# **Mapping Stem Rust Resistance Loci in Spring Wheat variety Linkert**

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#### Introduction

> Wheat stem rust caused by *Puccinia graminis f. sp. tritici* (*Pgt*) is one of the diseases that

threatens wheat productions worldwide.

> It can cause a significant seed yield reduction during its epidemics.

> Deploying a variety with one or more resistance genes for production is an economical and

environmentally safe method of controlling wheat stem rust disease.

➢ Variety 'Linkert' was released in 2013 by the University of Minnesota and became widely

grown in Minnesota and Eastern North Dakota by 2017. Linkert was one of the first varieties

released in the Northern United States with adult plant resistance to Ug99.

> In the present study, we report a QTL consistently associated with wheat stem rust resistance

across environments using the Linkert/Forefront and Linkert/LMPG-6 populations.

### Objectives

> To characterize the genetics of wheat stem resistance in variety 'Linkert'.

> To identify chromosome locations of QTLs associated with stem rust resistance.

## **Materials and Methods**

- Two doubled haploid populations were developed from three parents. The crosses were
   Forefront/Linkert and LMPG-6/ Linkert. LMPG-6 and Forefront are susceptible to Ug99.
- A total of 190 for lines for the Linkert/LMPG-6 population, and 107 lines for the Linkert/Forefront population were evaluated with their parents in the field in Ethiopia and Kenya for three years (2016-2018) against virulent *Pgt* races including the Ug99 race group.
- These populations were also evaluated at Rosemont, MN for three years (2015-2017) with four domestic stem rust fungus isolates such as QTHJC, QFCSC, TPMKC and RCRSC. Evaluation was also done with the leaf rust fungus both at the seedling stage and in the field in St. Paul, MN.

# Table 1. QTL detected for wheat stem resistance across environments in Ethiopia and Kenya for Linkert/Forefront and Linkert/LMPG-6 doubled haploid populations.

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Year	Trait	QTL position	Chr	Marker @ QTL	Left Flanking	Right flanking	LOD	% variance	population
				0				evplained	
								by QTL	
DZ 2017	COI	1.86	2B	wsnp_Ku_c48_103915	Tdurum_contig29563_109	GENE-0818_347	8.11	9.67	Linkert/Forfront
DZ 2018	COI	1.86	2B	wsnp Ku c48 103915	Tdurum contig29563 109	wsGENE-0818 347	4.52	9.67	Linkert/Forfront
						_			
DZ 2017	COI	2.63	4A2	CAP12_c2972_140	wsnp_BG313770B_Ta_1_1	Kukri_c17417_407	4.30	16.62	Linkert/LMPG-6
DZ 2017	COI	53.00	4D	-	wsnp_Ex_c34252_42593715	RAC875_c67855_529	3.10	11.18	Linkert/LMPG-6
DZ 2017	COI	125.91	5B	CAP12_c2189_159	BS00022662 51	RFL Contig4205 679	3.55	13.11	Linkert/LMPG-6
DZ 2018	COI	52.0	4D	-	wsnp_Ex_c34252_42593715	RAC875_c67855_529	5.44	9.04	Linkert/LMPG-6
DZ 2018	COI	59.57	6A	IACX3586	Ra_c8185_676	Excalibur_c26057_1049	3.75	3.03	Linkert/Forfront
Ken 2017	COI	25.0	1A	-	Kukri_c56494_585	BobWhite c20553_364	3.29	11.47	Linkert/Forfront
	COI	0.0	2B	Tdurum_contig29563_109	Tdurum_contig29563_109	GENE-0818-347	3.14	11.04	Linkert/Forfront
Ken 2018	COI	1.86	2B	BS00064164_51	Tdurum_contig29563_109	GENE-0818-347	4.37	9.02	Linkert/Forfront
Ken 2018	COI	11.1	1B2	BS00029539_51	Ra_c40444_243	BobWhite_c27474_154	3.02	4.46	Linkert/LMPG-6
2018	COI	32.0	4D	-	wsnp_BF473052D-Ta21	Kukri_c159-61-70	4.12	1.57	Linkert/LMPG-6
Ken 2018	COI	128.01	5B	Kukri_c57954_369	Tdurum_contig58442_188	RFL_Contig4205_679	4.09	3.33	Linkert/LMPG-6

# Table 2. QTL identified for RCRSC and TMPKC stem rust races evaluated at Rosemont, MN with Linkert/Forefront and Linkert/LMPG-6 doubled haploid populations.

Down	Daga	Vaam	Chr	OTL pos	Marker @ OTI	Left Flanking	Pight flanking	LOD	Permutation I OD (5%) threshold	%Variance explained
Popn	Race	rear	Cill		Marker @ QTL	Left Flanking	Right hanking	LOD	remutation LOD (576) uneshold	70 v ariance explained
				(cM)						
linkert/Forefront	RCRS	2017	1B	52.0	-	RAC875_c25125_210	GENE-0165_389	14.12	2.85	4.85
			3A	96.0	-	RAC875_rep_c109228_400	IAAV9044	23.6	2.85	2.93
Linkert/LMPG-6	RCRS	2015	5B	122.23	BS00000848 51	Tdurum contig47816 258	BS00080474 51	4.92	0.51	1.03
		2015	1B2	10.57	BobWhite_c2092_519	Ra_c40444_243	BobWhite_c27474_154	2.48	0.51	1.81
		2016	3A2	5.82	BobWhite_c11935_137	RAC875_c15390_459	BS00004149_51	5.82	0.51	1.28
		2016	4A2	2.63	CAP12 c2972 140	wsnp BG313770B Ta 1 1	Kukri c17417_407	2.63	0.51	1.97
		2017	5B	121.69	Excalibur_rep_c105964_928	Ex_c67086_584	Excalibur_rep_c88310_1394	4.12	0.51	1.94
		2017	3A2	1.83	CAP7_c1467_220	RAC875_c15390_459	RAC875_rep_c77067_347	2.09	0.51	0.72
Linkert/Forefront	TMPK	2015	7A	157.0	-	wsnp Ex c8692 14557179	Ra c9427 300	18.57	1.71	10.61
		2015	2B	24.86	BS00098490 51	RAC875_c16675_580	-	2.38	1.71	14.91
		2016	2A	8.0	-	GENE-1177_195	-	2.75	1.71	17.32
		2017	1B	79.00	Tdurum_contig81102_102	Tdurum_contig57731_412	Tdurum_contig81102_102	3.08	1,71	2.97
Linkert/LMPG-6	TMPK	2015	4B	45.00	-	RAC875_c2542_815	BobWhite_c42663_70	63.8	0.74	2.76
		2016	1B	0.0	wsnp_RFL_Contig3951_4390396	BobWhite_c23617_167	TA003668-0364	2.74	0.74	5.04
		2016	1B2	6.00	-	BS00022323_51	BobWhite_c2092_519	2.76	0.74	1.97
		2016	5A	47.0	Tdurum contig82190 124	-	-	2.39	0.74	6.31
		2016	5B	123.8	BS00080474_51	wsnp_Ex_c58091_59534826	RFL_Contig4205_679	2.01	0.74	6.18
		2016	7A	27.02	Ku_c6386_1034	CAP12_c2951_105	Excalibur c8066 791	2.79	0.74	4.56

#### Table 3. QTL identified for leaf rust resistance in the field

Year	QTL position	Chr	Marker @ QTL	Left Flanking	Right flanking	LOD	Permutation LOD (5%) threshold	Population
2017	5.27	4A2	Kukri_c17417_407	wsnp_BG313770B_Ta_1_1	Kukri_c17417_407	3.04	7.83	Linkert/LMPG-6
2017	5.28	4D	IAAV1324	tplb0038a13_900	wsnp_BF473052D_Ta_2_ 1	3.73	15.55	Linkert/LMPG-6
2018	58.5	6A	GENE_4052_338	wsnp_Ex_c34545_42832894	Ku_c56003_719	3.74	11.31	Linkert/LMPG-6
2018	115.7	6B	Excalibur_c64024_119	BS00034554_51	Tdurum_contig3203_291	4.10	14.70	Linkert/LMPG-6

- Both mapping populations were genotyped at the USDA-ARS small grains genotyping lab in Fargo, North Dakota, with the iSelect 90k SNP assay developed by Wang et al. (2014).
- > The raw 90K SNP data was processed using Illumina GenomeStudio software version 2.0.
- Linkage maps were constructed for each population with ASMap R package (Taylor and Butler, 2017) with a total of 1091 and 1552 high quality SNPs for Linkert/Forefront and Linkert/LMPG-6 populations, respectively.
- Quantitative trait loci (QTL) analysis was conducted in R package RQTL with composite interval mapping (CIM) method.

#### Results

- In most cases the phenotypic correlation coefficients among environments are positive (Fig.1).
- We found QTL consistently associated with wheat stem rust resistance on chromosome 2BS for the Linkert/Forefront population both in Ethiopia and Kenya (Table 1).
- Another reliable QTL was detected consistently on chromosomes 5BL (125.91 cM) and 4AL (*Sr7a*) for the Linkert/ LMPG population in Ethiopia and Kenya. The QTL on 5BL also provided resistance against races RCRSC and TPMKC that were evaluated in the field at Rosemont, MN (Table 2).
- A QTL was detected in the Sr7a region of chromosome 4AL of Linkert/LMPG that was effective to leaf rust in the field (Table 3). Different QTL identified in the two populations reflect the importance of examining the genetics of resistance in a population derived from adapted germplasm (Forefront) in addition to a genetic stock.
- The QTL detected in this study were population specific despite Linkert being used as a common parent between the two populations.

Fig.1. Phenotypic correlation coeffects among environments for Linkert/Forefront doubled haploid population evaluated for wheat stem resistance in Ethiopia and Kenya.



# Stable QTL linked with wheat stem rust resistance was identified using two doubled haploid populations. The QTL identified on chromosome 4AL in the Linkert/LMPG-6 population is likely conferred by *Sr7a*. The detected QTL were population specific though Linkert was used as the resistant parent in both populations. The QTL linked SNPs can be converted into breeder friendly markers to transfer resistance conferring QTL to adapted wheat lines.

# References 1. Taylor, J., Butler. R Package ASMap: Efficient Genetic Linkage Map Construction and Diagnosis. Journal of Statistical Software, D. (2017); 79(6), 1-29. 2. Wang, S., Wong, D., Forrest, K., Allen, A., Chao, S., Huang, B. E., et al. Characterization of polyploid wheat genomic diversity using a high-density 90,000 single nucleotide polymorphism array. Plant Biotechnol. J. (2014); 12, 787-796. doi: 10.1111/pbi.12183 3. Wu Y, Bhat PR, Close TJ, and Lonardi S. Efficient and accurate construction of genetic linkage maps from the minimum spanning tree of a graph. PLoS Genet. (2008); 4: e1000212.