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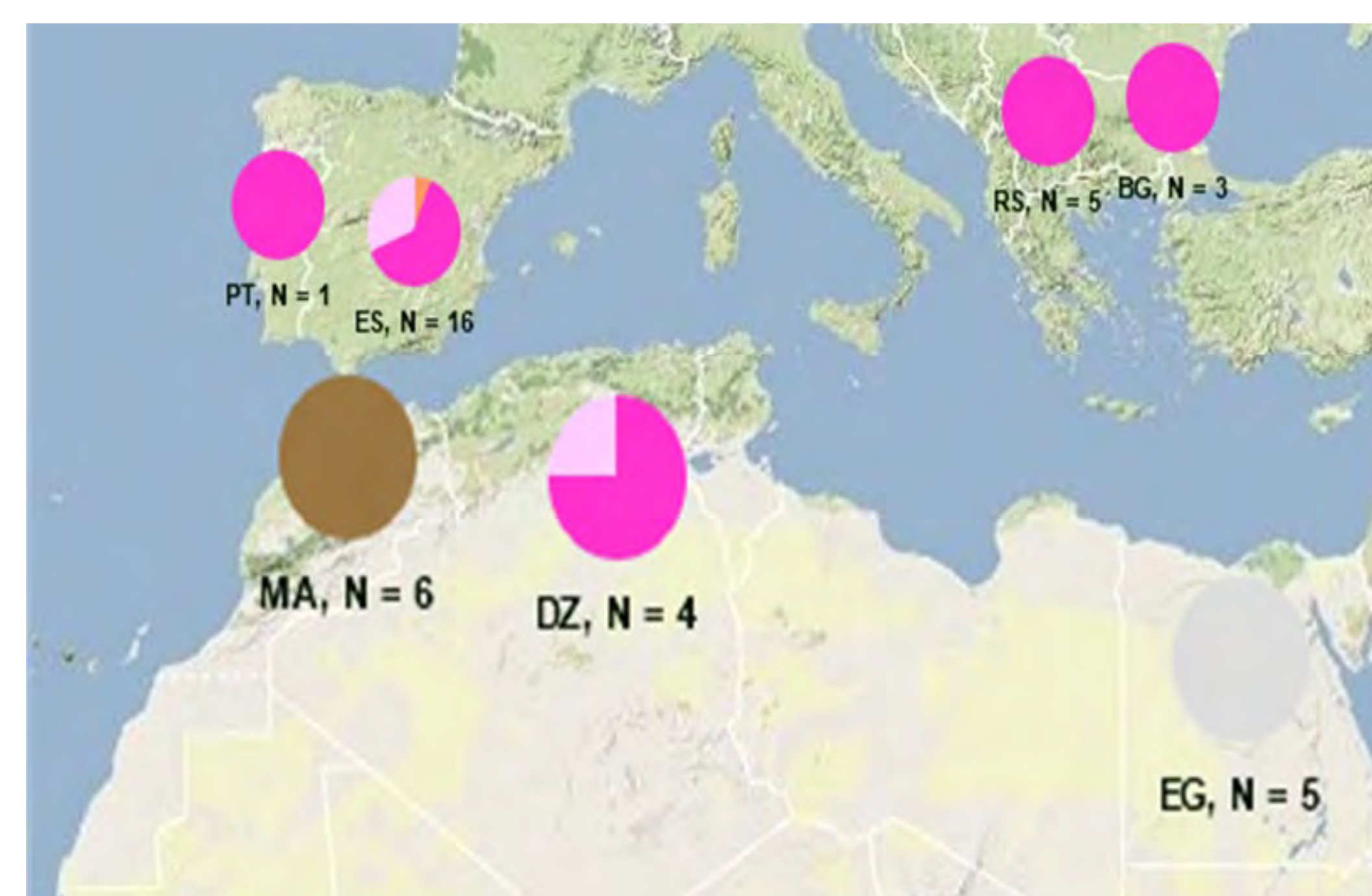
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ABSTRACT

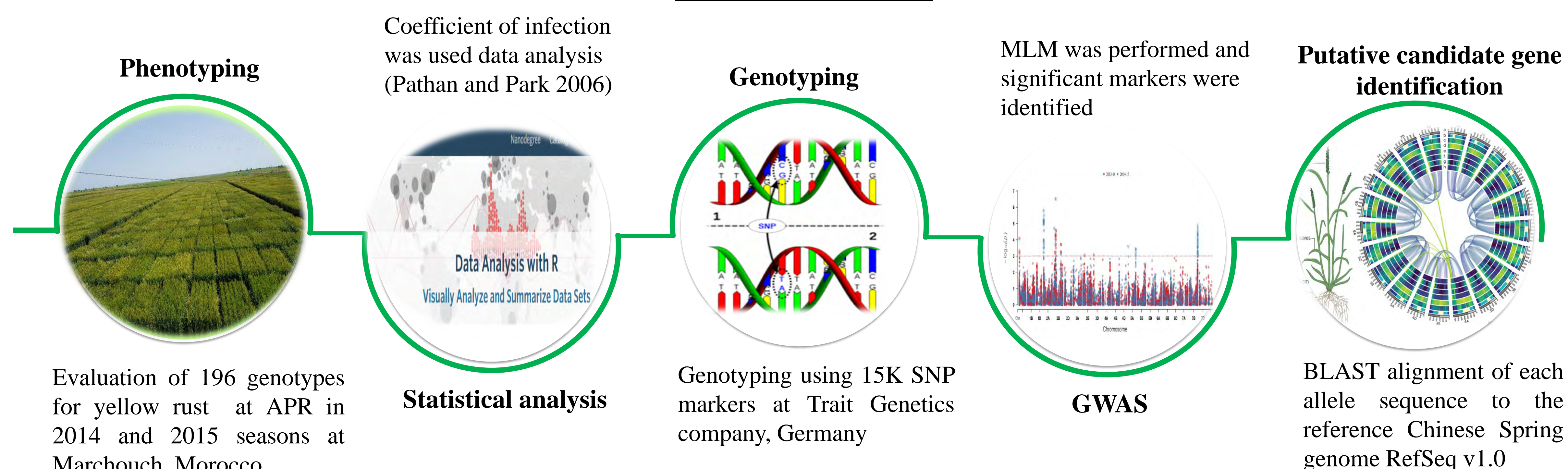
Yellow rust, caused by *Puccinia striiformis* f. sp. *tritici*, is a common and serious fungal disease of wheat (*Triticum aestivum* L.) all over the world and particularly in the Central and West Asia and North Africa region. A cultivars' resistance can break down quickly when new virulent pathotypes evolve in the ongoing arms race between host plant and pathogen. We investigated the disease development of 196 bread wheat genotypes under field conditions for two years 2014-2015 at ICARDA station, Marchouch, Morocco. The severity and the response rating were scored for adult plant field reaction following modified Cobb's scale. The Warrior (PstS7) race was prevalent in 2013 in Morocco while the virulence in the next two years was unknown. However, in 2016, a sampling was done systematically, and a new distinct race (PstS14) was detected along with PstS10 known as Warrior (-) previously reported in Algeria and Spain in 2014 and perhaps in Morocco as well but no data is available to confirm. Given that the breakdown of the resistance to stripe rust in a widely grown cultivar "Arrihane" in Morocco, which used to have moderate resistance to stripe rust in the past few years, became highly susceptible and scored 70-90S, and the resistance rating that dropped from 147 resistant genotypes in 2014 to 96 in 2015 might indicate that PstS10 and PstS14 (or may be other unknown races) possibly contributed to variation in the reaction type and the resistance in 2015. GWAS using mixed linear model identified 23 markers on chromosomes 2A, 2B, 2D and 7B significantly associated with adult plant resistance at false discovery rate (FDR-adjusted ≤ 0.05). BLAST analysis confirmed that YrR61 and Yr17 were mostly the candidate genes linked to the marker Tdurum_contig29983_490 on chromosome 2A and the marker Ku_c7740_879 overlapped with the QTL QYr.cim-2BS_Francolin designed as YrF previously reported on chromosome 2B.



● **Warrior (PstS7)** race was confirmed in **2013** in Morocco and continue to be spread widely in the Northern African countries, Europe and East Asia
 ● **PstS10 (Warrior⁽⁻⁾)** was also reported in Algeria and Spain in **2014**
Virulence in Morocco was unknown in 2015
 ● **PstS14** in **2016** in Morocco

Figure 3: Relative distribution of the emerged *P. striiformis* races from divergent lineages in Northern Africa and southern Europe during the period 2013-2016.

METHODOLOGY



RESULTS

- The analysis of variance for coefficient of infection (CI) scores revealed significant effect of the 2 years and genotypes as well as significant G × E interaction in response to stripe rust infection.
- 147 and 96 genotypes showed strong to moderate resistance based on the disease intensity in the first and second year
- The Moroccan check Arrihane is becoming highly susceptible in the second year and scored 70-90S
- 23 MTAs associated with stripe rust resistance passed a threshold of FDR ≤ 0.05 (El Hanafi et al. 2021).
- BLAST analysis and anchoring the flanking markers of stripe rust resistance locus on the reference genomes identified two markers Tdurum_contig29983_490 and Ku_c7740_879 linked to previously reported genes and QTL and novel potential marker RAC875_c34939_86
- Ku_c7740_879 reduced the LOD score from 6.49 to 4.49 in the first and the second year, respectively.



Figure 1: Yellow rust resistant lines in the middle of two susceptible lines

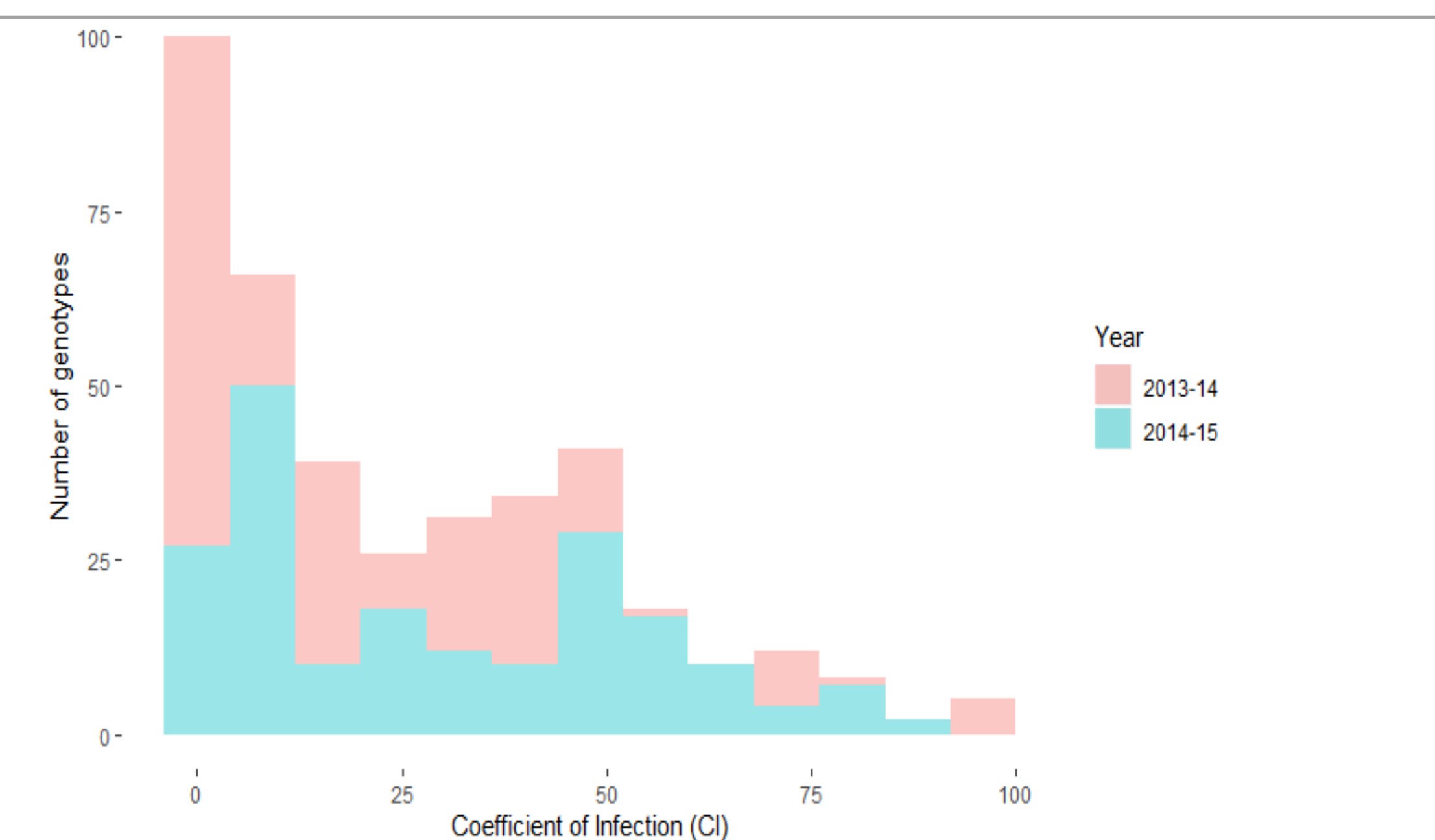


Figure 2: Coefficient of infection of the 196 spring wheat genotypes to yellow rust at Marchouch station (Morocco) during 2013-2014 and 2014-2015 cropping seasons

Table 1 Identification of genes and NLR of yellow rust resistance underlying QTLs +/- LD

Chr	Marker	-Log(p)	Left flanking position	Right flanking position	Number of genes	Published YR in region	NLR annotator
2A	Tdurum_contig29983_490	5.76	0	6259186	153	YrR61/BV211615, YR17	
2B	Ku_c7740_879	6.49	154217138	166217138	112	QYr.cim-2BS_Francolin	NLR43; NLR143
7B	RAC875_c34939_86	4.87	735577327	747577327	155	?	NLR80; NLR146; NLR147

Conclusion

- *PstS10* and *PstS14* (or may be other unknown races) possibly contributed to variation in the reaction type and the resistance in 2015.
- The identified significant markers overlapped with genes involved in plant disease resistance and defense mechanism (El Hanafi et al. 2021)
- The novel markers found might be useful in marker assisted selection but needs to be confirmed using an allelism test (El Hanafi et al. 2021)

References

- Pathan AK, Park RF (2006) Evaluation of seedling and adult plant resistance to leaf rust in European wheat cultivars: Leaf rust resistance in European wheat cultivars. *Euphytica* 149:327-342. <https://doi.org/10.1007/s10681-005-9081-4>
- El Hanafi S, Backhaus AE; Bendaou N, Sanchez-Garcia M, Al-Abdallat A, Tadesse W (2021) Genome-Wide Association Study for Adult Plant Resistance to Yellow Rust in Spring Bread Wheat (*Triticum Aestivum* L.). *Euphytica*, 217(87).