



A wheat-rye translocation 1AL.1RS involved in wheat resistance to common bunt (preliminary results)

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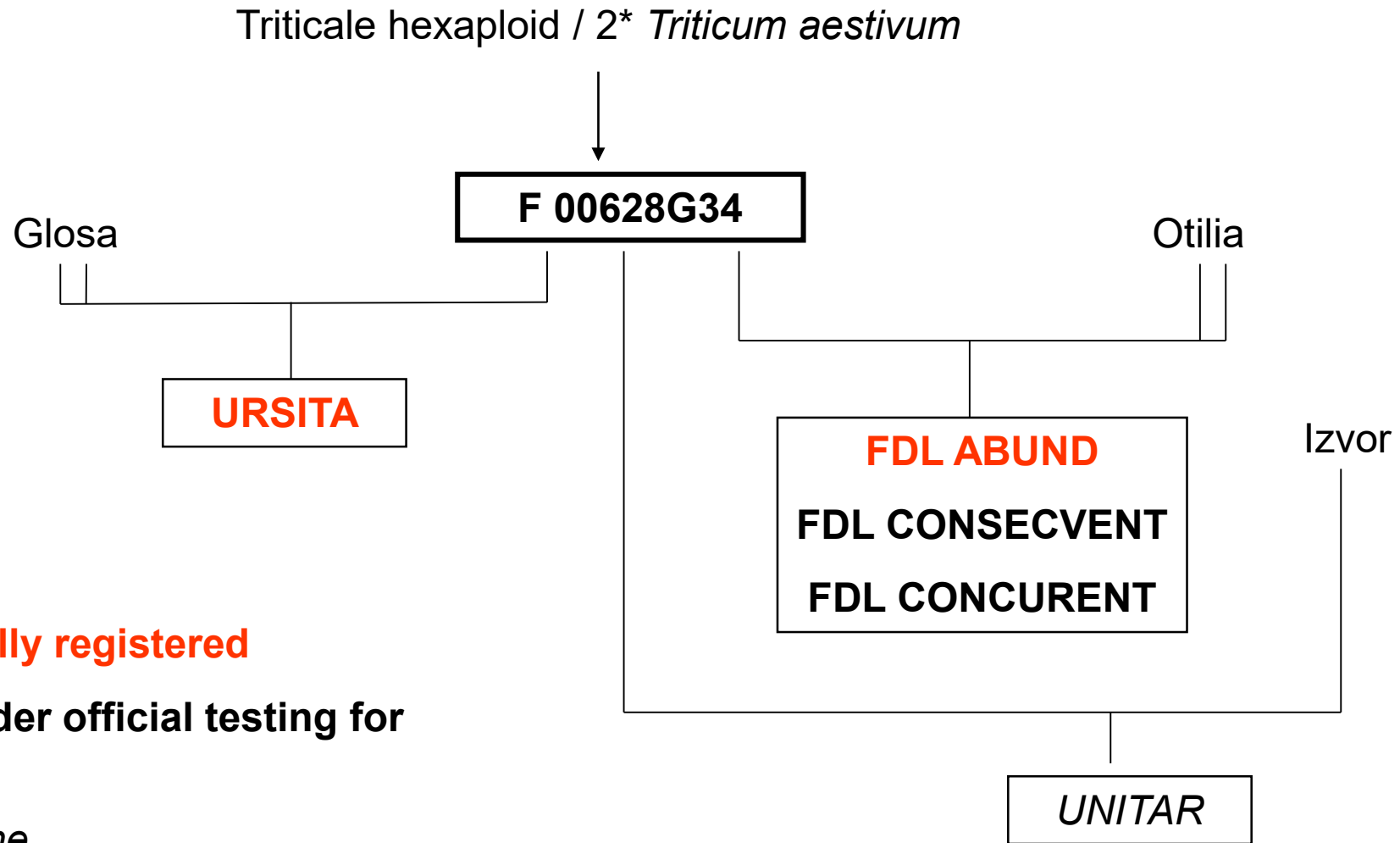


Common bunt - disease characteristics:

- In most of the cases, not all the plants with the susceptible genotypes are attacked, even if a good artificial infection is obtained;
- The level of bunt infection is strongly influenced by the autumn environmental conditions, which makes the heritability relatively low;
- The resistant genotypes are rarely completely immune. Different authors define as resistant the genotypes that are attacked at a level less than 5 to 10%;
- The existence of modifying genes can influence the infection level;
- Many of the resistance genes present a partial dominance.

The discovery of new sources of resistance to common bunt is an important task for researchers and breeders.

Winter wheat line-F00628G-34 with 1A:1R



Cultivars - officially registered

Wheat lines – under official testing for registration

Wheat breeding line

Previous studies

Results of testing bunt resistance of line F00628G34-1 in Romania and other European countries (in the European *Tilletia* Ring test) (Saulescu et al., 2011)

Location	Contributor	Year	<i>Tilletia</i> source	% bunted spikes	
				Susceptible check	F00628G
Ro, Fundulea	Ittu, M	2005	Mix of spores	45.4	0
Ro, Fundulea	Ittu, M	2007	Mix of spores	46.8	0
Ro, Fundulea	Ittu, M	2007	FUN	66.7	0
Ro, Fundulea	Ittu, M	2007	SIM	83.5	0
Ro, Fundulea	Ittu, M	2007	SUA	80.3	0
Ro, Fundulea	Ittu, M	2008	Mix of spores	59.9	0
Ro, Fundulea	Ittu, M	2009	Mix of spores	97.6	0
CH, Nyon	Mascher Frutschi, F.	2007	Mix-CH	83.7	2.7
CH, Nyon	Mascher Frutschi, F.	2007	Wilchingen-CH	90.9	0.5
G, Dottenfelderhof	Spieß, H.	2007	Local	48.6	0
A, Tulln	Buerstmayr, H.	2007	Mix-A	50.4	11.5
Denmark, Slagelse	Nielsen, B	2007	Mix-DK	24.8	1.5
UKR, Odessa	Babayants, O.	2007	Race T7	100.0	7.4
UKR	Babayants, O.	2007	Race T9	91.5	4.2
UKR	Babayants, O.	2007	Race T17	98.3	9.3
UKR	Babayants, O.	2007	Race T02	95.6	4.7
G, Darzau	Timmerman, M	2007	Mix-G	8.3	0
A, Tulln	Buerstmayr, H.	2008	Mix-A	64.0	0

RO – Romania, CH – Switzerland, DE (G)– Germany, AT (A) – Austria, UA (UKR)– Ukraine, DK – Denmark

Previous studies

In Kazakhstan (Southeastern part), an infection rate of 4,9% has been reported in line F00628G34, following artificial inoculation with a mixture of common bunt teliospores (Tagayev et al., 2018).

Name	Plant height, (cm)	Head Length (cm)	Spike number	Gr nr/sp.	Grain weight/sp.	TKW g	TotalGrain weight (g)	Bunted Ears (%)	Yield
F00628G34-1	80,7	10,0	18,0	80,0	3,1	38,7	24,1	4,9	3,53

Previous studies

The line F00628G34 was previously characterized as carrying rye chromatin - 1RS:1AL translocation, using hybridization techniques (GISH and FISH) at Research Institute of the Hungarian Academy of Sciences, Martonvásár, Hungary (Marta Molnar-Lang's Department) by Constantina Banica (personal communication, 2008).

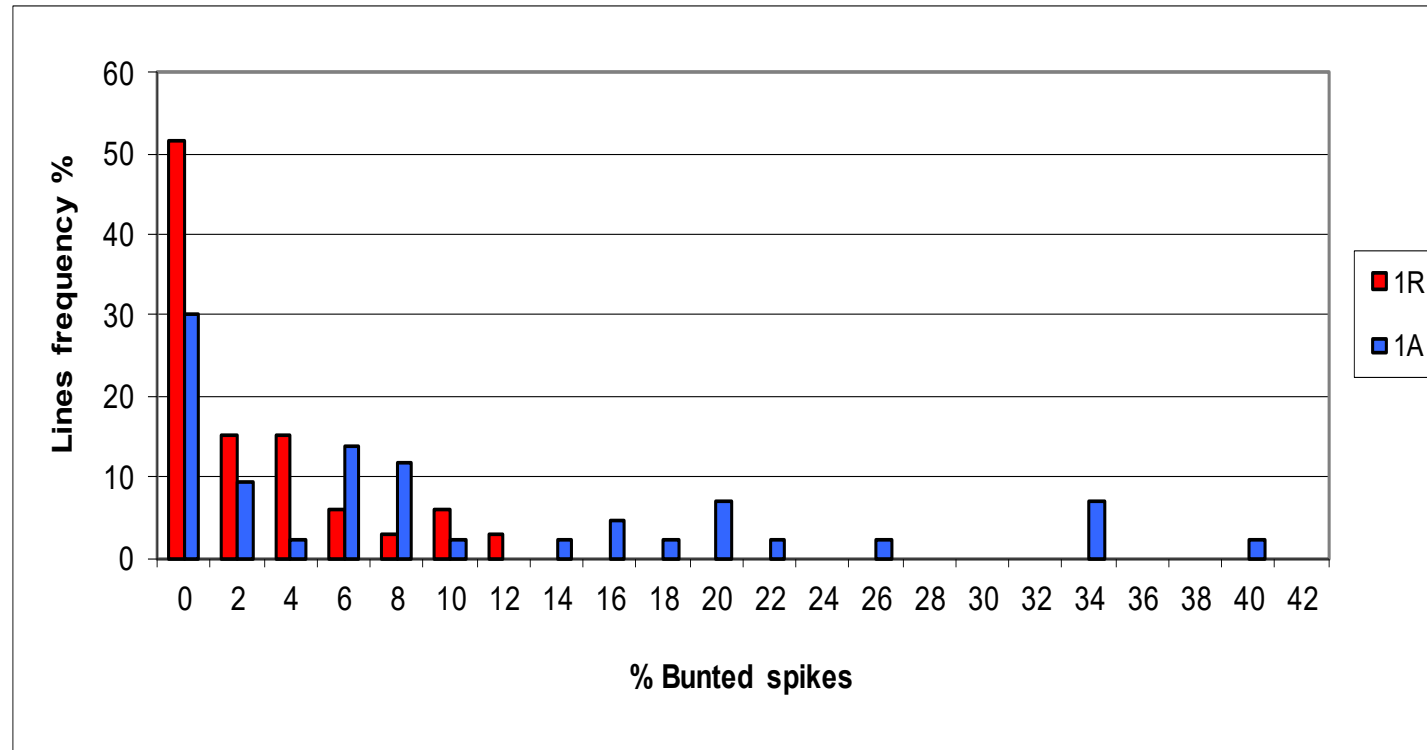
Study of 68 lines (F4 generation) randomly extracted from the cross Litera (susceptible parent) /F00628G34 showed 18 progenies lines non-bunted (0%) and 50 progenies lines differently degrees bunted (9-80%), while the susceptible parent, Litera expressed a 65% of attack. Also, partially bunted spikes and seeds were observed (NARDI Fundulea, 2010).

Molecular analysis with 21 specific markers for rye chromatin including: F3/R3, SCM9, STS-IAG95, *Sec-1* and GWM1223 showed the presence of 1RS:1AL translocation.

The bunt resistance identified in the F00628G34 line was associated with the presence of rye chromatin.

Current studies

Rye-wheat translocation (1RS:1AL) and percent of *Tilletia* sp. infection (Fundulea, 2022)



76 DH lines (F00628/Izvor) (Aurel Giura protocol (2011))

- lines with 1RS:1AL translocation - 0-11% spikes bunted (average 3,18);
- The presence of 1RS:1AL translocation was highlighted using molecular markers: SCM9, TSM106, TSM592 and GWM1223.
- lines without rye chromatin - 40% (average 9,28).

- F00628 ~7%;
- Izvor ~53%;
- Doina ~30-87%.

ONGOING STUDIES

RGA markers:

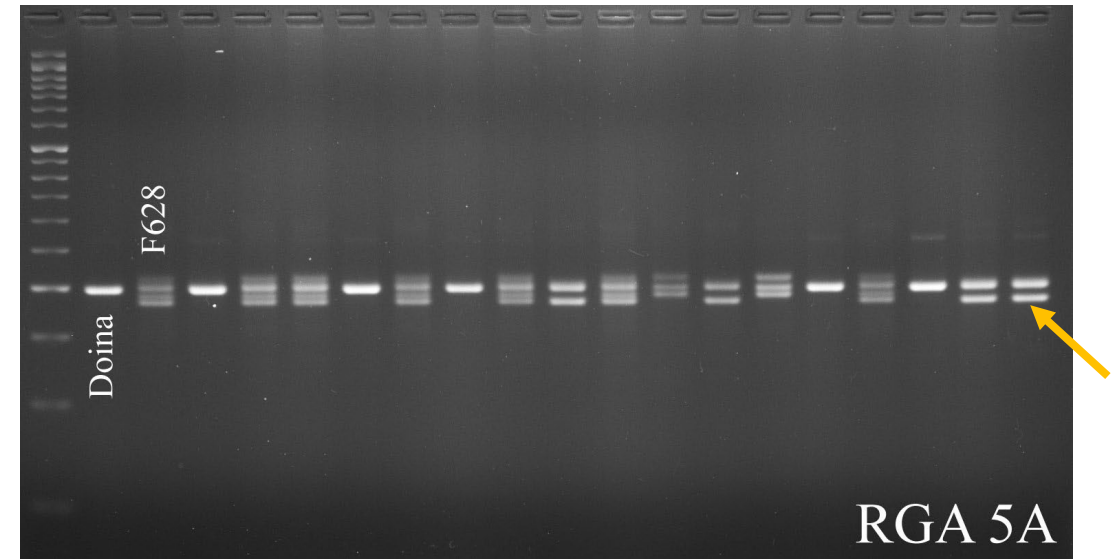
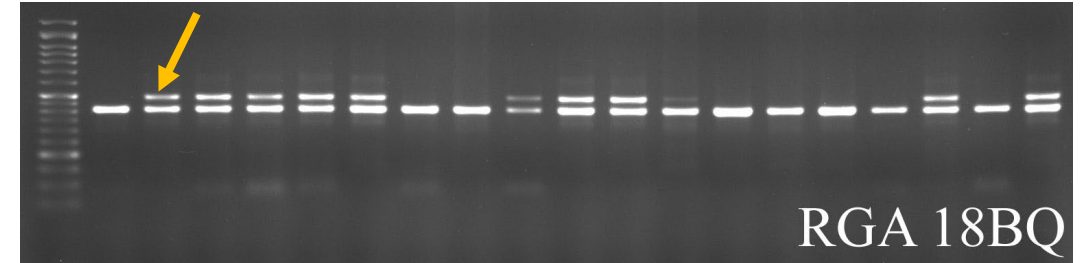
(1) Resistance gene analog-expressed sequence tag (RGA-EST)-based markers for NBS regions of wheat sequences of the NBS-LRR class (Karakas et al., 2011):

- RGA 18BQ (18-BQ579469)- PCR product ~ 500bp

(2) Markers targeting intron length polymorphism of resistance gene analogues (RGA-ILP) (Shang et al., 2010):

- RGA5a – EST accession-TC193589 and putative function-Receptor-like kinase Xa21- binding protein 3.
- amplified more than one orthologous or paralogous loci (Shang et al., 2010)
- PCR product ~183bp

Could be RGA5a_183bp allele the rye resistance allele to common bunt?



Alleles	No. samples	Average rate of infection
1R+RGA5a_183	31	2%
1R	3	4%
wheat	45	11%



Conclusions:

- The line F00628G34 could be a new source in breeding for resistance to common bunt;
- The 1A-1R translocation carries a bunt resistance gene, yet unnamed (should it be named?);
- Being associated with a convenient molecular marker, the 1A-1R bunt resistance gene can be easily combined with other known *Bt* resistance genes, to improve the level and durability of resistance to common bunt;
- The bunt resistance associated with 1A-1R translocation does not seem to involve any yield penalty, as suggested by the two recently released cultivars, being among the highest yielders.

Question:

Could the bunt resistance of the 1A-1R carrier cultivars be related with their allelopathic capacity i.e. could the allelopathic compounds reduce/stop the germination of *Tilletia* spores?

Acknowledgments

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Thank you for your attention!

