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# Inheritance of *Triticum militinae* Zhuk. derived leaf rust and stem rust resistance in common wheat

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**Abstract**

**The rust resistant hexaploid stocks, Selection (Sel.) T 2600 and Sel. T 216-1 derived from *T. aestivum* × *T. militinae* cross were analysed to study the mode of inheritance and to establish the identity of genes conditioning seedling resistance to the leaf rust pathotype 77-5 and stem rust pathotype 40-1. The genetic analysis of different filial generations *viz.*, $P_1$, $P_2$, $F_1$, $F_2$ and $BC_1$ $F_1$ of the crosses Agra Local × Sel. T 2600, Lal Bahadur × Sel. T 2600, Chinese Spring × Sel. T 2600, Agra Local × Sel. T 216-1, Kalyansona × Sel. T 216-1 and Chinese Spring × Sel. T 216-1 revealed that the resistance to leaf rust and stem rust was controlled by a single dominant gene. The test of allelism indicated that the gene governing leaf rust resistance in Sel. T 2600 was different from the known genes *Lr*19, *Lr*24 and *Lr*28 and that of Sel. T 216-1 from *Lr*9, *Lr*19 and *Lr*28. The gene for leaf rust resistance in Sel. T 2600 and Sel. T 216-1 was allelic to *Lr*9 and *Lr*24, respectively. The stem rust resistance present in Sel. T 216-1 was distinctly different than that of *Sr*24 and *Sr*26 as established through the test of allelism and the pattern of infection type.**

**Key words:** *Triticum militinae*, rust resistance, seedling test, inheritance, test of allelism

## Introduction

Wild progenitors of common wheat, *Triticum aestivum*, allied genera and related species constitute a vast reservoir of potentially useful genes for disease resistance, particularly rusts [1, 2]. Several useful genes have been transferred from these wild species to common wheat. Wild emmer and Timopheevi group of wheats have enormous genetic diversity with regards to many desirable characteristics. Amongst them, *T timopheevi* and its free threshing mutant *T. militinae* Zhuk. Et. Migush. (2n = 4x = 28, genome AAGG) holds great potential for disease resistance, particularly rusts and powdery mildew [3]. *T. militinae* was isolated as a spontaneous mutant from collection plots of *T. timopheevi* by Zhukovskyi [4]. Selections derved from an interspecific hybrid between *T. aestivum* and *T. militinae* exhibited high resistance to leaf and stem rust races prevailing in the Nilgiri region, Tamil Nadu India [5]. The present paper reports the mode of inheritance of resistance derived from *T. militinae* to leaf and stem rusts in selection Sel. T 2600 and Sel. T 216-1 of common wheat, and the identity of gene(s) in these selections in relation to other genetic stocks carrying different genes for resistance derived from alien sources.

## Materials and methods

The experimental material comprised of Sel. T 2600 and Sel. T 216-1, which were selected from the crosses C 306 / *T. militinae* //C 306 and Sonalika / *T. militinae* //Sonalika respectively, followed by five generations of selfing. Both the selections showed resistance of high degree to leaf rust (5MR) and to stem rust (10MRMS).

In order to study the inheritance pattern of *T. militinae* derived stem rust and leaf rust resistance, the wheat cultivars *viz.*, Agra Local (AL), Kalyansona (KS), Chinese Spring (CS) and Lal Bahadur (LB) were used as one of the rust susceptible parents. The near-isogenic lines (NILs) and stocks carrying known genes in use as differentials in India for pathotype analysis of leaf rust pathogen, *Puccinia recondita* f sp. *tritici* [6] and stem rust pathogen, *P. graminis* f sp. *tritici* [7] were considered in the present study. The initial inoculum of different pathotypes, 77-5 of leaf rust pathogen and 40-1 of stem rust pathogen was obtained from DWR, Regional Station, Flowerdale, Shimla and the same was used for genetic analysis of resistance gene(s) in Sel. T 2600 and Sel. T 216-1. Both Sel. T 2600 and Sel. T 216-1 were crossed to rust susceptible genotypes mentioned above. The resistant genotypes were also crossed with NILs carrying specific gene, *Lr*9, *Lr*19, *Lr*24 and *Lr*28 for leaf rust resistance and *Sr*24, *Sr*25 and *Sr*26 for stem rust resistance to test the identity of gene(s). The $F_1$, $F_2$ and $BC_1$ $F_1$ generations of the crosses along with parents were tested with pathotypes 77-5 of *P. recondita* and 40-1 of *P. graminis tritici*, while only $F_2$ generation of the crosses involving NILs were tested with above mentioned pathotypes at seedling stage. Seedling tests were conducted in glass house at mean temperature ranging

**Table 1.** Infection types (ITs) of selected pathotypes of *Puccinia recondita* and *P. graminis.* f sp. *tritici* on Sel. T 2600, Sel. T 216-1 and different stocks at seedling stage

| Genotypes | Pathotypes | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Leaf rust | | | | | | | | Stem rust | | | | | | |
| | 12A | 12-1 | 12-2 | 77-2 | 77-5 | 77-6 | 104-2 | 106 | 11 | 40 | 40A | 40-1 | 117A | 117-3 | 117-6 |
| Sel. T 2600 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | ;1 | ;1+ | ;1 | ;1+ | ;1 | ;1 | ;1 |
| *T. militinae* | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0; | ; | 0 | ; | ; | ; |
| C 306 | 3+ | 3+ | 33+ | 3+ | 3+ | 3+ | 33+ | 3+ | 3+ | 3+ | 4 | 33+ | 3+ | 33+ | 3+ |
| Agra local | 3+ | 3+ | 33+ | 3+ | 3+ | 3+ | 33+ | 3+ | 3+ | 3+ | 4 | 33+ | 3+ | 33+ | 4 |
| Lal Bahadur | 3+ | 3+ | 33+ | 3+ | 3+ | 3+ | 3+ | 3+ | 3+ | 3+ | 3+ | 4 | 3+ | 4 | 33+ |
| Sel. T 216-1 | - | - | ; | ;1 | ;1N | ;1 | ;1 | - | - | ;1 | ;1+ | ;1 | - | - | ; |
| Sonalika | ;12+ | X+ | X+ | 3+ | 3+ | 3+ | X+ | - | ;1 | 3+ | 4 | 3+ | ;12+ | - | - |
| Chinese spring | 33+ | 3+ | 33+ | 3+ | 3+ | 3+ | 33+ | - | 3+ | 3+ | 3+ | 3+ | 33+ | 4 | 3+ |
| Kalyansona | | | 3+ | 3+ | 3+ | 3+ | 33+ | - | | 3+ | 3+ | 33+ | 3+ | - | 3+ |
| Sunstar*6/C80-1 | 0; | ; | ; | 0; | ; | ; | ; | 0 | - | ;1 | ;1 | ;1+ | ; | ;1 | ;1 |
| HW 2051 | 0 | 0 | 0; | 0; | 0 | 0 | 0 | 0 | - | 3+ | 3+ | 3+ | ;1 | ;1 | - |
| HW 2033 | ; | 0 | 0 | ; | 0 | ; | 0 | 0 | 3+ | 3+ | 3+ | ;12 | 3+ | 3+ | - |
| Agent | ;N | ;1 | ;1 | ;1N | ;1-N | ; | ;1+ | ; | ; | 0 | ; | 3+ | ; | ; | ;1 |
| DARF | ; | ;1 | ;1 | ; | ;+ | ; | ;1 | ; | ;1 | 0 | ; | ;1+ | ;1 | ;1 | ; |

- = not tested

from 12°C to 30°C. Ten seeds were sown in each of ten rows in rectangular trays (27 × 10 × 7.5 cm) filled with soil. A week old seedlings were inoculated with uredospores of 77-5 and 40-1 according to the procedure described by Joshi *et al.* [8] and incubated in humidity chambers for 48h. Thereafter trays were shifted to the benches in glass house. Rust reactions were recorded according to the scale described by Stakman *et al.* [9] after ten days of inoculation. Seedlings were categorised on the basis of reaction pattern ';' to '2' as resistant (R) and '3' to '4' as susceptible (S). The chi-square ($\chi^2$) test was used to establish validity of expected ratios in segregating generations.

## Results and discussion

The results obtained in seedling tests on parental lines, $F_1$, $F_2$ and $BC_1$ $F_1$ generations are presented in Tables 1-4. The genetic analysis on resistance to leaf rust and stem rust is presented separately.

### Leaf rust resistance

Genetic analysis on resistance in Sel. T 2600 to leaf rust pathotype 77-5 was carried out based on three crosses each involving a different susceptible parent *viz.*, Agra Local, Lal Bahadur and Chinese Spring (Table 2). The resistant reaction in all $F_1$ plants tested and segregation of $F_2$ population into 3 resistant : 1 susceptible ratio in the cross Agra Local × Sel. T 2600 indicated the monogenic nature of resistance. The $BC_1$ $F_1$ progenies segregated into 1R : 1S ratio with good fit, which further validated the hypothesis. The same trend was observed in $F_1$, $F_2$ and $BC_1$ $F_1$ generations of the other two crosses Lal Bahadur × Sel. T 2600 and Chinese Spring × Sel. T 2600 indicating monogenic dominant control for leaf rust resistance in Sel. T 2600. These results indicated that the parents in each cross differed at only one locus governing the resistance to the pathotype of *Puccinia recondita.*

Similarly, the genetics of resistance to leaf rust in Sel. T 216-1 was determined in the crosses, *viz.*, Agra Local × Sel. T 216-1, Kalyansona × Sel. T 216-1 and Chinese Spring × Sel. T 216-1 (Table 2). The $F_1$, $F_2$ and $BC_1$ $F_1$ generations derived from the above mentioned crosses showed concordant segregation pattern across the crosses. The observations, where all $F_1$ plants with resistance indicated dominant nature of resistance and segregation in $F_2$ population with good fit to the expected ratio of 3R : 1S revealed monogenic control for resistance. Further segregation in $BC_1$ $F_1$ progenies fitting well to the expected 1R : 1S ratio again confirming the dominant monogenic control for resistance to 77-5 pathotype of leaf rust in Sel. T 216-1. Studies of similar nature on wheat × *T. militinae* derivatives have earlier been conducted [10-12] and single dominant gene imparting resistance to leaf rust pathotypes was reported. However, the plant material as well as the type of races of *Puccinia recondita* used were different in their studies.

### Stem rust resistance

Both *T. militinae* derivatives, Sel. T 2600 and Sel. T 216-1 showed resistance to 40-1 pathotype of *Puccinia graminis tritici.* Genetic analysis was, therefore, carried out to find out the nature of inheritance and number of genes governing. resistance to this particular pathotype 40-1 of stem rust. Table 3 indicate that all the $F_1$ plants of the crosses, Agra Local × Sel. T 2600, Lal Bahadur × Sel. T 2600 and Chinese Spring × Sel.

T 2600 showed resistant reaction in seedling stage indicating that the resistance to stem rust pathotype 40-1 in Sel. T 2600 is controlled by the dominant gene(s). The $F_2$ population in all the crosses segregated in good fit ratio of 3R : 1S demonstrating that the resistance is monogenically controlled. In the progeny of crosses of all $F_1$ with susceptible parent(s), an expected segregation ratio of 1R : 1S with non-significant Chi-square value was observed. Considering all these observations recorded in $F_1$, $F_2$ and $BC_1$ $F_1$ generations it was confirmed that the resistance in Sel. T 2600 against stem rust pathotype 40-1 is determined by a single dominant gene.

In order to understand the inheritance of resistance in Sel. T 216-1 to stem rust pathotype 40-1, different generations derived from the crosses Agra Local × Sel. T 216-1, Kalyansona × Sel. T 216-1 and Chinese Spring Sel. × T 216-1 and the test crosses were analysed genetically. The $F_1$ plants in all the three crosses exhibited resistance revealing dominance nature of resistance. The segregation pattern in $F_2$ population fitted well to the expected ratio of 3R : 1S and the segregation in $BC_1$ $F_1$ progenies was also in agreement with the expected ratio of 1R : 1S. (Table 3). Based on the pattern of segregation in $F_2$ and $BC_1$ $F_1$ generations and the resistant reaction in $F_1$ plants it could be ascertained that the Sel. T 216-1 also carries a single dominant gene for resistance to 40-1 pathotype of stem rust. Most of the designated stem rust resistance genes in wheat are of dominant nature [13]. Sinha *et al.* [14] reported a similar genetic control for stem rust resistance in hexaploid derivatives of wheat × *T. militinae*.

**Inter-relationship among the rust resistant parents**

Both Sel. T 2600. involving C-306 and Sel. 216-1 having Sonalika in the pedigree, confer resistance to leaf rust pathotype 77-5 and stem rust pathotype 40-1. The $F_1$ plants of the cross Sel. T 2600 × Sel. 216-1 did not survive because of progressive hybrid necrosis genes $Ne_1$ and $Ne_2$, which are reported from the cultivar C 306 and Sonalika respectively [14]. However, the

**Table 2.** Segregation of seedlings in $F_2$ and $BC_1F_1$ generations of different crosses tested with the leaf rust pathotype 77-5

| Parents/crosses | Generation | Number of seedlings | | | Expected ratio | $\chi^2$ | P value |
|---|---|---|---|---|---|---|---|
| | | Resistant (IT : 0-2) | Susceptible (IT : 3-4) | Total | | | |
| Agra Local (AL) | $P_1$ | 0 | 26 | 26 | | | |
| Sel. T 2600 | $P_2$ | 31 | 0 | 31 | | | |
| AL / Sel. T 2600 | $F_1$ | 12 | 0 | 12 | | | |
| | $F_2$ | 181 | 51 | 232 | 3R: 1S | 1.126 | 0.50-0.25 |
| AL / Sel. T 2600 // AL | $BC_1$ $F_1$ | 15 | 11 | 26 | 1R : 1S | 0.615 | 0.50-0.25 |
| Lal Bahadur (LB) | $P_1$ | 0 | 25 | 25 | | | |
| Sel. T 2600 | $P_2$ | 28 | 0 | 28 | | | |
| LB / Sel. T 2600 | $F_1$ | 10 | 0 | 10 | | | |
| | $F_2$ | 176 | 59 | 235 | 3R: 1S | 0.001 | 0.95-0.90 |
| LB / Sel. T 2600 // LB | $BC_1$ $F_1$ | 20 | 15 | 35 | 1R : 1S | 0.714 | 0.50-0.25 |
| Chinese Spring (CS) | $P_1$ | 0 | 21 | 21 | | | |
| Sel. T 2600 | $P_2$ | 17 | 0 | 17 | | | |
| CS / Sel. T 2600 | $F_1$ | 12 | 0 | 12 | | | |
| | $F_2$ | 86 | 33 | 119 | 3R: 1S | 0.473 | 0.50-0.25 |
| CS / Sel. T 2600 // CS | $BC_1$ $F_1$ | 14 | 17 | 31 | 1R : 1S | 0.290 | 0.75-0.50 |
| AL | $P_1$ | 0 | 17 | 17 | | | |
| Sel. T 216-1 | $P_2$ | 22 | 0 | 22 | | | |
| AL / Sel. T 216-1 | $F_1$ | 10 | 0 | 10 | | | |
| | $F_2$ | 85 | 22 | 107 | 3R : 1S | 1.125 | 0.50-0.25 |
| AL / Sel. T 216-1 // AL | $BC_1$ $F_1$ | 20 | 13 | 33 | 1R : 1S | 1.485 | 0.25-0.10 |
| Kalyansona (KS) | $P_1$ | 0 | 8 | 8 | | | |
| Sel. T 216-1 | $P_2$ | 11 | 0 | 11 | | | |
| KS / Sel. T 216-1 | $F_1$ | 7 | 0 | 7 | | | |
| | $F_2$ | 1 | 8 | 39 | 3R : 1S | 0.419 | 0.75-0.50 |
| KS / Sel. T 216-1 // KS | $BC_1$ $F_1$ | 15 | 21 | 36 | 1R : 1S | 1.000 | 0.50-0.25 |
| CS | $P_1$ | 0 | 16 | 16 | | | |
| Sel. T 216-1 | $P_2$ | 19 | 0 | 19 | | | |
| CS / Sel. T 216-1 | $F_1$ | 10 | 0 | 10 | | | |
| | $F_2$ | 52 | 23 | 75 | 3R : 1S | 1.284 | 0.50-0.25 |
| CS / Sel. T 216-1 // CS | $BC_1$ $F_1$ | 24 | 17 | 41 | 1R : 1S | 1.195 | 0.50-0.25 |

**Table 3.** $F_2$ and $BC_1F_1$ segregation for resistance in Sel. T 2600 and Sel. T 216-1 to stem rust pathotype 40-1 at seedling stage

| Parent/Cross | Generation | Number of seedlings | | | Expected ratio | $\chi^2$ | P-value |
|---|---|---|---|---|---|---|---|
| | | Resistant (IT : 0-2) | Susceptible (IT : 3-4) | Total | | | |
| Agra Local (AL) | $P_1$ | 0 | 21 | 21 | | | |
| Sel. T 2600 | $P_2$ | 31 | 0 | 31 | | | |
| AL / Sel. T 2600 | $F_1$ | 9 | 0 | 9 | | | |
| | $F_2$ | 66 | 16 | 82 | 3R : 1S | 1.317 | 0.50-0.25 |
| AL / Sel. T 2600 // AL | $BC_1F_1$ | 21 | 16 | 37 | 3R : 1S | 0.675 | 0.50-0.25 |
| Lal Bahadur (LB) | $P_1$ | 0 | 23 | 23 | | | |
| Sel. T 2600 | $P_2$ | 26 | 0 | 26 | | | |
| LB / Sel. T 2600 | $F_1$ | 10 | 0 | 10 | | | |
| | $F_2$ | 110 | 30 | 140 | 3R : 1S | 0.952 | 0.50-0.25 |
| LB / Sel. T 2600 // LB | $BC_1F_1$ | 20 | 14 | 34 | 1R : 1S | 1.059 | 0.50-0.25 |
| Chinese Spring (CS) | $P_1$ | 18 | 0 | 18 | | | |
| CS / Sel. T 2600 | $F_1$ | 18 | 0 | 18 | | | |
| | $F_2$ | 69 | 26 | 95 | 3R : 1S | 0.284 | 0.75-0.50 |
| CS / Sel. T 2600 // CS | $BC_1F_1$ | 12 | 17 | 29 | 1R : 1S | 0.862 | 0.50-0.25 |
| AL | $P_1$ | 0 | 19 | 19 | | | |
| Sel. T 216-1 | $P_2$ | 11 | 0 | 11 | | | |
| AL / Sel. T 216-1 | $F_1$ | 7 | 0 | 7 | | | |
| | $F_2$ | 26 | 5 | 31 | 3R : 1S | 1.831 | 0.25-0.10 |
| AL / Sel / T 216-1 // AL | $BC_1F_1$ | 16 | 22 | 38 | 1R : 1S | 0.947 | 0.50-0.25 |
| Kalyansona (KS) | $P_1$ | 0 | 15 | 15 | | | |
| Sel. T 216-1 | $P_2$ | 12 | 0 | 12 | | | |
| KS / Sel. T 216-1 | $F_1$ | 9 | 0 | 9 | | | |
| | $F_2$ | 26 | 5 | 31 | 3R : 1S | 1.830 | 0.25-0.10 |
| KS / Sel. T 216-1 // KS | $BC_1F_1$ | 20 | 17 | 37 | 1R : 1S | 0.243 | 0.75-0.50 |
| CS | $P_1$ | 0 | 14 | 14 | | | |
| Sel. T 216-1 | $P_2$ | 18 | 0 | 18 | | | |
| CS / Sel. T 216-1 | $F_1$ | 13 | 0 | 13 | | | |
| | $F_2$ | 48 | 20 | 68 | 3R : 1S | 0.706 | 0.50-0.25 |
| CS / Sel. T 216-1 // CS | $BC_1$ $F_1$ | 17 | 14 | 31 | 1R : 1S | 0.290 | 0.75-0.50 |

infection types on Sel. T 2600 and Sel. 216-1 (Table 1) to selected pathotypes of leaf rust were different. Although both these belong to resistant category, the differential reaction pattern provides an indication of genetic diversity among the derivatives.

*Test of allelism*: The segregation frequency in $F_2$ population of the crosses Sunstar*6 / C80-1 (*Lr*19) // Sel. T 2600, Agent (*Lr*24) × Sel, T 2600 and HW 2033 (*Lr*28) × Sel. T 2600 had good fit to the expected ratio of 15R : 1S. The appearance of susceptible plants and segregation in $F_2$ into 15R : 1S ratio confirmed that the leaf rust resistance identified in Sel. T 2600 is conferred by genes different than *Lr*19, *Lr*24 and *Lr*28. However, absence of susceptible seedlings in $F_2$ plants from the cross HW 2051 (*Lr*9) × Sel. T 2600 demonstrate that the resistance gene in Sel. T 2600 is allelic to *Lr*9 present in HW 2051. The gene *Lr*9 is derived from *Aegilops umbellulata* (2n = 2x = 14, genome UU), while the resistance identified in Sel. T 2600 is transferred from *T. militinae* (2n = 4x = 28, genome AAGG), the possibility of both genes being identical is less. Although Enno *et al.* [12] reported that the resistance derived from *T. militinae* and *T. timopheevi* was identical with that of imparted by *Lr*23 from emmer wheat. Testing of Sel. T 2600 with recently identified virulence, which has knocked down *Lr*23, *Lr*26 and *Lr*9 genes will help in establishing the correct identity of resistance in present stock. Techniques like chromosome banding, in situ hybridization or the use of molecular markers specific to *Lr*9 gene can help establishing the correct identity of the gene.

The $F_2$ population of the crosses HW 2051 (*Lr*9) × Sel. T 216-1, Sunstar*6 / C80-1 (*Lr*9) × Sel. T 216-1 and HW 2033 (*Lr*28) × Sel. T 216-1 segregated into expected ratio of 15R : 1S indicating that the leaf rust resistance gene possessed by Sel. T 216-1 is different from *Lr*9, *Lr*19 and *Lr*28. However, all 80 $F_2$ plants from Agent (*Lr*24) × Sel. T 216-1 showed resistance. The identity of resistance in Sel. T 216-1

**Table 4.** Segregation pattern in $F_2$ in the crosses of resistant parents to leaf rust and stem rust pathotypes 77-5 and 40-1, respectively

| Cross | Number of seedlings | | | Expected ratio | $\chi^2$ | P-value |
|---|---|---|---|---|---|---|
| | Resistant (IT : 0-2) | Susceptible (IT : 3-4) | Total | | | |
| Seedling test with leaf rust pathotype 77-5 | | | | | | |
| HW 2051 (*Lr*19) // Sel. T 2600 | 161 | 0 | 161 | 15R : 1S | 10.733 | < 0.01 |
| Sunstar*6 / C80-1 (*Lr*19) // Sel. T 2600 | 90 | 7 | 97 | 15R : 1S | 0.155 | 0.75-0.50 |
| Agent (*Lr*24) / Sel. T 2600 | 77 | 6 | 83 | 15R : 1S | 0.136 | 0.75-0.50 |
| HW 2033 (*Lr*28) / Sel. T 216-1 | 77 | 4 | 81 | 15R : 1S | 0.297 | 0.75-0.50 |
| HW 2051(*Lr*9) / Sel. T 216-1 | 84 | 7 | 91 | 15R : 1S | 0.323 | 0.75-0.50 |
| Sunstar*6 / C80-1 (*Lr*19) // Sel. T 216-1 | 61 | 6 | 67 | 15R : 1S | 0.837 | 0.50-0.25 |
| Agent (*Lr*24) / Sel. T 216-1 | 73 | 0 | 73 | 15R : 1S | 4.867 | < 0.01 |
| HW 2033 (*Lr*28) / Sel. T 216-1 | 75 | 7 | 82 | 15R : 1S | 0.732 | 0.50-0.25 |
| Seedling test with stem rust pathotype 40-1 | | | | | | |
| Agent (*Sr*24) | 0 | 10 | 10 | | | |
| Agent/Sel. T 216-1 | 60 | 23 | 83 | 3R : 1S | 0.325 | 0.75-0.50 |
| DARF (*Lr*24,*Sr*24,*Sr*26) / Sel. T 216-1 | 93 | 8 | 101 | 15R : 1S | 0.481 | 0.50-0.25 |

could be established based on the source of resistance as *Lr*24 has been introgressed from *Agropyron elongatum* [15].

*Diversity for stem rust resistance in Sel. T 2600 and Sel. T 216-1*: Reference to Table 1 reveals that both Sel. T 2600 and Sel. T 216-1 exhibited resistance to five stem rust pathotypes. However, the infection types recorded in both these genotypes were different indicating genetic diversity among the derivatives. The $F_2$ population from the cross Agent (*Sr*24) × Sel. T 216-1 was subjected to seedling test with stem rust pathotype 40-1. The plants in $F_2$ generation segregated in a ratio of 3 resistant : 1 susceptible emanating that gene(s) present in both the parents are not identical. The gene *Sr*24 has been reported ineffective [16] against stem rust pathotype 40-1 (62G29-1). The resistant reaction exhibited by Sel. T 216-1 and segregation in $F_2$ population of the cross Agent (*Sr*24) × Sel. T 216-1 suggest that Sel. T 216-1 carry a stem rust resistance gene different than *Sr*24. The Sel. T 216-1 was also crossed with DARF carrying rust resistance gene *Sr*26 from *Agropyron elongatum*. The $F_2$ population segregated into 15R : 1S ratio revealing that the resistance gene present in Sel. T 216-1 is different than that of *Sr*26. Besides, Sel. T 216-1 exhibited resistance to selected pathotypes of stem rust, *viz.*, 11, 40-1, 40A, 17-6 and 122. None of the wheat genes except those originated from allied and alien species showed resistance to all those above mentioned pathotypes [17-20].

The results of the present investigation showed that the resistance in Sel. T 2600 and Sel. T 216-1 to leaf rust pathotype 77-5 and stem rust pathotype 40-1 were imparted by an independent gene. The tetraploid species, *T. militinae*, which shares one genome (AA) with *T. aestivum* and greater homology between B genome of *T. aestivum* and G genome of *T. militinae*, introduced additional genetic variability, which can be exploited in breeding for host plant resistance.

## Conclusions

From the breeders' perspective, this study opens up the hcoice of diverse material for utilization in wheat improvement, particularly, for rust resistance. The study has also revealed that allied species *Triticum malitinae* is a potential donor for stem rust and leaf rust resistance genes. Genetic analysis and location of leaf rust and stem rust resistance gene(s) on chromosomes 6B and 1B respectively would stimulate interest in conventional breeding programmes. Partial genomic affinities between the B genome of wheat (*T. aestivum*) and G genome of *T. militinae* have been observed by earlier workers also [12, 21]. It is presumed that chromosome of B/G genomes are frequently involved in spontaneous translocations and have acquired natural polymorphism for translocations. The involvement of 1B/1G is also evident from the morphology as the colour of glumes in sel. T 2600 is black, which indeed is transferred from *T. militinae*. Similarly, the leaves of Sel. T 216-1 are pubescent like that of *T. militinae*. The study has illustrated that distant hybridization is an useful method for transferring desirable genes [22], which may be suitable for exploitation in wheat improvement and ultimately benefit the breeders.

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## References


1. **Dhaliwal H. S., Gill K. S. Singh P., Multani D. S. and Singh B.** 1986. Evaluation of germplasm of wild wheats and *Aegilops, Agropyron* for resistance to various diseases. Crop Improv. **13**: 107-112.
2. **Tomar S. M. S. and Kochumadhavan M.** 1996. Genetic resources for disease resistance in wild diploid *Triticum* and *Aegilops* species. Indian J. Pl. Genet. Resources, **9**: 53-61.
3. **Tomar S. M. S., Kochumadhavan M. and Nambisan P. N. N.** 1988. Evaluation of *Timopheevi* wheats for resistance to rusts and powdery mildew. Indian J. Genet., **48**: 69-73.
4. **Zhukovskyi P. M.** 1971. Cultivated plants and their wild relatives: Systematics, geography, cytogenetics, immunity, origin and use (In Russian). Kolos, Leningrad, p 121.
5. **Tomar S. M. S., Sinha V. C. and Menon M. K.** 1997. Transfer of leaf rust resistance from *Triticum militinae* to common wheat. *In*: Inter. Group Meet. On Wheat Research Needs Beyond 2000AD. (Abst.) DWR, Karnal India
6. **Nagarajan S., Nayar S. K. and Bahadur P.** 1983. The proposed brown rust of wheat (*Puccinia recondita* f sp. *tritici*) virulence monitoring system. Curr. Sci., **52**: 413-416.
7. **Bahadur P., Nagarajan S. and Nayar S. K.** 1985. A proposed system of virulence designation in India. II. *Puccinia graminis* f sp. *tritici*. Proc. Indian Acad. Sci. (Plant Science), **95**: 29-33.
8. **Joshi L. M., Singh D. V. and Srivastava K. D.** 1988. Manual of Wheat Diseases. Malhotra Publishing House, New Delhi: pp 75.
9. **Stakman E. C., Stewart D. M. and Loegering W. Q.** 1962. Identification of physiological races of *Puccinia graminis* var. *tritici*. USDA, Agric. Res. Serv. E617 (Rev.): pp 53.
10. **Sibikeev S. N., Sibikeeva-Yu-Ye and Yelesin V. A.** 1994. Study of four hybrids of common wheat and *Aegilops speltoides* Tausch. and *T. militinae* Zhuk., Russian Agriculture Sciences, **9**: 14.
11. **Peusha H., Enno T. and Priilinn O.** 1996. Gnetic analysis of disease resistance in wheat hybrids, derivatives of *Triticum timopheevi* and *Triticum militinae*. Acta Agronomica Hungarica, **44**: 237-244.
12. **Enno T., Peusha H., Timofeyeya L. Tohver M., Yakovson I. and Priilinn O.** 1998. Identification of chromosomal translocations in common wheat, derivatives of *T. timopheevi*. Acta Agronomica Hungarica, **46**: 209-216.
13. **McIntosh R. A., Hart G. E. and Gale M. D.** 1995. Catalogue of gene symbols for wheat. Proc. 8th Int. Wheat Genet. Symp., Beijing, China, pp. L333-1500.
14. **Sinha V. C., Tomar S. M. S. and Nanthakumar G.** 2001. Introgression of rust resistance from tetraploid wild species to common wheat. (Abst.) Diamond Jubilee Symp. Nov. 6-9, 2000, Indian Society of Genetics and Plant Breeding, New Delhi.
15. **McIntosh R. A., Dyck P. L. and Green G. J.** 1997. Inheritance of leaf and stem rust resistance in wheat cultivars Agent and Agatha. Aust. J. Agric. Res., **28**: 37-45.
16. **Bhardwaj S. C., Nayar S. K., Prashar M., Kumar J., Menon M. K. and Singh S. B.** 1990. A pathotype of *Puccinia graminis* f sp. *tritici* on *Sr*24 in India. Cereal Rusts and Powderv Mildew Bull., **18**: 35-37.
17. **Sawhney R. N. and Goel L. B.** 1981. Race specific interaction between wheat genotypes and Indian culture of stem rust. Theo. Appl. Genet., **60**: 161-166.
18. **Sharma J. B. and Singh D.** 2000. Assessment of Selection 212 - A wheat-rye recombinant line for resistance to leaf and stem rusts. Indian J. Genet., **60**: 5-14.
19. **Tomar S. M. S. and Menon M. K.** 2000. Evaluation of stem rust resistance genes in bread wheat and introgression of *Sr*26 into adapted cultivars. Proc. Int. Conf. on Integrated Plant Disease Management for sustainable Agriculture, Indian Phytopathological Society, New Delhi, pp. 650-653.
20. **Gandhikumar N., Bahadur P. and Ram Charan.** 2002. Effect of host genotypes and specific pathotypes of stem rust on *Sr*-genes in five bread wheats. Indian Phytopath., **55**: 438-443.
21. **Enno T. M., Peusha H., Jarve K., Tomofeyeva L., Tsimbalova E. and Priilinn O.** 1995. Introduction of genetic variation by means of interspecific hybridization. Proc. 9th EWAC Conference, pp. 65-67.
22. **Badaeva E. D., Badaeva N. S., Enno T. M., Zeller F. J. and Peusha H. O.** 1995. Chromosome substitution in progeny of hybrids *Triticum aestivum* × *Triticum timopheevi*, resistant to brown rust and powdery mildew. Russian J. Genet., **31**: 75-77.