Supporting Information

Rapid divergence and expansion of the X chromosome in papaya

Andrea R. Gschwend[a], Qingyi Yu[b,c,1], Eric J. Tong[c], Fanchang Zeng[a], Jennifer Han[a], Robert VanBuren[a], Rishi Aryal[a], Deborah Charlesworth[d], Paul H. Moore[c], Andrew H. Paterson[e], Ray Ming[a,1]

[a] Department of Plant Biology, University of Illinois at Urbana-Champaign, Urbana, IL 61801

[b] Texas AgriLife Research Center, Department of Plant Pathology and Microbiology, Texas A&M University, Weslaco, TX 78596

[c] Hawaii Agriculture Research Center, Kunia, HI 96759

[d] Institute of Evolutionary Biology, University of Edinburgh, Edinburgh EH9 3JT, United Kingdom

[e] Plant Genome Mapping Laboratory, University of Georgia, Athens, GA 30606

[1] To whom correspondence should be addressed. E-mail: rming@life.illinois.edu; QYu@ag.tamu.edu

SI Appendix

Synteny analysis. A dot plot, cycle schematic, and sequence alignment detected 3 syntenic regions between the papaya X-specific BACs and the corresponding *V. monoica* BACs (Fig. S2*a* and S2*b*). The first region (syntenic region 1), corresponding to *V. monoica* BACs MN13O12-MN74M10 and papaya Ctg11941-SH55B21, is located in the region between border A (at the left of the X physical map and the gap in the X physical map, which could not be filled using chromosome walking, due to its repetitive nature (Fig. S4); this region is 402kb larger (45%) in papaya (Fig. S3*a* and Table S12). The second region of synteny (syntenic region 2), corresponds to *V. monoica* BACs MN67D07-MN20D10 and papaya BACs SH54M13-SH49A07, which span a region from the aforementioned gap to the region just inside border B of the papaya X physical map; this region is 320kb larger (56%) in papaya. Syntenic region 3 corresponds to *V. monoica* BAC MN81D10 and the papaya BAC SH86B16, which spans border B of the X-specific region, the first 80kb falling within the sex-specific region and the last 102kb outside this region, into an area that is homologous with the Y^h chromosome (17). This syntenic region is 1.4kb (5%) larger in *V. monoica* than papaya. Overall, the syntenic papaya X-specific region is 721kb larger than *V. monoica* (i.e. it has additional sequence equal to 48% of the *V. monoica* size). When comparing the papaya autosomal BAC DM105M02 and its *V. monoica* homolog, BAC MN15I14, a single syntenic region was seen, although the *V. monoica* sequence is 62kb longer (Fig. S3*b* and Table S12).

Sequence expansion. Five X-specific regions (blocks) have longer sequences in papaya than in *V. monoica* (Fig. 1*c* and Table S5). Blocks 1-3 are located in syntenic region 1. Block 1, which corresponds to *V. monoica* BAC MN13O12 and papaya contigs Ctg11941-Ctg08318, is 64 kb (32.8%) larger in papaya. The second block, corresponding to *V. monoica* BAC MN82C19 and papaya BAC SH80F18, is also larger in papaya (by a total of 178 kb, or 57.1% expansion). Block 3, corresponding to *V. monoica* BAC MN96C09 and papaya BAC SH79M13 and SH55B21 has the greatest size difference in syntenic region 1, being a total of 251 kb (73.5%) larger in papaya. Blocks 4 and 5 correspond to syntenic region 2. Block 4, which corresponds to *V. monoica* BAC MN67D07 and papaya BAC SH54M13, is 37kb larger in papaya (56.1%). Block 5, which corresponds to *V. monoica* BACs MN25J07 and MN20D10 and papaya BACs SH53E18 and SH49A07, is 266 kb larger (46.9%) in papaya compared to *V. monoica*.

BAC sequence re-ordering. Two *V. monoica* BACs, MN15I14 and MN20D10, which are in 4 and 5 contigs, respectively, were both re-ordered after being aligned to the corresponding completed papaya BACs. This resulted in some changed X-specific (Table S2) and autosomal gene locations (Table S3) from those of the BACs submitted to NCBI, which were unordered upon submission. Refer to Table S11 for a complete list of BACs and NCBI accession numbers.

Gene prediction. Genes were predicted in *V. monoica* BACs MN96C09-MN20D10 and SH79M13-SH49A07, which correspond to regions that fall within the non-recombining HSY-specific region in papaya (Table S1). The other *V. monoica* and papaya BACs not analyzed here correspond either to regions that lie on or beyond Borders A and B defined by the HSY physical map. Genes were annotated in the 703 kb of *V. monoica* sequence, and the 1,820 kb of papaya X sequence corresponding to the BACs mentioned above.

Divergence time analysis. Ten genes are shared between *V. monoica*, the papaya X, and the papaya HSY. Divergence time analyses were performed on seven of the 10 shared genes (Table S9). Three genes, $CpXY^h20$, $CpXY^h29$, and $CpXY^h37$, were excluded from the analysis due to incomplete sequences of their introns. The K_{sil} values range from 0.132-0.215 between *V. monoica* and the papaya X and 0.141-0.215 between *V. monoica* and the papaya HSY. $CpXY^h4$, $CpXY^h8$, and $CpXY^h12$ are pseudogenes, but are still suitable for estimating divergence times from silent site differences. The *V. monoica* copy of $CpHY^h23$ is truncated compared to the papaya copies, but is still transcribed and contains a complete conserved domain, and so we included silent sites in the portion of sequence that is available. Divergence times were also estimated for 3 of the 5 autosomal gene pairs. Expansion within the introns of the *V. monoica* copy of VmA2 prevented an estimate of K_{sil} for this gene and CYC-b is a single exon gene, so K_{sil} analyses could not be preformed. The K_{sil} values for the remaining three autosomal genes suggest divergence times ranging from 22.4-24.1 MYA.

Repetitive element content. The larger size of the papaya X-specific region is due to retrotransposon insertions and duplications. About 60% of the *V. monoica* sequences consist of repetitive elements for both the BACs corresponding to the papaya X-specific and to the autosomal regions (Table S6), whereas the papaya X-specific region has an average of 65.4% of repetitive elements, a 5.4% increase, mainly due to an increase of retroelements, specifically long terminal repeat (LTR) elements. Figure 1*a* depicts the papaya X region in which these duplications are highly abundant. Two regions of *V. monoica* sequence have extensive duplications of *Gypsy* LTRs in papaya, occupying the gap in synteny between syntenic regions 1 and 2 in *V. monoica* and the papaya X-specific region (Fig. S3*a*).

***V. monoica* genome size**. The genome size of *Vasconcellea monoica*, Accession# HCAR171, was determined through flow cytometry by the Flow Cytomerty and Imaging Core Laboratory at the Virginia Mason Research Center, Seattle, WA, following the protocol reported by VanBuren et al. (2011). Internal standards of chicken red blood cells (2.5 pg/2C), *Glycine Max* (2.35 pg/2C), *Oryza sativa* cv Nipponbare (0.96 pg/2C), and *Arabidopsis thaliana* (0.36 pg/2C) were utilized to determine genome size.

References

VanBuren R, et al. (2011) Longli is not a hybrid of Longan and Lychee as revealed by genome size analysis and trichome morphology. *Trop Plant Biol* 4:228-236.

Na J-K, et al. (2012) Rapid expansion of the hermaphrodite specific region of Y^h chromosome (HSY) in papaya. *BMC Genomics* (in press).

Ming R, et al. (2008) The draft genome of the transgenic tropical fruit tree papaya (*Carica papaya* Linnaeus) *Nature* 452:991-996.

Supplemental Figures

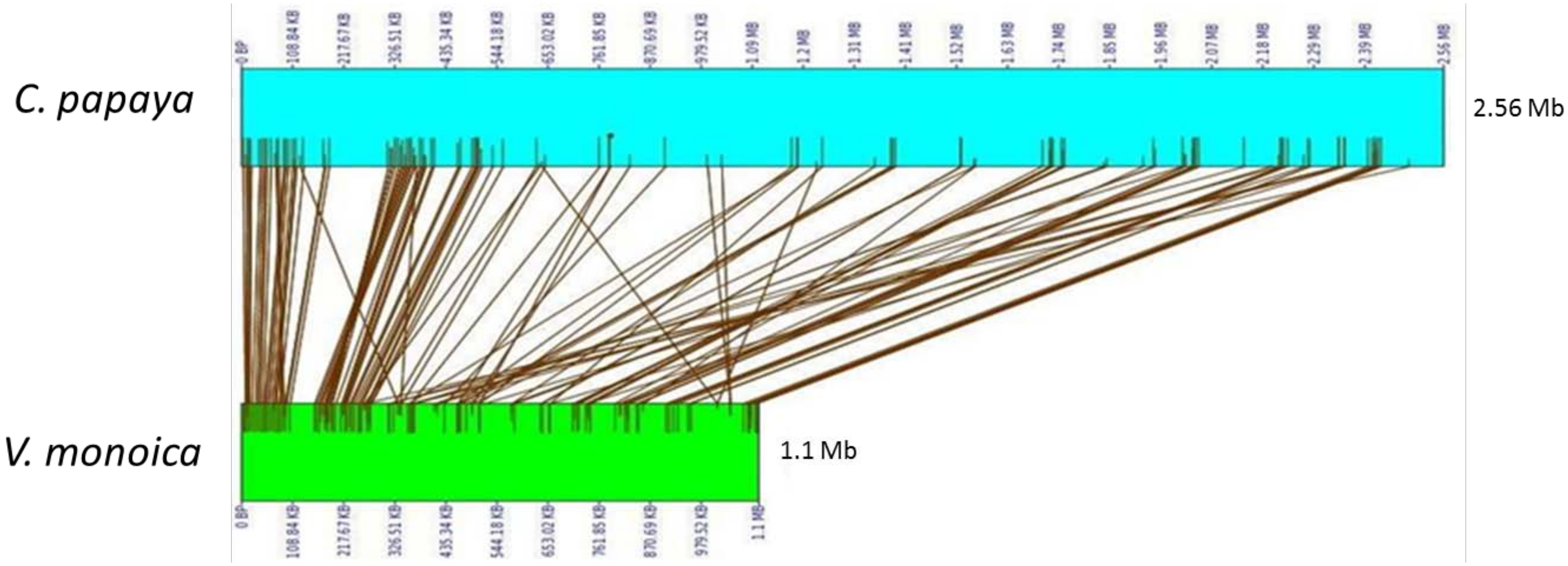

Fig. S1. The alignment of the papaya X-specific pseudomolecule and the corresponding *V. monoica* pseudomolecule. Brown lines denote alignable regions, and the locations of these regions in the pseudomolecules.

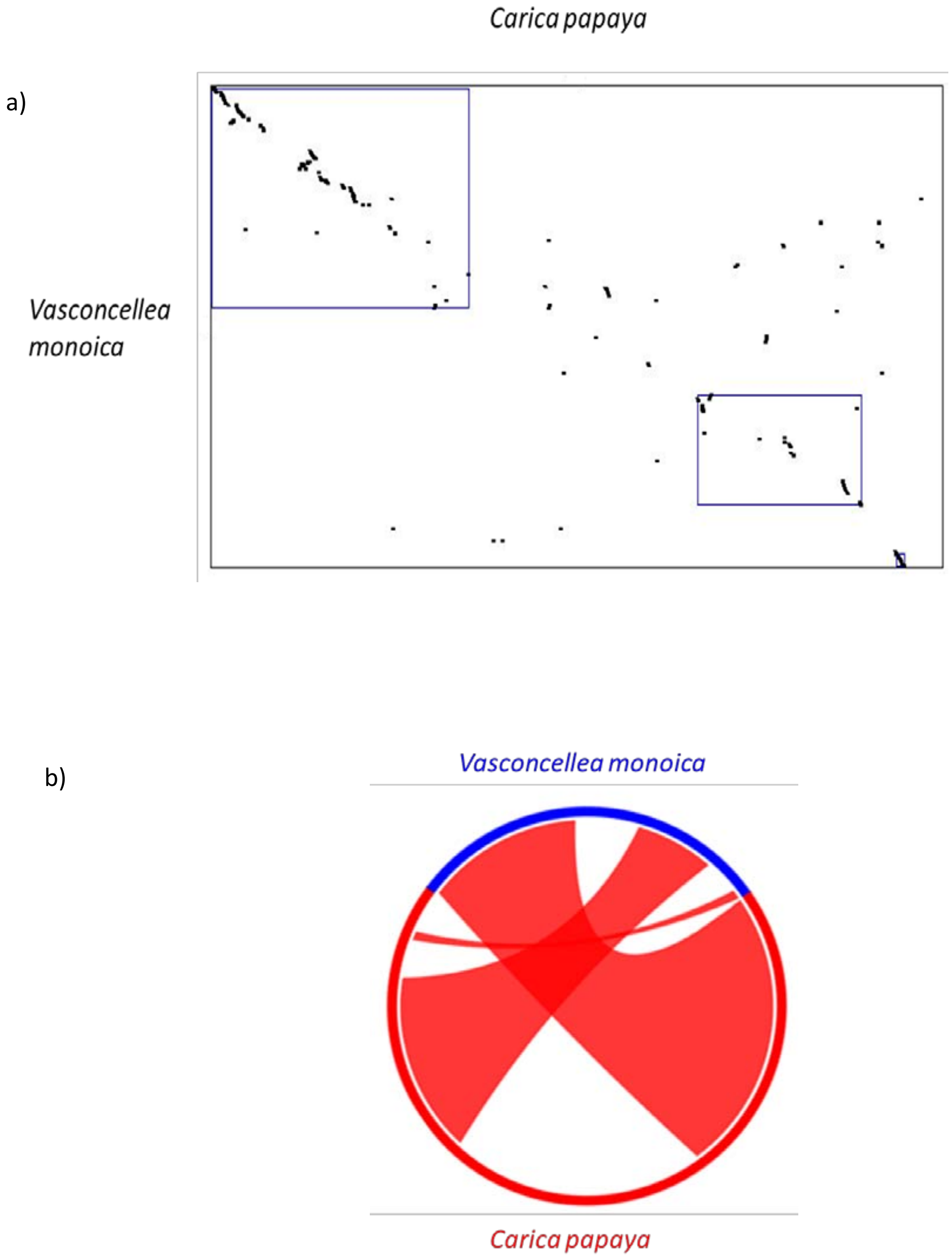

Fig. S2. The syntenic regions shared between the X-specific region in *C. papaya* and the corresponding regions of *V. monoica*. (A) Dot plot alignment map, with boxes denoting the three syntenic regions. (B) Cycle schematic view with the three syntenic regions represented.

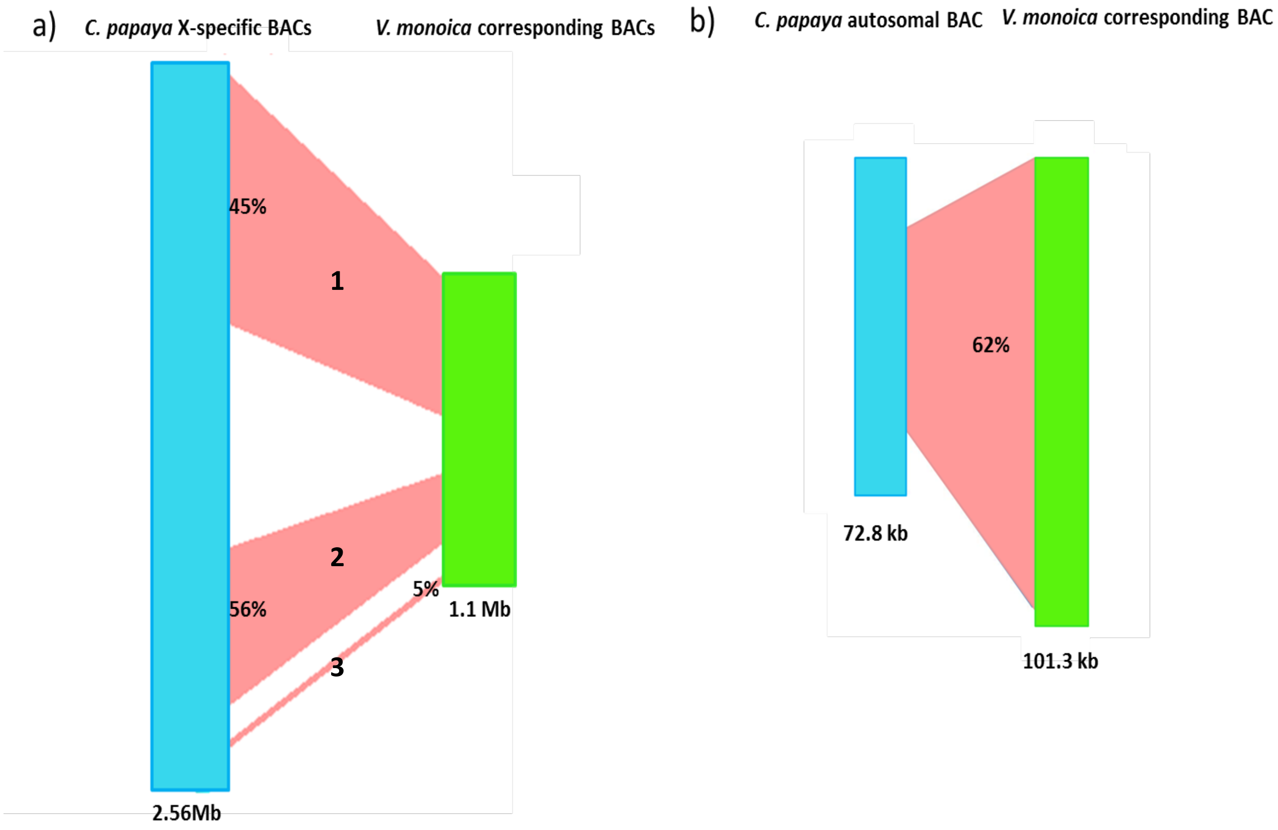

Fig. S3. Size differences in the syntenic regions of *C. papaya* and *V. monoica*. (a) Syntenic regions of the papaya X-specific pseudomolecule compared with the corresponding *V. monoica* pseudomolecule. (b) The syntenic region of one *V. monoica* autosomal BAC compared to its corresponding papaya autosomal BAC.

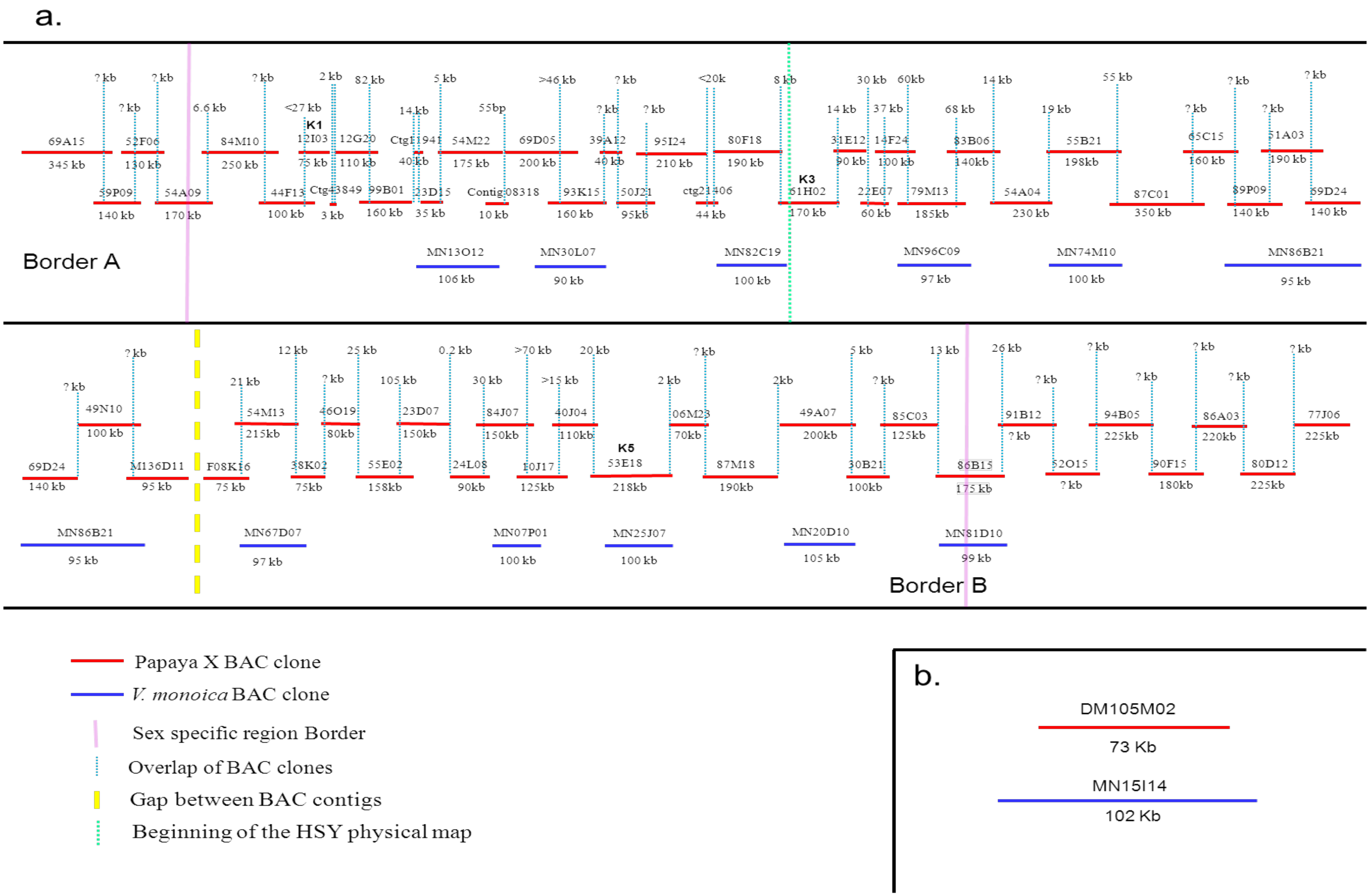

Fig. S4. Physical map locations of the *C. papaya* and *V. monoica* BACs. (A) The papaya X physical map published by Na et al. (2012) and the relative positions of the *V. monoica* BACs carrying homologous sequences. (B) The papaya autosomal BAC with the corresponding *V. monoica* BAC.

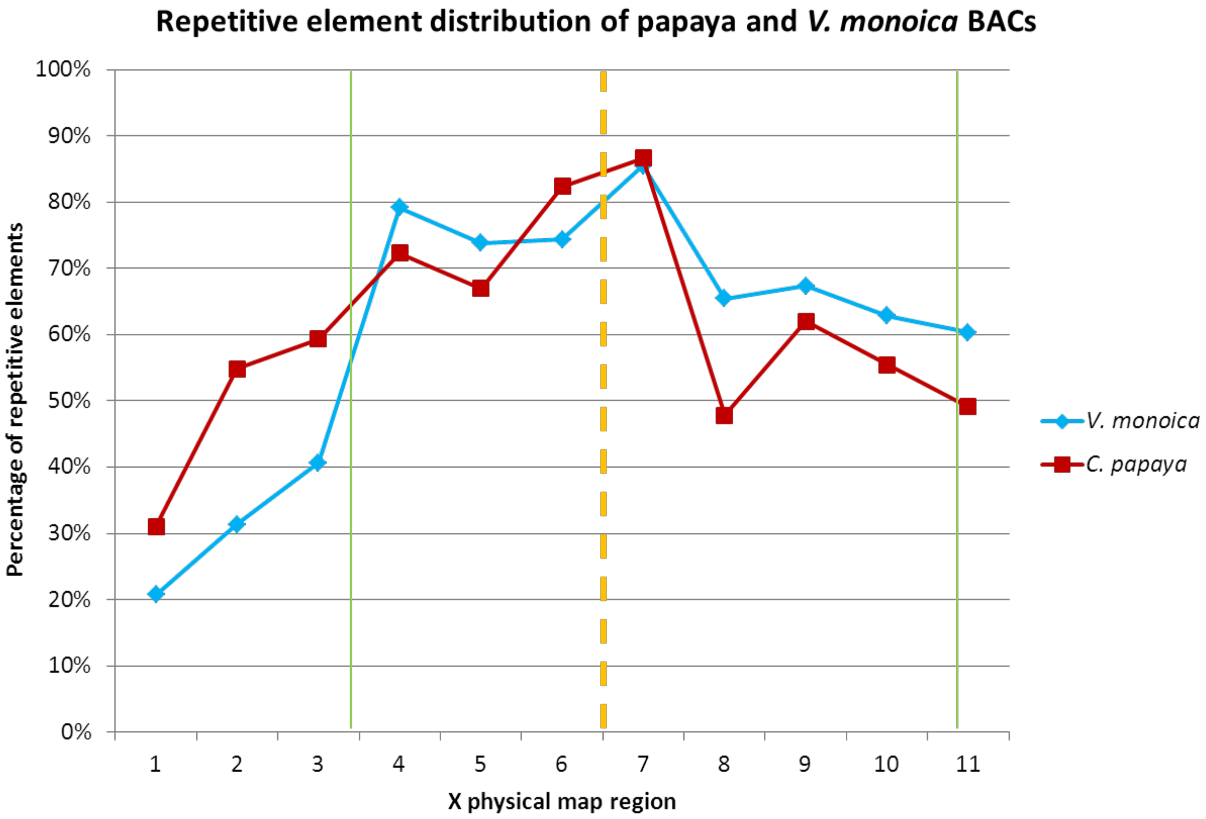

Fig. S5. The distribution of repetitive elements surrounding the gap on the papaya X physical map in both *C. papaya* and *V. monoica* is an indication of a conserved centromeric location between the two species. The vertical green lines represent the borders of the fully sex-specific region of the papaya X, and the dashed yellow vertical line represents the location of the gap in the X physical map.

Supplemental Tables

Table S1. Size and positions of the *V. monoica* BACs and corresponding *C. papaya* X BACs in the pseudomolecule used for the alignment, synteny, and repeat analyses.

BAC Order	*V. monoica* BACs	Size (bp)	Position on *V. monoica* pseudomolecule (kb)	Corresponding *C. papaya* X BACs	Size (bp)	Position on *C. papaya* X pseudomolecule (kb)
1	MN13O12	106,282	0-106	Ctg11941_SH23D15_SH54M22_Ctg08318	185,988	1-186
2	MN30L07	90,139	106-199	SH95K15	185,675	186-376
3	MN82C19	100,125	199-299	SH80F18	183,386	376-559
4	MN96C09	96,693	299-396	SH79M13	153,799	559-713
5	MN74M10	99,940	396-496	SH55B21	198,483	713-911
6	MN86B21	94,895	496-591	SH65C15_SH50M24_SH51A03_SH69D24_M136D11	572,951	911-1,484
7	MN67D07	108,986	591-699	SH54M13	216,367	1,484-1,701
8	MN07P01	97,045	699-797	SH84J07	222,899	1,701-1,924
9	MN25J07	100,458	797-897	SH53E18	252,668	1,924-2,176
10	MN20D10	104,999	897-1,002	SH49A07	203,300	2,176-2,379
11	MN81D10	98,788	1,002-1,101	SH86B15	182,222	2,379-2,561
	Total length	1,098,350			2,558,338	

Table S2. List of *V. monoica* (Vm) and *C. papaya* (Cp) genes located on BACs corresponding to the papaya X-specific region in the order they appear on the papaya X physical map.

Species/Sex chromosome	Gene Symbol	Putative Function	Number of exons			Coding Sequence Length			Intron Length			Autosome Homolog			BAC								
												Cp Linkage Group	Cp super-contig	Vm whole genome support	Position	ID	Accession Number	Position	ID	Accession Number	Position	ID	Accession Number
			Vm	CpX	CpHSY	Vm	CpX	CpHSY	Vm	CpX	CpHSY				Vm			CpX			CpHSY		
Vm	VmX1	uncharacterized protein	1			217			NA			1	123	+	7537-7755	MN96C09	JN088508						
Vm	VmX2	---NA---	1			888			NA					+	60091-60978	MN96C09	JN088508						
CpX	CpX-10	---NA---		2			432			532								51828-52791	SH79M13	AC239204			
CpX	CpX-11	---NA---		1			207			NA								58107-58313	SH79M13	AC239204			
Vm, CpX, CpHSY	CpXY^{h}5	4-nitrophenylphosphatase	8	8	8	829	807	816	2490	2444	2448			+	68216-71534	MN96C09	JN088508	66241-69491	SH79M13	AC239204	95427-98690	SH69E13	AC238619
Vm*, CpX, CpHSY	CpXY^{h}8	SYN4 (SISTER CHROMATID COHESION 1 PROTEIN 4)	14	15	15	3630	3618	3612	14247	10486	9256			+	13491-31367	MN74M10	JN088503	97208-111312	SH55B21	FJ429367	73441-86309	SH81012	AC239165
CpX	PCpX-4	---NA---		1			352			NA								65772-66123	SH51A03	AC238603			
CpX, CpHSY	PY^{h}CpXY^{h}22	Vps51/Vps67 family protein		6	5		3240	3045		16497	16473			+				178754-180952	SH51A03	AC238603	6062-25579	SH23L24	AC238593
CpX, CpHSY	PXY^{h}CpXY^{h}1	universal stress protein (USP) family protein		4	4		852	840		37086	34346							69753-107690	SH69D24	AC239162	57117-92302	SH53G04	AC238607
CpX, CpHSY	PY^{h}CpXY^{h}23	Hypothetical protein		1	1		339	326		NA	NA							86822-87160	SH69D24	AC239162	71268-71593	SH53G04	AC238607
CpX, CpHSY	CpXY^{h}11	PWWP domain-containing protein		1	1		3126	3111		NA	NA							110760-113885	SH69D24	AC239162	95120-98230	SH53G04	AC238607
Vm	VmX3**	---NA---	3			471			372					+	4398-5241, 53985-54827	MN86B21	JN088507						
Vm*, CpX, CpHSY	CpXY^{h}12	ADP-ribosylation factor A1B	4	5	6	461	552	558	2928	6244	7526			+	57666-61054	MN67D07	JN088502	159681-166476	SH54M13	AC238609	32224-40307	SH81O12	AC239165
Vm, CpX, CpHSY	CpXY^{h}20	MBD9; DNA binding / methyl-CpG binding	10	11	11	6568	6612	6609	31662	22522	37067			+	6198-44427	MN07P01	JN88494	166625-195755	SH84J07	AC238629	91204-134880	SH88A07	AC239168

Species/Sex chromosome	Gene Symbol	Putative Function	Number of exons			Coding Sequence Length			Intron Length			Autosome Homolog			BAC								
												Cp Linkage Group	Cp super-contig	Vm whole genome support	Position	ID	Accession Number	Position	ID	Accession Number	Position	ID	Accession Number
			Vm	CpX	CpHSY	Vm	CpX	CpHSY	Vm	CpX	CpHSY				Vm			CpX			CpHSY		
Vm[†], CpX, CpHSY	CpXY^{h}27	protein kinase	13	20	20	1683	2091	2088	3261	9032	88988			+	82044-86987	MN86B21	JN088507	19577-30698	SH53E18	EF661026	34767-45842	SH64O06	AC239158
Vm	VmX4	---NA---	1			270								+	49607-49876	MN07P01	JN88494						
Vm	VmX5	unnamed protein	8			3135			3151			9	1	+	8023-14308	MN25J07	JN088499						
Vm	VmX6	cation/H(+) antiporter	3			2307			220			unknown, 9,9	381, 1, 476	+	19361-21887	MN25J07	JN088499						
Vm*, CpX, CpHSY	CpXY^{h}29	N-acetylglucosamine-phosphate mutase	9	9	7	1574	1686	1362	27958	32248	19588			+	50651-92897	MN25J07	JN088499	86982-119229	SH53E18	EF661026	87673-107260	SH59O17	AC239154
CpX, CpHSY	CpXY^{h}30	NUC (nutcracker); nucleic acid binding / transcription factor/ zinc ion binding		1	1		209	312		NA	NA							92981-93289	SH53E18	EF661026	92916-93227	SH59O17	AC239154
Vm	VmX7	hypothetical protein	6			963			1611					+	64502-67075	MN25J07	JN088499						
Vm	VmX8	---NA---	1			264			NA					+	74529-74792	MN25J07	JN088499						
Vm	VmX9	hypothetical protein	3			423			1638					+	81854-83914	MN25J07	JN088499						
Vm, CpX, CpHSY	CpXY^{h}34	metal-dependent phosphohydrolase HD domain-containing protein	18	19	18	1419	1413	1413	16386	7477	7339			+	4950-22754	MN20D10	JN088497	155987-164916	SH49A07	AC239150	151017-159769	SH75H06	AC238771
Vm, CpX, CpHSY	CpXY^{h}35	calcium homeostasis regulater-like protein CHoR1	3	3	3	819	819	819	801	873	883			+	28936-30555	MN20D10	JN088497	150401-152093	SH49A07	AC239150	145436-147128	SH75H06	AC238771
Vm, CpX, CpHSY	CpXY^{h}36	formate dehydrogenase	6	6	6	1149	1149	1149	1627	1496	1497			+	31040-33815	MN20D10	JN088497	147308-149953	SH49A07	AC239150	142343-144988	SH75H06	AC238771
Vm*, CpX, CpHSY	CpXY^{h}37	ERA1 (ENHANCED RESPONSE TO ABA 1); farnesyltranstransferase/ protein farnesyltransferase	14	14	14	1299	1299	1299	17761	5840	5859			+	40595-59654	MN20D10	JN088497	100081-107219	SH49A07	AC239150	95081-102238	SH75H06	AC238771

* Vm pseudogene

** Gene is duplicated

† Gene is truncated

Table S3. List of *V. monoica* (Vm) and *C. papaya* (Cp) genes located on the papaya autosomal BAC and corresponding *V. monoica* BAC.

Species	Gene Symbol	Putative Function	Number of Exons		Coding Sequence Length		Intron length		BAC					
									Position	ID	Gene Bank Accession No.	Position	ID	Gene Bank Accession No.
			Vm	Cp	Vm	CpA	Vm	CpA	Vm			Cp		
Vm, Cp	CYC-b	capsanthin capsorubin synthase	1	1	1485	1485	0	0	1923-3407	MN15I14	JN88496	16714-18198	AM105M02	GQ478572
Vm, Cp	VmA2	uncharacterized protein	10	10	1290	1209	47948	16040	28786-76733	MN15I14	JN88496	19330-36579	AM105M02	GQ478572
Vm, Cp	VmA3	protein	3	3	638	648	687	351	78861-80185	MN15I14	JN88496	38581-39580	AM105M02	GQ478572
Vm, Cp	VmA4	otu-like cysteine type protease	4	4	990	1030	5550	6217	82441-88980	MN15I14	JN88496	41230-48477	AM105M02	GQ478572
Vm, Cp	VmA5	mrna-decapping enzyme-like protein	4	4	457	479	2025	2142	91960-94441	MN15I14	JN88496	50781-53402	AM105M02	GQ478572

Table S4. Gene densities of the syntenic regions of the *C. papaya* and *V. monoica* BACs.

Species	Sequence length (in kb)	Gene Density* (kb/1 gene)
V. monoica	703	**46.9**
C. papaya homologous region on the X chromosome	1,820	**130**
V. monoica	99	**19.80**
C.papaya autosomal homologous region	37	**7.40**

***** Pseudogenes were excluded from the calculation of gene density.

Table S5. The five blocks in which the *C. papaya* X-specific region is larger than the corresponding *V. monoica* region.

Block	Location in the *V. monoica* pseudomolecule	*V. monoica* expansion (bp)	*Location in the C. papaya* pseudomolecule	*C. papaya* expansion (bp)	Percent expansion on *C. papaya* X
1	4,955-4,7967	43,012	547-64,514	63,967	32.8%
2	200,482-276,850	76,368	380,431-558,631	178,200	57.1%
3	319,495-385,985	66,490	598,837-850,064	251,227	73.5%
4	627,652-643,872	16,220	1,502,467-1,539,407	36,940	56.1%
5	818,282-959,856	141,574	2,013,403-2,279,781	266,378	46.9%

Table S6. Repetitive element content of the *C. papaya* X-specific BACs and corresponding *V. monoica* BACs, as well as the *V. monoica* autosomal BAC and the *C. papaya* whole genome.

Sequence source	*V. monoica* X region BACS (1,082,404 bp)		*C. papaya* X-specific BACS (2,545,160 bp)		*V. monoica* autosome BAC (101,746 bp)		Complete papaya genome[1] (271,000,000 bp)	
Repeat class/family	Length occupied (bp)	Percentage of sequences	Length occupied (bp)	Percentage of sequences	Length occupied (bp)	Percentage of sequences	Length occupied (bp)	Percentage of sequences
Retroelements[2]	351,499	32.5%	1,181,757	46.4%	28,622	28.1%	115,601,100	42.7%
LINEs	15,266	1.4%	21,724	0.9%	7,644	7.5%	2,700,000	1.0%
LTR elements	336,233	31.1%	1,160,033	45.6%	20,978	20.6%	90,900,000	33.5%
DNA transposons	11,548	1.1%	2,371	0.1%	701	0.7%	534,200	0.2%
Unclassified	286,822	26.5%	480,122	18.9%	32,469	31.9%	24,298,200	9.0%
Total interspersed repeats	649,869	60.0%	1,664,250	65.4%	61,792	60.7%	140,433,500	51.8%

[1] Papaya genome repetitive element values were obtained from Ming et al. (2008).

[2] Retroelement totals include SINEs and Others as well as LTRs and LINEs.

Table S7. Repetitive element content of the *C. papaya* X-specific BACs.

C. papaya BAC ID	BAC size (bp)	Total Repeats	Percentage of repetitive elements
C. papaya X-specific BACs			
contig08318	10,102	1,664	16.47%
contig11941	163,794	88,598	54.09%
SH23D15	19,615	1,511	7.70%
SH49A07	202,700	112,384	55.44%
SH50M24	144,145	142,546	98.89%
SH51A03	183,721	169,862	92.46%
SH53E18	251,868	156,259	62.04%
SH54M13	215,667	186,841	86.63%
SH54M22	167,852	77,269	46.03%
SH55B21	197,783	132,471	66.98%
SH65C15	153,279	127,473	83.16%
SH69D24	143,655	83,279	57.97%
SH79M13	153,099	110,711	72.31%
SH80F18	182,686	108,373	59.32%
SH84J07	222,249	106,359	47.86%
SH86B15	182,222	89,558	49.15%
SH93K15	185,581	101,727	54.82%
AM136D11	89,095	70,606	79.25%
Autosomal BAC			
DM105M02	72,846	16,226	22.27%

Table S8. Repetitive element contents of individual *V. monoica* BACs.

V. monoica BAC ID	BAC size (bp)	Total Repeats	Percentage of repetitive elements
BACs corresponding to the *C. papaya* X-specific region			
MN07P01	98,296	64,289	65.40%
MN13O12	106,282	22,079	20.77%
MN20D10	102,599	64,450	62.82%
MN25J07	99,658	67,121	67.35%
MN30L07	89,446	28,021	31.33%
MN67D07	107,683	92,084	85.51%
MN74M10	95,940	70,831	73.83%
MN81D10	96,388	58,140	60.32%
MN82C19	99,325	40,400	40.67%
MN86B21	92,495	68,799	74.38%
MN96C09	94,292	74,655	79.17%
Total	108,2404	650,869	60.13%
Autosomal BAC			
MN15I14	101,746	62,126	61.06%

Table S9. Estimated age of divergence of the genes shared by the *C. papaya* HSY, X, and *V. monoica* in regions of synteny.

Gene ID	Silent Sites		Silent mutations		Silent divergence (K_{sil})		Estimated age (MYA)		Average Estimated Age (MYA) ± (SD)	
	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY
CpXY^{h}5	2,560.92	2,547.75	309	328	0.132	0.141	16.450	17.675	21.439* ± 2.988	21.677* ± 3.648
CpXY^{h}8	9,396.75	9,310.67	1,487	1,469	0.178	0.177	22.220	22.145		
CpXY^{h}12	1,827.5	1,819.5	237	237	0.142	0.143	17.798	17.884		
CpXY^{h}27	3,579.75	3,581.5	476	488	0.147	0.151	18.318	18.818		
CpXY^{h}34	7,525.25	7,303.33	1,332	1,207	0.202	0.187	25.250	23.336		
CpXY^{h}35	647.75	651.58	121	122	0.215	0.215	26.854	26.926		
CpXY^{h}36	1,673.33	1,688.83	275	296	0.186	0.200	23.188	24.954		
Vm vs Cp autosome										
VmA3	480.17		78		0.184		23.051		23.181±0.886	
VmA4	5,074.42		863		0.193		24.125			
VmA5	2,003.83		319		0.179		22.368			

*The average age was estimated only to easily compare the X and HSY K_{sil} and does not reflect an accurate divergence time. See the autosomal average estimated age for the divergence time between *V. monoica* and *C. papaya*

Table S10. Total numbers of mutations and K_a/K_s values for 5 pairs of transcripts shared between *V. monoica* (Vm), the papaya X-specific region (X), and the papaya HSY-specific region (HSY), as well as for 5 gene pairs compared between the *V. monoica* and papaya autosomal BACs.

Gene ID	No. Sites (bp)				No. Mutations								Ks		Ka		Ka/Ks		Average Ka/Ks ± (SD)	
	Total sites		Total coding sites analyzed		Syn sites		Non-Syn sites		Syn mutations		Non-Syn mutations									
	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY	Vm vs X	Vm vs HSY
$\text{CpXY}^{h}5$	3,319	3,319	804	801	190.58	188.42	613.42	612.58	31	34	27	34	0.183	0.209	0.045	0.057	0.247	0.273	0.220 ± 0.089	0.227 ± 0.092
$\text{CpXY}^{h}20$	38,230	38,230	6,600	6,600	1490.08	1488.75	5109.92	5111.25	209	203	265	261	0.155	0.151	0.054	0.053	0.347	0.350		
$\text{CpXY}^{h}34$	17,805	17,805	1,410	1,410	311.92	313.00	1098.08	1097.00	54	54	41	42	0.195	0.194	0.038	0.039	0.194	0.200		
$\text{CpXY}^{h}35$	1,196	1,196	813	813	187.33	187.33	625.67	625.67	39	39	31	31	0.244	0.244	0.051	0.051	0.210	0.210		
$\text{CpXY}^{h}36$	2,776	2,776	1,143	1,143	268.33	268.33	874.67	874.67	53	53	20	20	0.229	0.229	0.023	0.023	0.101	0.101		
Vm vs Cp autosome																				
CYC-b	1,485		1,308		308.5		999.5		65.83		51.17		0.251		0.053		0.211		0.205 ± 0.07	
VmA2	1,915		1,191		286.83		904.17		37.75		39.25		0.145		0.045		0.309			
VmA3	1,323		624		152.42		471.58		51		24		0.443		0.053		0.119			
VmA4	6,540		987		231.5		755.5		40		25		0.196		0.034		0.172			
VmA5	2,482		456		98.08		348.92		23		20		0.281		0.060		0.212			

Table S11. NCBI accession numbers of the *V. monoica* and *C. papaya* BACs.

***Vasconcellea monoica* BACs**	**Accession numbers**
MN07P01	JN88494
MN13O12	JN088495
MN15I14	JN88496
MN20D10	JN088497
MN25J07	JN088499
MN30L07	JN088501
MN67D07	JN088502
MN74M10	JN088503
MN81D10	JN088505
MN82C19	JN088506
MN86B21	JN088507
MN96C09	JN088508
***Carica papaya* BACs**	**Accession numbers**
SH05K22	AC239135
SH23D15	AC239144
SH23L24	AC238593
SH49A07	AC239150
SH50M24	JN088493
SH51A03	AC238603
SH53E18	EF661026
SH53G04	AC238607
SH54M13	AC238609
SH54M22	AC239202
SH55B21	FJ429367
SH59O17	AC239154
SH64O06	AC239158
SH65C15	AC239160
SH69D24	AC239162
SH69E13	AC238619
SH75H06	AC238771
SH79M13	AC239204
SH80F18	AC238626
SH81O12	AC239165
SH84J07	AC238629
SH86B15	AC239167
SH93K15	AC239170
AM105M02	GQ478572
AM136D11	AC239253

Table S12. **Sizes of the syntenic regions of the *C. papaya* X-specific region compared to the corresponding *V. monoica* region, as well as the *C. papaya* autosomal region compared with the corresponding *V. monoica* autosomal region.**

	C. papaya syntenic region (bp)	*V. monoica* syntenic region (bp)	Percent expansion in *C. papaya* X	Percent expansion in *V. monoica*
X chromosome				
Block 1	900,826	499,232	45%	
Block 2	571,348	250,963	56%	
Block 3	28,672	30,057		5%
Total expansion of the X region	1,500,846	780,252	48%	
Autosome				
Block 1	37,180	98,904		62%