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Development of bread wheat genotypes for multiple resistance to foliar diseases

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Introduction

Global food security and sustainable wheat production are both constantly threatened by increased human population. Yellow rust (*Puccinia striiformis* f. sp. tritici) stem rust (*P.graminis* f. sp. tritici) and Septoria tritici blotch , ((*Zymoseptoria tritici*) are the major challenges for sustainable wheat production in different countries around the world. The three wheat rusts are the most damaging diseases in world and continue threatening global food security (Bhavani *et al*. 2022). Genetic resistance is the key objective of the bread breeding program. Many varieties are released in many countries and losses of resistance mainly for new races of pathogens causing SR and YR is a key challenge (Fedak *et al*. 2021). The breeding program is developing elite germplasm combining resistance to two or more diseases. Therefore, the objective of this work was to develop multiple resistance to key foliar diseases targeting different agro-ecologies.

Materials and methods

Two hundred-thirty-three elite genotypes from ICARDA bread wheat breeding program was evaluated for their resistance to Yellow rust (YR), stem rust (SR) and *Septoria tritici* blotch (STB) under controlled conditions. The genotypes were sown in two replications. Seedlings were exposed to a mixture of virulent pathogen populations of the three diseases collected from infected bread wheat plants in Morocco. For STB screening, a mixture of six isolates were multiplied on YMDA (yeast extract + malt extract + dextrose + agar) medium. Two-weeks-old seedlings were inoculated with spore suspension.

For yellow and stem rusts pathogens, uredospores were mixed with talcum powder and 12 days seedlings with first leaves fully unfolded were inoculated. Inoculated seedlings were incubated for 24 h in growth chamber under darkness and at 8^{O}C for yellow rust and 20^{0}C for stem rust. After 24 h of incubation, the seedlings were kept at 16h light for 17 days for yellow rust and 12 days for stem rust.

Disease evaluations: A seedling infection score for STB was scored based on the visually estimated percentage of necrotic lesions containing pycnidia on the infected leaves (Zwart et al. 2010) after 21 days post-inoculation using 1–5 scale where 1 = highly resistant and 5= highly susceptible. For YR, seedlings were evaluated after 17 days using 1-9 rating scale where 1= highly susceptible and 9= highly susceptible. Stem rust seedlings evaluations were done using 0-4 rating scale (Stakman et al. 1962). where 0 to 2 and 2+ were considered low IT (resistance) and 3 to 4 were considered as high IT (susceptible).

References

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Results

Genotypes showed varying levels of responses for the three diseases (Figs. 1 & 4)

- 137 genotypes were resistant to YR and 92 genotypes were resistant to SR (Fig 2)
- 92 genotypes were resistant to SR .
- 91 genotypes were resistant to STB
- 33 genotypes showed resistant to STB &SR (Fig.2).
- 65 genotypes showed resistance to YR&SR.
- 62 genotypes showed resistance to YR& STB(Fig. 2)
- 26 genotypes have resistant to the three diseases (Fig.2)
- We showed a positive correlation exists between STB and YR, as well as between STB and SR. However, there is a negative correlation between YR and SR. Furthermore, genotypes grouped into four distinct clusters based on their variability to the three diseases, as illustrated in (Figs. 6)

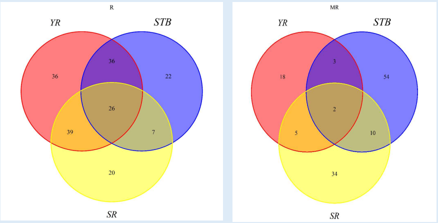

Figure 1 : Venn diagram of infection responses (R and MR) of 233 BW wheat genotypes to the three diseases Septoria (STB), stem rust (SR) and Leaf Rust (LR), under controlled conditions

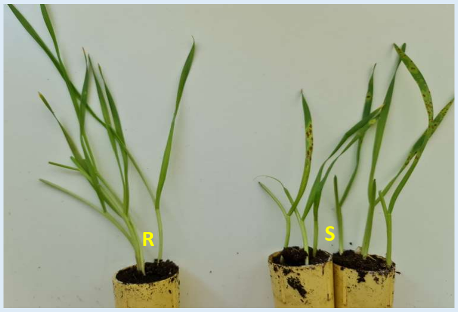

Figure 3: Stem rust

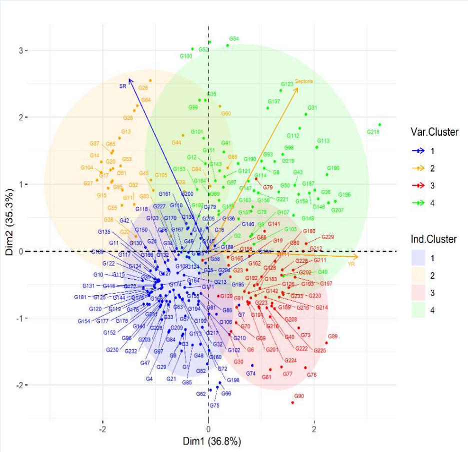

Figure 4: Biplot of 233 bread genotypes for the three diseases under controlled condition

Figure 2: Yellow rust S= susceptible and R= resistant

Figure 5: *Septoria tritici*

Conclusion

- The genotypes evaluated showed high diversity for resistance to single and more diseases.
- Genotypes with multiple resistance will be given high priority to share to national program.
- Further evaluations under field conditions are required and markers can be applied to identify multiple resistance genes in the selected genotypes.