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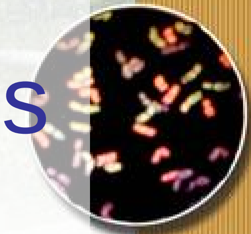

New Sources of Resistance to Fusarium Head Blight and Indicators of Their Mode of Action

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120 BC2F3 entries x 3 reps – Ottawa ON

Greenhouse misting

Cabinet misting system

Outline

Fusarium head blight resistance from wide crosses

- Hexaploid wheat
  - *Tritium monococcum*
  - *Aegilops speltoides*
  - *Triticum timopheevi*
  - *Triticum miguschovae*
  - *Aegilops cylindrica*
- Tetraploid wheat
  - *Tritordeum*
  - *Triticum carthlicum*
- Triticale

Thinopyrum elongatum

- GFP studies
- Microarray analysis

- Accession PI343447 crossed & backcrossed to Crocus.

- 535 plants advanced to F7 by SSD.

- TC67 selected.

- Mapping population of 230 F7 RIL lines produced from TC67 X Brio cross

Spikes of a *T. timopheevi* derivative at 21 days after point inoculation

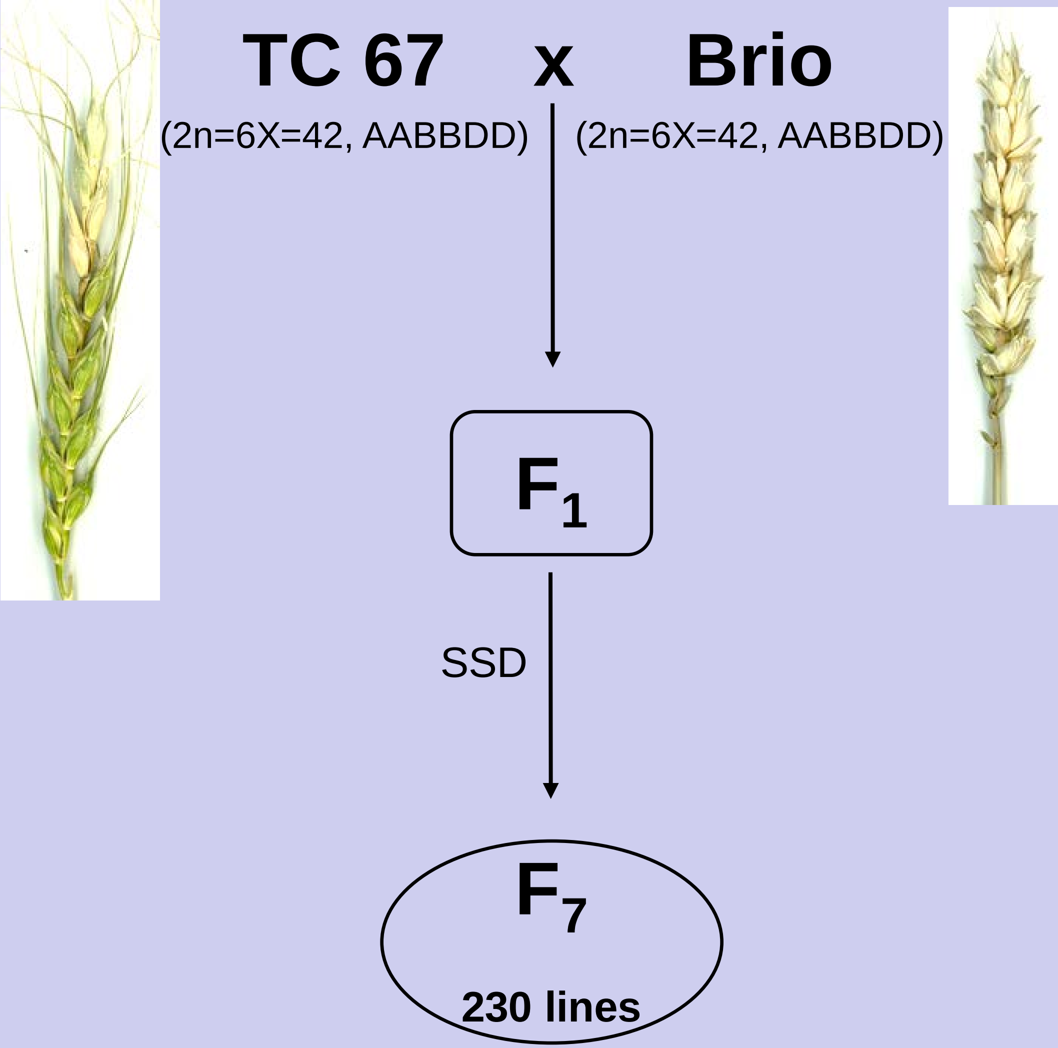
FHB symptoms on TC67(*T. timopheevi* derivative) and check cultivars(2 year data)

Line	Incidence	Severity	FDK(%)	DON (ppm)
Sumai3	14.8	6.3	9.5	6.6
Hy644	42.6	20.0	35.1	25.3
Roblin	90.7	81.9	66.1	35.0
TC67	29.4	16.9	14.5	7.7

A QTL on 5A Chromosome in TC 67

Materials and Methods

Development of plant materials



TC 67 x **Brio**

(2n=6X=42, AABBDD) (2n=6X=42, AABBDD)

F_1

SSD

F_7

230 lines

Materials and Methods

Field evaluation

- **To detect resistance to:**

- initial infection (type I)
- disease spread (type II)
- DON accumulation (type III)
- FDK (type IV)

- Spray inoculation was used

- Disease incidence, severity, index, DON accumulation, and FDK were measured

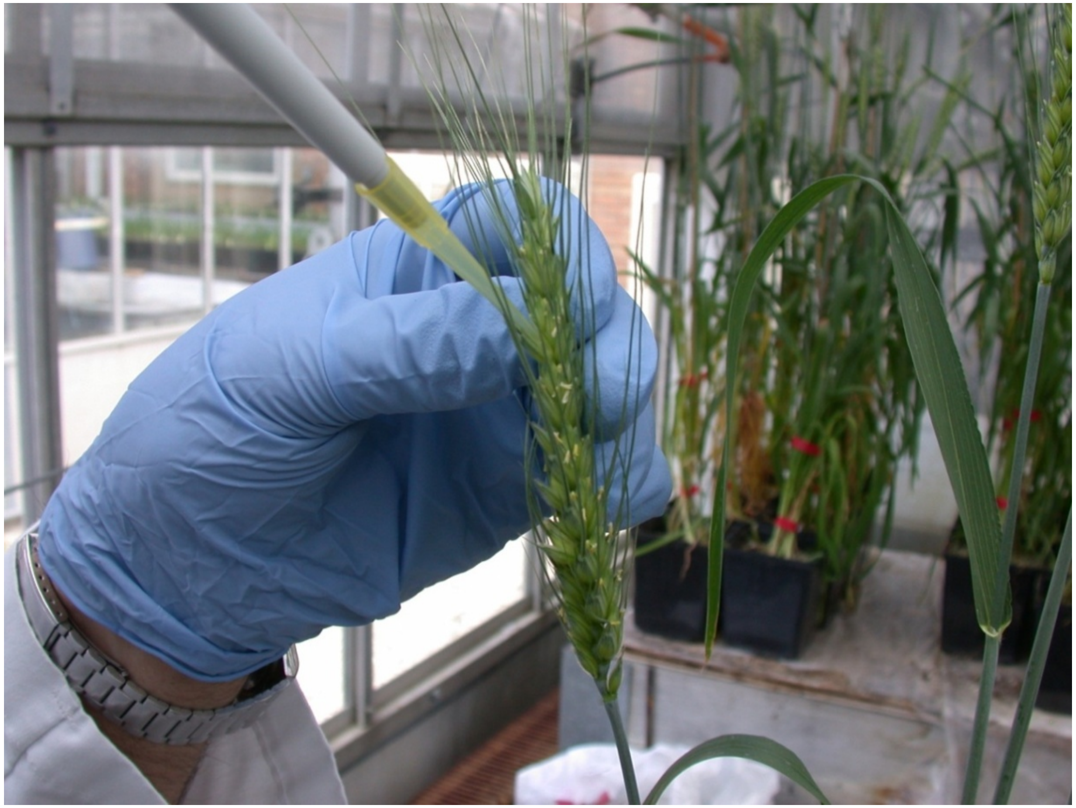
Materials and Methods

Greenhouse evaluation

- **To detect resistance to:**

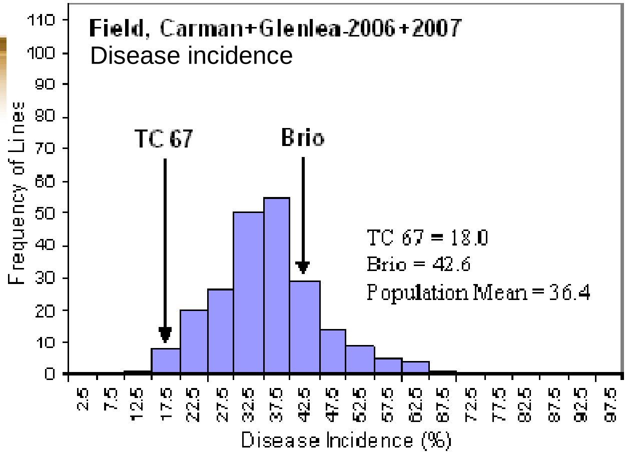
- disease spread (type II)

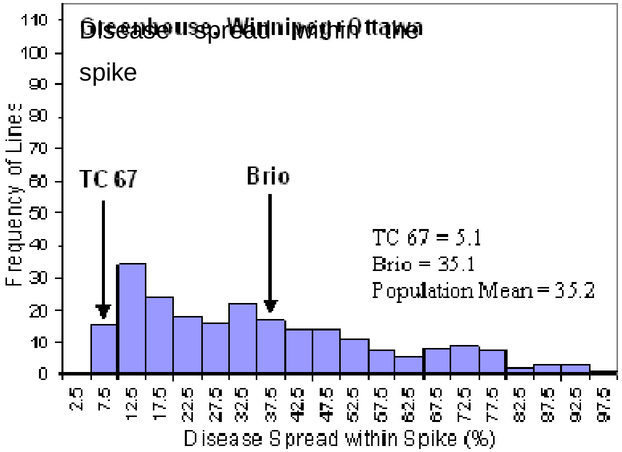
- Single-floret inoculation was used
- Disease spread was measured

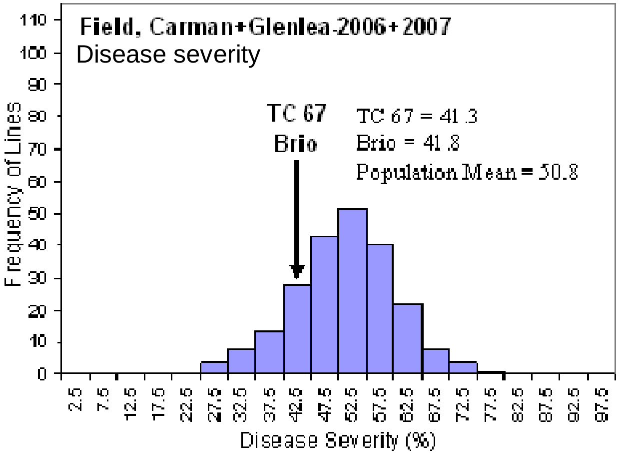


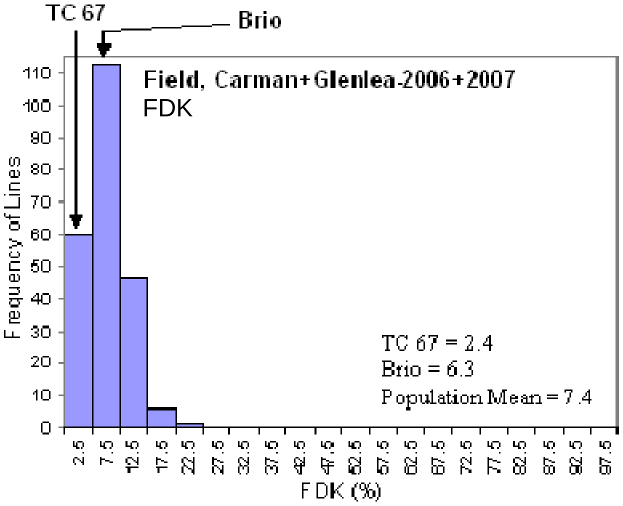
Results and Discussion

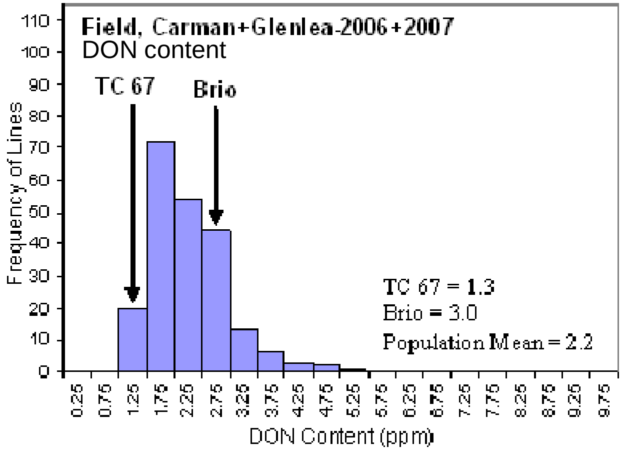
Frequency distribution











Materials and Methods

Statistical analysis

- SAS®

Genotypic data collection

- DNA extraction
- DNA amplification: SSRs
- PCR products: ABI Analyzer

Bulked segregant analysis

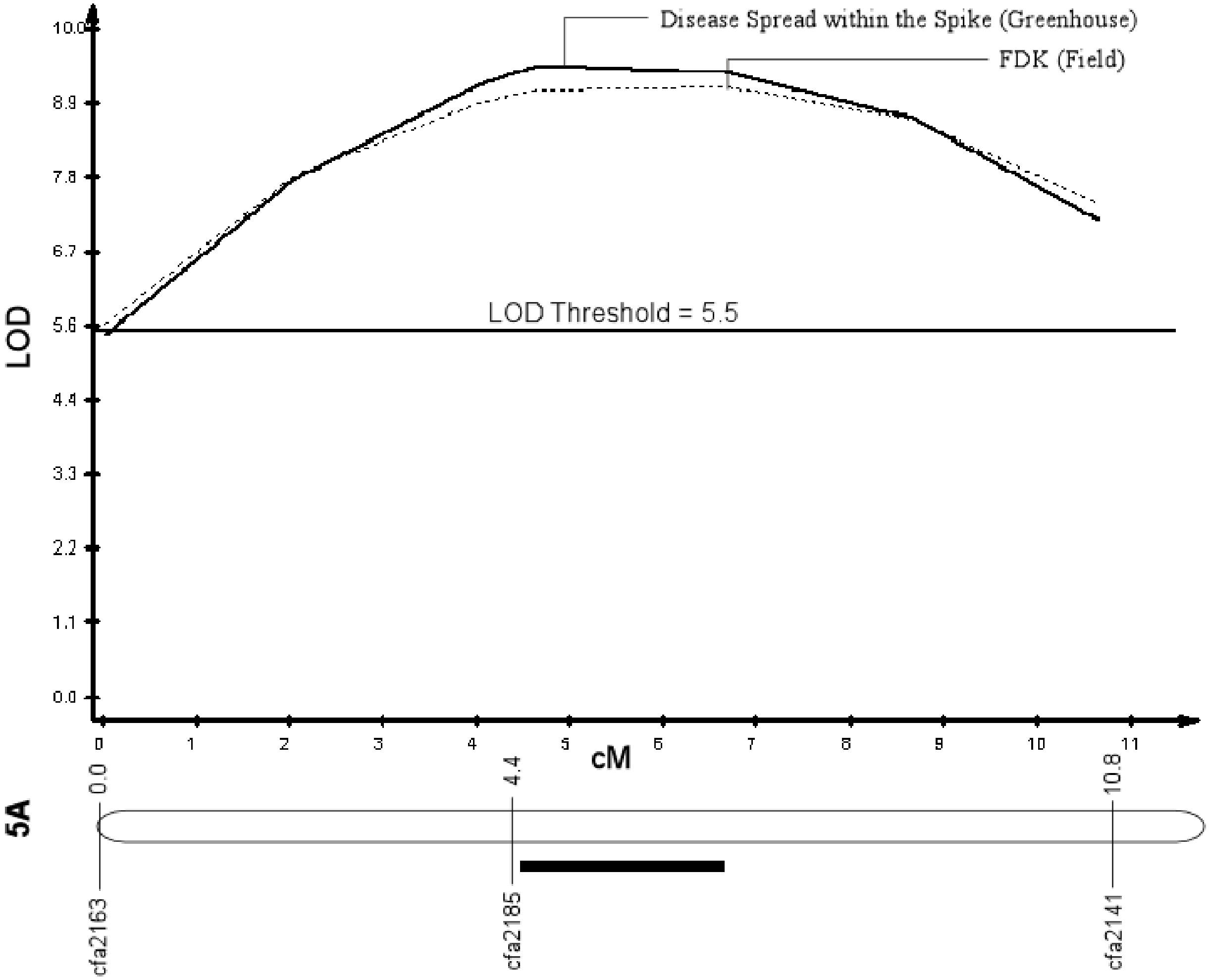
- 851 SSR primers
- Primers screened on: RP, SP, RB, and SB
- Polymorphic markers screened on: individuals of RB and SB
- Highly polymorphic markers screened on: entire population

QTL mapping

- MAPMAKER/EXP
- QTL Cartographer

Results and Discussion

QTL mapping



- 200 accessions screened.

- Accession 10-1 crossed & backcrossed to AC Superb.

- DH mapping population produced from cross to AC Superb

T. monococcum

- 50 accessions screened, 3 backcrosses to AC Superb required to restore fertility.

- DH mapping population produced from cross to AC Superb.

Aegilops speltoides

Average metaphase I chromosome pairing in F1 hybrids between *Triticum aestivum* (c.v Superb) and *Aegilops speltoides* accession

		Metephase I configurations					
		II					
I	Rod	Rings	Total	III	IV	Xta freq.	No of cells
9.55	4.82	2.40	7.22	1.29	0.14	11.90	88
10.80	4.60	3.10	7.70	0.36	0.18	12.62	112

FHB symptoms and DON content of progenies from interspecific crosses with bread wheat (AC Superb) (field data, 2005)

Source of resistance	Generation	Number of lines	FHB Index (range)	DON Level (range) ppm
T. monococcum	BC_2F_6	22	0.3-3.0	0.1-1.7
Ae. speltoides	BC_3F_6	70	0.3-7.5	0.3-2.0
Checks				
Roblin			76.5	9.1
Superb			24.0	9.2
Fukuho			1.5	1.9
Sumai3			1.3	2.9

Agronomic characteristics of FHB resistant lines obtained from wide crosses

Genotypes	Yield (kg/ha)	Days to heading	TSTWT (kg/hl)	TKW (g)	HT (cm)	Protein (%)	Flour (%)	DON (ppm)
Sumai3	2895	70	--	33.0	88.5	13.0	--	2.1
M 321	3272	64	79.3	34.4	76	13.9	57.5	5.5
S 184	3246	61	80.3	35.0	86	13.3	67.2	3.4
AC Barrie	3304	61	80.5	34.6	79	13.7	66.8	6.5
Hoffman	4597	61	82.0	44.0	89	10.9	61.9	15.2
Roblin	--	--	--	--	--	--	--	17.2

M 321

S 184


AC Barrie

M 321

- Single accession crossed & backcrossed to AC Superb & progeny advanced to F6 by SSD.

- Resistant line selected.

- DH production in progress.

Triticum miguschovae

Average metaphase I chromosome pairing in F1 hybrids between *Triticum aestivum* (c.v.Superb) and *T. miguschovae* (AGD genome)

Metaphase I configurations							
	II						
I	Rod	Rings	Total	III	IV	Xta freq.	No of cells
4.61	3.81	13.75	17.56	0.57	0.14	32.87	150

FHB symptoms and DON content in progenies from intercrosses of bread wheat with *T. miguschovae* (AGD) (field data 2005)

Generation	**Number of lines**	**FHB Index (range)**	**DON Content (range) ppm**
BC_3F_4	7	0.3-4.0	0.2-3.4
Checks			
Roblin	–	81.0	9.1
Superb		13.5	9.2
Fukuho		0.5	1.9

Symptoms on BC2 spike of hybrid between Superb and *T. miguschovae* at 21 days after point inoculation

Fusarium Head Blight Resistant Lines Derived From Hybrids with *Aegilops cylindrica*

Hybrid combination	Generation	Number of lines
AC Superb X 1/74-91 X 5/20-91	F6	220
Teal	F2-F5	bulks
AC Barrie		
Domain		
Elsa		
H4644		
Glenlea		
Alsen		

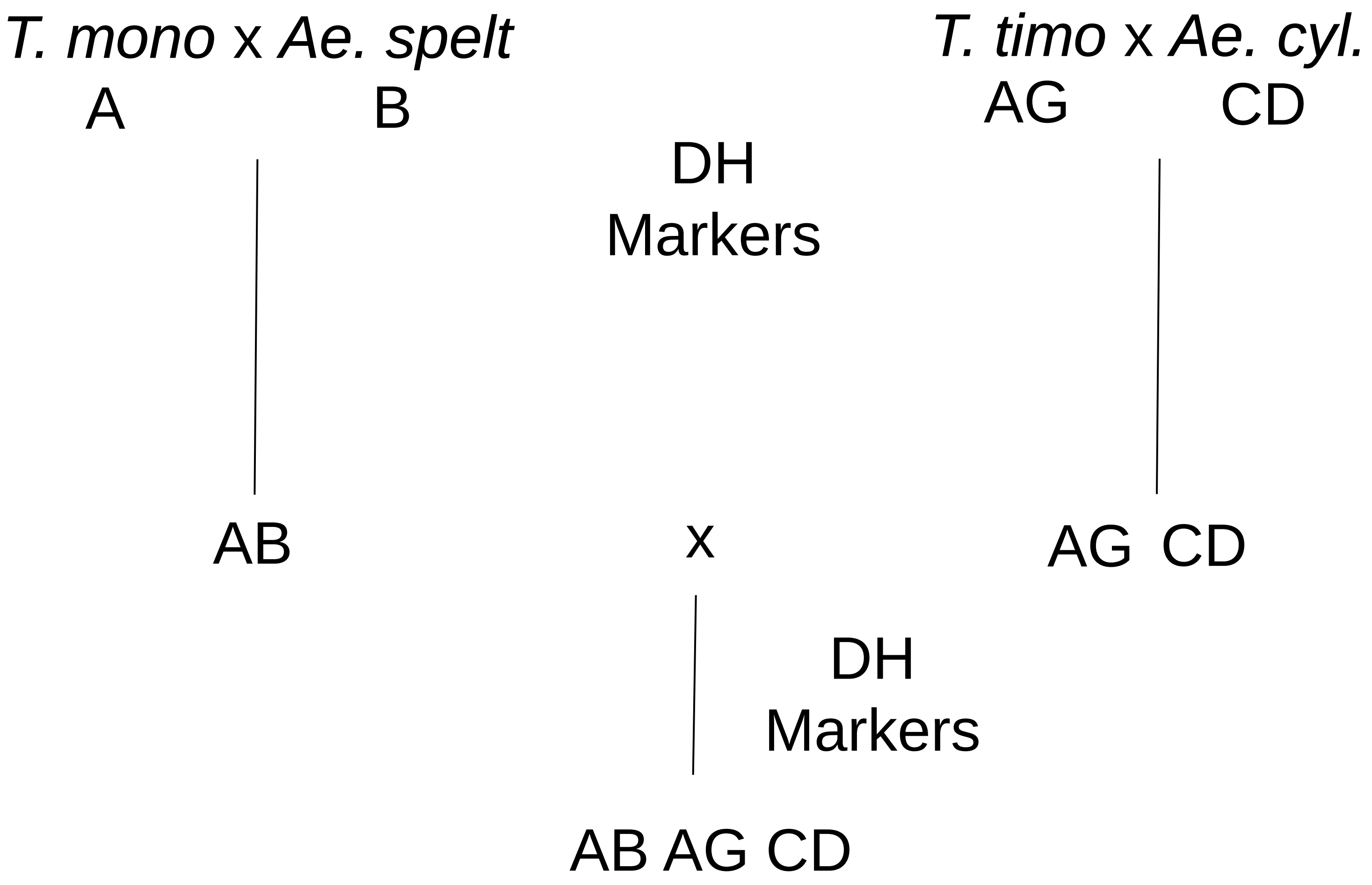
FHB Symptoms in Derivaties from *Triticum miguschovae* and *Aegilops cylindrica*

Line	**FHB Index (%)**	**DON (ppm)**
MSB 16	17.7	37.7
MSB 55	9.0	10.8
Odessa-129-2	7.8	9.6
Superb	46.3	47.2
Sumai 3	2.6	3.9

Markers assignments to FHB resistance QTLs obtained from alien sources

Source of resistance	**Chromosome location**	**Markers**	**References**
T. monococcum (A)	5A (M321)	wmc 705	--
	3A (Frontana)	gwm5	--
Ae. cylindrica (CD)	1D	cfd65	--
	4D	wmc457, wmc622	--
	5D	gwm 292	--
	6D	barc 96	--
T. carthlicum (AB)	6B	wmc 397	Somers et al., 2006
	2B (Strongfield)	gwm 55	Somers et al., 2006
	1A	cfe2153	Singh et al., 2008
T. timopheevii (AG)	5A (Tc 67)	Cfa 2185	Malihipour et al., 2008

Pyramiding Sources of FHB Resistance



T. mono x *Ae. spelt*
A B

T. timo x *Ae. cyl.*
AG CD

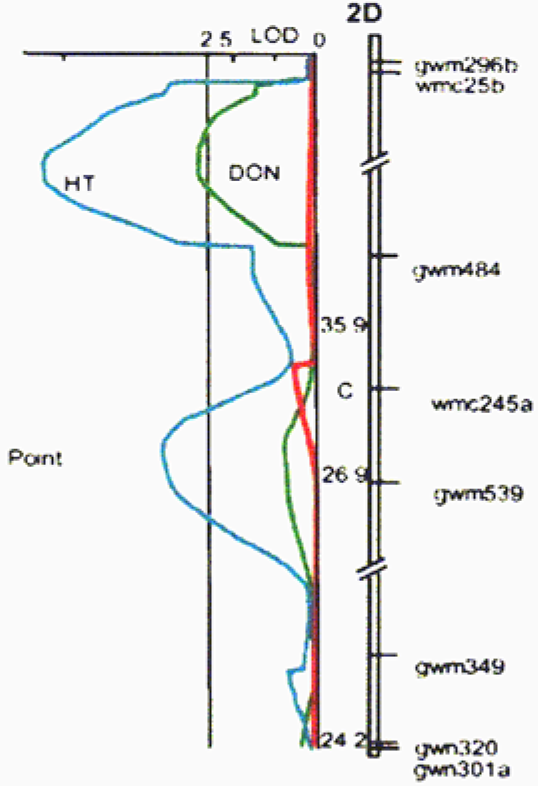
DH
Markers

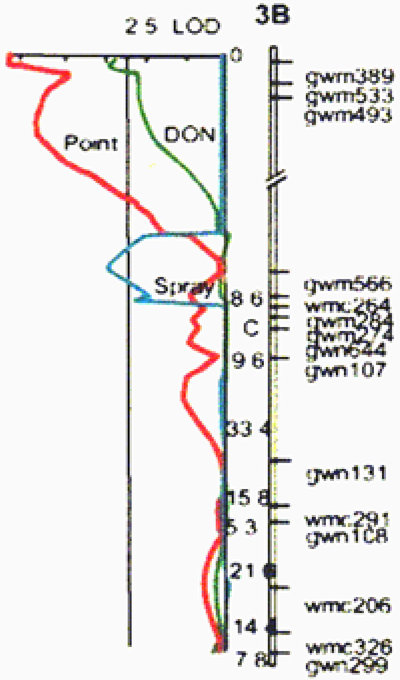
AB x AG CD

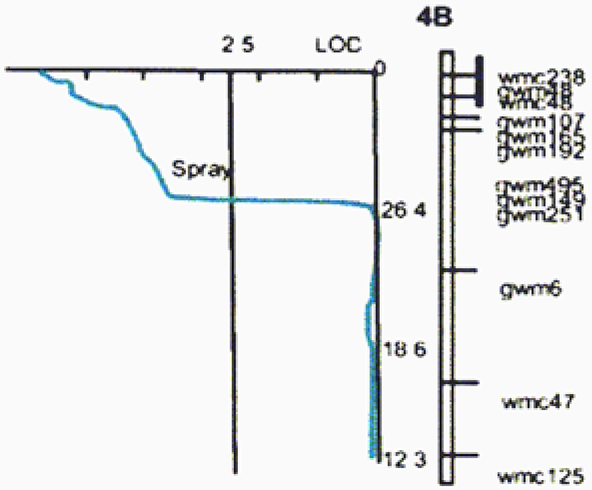
DH
Markers

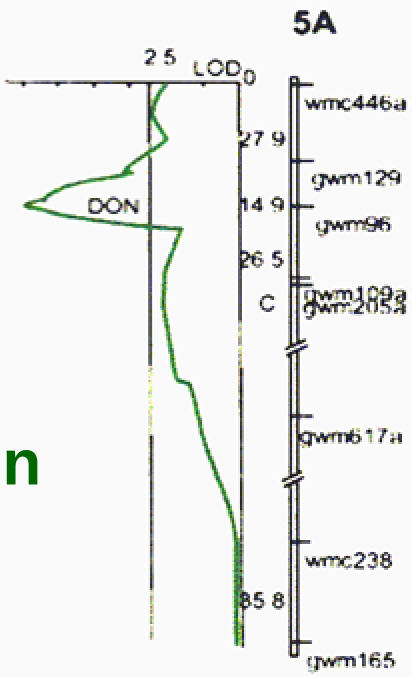
AB AG CD

Wuhan/NuBay
Mapping Population
91 DH lines









FHB index and DON contents of 15 WS lines with their parents Sumai3 and Snowbird and 6 checks in the field FHB nursery of 2009, 2010 and 2011

Line	**2009**		**2010**		**2011**		**Averge**		**QTLs**
	Index (%)	**DON (ppm)**	**Index (%)**	**DON (ppm)**	**Index (%)**	**DON (ppm)**	**Index (%)**	**DON (ppm)**	
Snowbird	36.67	14.30	36.67	31.23	41.67	7.20	38.34	17.58	x, x, x
Sumai3	3.00	0.67	30..	1.50	2.17	0.77	2.72	0.98	3B,5A,6B +
WS-44	3.33	1.33	3.00	2.73	3.50	0.53	3.28	1.53	3B, x, 6B +
WS-84	11.33	8.77	5.67	11.17	4.67	4.47	7.22	8.13	3B, x, 6B +
WS-131*	3.33	2.67	3.00	9.30	4.17	3.63	3.50	5.20	x, 5A, 6B +
WS-175	8.00	2.20	2.67	3.03	2.43	1.20	4.37	2.14	x, 5A, 6B +
WS-246	30.00	8.67	6.00	8.70	27.17	5.13	21.06	7.50	3B,5A, x -
WS-321*	15.65	5.67	3.00	8.67	10.93	5.23	9.87	6.52	3B, x, 6B +
WS-385	15.67	4.77	8.67	6.50	3.83	2.70	9.39	4.66	x, 5A, 6B +
WS-420	31.33	8.80	5.67	28.03	11.67	3.60	16.22	13.48	3B,5A, x H
WS-447	16.00	6.50	3.33	15.67	2.50	2.07	7.28	8.08	3B,5A, x -
WS-481*	3.00	0.53	2.67	28.67?	1.83	1.30	2.50	10.17	3B, x, 6B H
WS-630	21.00	6.80	7.00	16.80	3.50	4.67	10.50	9.42	3B,5A, x H
WS-745	14.67	5.63	3.67	4.97	3.67	3.43	7.34	4.68	3B,5A, x H
WS-795	3.00	4.27	7.67	8.70	30.17	7.43	13.61	6.80	3B, x, 6B +
WS-830	8.67	8.33	7.67	7.17	35.00	7.83	17.11	7.78	x, 5A,6B H
WS-886	7.00	2.07	8.33	3.13	2.10	1.07	5.81	2.42	3B,5A,6B +
ACS53619	33.33	17.63	61.67	15.47	66.67	9.47	53.89	14.19	x, x, x
AC Vista	90.00	35.93	91.67	28.10	98.33	19.57	93.33	27.87	x, x, x
Snowstar	-	-	43.33	18.47	56.67	3.93	50.00	11.20	x, x, x
AC Formost	-	-	98.33	22.80	100.00	13.60	99.17	18.20	x, x, x
AC Barrie	-	-	21.67	3.20	26.67	4.40	24.17	3.80	?
FL62R1	-	-	4.00	1.87	2.67	1.53	3.33	1.70	?

Spike symptoms of: **1**) Roblin, **2**) P1131-5, **3**) P1142-1-2-6, **4**) P1142-2-9, **5**) P1142-2-5, **6**) P1142-2-15, **7**) P1142-3-B, **8**) P1142-3-E, **9**) P1142-3-1-5 at 21 days after inoculation with *Fusarium graminearum* spores

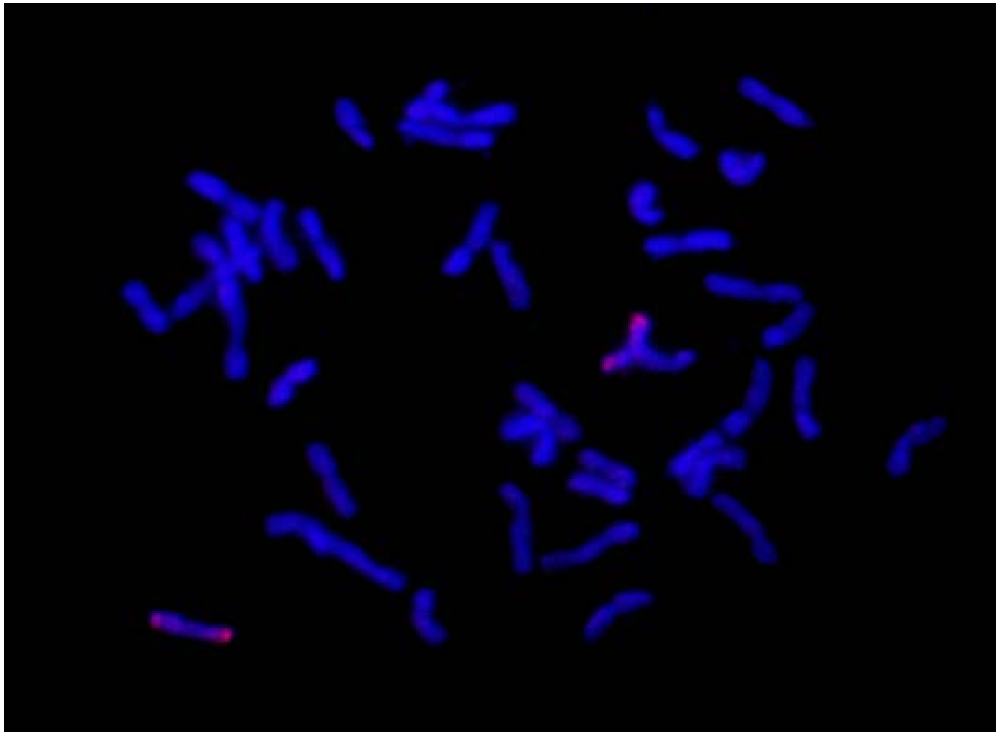
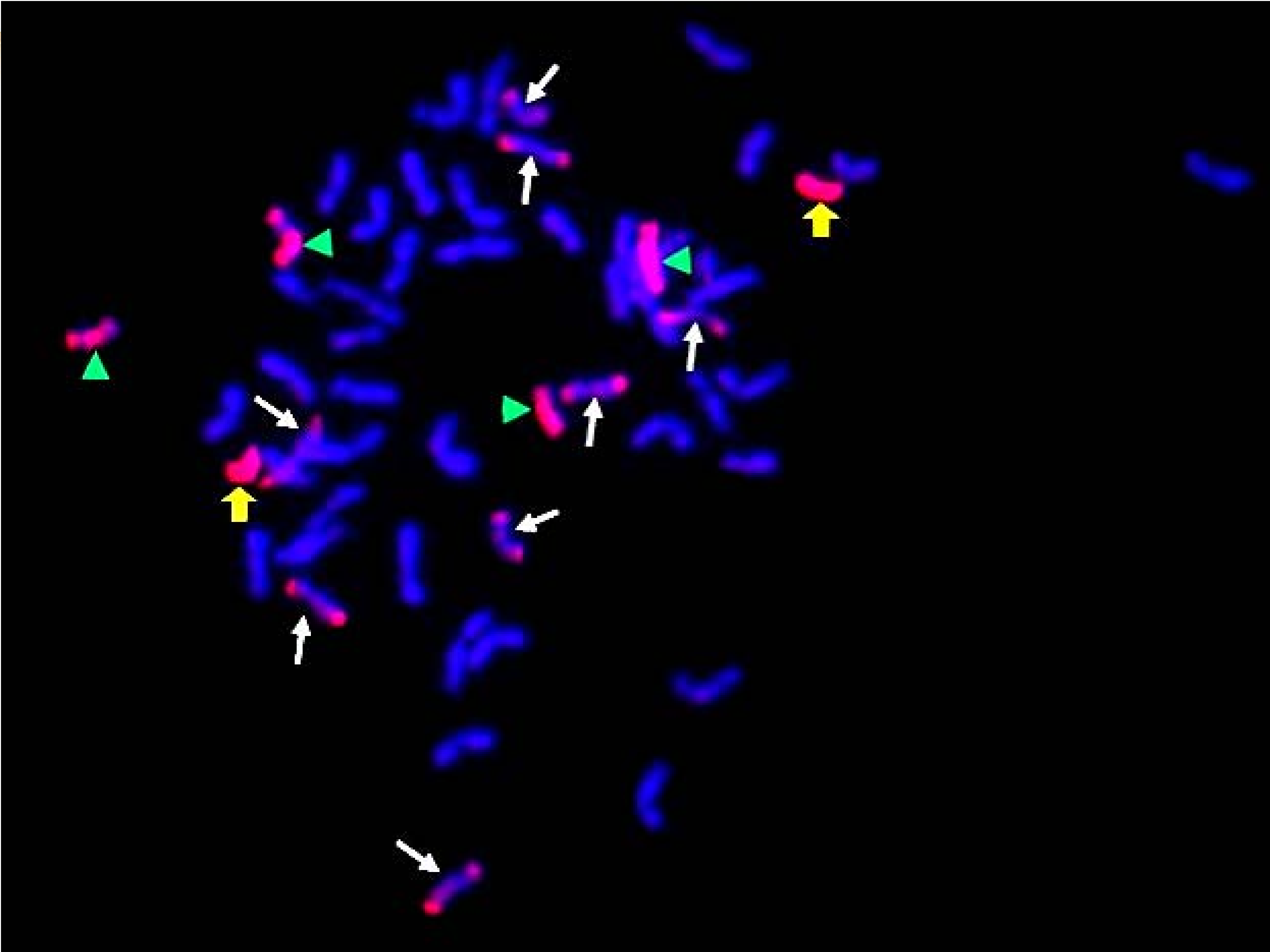


Fig. 3. P1142-3-1 (2n = 42) with two terminal translocation chromosomes (white arrows).



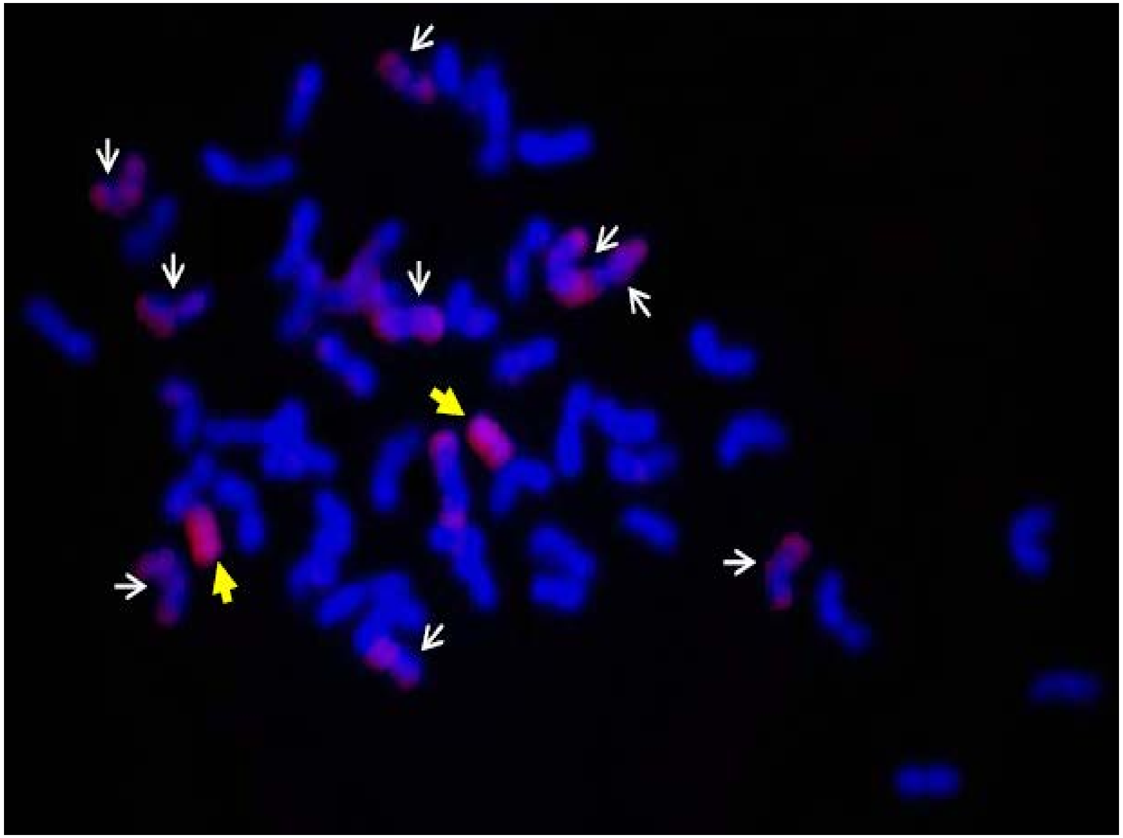


Fig. 2. P1142-2 (2n = 54) with 10 terminal translocation chromosomes (white arrows) and two entire chromosomes from *E. repens* (yellow arrows).

FHB symptoms on spikes of *Tritordeum* (durum x *Hordeum bogdanii* - ABH genomes) lines at 21 days after inoculation.

Roblin ***Tritordeum***

FHB symptoms and DON content in progenies of interspecific crosses between AC Strongfield and strains of *Tritordeum* (ABH) (field data 2005)

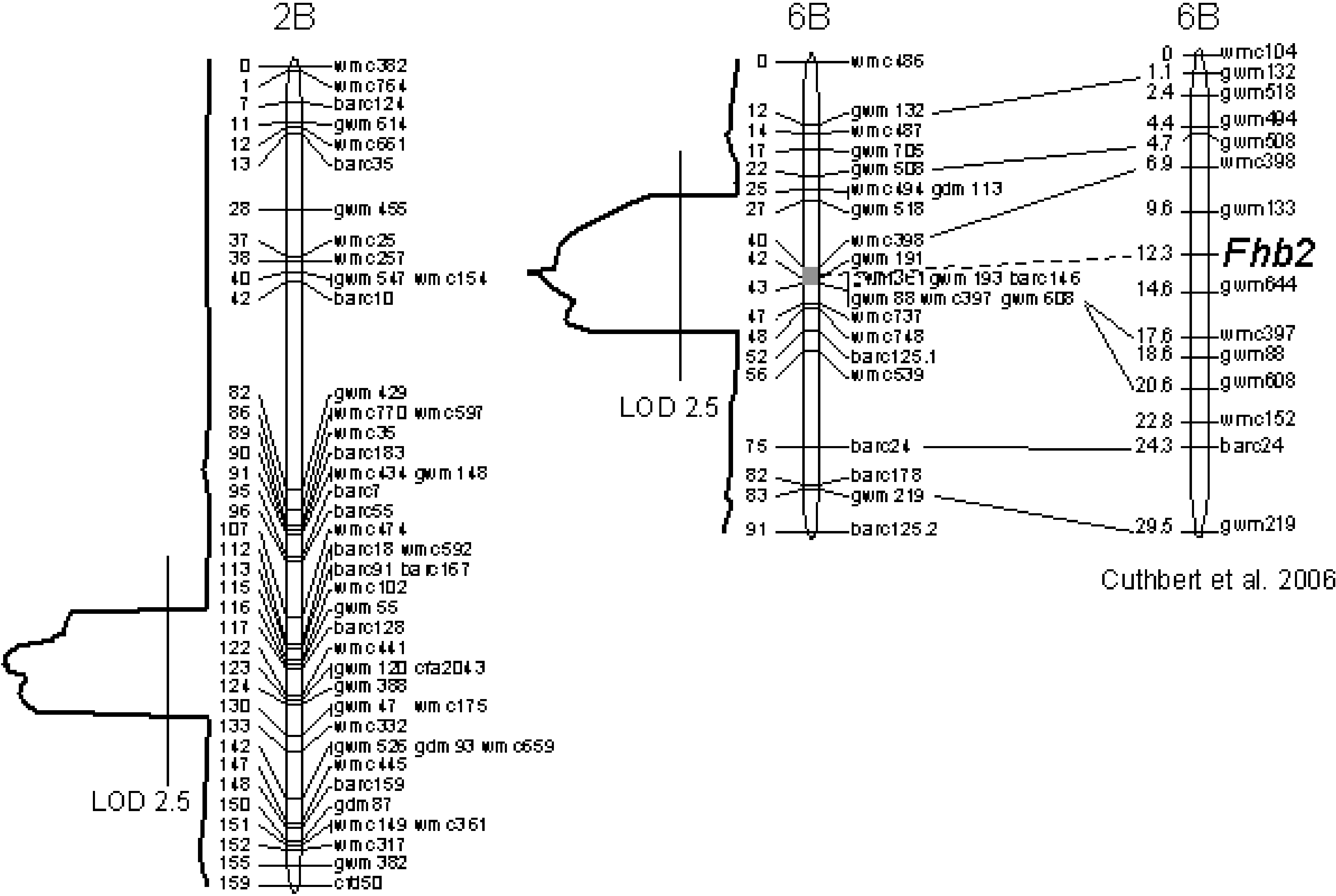
Generation	Number of lines	FHB Index (range)	DON Content (range) ppm
BC_3F_4	27	0.5-10.5	0.8-5.5 7.4-11.9
Check			
AC Strongfield	–	6.8	16.5

FHB symptoms on *Tritordeum* X AC Strongfield derivative

Trito-1-34 **AC Strongfield**

- Resistant accession identified.
- Mapping population of 100 RIL developed from cross to AC Strongfield

***Triticum carthlicum (AB* genome)**



Cuthbert et al. 2006

FHB symptoms on a spike of Triticale TMP16315 at 21 days after point inoculation.

TRITICALE FHB MAPPING

- TMP16315 x AC Ultima
- 100 DH lines
- Phenotyped at three locations

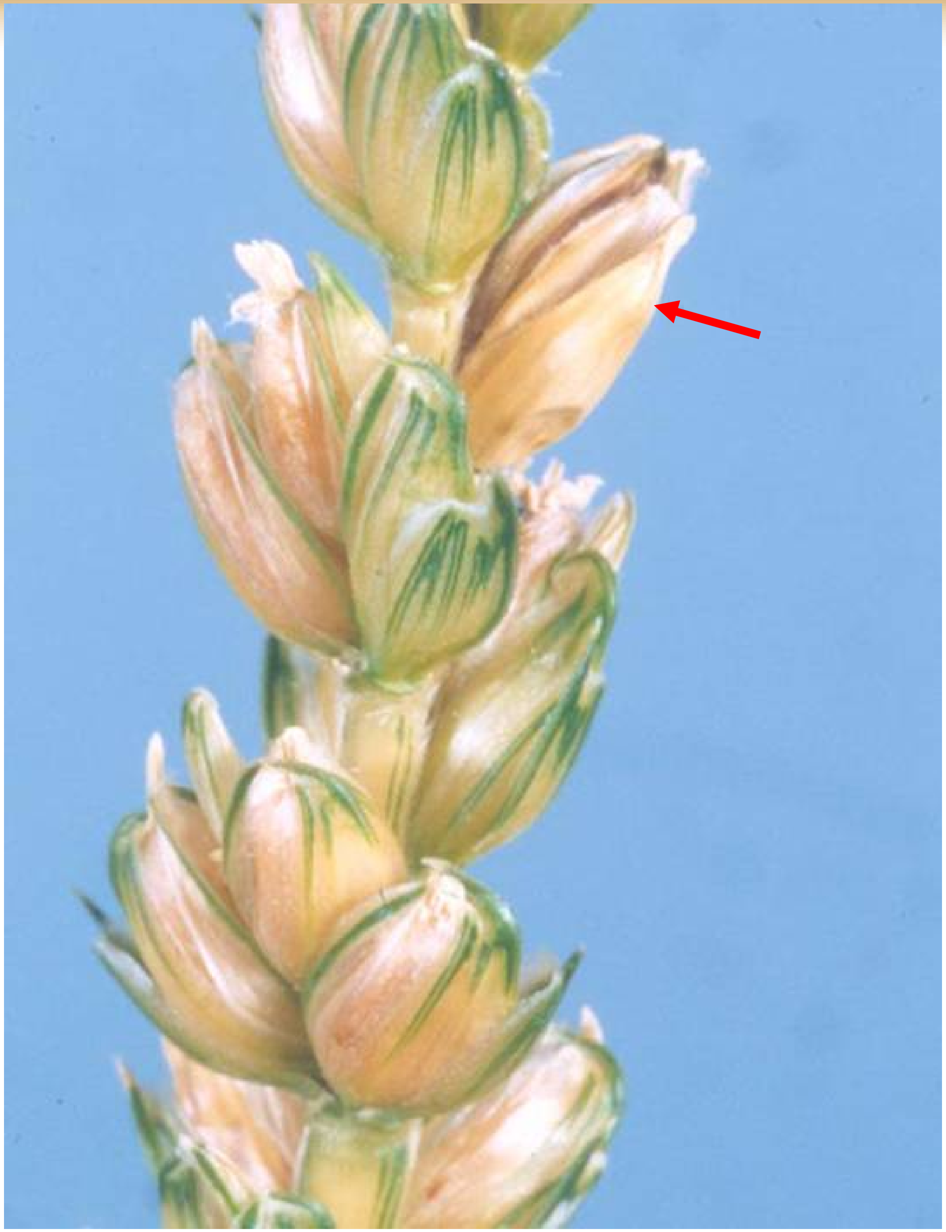
Infected spikelet of Triticale at 21 days after inoculation

FHB Symptoms and DON Levels in Triticale lines(2 years average)

Line	Incidence(%)	Severity(%)	DON(ppm)
TMP16315	17.5	12.5	4.1
AC Ultima	6.0	47.5	17.5
Sumai3	5	5	1.2

FHB symptoms at 21 days after point inoculation

Thinopyrum elongatum **(E genome, 2n=14)**

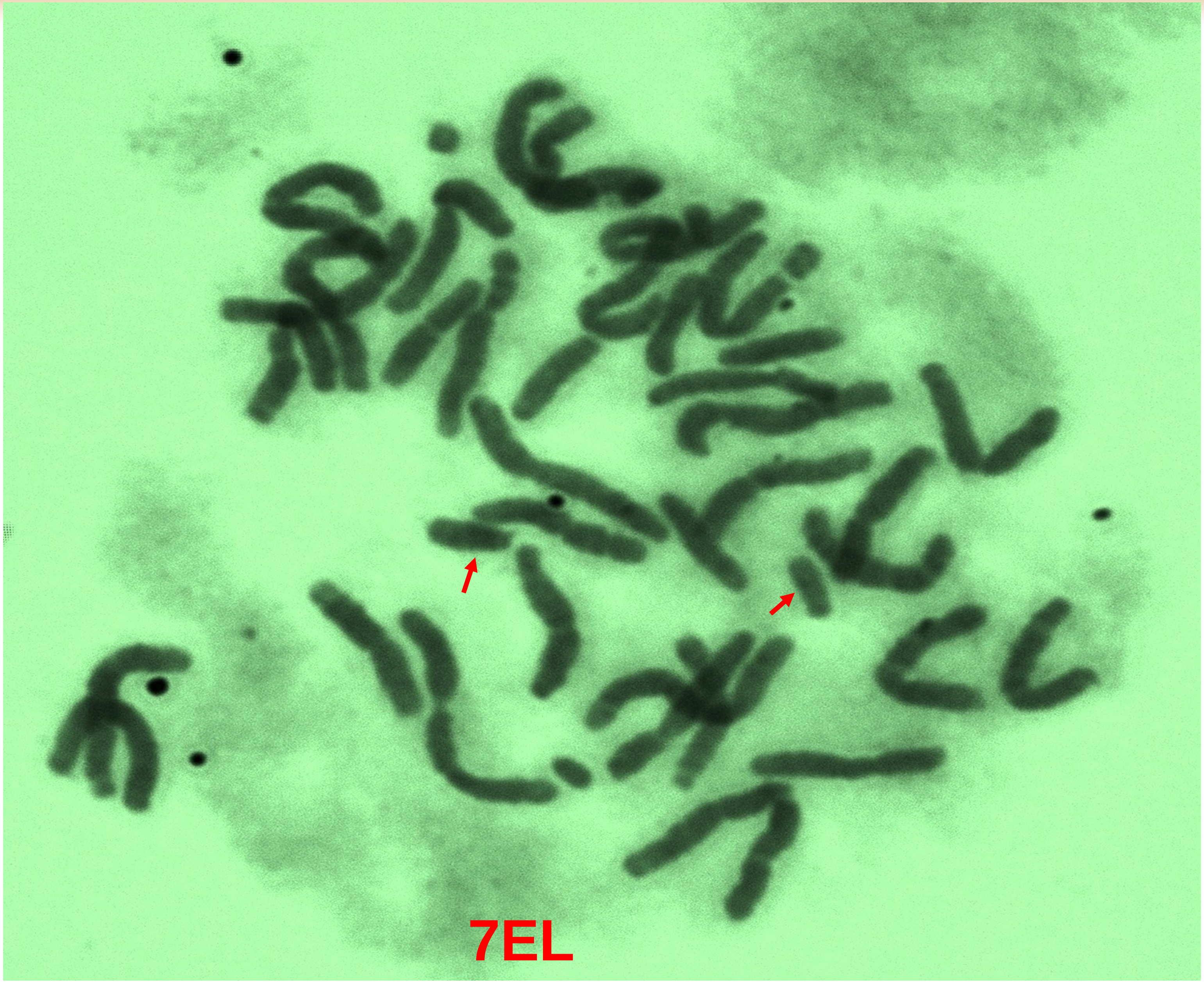


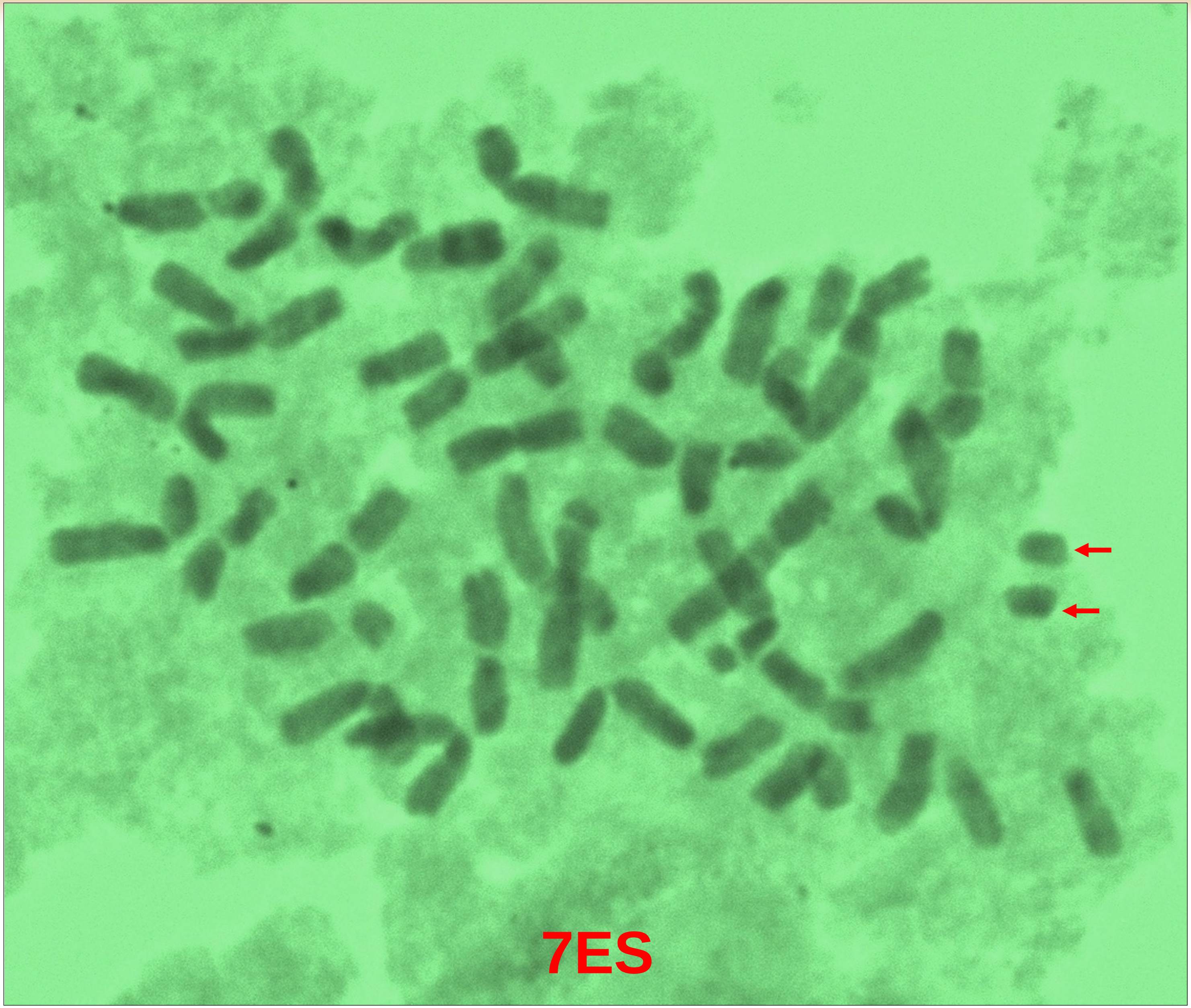
CS – 7E addition


Roblin
8801
8802
8803

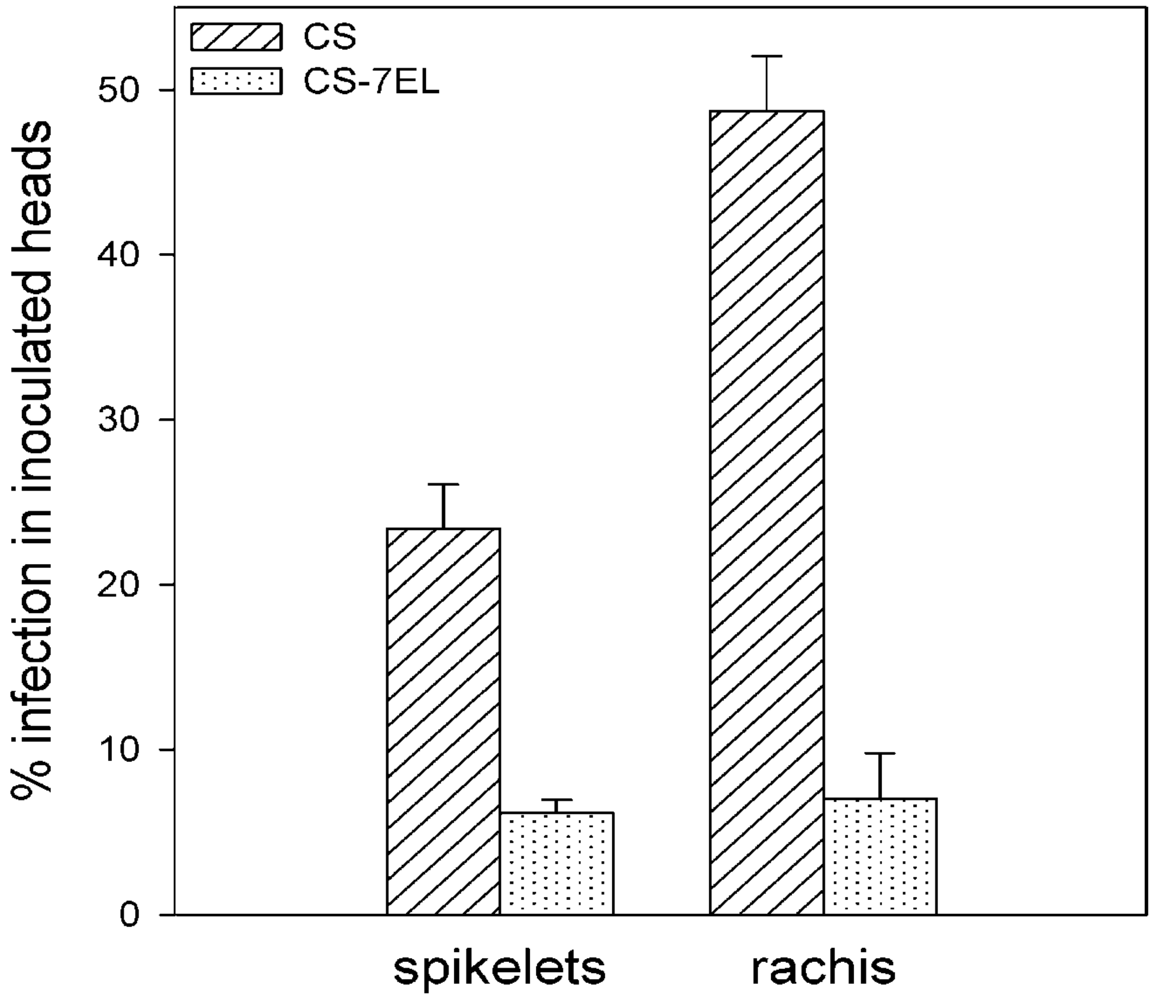
FHB symptoms on 7E lines following point inoculation

Aneuploid Lines	Severity % infected florets
7EL disomic addition 2n = 42 +2t	9.6
7ES disomic addition 2n = 42+2t	86.5
7E disomic addition 2n = 44	14.5
7E(7A) disomic substitution 2n =42	18.8
7E(7B) disomic substitution 2n = 42	5.8
7E(7D) disomic substitution 2n = 42	8.0
Chinese Spring parent	57.5
Sumai 3	2.8

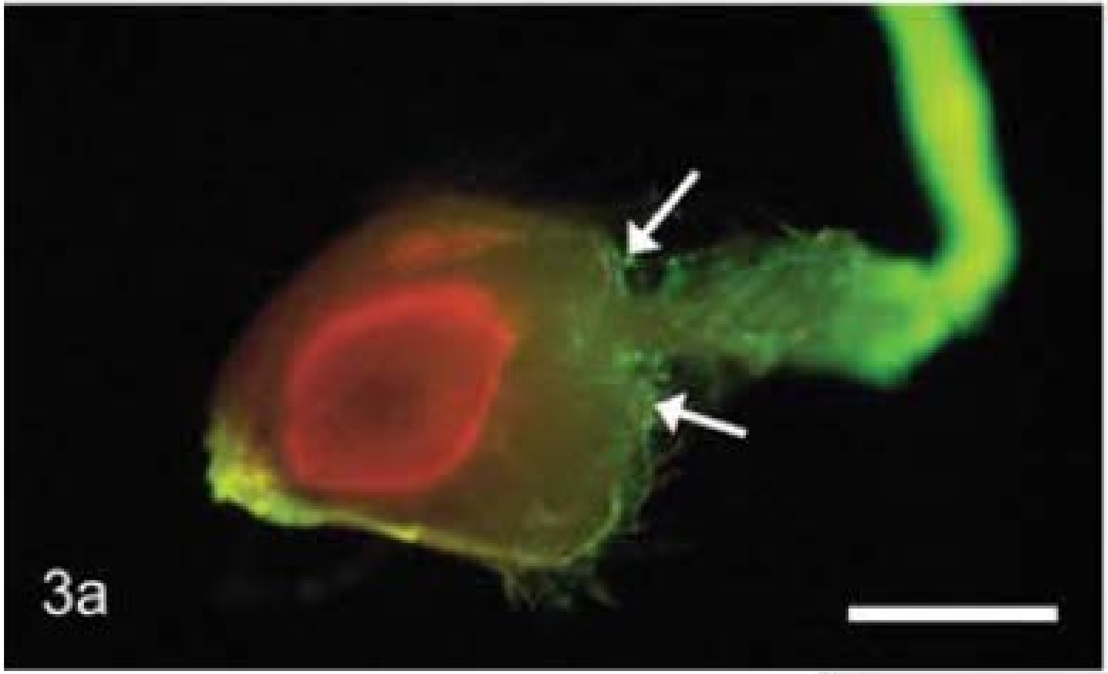

7EL


7ES

Spikes of CS (a) and CS-7EL(b) 4 days after inoculation. Arrows indicate inoculated spikelets. c,d) Rachis with florets removed above and below point of inoculation, 21 days after inoculation. c) CS, d) CS-7EL.



Average disease ratings for CS (n=19) and CS-7EL (n=23) inoculated heads, at 21 dpi. Inoculations were done with a suspension of 50,000 spores/ml.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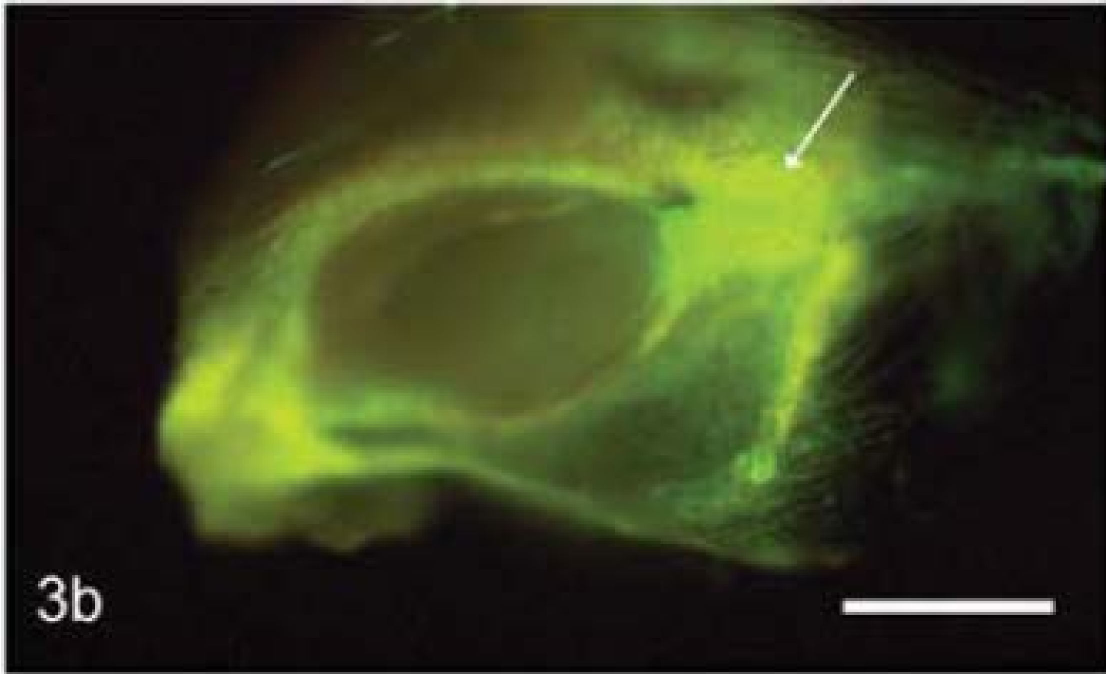
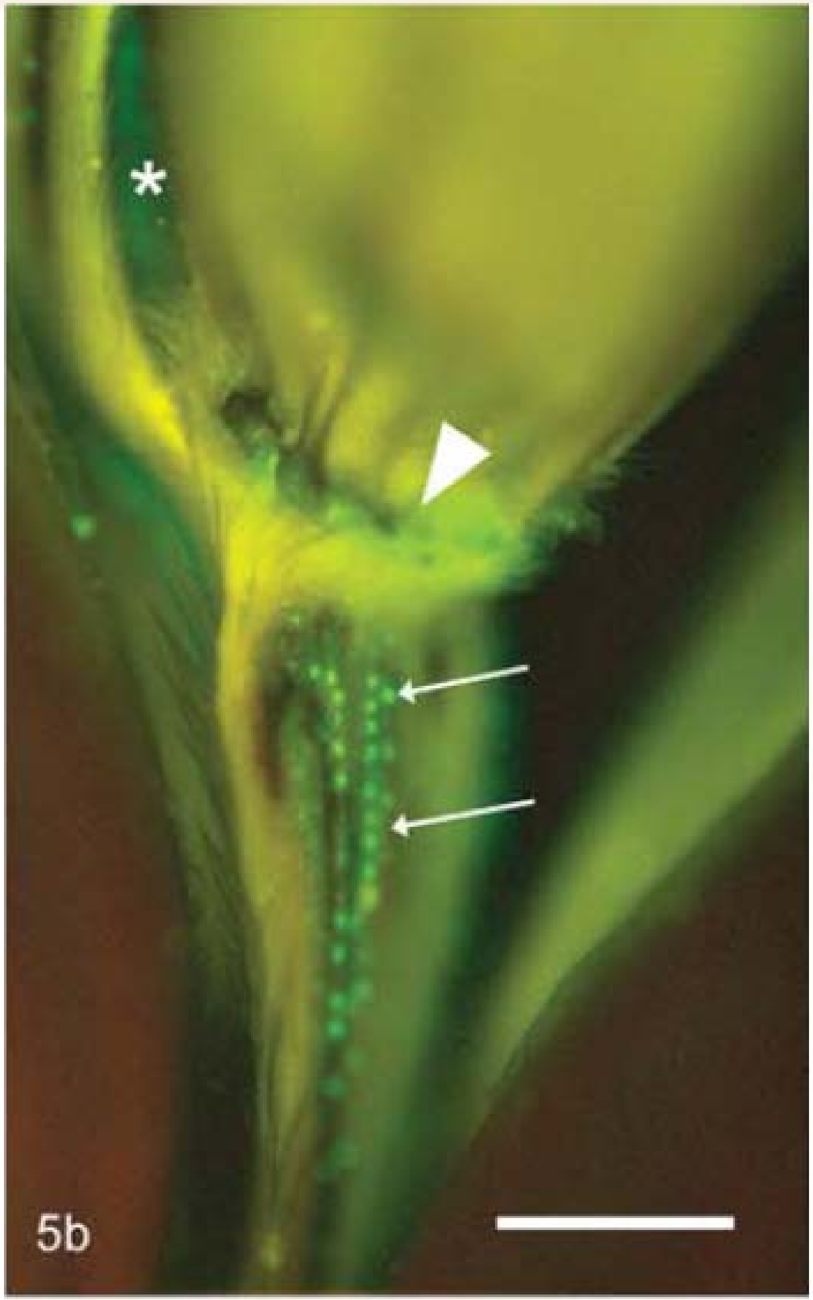

3b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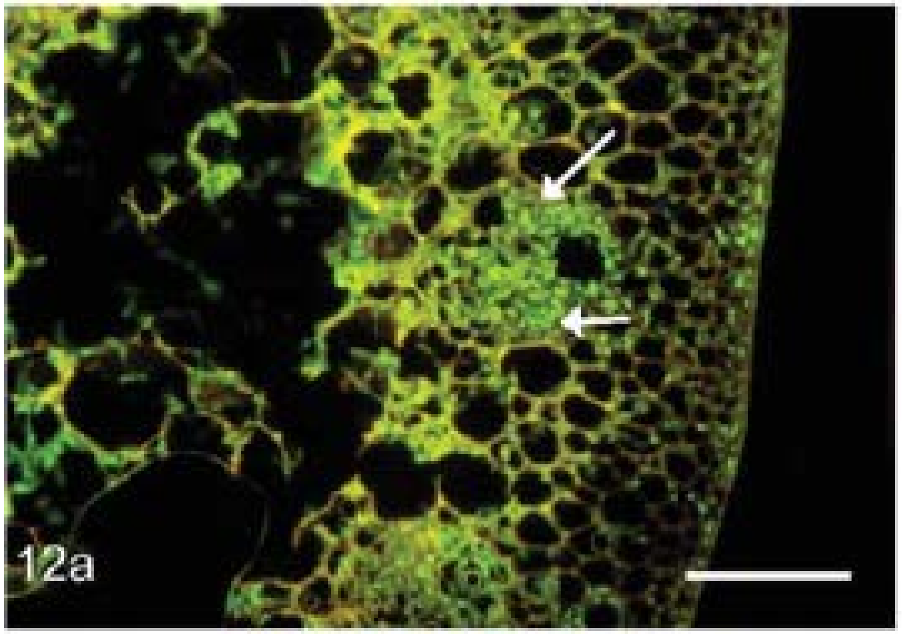
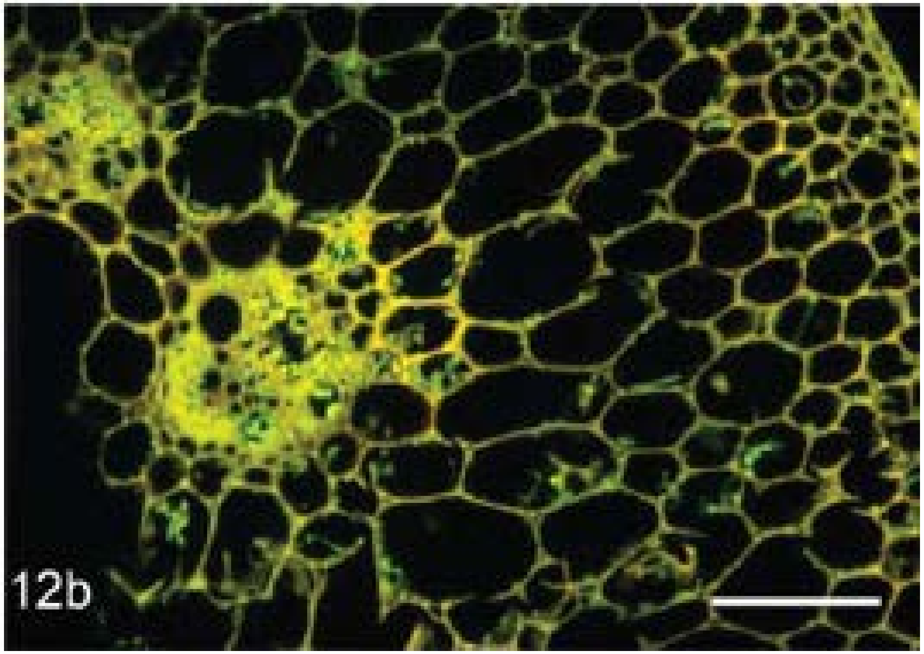
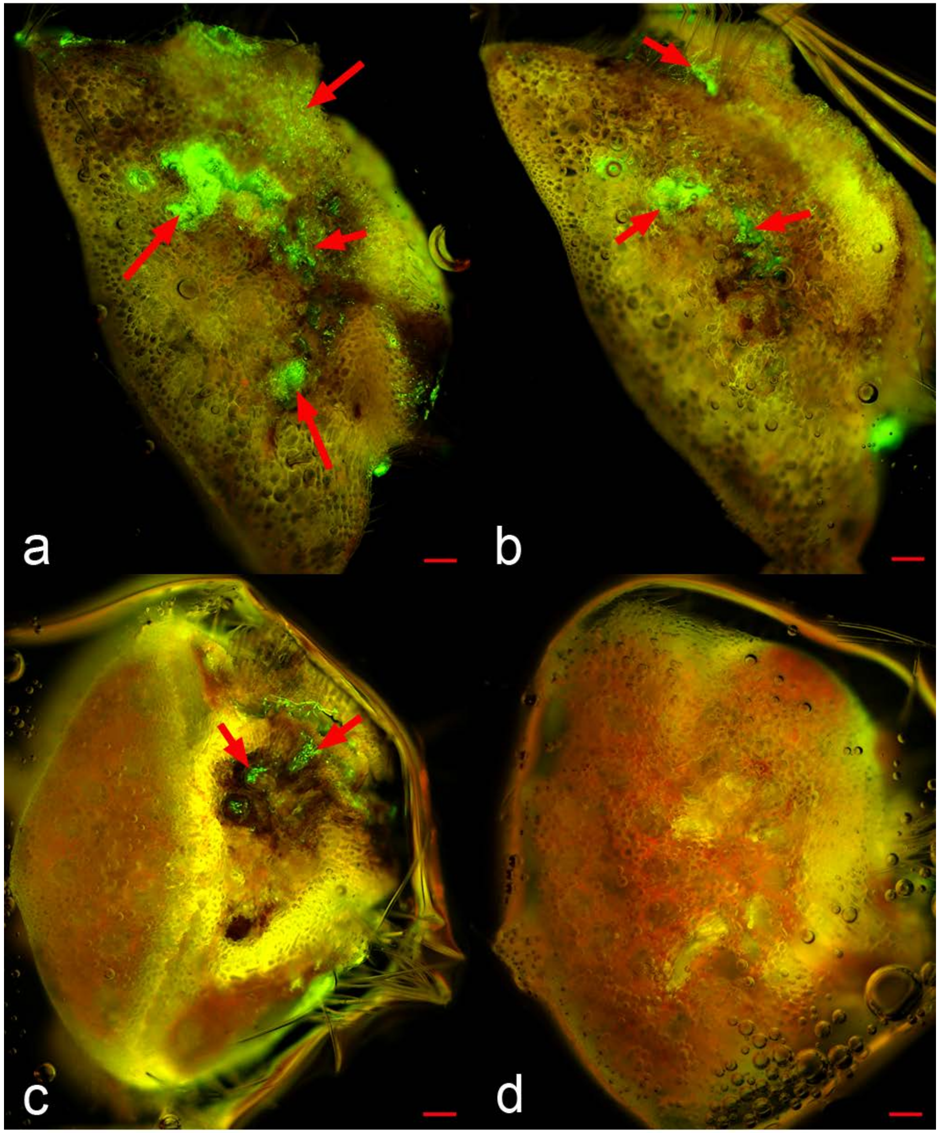
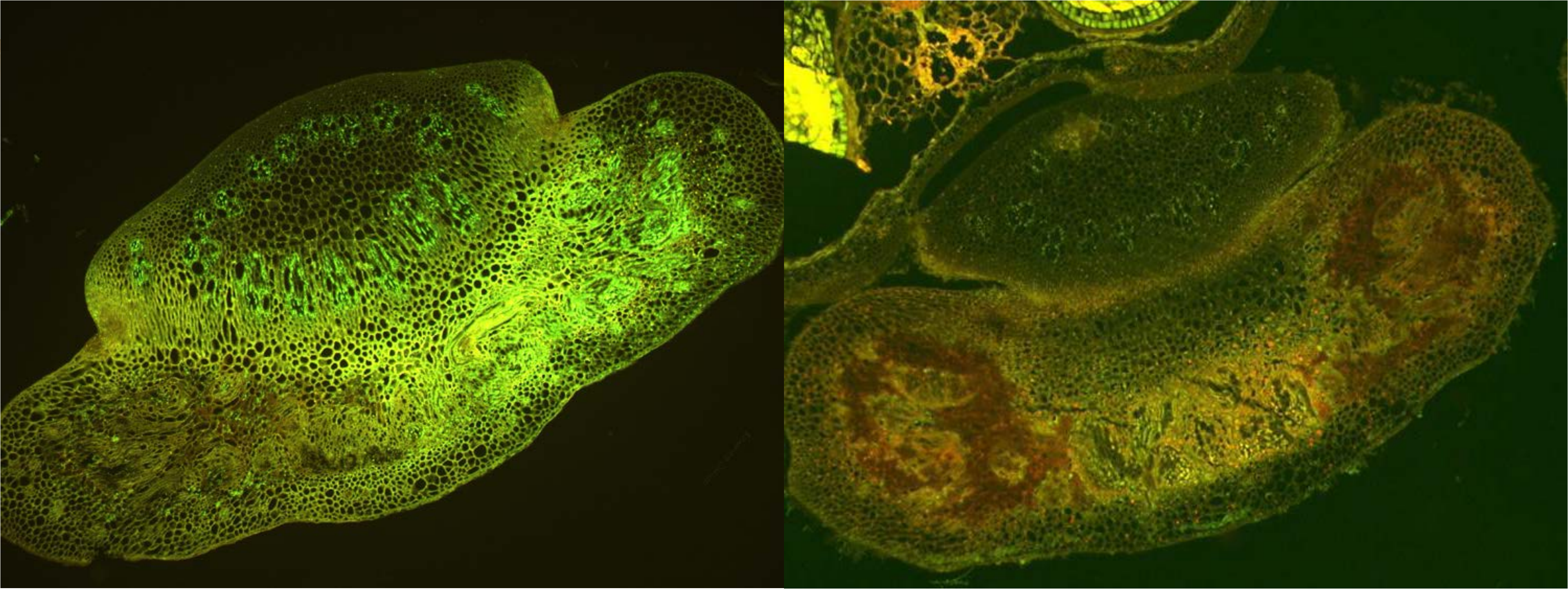
5b


12a


12b



Hand sections through the node bearing the inoculated floret at 6 dpi. a) CS, top of the node (closest to point of inoculation) b) CS, bottom of the same node section, c) CS-7EL, top of the node (closest to point of inoculation) d) CS-7EL, bottom of the same node section. Bars = 200 µm.

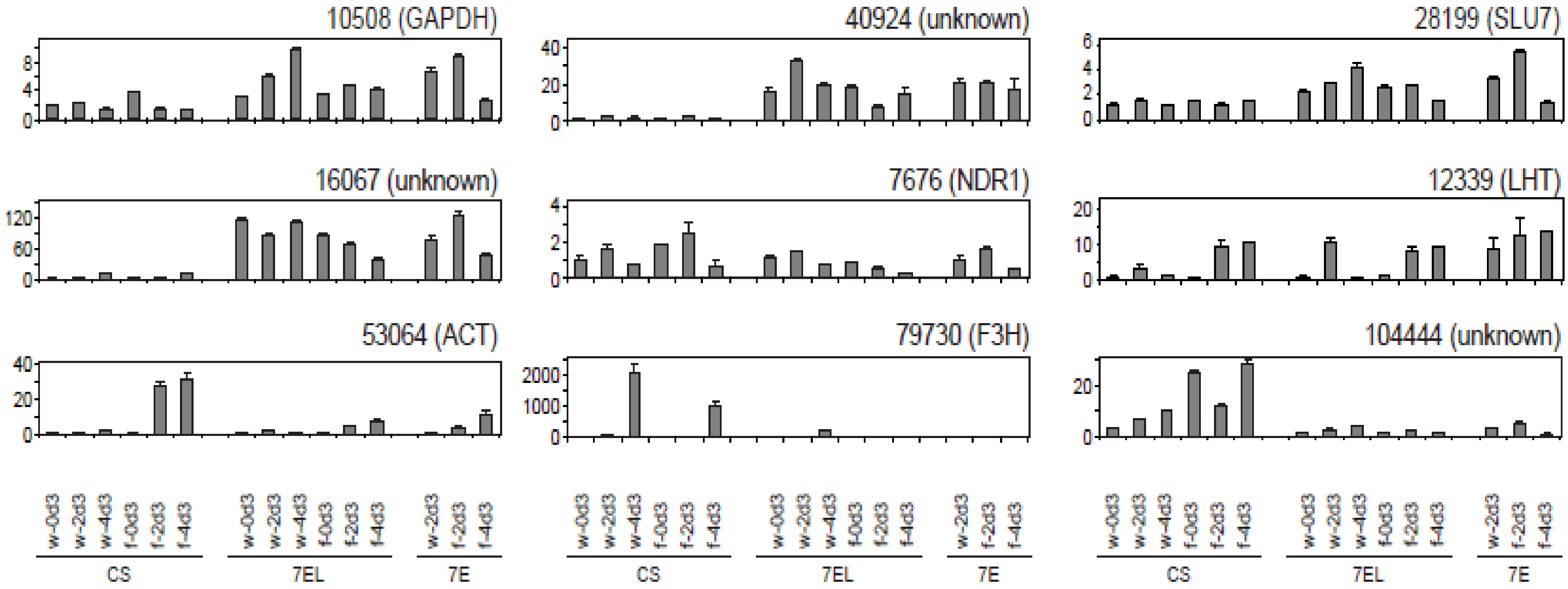


Chapais

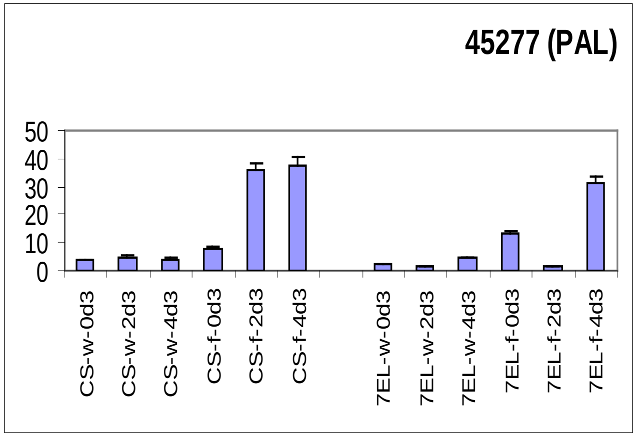
Chevron

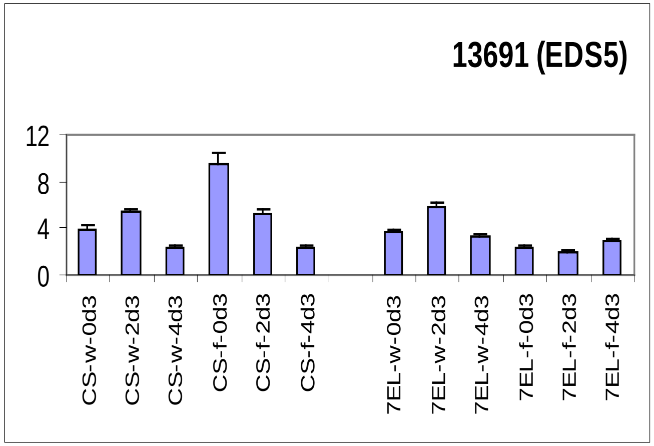
Barley. Node at base of inoculated floret, 11 days post inoculation

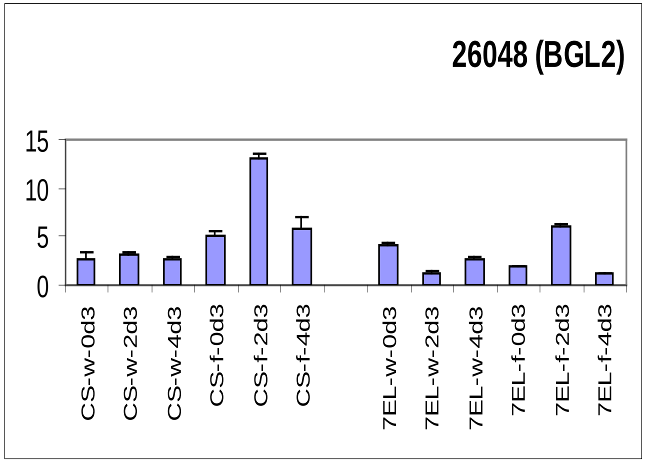
RT-g PCR validation of expression profiles on nine genes

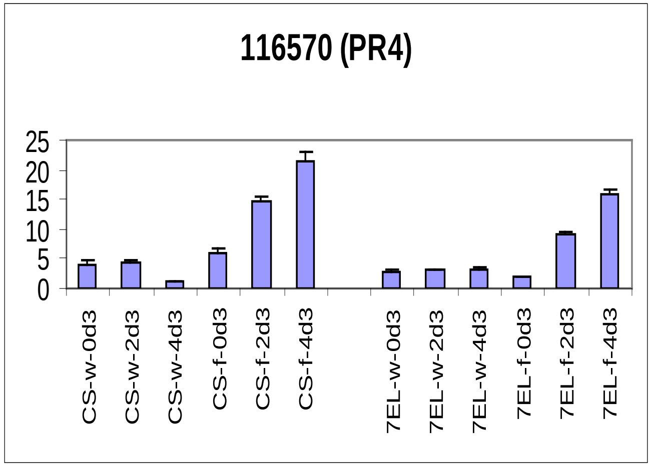


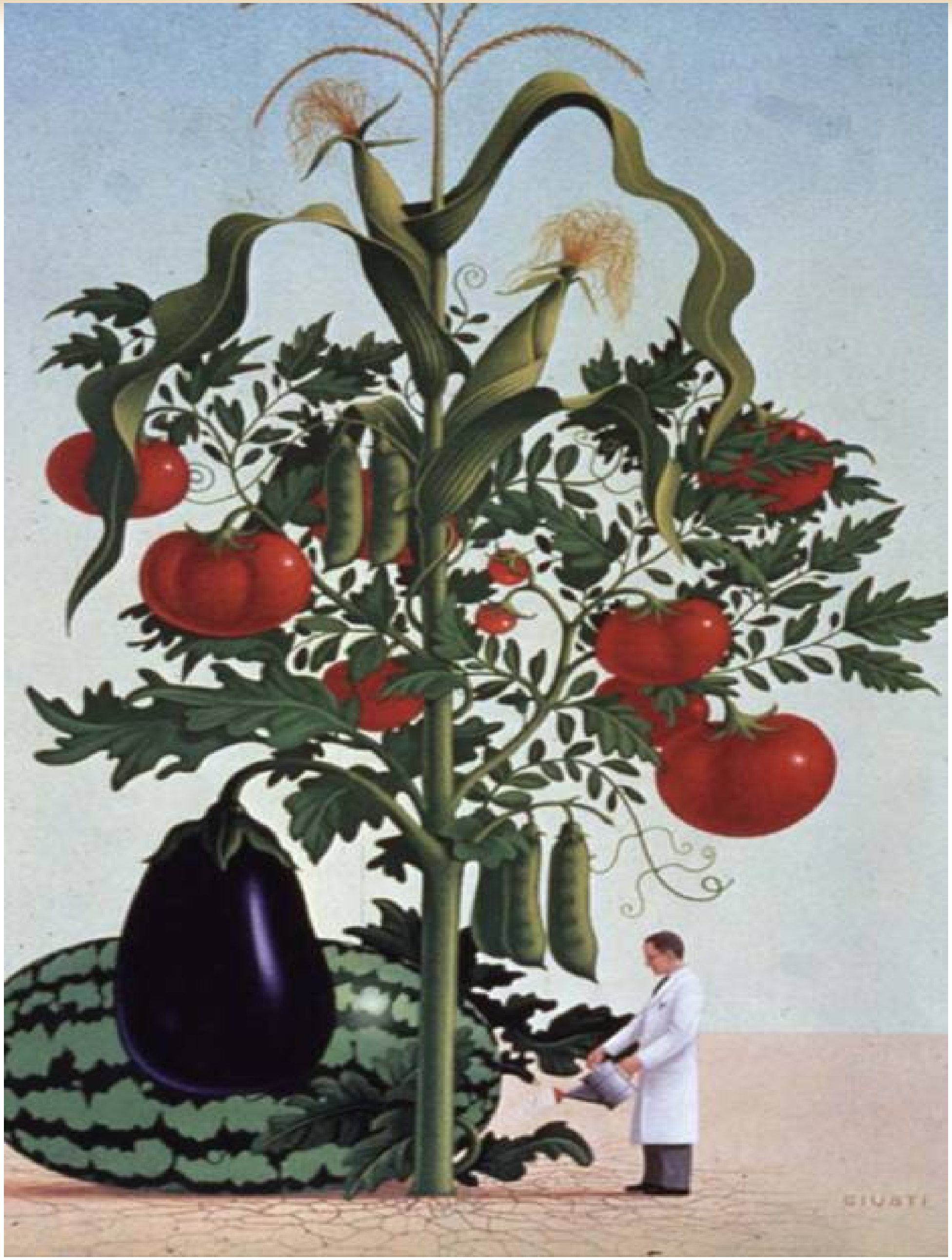
Comparison of gene expression profiles of selected defence response genes between CS and CS-7EL by RT-qPCR analysis.







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Thank You

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