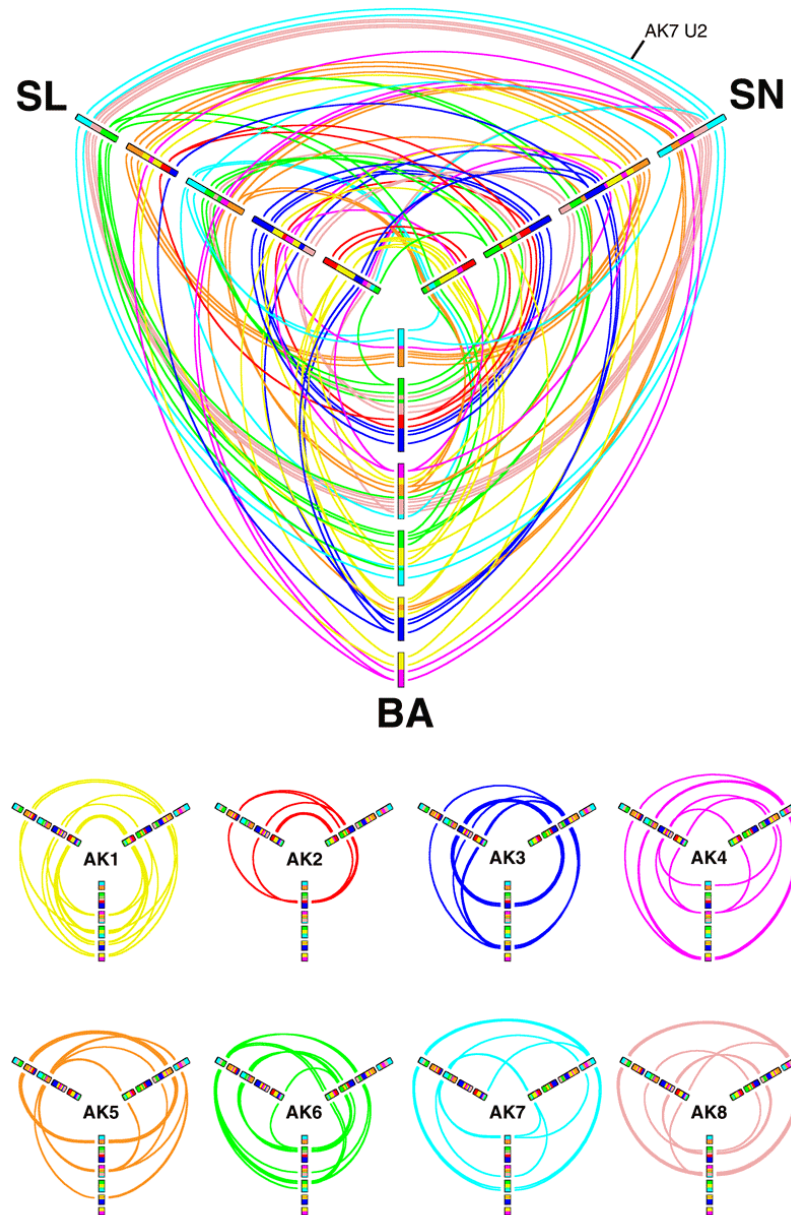
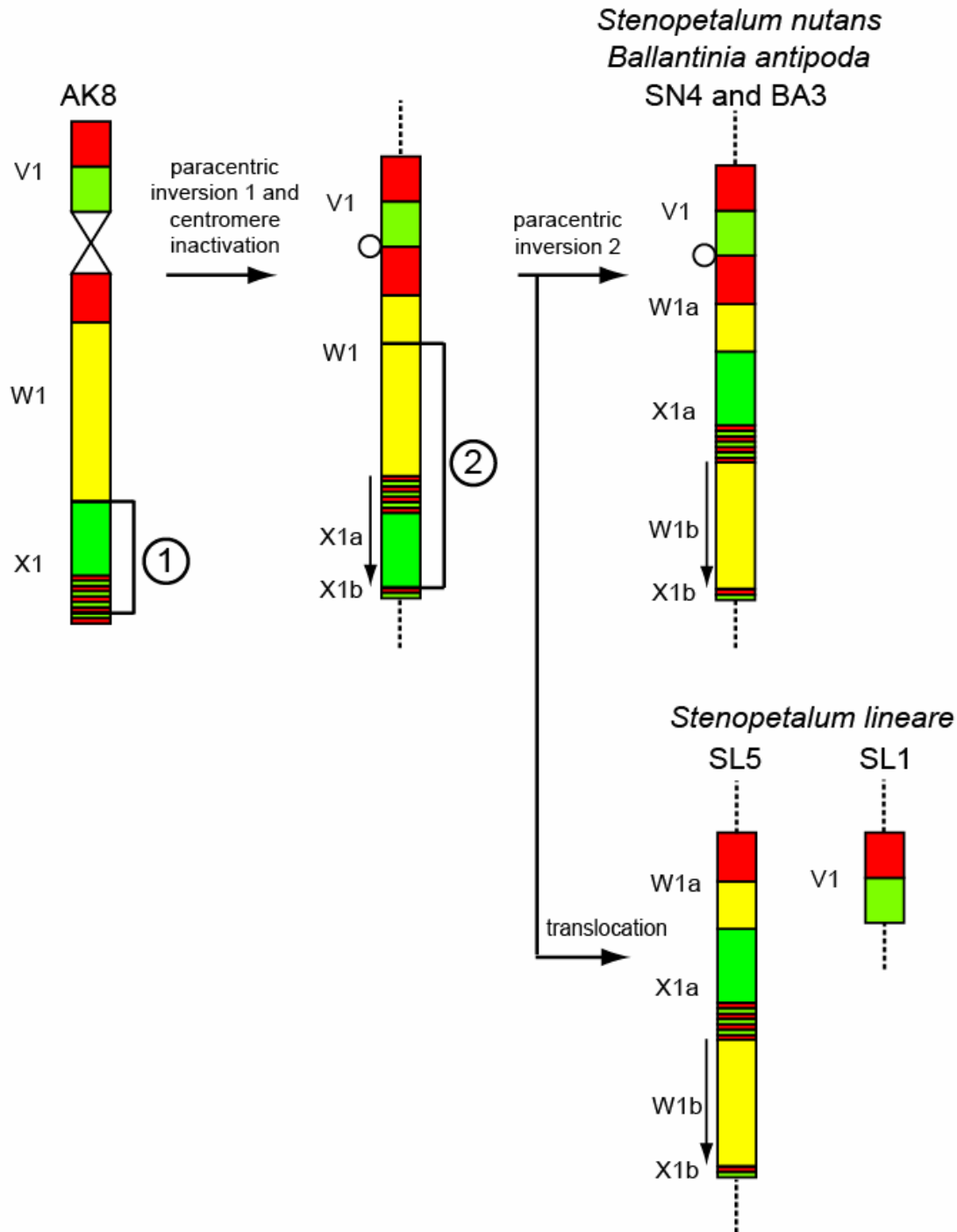


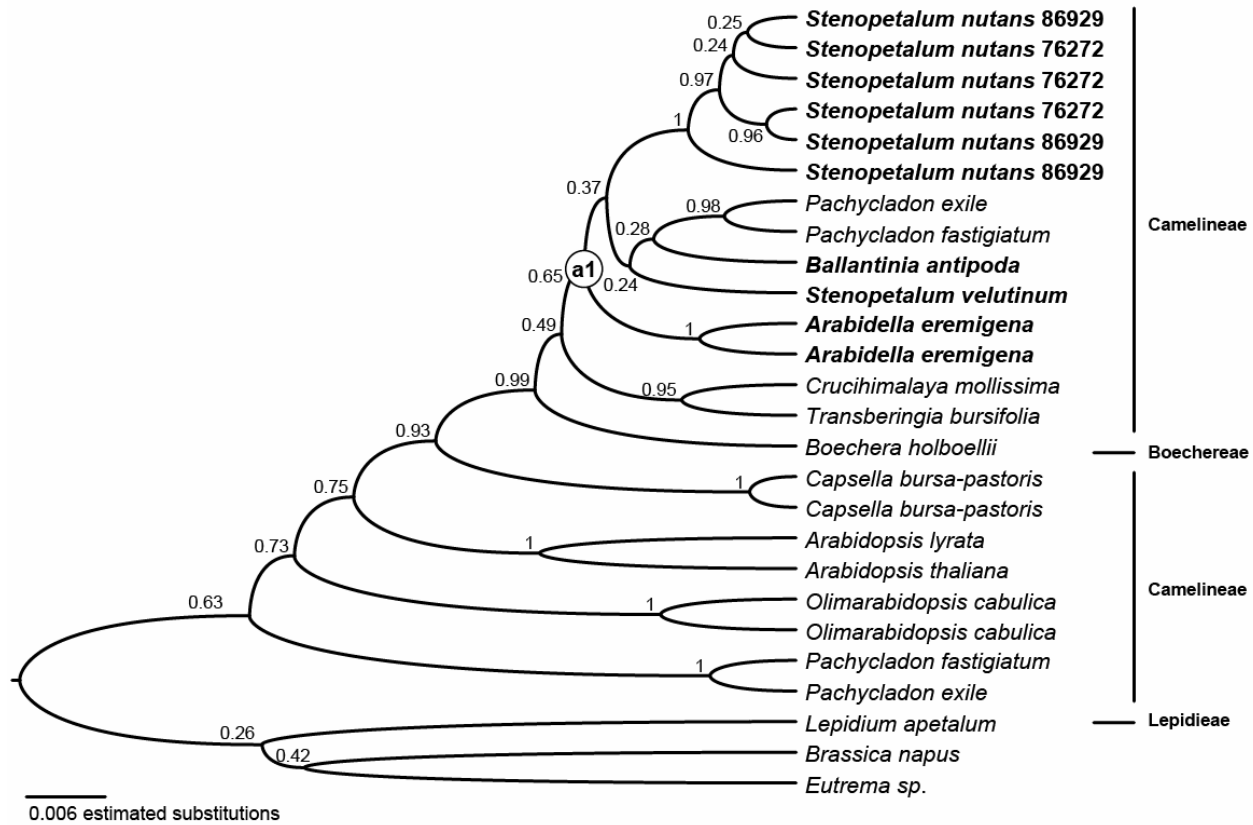
Supplemental Figure 1. A Three-Way Comparison of the Relative Position of Corresponding Synteny Blocks of *Stenopetalum nutans* (SN), *S. lineare* (SL) and *Ballantinia antipoda* (BA) Relative to the Reference Ancestral Crucifer Karyotype (ACK). In the main panel of the image, each of the three modern karyotypes is presented in a radial layout. Within each of the three karyotypes, ideograms are ordered and oriented in the outward direction (corresponding to the same counter-clockwise scale progression of Figure 3). Each line connects a pair of genomic positions on two different modern genomes that are syntenically related to the same genomic block in the ACK. For example, the light-blue line at the top of the figure between SL and SN corresponds to synteny with the genomic block U2 on AK7. Each of the eight small panels shows synteny relationships between the three modern genomes for a specific ancestral chromosome (AK1-8).



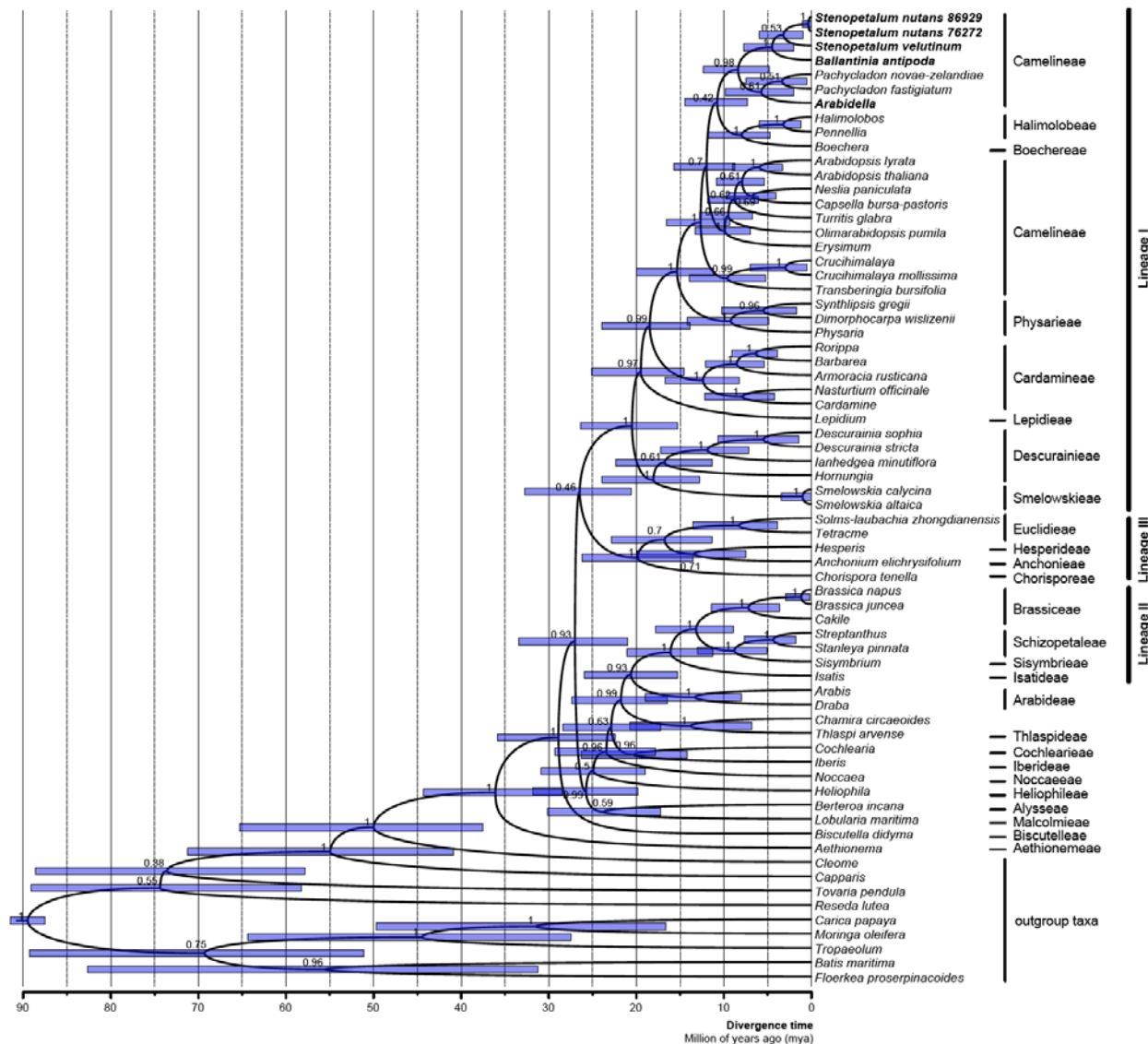
Supplemental Figure 2. The Unique Rearrangement of the AK8(#1)-like Homoeologue Shared by All Analyzed Species. This rearrangement was mediated by two subsequent paracentric inversions involving two thirds of genomic block W1 and a major part of X1. In *S. lineare*, block V1 underwent a secondary translocation to another chromosome. The rearrangement not shown for *Arabidella eremigena* and *Blennodia canescens*.



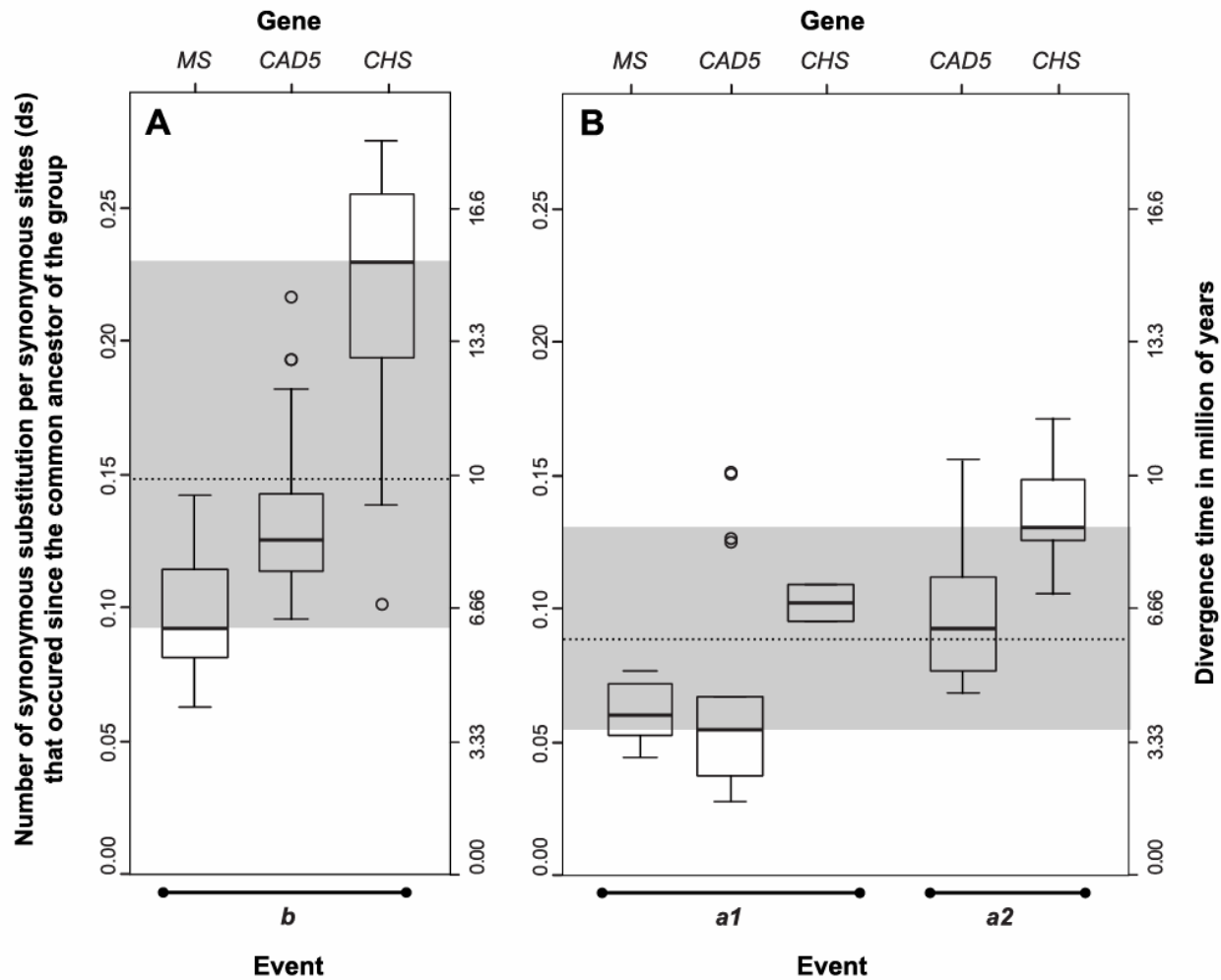
Supplemental Figure 3. Phylogeny of the Malate Synthase (*MS*) (TrN + Γ + I) Showing the Position of Sequences from the Australian Species (in Bold) in the Context of Other Brassicaceae Taxa. Clade posterior probabilities < 0.5 are not shown. Tribal classification follows Al-Shehbaz et al. (2006). 'a1' identifies the Camelinae gene copy present in the genomes of Australian Brassicaceae (a2 gene copy was not detected in this analysis).



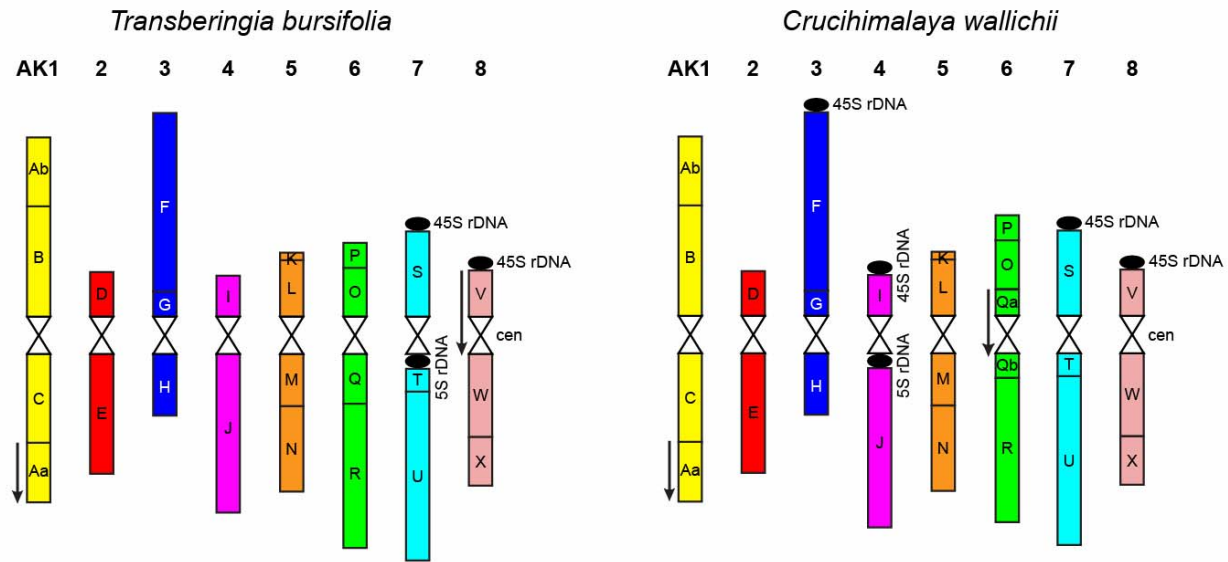
Supplemental Figure 4. Maternal Phylogeny (Chronogram) of Australian Genera *Stenopetalum*, *Ballantinia*, and *Arabidella* in the Context of Other Brassicaceae Taxa Resulting from the Partitioned Analysis of the Genes *rbcL* (K81uf + Γ + I), *nad4* (TVMef + Γ + I), *matK* (TVM + Γ + I), and *ndhF* (TVM + Γ + I) in BEAST. Clade posterior probabilities < 0.5 are not shown. The analysis included representatives of the three major Brassicaceae phylogenetic lineages (I-III; Al-Shehbaz et al., 2006; Couvreur et al., 2010) and nine outgroup taxa representing the crown group of the Brassicales (Wang et al., 2009), i.e. *Batis*, *Floerkea*, *Tropaeolum*, *Moringa*, *Carica*, *Reseda*, *Tovaria*, *Capparis*, and *Cleome*. Tribal classification follows Al-Shehbaz et al. (2006) and Couvreur et al. (2010).



Supplemental Figure 5. Comparison of the Estimated Time of Original Divergence Between the Parents that Were Involved in the Allopolyploid Event (A) and the Estimated Time of the Event (B) Based on the Analysis of Three Nuclear Genes. The dashed vertical lines represent the mean of median estimates. The ‘b’ represents the divergence between the two parental genome copies prior to the WGD, whereas ‘a1’ and ‘a2’ represent the two genome copies present in the Australian Camelineae species and suggest a minimal age for the mesopolyploid event(s) (see Figure 4). *Stenopetalum velutinum*, involved in a more recent polyploid event, was not included in the estimations.



Supplemental Figure 6. Reconstructed Karyotypes of *Transberingia bursifolia* ($n = 8$) and *Crucihimalaya wallichii* ($n = 8$). The karyotypes resembling the Ancestral Crucifer Karyotype (ACK) were reconstructed by comparative chromosome painting using *Arabidopsis thaliana* BAC contigs as probes. The 24 genomic blocks (GB) are indicated by uppercase letters (A to X) and colored according to their positions on chromosomes AK1 to AK8 of the ACK (Figure 1D). Downward-pointing arrows indicate the opposite orientation of GBs compared with the position in the ACK, i.e. inversions.



Supplemental Table 1. Ancestral Genomic Blocks (GB) of the Ancestral Crucifer Karyotype (ACK) identified on chromosomes of *Stenopetalum nutans* (chromosomes SN1-SN4), *S. lineare* (SL1-SL5) and *Ballantinia antipoda* (BA1-BA6). Details on corresponding BAC contigs of *Arabidopsis thaliana* are given.

SN/SL/BA Chromosome	GB	Position of GB on Ancestral Chromosomes ^a	<i>A. thaliana</i> Boundary BAC Clones ^b		No. of Used <i>A. thaliana</i> BAC Clones	<i>A. thaliana</i> BAC Contig Size (bp) ^b
<i>Stenopetalum nutans</i> (n = 4)						
SN1	O1	AK6	F6N15	T1J1	24	2500000
	N1a	AK5	T26I12	F24M12	12	1470000
	M1b	AK5	F3A4	T3A5	2	570000
	T1	AK7	F25E4	F18A5	12	1100000
	S1	AK7	F5H8	MPK23	30	2400000
	R1a	AK6	F7J8	F15N18	17	3700000
	A1a	AK1	F22M8	T29M8	29	6000000
	B1b	AK1	T16E15	T23E23	3	950000
	A1b	AK1	T25K16	T1N6	2	700000
	B1c	AK1	F3I6	F12K21	21	3800000
	B1a	AK1	F6F9	F16L1	5	950000
	J2a	AK4	T6A23	F18A8	20	3280000
	D2	AK2	T12P18	F12K22	17	2300000
	E2	AK2	T23K8	F23A5	29	6200000
SN2	R2	AK6	F7J8	T6G21	33	7400000
	Q2	AK6	T20O7	T8M17	17	2600000
	E1b	AK2	F1B16	F23A5	9	1550000
	A2	AK1	T25K16	T29M8	31	6700000
	P2	AK6	T3H13	F8L21	11	1300000
	O2	AK6	F6N15	T1J1	24	2500000
	V2	AK8	K23F3	MBD2	28	2400000
	E1a	AK2	F25A4	T23K8	20	4650000
	D1	AK2	T12P18	F12K22	17	2300000
	H2	AK3	T10F5	F5H14	16	3200000
	G2	AK3	F1O13	T25N22	5	1300000
	F2	AK3	MWL2	T4P13	46	9200000
SN3	W2	AK8	K21P3	K9B18	26	4300000
	X2	AK8	MSL3	K9I9	14	2500000
	R1b	AK6	MXC9	T6G21	16	3700000
	Q1	AK6	T20O7	T8M17	17	2600000
	P1	AK6	T3H13	F8L21	11	1300000
	N1b	AK5	T26I12	F16M2	12	2900000
	F1	AK3	T4P13	MWL2	46	9200000
	G1	AK3	F1O13	T25N22	5	1300000
	H1	AK3	F5H14	T10F5	16	3200000
	I2	AK4	F3K23	F8N16	16	1640000
	C1	AK1	T6H22	F2J6	25	4600000
	B2	AK1	F6F9	F12K21	29	5700000
	J2b	AK4	F13I13	T8I13	15	3280000
	C2	AK1	F2J6	T6H22	25	4600000

Supplemental Data. Mandáková et al. (2010). Plant Cell 10.1105/tpc.110.074526

SN/SL/BA Chromosome	GB	Position of GB on Ancestral Chromosomes ^a	<i>A. thaliana</i> Boundary BAC Clones ^b		No. of Used <i>A. thaliana</i> BAC Clones	<i>A. thaliana</i> BAC Contig Size (bp) ^b
	K2	AK5	F2I9	F3C11	7	400000
	L2	AK5	MJL14	T4A2	28	2900000
	M2	AK5	T10D17	F3A4	12	2700000
	N2	AK5	F24M12	F16M2	18	4400000
SN4	U1	AK7	T5J17	T6K21	38	8700000
	L1	AK5	MJL14	T4A2	28	2900000
	K1	AK5	F2I9	F3C11	7	400000
	M1a	AK5	T10D17	F2K15	11	2160000
	I1	AK4	F3K23	F8N16	16	2100000
	J1	AK4	F6K5	T8I13	35	8200000
	X1b	AK8	K14B20	K9I9	5	500000
	W1b	AK8	MGN6	K9B18	14	2900000
	X1a	AK8	K19O4	MUP24	9	2000000
	W1a	AK8	MNC6	K21P3	13	1400000
	V1	AK8	MBD2	K23F3	28	2400000
	S2	AK7	F5H8	MPK23	30	2400000
	T2	AK7	F25E4	F18A5	12	1100000
	U2	AK7	T6K21	T5J17	38	8700000
<i>Stenopetalum lineare</i> (n = 5)						
SL1	R2b	AK6	F7J8	F15N18	17	3700000
	S2	AK7	F5H8	MPK23	30	2400000
	V1	AK8	MBD2	MGC1	28	2400000
	J2b	AK4	F3G5	T8I13	17	2700000
	G1	AK3	F1O13	T25N22	5	1300000
	F1b	AK3	MWL2	F11B9	30	4600000
	A1	AK1	T25K16	T29M8	31	6700000
	B1	AK1	F6F9	F12K21	29	5700000
	D2	AK2	F12K22	T12P18	17	2300000
	E2	AK2	T23K8	F23A5	29	6200000
SL2	X2	AK8	K9I9	MSL3	14	2500000
	W2	AK8	K9B18	K21P3	26	4300000
	H1	AK3	F5H14	T10F5	16	3200000
	C1	AK1	F2J6	T6H22	25	4600000
	I2	AK4	F3K23	F19L18	16	2100000
	J2a	AK4	F18A8	F13K3	18	2700000
	D1	AK2	F12K22	T12P18	17	2300000
	A2	AK1	T29M8	T25K16	31	6700000
	H2	AK3	F5H14	T10F5	16	3200000
	G2	AK3	F1O13	T25N22	5	1300000
	F2	AK3	MWL2	T4P13	46	9200000
	N1	AK5	F24M12	F16M2	18	4400000
	M1	AK5	T10D17	F3A4	12	2700000
	L1	AK5	T4A2	MJL14	28	2900000
	K1	AK5	F2I9	F3C11	7	400000
	I1	AK4	F3K23	F19L18	16	2100000
	J1a	AK4	F18A8	F13K3	18	2700000

Supplemental Data. Mandáková et al. (2010). Plant Cell 10.1105/tpc.110.074526

SN/SL/BA Chromosome	GB	Position of GB on Ancestral Chromosomes ^a	<i>A. thaliana</i> Boundary BAC Clones ^b		No. of Used <i>A. thaliana</i> BAC Clones	<i>A. thaliana</i> BAC Contig Size (bp) ^b	
SL3	O2	AK6	F6N15	T1J1	24	2500000	
	V2	AK8	MGC1	MBD2	28	2400000	
	Q2	AK6	T8M17	T20O7	17	2600000	
	R2a	AK6	MXC9	T6G21	16	3700000	
	U1	AK7	T5J17	T6K21	38	8700000	
	T1	AK7	F25E4	F18A5	12	1100000	
	S1	AK7	F5H8	MPK23	30	2400000	
SL4	F1a	AK3	T4P13	F13M14	16	4600000	
	E1	AK2	T23K8	F23A5	29	6200000	
	B2	AK1	F6F9	F12K21	29	5700000	
	J1b	AK4	F3G5	T8I13	17	2700000	
	C2	AK1	F2J6	T6H22	25	4600000	
	K2	AK5	F2I9	F3C11	7	400000	
	L2	AK5	MJL14	T4A2	28	2900000	
	M2	AK5	T10D17	F3A4	12	2700000	
SL5	N2	AK5	F24M12	F16M2	18	4400000	
	O1	AK6	F6N15	T1J1	24	2500000	
	P1	AK6	T3H13	F8L21	11	1300000	
	R1	AK6	F7J8	T6G21	33	7400000	
	X1b	AK8	K14B20	K9I9	5	500000	
	W1b	AK8	MGN6	K9B18	14	2900000	
	X1a	AK8	K19O4	MUP24	9	2000000	
	W1a	AK8	MNC6	K21P3	13	1400000	
<i>Ballantinia antipoda</i> (n = 6)	T2	AK7	F25E4	F18A5	12	1100000	
	U2	AK7	T6K21	T5J17	38	8700000	
	BA1	T1	AK7	F25E4	F18A5	12	1100000
		U1	AK7	T6K21	T5J17	38	8700000
		I2	AK4	F3K23	F8N16	16	2100000
		L2	AK5	MJL14	T4A2	28	2900000
		K2	AK5	F2I9	F3C11	7	400000
		M2	AK5	T10D17	F3A4	12	2700000
		N2	AK5	F24M12	F16M2	18	4400000
	BA2	R2	AK6	F7J8	T6G21	33	7400000
		Q2	AK6	T20O7	T8M17	17	2600000
		V2	AK8	MBD2	K23F3	28	2400000
O2		AK6	F6N15	T1J1	24	2500000	
W2		AK8	K21P3	K9B18	26	4300000	
X2		AK8	MSL3	K9I9	14	2500000	
E		AK2	F23A5	T23K8	29	6200000	
D		AK2	F12K22	T12P18	17	2300000	
H2		AK3	F5H14	T10F5	16	3200000	
G2		AK3	F1O13	T25N22	5	1300000	
F2		AK3	MWL2	T4P13	46	9200000	
	J2	AK4	F6K5	T8I13	35	8200000	
	B1b	AK1	F13K9	F5D14	9	1900000	

Supplemental Data. Mandáková et al. (2010). Plant Cell 10.1105/tpc.110.074526

SN/SL/BA Chromosome	GB	Position of GB on Ancestral Chromosomes ^a	<i>A. thaliana</i> Boundary BAC Clones ^b		No. of Used <i>A. thaliana</i> BAC Clones	<i>A. thaliana</i> BAC Contig Size (bp) ^b
BA3	A2b	AK1	F17F16	T29M8	6	2200000
	M1	AK5	T10D17	F3A4	12	2700000
	N1	AK5	F24M12	F16M2	18	4400000
	R1b	AK6	T20K14	T2K12	10	1850000
	X1b	AK8	K14B20	K9I9	5	500000
	W1b	AK8	MGN6	K9B18	14	2900000
	X1a	AK8	K19O4	MUP24	9	2000000
	W1a	AK8	MNC6	K21P3	13	1400000
	V1	AK8	MBD2	K23F3	28	2400000
	S	AK7	F5H8	MPK23	30	2400000
BA4	O1	AK6	F6N15	T1J1	24	2500000
	P1	AK6	T3H13	F8L21	11	1300000
	Q1	AK6	T20O7	T4C12	17	2600000
	R1a	AK6	T6G21	T20K14	11	3700000
	C2	AK1	F2J6	T6H22	25	4600000
	A1a	AK1	T25K16	F19K19	25	4500000
	B1c	AK1	F6N18	F12K21	6	1900000
	T2	AK7	F25E4	F18A5	12	1100000
	R1c	AK6	F7J8	T2K12	13	1850000
	U2	AK7	T6K21	T5J17	38	8700000
BA5	B1a	AK1	F28L5	F6F9	14	1900000
	A1b	AK1	F17F16	T29M8	6	2200000
	L1	AK5	MJL14	T4A2	28	2900000
	K1	AK5	F2I9	F3C11	7	400000
	C1	AK1	F2J6	T6H22	25	4600000
	H1	AK3	F5H14	T10F5	16	3200000
	G1	AK3	F1O13	T25N22	5	1300000
	F1	AK3	MWL2	T4P13	46	9200000
BA6	A2a	AK1	T25K16	F3O9	25	4500000
	B2	AK1	F6F9	F12K21	29	5700000
	I1	AK4	F3K23	F8N16	16	2100000
	J1	AK4	F6K5	T8I13	35	8200000

^a 24 genomic blocks (A-X) on the eight ancestral chromosomes (AK1-8) of the ACK (Schranz et al., 2006).

^b <http://www.arabidopsis.org>

Supplemental Table 2. Structure and Position of the Eight Ancestral Chromosomes (AK1-AK8) and 24 Genomic Blocks (GBs) of the Ancestral Crucifer Karyotype (n = 8) Within Duplicated Genomes of *Stenopetalum* and *Ballantinia* Species. AK-like association refers to the GB association corresponding to an entire AK chromosome, whereas partial AK-like association indicates the GB association corresponding to an arm of AK chromosome. Ⓜ: conserved GB not forming any AK-like association, split ⌘: GB split into two (a+b) or three (a+b+c) sub-blocks, ✕: GB lost.

AK Chromosome	Genomic Block	<i>S. nutans</i> (n = 4)	<i>S. lineare</i> (n = 5)	<i>B. antipoda</i> (n = 6)
AK1(#1)	A1	partial AK1-like assoc. (split ⌘ by secondary inversions)	partial AK1-like assoc.	split ⌘ (a+b)
	B1			split ⌘ (a+b+c)
	C1			Ⓜ
AK1(#2)	A2	Ⓜ	Ⓜ	partial AK1-like assoc. (part of A2 translocated)
	B2	Ⓜ	Ⓜ	
	C2	Ⓜ	Ⓜ	
AK2(#1)	D1	Ⓜ	Ⓜ	✕
	E1	⌘ split (a+b)	Ⓜ	✕
AK2(#2)	D2	AK2-like assoc.	AK2-like assoc.	AK2-like assoc. [†]
	E2			
AK3(#1)	F1	AK3-like assoc.	⌘ split (a+b)	AK3-like assoc.
	G1		Ⓜ	
	H1		Ⓜ	
AK3(#2)	F2	AK3-like assoc.	AK3-like assoc.	AK3-like association
	G2			
	H2			
AK4(#1)	I1	AK4-like assoc.	Ⓜ	AK4-like assoc.
	J1		⌘ split (a+b)	
AK4(#2)	I2	Ⓜ	Ⓜ	Ⓜ
	J2	⌘ split (a+b)	⌘ split (a+b)	Ⓜ
AK5(#1)	K1	partial AK5-like assoc.	AK5-like assoc.	partial AK5-like assoc.
	L1			
	M1			⌘ split (a+b)
	N1			⌘ split (a+b)
AK5(#2)	K2	AK5-like assoc.	AK5-like assoc.	AK5-like assoc.
	L2			
	M2			
	N2			
AK6(#1)	O1	Ⓜ	partial AK6-like assoc.	partial AK6-like assoc.
	P1	Ⓜ	✕	✕ [‡]
	Q1	Ⓜ	Ⓜ	⌘ split (a+b+c)
	R1	⌘ split (a+b)	Ⓜ	
AK6(#2)	O2	partial AK6-like assoc.	Ⓜ	Ⓜ
	P2		✕	✕
	Q2	partial AK6-like assoc.	Ⓜ	partial AK6-like assoc.
	R2		⌘ split (a+b)	
AK7(#1)	S1	Ⓜ	AK7-like assoc.	✕
	T1	Ⓜ		partial AK7-like assoc.
	U1	Ⓜ		
AK7(#2)	S2	AK7-like assoc.	Ⓜ	Ⓜ [†]
	T2		partial AK7-like assoc.	Ⓜ
	U2			Ⓜ

Supplemental Data. Mandáková et al. (2010). Plant Cell 10.1105/tpc.110.074526

AK8(#1)	V1	AK8-like assoc. (split \bowtie by secondary inversions)	Ⓛ	AK8-like assoc. (split \bowtie by secondary inversions)
	W1		partial AK8-like assoc. (split \bowtie by secondary inversions)	
	X1			
AK8(#2)	V2	Ⓛ	Ⓛ	Ⓛ
	W2	partial AK8-like assoc.	partial AK8-like assoc.	partial AK8-like assoc.
	X2			

† As paralogues of these GBs were lost, the assignment as the #2 copy of AK2 and AK7 is tentative and based on the comparison with other two species.

‡ $\approx 33\%$ (0.9 Mb in the *Arabidopsis thaliana* genome) of the block Q1 (2.6 Mb) were lost.

Supplemental Table 3. Bayes Factor (BF) Scores for Different Evolutionary Hypotheses Regarding the Number of Independent Polyploid Events at the Origin of the Australian Species Relative to the Null Hypothesis of Four Independent Origins. Genera within brackets indicate that they share the same polyploid origin for a given hypothesis (they were constrained to be monophyletic in the phylogenetic hypothesis); A – *Arabidella*, B – *Ballantinia*, S – *Stenopetalum*, P – *Pachycladon*. A $|BF| > 2$ is considered decisive and a positive score means that the alternative hypothesis is better.

Hypothesis	No. Origins	<i>mat</i>	<i>CHS</i>	<i>CAD5</i>	<i>MS</i>
(ABSP)	1	-0.119	0.167	0.078	0.052
(BSP)	2	-0.338	0.07	-0.09	0.014
(ASP)	2	0.542	-0.018	-0.018	0.013
(ABP)	2	-0.351	0.028	0.012	0.086
(ABS)	2	-0.017	0.025	-0.068	0.015
(AB) (SP)	2	0.243	0.039	-0.175	-0.033
(AS) (BP)	2	0.111	0.106	-0.04	0.008
(AP) (BS)	2	0.175	-0.125	-0.129	0.016
(SP)	3	-0.013	0.079	-0.111	0.036
(BP)	3	1.192	0.084	-0.084	0.029
(BS)	3	0.092	0.032	-0.051	-0.033
(AP)	3	1.102	0.101	-0.034	-0.139
(AS)	3	0.041	0.124	-0.114	0.008
(AB)	3	0.002	0.16	-0.152	0.064

Supplemental Table 4. Collection Data of Australian Crucifer Species Used in the Present Study.

Species	Collector/Accession No./Herbarium Sheet No.	Origin
<i>Arabidella eremigena</i> (F. Muell.) E.A. Shaw	N. Scarlett	Australia, Victoria, Western Creek, Millmerran Old
<i>Ballantinia antipoda</i> (F. Muell.) E.A. Shaw	MEL 2280901 (J. Thomas 2005, JAJ1421)	Australia, Victoria, Mount Alexander Regional Park
<i>Blennodia canescens</i> R. Br.	MSB 0288114	Australia, Northern Territory, 27.3 km south of Alice Springs, Airport Road along Old South Road
<i>Crucihimalaya wallichii</i> (Hook. f. & Thoms.) Al-Shehbaz, O'Kane & Price	M. Hoffmann	Uzbekistan, Shurob (Lysak et al. 2003)
<i>Stenopetalum anfractum</i> E.A. Shaw	MSB 288363	Australia, Northern Territory, 24°04'07''S, 133°59'30''E
<i>Stenopetalum lineare</i> R. Br. ex DC.	N. Wong per N. Scarlett, La Trobe University	Australia, Victoria, Terrick Terrick
<i>Stenopetalum nutans</i> F. Muell.	MSB 76272	Australia, Northern Territory, 22°2'S, 133°27'E
<i>Stenopetalum nutans</i>	MSB 86929	Australia, Queensland, 25°15'40''S, 142°39'50''E
<i>Stenopetalum velutinum</i> F. Muell.	MSB 288181	Australia, Northern Territory, 24°08'36''S, 134°00'14''E
<i>Transberingia bursifolia</i> (de Candolle) Al-Shehbaz & O'Kane	E. Schranz (ES 1081)	USA, Idaho, Upper Hot Springs, 45°18'11.6''N, 114 20'28.7''W

MEL - National Herbarium of Victoria, Royal Botanic Gardens, Melbourne

MSB - Millenium Seed Bank, Royal Botanic Gardens, Kew

NT - Northern Territory Herbarium, Alice Springs

Supplemental Table 5. GenBank Accession Numbers for Sequences Used in the Phylogenetic Analyses of the Nuclear Genes *CHS*, *CAD5*, and *MS*.

Species	<i>CHS</i>	<i>CAD5</i>	<i>MS</i>
<i>Aethionema grandiflora</i>	AF112082	---	---
<i>Arabidella eremigena</i>	GQ926526, GQ926528, GQ926529	GQ926501, GQ926503 - GQ926505	GQ926548, GQ926552
<i>Arabidopsis arenosa</i>	AY612781	---	---
<i>Arabidopsis halleri</i>	AJ619906	---	---
<i>Arabidopsis lyrata ssp. lyrata</i>	AJ619890	FJ645063	FJ645118
<i>Arabidopsis thaliana</i>	NC003076	NM_119587.3	NM_120467
<i>Arabis hirsuta</i>	AF112096	---	---
<i>Ballantinia antipoda</i>	GQ926531, GQ926532	GQ926508 - GQ926510	GQ926554
<i>Barbarea vulgaris</i>	AF112108	---	---
<i>Boechera fendleri</i>	AF112090	---	---
<i>Boechera holboellii</i>	FJ645081	FJ645074	FJ645133
<i>Boechera lyallii</i>	AF112099	---	---
<i>Boechera parishii</i>	AF112101	---	---
<i>Boechera stricta</i>	AY612784	---	---
<i>Brassica rapa</i>	---	AC189325	---
<i>Brassica oleracea</i>	AY228486	---	---
<i>Brassica napus</i>	---	---	J04468
<i>Capsella bursa-pastoris</i>	AY612785	FJ645064	FJ645128 - FJ645129
<i>Capsella rubella</i>	AF112106	---	---
<i>Cardamine amara</i>	DQ209008	---	---
<i>Cochlearia danica</i>	AF144542	---	---
<i>Transberingia bursifolia ssp. bursifolia</i>	FJ645087	FJ645073	FJ645144
<i>Crucihimalaya himalaica</i>	AY612786	---	---
<i>Crucihimalaya mollissima</i>	FJ645084 - FJ645086	FJ645072	FJ645138
<i>Erysimum handel-mazzettii</i>	DQ409238	---	---
<i>Eutrema sp.</i>	FJ645115	---	FJ645123
<i>Ionopsidium abulense</i>	AF144542	---	---
<i>Leiospora pamirica</i>	DQ409231	---	---
<i>Lepidium apetalum</i>	FJ645109	FJ645077 - FJ645078	FJ645153
<i>Lepidium campestre</i>	AF144534	---	---
<i>Olimarabidopsis cabulica</i>	AF144533	FJ645071	FJ645149 - FJ645150
<i>Olimarabidopsis pumila</i>	AF112092, AF112093	---	---
<i>Pachycladon exile</i>	FJ645093, FJ645094	FJ645069 - FJ645070	FJ645161 - FJ645162
<i>Pachycladon fastigiatum</i>	FJ645091, FJ645092	FJ645067 - FJ645068	FJ645158 - FJ645159
<i>Parrya nudicaulis</i>	DQ409229	---	---
<i>Physaria fendleri</i>	FJ645107, FJ645108	---	---
<i>Raphanus sativus</i>	EF408924	---	---
<i>Rorippa amphibia</i>	AF144530	---	---
<i>Sisymbrium irio</i>	AF144541	---	---
<i>Solms-laubachia eurycarpa</i>	DQ409240	---	---

Supplemental Data. Mandáková et al. (2010). Plant Cell 10.1105/tpc.110.074526

Species	CHS	CAD5	MS
<i>Solms-laubachia linearis</i>	DQ409230	---	---
<i>Stenopetalum nutans</i> 76272	GQ926536	GQ926511 - GQ926513	GQ926561 - GQ926563
<i>Stenopetalum nutans</i> 86929	GQ926538, GQ926541	GQ926514 - GQ926517	GQ926564, GQ926566, GQ926568
<i>Stenopetalum velutinum</i>	GQ926542 - GQ926546	GQ926519, GQ926520, GQ926522, GQ926523	GQ926556
<i>Thlaspi arvense</i>	AF144535	---	---
<i>Turritis glabra</i>	AF112091	---	---

Supplemental Table 6. GenBank Accession Numbers, Lineage and Tribal Assignments for Taxa Included in the Maternal Phylogenetic Analysis.

Genus / Species	Lineage ^a	Tribe ^a	<i>rbcL</i>	<i>nad4</i>	<i>matK</i>	<i>ndhF</i>
<i>Aethionema</i>	Aethionema	Aethionemeae	AP009367 [grandiflorum]	EU931343 [arabicum]	AF144354 [grandiflorum]	DQ288726 [saxatile]
<i>Biscutella didyma</i>	Unassigned	Biscutelleae	---	FN594818	GQ424575 [didyma]	DQ288738
<i>Berteroa incana</i>	Unassigned	Alysseae	---	EU931348	GQ424574	AY330097
<i>Lobularia maritima</i>	Unassigned	Malcolmieae	AP009375	GQ424689	GQ424591	DQ288791
<i>Heliophila</i>	Unassigned	Heliophileae	AM234933 [pubescens]	EU931361 [linearis]	GQ424588 [variabilis]	DQ288775 [sp.]
<i>Noccaea caerulescens</i>	Unassigned	Noccaeae	FN594826	EU931379	GQ424598	DQ288804 [cochleariforme]
<i>Cochlearia acaulis</i> [= <i>Ionopsidium acaule</i>]	Unassigned	Cochlearieae	FN594827	EU931369	AF144369 [prolongoi]	DQ288785
<i>Iberis amara</i>	Unassigned	Iberideae	FN594828	EU931367	GQ424589	DQ288781 [semperivens]
<i>Thlaspi arvense</i>	Unassigned	Thlaspidiae	FN594829	EU931392	GQ424602	DQ288839
<i>Chamira circaeoides</i>	Unassigned	Unassigned	AM234932	FN594819	---	---
<i>Arabis alpina</i>	Unassigned	Arabideae	D88903 [stelleri]	EU931347	AF144328	DQ288731
<i>Draba</i>	Unassigned	Arabideae	AP009373 [nemorosa]	EU931357 [altaica]	NC009272 [nemorosa]	DQ288765 [altaica]
<i>Isatis</i>	Lineage II	Isatideae	FN594830	EU931370 [brevipes]	AB354278 [tinctoria]	DQ288786 [tinctoria]
<i>Sisymbrium</i>	Lineage II	Sisymbrieae	AY167982 [irio]	EU931385 [loeselii]	AF144366 [irio]	DQ288826 [altissimum]
<i>Stanleya pinnata</i>	Lineage II	Schizopetaleae	AY483263	GQ424647	AY483226	DQ288832
<i>Streptanthus</i>	Lineage II	Schizopetaleae	FN594831 [glandulosus]	EU931387 [platycarpus]	---	DQ288835 [squamiiformis]
<i>Brassica juncea</i>	Lineage II	Brassicaceae	AY167979	AF095246	---	---
<i>Brassica</i>	Lineage II	Brassicaceae	AF267640 [napus]	AF095244 [rapa ssp. chinensis]	---	---
<i>Cakile</i>	Lineage II	Brassicaceae	AY167981 [maritima]	EU931351 [lanceolata]	GQ424577 [maritima]	DQ288745 [maritima]
<i>Solms-laubachia zhongdianensis</i>	Lineage III	Euclidieae	---	GQ424645	DQ409250	DQ288830
<i>Tetracme quadricornis</i>	Lineage III	Euclidieae	FN594832	EU931390	---	DQ288837 [pamirica]
<i>Chorispora tenella</i>	Lineage III	Chorisporaeae	FN594833	EU931353	---	DQ288753
<i>Anchonium elichrysofolium</i>	Lineage III	Anchonieae	FN594834	EU931346	---	---
<i>Hesperis</i>	Lineage III	Hesperideae	FN594835 [sibirica]	GQ424638 [sibirica]	---	DQ288776 [matronalis]
<i>Smelowskia</i>	Lineage I	Smelowskieae	FN594836 [altaica]	EU931360 [altaica]	---	DQ288774 [tibetica]
<i>Smelowskia calycina</i>	Lineage I	Smelowskieae	FN594837	EU931386	---	DQ288828
<i>Descurainia stricta</i>	Lineage I	Descurainieae	FN594838	EU931355	---	---
<i>Descurainia sophia</i>	Lineage I	Descurainieae	---	GQ424737	GQ424581	DQ288759
<i>Ianhedgea minutiflora</i>	Lineage I	Descurainieae	FN594825	EU931366	---	DQ288780
<i>Hornungia</i>	Lineage I	Descurainieae	DQ310538 [alpina]	EU931365 [petraea]	---	DQ288779 [procumbens]
<i>Lepidium</i>	Lineage I	Lepidieae	AM234934 [africanum]	EU931371 [latifolium]	AF144359 [campestre]	DQ288790 [draba]
<i>Armoracia rusticana</i>	Lineage I	Cardamineae	AF020323	GQ424684	FN597648	---
<i>Barbarea verna</i>	Lineage I	Cardamineae	AP009370	GQ424683	AF144330 [vulgaris]	DQ288737
<i>Cardamine</i>	Lineage I	Cardamineae	AF020324 [pennsylvanica]	AF095252 [scutata]	AF144365 [rivularis]	AF198139 [angustata]
<i>Nasturtium officinale</i>	Lineage I	Cardamineae	AP009376	GQ424688	FN597649	DQ288801
<i>Rorippa</i>	Lineage I	Cardamineae	AF020328 [sylvestris]	AF095250 [indica]	AF144355 [palustris]	AF198138 [curvipes]
<i>Dimorphocarpa</i>	Lineage I	Physarieae	FN594839	GQ424680	---	DQ288763

Supplemental Data. Mandáková et al. (2010). Plant Cell 10.1105/tpc.110.074526

Genus / Species	Lineage ^a	Tribe ^a	<i>rbcL</i>	<i>nad4</i>	<i>matK</i>	<i>ndhF</i>
<i>wislizeni</i>						
<i>Physaria</i>	Lineage I	Physarieae	FN594840 [fendleri]	GQ424677 [purpurea]	---	DQ288813 [floribunda]
<i>Synthlipsis greggii</i>	Lineage I	Physarieae	FN594841	GQ424753	---	EU907365
<i>Crucihimalaya mollissima</i>	Lineage I	Camelineae	FN594843	GQ424831	---	---
<i>Crucihimalaya</i>	Lineage I	Camelineae	D88902 [himalaica]	GQ424734 [rupicola]	AF144356 [himalaica]	AP009372 [wallichii]
<i>Transberingia bursifolia</i>	Lineage I	Camelineae	FN598779	---	DQ406759	---
<i>Erysimum</i>	Lineage I	Camelineae	AY167980 [capitatum]	GQ424669 [canescens]	DQ409262 [handel-mazzettii]	DQ288766 [capitatum]
<i>Olimarabidopsis pumila</i>	Lineage I	Camelineae	NC_009267	GQ424672	AF144345	DQ288807
<i>Turritis glabra</i>	Lineage I	Camelineae	DQ310542	GQ424673	AF144333	DQ288840
<i>Arabidopsis lyrata</i>	Lineage I	Camelineae	FN594842	---	AF144342	DQ288730
<i>Arabidopsis thaliana</i>	Lineage I	Camelineae	NC_000932	Y08501	AF144348	NC_000932
<i>Capsella bursa-pastoris</i>	Lineage I	Camelineae	FN594844	GQ424665	GQ424578	DQ288748
<i>Nestia paniculata</i>	Lineage I	Camelineae	DQ310541	GQ424748	GQ424597	---
<i>Boechera</i>	Lineage I	Boechereae	FN594845 [holboellii]	EU931349 [stricta]	AF144343 [stricta]	DQ288739 [laevigata]
<i>Halimolobos</i>	Lineage I	Halimolobeae	FN594846 [diffusus]	EU931359 [diffusus]	AF144346 [perplexus]	EU718621 [diffusus]
<i>Pennellia micrantha</i>	Lineage I	Halimolobeae	FN594847 [micrantha]	EU931381 [micrantha]	---	DQ288811 [brachycarpa]
Australian endemic species						
<i>Arabidella</i>			FN597049 [eremigena]	FN594822 [glaucescens]	---	---
<i>Ballantinia antipoda</i>			FN597048	FN594823	---	---
<i>Stenopetalum nutans</i>			FN594849 [nutans]	FN594820 [nutans]	---	DQ288833
<i>Stenopetalum nutans</i>			FN594848 [nutans]	FN594824 [nutans]	---	DQ288833
<i>Stenopetalum velutinum</i>			FN594850	FN594821	---	---
New Zealand endemic species						
<i>Pachycladon fastigiatum</i>			FN594851	GQ424668	---	---
<i>Pachycladon novae-zelandiae</i>			FN594852	GQ424667	---	---
outgroups						
<i>Batis maritima</i>			L22438	GQ449679	AY483219	EU002199
<i>Capparis</i>			AY167985 [spinosa]	AF451591 [lanceolaris]	EU371772 [spinosa]	EU002208 [flexuosa]
<i>Carica papaya</i>			M95671	NC_012116	AY483221	AY483248
<i>Cleome</i>			AY483268 [viridiflora]	AF451588 [viscosa]	EU371806 [viscosa]	DQ288755 [rutidosperma]
<i>Floerkea proserpinacoides</i>			L12679	GQ449678	EU002178	---
<i>Tropaeolum</i>			L14706 [majus]	GQ449676 [minus]	AY483224 [majus]	AJ236281 [majus]
<i>Reseda lutea</i>			FJ212219	GQ449675	AY483241	EU002256
<i>Moringa oleifera</i>			L11359	AF451593	AY483223	AY122405
<i>Tovaria pendula</i>			FJ212209	---	AY483242	AY122407

^a Assignment to main phylogenetic lineages and tribal assignment follow Al-Shehbaz et al. (2006) and Couvreur et al. (2010).

Phylogenetic relationships and comparison with previous studies. Up to now the phylogenetic affiliation of the analyzed Australian species was unclear. Phylogenetic analysis of *Stenopetalum* placed the taxon within the crucifer Lineage I (Couvreur et al., 2010), perhaps into Camelinae (Beilstein et al., 2008; Al-Shehbaz et al., 2006); *Arabidella* was only tentatively assigned to Cardamineae (Al-Shehbaz et al., 2006). The present study shows that in all inferred phylogenies the Australian and *Pachycladon* species are interspersed within the Camelinae, Boechereae and Halimolobeae of Lineage I (Figure 4 and Supplemental Figure 3 and 4). The same genera and tribes were also found as the closest relatives of the few Australian and New Zealand genera included in the eight marker data set of Couvreur et al. (2010). As the latter two tribes are morphologically, cytogenetically and geographically well-defined (Koch et al., 2001), *Arabidella* (6 species), *Ballantinia* (1 sp.), *Stenopetalum* (12 spp.) and *Pachycladon* (11 spp.) should be included into the polyphyletic Camelinae.

As the closest relatives of the Australian Camelinae genera were identified the New Zealand *Pachycladon* species (n = 10). Together the two groups form a monophyletic clade in the *MS* and combined maternal phylogenies. This raises the question whether the two groups descended from a common allopolyploid ancestor, with *Pachycladon* species not having undergone the same chromosome number reduction seen in the Australian genera. This question remains unanswered given that Bayes factor analyses (Supplemental Table 3) were unable to find conclusive evidence for more than one WGD event.

Although less taxa have been analyzed in the nuclear gene analyses, the topology of the nuclear gene trees generally agrees with the maternal phylogeny with the exception of the Physarieae which are placed within Lineage I in the maternal phylogeny (Supplemental Figure 4; see also Couvreur et al., 2010; Koch et al., 2001) but outside Lineage I (along with *Aethionema*) as sister to the rest of the Brassicaceae in the *CHS* tree (Figure 4). Some minor incongruencies in tree topology between nuclear and maternal DNA phylogenies have also been observed by Koch et al. (2001), and interestingly, for the position of *Physaria* by Beilstein et al. (2008). For the maternal phylogeny we have used a more comprehensive taxon sampling than for the nuclear gene trees. It has been shown earlier that an increased taxon sampling greatly reduces phylogenetic errors (Zwickl and Hillis, 2002). Hence, an increased taxon sampling could eventually change the position of *Physaria* in the nuclear gene trees.

Supplemental References

- Al-Shehbaz, I.A., Beilstein, M.A., and Kellogg, E.A.** (2006). Systematics and phylogeny of the Brassicaceae (Cruciferae): an overview. *Plant Syst. Evol.* **259**: 89–120.
- Beilstein, M.A., Al-Shehbaz, I.A., Mathews, S., and Kellogg, E.A.** (2008). Brassicaceae phylogeny inferred from phytochrome A and *ndhF* sequence data: tribes and trichomes revisited. *Amer. J. Bot.* **95**: 1307–1327.
- Couvreur, T.L.P., Franzke, A., Al-Shehbaz, I.A., Bakker, F.T., Koch, M.A., and Mummenhoff, K.** (2010). Molecular phylogenetics, temporal diversification and principles of evolution in the mustard family (Brassicaceae). *Mol. Biol. Evol.* **27**: 55–71.
- Koch, M., Haubold, B., and Mitchell-Olds T.** (2001). Molecular systematics of the Brassicaceae: evidence from coding plastidic *matK* and nuclear *Chs* sequences. *Amer. J. Bot.* **88**: 534–544.
- Lysak, M.A., Pecinka, A., and Schubert, I.** (2003). Recent progress in chromosome painting of *Arabidopsis* and related species. *Chromosome Res.* **11**: 195-204.
- Schranz, M.E., Lysak, M.A., and Mitchell-Olds, T.** (2006). The ABC's of comparative genomics in the Brassicaceae: Building blocks of crucifer genomes. *Trends Plant. Sci.* **11**: 535–542.
- Wang, H., Moore, M.J., Soltis, P.S., Bell, C.D., Brockington, S.F., Alexandre, R., Davis C.C., Latvis, M., Manchester, S.R., and Soltis, D.E.** (2009). Rosid radiation and the rapid rise of angiosperm-dominated forests. *Proc. Natl. Acad. Sci. USA* **106**: 3853–3858.
- Zwickl, D.J., and Hillis, D.M.** (2002). Increased taxon sampling greatly reduces phylogenetic error. *Systematic Biology* **51**: 588–598.