

Assessing Genetic variation associated with stripe rust resistance in Indian wheat genotypes using linked markers

Reema Rani^{1,3}*, Shikha Yashveer¹, Rajender Singh², and Neelam R. Yadav¹

¹Department of Molecular Biology, Biotechnology & Bioinformatics, ² Department of Plant Pathology, Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana-125004, India

³ICAR-Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur, Rajasthan-321303, India

* Corresponding author: reemasherwal@gmail.com



Background

Stripe rust, commonly known as yellow rust (*Yr*) or "Pilliya" in India is caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*) fungi which is causing severe yield losses in the wheat production in the country. The analysis of genetic diversity in breeding material helps plant breeders in selection and prediction of potential genetic gain for sustainable breeding program. More diversity of genotypes provides the breeder better options for selecting parents to utilize directly in resistance breeding.

Material and Methods

Wheat materials: Sixty eight wheat genotypes were used for screening purposes.

Molecular markers: A total of 38 polymorphic SSR markers linked with *Yr* resistance genes were used.

Stripe rust phenotyping: All of these 68 wheat genotypes were evaluated under natural field conditions for yellow rust reaction

Genetic diversity analysis: The dendrogram was constructed and Principal component analysis (PCA) was done by NTSYS-PC software.

Results

A Total of 115 alleles were scored. The number of alleles per locus varied from 2 to 8 with an average of 3.02 alleles per locus. Maximum 8 alleles were identified in marker *Xgwm273* and *Wmc44*. The PIC values ranged from 0.0 to 0.872 with an average value of 0.534 among SSR loci. Maximum PIC (0.872) was identified in *Xgwm582* followed by (0.789) in *Xgwm526*. Least PIC (0.0) was found in *S26M49* and *Owm45F3R3* followed by (0.1) in *Xgwm533*. Estimates of genetic distance based on Jaccard's similarity coefficients ranged from 0.58 to 0.95 indicated the wide range of genetic diversity at genotypic level. Two-dimensional PCA and Three-dimensional PCA analysis also showed the clustering of yellow rust susceptible and resistant genotypes into separate groups. Under epiphytotic conditions, Coefficient of infection ranged from 0-60 among all wheat genotypes. Fifty three genotypes were found resistant (ITs 0), accounting for 77.94% of total genotypes, 3 genotypes (4.4%) showed trace resistance (ITs 1), 7 genotypes (10.3) were moderately susceptible (ITs 3) and 5 genotypes (7.35 %) were susceptible (ITs 4).

| S. No. | Marker name | PIC | S. No. | Marker name | PIC |
|--------|---------------------|-------|--------|--------------------|-------|
| 1 | <i>Xgwm498-1B</i> | 0.553 | 20 | <i>Wmc219-4A</i> | 0.500 |
| 2 | <i>Barc8-1B</i> | 0.224 | 21 | <i>Wmc313-4A</i> | 0.424 |
| 3 | <i>Barc181-1B</i> | 0.452 | 22 | <i>S26M49-4B</i> | 0.000 |
| 4 | <i>Wmc44-1B</i> | 0.492 | 23 | <i>Cfd23-4D</i> | 0.500 |
| 5 | <i>Xgwm259-1B</i> | 0.636 | 24 | <i>Cfd71-4D</i> | 0.740 |
| 6 | <i>Xgwm413-1B</i> | 0.663 | 25 | <i>Be492011-5A</i> | 0.500 |
| 7 | <i>Barc187-1B</i> | 0.668 | 26 | <i>cfa2149-5A</i> | 0.500 |
| 8 | <i>Xgwm582-1B</i> | 0.876 | 27 | <i>SN/A2-5A</i> | 0.589 |
| 9 | <i>Xgwm273-1B</i> | 0.800 | 28 | <i>cfb309-5B</i> | 0.494 |
| 10 | <i>Wmc198-2A</i> | 0.636 | 29 | <i>Xfbb276-5D</i> | 0.493 |
| 11 | <i>Xgwm249-2B</i> | 0.760 | 30 | <i>ASA-6B</i> | 0.560 |
| 12 | <i>Xgwm526-2B</i> | 0.789 | 31 | <i>Barc101-6B</i> | 0.600 |
| 13 | <i>S19M93-2B</i> | 0.459 | 32 | <i>Xpsp3000-7B</i> | 0.700 |
| 14 | <i>IB267-2B</i> | 0.556 | 33 | <i>Barc32-7B</i> | 0.633 |
| 15 | <i>Barc349-2B</i> | 0.722 | 35 | <i>Wmc557-7B</i> | 0.495 |
| 16 | <i>Xgwm501-2B</i> | 0.731 | 36 | <i>cslv34-7B</i> | 0.500 |
| 17 | <i>Xgwm102-2D</i> | 0.600 | 37 | <i>Wmc364-7B</i> | 0.189 |
| 18 | <i>Xgwm533-3B</i> | 0.125 | 38 | <i>Wmc219-4A</i> | 0.500 |
| 19 | <i>Owm45F3R3-4A</i> | 0.000 | | | |

Table:1 PIC information content of molecular markers used for analysis

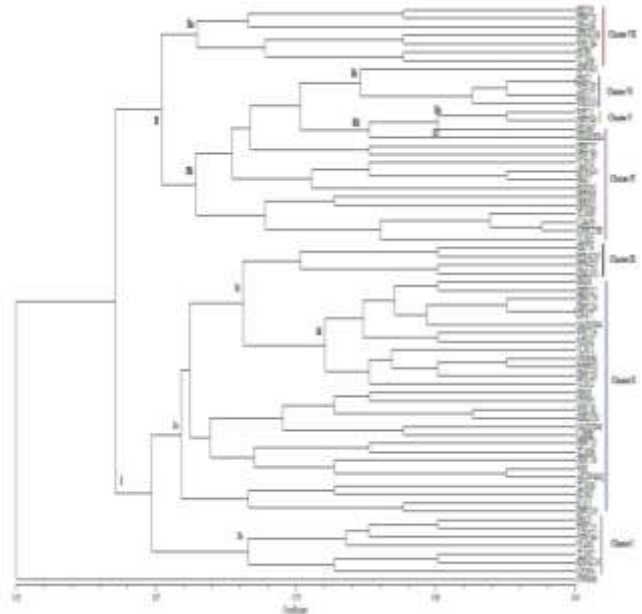


Figure:1 Dendrogram of 68 wheat genotypes based on 38 SSR loci

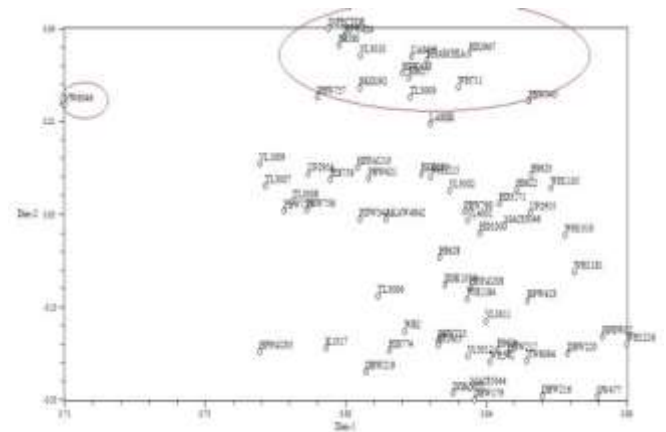


Figure:2 Three dimensional PCA scaling of 68 wheat genotypes based on 38 SSR loci

Conclusion and Discussion

- Wheat Genotypes with more alleles favorable to resistance also exhibited higher levels of resistance to stripe rust in the field conditions.
- Molecular markers linked with *Yr* genes can be utilized for diversity analysis and MAS purposes.
- The information generated in this study can be used in hybridization programmes in such a way that the parent belonging to different clusters with maximum divergence could be utilized to get desirable transgressive segregants.

References

1. Evaluating stripe rust resistance in Indian wheat genotypes and breeding lines using molecular markers (2019) Comptes Rendus Biologies, Volume 342: 5–6
2. MAS Wheat, database available at (http://maswheat.ucdavis.edu/protocols/FunctionalMarkers/FM_disease.htm)
3. Rohlf, F.J. (2000) NTSYS-PC, numerical taxonomy and multivariate analysis system. Version 2.02, Applied