Supporting Information

Ahmed et al. 10.1073/pnas.0902213106

SI Text

Genetic Diversity. Departures from Hardy-Weinberg expectations and linkage disequilibrium were estimated using Genepop 3.4 (1) with sequential Bonferroni correction applied to adjust the critical probability for multiple comparisons. Four of the six loci showed significant departure from Hardy-Weinberg expectations (Table S5). The possibility of allelic drop-out or the presence of null alleles was tested using the program MICRO-CHECKER (2), which detects nulls by comparison of the observed allele frequencies rather than genotype frequencies expected under Hardy-Weinberg equilibrium. Using this software, only one locus, *Fsyc13*, was suggested to have null alleles present. Large-allele drop-out was not detected and was considered unlikely because the largest allele was 301 bp and allele size ranges were narrow for all loci.

The overall positive F_{IS} value indicates that there was inbreeding present in the adult population. This value can be used to estimate a rate of inbreeding in the population of ≈5% from $F_{IS} = S/(2–S)$ (3), where S is the proportion of offspring produced by selfing (excluding locus *Fsyc13*). Although we did not see any evidence of selfing in the progeny that we collected, it could be that selfing is more common in the summer season, when fruit crops are larger and less synchronized than in the winter, when our sample was collected. Furthermore, the observed F_{IS} value was derived from the adult population and so may reflect past inbreeding, which is not reflected in the present mating pattern. No significant linkage disequilibria were detected among the six loci (see Table S5) used in this study.

Paternity Analysis. The paternity analyses we performed in the program CERVUS 2 (4). We used the option for paternity assignment where one parent is known: as we had collected the seeds directly from the trees, we could be confident of the mother. Three out of 94 seedlings, all offspring of mother 1, were mismatched with the mother at *Fsyc* 6 (mother genotype for *Fsyc* 6: 193 homozygote, three mismatching offspring genotypes for *Fsyc 6*: 180/189, 170/175, 171/180). As we were not certain whether the mismatches were a result of scoring errors or incorrect maternal labeling, they were omitted from the paternity analysis. No other mother-offspring mismatches were observed. However, had these three been included, this would indicate a scoring error rate of 0.54%. Therefore, we investigated the effect of applying an error rate of between 0 and 0.54%, and we observed no change in paternity assignment.

The critical LOD score in CERVUS was estimated by simulation of offspring data given the parental allele frequencies. The program generates two parents from the allele frequencies supplied, as well as a number of unrelated individuals and an offspring. The likelihood ratio is then calculated comparing the true simulated parent with the other candidate parents. This simulation was repeated for 5 sets of 1,000,000 offspring to give a critical LOD score, which must be achieved to assign paternity. Other parameters considered in the simulation are the scoring error rates and the proportion of sampled parents. We varied the error rate as described above, and we set the proportion of candidate parents sampled at 80%; this was considered conservative because we sampled all accessible trees in the study area, the most upstream maternal tree was ≈50 km from the end of our study site, and there were no trees in the remaining 10 km of the study site upstream of the last tree identified.

Simulation of Directional Dispersal. We simulated the expected distribution of paternities under panmixia by drawing the observed number of mothers at random from the total set of 79 sampled adult trees and then assigning paternities at random (excluding self-fertilization) to give the observed numbers of offspring per mother. Fathers could be up or down river of the mothers and simulations included 1,000 random draws.

1. Raymond M, Rousset F (1995) Genepop (Version-1.2)—Population genetics software for exact tests and ecumenicism. *J Hered* 86:248–249.
2. Van Oosterhout C, Hutchinson WF, Wills DPM, Shipley P (2004) MICRO-CHECKER: Software for identifying and correcting genotyping errors in microsatellite data. *Mol Ecol Notes* 4:535–538.
3. Hedrick PW (2004) *Genetics of Populations* (Jones and Bartlett, Sudbury) 3rd Ed, p 737.
4. Marshall TC, Slate J, Kruuk EB, Pemberton JM (1998) Statistical confidence for liklihood-based paternity inference in natural populations. *Mol Ecol* 7:637–655.

Table S1. Locations of *Ficus sycomorus* trees in the Ugab study site

		South		East	
Tree ID	River location	Degrees	Minutes	Degrees	Minutes
1	Ugab	21	9.034	13	41.960
2	Ugab	20	59.472	14	28.004
3	Ugab	20	59.124	14	29.068
4	Ugab	20	58.953	14	30.036
5	Ugab	20	59.185	14	30.905
6	Ugab	20	58.552	14	31.321
7	Ugab	20	58.502	14	32.089
8	Ugab	21	0.805	14	41.380
9	White Lady	21	6.239	14	39.993
10	White Lady	21	6.400	14	39.980
11	White Lady	21	6.500	14	39.830
12	White Lady	21	6.560	14	39.745
13	White Lady	21	6.620	14	39.660
14	White Lady	21	6.620	14	39.650
15	White Lady	21	6.640	14	39.630
16	White Lady	21	6.657	14	39.581
17	White Lady	21	6.680	14	39.550
18	White Lady	21	6.693	14	39.534
19	White Lady	21	6.693	14	39.534
20	White Lady	21	6.700	14	39.515
21	Ugab	21	0.726	14	43.177
22	Ugab	21	0.470	14	44.429
23–25	Ugab	21	0.483	14	44.514
26	Ugab	21	0.430	14	44.663
27	Ugab	21	0.346	14	44.774
28	Ugab	21	0.251	14	44.980
29	Ugab	21	0.300	14	45.383
30	Ugab	20	58.643	14	49.069
31	Ugab	20	57.057	14	50.176
32	Ugab	20	55.730	14	52.767
33	Ugab	20	55.364	14	52.913
34	Ugab	20	54.964	14	54.445
35	Ugab	20	54.969	14	54.451
36–37	Ugab	20	55.062	14	55.596
38	Ugab	20	54.091	14	55.531
39	Ugab	20	52.649	14	57.458
40	Ugab	20	51.534	14	58.758
41	Ugab	20	51.510	14	58.941
42–43	Ugab	20	49.155	15	1.041
44–45	Ugab	20	48.576	15	2.229
46	Ugab	20	48.048	15	2.578
47	Ugab	20	47.763	15	3.020
48	Ugab	20	47.279	15	4.459
49–50	Ugab	20	44.972	15	7.670
51	Ugab	20	43.597	15	9.520
52–53	Ugab	20	43.426	15	9.684
54–55	Ugab	20	43.333	15	9.779
56	Ugab	20	43.033	15	9.563
57–60	Ugab	20	42.291	15	10.289
61–73	Ugab	20	41.602	15	10.759
74–75	Ugab	20	41.126	15	10.934
76	Ugab	20	41.006	15	11.035
77	Ugab	20	40.419	15	11.980
78	Ugab	20	40.358	15	12.123
79	Ugab	20	40.007	15	12.699
end	Omaowa settlement	20	38.500	15	16.000

Tree identification numbers are indicated along with river location. South and East coordinates are shown in degrees and minutes.

Table S2. Genotypes of adult trees

	MFC 2		*Fsyc02*		*Fsyc06*		*Fsyc08*		*Fsyc09*		*Fsyc13*	
Tree ID	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2
1	158	174	173	182	193	193	195	195	195	203	301	301
2	158	174	145	180	189	193	195	195	185	203	293	301
3	158	158	180	182	189	193	195	239	185	195	301	301
4	164	174	145	173	193	193	195	203	195	203	293	301
5	176	184	180	186	171	171	239	250	195	195	301	301
6	148	174	173	180	175	193	195	195	195	195	301	301
7	158	170	180	182	180	193	207	239	195	195	293	301
8	148	158	180	180	173	180	199	219	195	195	293	293
9	170	178	173	173	180	180	195	195	195	197	301	301
10	148	158	180	180	171	180	195	195	195	195	293	293
11	150	168	173	173	171	180	203	203	195	195	293	301
12	154	164	173	173	171	180	239	247	195	195	301	301
13	158	178	173	173	180	193	239	247	195	203	301	301
14	162	178	173	173	171	189	247	247	195	195	293	293
15	158	166	173	182	189	193	195	195	185	197	293	293
16	154	174	173	180	180	189	199	207	195	195	293	293
17	154	174	173	173	171	189	239	243	185	195	293	301
18	−1	−1	−1	182	−1	−1	−1	−1	195	195	301	301
19	174	186	173	180	195	195	203	219	195	195	293	301
20	154	158	173	173	180	193	197	239	187	187	293	301
21	145	154	173	180	189	197	195	195	185	195	301	301
22	162	170	173	173	189	189	195	203	195	197	301	301
23	158	168	173	180	189	193	195	203	195	195	297	301
24	148	158	145	182	180	193	195	195	195	195	297	301
25	148	166	173	173	171	189	239	247	185	195	301	301
26	158	174	173	173	171	171	195	203	185	195	293	293
27	174	174	160	173	175	189	239	247	195	197	293	297
28	148	158	173	180	180	189	239	258	195	195	301	301
29	158	174	173	180	171	180	195	195	195	195	301	301
30	160	162	173	173	180	189	195	247	195	197	301	301
31	154	166	173	186	189	193	243	250	195	195	293	301
32	150	166	173	173	171	189	203	247	185	195	301	301
33	166	176	173	180	171	171	195	239	185	195	301	301
34	158	174	173	173	171	189	195	239	195	195	301	301
35	158	178	173	173	171	193	195	199	195	197	297	301
36	158	176	145	182	171	189	195	247	185	195	301	301
37	154	162	180	182	171	193	195	247	197	197	297	301
38	172	172	160	173	175	189	239	247	195	197	293	297
39	154	168	173	180	189	201	199	203	185	195	293	301
40	162	176	160	173	175	189	203	203	195	197	293	301
41	148	174	180	186	171	175	195	203	195	195	301	301
42	148	162	173	173	195	195	203	203	195	206	297	301
43	154	164	173	186	171	180	239	247	195	195	293	293
44	162	162	180	180	171	171	195	235	185	195	293	301
45	158	178	180	182	180	189	239	258	195	195	301	301
46	174	174	173	186	171	180	195	247	195	195	297	301
47	168	184	145	182	171	175	239	247	185	195	293	293
48	148	158	173	180	177	180	195	247	195	197	297	301
49	158	180	180	180	193	193	239	247	190	195	293	301
50	148	162	173	180	171	201	239	247	195	197	301	301
51	154	180	160	173	171	180	195	239	195	197	297	297
52	148	154	173	180	171	189	195	195	195	195	297	301
53	148	158	145	173	180	193	243	247	195	197	297	301
54	148	158	173	173	180	189	239	239	195	203	301	301
55	166	176	173	182	175	189	195	247	195	203	297	301
56	174	174	173	180	171	171	235	235	195	195	293	301
57	172	188	173	180	−1	−1	195	203	195	197	293	301
58	178	180	173	186	189	193	239	247	185	197	301	301
59	172	174	173	173	171	180	239	239	195	195	297	301
60	166	178	173	180	189	193	207	239	195	203	293	297
61	148	174	145	173	189	189	195	239	185	195	301	301
62	142	142	165	173	175	175	195	239	195	203	282	282
63	148	188	173	173	171	180	195	239	195	195	301	301

	MFC 2		*Fsyc02*		*Fsyc06*		*Fsyc08*		*Fsyc09*		*Fsyc13*	
Tree ID	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2
64	178	178	173	173	180	201	195	247	195	195	293	297
65	180	182	160	173	180	189	195	195	195	195	293	293
66	158	180	173	173	171	180	195	247	195	203	293	293
67	174	174	145	180	180	189	195	203	185	195	293	301
68	158	166	173	182	171	171	195	203	185	195	282	282
69	174	176	145	173	180	189	199	203	185	195	301	301
70	182	182	173	173	189	189	195	203	195	195	293	301
71	178	178	173	180	171	180	203	247	195	195	293	301
72	174	184	145	173	189	189	239	247	195	197	293	301
73	178	178	173	180	175	175	203	247	195	197	293	301
74	148	168	173	173	180	180	195	239	195	195	293	297
75	148	158	173	173	180	189	195	203	195	195	301	301
76	148	160	173	182	171	171	235	239	195	195	301	301
77	148	158	173	180	177	195	195	195	195	197	301	301
78	154	166	173	180	171	177	239	247	195	195	297	301
79	168	178	173	180	193	193	247	247	195	195	293	293

Tree identification numbers are indicated. The six microsatellite loci used in the study are identified, with the sequence-length identity of allele 1 and allele 2 present in each individual. Missing data are denoted by −1.

Table S3. Genotypes of offspring

Mother ID	Offspring ID	*MFC2*		*Fsyc02*		*Fsyc06*		*Fsyc08*		*Fsyc09*		*Fsyc13*	
		Allele 1	Allele 2	Allele1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2
1	1.111	170	174	180	182	193	193	195	203	195	195	301	301
1	1.1141	158	162	173	173	171	193	195	203	185	203	301	301
1	1.1171	145	174	173	173	193	193	195	203	195	203	301	301
1	1.121	158	158	173	180	193	193	195	195	195	203	301	301
1	1.211	158	158	173	182	171	193	195	195	195	203	301	301
1	1.221	158	178	173	173	171	193	195	203	195	195	301	301
1	1.331	174	174	173	182	171	193	195	203	195	195	301	301
1	1.431	148	158	173	186	171	193	195	247	195	195	301	301
1	1.441	148	158	182	186	171	193	195	247	185	195	301	301
1	1.511	158	170	182	182	171	193	195	247	195	195	301	301
1	1.551	148	158	173	186	171	193	195	195	195	195	301	301
1	1.561	148	158	173	186	171	193	195	247	195	203	301	301
1	1.33	174	178	173	182	171	193	195	203	195	195	301	301
1	1.37	148	158	173	182	171	193	195	195	195	195	301	301
1	1.31	158	158	173	180	180	193	195	239	195	195	297	301
1	1.312	158	166	182	182	180	193	195	195	195	195	301	301
1	1.311	158	182	173	182	−1	−1	195	203	195	203	297	301
1	1.32	158	178	173	173	193	193	195	247	195	195	297	301
1	1.13	158	166	173	180	189	193	195	195	195	195	297	301
1	1.45	158	182	173	173	189	193	195	195	195	195	301	301
1	1.44	158	158	173	182	189	193	195	203	195	195	301	301
1	1.413	174	174	182	186	171	193	195	247	195	195	301	301
1	1.451	158	158	173	182	180	193	195	195	195	203	301	301
1	1.46	148	158	173	173	171	193	195	239	195	195	301	301
1	1.57	158	158	173	173	189	193	195	195	195	195	301	301
1	1.6	158	158	173	173	171	193	195	195	195	195	301	301
1	1.7	158	174	173	182	171	193	195	195	195	195	301	301
1	1.2.2	158	158	173	171	171	193	195	203	195	195	301	301
1	1.2.7	148	158	173	182	171	193	195	195	195	195	301	301
1	1.2.8	158	182	173	182	171	193	195	195	195	195	293	301
1	1.2.9	174	182	173	173	189	193	195	203	195	195	293	301
1	1.2.10	158	174	173	180	171	193	195	239	195	195	297	301
1	1.2.13	148	174	180	182	189	193	195	195	195	195	301	301
1	1.2.6	168	174	173	173	171	193	195	195	195	195	301	301
1	1.2.4	158	158	173	173	180	193	195	247	195	195	301	301
1	1.2	158	174	180	182	171	193	195	195	195	195	301	301
1	1.4.10	148	158	173	173	171	193	195	247	195	203	301	301
3	4.3.5	158	168	180	182	193	193	239	258	195	203	301	301
3	4.4.3	158	166	173	180	193	−1	195	239	195	195	301	301
3	4.9.6	148	158	182	182	193	193	195	195	195	195	−1	−1
3	4.21	158	180	173	182	180	193	239	247	195	195	301	301
3	4.22	158	166	173	180	189	193	203	239	195	195	301	301
3	4.23	158	166	173	182	180	193	203	239	195	195	301	301
3	4.24	158	158	173	180	180	193	203	239	185	195	301	301
3	4.25	158	158	173	182	189	189	239	247	195	195	301	301
3	4.26	158	166	173	180	189	189	195	203	185	195	301	301
3	4.27	158	158	173	182	180	189	239	247	195	−1	301	301
3	4.29	158	158	182	193	193	193	239	239	185	195	301	301
3	4.10.7	158	158	173	180	180	193	−1	−1	185	195	297	301
3	4.6.5	150	158	180	182	171	189	195	239	195	195	301	301
4	5.3	158	164	145	173	189	193	203	247	195	195	293	293
4	5.4.1	148	174	145	173	193	193	195	203	195	195	−1	−1
4	5.4.2	158	164	145	173	180	193	203	247	195	195	293	293
4	5.41	148	174	173	173	171	193	203	247	195	195	293	293
4	5.2	−1	−1	145	173	180	193	195	203	195	195	293	301
6	7.01	148	158	173	173	175	180	195	247	195	195	293	301
6	7.31	148	158	173	180	175	193	195	203	185	195	301	301
6	7.33	148	158	145	180	175	193	195	247	−1	−1	301	301
8	12.01	148	158	180	180	170	180	203	219	195	195	293	301
8	12.4	148	174	173	180	180	201	219	239	195	195	293	301
13	17.11	178	178	173	182	175	180	203	239	195	195	301	301
17	21.1	148	154	173	173	171	171	195	239	195	195	293	301
17	21.2	174	174	173	180	175	189	197	239	195	195	301	301

Mother	Offspring	*MFC2*		*Fsyc02*		*Fsyc06*		*Fsyc08*		*Fsyc09*		*Fsyc13*	
ID	ID	Allele 1	Allele 2	Allele1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2	Allele 1	Allele 2
17	21.21	154	162	173	173	171	189	203	239	195	195	293	301
17	21.4	154	158	173	180	189	189	195	239	185	195	293	301
17	21.7	148	154	173	186	171	189	195	239	195	195	293	301
28	34.3	148	148	173	182	171	180	203	239	195	195	301	301
28	34.5	148	170	173	182	171	180	239	258	195	195	301	301
28	34.7	158	170	173	182	171	189	203	239	195	195	301	301
28	34.6	158	172	173	182	171	180	239	258	195	195	301	301
28	34.1	148	180	173	182	171	180	203	258	195	195	301	301
28	34.9	148	188	173	182	171	189	239	239	195	195	301	301
28	34.2	148	148	180	182	171	180	239	239	195	195	301	301
28	34.9.1	158	158	173	182	171	180	203	239	195	195	301	301
28	34.4.1	148	158	173	182	171	180	203	239	195	195	301	301
28	34.8	158	158	180	182	171	189	195	239	195	195	301	301
28	34.4.2	158	158	180	182	171	180	203	239	195	195	301	301
40	46.4.6	162	168	160	173	−1	−1	203	247	195	195	297	301
40	46.9.7	148	162	173	173	180	189	195	203	195	195	−1	−1
41	47.1.9	148	172	182	186	175	180	195	203	195	195	293	301
41	47.2.4	148	174	173	186	171	193	195	203	195	197	297	301
41	47.5.6	148	148	180	186	171	171	195	239	195	197	301	301
41	47.1.6	148	172	173	180	175	180	195	195	195	195	293	301
41	47.1.3	148	148	182	186	171	180	195	203	195	195	293	301
41	47.6.1	148	172	173	186	175	180	195	203	195	195	293	301
41	47.2.2	148	158	180	182	171	175	203	239	195	195	297	301
41	47.7.4	−1	−1	173	186	171	180	195	239	195	203	297	301
41	47.7.7	148	168	173	180	171	180	195	239	195	195	297	301
41	47.8.6	−1	−1	173	186	171	180	195	203	195	195	301	301
41	47.8.10	−1	−1	173	186	171	180	195	195	195	203	297	301

Tree identification numbers are indicated. The six loci microsatellite loci used in the study are identified, with the sequence-length identity of allele 1 and allele 2 present in each individual. Missing data are denoted by −1.

Table S4. Paternity assignments made in CERVUS

Offspring ID	Mother ID	Father ID	Second parent NEP	Trio LOD	Trio C	D (km)
1.46	1	76	2.12E-02	4.53E+00	+	164.7
1.44	1	75	2.21E-02	4.44E+00	+	163.8
1.221	1	71	1.13E-02	4.52E+00	+	163.2
1.33	1	71	1.23E-02	4.38E+00	+	163.2
1.37	1	63	3.46E-02	3.91E+00	+	163.2
1.45	1	70	5.20E-03	6.61E+00	*	163.2
1.2.7	1	63	3.46E-02	3.91E+00	+	163.2
1.2.9	1	70	1.51E-03	8.12E+00	*	163.2
1.2.13	1	52	1.58E-02	4.27E+00	+	161.7
1.413	1	46	2.09E-03	6.46E+00	*	150.8
1.551	1	41	2.98E-03	6.01E+00	+	143.6
1.2	1	29	3.80E-02	4.66E+00	+	120.2
1.211	1	29	4.96E-02	3.49E+00	+	120.2
1.451	1	29	4.27E-02	3.66E+00	+	120.2
1.6	1	29	4.42E-02	3.70E+00	+	120.2
1.7	1	29	8.15E-02	3.64E+00	+	120.2
1.4.10	1	25	1.95E-02	3.89E+00	+	110.6
1.2.4	1	13	2.24E-02	3.80E+00	+	100.8
1.121	1	3	1.48E-02	4.31E+00	+	85.3
4.24	3	75	1.91E-02	4.57E+00	+	80.8
4.22	3	32	1.07E-02	4.51E+00	+	42.8
4.26	3	32	7.69E-03	5.52E+00	+	42.8
4.9.6	3	24	4.99E-03	5.88E+00	+	27.4
4.27	3	13	2.49E-02	4.11E+00	+	24.2
5.4.2	4	66	1.47E-02	4.35E+00	+	78.5
5.4.1	4	24	3.50E-02	3.53E+00	+	24.7
7.01	6	66	1.37E-02	4.45E+00	+	75.7
7.33	6	53	4.03E-03	4.82E+00	+	71.4
12.01	8	41	3.88E-02	3.52E+00	+	51.1
21.1	17	63	3.86E-02	3.64E+00	+	71.5
21.7	17	41	6.15E-03	4.93E+00	+	43.8
21.4	17	3	2.81E-02	4.04E+00	+	23.8
21.21	17	22	1.52E-02	4.56E+00	+	14.2
34.2	28	76	4.19E-03	6.42E+00	*	57.4
34.8	28	36	8.73E-03	4.21E+00	+	20.6
46.9.7	40	74	3.40E-02	4.34E+00	+	27.9
47.7.7	41	74	1.68E-03	7.38E+00	*	29.1
47.1.6	41	57	3.74E-03	3.50E+00	+	26.1
47.6.1	41	57	4.87E-03	3.83E+00	+	26.1
47.5.6	41	50	3.07E-03	5.60E+00	+	22.3

Offspring ID; Mother ID; Assigned father ID; Paternal nonexclusion probability (NEP); Trio LOD score, trio confidence (C) level 80% confidence interval (+) and 95% confidence interval (*), mother-assigned father distance (D) in kilometers.

Table S5. Microsatellite summary statistics

Locus	*k*	N	*Ho*	*He*	HW departure	*F*is
MFC2	21	78	0.846	0.912	*	0.07
Fsyc02	7	79	0.658	0.636	—	−0.04
Fsyc06	10	77	0.727	0.814	*	0.11
Fsyc08	12	78	0.744	0.797	*	0.07
Fsyc09	7	79	0.544	0.505	—	−0.08
Fsyc13	4	79	0.456	0.587	*	0.22
Mean	10.167	—	0.663	0.708	—	0.06

The locus identity, number of alleles (*k*), number of individuals (N), observed heterozygosity (*Ho*), expected heterozygosity (*He*), Hardy-Weinberg probability test (HW). Loci showing significant heterozygote deficiency under a sequential Bonferonni correction for multiple comparisons are denoted by *, and Weir and Cockerham inbreeding coefficient (*F*is) both estimated in Genepop 3.4 [Raymond M, Rousset F (1995) Genepop (Version-1.2) - Population genetics software for exact tests and ecumenicism. *Journal of Heredity* 86:248–249.].