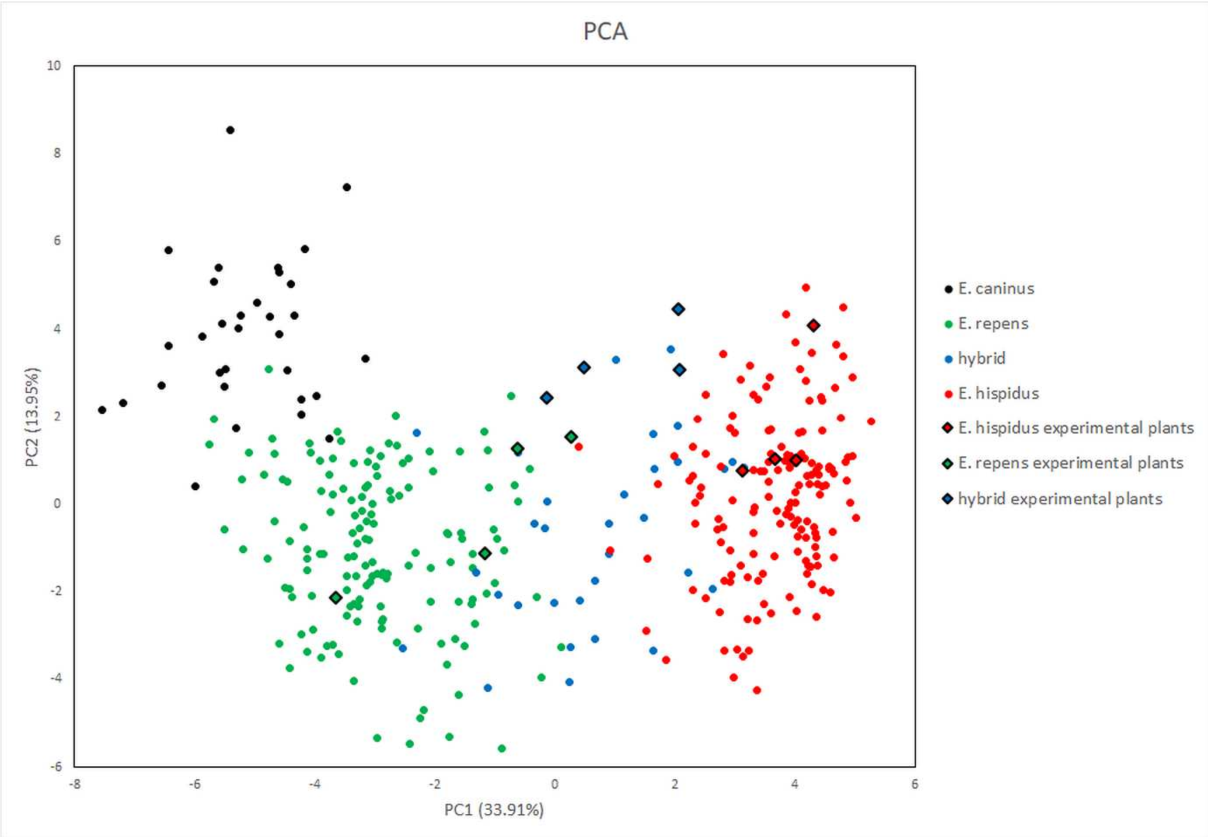
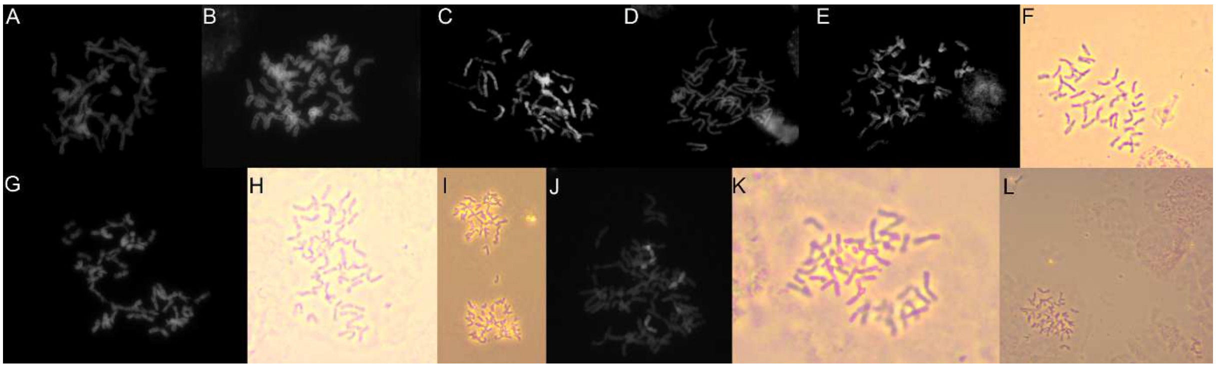
Urfusová R., Mahelka V., Krahulec F., Veškrna O. & Urfus T. (2022) The mentor effect increases the rate of selfing in couchgrasses. – Preslia 94: 377–397.

Electronic Appendix 1. – Parental plants in pollination experiments, their absolute genome sizes (GS; in pg) and ploidy levels. Ploidy of *Elymus* plants were verified by chromosome counts, ploidy levels of crops were verified by their producers – the breeding stations Selgen and Danko. *Elymus* taxa were morphologically determined and their identity was confirmed by morphometrics (following Urfusová et al. 2021).

Parental plant	Species	GS (pg)	ploidy level
MO24c	*E. repens*	25.02	6x
CS22a	*E. repens*	24.50	6x
T14P4	*E. hispidus*	27.77	6x
CS1f	*E. hispidus*	27.85	6x
MO5b	hybrid	26.74	6x
T13P12	hybrid	28.77	6x
T10P7	*E. repens*	30.81	7x
T14P8	*E. repens*	30.22	7x
T9P1	hybrid	30.50	7x
T1P1	hybrid	35.44	8x
T4P4	*E. hispidus*	33.18	8x
T4P5	*E. hispidus*	32.71	8x
Secale Gadello	*Secale cereale*	17.55	2x
JJ 6R 610 A	*Hordeum vulgare*	10.84	2x
Lancelot	*Hordeum vulgare*	10.84	2x
JJ cross 43	*Hordeum vulgare*	11.21	2x
Triticum monococcum	*Triticum monococcum*	12.61	2x
K1 Bohemia	*Triticum aestivum*	37.74	6x
SG-U2078-18	*Triticum aestivum*	36.48	6x
K2 Illusion	*Triticum aestivum*	35.71	6x
(SG-S1500-14) Lorien	*Triticum aestivum*	36.49	6x
SG-U5003-16	*Triticum aestivum*	35.76	6x
Viriato	*Triticum aestivum*	38.12	6x
Triticale MAMUT	*Triticale*	43.40	6x
Triticale PORTO	*Triticale*	42.08	6x



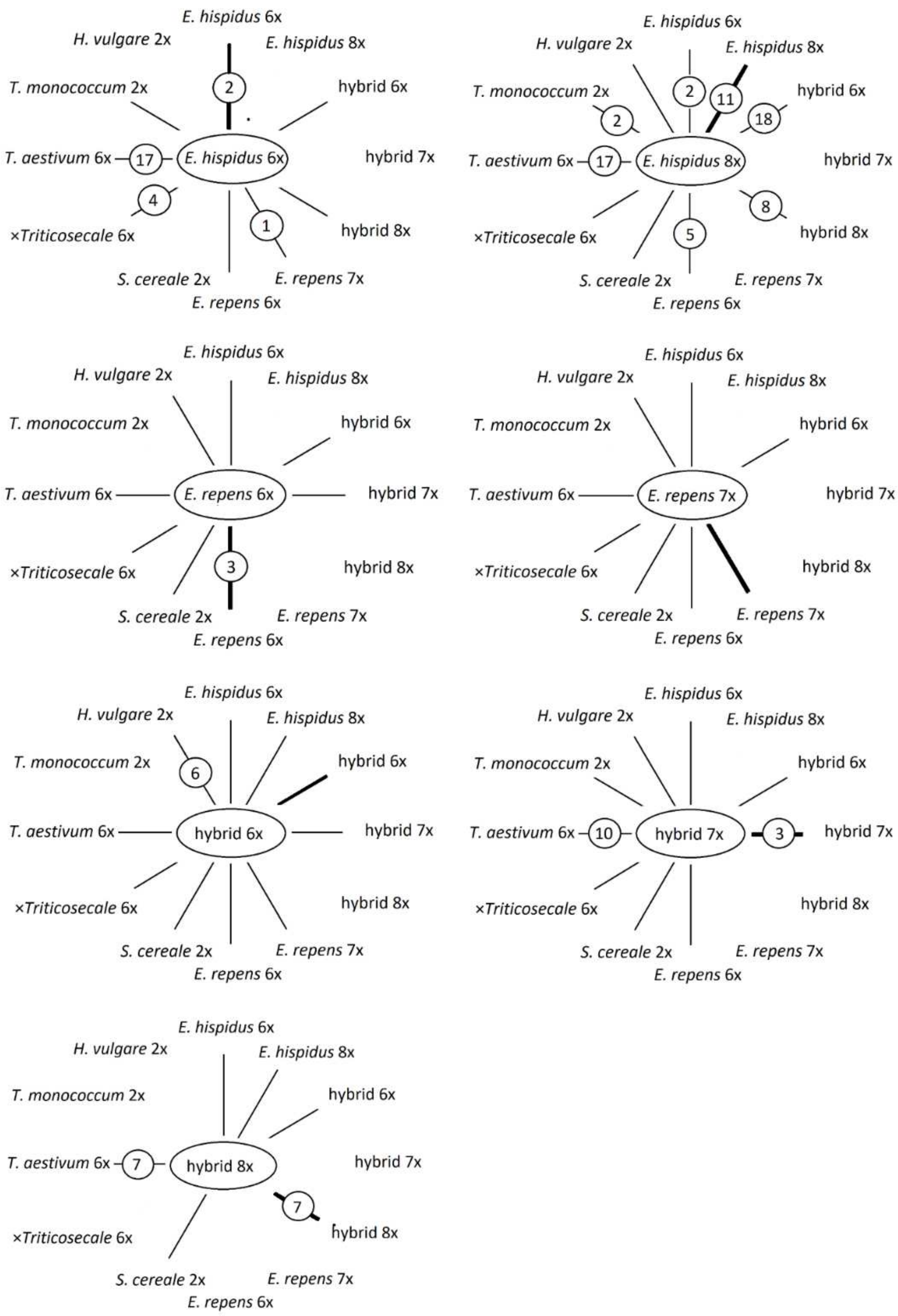
Electronic Appendix 2. – Ordination diagram of principal component analysis (PCA) of individuals from the study of Urfusová et al. (2021), with added *Elymus* plants used in this study – encircled in black.



Electronic Appendix 3. – Chromosomes of parental plants. A, B – hexaploid *E. repens*; C, D – hexaploid hybrid; E, F – hexaploid *E. hispidus*; G, H – heptaploid *E. repens*; I – heptaploid hybrid; J – octoploid hybrid; K, L – octoploid *E. hispidus*. Black-and-white images – magnification 600×, colour images – 400×.

Electronic Appendix 4. – *Elymus* species used in the open-pollination control experiment. The ploidy levels of part of these plants were confirmed by chromosome counts.

sample	**species**	**GS (pg)**	**ploidy**
Rum17-3c	*E. repens*	24.77	6x
MO24c	*E. repens*	25.02	6x
Mol17-3b	*E. repens*	25.09	6x
CS1f	*E. hispidus*	27.85	6x
SR17-1a	*E. hispidus*	28.11	6x
Ukr17-3c	*E. hispidus*	30.01	6x
Ukr17-7b	*E. hispidus*	29.55	6x
Ukr17-3ch	*E. hispidus*	29.12	6x
MO5b	hybrid	26.74	6x



Electronic Appendix 5. – Schematically expressed pollination experiment based on maternal plants (marked by ellipse) and realized crossings linked to pollen donor taxa/ploidal cytotypes. The thin line corresponds to induced selfing and the thick line to core selfing. Successful pollinations are marked by numbers of developed seeds in a circle.

Electronic Appendix 6. – Results of particular generalized linear mixed-effects models (GLMM) testing the effect of ploidy level and species of maternal plant and paternal plant and type of selfing on seed set with Tukey Contrasts. Seed set refers to number of seeds/number of florets ratio of each single pollinated spike. Maternal plant individual was used as random effect.

GLMM				
Seed set: entire				
maternal plant ploidy level (regardless of species):	$\chi 2$ (2) = 14.884, Df resid = 257, p = 0.0005862			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
7x - 6x == 0	0.8363	0.9745	0.858	0.66326
8x - 6x == 0	-2.5969	0.8476	-3.064	0.00620
8x - 7x == 0	-3.4331	1.1140	-3.082	0.00601
maternal plant species (regardless of ploidy level):	$\chi 2$ (2) = 17.474 Df resid = 257, p = 0.0001605			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
E. repens - *E. hispidus* == 0	3.875	1.050	3.692	< 0.001
hybrid - *E. hispidus* == 0	2.027	0.681	2.976	0.00789
hybrid - *E. repens* == 0	-1.848	1.032	-1.790	0.16802
maternal plant species combined with ploidy level:	$\chi 2$ (6) = 30.193, Df resid = 253, p = 3.613e^{-05}			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
E. hispidus 8x - *E. hispidus* 6x == 0	-1.6108	0.8830	-1.824	0.48151
E. repens 6x - *E. hispidus* 6x == 0	2.0220	1.2307	1.643	0.60732
E. repens 7x - *E. hispidus* 6x == 0	21.4800	256.0000	0.084	1.00000
hybrid 6x - *E. hispidus* 6x == 0	2.6343	1.0456	2.519	0.12578
hybrid 7x - *E. hispidus* 6x == 0	0.6897	1.0368	0.665	0.99271
hybrid 8x - *E. hispidus* 6x == 0	-0.0712	0.9711	-0.073	1.00000

	Estimate	Std. Error	z value	Pr(>|z|)
E. repens 6x - *E. hispidus* 8x == 0	3.6328	1.2579	2.888	0.04713
E. repens 7x - *E. hispidus* 8x == 0	23.0908	256.0014	0.090	1.00000
hybrid 6x - *E. hispidus* 8x == 0	4.2451	1.1118	3.818	0.00199
hybrid 7x - *E. hispidus* 8x == 0	2.3005	1.0811	2.128	0.29182
hybrid 8x - *E. hispidus* 8x == 0	1.5396	0.9884	1.558	0.66597
E. repens 7x - *E. repens* 6x == 0	19.4580	256.0028	0.076	1.00000
hybrid 6x - *E. repens* 6x == 0	0.6123	1.3761	0.445	0.99922
hybrid 7x - *E. repens* 6x == 0	-1.3323	1.3697	-0.973	0.94967
hybrid 8x - *E. repens* 6x == 0	-2.0932	1.3211	-1.584	0.64770
hybrid 6x - *E. repens* 7x == 0	-18.8457	256.0020	-0.074	1.00000
hybrid 7x - *E. repens* 7x == 0	-20.7903	256.0019	-0.081	1.00000
hybrid 8x - *E. repens* 7x == 0	-21.5512	256.0018	-0.084	1.00000
hybrid 7x - hybrid 6x == 0	-1.9446	1.1874	-1.638	0.61135
hybrid 8x - hybrid 6x == 0	-2.7055	1.1746	-2.303	0.20547
hybrid 8x - hybrid 7x == 0	-0.7609	1.1511	-0.661	0.99295
autonomous vs. induced selfing:	$\chi 2$ (1) = 8.3748, Df resid = 258 , p = 0.003805			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
autonomous selfing - induced selfing== 0	0.7188	0.2576	2.79	0.00527

Seed set: <u>hexaploid maternal plant</u>				
<u>maternal plant species:</u>	$\chi 2$ (2) = 9.7565, Df resid = 126, p = 0.00761			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
E. repens - *E. hispidus* == 0	2.0225	1.2586	1.607	0.2395
hybrid - *E. hispidus* == 0	2.6777	1.1345	2.360	0.0469
hybrid - *E. repens* == 0	0.6551	1.4544	0.450	0.8930
autonomous vs. induced selfing:	$\chi 2$ (1) = 2.9208, Df resid = 128, p = 0.08745			

Seed set: **maternal plant *E. hispidus***

maternal plant ploidy level:	$\chi 2$ (1) = 4.407, Df resid = 79, p = 0.03579			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
8x - 6x == 0	-1.3904	0.6583	-2.112	0.0347
autonomous vs. induced selfing:	$\chi 2$ (1) = 0.0006874, Df resid = 79, p = 0.00176			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
selfing - induced== 0	1.0201	0.3261	3.128	0.00176

Seed set: **maternal plant *E. repens***

maternal plant ploidy level:	$\chi 2$ (1) = 4.1199, Df resid = 64, p = 0.04238
autonomous vs. induced selfing:	$\chi 2$ (1) = 3.9436, Df resid = 64, p = 0.04705

Seed set: **maternal plant hybrid**

maternal plant ploidy level:	$\chi 2$ (2) = 6.0933, Df resid = 108, p = 0.04752			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
7x - 6x == 0	-2.333	1.745	-1.337	0.3744
8x - 6x == 0	-3.761	1.826	-2.060	0.0983
8x - 7x == 0	-1.428	1.833	-0.779	0.7159
autonomous vs. induced selfing:	$\chi 2$ (1) = 0.61782, Df resid = 109, p = 0.4319			

Seed set: **autonomous selfing**

maternal plants species (regardless on ploidy level):	$\chi 2$ (2) = 6.407, Df resid = 112, p = 0.04062			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
E. *repens* - *E. hispidus* == 0	1.7988	0.7542	2.385	0.0442
hybrid - *E. hispidus* == 0	0.9651	0.5575	1.731	0.1906

hybrid - *E. repens* == 0	-0.8337	0.7445	-1.120	0.4979
ploidy level of maternal plants (regardless on species):	χ2 (2) = 7.2812, Df resid = 112, p = 0.02624			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
7x - 6x == 0	0.3314	0.8441	0.393	0.9178
8x - 6x == 0	-1.3140	0.6528	-2.013	0.1076
8x - 7x == 0	-1.6454	0.7852	-2.095	0.0894

Seed set: induced selfing

diploid vs. polyploid paternal plant	χ2 (1) = 1.941, Df resid = 142, p = 0.1636			
ploidy level of maternal plants (regardless on species):	χ2 (2)= 8.2165, Df resid = 141, p = 0.01644			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate Std.	Error	z value	Pr(>|z|)
7x - 6x == 0	1.157	1.431	0.809	0.6935
8x - 6x == 0	-2.995	1.209	-2.478	0.0344
8x - 7x == 0	-4.152	1.653	-2.511	0.0315
maternal plants species (regardless on ploidy level)	χ2 (2) = 17.269, Df resid = 141, p = 0.0001779			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
E. repens - *E. hispidus* == 0	20.341	6311.326	0.003	0.99999
hybrid - *E. hispidus* == 0	3.087	1.085	2.846	0.00883
hybrid - *E. repens* == 0	-17.253	6311.326	-0.003	1.00000
diploid vs. polyploid paternal plant	χ2 (1) = 1.941, Df resid = 142, p = 0.1636			
ploidy level of paternal plants (regardless on species):	χ2 (3)= 15.142, Df resid = 140, p = 0.0017			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)

6x - 2x == 0	0.9742	0.3805	2.560	0.0434
7x - 2x == 0	1.4377	1.1397	1.261	0.5545
8x - 2x == 0	-0.9016	0.8214	-1.098	0.6617
7x - 6x == 0	0.4635	1.0894	0.425	0.9704
8x - 6x == 0	-1.8758	0.7328	-2.560	0.0434
8x - 7x == 0	-2.3394	1.3094	-1.787	0.2511

<u>paternal plants species (regardless on ploidy level):</u>	$\chi2$ (7) = 29.389, Df resid = 136, p = 0.0001229			
Multiple Comparisons of Means: Tukey Contrasts:				
	Estimate	Std. Error	z value	Pr(>|z|)
E. repens - *E. hispidus* == 0	0.35335	0.98805	0.358	1.0000
Hordeum vulgare - *E. hispidus* == 0	-1.12641	0.99041	-1.137	0.9398
hybrid - *E. hispidus* == 0	0.01617	0.91425	0.018	1.0000
Secale cereale - *E. hispidus* == 0	-0.03220	1.05058	-0.031	1.0000
T. aestivum - *E. hispidus* == 0	1.11796	0.94695	1.181	0.9271
T. monococcum - *E. hispidus* == 0	0.84444	1.18872	0.710	0.9960
×*Triticosecale* - *E. hispidus* == 0	0.92341	1.05152	0.878	0.9855
Hordeum vulgare - *E. repens* == 0	-1.47975	0.57292	-2.583	0.1436
hybrid - *E. repens* == 0	-0.33717	0.52468	-0.643	0.9979
Secale cereale - *E. repens* == 0	-0.38555	0.68130	-0.566	0.9991
T. aestivum - *E. repens* == 0	0.76462	0.55956	1.366	0.8545
T. monococcum - *E. repens* == 0	0.49110	0.86670	0.567	0.9990
×*Triticosecale* - *E. repens* == 0	0.57007	0.70786	0.805	0.9913
hybrid - *Hordeum vulgare* == 0	1.14258	0.45951	2.487	0.1796
Secale cereale - *Hordeum vulgare* == 0	1.09420	0.53618	2.041	0.4211
T. aestivum - *Hordeum vulgare* == 0	2.24437	0.48971	4.583	<0.001
T. monococcum - *Hordeum vulgare* == 0	1.97085	0.76714	2.569	0.1487
×*Triticosecale* - *Hordeum vulgare* == 0	2.04982	0.69743	2.939	0.0567
Secale cereale - hybrid == 0	-0.04837	0.58803	-0.082	1.0000
T. aestivum - hybrid == 0	1.10179	0.36763	2.997	0.0479

T. monococcum - hybrid == 0	0.82827	0.80150	1.033	0.9637
×*Triticosecale* - hybrid == 0	0.90724	0.57101	1.589	0.7299
T. aestivum - *Secale cereale* == 0	1.15016	0.61234	1.878	0.5319
T. monococcum - *Secale cereale* == 0	0.87664	0.85208	1.029	0.9646
×*Triticosecale* - Secale cereale == 0	0.95561	0.78691	1.214	0.9162
T. monococcum - *T. aestivum* == 0	-0.27352	0.82062	-0.333	1.0000
×*Triticosecale* - *T. aestivum* == 0	-0.19455	0.62448	-0.312	1.0000
×*Triticosecale* - *T. monococcum* == 0	0.07897	0.95564	0.083	1.0000

Electronic Appendix 7. – Results of generalized linear mixed-effects models (GLMM) testing the effect of ploidy level and species of maternal plant and species of paternal plant on seed set and germination rate. Seed set refers to number of seeds/number of florets ratio of each single pollinated spike.

Model used	GLMM	GLMM
dataset	seed set: entire	germination rate: entire
Maternal plant:		
maternal plant species	$\chi 2$ (2) = 12.247, Df resid = 246, p = 0.002191	$\chi 2$ (2) = 0.0631, Df resid = 37, p = 0.9689
maternal plant ploidy	$\chi 2$ (2) = 5.3194, Df resid = 246, p = 0.06997	$\chi 2$ (2) = 0.0851, Df resid = 37, p = 0.9584
Paternal plant:		
paternal plant species	$\chi 2$ (6) = 26.31, Df resid = 250, p = 0.0001949	$\chi 2$ (6) = 0.2, Df resid = 41, p = 0.9998
paternal plant ploidy	$\chi 2$ (2) = 0.8474, Df resid = 246, p = 0.6546	$\chi 2$ (2) = 0.2279, Df resid = 37, p = 0.8923
autonomous vs. induced selfing	$\chi 2$ (1) = 0.4382, Df resid = 245, p = 0.508	$\chi 2$ (1) = 0.0011, Df resid = 36, p = 0.9733
ploidy of pollination (homo x heteroploid)	$\chi 2$ (1) = 0.2986 , Df resid = 245, p = 0.5848	$\chi 2$ (1) = 0.0544, Df resid = 36, p = 0.8156

Maternal plant individual was treated as a random factor in GLMM models. Numbers are $\chi 2$ values obtained from LRT tests (GLMM).

Electronic Appendix 8. – Results of GLMM analysis of entire dataset only with presence or absence of evolved seeds (successful vs. unsuccessful crosses) and GLMM analysis of the successful crosses only.

GLMM

Seedset: entire seedset; 0/1 seeds	
maternal plant species	$\chi 2$ (2) = 19.401, Df resid = 246, p = 6.127e-05
maternal plant ploidy	$\chi 2$ (2) = 4.7052, Df resid = 246, p = 0.09512
paternal plant species	$\chi 2$ (6) = 9.7404, Df resid = 250, p = 0.136
paternal plant ploidy	$\chi 2$ (2) = 0.9692, Df resid = 246, p = 0.616
autonomous vs. induced selfing	$\chi 2$ (1) = 2.4503, Df resid = 245, p = 0.1175
ploidy of pollination (homo x heteroploid)	$\chi 2$ (1) = 0.008, Df resid = 245, p = 0.9287

Seedset: only successful pollinated spikes; number of seeds combined with number of florets	
maternal plant species	$\chi 2$ (2) = 0.5825, Df resid = 37, p = 0.7473
maternal plant ploidy	$\chi 2$ (2) = 5.0465, Df resid = 37, p = 0.0802
paternal plant species	$\chi 2$ (6) = 16.055, Df resid = 41, p = 0.01346

paternal plant ploidy	$\chi2$ (2) = 1.2398, Df resid = 37, p = 0.538
autonomous vs. induced selfing	$\chi2$ (1) = 7.6176, Df resid = 36, p = 0.00578
ploidy of pollination (homo x heteroploid)	$\chi2$ (1) = 1.2693, Df resid = 36, p = 0.2599

Maternal plant individual was treated as a random factor in GLMM models. Numbers are $\chi2$ values obtained from LRT tests (GLMM).