

Spot blotch QTLs in barley germplasm from Latin America

Lucía Gutiérrez¹, Natalia Berberían¹, Flavio Capettini², Darío Fros³, Silvia Germán⁴, Silvia Pereyra⁴, Carlos Pérez³, Sergio Sandoval-Islas⁵, Ariel Castro^{6*}

¹Departamento de Estadística, Facultad de Agronomía, Universidad de la República, Garzón 780, Montevideo 12900, Uruguay; ²ICARDA, Syria; ³Departamento de Protección Vegetal, Facultad de Agronomía, Uruguay; ⁴INIA La Estanzuela, Colonia, Uruguay; ⁵COLPOS, Chapingo, México; ⁶Departamento de Producción Vegetal, Est. Exp. "Dr. Mario A. Cassinoni", Facultad de Agronomía, Universidad de la República, Ruta 3 Km 363, Paysandú, 60000, Uruguay (vontruch@fagro.edu.uy)

MAIN GOAL

To identify and map new resistance QTLs to spot blotch (SB) in a barley germplasm collection including genotypes developed by ICARDA and breeding programs from Latin America

MATERIALS AND METHODS

Plant Material: 343 genotypes including materials developed by ICARDA and breeding programs from different countries in South America.

Genotyping: 1536 SNPs using an Illumina oligonucleotide pool assay developed by the Barley CAP (BOPA1).

Phenotyping: Spot blotch severity at seedling and adult plant stages at INIA La Estanzuela- Colonia (EELE) and Paysandú (EEMAC) in Uruguay. Seedlings were inoculated and assessed according to Fetch and Steffenson (1999). For adult plant characterization, genotypes were planted in the field, either in two-row plots of 1-m long or hill-plots at La Estanzuela. Plants were evaluated in winter/spring and summer nurseries in the period 2009-2010. Plots were inoculated at GS45-49, once or twice with the same isolates used for seedling tests. A concentration of 8×10^3 conidia/ml at a rate of 50 ml/m² was used. SB severity was measured based on visual assessment of the percentage of diseased area (severity) on a plot basis at GS71-79.

Analysis: Genome-wide association analysis using a mixed model:

$$Y = X\beta + Qv + Ku + e$$

X: Matrix with molecular marker scores

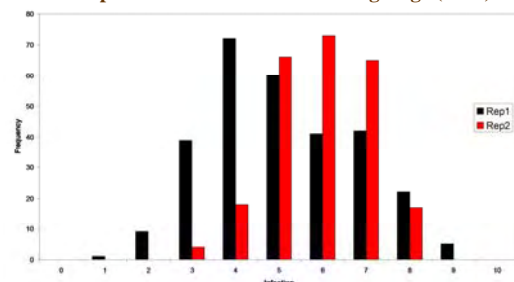
Q: PCA matrix

K: Kinship matrix

Analysis was performed on R (version 2.10.1)

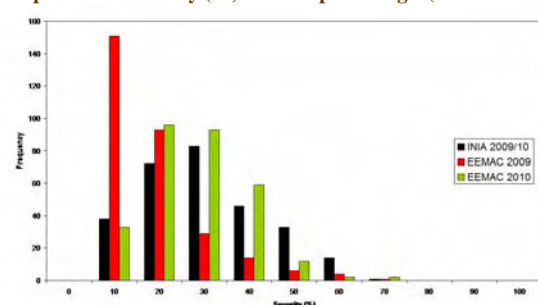
RESULTS

Spot blotch infection at seedling stage (2009)



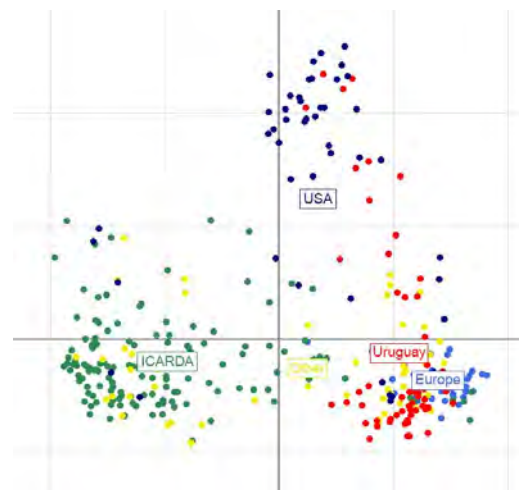
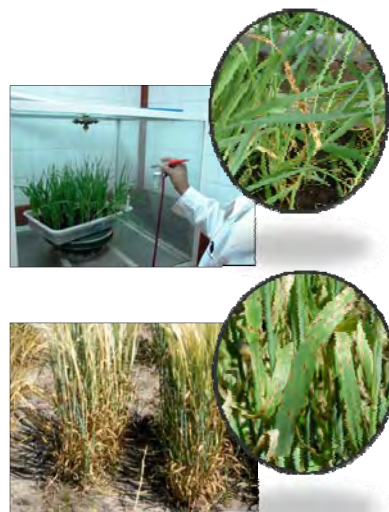
No significant associations were detected for SB resistance at the seedling stage

Spot blotch severity (%) at adult plant stage (2009 – 2010)



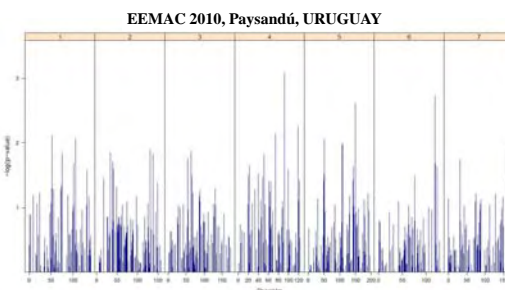
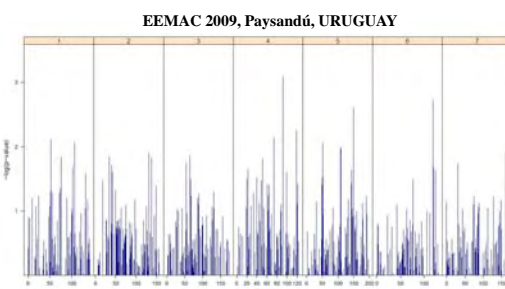
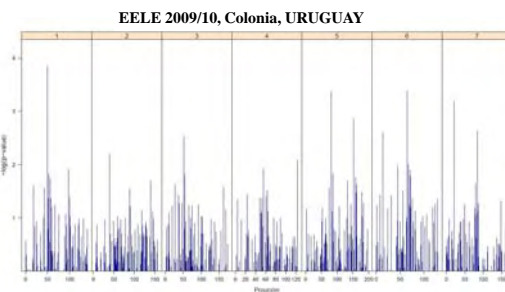
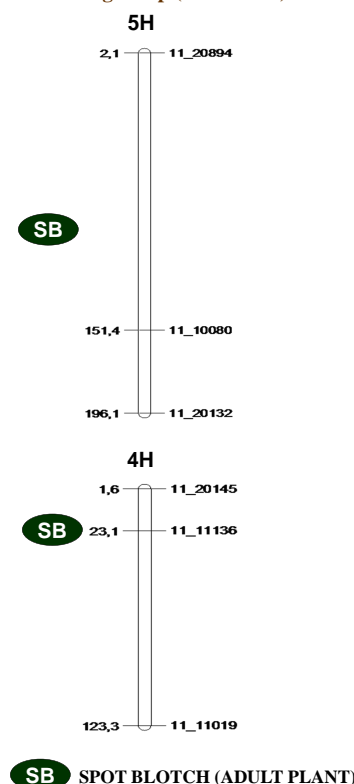
REFERENCES

Fetch T. G. JR, Steffenson B. J. 1999. Rating scales for assessing infection responses of barley infected with *Cochliobolus sativus*. Plant Dis. 83:213-217.



PCA analysis of the marker data (PC1 and PC2 represented) with genotypes identified according to their origin.

Linkage Map (5H and 4H)



Association Mapping – Mixed Model (fixed PCA matrix, random Kinship matrix). Possible resistance QTLs (threshold 4.32)

CONCLUSIONS

- Preliminary results show marker-trait associations for SB severity in the adult plant stage in several chromosomes (see figures)
- Most detected associations were environment- or model-dependant
- Higher infection levels of SB at the field nurseries would aid in confirming results.
- Better models are being developed to further study these associations.