

Supplementary Information

Supplementary Figure Legends

Figure S1. Reduced read mapping bias when mapping against reconstructed parental haplotypes. Genomic ratios (*C. bursa-pastoris* A homeolog/Total; or *C. rubella*/Total for diploid F1s) obtained when genomic reads for genes expressed in flower buds were mapped against the parental haplotypes (A, C, E, F) or the *C. rubella* reference genome (B, D, F, H). Separate histograms are shown for CbpGY (A,B), CbpDE (C, D), Inter13 (E, F) and Inter14 (G, H). The equal ratio (0.5) is indicated by a red line, whereas the median of the genomic ratios is plotted in grey. A strong bias towards the *C. bursa-pastoris* A homeolog or the *C. rubella* allele can be observed when mapping against the *C. rubella* reference.

Figure S2. Reduced read mapping bias when mapping against reconstructed parental haplotypes. Genomic ratios (*C. bursa-pastoris* A homeolog/Total; or *C. rubella*/Total for diploid F1s) obtained when genomic reads for genes expressed in leaves were mapped against the parental haplotypes (A, C, E, F) and the *C. rubella* reference genome (B, D, F, H). Separate histograms are shown for CbpGY (A,B), CbpDE (C, D), Inter13 (E, F) and Inter14 (G, H). The equal ratio (0.5) is indicated by a red line, whereas the median of the genomic ratios is plotted in grey. A strong bias towards the *C. bursa-pastoris* A homeolog or the *C. rubella* allele can be observed when mapping against the *C. rubella* reference.

Figure S3. Effect of heterozygous transposable element (TE) insertion on expression in diploid F1 hybrids. The boxplots show the relative allelic expression (ratio of the expression of the haplotype where the TE was inserted to total expression) for genes with TE insertions from 200 bp to 10 kb. Patterns for flower buds (A, C) and leaves (B, D) for Inter13 (A, B) and Inter14 (C, D).

Figure S4. Heatmap for FDR (A) and the odds ratio (B) of the association of expression bias with heterozygous transposable elements (TEs) in flower buds (F) and leaves (L) for all genes amenable to analyses in the interspecific F1s. The corresponding value for the color of the FDR-values (A) can be found in C, and the corresponding values to the odds ratio (B) can be found in D.

Figure S5. The direction of homeolog expression bias in *C. bursa-pastoris* reflects the direction of allelic expression bias in diploid F1 hybrids. The boxplots show the ratio of the expression of the *C. bursa-pastoris* A homeolog to total, for genes that show allelic expression bias toward *C. rubella* or *C. orientalis* in the diploid hybrid, separately for leaves and flower buds.

Supplementary Tables

Table S1. Geographic origin of four *C. bursa-pastoris* (Cbp) accessions used.

Accession name	Accession designation	Species	Geographic origin
CbpDE	CbpWEDE9.136	<i>C. bursa-pastoris</i>	Regensburg, Germany
CbpGR	CbpWEGR89.6	<i>C. bursa-pastoris</i>	Koukouli, Zagory, Greece
CbpKMB	CbpChKMB205	<i>C. bursa-pastoris</i>	Kunming, Yunan, China
CbpGY	CbpChGY36	<i>C. bursa-pastoris</i>	Guiyang, Guizhou, China

Table S2. Geographic origin of seed an pollen parent of interspecific F1s

Accession designation	Seed parent	Geographic origin seed parent	Pollen parent	Geographic origin pollen parent
Inter13	Co1979-9	Loktevsk raion, Altai Kraj, Siberia, Russia	Cr75-2-3	Trapeza, Greece
Inter14	Co1719-11	Bayan-Olgii Aymag, Mongolia	Cr39-1	Sicily, Italy

Table S3. Yield and quality of transcriptomic data in Gbases

Sample	Yield PF (Gbp)	Q \geq 30 (%)	Yield Q \geq 30 (Gbp)
CbpGY-KS1-F	10.6	91.4	9.7
CbpGY-KS1-L	9.4	92	8.7
CbpGY-KS2-F	9	92.45	8.3
CbpGY-KS2-L	8.8	91.6	8
CbpGY-KS3-F	10	92.55	9.3
CbpGY-KS3-L	10.4	91.7	9.5
CbpDE-KS1-F	8	92.35	7.5
CbpDE-KS1-L	7.6	92.5	7
CbpDE-KS2-F	8.8	92.4	8.2
CbpDE-KS2-L	9.4	92.65	8.7
CbpDE-KS3-F	8	92.05	7.4
CbpDE-KS3-L	9.2	92.7	8.6
CbpGR-KS1-F	10.4	92.45	9.7
CbpGR-KS1-L	9.8	91.85	9
CbpGR-KS2-F	9.6	92.3	8.8
CbpGR-KS2-L	9	91.85	8.3
CbpGR-KS3-F	8.2	92.3	7.6
CbpGR-KS3-L	9.2	92.55	8.5
CbpKMB-KS1-F	9.8	91.55	9
CbpKMB-KS1-L	10.2	92.1	9.3
CbpKMB-KS2-F	11.4	91.2	10.5
CbpKMB-KS2-L	7.8	91.85	7.2
CbpKMB-KS3-F	10	91.85	9.2
CbpKMB-KS3-L	10.6	92.15	9.8
Inter13-KS1-F	10	93.2	9.3
Inter13-KS1-L	10.4	92.45	9.6
Inter13-KS2-F	6.6	92.85	6.2
Inter13-KS2-L	9.8	92.4	9
Inter13-KS3-F	10.6	91.35	9.7
Inter13-KS3-L	9.8	92.1	9.1
Inter14-KS1-F	10.8	91.1	9.9
Inter14-KS1-L	8.8	92.25	8.1
Inter14-KS2-F	10.2	91.35	9.3
Inter14-KS2-L	10.8	91.95	9.9
Inter14-KS3-F	10.8	91.55	9.9
Inter14-KS3-L	10.6	92.3	9.8

Table S4. Yield and quality of genomic data in Gbases

Sample	Yield Gbp	Q \geq 30 (%)	Yield Q \geq 30 Gbp
CbpGY	11.6	93.28	10.8
CbpKMB	9.2	92.43	8.6
CbpD	10.8	92.93	10.1
CbpGR	10.4	93.05	9.8
Co1719-11	6	90.00	5.4
Co1979-9	9	93.33	8.4
Cr75-2-3	10.4	92.40	9.4
Inter13	9	92.30	8.3
Inter14	10.4	91.88	9.4

Table S5. Transposable element (TE) abundance in the parents of the interspecific F1s

TE insertion	Co1719-11	Co1979-9	Cr39-1	Cr75-2-3
CACTA	46	43	92	98
Copia	312	333	552	661
Gypsy	576	542	970	1301
Harbinger	84	99	149	197
hAT	30	39	69	85
Helitron	104	141	207	286
LINE	55	66	149	229
MuDR	78	81	177	203
SINE	35	48	47	132
Total	1320	1392	2412	3192

Table S6. Transposable Element (TE) abundance in the interspecific F1s and *C. bursa-pastoris* accesions

	Inter13		Inter14		CbpDE		CbpGR		CbpKMB		CbpGY	
	homTE	hetTE	homTE	hetTE	homTE	hetTE	homTE	hetTE	homTE	homTE	homTE	hetTE
CACTA	53	44	61	42	56	47	59	56	32	28	37	35
Copia	291	471	327	477	346	577	353	562	304	577	348	602
Gypsy	728	526	776	616	606	500	652	559	513	426	562	481
Harbinger	103	136	112	132	93	107	108	120	77	86	82	88
hAT	37	40	40	37	44	29	42	38	26	24	32	22
Helitron	154	124	161	155	127	129	141	132	108	102	136	111
LINE	94	119	104	141	92	141	98	147	59	88	67	94
MuDR	139	69	149	80	110	79	134	97	99	60	116	58
SINE	33	53	31	86	23	51	37	44	23	44	21	54
SUM	1632	1582	1761	1766	1497	1660	1624	1755	1241	1435	1401	1545

Table S7. Total number of genes amenable to analysis of ASE in flower bud and leaf samples from the two *C. orientalis* x *C. rubella* F1s,,counts of genes with evidence for allele-specific expression (ASE) and the estimated false discovery rate (FDR) and proportion of genes with ASE.

Sample designation	Sample	Genes amenable to ASE analysis ¹	Analyzed genes ²	Heterozygous SNPs in analyzed genes	Number of genes with ASE PP ≥ 0.95 ³	FDR	ASE proportion ⁴
Inter13	Flower buds	14443	14039	100245	5247	0.00345	0.549
Inter14		14120	13789	95779	5751	0.00339	0.587
Inter13	Leaves	14443	14037	100230	4585	0.00289	0.481
Inter14		14120	12814	90820	3924	0.00274	0.456

¹Total number of genes with heterozygous SNPs in coding regions remaining after filtering.

²Number of genes amenable to ASE analyses with expression data in at least one of the replicates of the sample.

³Genes with evidence for ASE (posterior probability ≥ 0.95).

⁴Direct estimate of the ASE proportion independent of significance cutoffs.

Table S8. Association of genes with significant expression bias (posterior probability for ASE or HSE ≥ 0.95) with presence of heterozygous transposable element (TEs) insertions in interspecific F1 hybrids. All genes amenable to ASE analyses in each F1 hybrid were included in these analyses. None of the associations were significant at an of FDR ≤ 0.05 .

Individual	Tissue	Window	+ASE, +TE	+ASE, -TE	-ASE, +TE	-ASE, -TE	Odds ratio	
Inter13	Flower buds	10000	1307	3691	2080	6257	1.065	
		5000	448	4213	735	7129	1.031	
		2000	434	4758	620	8059	1.186	
		1000	283	4926	410	8313	1.165	
		200	142	5080	190	8553	1.258	
	Leaves	10000	1132	3236	2264	6704	1.036	
		5000	370	3698	813	7640	0.940	
		2000	383	4150	674	8662	1.186	
	Flower buds	1000	256	4299	441	8934	1.206	
		200	130	4436	203	9194	1.327	
Inter14		10000	1063	4490	1482	6308	1.008	
		5000	324	5028	483	7051	0.941	
		2000	320	5393	421	7560	1.066	
		1000	219	5508	263	7739	1.170	
		200	123	5610	122	7894	1.419	
Leaves	10000	698	3094	1640	6973	0.959		
	5000	213	3443	513	7810	0.942		
	2000	210	3692	466	8357	1.020		
	1000	141	3773	302	8541	1.057		
	200	79	3837	148	8710	1.212		