ASSOCIATION MAPPING FOR STRIPE RUST (PUCCINIASTRIIFORMIS F. SP. TRITICI) IN BREAD WHEAT

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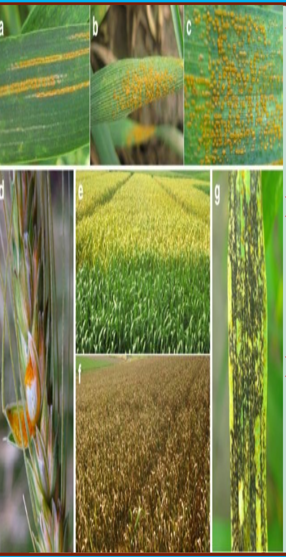
Introduction



- Wheat stripe rust , caused by *Puccinia striiformis* Westend. f. sp. *Tritici,* is a devastating fungal disease that threatens most of the world's wheat production.
- New resistance genes must be identified and introgressed into future wheat cultivars to tackle the current and newly emerging races of this pathogen.
- In this study, we conducted a genome-wide association study (GWAS) using 9523 single nucleotide polymorphism (SNPs) markers identified from 245 wheat lines to identify the genetic basis of stripe rust resistance.

Objectives

General objectives:

This research is aimed to find the novel loci responsible for *Pst* resistance on spring bread wheat germplasm to contribute substantial input for durable rust-resistant variety development program against the *Pst*.

Specific Objectives:

1. To evaluate bread wheat varieties for their resistance against yellow rust under natural disease pressure.
2. To identify and map QTLs associated with yellow rust through genome-wide association mapping.
3. To assess the nature and extent of genetic diversity of globally collected bread wheat germplasms.

Materials and methods

Study Area

Field screening was conducted during 2018 and 2019 main cropping seasons at Kulumsa Agricultural Research Center (KARC), in Ethiopia

Plant Material

This research used a panel of 245 elite spring wheat breeding lines (*T. aestivum*) from International Center for Agricultural Research in Dry Areas (ICARDA).

Genetic Diversity

Genetic diversity was discovered based on polymorphic information content (PIC), heterozygosity, and Nei's gene diversity using the whole set of SNP markers from PowerMarker 3.25 software (K. Liu & Muse, 2005).

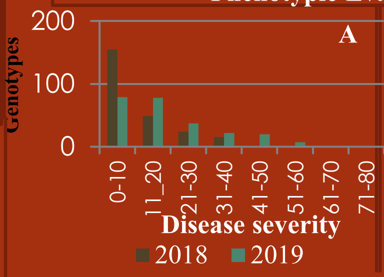
Genome-Wide Association

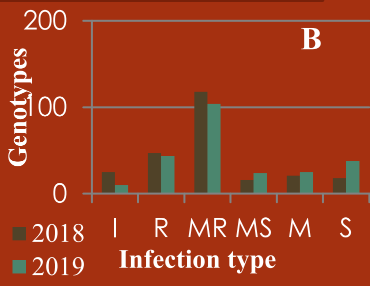
The mixed linear model (MLM) in TASSEL 5.2 software was used to examine marker-trait association (MTAs) between BLUEs value of CI and SNP genotypic data. Mixed linear model in which genetic markers were used as a covariance matrix between individuals along with population structure and kinship matrix

MTAs were declared significant at a threshold value of $-log_{10}(p) \geq 2.5$ (corresponding p $value \leq 0.05$).

Results and Discussions

Phenotypic Evaluation results





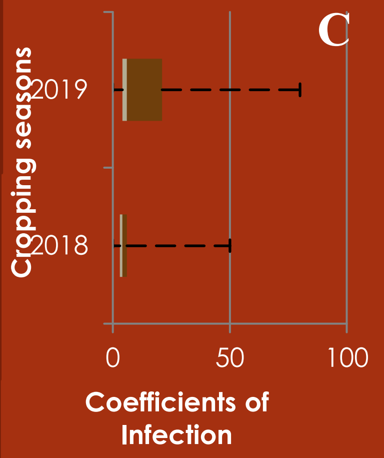


Fig 2 – Phenotypic distribution of 245 wheat lines against stripe rust under natural disease pressure as infection type (IT), disease severity (DS), and coefficient of infection (CI) in corresponding two environments (2018 and 2019). (A) Frequency of genotypes for DS in percentage; (B) frequency of genotypes for IT; (C) Frequency of genotypes for CI on the scale of 0-100 Each environment is represented with different colors as indicated by the color legend.

Genotypic Analysis

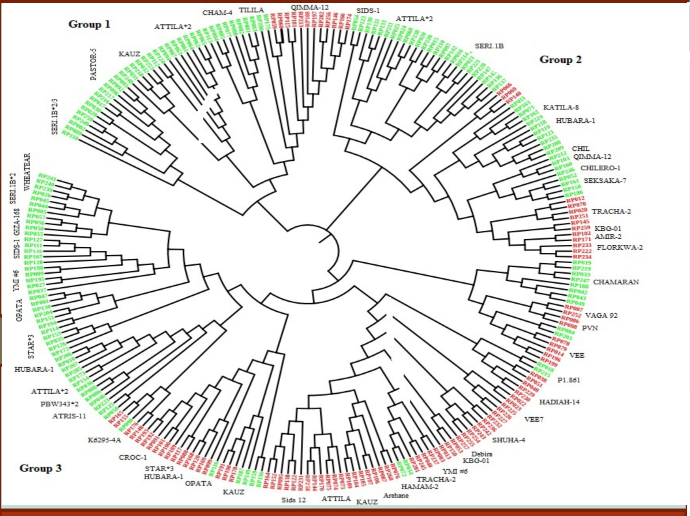


Figure 2- A dendrogram illustrating the clusters of wheat lines based on Nei's genetic distance. The lines were color-coded with STRUCTURE probability distribution.

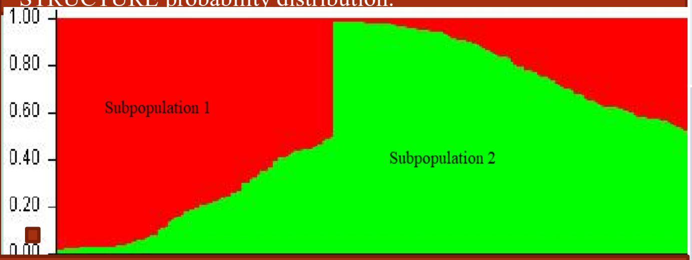


Fig 3 – Structure clustering and principal components of 245 wheat lines based on 9523 SNP markers. K_probability of population group based on K=2; a

Table 1-Summary of the MTAs detected in the 245 wheat breeding lines for stripe rust resistance

	Name of QTLs	Position	P-value	R2	*Yr/QTL*	Reference
Name of QTLs Potential candidate for representing alleles of the same genes.	EWYY1B.3 EWYY1B.5 EWYY2B.2 EWYY2B.3 EWYY3B EWYY4B.1 EWYY4B.2 EWYY5B.1 EWYY7B.1 EWYY7B.2	60.62 139.53 141.48 169.3 5.79 61.84-75.65 71.37-75.65 126.35-129.24 63.09-71.33 73.39 -73.79	2.978811 2.928118 3.807739 2.844664 2.638272 2.779892 3.929556 2.551294 4.404724 4.003423	5.768 4.424 7.457 5.522 5.129 5.377 7.683 5.527 7.088 7.733	Yr24/26, Yr64,Yr65 *Lr46/Yr29* *Yr43, Yr53* *Yr3* Yr4, Yr57 , Yr30 Yr50 Yr62 YrExp2 Yr39 Yr39	Cheng *et al.*, 2014 Rosewarne *et al.* 2012 Xu *et al.*, 2013 Wheat Catalogue Suenaga *et al.*, 2003 Liu *et al.*, 2013 Lu *et al.*, 2014 Wheat Catalogue Lin & Chen 2007 Lin and Chen 2007
Potential candidate for representing alleles of the same QTLs for *Pst* resistance	EWYY1B.1 EWYY1B.2 EWYY2B.1 EWYY6B.2 EWYY7B.4	27.62 43.86 76.7-80.77 73.24 133.59	3.340569 2.616185 3.280868 3.03323 2.821023	5.163 5.056 5.716 5.500 5.496	QYr.cau-1BS_AQ 24788-53 QYr.cau-1BS_AQ 24788-53 QYr.ucw-2B_UC1110 QYr.ucw-6B QYr-7B_Tiritea	Lukaszewski, 2000 Quan *et al.*, 2013 Lowe *et al.*, 2011 Maccaferri *et al.*, 2015 Imtiaz *et al.*, 2004
Potentially novel significant QTLs identified in this study	EWYY1B.4 EWYY2A EWYY4A EWYY5A.1 EWYY5A.2 EWYY5B.2 EWYY6B.1 EWYY7B.3	95.12 62.81 74.96 67 93.23 176.61 64.08 89.64	2.539102 2.866461 2.500313 2.886057 3.461778 2.809668 3.0 3.249414	5.063 4.294 3.634 5.588 6.745 5.436 5.811 6.311		This study This study This study This study This Study This study This study This study