Supporting Information

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SI Materials and Methods

Selection of Haplogroups. We chose haplogroups in each region based on prior TMRCA affiliation with either the Holocene, Last Glacial, or Upper Paleolithic periods. In each case, we used haplogroups on both sides of the major phylogenetic divisions to minimize lineage-specific biases: both M and N in eastern Asia; both R and non-R lineages in Europe (H and non-H); and L0 vs. L2/3 in Africa. The haplogroups from the Holocene, Last Glacial, and Upper Paleolithic collections are all representative of populous lineages within their respective continents (1–3).

Europe. We chose haplogroups associated with an origin in Near Eastern populations during the Holocene: T1, T2, J1a, K2a, and H4a. These haplogroups (T1, T2, J1a, and K) all appear to have Near Eastern founders that migrated to Europe after the Younger Dryas (2). After inspecting the haplogroup K network in Behar et al. (4), we chose the subgroup K2a, which appears to be present in the Near East (including non-Ashkenazi Jews) and European populations (but not North Africa). Haplogroup H4a is thought to have expanded throughout Europe during the Neolithic (5). However, the location of its origin is still not certain (6). Removing H4a from the Skyline analysis did not substantively change the timing of Holocene period expansion (results not shown). European haplogroups U5, V, and 3H are associated with an indigenous origin in Europe (2). Haplogroups U5a, U5b1, V, and 3H have all been attributed a TMRCA during the Last Glacial Period (2, 7–9).

Africa. Haplogroups associated with the Neolithic expansion in Africa include L0a2, L2a1, L3d, and L3e2. L0a2 (formerly L1a2) has been associated with a Holocene origin in tropical Africa, then eastern and southeastern dispersals of the Bantu-speaking populations (3). Haplogroup L2a1 has an origin in western Africa, but a current pan-African distribution. There is a clear signature of L2a1 in Bantu-speaking groups (3). Haplogroup L3d originated 30,000 ya, likely in western Africa, and has been associated with the Bantu-speaking migration into southern Africa (3, 10).

Eastern Asia. Haplogroups associated with Holocene period migrations in eastern Asia include B4a1, F1a, and E1. Haplogroup B4a1 and its subgroups are most well known for their association with the Polynesian agricultural expansion. B4a is present in China, Taiwan, Japan, and Mainland/Island Southeast Asia (1, 11). B4a1a and subgroups appear to coalesce at/or less than 12Kya (12, 13). F1a is distributed throughout China, Island Southeast Asia, Taiwan, Japan, and Thailand (1, 11). The primary subgroups of F1a (i.e., F1a1a, F1a2, F1a3, F1a4) are all younger than 10 Kya (1). Subhaplogroups E1a and E1b (the only two subgroups of E1) have been recently accorded a phylogeographic origin in island southeastern Asia (e.g., Taiwan, Indonesia, Melanesia) dating to <12 Kya (13, 14).

Papua New Guinea. To investigate a signal of Asian population growth that should clearly predate the Holocene, we looked to lineages known to be indigenous to highland Papua New Guinean populations. Haplogroups P1, P2, P4a, and Q3 are derived from the initial Upper Paleolithic settlement of Oceania >40 Kya (15).

After determining the set of haplogroups for analysis, we searched for these select haplogroups in a database built from publicly available complete mitochondrial coding region sequences in GenBank. We assigned a precise haplogroup affiliation for each individual by our own internal algorithm, which may differ from the recorded GenBank affiliation if it was included in the accession information.

We would have liked to include Native American lineages in this analysis, because there is a well-supported archaeological record for the independent development of agriculture in the Americas. However, few American haplogroups are specifically associated with regions where agriculture developed 5,000 ya. Additionally, there is a paucity of complete mitochondrial coding region sequences in regions of large-scale agricultural production (central America and the Andean highlands). Recent Bayesian Skyline analysis of all Native American haplogroups reflects the expansion of these lineages after the initial colonization of the Americans during the Last Glacial Period (16, 17).

Accession Information for All Samples. European Neolithic sample (n = 144):

EF177410, EF657445, AY495286, AY495275, AY495281, EF657401, EF660992, DQ523649, EF657755, EF657285, AY495282, AY195767, EF657345, EF657455, AY495304, AY495302, EF661001, EU007862, DQ112814, EF660978, AY495277, EF657604, AY339568, AY495291, EF657448, AY495289, EF657427, EF657777, DQ112892, AY495288, AY495290, AY495297, EF657397, EF177409, EF657240, AF382006, DQ112817, DQ112943, AY339570, EF657686, AY495292, AY339574, EF657430, AY339572, AY339575, AY339576, EF177431, DQ112800, AY495201, DQ358973, EF657649, AY495222, AY495211, AY339585, EF657620, AY495230, AY495212, EF657300, EF657560, AY495195, AY495217, AY495226, AY495216, AY495229, DQ112793, AY339587, AY495228, EF660981, AY495221, DQ523659, EF657573, AY495192, EU130562, EF657656, AY495193, EF449507, EU130942, AY495190, AY339423, EF657619, AY495191, EF657456, EF657787, AY495189, AY339425, AY495188, EU215517, EF657479, EU200235, AY495194, AY738972, EF177447, AY339422, EF657629, EF657721, AY339424, EF609015, AY495178, EF657496, EF657776, AY495183, AY495184, AY495123, EF657298, EF660991, EF657270, DQ523646, EF657591, EF657783, EU200347, AY495181, EF657469, AY495179, AY495095, EF657767, DQ358977, AY495111, AY495186, EF177440, EF657728, EU051827, DQ282493, DQ282501, AY495246, DQ282502, AY495244, AY495247, DQ282504, EF657602, EU130564, AY495241, DQ282495, EF657526, EF657610, DQ282497, EF657244, DQ282499, AY495252, AY495242, EF657273, EF657453, AY495249, DQ282498, DQ282503

European Last Glacial Period sample (n = 65):
EF657653, EF657646, EF660946, AY495310, EF657696, AY738947, EF657467, EF661005, EF657709, EF657444, AY495325, EF657364, AM260578, AY738986, AM260575, EU140330, AY495323, AY339442, AY738991, AY339440, AY882411, EF657233, EF660930, AM260562, AY738990, EF397754, EF657259, EF657784, AY495322, EF657328, DQ112837, AY339526, AM260564, EU140744, AM260591, AY882409, AY495317, AY339434, AY495313, EF657684, AY339441, DQ661681, AM260576, EF177435, EF177419, EF660950, EF657245, EF657594, EF657320, AY339523, EF657657, AY882399, AM260572, AY882410, EF657274, AY339437, DQ112808, EF660980, AY495319, AY339445, DQ489521, AY339435, EU140332, DQ112890, EF657616

African Neolithic sample (n = 84):
AF346967, AF346977, AF346994, AF346998, AF346999, AF347014, AF347015, AF381998, AM711903, AY195782, DQ112686, DQ112687, DQ112688, DQ112689, DQ112713,

DQ112714, DQ112715, DQ112716, DQ112722, DQ112739, DQ112744, DQ112747, DQ112756, DQ112847, DQ112848, DQ112851, DQ112853, DQ112857, DQ112884, DQ112901, DQ112904, DQ112906, DQ112917, DQ112918, DQ112923, DQ112949, DQ112953, DQ304968, DQ304969, DQ304970, DQ304971, DQ304972, DQ304973, DQ304974, DQ304975, DQ304976, DQ304977, DQ304998, DQ304999, DQ305002, DQ305004, DQ305005, DQ305007, DQ305009, DQ305010, DQ305012, DQ305013, DQ305015, DQ305016, DQ305017, DQ305018, DQ305019, DQ305020, DQ305022, DQ305023, DQ341058, DQ341070, DQ341071, DQ341072, EF184602, EF184603, EF184604, EF184605, EF184606, EF184607, EF184608, EF184623, EF184628, EF184641, EF657277, EF657286, EF657544, EF657580, HUMMTA

African Upper Paleolithic sample (n = 38):
EF184592, EF184586, EF184593, EF184591, EF184590, AY195777, EF184594, EF184610, AF347009, AF347008, EF184611, EF184609, L498, L488, L500, L490, L583, L491, L503, L342, L487, L501, L334, L505, L524, L502, L493, L521, L520, L504, L516, L499, L492, L441, L515, L506, L496, L513

East Asian Neolithic sample (n = 72):
AF347007, AJ842744, AJ842745, AJ842746, AJ842747, AJ842748, AJ842749, AP008257, AP008279, AP008338, AP008347, AP008384, AP008475, AP008567, AP008658, AP008667, AP008679, AP008691, AP008701, AP008733, AP008774, AP008798, AP008906, AY195770, AY195791, AY255175, AY289068, AY289069, AY289076, AY289077, AY289080, AY289083, AY289093, AY289094, AY289099, AY289102, AY519492, AY519495, AY950289, AY963572, AY963574, DQ272120, DQ272124, DQ372871, DQ372873, DQ372874, DQ372875, DQ372877, DQ372878, DQ372881, DQ372886, DQ834261, EF061151, EF061152, EF093535, EF093536, EF093538, EF093539, EF093540, EF093544, EF093548, EF093551, EF093552, EF093553, EF093556, EF093557, EF093558, EF114270, EF114271, EF114272, EF114288, EF114289

Papua New Guinea Upper Paleolithic sample (n = 20):
DQ112896, DQ112895, AY289079, DQ112898, AY289089, AY289078, EF061158, EF061155, DQ372870, EF495215, DQ372872, AY289084, AY289088, DQ112897, AF347002, AF347004, AY289087, AY289086, AF347005, AY289092

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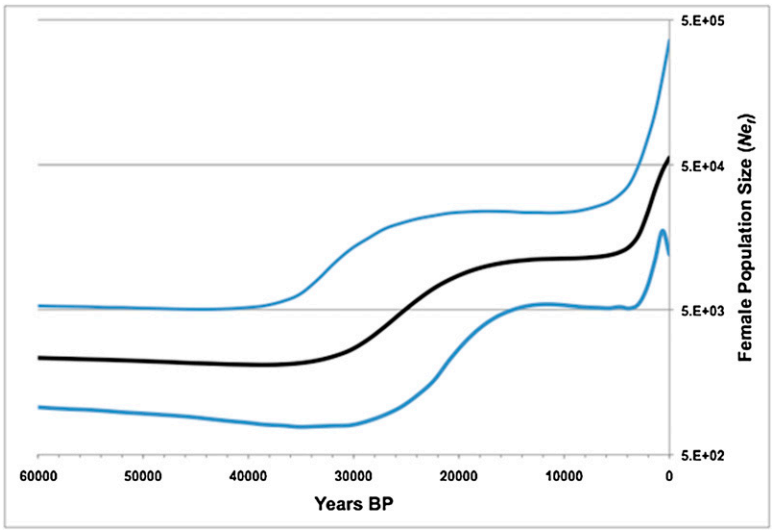

Fig. S1. Bayesian Skyline Plot showing effective female population size changes using our sub-Saharan African Holocene sample (Table S1). The *y* axis represents the female effective population size, only a fraction of the actual population size. The *x* axis represents time in years. Skyline curves were independently corrected for the time dependency of mtDNA mutation rate estimates to accurately compare the timing of genetic growth estimates and archaeological dates for population events. The initial growth at ≈30 Kya was detected before in (18, 19) and may represent the initial occupation in western Africa.

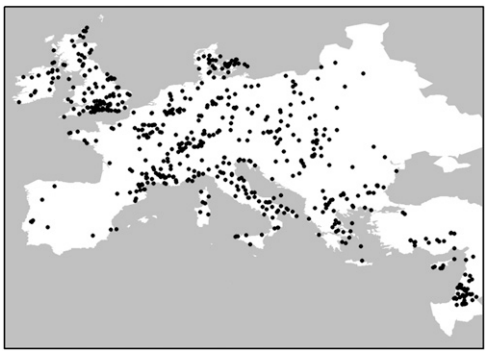

Fig. S2. Locations of the 665 archaeological sites used to create the contour plots seen in Fig. 2 (20).

Table S1. Haplogroup and ethnic information by sample set

Sample set	*n*	Haplogroups	Origin
European Holocene	144	T1, T2, J1a, H4a, K2a	Western Europe, Northern Europe, Mediterranean Europe, United States (European origin)
European Last Glacial	65	U5a, U5b1, V, 3H	Western Europe, Northern Europe, United States (European origin), European (unspecified)
African Holocene	84	L0a2, L3e2, L2a1, L3d	United States (African-American), Eastern Africa, Western Africa
African Upper Paleolithic	38	L0d, L0k	Southern Africa
Southeast Asian Holocene	72	B4a1, F1a, E1	Polynesia, Eastern Asia, Peninsular and Island Southeastern Asia, coastal Papua New Guinea
Papua New Guinea Upper Paleolithic	20	Q3, P1, P2, P4a	Papua New Guinea, Trobriand Islands