

Table 4: Relative proportion of the gliadins and gluteins present in T2 seeds from the lines in class #1 intended for release. All data is expressed as a % of total seed protein content and the errors given are standard error form 3 independent determinations.

Fraction	Line							
	Controls		Transgenics					
			gamma RNAi				alpha RNAi	
Line name	b3.3	2D2 3.1 O	1C2 1.1 C	2A1 1.1 B	2D2 3.1b O	5b2 2.1 7	3c1 2.1c	4d3 1.1m
% protein	13.8	14.6	19.5	11.3	13.5	12.7	19.5	10.9
HMW-GS	6.8 ± 0.5	6.9 ± 1.8	11.6 ± 1.4	11.0 ± 1.0	12.8 ± 0.6	15.8 ± 0.1	10.1 ± 1.4	7.0 ± 0.8
LMW-GS	16.3 ± 0.5	17.3 ± 1.8	20.4 ± 1.4	21.0 ± 1.0	23.2 ± 0.6	26.0 ± 0.2	21.3 ± 1.3	19.8 ± 0.8
α/β gliadins	24.7 ± 0.8	24.1 ± 1.0	33.8 ± 0.6	34.4 ± 0.5	31.4 ± 0.7	34.2 ± 0.3	14.3 ± 2.2	22.9 ± 0.1
γ gliadins	19.8 ± 0.8	20.5 ± 1.3	4.8 ± 0.7	3.4 ± 0.9	5.2 ± 0.9	2.7 ± 0.1	18.8 ± 1.3	20.1 ± 0.9
ω gliadins	9.2 ± 0.3	9.1 ± 0.8	10.6 ± 0.1	10.8 ± 1.4	10.5 ± 0.3	10.9 ± 0.1	12.1 ± 0.9	10.1 ± 0.9

Table 5: Relative proportion of the gliadins and gluteins present in T3 seeds from the lines in class #1 intended for release. All data is expressed as a % of total seed protein content and the errors given are standard error form 3 independent determinations. Note the T3 seeds from line 5b2 2.1 7 have not been analysed by HPLC yet, however, ACID-PAGE analysis of the gliadin composition indicates that the gamma gliadins are suppressed.

Fraction	Line							
	Controls		Transgenics					
			gamma RNAi				alpha RNAi	
Line name	b3.3	2D2 3.1 O	1C2 1.1 C	2A1 1.1 B	2D2 3.1b O	5b2 2.1 7	3c1 2.1c	4d3 1.1m
% protein	13	12.9	14.4	13.3	11.9		14	12.1
HMW-GS	7.4 ± 0.1	8.4 ± 0.2	12.8 ± 0.8	11.6 ± 0.3	11.3 ± 0.1		10.3 ± 0.1	6.9 ± 0.1
LMW-GS	15.0 ± 0.1	16.8 ± 0.2	21.5 ± 0.5	21.5 ± 1.0	20.1 ± 0.1		19.9 ± 0.1	14.6 ± 0.1
α/β gliadins	24.5 ± 0.1	26.2 ± 0.3	31.7 ± 0.5	31.9 ± 0.3	29.7 ± 0.1		16.3 ± 0.1	24.6 ± 0.1
γ gliadins	18.9 ± 0.2	16.0 ± 0.2	4.6 ± 0.1	3.9 ± 0.6	6.3 ± 0.2		18.8 ± 0.1	19.0 ± 0.1
ω gliadins	9.3 ± 0.1	9.2 ± 0.1	10.0 ± 0.2	9.1 ± 0.2	9.9 ± 0.1		9.4 ± 0.1	9.4 ± 0.1

Table 6: Analysis of composition of T3 seeds from the SMEA RNAi lines relative to negative segregant lines. After weighing, seeds were pooled and milled to wholemeal flour for component analyses. Data are expressed as percentage of seed weight and are the mean of three technical replicates (SD = standard deviation). hp and NS positive and negative segregants respectively.

line	100 seeds (g) (SD)	total protein (SD)	total starch (SD)
3A-1-1 hp	5.16 (0.68)	19.31 (1.54)	56.45 (2.85)
3A-1-1 NS	5.37 (0.67)	20.66 (1.77)	56.63 (1.45)
3F-1 hp	5.16 (0.37)	16.83 (1.48)	63.45 (0.56)
3F-1 NS	5.10 (0.48)	16.36 (1.34)	62.81 (3.87)

Raw data on compositional analyses of wheat and barely transgenic lines

Line name	Moisture (% of flour)		Sucrose (% of flour)		Fructose (% of flour)		Glucose (% of flour)		Ash (% of flour)		Protein (% of flour)		Total FAT (% of flour)	
	R1	R2	R1	R2	R1	R2	R1	R2	R1	R2	R1	R2	R1	R2
85.2c (Wheat transgenic line)	8.5	8.4	1.1	1.0	0	0	0	0	2.4	2.2	15.8	15.2	3.8	3.7
12 (Wheat transgenic line)	7.4	7.4	1.1	1.2	0.2	0.2	0	0	1.9	1.8	11.2	11.3	4.5	4.5
H7 (Wheat transgenic line)	8.2	8.2	0.8	0.7	0.1	0.1	0	0	1.7	1.8	12.1	12.0	3.3	3.5
B1- Wheat control	8.5	8.5	0.7	0.6	0	0	0	0	2.3	1.9	12.7	13.2	2.9	2.8
BC10.5 (Barley transgenic line)	5.5	5.5	1.6	1.7	0.1	0.1	0	0	2.4	2.5	12.3	12.2	4.9	5.0
Golden promise (Barley control)	6.5	6.1	0.9	1.1	0.1	0.1	0.1	0.1	2.3	2.3	9.0	9.2	3.1	3.1

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