

# Genetics of Stem Rust Resistance in 'Gage' Hard Red Winter Wheat

## Abstract

Gage is a Nebraska hard red winter wheat cultivar, released in 1963 mainly for its excellent field resistance to wheat stem rust (*Puccinia graminis* f.s. *tritici*). Resistance in Gage remains unexplained by breeders and pathologists. The results reported represent an effort to understand the stem rust resistance in Gage. The Sr2 marker phenotype from F<sub>2</sub> plants validated the involvement of adult plant resistance gene. Segregation of seedling resistance to races QFCSC among F<sub>2:3</sub> families suggested the resistance is conferred by gene/s in addition to Sr2.

## Materials and Methods

Initial screening of seedling Gage and 'Bill Brown', along with the check cultivar 'Scout 66', was conducted at the CDL. Gage was evaluated with molecular markers for known major stem resistance genes at the USDA-ARS Eastern Regional Genotyping Laboratory.

Stem rust reaction in 245 F<sub>2</sub> and F<sub>2:3</sub> families from a cross between susceptible cultivar 'Bill Brown' and Gage was evaluated. F<sub>2</sub> plants were screened with the csSr2 CAPS marker and stem rust race QFCSC at adult plant stage in greenhouses of the University of Nebraska Lincoln. For two sets of F<sub>2:3</sub> seedling (one for each race) evaluated at the USDA-ARS Cereal Disease Laboratory in St. Paul, MN; 10 to 20 seeds were grown in greenhouse during February 2012. Seedlings were inoculated with TTKSK and QFCSC races separately in different inoculation booths. Infection type was rated according to the Stakeman method and then linearized according to Zhang (Zhang et. al., 2011). Families rated between 5 and 6 are classified as resistant; between 6 and 8 as heterozygous, and between 8 and 9 as susceptible. Observed segregation ratios were compared to expected ratio and probabilities were determined using  $\chi^2$  goodness of fit test with  $\alpha = 0.05$ .

## Results and Discussion

**Stem Rust Resistance of Gage.** In seedling resistance screening, Gage was more resistant than Scout66 to Ug99 and variants and to North American race QFCSC (Table 1). Gage was not positive for known stem rust resistance molecular markers for: *Sr6*, *Sr9a*, *SrWeb*, *Sr24*, *1BL:1RS*, *Sr26*, *Sr36*, *Sr42*, *Sr54*, or *Lr19/Sr25*. Gage and Scout66 share cultivar 'Hope' in their pedigree which has extensively been used as source of resistance in North America and Australia due to its high field resistance to stem rust (Mcintosh, et al., 1967).

**Sr2 Marker Analyses.** The Sr2 marker phenotype from F<sub>2</sub> plants of Gage x Bill Brown (Figure 1) segregated 3:1 ratio as expected (Table 2). Bill Brown has the null allele for the csSr2 marker; therefore the marker segregates as a dominant marker.

**Table 1. Seedling reaction of Gage (resistant parent), Bill Brown (susceptible parent), Scout 66 (resistant cultivar) and LMPG-6 (susceptible cultivar)**

Cultivar	Pathotype														
	Ug99					United States race									
	Ug99 race	Ug99 race	Ug99+Sr24 race	Ug99+Sr36 Race	Yemen race	TTTTF	TPMKC	RKQQC	RCRSC	QTHJC	QFCSC	MCCFC	QCCSM	QCCJB	SCCCSC
Gage	2	2	22+	22+	3+	4	4	2+3	32+	3	2	4	13-	3	32+
Scout 66	22+	2+/3+	2+	2+/3+	3+	4	4/0;1	3+/32+	4	4	3+/0;	4	33+	4/0;1	3+
Bill Brown	3+	3+	3+	3+	3+	4/0;1+	4	4	4	4	4	4	33+	4	3+
LMPG-6	3+	3+	3+	3+	3+	4	4	4	4	4	4	4	4/;3+Y	4	4

**Fig 1. csSr2 CAPS marker segregating on F<sub>2</sub> population**



**Table 2. Chi-square analysis of csSr2 marker segregation on F<sub>2</sub> population derived from the cross Bill Brown by Gage**

Category	Observed	Expected	$\chi^2$	P-value
Present	174	183.75	2.07	0.15 <sup>†</sup>
Absent	71	61.25		

<sup>†</sup> molecular marker phenotype fits the expected 3:1 ratio

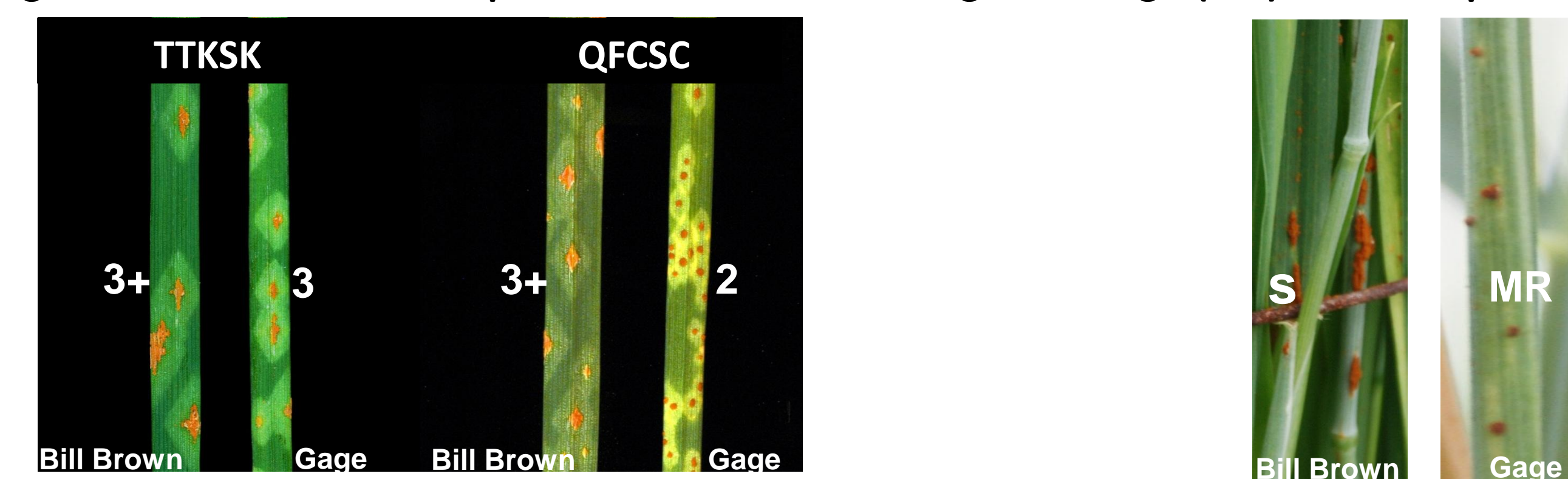
**F<sub>2</sub> Adult Plant Reaction.** Infection type to race QFCSC in the greenhouse did not clearly distinguish intermediate infection types from susceptible reactions. F<sub>2</sub> adult plant reaction was categorized as resistant or susceptible/intermediate. csSr2 marker segregation was not independent of infection type segregation (Table 3) validating the involvement of Sr2.

**Table 3. Chi-square test of segregation independence between adult plant F<sub>2</sub> infection type and csSr2 marker.**

csSr2 marker	Adult plant QFCSC infection type	
	Susceptible/Intermediate	Resistant
+Marker	118	56
-Marker	60	11

$\chi^2 = 7.07^{**}$

**Fig 2. Stem rust infection response of Bill Brown and Gage Seedlings (left) and adult plant (right)**



**F<sub>2:3</sub> Seedling Reaction.** From total 238 F<sub>2:3</sub> families, 51 were resistant, 114 were heterogeneous and 74 were susceptible. This classification among families fits a single gene model. Seedling infection phenotype segregated independently from csSr2 marker phenotype (Table 4) suggesting the seedling resistance is not from Sr2.

**Table 4. Chi-square test of segregation independence between F<sub>2:3</sub> seedling infection & csSr2 marker**

csSr2 marker	Seedling QFCSC infection		
	Resistant	Heterogeneous	Susceptible
+Marker	36	80	51
-Marker	15	34	22

$\chi^2 = 0.0075$  (ns)

F<sub>2</sub> plants expressing adult plant resistant phenotypes gave rise to F<sub>2:3</sub> families with resistant, heterogeneous, and susceptible seedling reactions, which indicates that separate genes adult plant and seedling genes are acting in the population. However, infection phenotype segregation from F<sub>2:3</sub> seedlings and from the corresponding F<sub>2</sub> adult plants are not independent which is an indication that stem rust seedling and adult plant resistance in Gage are linked (Table 5).

**Table 5. Chi-square test of segregation independence between F<sub>2:3</sub> seedlings & F<sub>2</sub> Adult plant infection**

F <sub>2</sub> Adult plant infection	F <sub>2:3</sub> Seedling QFCSC infection		
	Resistant	Heterogeneous	Susceptible
Resistant	15	74	9
Susc/intermediate	36	40	64

$\chi^2 = 11.93^{**}$

## Conclusions

- The study indicated that the stem rust resistance in Gage involves more than one gene.
- Seedling resistance in Gage is attributed to gene different from, but possibly linked to Sr<sub>2</sub>.
- From genetic marker analysis and infection response to several races, the gene/s involved are most likely different from known major stem rust genes such as *Sr6*, *Sr9a*, *SrWeb*, *Sr24*, *1RS*, *Sr26*, *Sr36*, *Sr42*, *Sr54* and *Lr19/Sr25*

## References

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