

Table 1 Suppl. Sequences of the primer pairs employed in this study. Ta - annealing temperature. Primers based on rye *ScMATE1* (*ScAACT1*) gene reported by Silva-Navas *et al.* (2012).

Primer	Sequence (5' → 3')	Ta	Purpose
AACT1-qPCR-1F	CCCACCGAGCCTTAAATCC	60°C	quantitative RT-PCR
AACT1-qPCR-1R	GAGCAGCAGGAATCCACACC		
cDNA-1F	CGAGCGAACCATCGGCTGATCGAC	56°C	full-length cDNA
cDNA-1R	TCACTTCCGGAGGAAAGCCCATGG		
cDNA-2F	GACCTCTCAGGCAAGCATCGATCC		

Table 2 Suppl. Software programs used to deduce the structure of ScMATE1 proteins.

Program	URL address	Reference
TopPred	http://mobyli.pasteur.fr/cgi-bin/MobyliPortal/portal.py?form=toppred	Claros and Von Heijne (1994)
SOSUI	http://bp.nuap.nagoya-u.ac.jp/sosui/	Hirokawa <i>et al.</i> (1998)
PSIpred	http://bioinf.cs.ucl.ac.uk/psipred/psiform.html	McGuffin <i>et al.</i> (2000)
TMHMM	http://www.cbs.dtu.dk/services/TMHMM/	Krogh <i>et al.</i> (2001)
HMMTOP	http://www.enzim.hu/hmmtop	Tusnády and Simon (2001)
DAS	http://mendel.imp.univie.ac.at/sat/DAS/DAS.html	Cserzo <i>et al.</i> (2002)

Table 3 Suppl. Diversity parameters obtained comparing eleven different sequences of cDNA from different rye cultivars (four from Lamego, two from Montalegre, and one from each of Ailés, Imperial, Linea V, Petkus, and Riodeva). *A* - and six different sequences of cDNA from six different species of *Secale* (one from each of *S. ancestrale*, *S. segetale*, *S. strictum*, *S. sylvestre*, *S. vavilovii*, and *S. cereale* cv. Imperial); *B* - using the *DnaSP* v. 5.0 software. Ex - exon, SWAG - sites with alignments gaps, IMS - invariable (monomorphic) sites, VPS - variable (polymorphic) sites, TNM - total number of mutations, SVS - singleton variable sites, PIS - parsimony informative sites, TNSC - total number of synonymous changes, TNRC - total number of replacement changes, Hd - haplotype (gene) diversity, ND (Pi) - nucleotide diversity, k - average number of nucleotide differences.

<i>A</i>	<i>Secale cereale</i>	Ex1	Ex2	Ex3	Ex4	Ex5	Ex6	Ex7	Ex8	Ex9	Ex10	Ex11	Ex12	Ex13	cDNA
	Exon size [bp]	200	122	207	194	136	97	101	164	72	117	96	122	43	1671
	SWAG	6	0	0	0	0	0	0	0	0	0	0	0	0	6
	IMS	179	118	204	185	135	95	101	157	70	114	93	120	43	1614
	VPS	15	4	3	9	1	2	0	7	2	3	3	2	0	51
	TNM	15	4	3	9	1	2	0	7	3	3	3	2	0	52
	SVS	7	3	3	7	1	2	0	2	2	3	3	2	0	35
	PIS	8	1	0	2	0	0	0	5	0	0	0	0	0	16
	TNSC	6	0	0	1	0	2	0	1	3	3	3	2	0	21
	TNRC	9	4	3	8	1	0	0	6	0	0	0	0	0	31
	Hd	0.964	0.345	0.345	0.727	0.182	0.345	0	0.491	0.491	0.491	0.182	0.345	0	1
	ND (Pi)	0.024180	0.007150	0.002640	0.00993	0.00134	0.00375	0	0.0122	0.00732	0.00466	0.00568	0.00298	0	0.00755
	k	4.691	0.873	0.545	1.927	0.182	0.364	0	2	0.527	0.545	0.545	0.364	0	12.564
<i>B</i>	<i>Secale</i> genus	Ex1	Ex2	Ex3	Ex4	Ex5	Ex6	Ex7	Ex8	Ex9	Ex10	Ex11	Ex12	Ex13	cDNA
	Exon size [bp]	197	122	207	194	136	97	101	164	72	117	96	122	43	1668
	SWAG	1	0	0	0	0	0	0	0	0	0	0	0	0	1
	IMS	184	116	201	188	131	92	99	147	70	112	89	121	43	1593
	VPS	10	6	6	6	5	5	2	17	2	5	7	1	0	72
	TNM	10	6	6	6	5	5	2	17	2	5	7	1	0	72
	SVS	8	5	3	6	2	3	2	5	1	4	3	1	0	43
	PIS	2	1	3	0	3	2	0	12	1	1	4	0	0	29
	TNSC	5	1	1	2	5	1	0	2	1	3	5	1	0	27
	TNRC	5	5	5	4	0	4	2	15	1	2	2	0	0	45
	Hd	1	1	1	0.8	0.933	0.933	0.6	0.933	0.733	0.8	1	0.333	0	1
	ND (Pi)	0.019930	0.018580	0.0132	0.01031	0.01765	0.02131	0.0066	0.05081	0.01204	0.01595	0.03403	0.00273	0	0.01842
	k	3.867	2.267	2.733	2	2.4	2.067	0.667	8.333	0.867	1.867	3.267	0.333	0	30.667

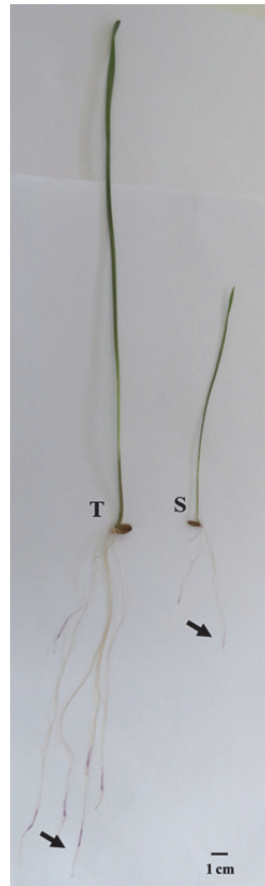


Fig. 1 Suppl. Example of a tolerant (T) (*S. segetale*) and a sensitive (S) (*S. sylvestre*) rye genotype. Arrows shows the root re-growth in the tolerant rye and the lacking re-growth in the sensitive one.

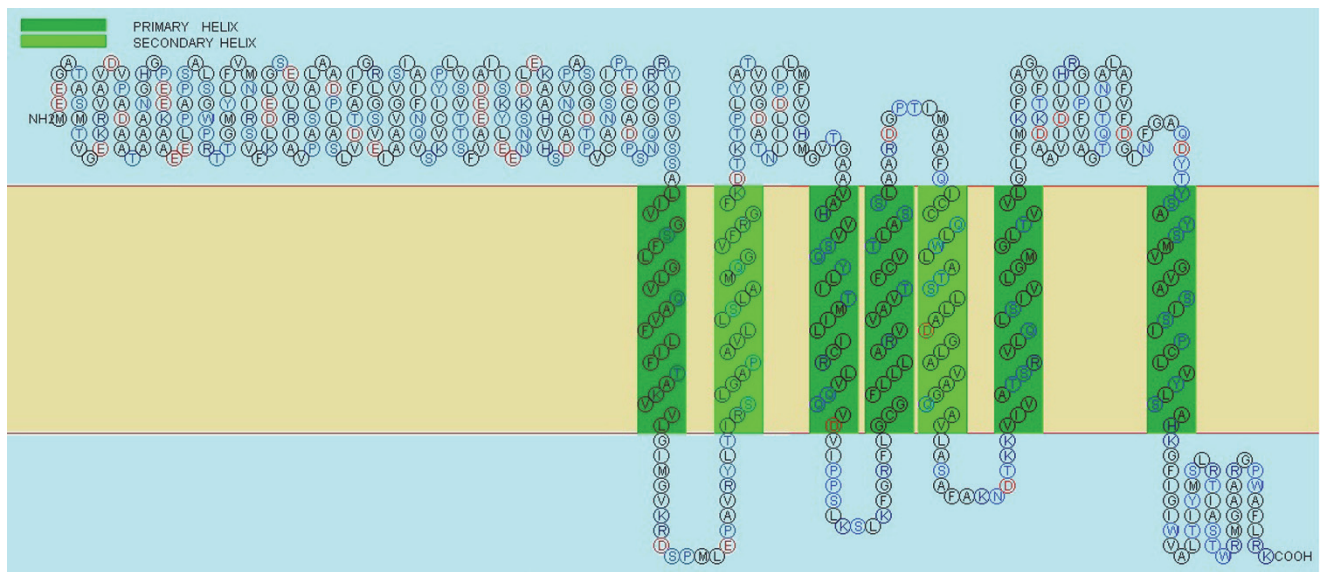


Fig. 2 Suppl. Transmembrane domains of the ScMATE1 proteins predicted by SOSUI software (Hirokawa et al. 1998). This software predicted seven transmembrane domains for all ScMATE1 protein analyzed except for *S. strictum* and *S. sylvestre*, with a prediction of eight transmembrane domains. The synonymous changes (blue circles), the conserved amino acids (yellow circles) and the non-synonymous changes (white circles) detected between the 12 hypothetical proteins analyzed are indicated.

References

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