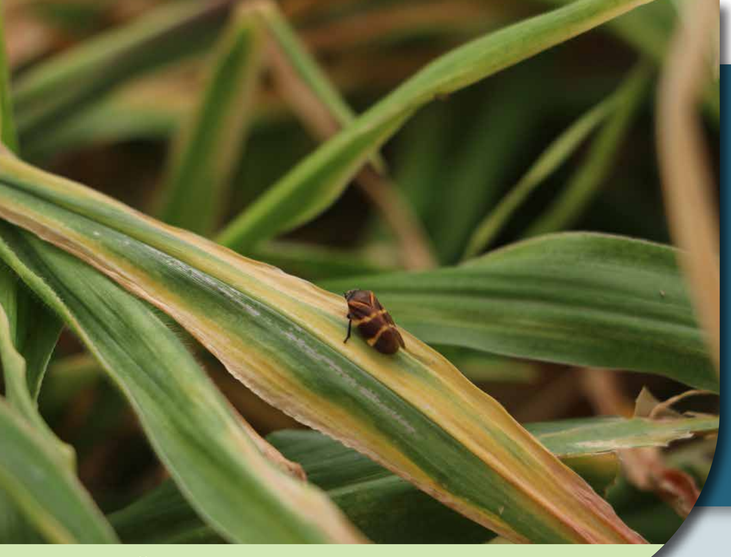

Paula Espitia/CIAT

Integrating spatial analysis and machine learning approaches into the protocol for assessing spittlebug (Hemiptera: Cercopidae) resistance in *Urochloa* sp.

Luis Miguel Hernández; Paula Espitia-Buitrago; Juan Cardoso; **Rosa Jauregui.**
International Center for Tropical Agriculture, Tropical Forages Program, Colombia.

Contact: r.jauregui@cgiar.orgz

Introduction

- Resistance of *Urochloa* hybrids to spittlebug infestations is a key trait in the interspecific *Urochloa* breeding program of the Alliance Bioversity-CIAT in Latin America (Miles et al., 2006).
- The current phenotyping methodology has enabled the program to achieve high genetic gains per year for spittlebug resistance in *Urochloa* hybrids, reaching 2.3% for plant damage and 7.4% for insect survival (Hernández et al., unpublished; Parsa et al., 2011).
- High-throughput phenotyping and robust data analysis techniques optimize the *Urochloa* breeding scheme by increasing spittlebug tolerance in the assessed population and enhancing genetic gain (Sweitzer et al., 2021) .

Objective

Integrate spatial statistical modelling and machine learning (ML) approaches into the protocol for assessing spittlebug resistance in interspecific *Urochloa* sp.

Methodology

A synthetic hybrid population "BR19" product of the 11th cycle of recurrent selection of the interspecific *Urochloa* breeding program, was evaluated for spittlebug resistance (Parsa et al., 2011). The experimental design utilized was a complete randomized block design with five infested replicates, considering the row-column position of each experimental unit. Plant damage (%) was quantified using digital images acquired in a controlled environment (photobox) 35 days after infestation (DAI), using an unsupervised ML model with a K-means algorithm (Hernández et al., 2022).

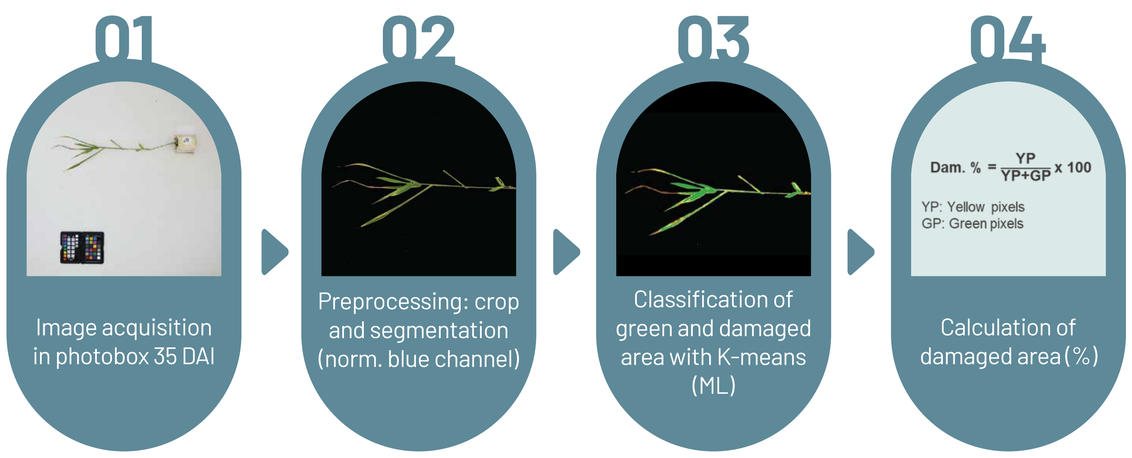

Figure 1. Pipeline for digital images processing and yellow pixels quantification

The data was analyzed using MrBean, an R-shiny web app for experimental plant breeding analysis, based on linear mixed models and spatial modelling (Aparicio, 2022). The genotype was treated as a random factor, to estimate the BLUPs (best linear unbiased predictions).

Results

The spatial analysis showed that there was variation in the experiment, that was modeled and considered in the BLUPs estimation in MrBean. The heritability for plant damage was 0.66, indicating high accuracy in the phenotyping of the response variable (Fig. 2).

The susceptible check (CIAT 606) showed the maximum value for plant damage, 48.7%, with most of the population expressing higher levels of tolerance ($\bar{X}$= 27.68%) (Figure 3). These results suggest that the genetic effects for resistance have accumulated over the recurrent selection cycles in the breeding program.

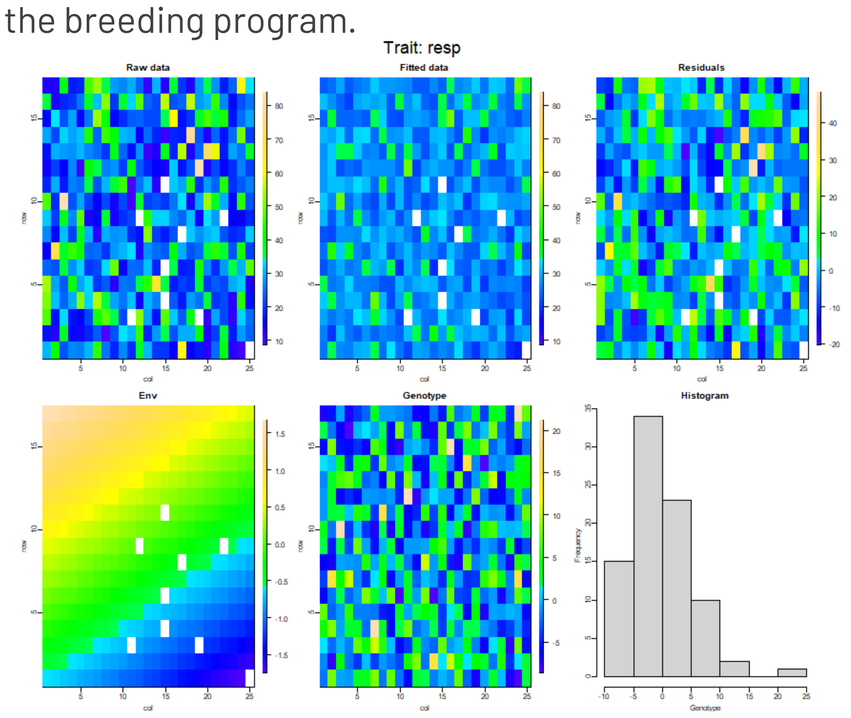

Figure 2. Space modeling of the experiment for the variable response plant damage (%) (MrBean)

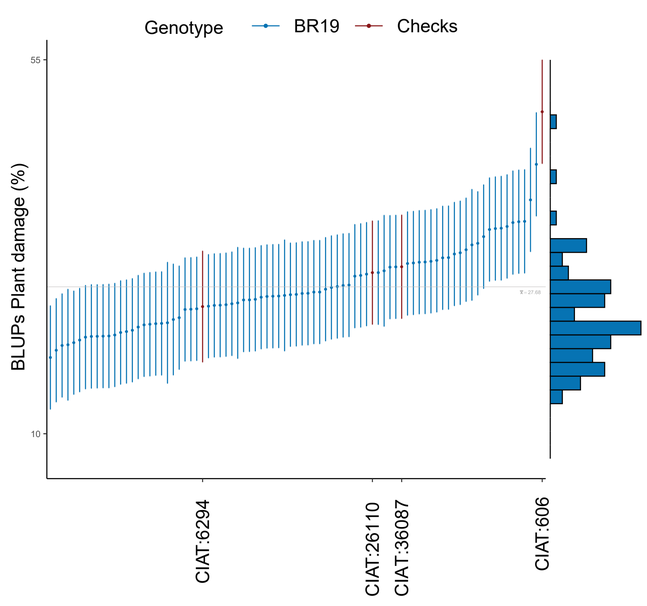

Figure 3. BLUPs of plant damage of the population

Paula Espitia/CIAT

Conclusions

The methodology using an unsupervised model of ML allowed the classification of genotypes according to the level of damage expressed, allowing to select for tolerant genotypes. The spatial statistical techniques enhanced the heritability of the trials.

References

Aparicio, J. (2022). MrBean: Web application for analyzing field experiments. R package version 2.0.9.

Hernández, L., Espitia, P., & Cardoso, J. A. (2022). Digital imaging outperforms traditional scoring methods for spittlebug tolerance in *Urochloa humidicola* hybrids. Tropical Grasslands-Forrajes Tropicales, 10(3), 271–279. https://doi.org/10.17138/TGFT(10)271-279

Miles, J. W., Cardona, C., & Sotelo, G. (2006). Recurrent selection in a synthetic brachiariagrass population improves resistance to three spittlebug species. Crop Science, 46(3), 1088–1093. https://doi.org/10.2135/cropsci2005.06-0101

Parsa, S., Sotelo, G., & Cardona, C. (2011). Characterizing herbivore resistance mechanisms: Spittlebugs on *Brachiaria* spp. as an example. Journal of Visualized Experiments, 52. https://doi.org/10.3791/3047

Sweitzer, E.; Hernandez, L.; Florian, D.; Notenbaert, A.; Burkart, S.; Arango, J.; Cardoso, J.; Peters, M.; Castiblanco, V. (2021) Review of *Urochloa* breeder's toolbox with the theory of change and stage gate system approach. Poster presented at the Joint XXIV International Grassland Congress and XI Rangeland 2021 Congress, Nairobi, Kenya, 25-29 October 2021. Cali (Colombia): Alliance of Bioversity and CIAT. https://uknowledge.uky.edu/igc/24/2-3/3/

Acknowledgments
This work was done as part of the CGIAR Accelerated Breeding Initiative (ABI), and is supported by The Papalotla Group. We thank all donors that globally support our research through their contributions to the CGIAR system.

Alliance Bioversity & CIAT
CGIAR INITIATIVE ON Accelerated Breeding
PAPALOTLA SEMILLAS
APBA African Plant Breeders Association

Poster prepared for:
APBA 2023
October 23-26, 2023
Benguerir (Morocco)