 1). Eighty F5-MAGIC contrast families for VW were selected from the 2020/21 phenotyping trial and phenotyped in another VW infested field in the EEA INTA Anguil (36° 32'17" S, 63° 59' 20" W) in the 2023/24 summer season (Figure 2).

Table 1. Vegetation indices implemented in each flight.

Vegetation Index	Season
Normalized Difference Vegetation Index (NDVI)	2020/21 - 2023/24
Normalized Water Vegetation Index (NWVI)	2020/21
Optimized Soil-Adjusted Vegetation Index (OSAVI)	2020/21
Leaf Chlorophyll Index (LCI)	2020/21
Green Normalized Difference Vegetation Index (GNDVI)	2023/24
Enhanced Vegetation Index (EVI)	2023/24
Normalized difference red edge index (NDRE)	2023/24
Green Red Vegetation Index (GRVI)	2023/24
Green Leaf Index (GLI)	2023/24
Plant Senescence Reflectance Index (PSRI)	2023/24
Differenced Vegetation Index (DVI)	2023/24
Visible Atmospherically Resistant Index (VARI)	2023/24
Chlorophyll Index Red Edge (CIRE)	2023/24

Figure 1. Aerial view of 2020/21 VW field.

Figure 2. 2023/24 plots.

VW incidence, severity and disease severity index (DSI) were recorded for each plot (one row of 5 m length). In the 2020/21 season, the trial was flown once during the flowering period (R5) using a Parrot Disco-Pro Ag drone (4 bands) with a flight altitude of 50 m. In the 2023/24 season, we used a Phantom 4 drone (5 bands), the flight altitude was 40 m and the trial was flown four times during the flowering and grain filling period from R1 to R9. The Table 1 indicates the vegetation indices (VIs) used.
Using the information from the spectral bands and the VIs, different machine learning models (MLM) were applied to classified each plot as susceptible or resistant to VW using the CARET library in R.

RESULTS AND DISCUSSION

The results confirmed the phenotypic variability of the MAGIC population for VW. Thirty three resistant MAGIC F5 families exhibiting a DSI below 5 % were identified as valuable candidates for future breeding purposes (Figure 3).

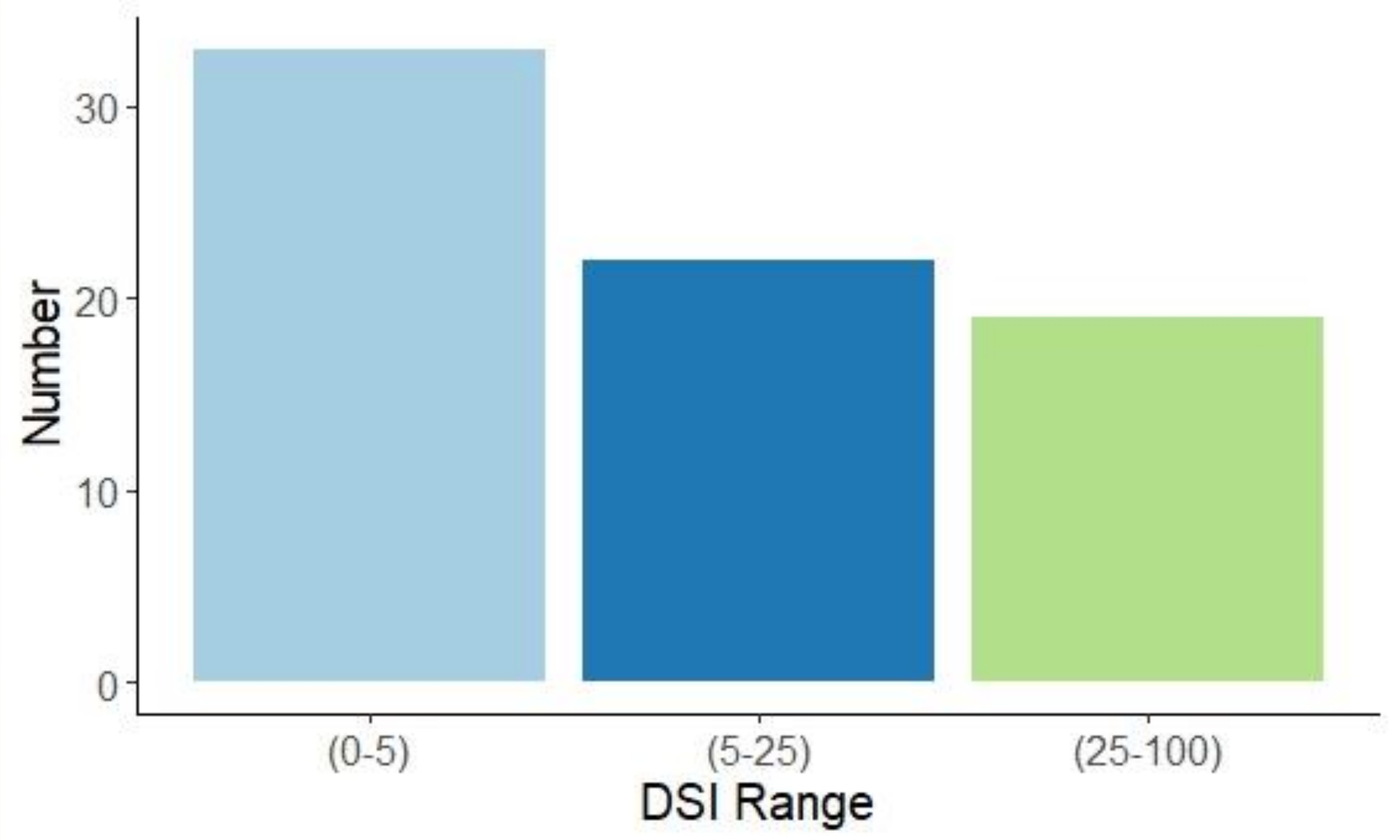

Figure 3. DSI range of the MAGIC F5 families evaluated in Anguil 2023/24

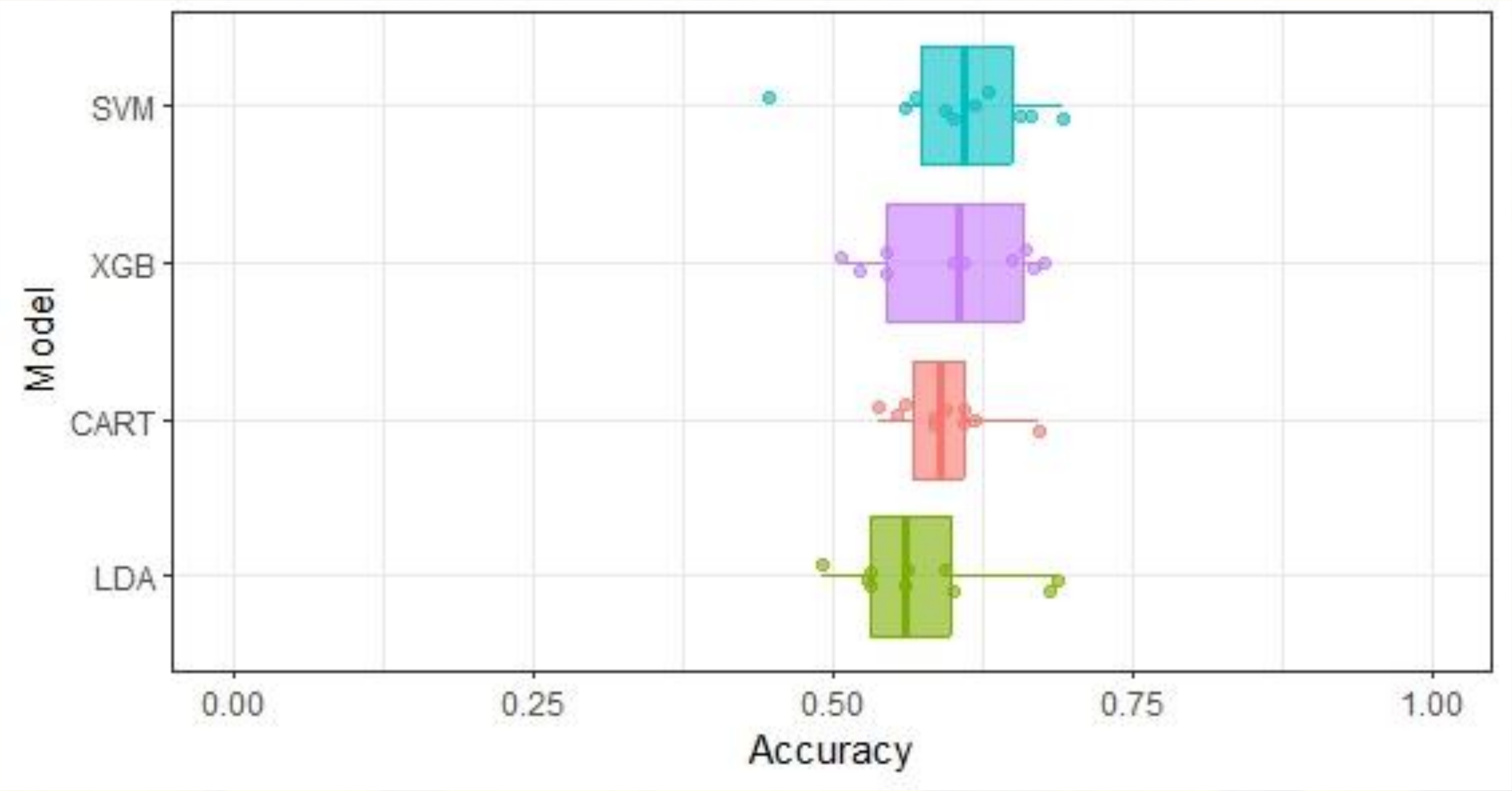

Figure 4. Accuracy of the prediction models in the 2020/21 trial.

The MLM achieved a prediction accuracy of about 65 % in both trials, with the SVM and XGBoost models showing the better prediction performance in the trials 2020/21 and 2023/24 (Figure 4 and Figure 5).

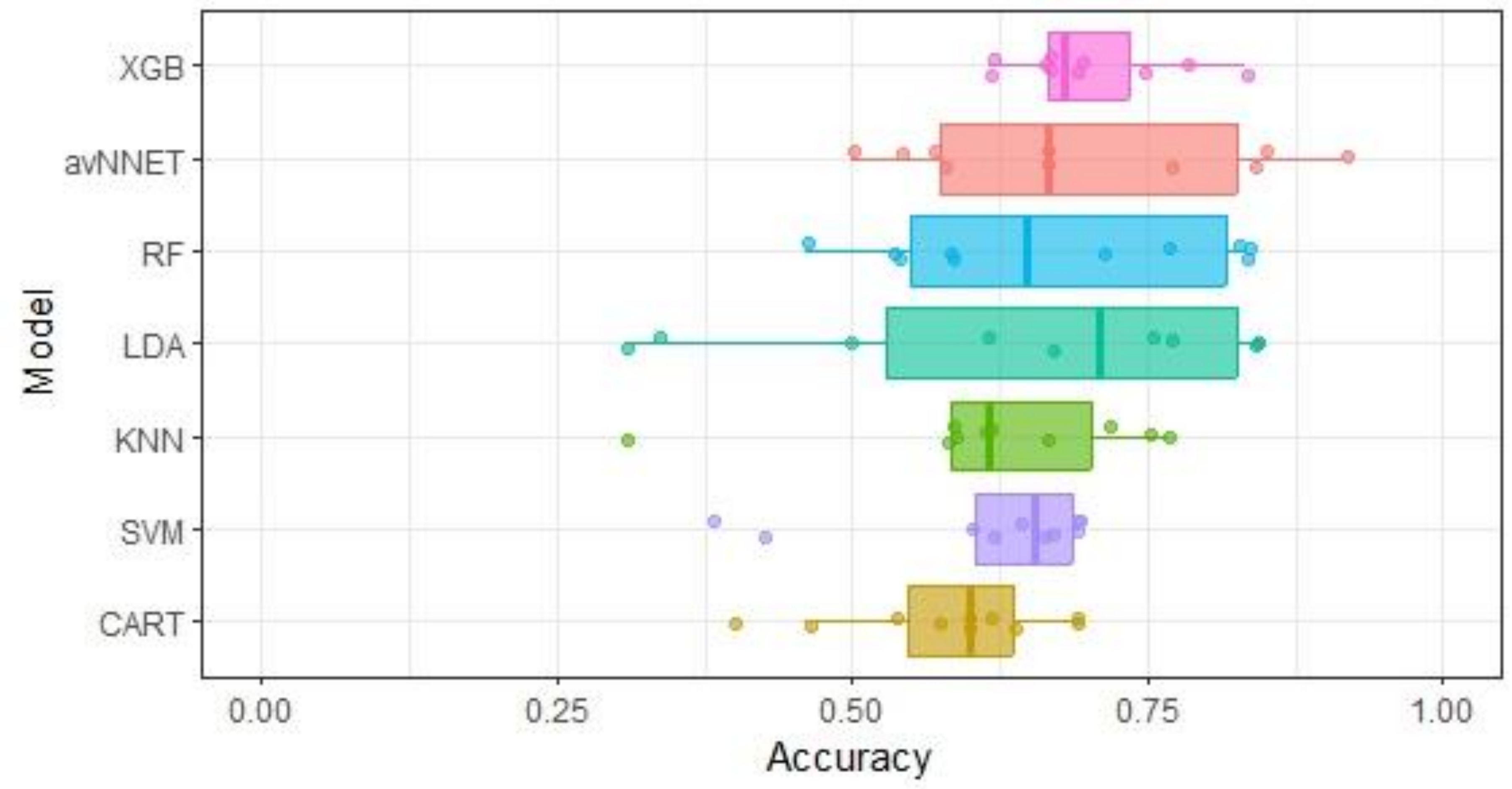

Figure 5. Accuracy of the prediction models in the 2023/24 trial.

These results highlight the potential of HTP for sunflower disease phenotyping and its applicability in the sunflower breeding programs. Furthermore, we identified more than 30 MAGIC lines with resistance against VW to incorporate in the breeding program.

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