

Evaluation and Association Mapping of Bread Wheat (*Triticum aestivum*) pre-breeding Lines for Reaction to Leaf Rust (*Puccinia triticina*)

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Amounane Fatima^{12*}, Backhaus Anna², Moulakat Adil², El jaboubi Muamar², Amri Ahmed², Belqadi Loubna¹, Kehel Zakaria²

¹Hassan II Agronomic and Veterinary Institute, Rabat.; ²International Centre for Agricultural Research in the Dry Areas (ICARDA), Rabat.

*Corresponding author: E-mail: fatimaamounane7@gmail.com

INTRODUCTION

- Bread wheat (BW) is the main crop produced and consumed in the world, accounting for 95% of all wheat grown [1].
- Early-stage leaf rust infections can lead to yield losses exceeding 50% [2].
- The genetic resources mainly wild relative species conserved in gene banks are important reservoirs of genes for breeding programs. However, they require pre-breeding efforts to meet breeders' objectives [3].

Objectives:

- Evaluate the resistance of 480 pre-selected BW lines to leaf rust at seedling stage.
- Identify genetic markers associated with leaf rust resistance through GWAS analysis.

METHODS AND MATERIALS

Plant material:



- Genotypes:** 480 BW pre-breeding lines
- Checks:** Achtar and Atlas
- Design:** Augmented design
- Blocks:** five blocks
- Fungal material:** mixture of three leaf rust isolates (*Puccinia triticina*)
- Scoring:** Stakman scale from 0 to 4 [4]

Analysis:



- MLM:** Lme4 R package
- GWAS:** GAPIT3 R package

RESULTS

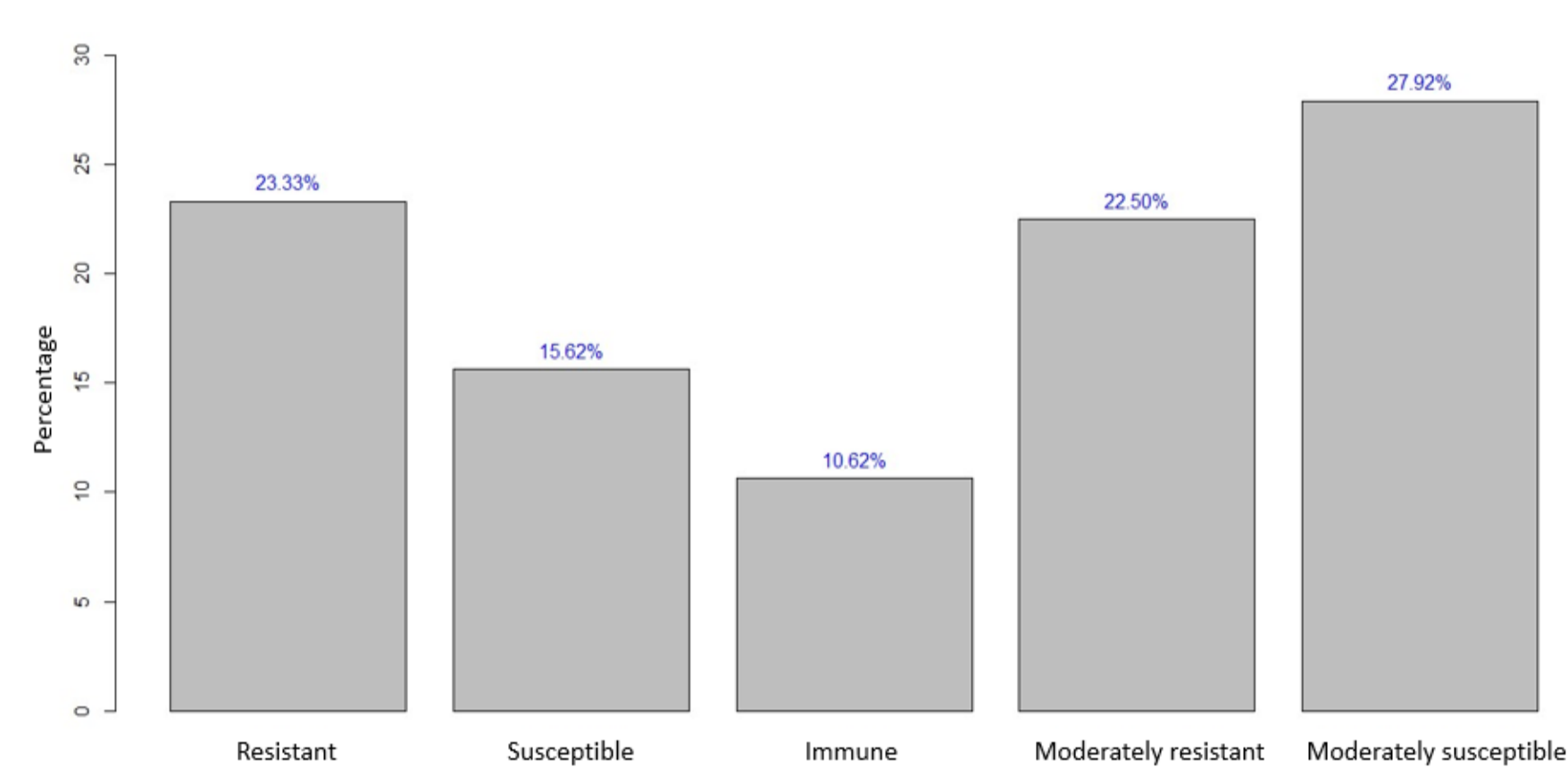


Fig1: Frequency of reactions of wheat lines to leaf rust under controlled conditions and at the seedling stage

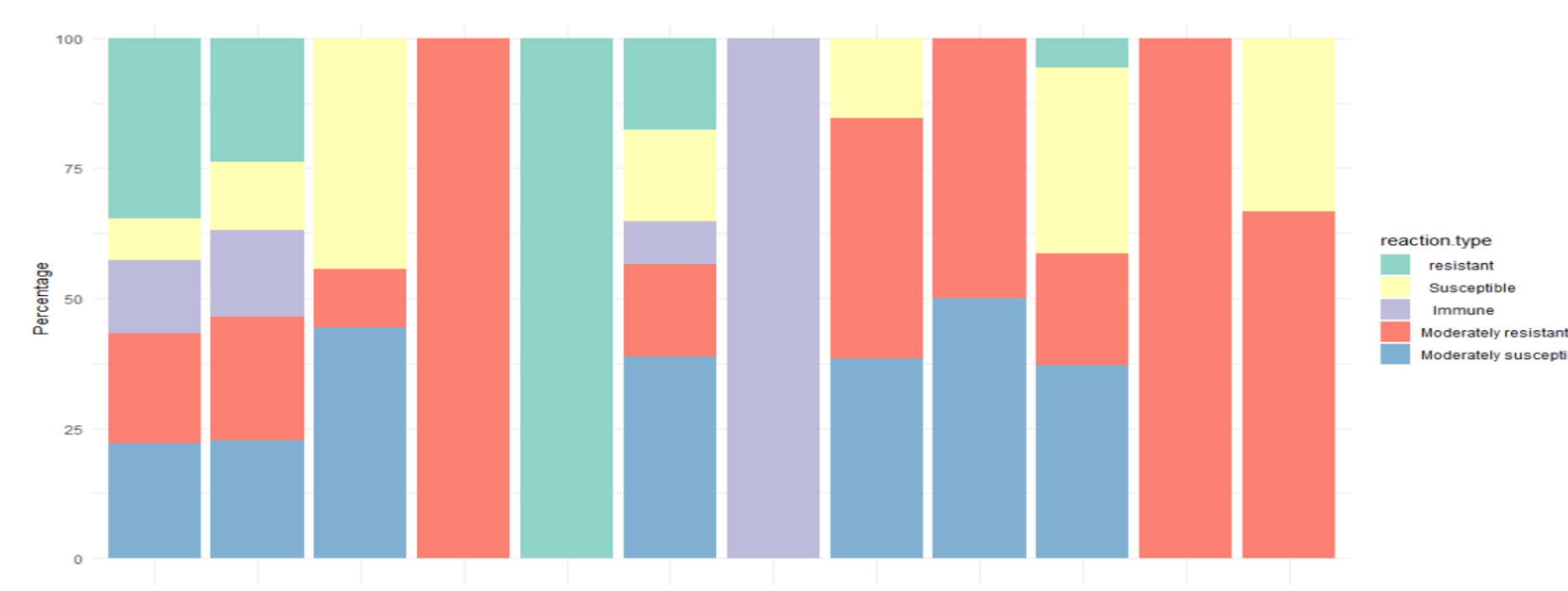


Fig2: Frequency of wheat genotype reaction by parents species

Tab1: Contribution of the species and the type of the first, second and third parent in the cross to the variance of the LR reaction

| Term | Contribution (%) |
|------------|------------------|
| Genotype | 90 |
| Type P1 | 30 |
| Species P1 | 34 |
| Type P2 | 30 |
| Species P2 | 27 |
| Type P3 | 34 |
| Species P3 | 22 |

Tab2: Trait-marker associations

| SNP | Chr | Pos | P value | MAF | Effect | -log(P) | Model |
|----------------|-----|-----------|----------|--------|--------|---------|-------|
| TaDArTAG009565 | 6D | 195467314 | 1,85E-05 | 0,2071 | 0,660 | 4,7 | MLM |
| TaDArTAG002251 | 3A | 488622202 | 5,84E-05 | 0,2273 | 0,574 | 4,2 | MLM |
| TaDArTAG006674 | 5A | 667872908 | 0,0003 | 0,2879 | -0,559 | 3,6 | MLM |
| TaDArTAG007418 | 1D | 280013775 | 0,0006 | 0,1641 | 0,555 | 3,2 | MLM |

- Approximately 34% of the lines showed resistance or immunity to leaf rust, 22% exhibited moderate resistance, and 43.54% displayed moderate susceptibility to susceptibility (Fig1).
- The highest number of lines expressing an Immune (I) and resistant (R) type of disease reaction was recorded in lines crossed with *Aegilops bicornis* var. *bicornis* (AB), *Aegilops ovata* (AO) and those crossed with *Triticum aestivum* subsp. *aestivum*+*Triticum aestivum* subsp. *compactum* (TEE+TEC) (Fig2).
- The effect of genotype explained a large proportion of the total variance (90%). The contribution of parent type is almost the same for all parents (P1 (30%), P2 (30%) and P3 (34%). While 34% of the genetic variance is expressed by the species of the first parent (Tab1).
- GWAS analysis revealed a remarkable set of 4 significant DarTag markers spread over chromosomes 3A, 5A, 1D and 6D (Tab2).

CONCLUSIONS

- Crop wild relatives (CWR) play a vital role in providing valuable traits, notably resistance to leaf rust, in the development of new bread wheat varieties.
- The associated markers presented here can improve the efficiency of breeding new resistant bread wheat varieties.
- To unlock the potential of crop wild relatives, pre-breeding efforts must connect with gene bank collections, focusing on economically important traits and targeted gene mobilization.

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