Table S1 Number of individuals in the test-cross progeny by seasons, line, rearing regimes, and chromosome

Season	Line	Chromosome X		Chromosome 2		Chromosome 3	
		Normal conditions	Desiccation hardening	Normal conditions	Desiccation hardening	Normal conditions	Desiccation hardening
Autumn	A1	251	266	234	261	223	230
	A2	256	239	258	232	244	248
	A3	244	262	240	247	238	235
	A4	283	269	269	262	254	253
	A5	272	236	238	239	233	234
	A6	263	241	225	245	247	230
	A7	251	239	303	230	246	257
Winter	W1	238	254	246	240	258	229
	W2	257	237	239	238	246	251
	W3	272	271	260	265	241	241
	W4	262	245	268	248	260	236
	W5	249	263	238	250	237	231
	W6	254	250	280	247	230	222
	W7	265	237	272	238	225	239

Text S2 Statistical analysis of crossover interference

Crossover interference was analyzed using a restricted maximum-likelihood approach. Recombination rates were estimated in the single-interval analysis and then handled as known parameters during the estimation of the coefficients of coincidence (C). Such an approach simplifies inference about the effects of season, treatment, and line on crossover interference. Thus, four vectors of parameters were estimated and compared:

$$\Theta_{ac} = (C_{ac1}, \ldots, C_{ac7}),\ \Theta_{at} = (C_{at1}, \ldots, C_{at7}),\ \Theta_{wc} = (C_{wc1}, \ldots, C_{wc7}),\ \text{and}\ \Theta_{wt} = (C_{wt1}, \ldots, C_{wt7}),$$

where the indices ac, at, wc and wt stand for autumn-control, autumn-treatment, winter-control, and winter-treatment combinations, respectively. In general, for a pair of consequent intervals flanked by three markers (m1–m2–m3), the log-likelihood function for a sample from test-cross progeny can be presented as

$$L(r_1, r_2, C) = n_{00}\cdot\ln(1-r_1-r_2+r_1\cdot r_2\cdot C) + n_{11}\cdot\ln(r_1\cdot r_2\cdot C) + n_{10}\cdot\ln(r_1-r_1\cdot r_2\cdot C) + n_{01}\cdot\ln(r_2-r_1\cdot r_2\cdot C),$$

where r_1 and r_2 are the recombination rates in m1–m2 and m2–m3 intervals; C is the coefficient of coincidence; n_{00} is the observed number of non-recombinants for both intervals; n_{10}, n_{01} and n_{11} are the numbers of recombinants for the first, the second, and both intervals, respectively. As indicated above, in our estimation of parameter C, we maximize the likelihood function $L(r_1, r_2, C)$ under the restriction that the values of r_1 and r_2 are already estimated in single-interval analysis. This allows avoiding situations when the estimate of recombination rate in a certain interval, obtained in three-locus analysis, depends on the second interval.

To estimate the effect of *season*, the log-likelihood functions were assumed dependent on vectors of seven variables, $\Theta_{ac} = (C_{ac1}, \ldots, C_{ac7})$ and $\Theta_{wc} = (C_{wc1}, \ldots, C_{wc7})$. H_0-hypothesis was that C does not depend on season or line within season, i.e., $C_{ac1} = \ldots = C_{ac7} = C_{wc1} = \ldots = C_{wc7}$. H_1-hypothesis implied that C depends only on season: $C_{ac1} = \ldots = C_{ca7}$ and $C_{wc1} = \ldots = C_{wc7}$. H_2-hypothesis implied that C depends on both season and line, so that all 14 parameters are needed in the general case. The estimates of C vectors for H_0, H_1, and H_2 required optimization of likelihood functions with one, two, and 14 parameters, respectively. To discriminate between the hypotheses, we used the likelihood-ratio test with df=1, 12, and 13 for the pairs H_0–H_1, H_1–H_2, and H_0–H_2, respectively.

The effect of *treatment* was estimated given the effects of season and line. Here, H_0-hypothesis assumed no difference in C between control and treatment for each of seven lines within each season (implying

seven model parameters per season). H_1-hypothesis assumed that *C* changes under treatment (implying 14 model parameters per season). The standard likelihood-ratio test with df=14–7=7 was used to discriminate between H_0 and H_1. However, the standard test is not sensitive to the direction of induced changes in *C*. As a result, if changes in all lines are pronounced but oppositely directed, then H_0 will be rejected even in the absence of an overall directed effect of treatment. To overcome this problem, the following test was used. Let

$Y = \sum Y_l/\sqrt{7}$, where $Y_l = \sqrt{X_l^2} \cdot \mathrm{sign}\left(C_{t,l} - C_{c,l}\right)$, $X_l^2 = 2[\log L(\mathrm{H}_1) - \log L(\mathrm{H}_0)]$, and index l stands for line.

Under H_0, X_l^2 has χ^2-distribution with df=1. When the effect of treatment has no consistent direction (i.e. when the treatment-control differences across lines within season have symmetric distribution), Y_l has an asymptotically normal distribution. Hence, under H_0 and the mentioned symmetry, *Y* is also normally distributed. If the absolute value of *Y* is lower than a critical value (even if X^2_{total} is higher than the critical value), we conclude that the significance of heterogeneity of stress response of *C* values is caused by the heterogeneity of lines' response direction rather than the overall direction of response.

Table S3 The effect of season on crossover rates (based on the Student's *t*-test for independent samples)

Interval	Recombination rate (%) ± SE		Effect of season		
	Autumn hybrids	Autumn hybrids	*t*	*p*	*p*(FDR)
Chromosome X					
y-cv	12.20 ± 0.49	10.97 ± 0.51	1.78	0.100	0.130
cv-v	19.18 ± 0.54	21.44 ± 0.53	-2.96	0.012	**0.022**
v-f	19.90 ± 0.70	23.29 ± 0.69	-3.432	0.005	**0.011**
Chromosome 2					
al-dp	7.39 ± 0.49	10.62 ± 0.45	-4.926	$4 \cdot 10^{-4}$	**0.002**
dp-b	24.90 ± 0.52	23.04 ± 0.60	2.374	0.035	**0.057**
b-pr	3.32 ± 0.34	3.95 ± 0.38	-1.312	0.214	0.253
pr-c	14.84 ± 0.49	19.85 ± 0.51	-6.901	$2 \cdot 10^{-5}$	$\mathbf{2 \cdot 10^{-4}}$
c-px	18.72 ± 0.42	21.95 ± 0.59	-4.522	0.001	**0.003**
px-sp	5.37 ± 0.31	3.68 ± 0.32	3.638	0.003	**0.010**
Chromosome 3					
ru-h	20.33 ± 0.34	20.25 ± 0.68	0.159	0.877	0.877
h-th	15.26 ± 0.28	17.23 ± 0.48	-3.583	0.004	**0.010**
th-sr	15.11 ± 0.43	15.51 ± 0.46	-0.641	0.534	0.579
sr-e	6.12 ± 0.12	7.00 ± 0.37	-2.266	0.043	**0.062**

FDR-corrected significances *p*(FDR)<0.1 are bolded

Table S5 Modulation of the effect of treatment (desiccation stress) on crossover rate by desiccation tolerance (based on the repeated-measure ANCOVA with treatment as the major factor and desiccation tolerance as the covariate)

Interval	Both seasonal cohorts			Autumn hybrids		Winter hybrids	
	F	*p*	*p*(FDR)	*F*	*P*	*F*	*p*
Chromosome X							
y-cv	9.317	0.010	**0.036**	0.132	0.731	3.184	0.134
cv-v	5.994	0.031	**0.081**	2.157	0.202	0.066	0.807
v-f	2.573	0.135	0.251	0.026	0.878	2.725	0.160
Chromosome 2							
al-dp	4.024	0.068	0.147	1.260	0.313	$4.1 \cdot 10^{-4}$	0.985
dp-b	1.061	0.323	0.420	0.838	0.402	1.091	0.344
b-pr	0.297	0.596	0.596	5.176	0.072	0.515	0.505
pr-c	11.081	0.006	**0.036**	0.004	0.953	0.040	0.850
c-px	1.762	0.209	0.313	0.127	0.736	0.072	0.799
px-sp	9.282	0.010	**0.036**	0.071	0.801	1.368	0.295
Chromosome 3							
ru-h	9.004	0.011	**0.036**	2.116	0.206	1.042	0.354
h-th	1.695	0.217	0.313	0.432	0.540	1.801	0.237
th-sr	0.542	0.476	0.563	0.096	0.769	0.519	0.503
sr-e	0.350	0.565	0.596	0.004	0.952	0.463	0.526

FDR-corrected significances $p(\text{FDR})<0.1$ are bolded

Tables S6 Marker segregation and changes in recombinant frequencies for the recombination-reactive intervals

Interval	Group	Number of offspring				Frequency of marker, %		Changes in frequency of recombinant, %	
		++	+*m1*	*m2*+	*m1m2*	*m1*	*m2*	+*m1*	*m2*+
Intervals with a significant effect of season (normal conditions)									
cv–v	Autumn	756	183	166	715	49.34	48.41	0.91	1.34
	Winter	737	197	188	675	48.53	48.02		
v-f	Autumn	743	179	184	714	49.07	49.34	2.30	1.08
	Winter	707	218	201	671	49.47	48.53		
al-dp	Autumn	867	58	72	770	46.86	47.65	1.32	1.92
	Winter	871	83	108	741	45.70	47.09		
dp–b	Autumn	728	211	229	599	45.84	46.86	-0.13	-1.70
	Winter	766	213	203	621	46.26	45.70		
pr-c	Autumn	799	146	117	705	48.16	46.52	2.44	2.53
	Winter	773	193	165	672	47.98	46.42		
c-px	Autumn	735	181	150	701	49.92	48.16	1.68	1.49
	Winter	723	215	180	685	49.92	47.98		
px-sp	Autumn	831	54	42	840	50.60	49.92	-1.11	-0.66
	Winter	868	35	31	869	50.14	49.92		
h–th	Autumn	745	132	125	683	48.37	47.95	0.36	1.60
	Winter	722	139	153	683	48.44	49.26		
sr–e	Autumn	815	56	47	767	48.84	48.31	0.33	0.57
	Winter	816	62	57	762	48.56	48.26		
Intervals with a significant effect of treatment (autumn hybrids)									
cv-v	Control	756	183	166	715	49.34	48.41	1.87	2.75
	Treatment	672	209	208	663	49.77	49.71		
v-f	Control	743	179	184	714	49.07	49.34	2.09	1.82
	Treatment	671	209	209	663	49.77	49.77		
pr-c	Control	799	146	117	705	48.16	46.52	1.99	1.83
	Treatment	727	176	145	668	49.18	47.38		
c-px	Control	735	181	150	701	49.92	48.16	1.59	1.94
	Treatment	669	203	179	665	50.58	49.18		
h–th	Control	745	132	125	683	48.37	47.95	1.06	1.30
	Treatment	732	150	147	658	47.90	47.72		
th–sr	Control	743	127	128	687	48.31	48.37	1.65	0.82

	Treatment	724	155	142	666	48.67	47.90		
Intervals with a significant effect of treatment (winter hybrids)									
cv–v	Control	737	197	188	675	48.53	48.02	0.99	1.89
	Treatment	683	210	217	647	48.78	49.17		
al–dp	Control	871	83	108	741	45.70	47.09	-0.26	-0.78
	Treatment	810	75	90	751	47.86	48.73		