

## POTENTIALLY NEW SOURCES OF GENES FOR RESISTANCE TO COMMON BUNT (*TILLETIA* spp.) IN WINTER WHEAT (*TRITICUM AESTIVUM* L.)

FRAGA ONCICĂ<sup>a</sup> and NICOLAE SĂULESCU<sup>b</sup>

<sup>a</sup>Agricultural Research & Development Station Simnic, 200721 Romania. E-mail: fragaoncica@yahoo.com

<sup>b</sup>National Agricultural Research & Development Institute, Department of Plant Breeding, Fundulea, 915200 Romania. E-mail: saulescu@incda-fundulea.ro

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Despite availability of efficient chemical control, common bunt, caused by *Tilletia laevis* Kühn and *Tilletia tritici* (Bjerk.) Wint., can produce important damages, especially in organic wheat production. Genetic resistance is the most efficient way of control, if pathogen's high ability to overcome resistance by new races can be counteracted by genetic diversity. Lines derived from crosses with related species or genera, bred at the National Agricultural Research & Development Institute Fundulea, were tested under artificial inoculation with bunt at the Agricultural Research & Development Station Simnic. Several bunt resistant lines were of special interest, because, their genealogy does not suggest presence of any previously known bunt resistance genes. Lines F96915G1-1, selected from a cross with WGRC 23 (a *Triticum monococcum* derivative) and three lines selected from cross F00628G, *Triticale*/wheat, are considered potentially new sources of bunt resistance and are recommended in breeding wheat for diversifying genetic basis of resistance.

*Key words:* Common bunt; Resistance; Wheat.

### INTRODUCTION

Common bunt of wheat, caused by *Tilletia laevis* Kühn and *Tilletia tritici* (Bjerk.) Wint., is one of the world's most destructive wheat diseases<sup>1</sup>. Despite availability of efficient chemical control, it can still cause important damages, when treatments are not applied, because of economic or ecologic reasons, or treatments are not correct. Organic farming, which prohibits the use of chemicals, might favor an increase of affected areas, especially because, according EU-regulation 2092/91, seed for organic farming must be produced without chemical treatments, year after year, increasing the risk of disease build-up<sup>2</sup>.

Genetic resistance is the most convenient way of controlling the disease, as it reduces both costs and environmental impact. However, bunt has been

known for its high ability to overcome resistance by new, more aggressive races, prompting continuous search for genetic diversity of resistance.

This paper presents semidwarf winter wheat lines, apparently not carrying previously known bunt resistance genes, and therefore representing potentially new sources of common bunt resistance.

### MATERIALS AND METHODS

To search for new sources of resistance, 26 winter wheat lines derived from crosses with related species or genera, bred at the National Agricultural Research & Development Institute (NARDI) Fundulea, and not previously selected for bunt resistance, were tested for two years (2005 and 2006) under artificial inoculation with bunt and Agricultural Research & Development Station Simnic. The crosses from which the tested lines were selected are presented in Table 1.

Table 1  
Genealogy of the tested lines

Cross	Genealogy
F00628G	Tcl191TR-1-1221Fu/ 2*wheat
F96915G	WGRC23 / DROPIA
F01097G	WGRC23 / DROPIA /Cadet
F01096G	WGRC23 / DROPIA // F96869G1-1
F01476G	Tcl191TR2-1010201 /236U1-101// Cadet
F01531G	Tcl92438T1-102/ Delabrad// wheat
F00310G	Tcl191TR2-1010201/Boema
F00626G	Tcl191TR-2-1111Fu/93042G2-1//wheat
F00634G	Tcl93024-3-1/92151G1-2// wheat
F01474G	Tcl191TR2-1010201/ 236U1-101// Cadet

Only lines identified as resistant in the first two years were additionally tested in 2007.

Inoculation was done by mixing and shaking common bunt teliospores with seeds in paper envelopes. Inoculation was done with spores from five sori for 100 grains. Inoculated seeds were planted on one meter long rows in three replications. Bunt inoculums represented mixtures of most aggressive common bunt races collected from the region.

At maturity, infected spikes (where at least one grain was replaced by bunt balls) were counted and expressed as percentage from total number of spikes.

## RESULTS

Along with confirming the efficiency of known bunt resistance genes *Bt5*, *Bt8*, *Bt10*, *Bt11*, *Bt12* and *Bt13*<sup>3</sup>, results of artificial inoculation tests identified several not related lines, with no infected spike (Table 2), when the percentage of infected spikes in susceptible checks varied between 47.9 and 64.3%.

Table 2

Results of testing under artificial inoculation with common bunt

Line	Infected spikes (%)			
	2005	2006	2007	Average
F00628G34-1	0	0	0	0
F00628G34-2	0	0	0	0
F96915G1	0	0	0	0
F00628G4-1	0	0.5	0	0.2
F00628G24-2	8.9	3.4	n.t.	6.1
F00628G30-1	8.2	6.7	n.t.	7.4
F01097G1-1	8.7	8.0	7.3	8
F00628G24-1	3.1	13.9	n.t.	8.5
F00628G12-2	6.9	11.7	n.t.	9.3
F01096G2-1	12.3	8.0	9.0	9.8

F01476G2-1	10.4	13.4	n.t.	11.9
F01531G2-1	16.1	9.0	n.t.	12.5
F00628G22-2	11.4	15.4	n.t.	13.4
F00628G22-1	13.5	13.5	n.t.	13.5
F00628G23-1	15.4	11.7	n.t.	13.5
F00310G1-1	12.2	14.7	n.t.	13.9
F01096G2-2	14.9	13.4	n.t.	14.1
F00628G12-1	11.2	21.2	n.t.	16.2
F00628G35-1	22.9	11.5	n.t.	17
F00628G20-1	26.0	19.6	n.t.	22.8
F00626GLF1	20.5	31.4	n.t.	25.9
F00634G2-21	27.7	24.4	n.t.	26
F00634G2-11	14.1	40.2	n.t.	27.1
F01474G1-1	29.2	28.5	n.t.	28.8
F00628G18-1	35.5	28.5	n.t.	32
F00628G13-1	37.7	27.0	n.t.	32.3
Susceptible check-Dropia	59.3	47.9	64.3	57.2

n.t. – not tested

The following lines, which confirmed high resistance during three years, were considered of special interest, because their genealogy does not suggest a possible presence of any of the previously known bunt resistance genes:

- F96915G1-1 selected from the cross WGRC 23/Dropia
- F00628G34-1, F00628G34-2 and F00628G4-1, all selected from a cross *Triticale* / 2\*wheat.

## DISCUSSION

Fifteen major resistance genes, effective against both dwarf and common bunt (*Bt1* through *Bt15*), have been identified, that follow the classic gene-for-gene system<sup>4</sup>. In addition, several highly resistant wheats, primarily land races originating from Eastern Turkey and Yugoslavia, were identified by screening thousands of bread wheat entries (*Triticum aestivum*) from around the world in the USDA National Small Grains Collections. They might represent new genes or gene combinations<sup>4</sup>.

Many of the known resistance genes have already been introduced in adapted semidwarf background, as part of a special program of breeding for bunt resistance<sup>3,5</sup>.

However, the search for new resistance sources continues to be necessary to provide more diversity for breeding programs.

Related species and genera have long been recognized as valuable sources of bunt resistance genes. Mamluk<sup>6</sup> presented data showing that *Triticum boeoticum*, *T. dicoccoides*, and *Aegilops* species represent excellent sources of resistance to common bunt. Babayants *et al.*<sup>7</sup> described several lines with bunt resistance derived from species of *Agropyron*, *Aegilops*, *Triticum erebuni*, *T. dicoccoides* etc. Rubiales *et al.*<sup>8</sup> showed that *H. chilense* accessions and hexaploid tritordeums were very resistant or immune to *Tilletia tritici*. He and Hughes<sup>9</sup> indicated the spelt wheat cultivars RL5407 and SK0263 as potentially new sources of bunt resistance.

Line F96915G1-1, was selected from a cross of the line WGRC23 (a breeding line obtained at Kansas State University Genetic Resource Center, from a cross involving *Triticum monococcum* accessions PI 266844 and PI 355520) with the cultivar Dropia (Figure 1). As Dropia is susceptible to bunt, it is probable that the bunt resistance gene in this line comes from the *T. monococcum* parents, and might be different from the already known genes.

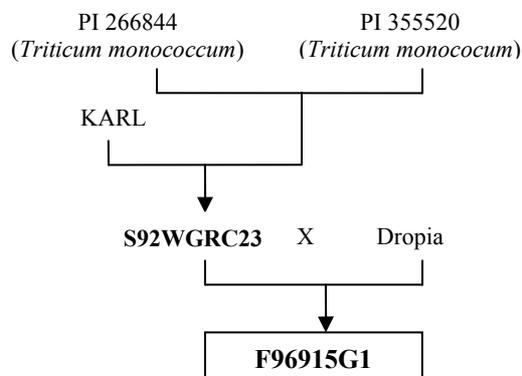


Fig. 1. Genealogy of line F96915G1.

Triticale was designated immune or highly resistant<sup>10, 11</sup>. Despite this, we do not know of any reported transfer of this resistance to wheat. The only indirect information comes from the work of Martinov *et al.*<sup>12</sup>, who, found that in the genealogies of Russian and Ukrainian cultivars in the northern region, the contributions of the wheat grass (*Agropyron glaucum*) and of the rye cultivar Eliseevskaya are significantly higher in the bunt resistant cultivars than in susceptible ones. On the other hand, by testing several cultivars carrying translocations from rye, Liatukas, and Ruzgas<sup>13</sup>

concluded that cultivars carrying complex translocation from *Secale cereale* did not possess effective resistance.

In our study, we identified three lines with excellent bunt resistance, F00628G34-1, F00628G34-2 and F00628G4-1, all selected from the same cross between a Triticale line and wheat (Fig. 2).

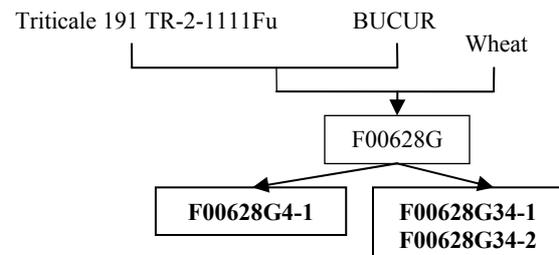


Fig. 2. Genealogy of cross F00628G.

Iuoraş *et al.*<sup>14</sup> found that the “universal marker” for rye chromatin<sup>15</sup> was present in several lines selected from the cross F00628G, and concluded that these lines carry rye translocation(s). On the other hand, these lines also have other traits (powdery mildew and *Septoria tritici* resistance), possibly inherited from rye. Therefore, it is possible that this line also inherited its bunt resistance from rye, although we cannot totally exclude a contamination with pollen from wheat carrying *Bt* resistance genes. Work is in progress for establishing the strength of association between bunt resistance and the presence of rye chromatin.

Further work is necessary to clearly establish the relationship of bunt resistance gene(s) present in these three lines with already known resistance genes. Nevertheless, data obtained so far indicate potential use of these lines in breeding programs and suggest that they could contribute to increased diversity of resistance.

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