

Supplementary information

On the origins and domestication of the olive: a review and perspectives

G. Besnard, J.F. Terral & A. Cornille

SI Appendix includes:

Table S1. Summary of the current genetic data used to infer histories of cultivated and wild olives, with associated methodologies, limitations and main conclusions, and the future genomic data required to test for the neutral and adaptive genomics of domestication in olive

Table S2. Data matrix for the 147 plastid DNA haplotypes identified in the olive complex with 71 loci

Figure S1. Reduced median networks of Mediterranean olive plastid DNA haplotypes

Figure S2. Median joining network of olive chlorotypes reconstructed with NETWORK

References

Table S1. Summary of the current genetic data used to infer histories of cultivated and wild olives, with associated methodologies, limitations and main conclusions, and the future genomic data required to test for the neutral and adaptive genomics of domestication in olive

Data availability	DNA information	Methodology	Main applications	Limitations	Main results relative to the Olive origins
Available	DNA fingerprint; mostly from the nuclear genome (i.e. RAPD, AFLP, ISSR)	<ul style="list-style-type: none"> - Genetic relatedness among individuals (phenetic analyses) - Population genetics estimates (AMOVA [61]) - Demographic inferences (BAPS [44]) 	<ul style="list-style-type: none"> - Cultivar identification [e.g. 22,75,86,100] - Taxonomy of wild olive relatives to the cultivated olive [70,99] - Population structure and phylogeography of wild and cultivated olives [25,70,89] - Among- populations and subspecies gene flow estimates [96] - Inferring cultivated olive origins [22,24,42,89] - Genetic map reconstruction for QTL mapping [49,102] 	<ul style="list-style-type: none"> - Dominant inheritance: inaccurate estimate of heterozygosity and allele frequencies, poorly suitable to perform demographic inferences - Potential amplification of non-Olive DNA, with putative lack of repeatability (e.g. RAPD) - Possible amplification of organellar DNA (e.g. RAPD, AFLP) 	<ul style="list-style-type: none"> - Distinction of two Mediterranean gene pools, first referred to as "East" and "West" [e.g. 6,25,70,96,99] - Evidence for close genetic relationship of most (but not all) olive cultivars with the eastern wild group [6,25] - Structure related to geographic origin and fruit use of cultivars [e.g. 22,24,42,89]
	Nuclear ribosomal DNA (i.e. ITS)	<ul style="list-style-type: none"> - Phylogenetic inferences (e.g. MrBayes, PAUP, BEAST [56,95]) 	<ul style="list-style-type: none"> - Identification of distinct phylogenetic lineages in wild olives based on a nuclear marker [34,70] 	<ul style="list-style-type: none"> - Complex sequence evolution due to concerted evolution, to selective pressures to maintain secondary structure for the maturation of nrRNA (high GC content), and to the presence of several pseudogenic variants [34] 	<ul style="list-style-type: none"> - Distinction of two ITS Mediterranean lineages (both on functional units and pseudogenes) sustaining the existence of two distinct taxa in West and East Mediterranean [33,34] - First molecular characterization of archeological olive remains [59]
	Nuclear repetitive DNAs and retrotransposons	<ul style="list-style-type: none"> - Estimation of the number of tandem repeats - Retrotransposon [69] 	<ul style="list-style-type: none"> - Distinction of groups based on their composition in tandem repeats [43] - Potential use for genotype identification [69] 	<ul style="list-style-type: none"> - Descriptive approach, poorly suitable for implementing evolutionary models 	<ul style="list-style-type: none"> - Distinction of two main groups in the Mediterranean Basin [43]
	Organellar plastid and mitochondrial DNAs (i.e. genomic sequences, RFLP, CAP and microsatellites)	<ul style="list-style-type: none"> - Population genetic estimates - Network analysis - Phylogenetic inferences with molecular dating (e.g. Network, BEAST, Batwing [12,56,101]) 	<ul style="list-style-type: none"> - Phylogeography of the olive complex with dating of the diversification and dispersal history of the maternal lineages [31] - Identification of hotspots of genetic diversity in Oleasters [31] - Cytoplasmic male sterility [32] 	<ul style="list-style-type: none"> - Low genetic variation [30,84] - Maternally inherited genomes data only [32] - Biases associated to potential selective sweep in the chloroplastic and mitochondrial genomes [11] 	<ul style="list-style-type: none"> - Distinction of three phylogenetic maternal lineages, referred to as E1 (East), E2 (West) and E3 (West), and Bayesian dating of their diversification [31] - Human-mediated spread of cultivated chlorotypes or mitotypes [31] - Maternal origins of invasive olives [26]

Table S1, continued

Data availability	DNA information	Methodology	Main applications	Limitations	Main results relative to the Olive origins
Available	Nuclear co-dominant markers (i.e. isozymes, RFLP, microsatellites)	<ul style="list-style-type: none"> - Parentage analyses, genetic relatedness between individuals and co-ancestry analyses [e.g. 54,85] - Population genetic diversity estimates, population structure and demographic inferences (STRUCTURE, ABC [18,92]) 	<ul style="list-style-type: none"> - Genetic discrimination among cultivars genotypes, identifications and parentage/paternity analyses [e.g. 10] - Accurate estimate of heterozygosity and allelic frequencies [36,51] - Population structure and inferences of demographic history of the cultivated olives and of its wild relatives [e.g. 10,20,21,54,65,105] - Detection of polyploids in wild olive trees [29,39,64] - Reconstruction of genetic maps (e.g. anchored reference loci) for QTL mapping [e.g. 49,102] 	<ul style="list-style-type: none"> - Sensitive to genotyping errors (limitations to combine SSR datasets generated independantly, for instance from different laboratories) - High mutation rate and homoplasmy (potential limitation for parentage analyses and phylogenetic analyses) - Limited number of loci usually used (< 30) - Possible strong selective pressures on isozymatic loci [81] 	<ul style="list-style-type: none"> - Identification of cultivated genotypes (varieties, rootstocks) [4,9,41,71,76,97], and somatic mutations [8,14,57,80] - Distinction of two wild Mediterranean gene pools referred to as WW (E-I) and WE (E-II) [27,38,54,82], as well three main clusters of cultivated olive (Q1, Q2, Q3) [19,27,50,68] (Box 2) - Core-collections for GWAS [19,58,68] - ABC modeling to test scenarios of population demography (e.g. relatedness among genepools, admixture and gene flow, bottleneck) [26,54] - Historical perspective on olive domestications with the reconstruction of cultivar pedigrees or networks [54,85]
Partially Available	ESTs, transcriptomes (Illumina sequencing, RNA-Seq, RT-PCR)	<ul style="list-style-type: none"> - Functional annotation of transcripts [88] - microRNAs [55,103] - Identification of SNPs between genotypes on ESTs [73] 	<ul style="list-style-type: none"> - Detection of gene expression differential associated to domestication regulatory networks for instance fruit size (e.g. miRNA in apples [104]) and oil content [13] - In olive, transcriptomes are available for different organs (e.g. different fruit and flower developmental stages [1,2,3,40,63,90], trichomes [77]) or different environmental conditions [17] 	<ul style="list-style-type: none"> - Require intensive experimental approaches (growth in control conditions, production of clones, genetically modified organisms) which are very limiting in perennials 	<ul style="list-style-type: none"> - Potential use for comparing transcriptomes of wild and cultivated olives (i.e. sequence and transcription variation of genes), and for the validation of candidate genes under selection during domestication
Partially available ^a	SNPs (Sequence, Chip SNP), or genomic profiling with reduced representation libraries [DArT, RAD-Seq; 47, 48]	<ul style="list-style-type: none"> - Population structure inferences (fastSTRUCTURE, CHROMOPAINTER, ADMIXTURE [5,78,93]) - GWAS (e.g. TASSEL; [37]) - Genomic association with environmental variables (e.g. BAYESCAN, Imm, [62,72,98]) - Phylogenetic inferences [e.g.56,95] 	<ul style="list-style-type: none"> - Genotype identification [e.g. 19], and potential use for parentage/paternity analyses - Genetic mapping [55] - Phylogenetics based on single or low copy genes (diversification of the Olives, and/or multigene families) [27,67] - Population structure and hybridization using a large number of markers (pre-requisite to test further hypotheses presented hereafter) - Genomic basis of domestication of the olive (candidate SNP associated to agronomic interest) - Detection of polymorphism involved in local adaptation to environmental conditions in wild and cultivated olives 	<ul style="list-style-type: none"> - Time-consuming genomic data processing (computing, bioinformatics) - Need of long and costly phenotyping for association mapping studies [e.g. 7,23] 	<ul style="list-style-type: none"> - Identification of cultivated olive varieties [19,35,73,87,94] - Identification of cultivated genepools [19] - High sequence variation in the Mediterranean olive, with the distinction of nuclear gene lineages attesting for a complex history of archaic and modern admixture in Oleasters [27] - Association mapping revealed markers significantly related to some important agronomic traits [74]

Table S1, end

Data availability	DNA information	Methodology	Main applications	Limitations	Main results relative to the Olive origins
Partly available ^a	Genomes (Single molecule Real Time Pacific Biosciences, Illumina sequencing, Exome capture, Pool Seq)	<ul style="list-style-type: none"> - Linkage disequilibrium estimation - Genome scans for candidates genes and introgressions - Demographic inferences (ABC [60], Diffusion [66], and N_e estimation over time [79]) 	<ul style="list-style-type: none"> - Reference Genome (i.e. “Golden path” [83]). - Genomic signs of local adaptation in the cultivated olives (outcomes for breeding programs) and in the wild olives (outcomes in conservation biology through the integrations of adaptive genetic variability) - Genomic signature of wild-to-crop gene flow (introgression along the genomes: heterogeneous versus homogeneous regions of introgressions) - Demographic inferences (i.e. effective populations size over times and scenarios of domestication) - Prerequisite to the analysis of epigenomes and archaeogenomes [46,52,91] 	<ul style="list-style-type: none"> - High frequency of repetitive DNA [15,16] - Complex admixture history in wild and cultivated olives (complex scenario to be tested) 	<ul style="list-style-type: none"> - First genome draft recently published [45]

Abbreviations: ABC: Approximate Bayesian Computation; AFLP: Amplification Fragment Length Polymorphism; CAPS: Cleaved Amplified Polymorphic Sequence; DArT: Diversity Arrays Technology; EST: Expressed Sequence Tag; GWAS: Genome-Wide Association Study; ISSR: Inter Simple Sequence Repeat; ITS: Internal Transcribed Spacer; N_e : Effective population size; QTL: Quantitative Trait Locus; RAD-Seq: Restriction-site Associated DNA Sequencing; RAPD: Random Amplified Polymorphic DNA; RFLP: Restriction Fragment Length Polymorphism; RNA-Seq: RNA sequencing; SNP: Single Nucleotide Polymorphism; SSR: Simple Sequence Repeat (or microsatellite).

Table S2. Data matrix of the 147 plastid DNA haplotypes identified in the olive complex with 71 loci [30]. Alleles of each locus are coded for the median joining network analysis (Fig. S1). Stretch size of the repeated motif is given for each microsatellite locus, while a binary code (0/1) has been defined for indels and single nucleotide. This coding was verified by sequencing alleles of a few haplotypes (for more details see [26,30,31]). The countries or regions where each haplotype were observed is given. For more convenience, sublineages were distinguished within lineages E1 and M defined by [34]: For E1, sublineages *e* (*europaea*), *I1* (*laperrinei*), *I2* (*laperrinei*) and *I3* (*cuspidata*); and for M, sublineages *m* (*maroccana*), *c* (*cerasiformis*), *g1* (*guanchica*) and *g2* (*guanchica*). Haplotypes of lineages E1-I1, E1-I2, E1-I3, M-m, M-c, M-g1 and M-g2 are unpublished data.

Haplotype	Xapl	ECORI	6C	6A	30B	45C	5A	26D	27C	11B	31A	15B	2A	48B	36A	24A	52B	57B-1	57B-2	54B-1	54B-2	39C	38B	46D	23D	19A	51C-1	51C-2	22C	59C	25A	28C	44A	53D	33D	21A	19A	11C-1	11C-2	42D	47D	41B	17B	49D	56D	28A	50C	58C	10D-1	10D-2	61E	4B	32B	12B	60D	3C	34A	35B	13C	55D	7D-1	7D-2	7D-3	14A	40A	20D	18B	43B	37A	62	8E	Countries
A.1	0	1	8	9	10	9	12	21	8	11	10	17	11	21	15	11	1	1	13	1	9	12	10	12	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	12	12	11	11	16	11	21	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	South Africa	
A.2	0	1	8	9	10	9	12	22	8	11	10	17	11	21	15	11	1	1	13	1	9	12	10	12	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	12	12	11	10	16	11	21	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	South Africa	
A.3	0	1	8	9	10	9	12	21	8	11	10	17	9	21	15	11	1	1	13	1	9	12	10	12	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	12	11	11	10	16	11	21	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	South Africa	
A.4	0	1	8	9	10	9	12	21	8	11	10	17	11	21	15	11	1	1	13	1	9	12	10	12	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	12	12	11	10	16	11	21	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	South Africa	
A.5	0	1	8	9	10	9	12	22	8	11	10	17	11	21	15	12	1	1	13	1	9	12	10	12	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	12	12	11	10	16	11	21	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	South Africa	
A.6	0	1	8	9	10	9	12	21	8	11	10	17	10	21	15	11	1	1	13	1	9	12	10	12	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	12	11	11	10	16	11	21	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	South Africa	
A.7	0	1	8	9	10	9	12	21	8	11	10	17	10	21	15	11	1	1	13	1	9	12	11	12	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	12	11	11	10	17	11	21	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	South Africa	
A.8	0	1	8	9	10	9	12	21	8	11	10	18	10	21	15	11	1	1	13	1	9	12	11	12	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	12	11	11	10	17	11	21	21	1	0	1	9	9	7	5	11	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	South Africa	
A.9	0	1	8	9	10	9	12	21	8	11	10	17	10	21	15	12	1	1	13	1	9	12	11	12	10	20	17	1	10	7	13	13	9	9	9	33	1	12	12	11	12	11	10	16	11	21	21	1	0	1	9	9	7	5	12	1	0	10	0	1	0	0	9	0	1	0	9	8	5	1	Zimbabwe	
A.10	0	1	8	9	10	9	12	21	8	11	10	17	10	21	15	12	1	1	13	1	9	11	12	10	20	17	1	10	7	13	13	9	9	9	34	1	12	12	12	12	11	10	16	11	21	21	1	0	1	9	9	7	5	12	1	0	10	0	1	0	0	9	0	1	0	9	8	5	1	Zimbabwe		
A.11	0	1	8	9	10	9	12	21	8	10	10	17	10	21	15	11	1	1	13	1	10	12	10	12	10	20	15	1	10	7	13	13	9	9	9	33	1	11	12	11	11	11	10	16	11	22	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	10	0	1	0	9	8	5	1	Mozambique	
A.12	1	1	8	9	10	9	12	21	8	11	11	18	11	21	15	12	1	1	13	1	9	12	10	12	10	20	16	1	10	7	13	13	9	10	9	34	1	11	12	12	12	11	10	16	11	21	21	1	0	1	9	9	7	5	11	1	0	11	0	0	0	9	0	1	0	9	8	5	1	Malawi		
A.13	1	1	8	9	10	9	12	21	8	11	10	19	10	20	15	11	0	1	13	1	9	12	10	12	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	12	11	11	10	16	11	21	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	Tanzania	
A.14	0	1	8	9	10	9	12	21	8	11	10	16	10	21	15	13	1	1	13	1	9	12	10	12	10	21	16	1	10	7	13	13	9	9	9	33	1	11	13	12	12	11	10	16	12	21	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	Mascareignes	
A.15	1	1	8	9	10	9	12	21	9	12	10	18	10	21	15	11	1	1	13	1	9	13	11	12	10	20	16	1	10	7	13	13	9	9	9	34	1	11	12	12	12	11	10	16	11	22	21	1	0	1	9	9	7	5	13	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	Kenya	
A.16	1	1	8	9	10	9	12	21	9	11	10	19	10	21	15	11	1	1	13	1	9	12	11	12	10	20	16	1	10	7	13	13	9	9	9	34	1	11	12	12	12	11	10	16	11	22	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	Kenya	
A.17	1	1	8	9	10	9	12	21	9	12	10	19	10	20	15	11	1	1	13	1	9	12	11	12	10	20	16	1	10	7	13	13	9	9	9	34	1	11	12	12	12	11	10	16	11	22	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	Kenya	
A.18	1	1	8	9	10	9	12	21	9	11	10	19	10	20	15	11	1	1	13	1	9	12	11	12	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	12	12	11	10	16	11	22	20	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	Kenya	
A.19	1	1	8	9	10	9	12	21	8	13	10	18	10	21	15	11	1	1	13	1	9	12	10	13	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	13	11	11	10	16	11	21	22	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	Kenya	
A.20	1	1	8	9	10	9	12	21	9	11	10	19	10	19	15	10	1	1	13	1	9	12	11	12	10	20	16	1	10	7	13	13	9	9	9	33	1	11	12	12	12	11	10	16	11	22	21	1	0	1	9	9	7	5	12	1	0	11	0	1	0	0	9	0	1	0	9	8	5	1	Kenya	
A.21	1	1	8	9	10	9	13	22	8	11	10	18	9	21	15	11	0	1	13	1	9	12	10	12	10	20	16	1	10	7	13	13	9	9	9	33	1	12	12	12	11	11	10	16	11	21	20	1</																								

Table S2. continued

Haplotype	XapI	ECORI	BC	16A	30B	45C	5A	26D	27C	1B	31A	15B	2A	48B	36A	24A	52B	57B-1	57B-2	54B-1	54B-2	39C	38B	46D	23D	9A	51C-1	51C-2	22C	59C	25A	28C	44A	53D	33D	21A	19A	11C-1	11C-2	42D	47D	41B	17B	49D	56D	29A	50C	58C	10D-1	10D-2	61E	4B	32B	12B	60D	3C	34A	35B	13C	55D	7D-1	7D-2	7D-3	14A	40A	20D	18B	43B	37A	62	BE	Countries
EI-/1.1	1	1	8	10	11	10	12	20	10	12	11	15	9	22	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	0	9	9	6	1	Algeria (Hoggar), Niger (Air)
EI-/1.2	1	1	8	10	11	10	12	20	10	12	11	15	9	22	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	12	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)	
EI-/1.3	1	1	8	10	11	10	12	20	10	13	11	15	9	22	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)	
EI-/1.4	1	1	8	10	11	10	12	20	10	12	11	15	9	22	15	11	1	1	14	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)	
EI-/1.5	1	1	8	10	11	10	12	20	10	12	11	15	9	21	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar), Niger (Air)	
EI-/1.6	1	1	8	10	11	10	12	20	10	12	11	15	9	22	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	14	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)	
EI-/1.7	1	1	8	10	11	10	12	20	10	12	11	16	9	22	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)	
EI-/1.8	1	1	8	10	11	11	12	20	10	12	11	16	9	22	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	12	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)	
EI-/1.9	1	1	8	10	11	10	12	20	10	11	15	15	9	22	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar), Niger (Air)	
EI-/1.10	1	1	8	10	11	10	12	20	10	11	15	15	9	22	15	11	1	1	15	1	10	13	10	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)	
EI-/1.11	1	1	8	10	11	10	12	20	10	11	15	9	22	15	11	1	1	15	1	10	13	11	11	10	21	17	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)		
EI-/1.12	1	1	8	10	11	10	12	20	10	11	15	15	9	22	15	11	1	1	15	1	10	13	11	11	10	20	17	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)	
EI-/1.13	1	1	8	10	11	10	12	20	10	11	15	15	9	22	15	11	1	1	15	1	10	13	11	11	10	20	18	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)	
EI-/1.14	1	1	8	10	11	10	12	20	10	11	15	9	22	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	32	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)		
EI-/1.15	1	1	8	10	11	10	12	20	10	11	15	15	9	22	15	11	1	1	16	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)	
EI-/1.16	1	1	8	10	11	10	12	20	10	10	11	15	9	22	15	11	1	1	16	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Algeria (Hoggar)	
EI-/1.17	1	1	8	10	11	10	12	20	10	11	15	15	9	22	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	34	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Niger (Air)	
EI-/1.18	1	1	8	10	11	10	12	20	10	11	15	15	9	22	15	11	1	1	15	1	10	12	11	11	10	21	18	1	13	7	13	12	9	9	11	10	34	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Niger (Air)	
EI-/1.19	1	1	8	10	11	10	12	20	10	11	15	10	22	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	34	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Niger (Air)		
EI-/1.20	1	1	8	10	11	10	12	20	10	11	11	15	9	22	15	11	1	1	15	1	10	13	11	11	10	21	18	1	13	7	13	12	9	9	11	10	34	0	12	11	11	11	10	10	16	11	21	20	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Niger (Air)	
EI-/2.1	1	1	8	10	11	10	12	20	10	12	10	15	11	23	15	11	1	1	15	1	8	13	10	11	10	21	18	1	13	7	13	12	9	9	11	10	35	0	12	12	12	12	10	10	16	11	21	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Sudan (Jebel Marra)	
EI-/2.2	1	1	8	10	11	10	12	20	10	12	10	15	11	23	15	11	0	1	15	1	8	13	10	11	10	21	18	1	13	7	13	12	9	9	11	10	35	0	12	12	12	12	10	10	16	11	21	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Sudan (Jebel Marra)	
EI-/3.1	1	1	8	10	11	10	12	20	10	13	10	18	12	21	15	11	1	1	14	1	9	12	10	11	10	22	18	1	13	7	13	12	9	9	12	10	34	0	12	12	11	11	10	10	16	11	21	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Egypt (Gebel Elba)	
EI-/3.2	1	1	8	10	11	10	12	20	10	12	10	17	12	21	15	11	1	1	14	1	9	13	10	11	10	22	18	1	13	7	13	12	9	9	11	10	36	0	12	12	11	11	10	10	16	11	21	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9				

Table S2. continued

Haplotype	XapI	ECORI	BC	16A	30B	45C	5A	26D	27C	1B	31A	15B	2A	48B	36A	24A	52B	57B-1	57B-2	54B-1	39C	38B	46D	23D	9A	51C-1	51C-2	22C	59C	25A	28C	44A	53D	33D	21A	19A	11C-1	11C-2	42D	47D	41B	17B	49D	56D	29A	50C	58C	100D-1	100D-2	61E	4B	32B	12B	60D	3C	34A	35B	13C	55D	7D-1	7D-2	7D-3	14A	40A	20D	18B	43B	37A	6Z	BE	Countries	
M-g1.1	0	1	8	10	11	10	12	20	11	10	10	15	10	21	15	13	1	1	13	1	9	13	11	11	10	21	14	1	12	7	13	12	9	8	10	10	35	1	12	13	10	12	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	0	9	9	6	1	canray Islands (West)
M-g1.2	0	1	8	10	11	10	12	20	11	10	10	15	10	21	15	13	1	1	13	1	9	13	11	11	10	21	14	1	12	7	13	12	9	8	10	10	34	1	12	13	10	12	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.3	0	1	8	10	11	10	12	20	11	10	10	15	10	21	15	13	1	1	13	1	9	13	10	11	10	21	14	1	12	7	13	12	9	8	10	10	34	1	12	13	10	12	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.4	0	1	8	10	11	10	12	20	11	10	10	15	10	21	15	13	1	1	13	1	9	13	11	11	10	21	14	1	12	7	13	12	9	9	10	10	34	1	12	13	10	12	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.5	0	1	8	10	11	10	12	20	11	10	10	15	10	21	15	13	1	1	13	1	9	13	11	11	10	21	14	1	12	7	13	12	9	9	10	10	34	1	12	13	10	12	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.6	0	1	8	10	11	10	12	20	11	10	10	15	10	21	15	13	1	1	13	1	9	13	11	11	10	21	14	1	12	7	13	12	9	9	10	10	33	1	12	13	10	12	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.7	0	1	8	10	11	10	12	20	11	10	10	15	10	21	15	13	1	1	13	1	9	13	11	11	10	21	15	1	12	7	13	12	9	9	10	10	34	1	12	13	10	12	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.8	0	1	8	10	11	10	12	21	11	10	10	15	10	21	15	13	1	1	13	1	9	13	11	11	10	21	15	1	12	7	13	12	9	9	10	10	34	1	12	13	10	12	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.9	0	1	8	10	11	10	13	20	11	10	10	15	10	21	15	13	1	1	13	1	9	13	11	11	10	22	14	1	12	7	13	12	9	9	10	10	34	1	12	13	10	13	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.10	0	1	8	10	11	10	13	20	11	10	11	15	10	21	15	13	1	1	13	1	9	13	11	11	10	22	14	1	12	7	13	12	9	9	10	10	34	1	12	13	10	13	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.11	0	1	8	10	11	10	13	20	11	10	11	15	10	20	15	13	1	1	13	1	9	13	11	11	10	22	14	1	12	7	13	12	9	9	10	10	34	1	12	13	10	13	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.12	0	1	8	10	11	10	13	20	11	10	11	15	10	21	15	13	1	1	13	1	9	13	11	11	10	22	14	1	12	7	13	12	9	9	10	10	34	1	13	13	10	13	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.13	0	1	8	10	11	10	13	20	11	10	11	15	9	21	15	13	1	1	13	1	9	13	11	11	10	22	14	1	12	7	13	12	9	9	10	10	34	1	13	13	10	13	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.14	0	1	8	10	11	10	13	20	11	10	11	15	10	21	15	13	1	1	13	1	10	13	11	11	10	22	14	1	12	7	13	12	9	9	10	10	34	1	12	13	10	13	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g1.15	0	1	8	10	11	10	12	19	11	10	10	15	10	21	15	13	1	1	13	1	9	13	11	11	10	21	14	1	12	7	13	12	9	9	10	10	34	1	12	13	10	13	10	10	16	12	23	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (West)	
M-g2.1	0	1	8	9	11	10	12	19	11	11	10	15	9	21	15	13	1	1	13	1	9	14	11	11	10	21	13	1	12	7	13	11	9	9	10	10	34	1	12	13	10	11	10	10	16	12	22	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	canray Islands (East)	
E1-e.1	1	0	8	10	11	10	12	20	10	12	10	15	10	21	15	11	1	1	15	1	9	13	10	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	12	11	11	10	10	16	11	21	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Mediterranean Basin	
E1-e.2	0	1	8	10	11	10	12	20	10	12	10	15	10	21	15	11	1	1	15	1	9	13	10	11	10	21	17	1	13	7	13	12	9	9	11	10	34	0	12	12	11	11	10	10	16	11	21	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Mediterranean Basin	
E1-e.3	1	1	8	10	11	10	12	20	10	12	10	15	10	21	15	11	1	1	15	1	9	13	10	11	10	21	17	1	13	7	13	12	9	9	11	10	33	0	12	12	11	11	10	10	16	11	21	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	Mediterranean Basin	
E1-e.4	1	1	8	10	11	10	12	20	10	12	10	15	10	21	15	11	1	1	15	1	9	13	10	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	12	11	11	10	10	16	11	21	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	East Mediterranean Basin	
E1-e.5	1	1	8	10	11	10	12	20	10	12	10	15	10	21	15	11	1	1	15	1	9	13	10	11	10	21	17	1	13	7	13	12	9	9	11	10	34	0	12	12	11	11	10	10	16	11	21	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	East Mediterranean Basin	
E1-e.6	1	1	8	10	11	10	12	20	10	12	10	15	10	21	15	11	1	1	15	1	9	13	10	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	12	11	11	10	10	16	11	21	22	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	East Mediterranean Basin	
E1-e.7	1	1	8	10	11	10	12	20	10	12	10	15	10	21	15	11	1	1	15	1	9	13	10	11	10	21	18	1	13	7	13	12	9	9	11	11	33	0	12	12	11	11	10	10	16	11	21	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	East Mediterranean Basin	
E1-e.8	1	1	8	10	11	10	12	20	10	12	10	15	10	21	15	11	1	1	15	1	10	13	10	11	10	21	18	1	13	7	13	12	9	9	11	10	33	0	12	12	11	11	10	10	17	11	21	21	1	0	1	10	9	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	East Mediterranean Basin	
E1-e.9	1	1	8	10	11																																																																			

Table S2. End

Haplotype	XapI	ECORI	6C	16A	30B	45C	5A	26D	27C	1B	31A	15B	2A	48B	36A	24A	52B	57B-1	57B-2	54B-1	54B-2	39C	38B	46D	23D	9A	51C-1	51C-2	22C	59C	25A	28C	44A	53D	33D	21A	19A	11C-1	11C-2	42D	47D	41B	17B	49D	56D	29A	50C	56C	10D-1	10D-2	61E	4B	32B	12B	60D	3C	34A	35B	13C	55D	7D-1	7D-2	7D-3	14A	40A	20D	18B	43B	37A	62	8E	Countries		
E2.1	1	1	8	10	11	10	12	20	10	11	9	16	11	21	16	11	1	0	13	0	9	13	11	10	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	10	10	10	15	11	21	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin
E2.2	0	1	8	10	11	10	12	20	10	11	9	16	11	21	16	11	1	0	13	0	9	13	11	10	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	10	10	10	15	11	21	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin
E2.3	1	1	8	10	11	10	12	20	10	11	9	16	11	21	16	11	1	0	13	0	9	13	11	10	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	10	10	10	15	11	21	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin
E2.4	0	1	8	10	11	10	12	20	10	11	9	16	11	21	16	11	1	0	13	0	9	13	11	10	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	10	10	10	15	11	21	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin
E2.5	1	1	8	10	11	10	12	20	10	11	9	16	10	21	16	11	1	0	13	0	9	13	11	10	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	10	10	10	15	11	21	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin
E2.6	1	1	8	10	11	10	12	20	10	11	9	16	10	21	16	11	1	0	13	0	9	13	11	9	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	10	10	10	15	11	21	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin
E2.7	1	1	8	10	11	10	12	20	10	11	9	16	11	21	16	11	1	0	13	0	9	13	12	10	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	10	10	10	15	11	21	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin	
E2.8	1	1	9	10	11	10	12	20	10	11	9	16	11	21	16	11	1	0	13	0	9	13	11	10	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	10	10	10	15	11	22	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin	
E2.9	1	1	9	10	11	10	12	20	10	11	9	16	11	21	16	11	1	0	13	0	9	13	11	10	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	11	10	10	15	11	22	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin	
E2.10	0	1	8	10	11	10	12	20	10	11	9	16	11	21	16	11	1	0	13	0	9	13	11	10	11	20	20	11	1	14	7	13	12	9	9	11	10	33	1	14	12	12	10	10	10	15	11	21	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin	
E2.11	1	1	8	10	11	10	12	20	10	11	9	17	11	21	16	11	1	0	13	0	9	13	11	10	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	10	10	10	15	11	21	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin	
E2.12	1	1	8	10	11	10	12	20	10	11	9	16	11	20	16	11	1	0	13	0	9	13	11	10	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	10	10	10	15	11	21	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin	
E2.13	0	1	8	10	11	10	12	20	10	11	9	16	12	21	16	11	1	0	13	0	9	13	11	10	11	20	20	11	1	13	7	13	12	9	9	11	10	32	1	14	12	12	10	10	10	15	11	21	21	0	0	1	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin	
E2.14	1	1	8	10	11	10	12	20	10	11	9	16	11	22	16	10	1	0	13	0	9	13	11	10	11	20	20	11	1	13	7	14	12	9	9	11	10	32	1	14	12	12	10	10	10	15	12	21	20	0	0	1	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin	
E3.3	0	1	8	10	11	10	12	20	11	10	10	16	11	22	15	12	0	1	13	1	9	13	11	11	10	21	18	1	12	6	11	11	9	10	11	10	33	1	11	12	13	9	11	11	15	11	21	21	1	0	0	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin		
E3.1	0	1	8	10	11	10	12	20	11	10	10	16	11	22	15	12	0	1	13	1	9	13	11	11	10	21	18	1	12	6	11	11	9	10	11	10	34	1	11	12	13	9	11	11	15	11	21	21	1	0	0	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin		
E3.2	0	1	8	10	11	10	12	20	11	9	10	16	11	22	15	12	0	1	13	1	9	13	11	11	10	21	18	1	12	6	11	11	9	10	11	10	34	1	11	12	13	9	11	11	15	11	21	21	1	0	0	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin		
E3.6	0	1	8	10	11	10	12	20	11	9	10	16	10	22	15	12	0	1	13	1	9	13	11	11	10	21	18	1	12	6	11	11	9	10	11	10	34	1	11	12	13	9	11	11	15	11	21	21	1	0	0	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin		
E3.5	0	1	8	10	11	10	12	20	11	10	10	16	12	22	15	12	0	1	13	1	9	13	11	12	10	21	18	1	12	6	11	11	9	10	11	10	34	1	11	12	13	9	11	10	15	11	21	21	1	0	0	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin		
E3.4	0	1	8	10	11	10	12	20	11	10	10	16	12	22	15	12	0	1	13	1	9	13	11	12	10	21	18	1	12	6	11	11	9	10	11	10	33	1	11	12	13	9	11	11	15	11	21	21	1	0	0	10	9	8	8	5	12	1	1	10	1	1	0	0	9	0	0	9	9	6	1	West & Central Mediterranean Basin		

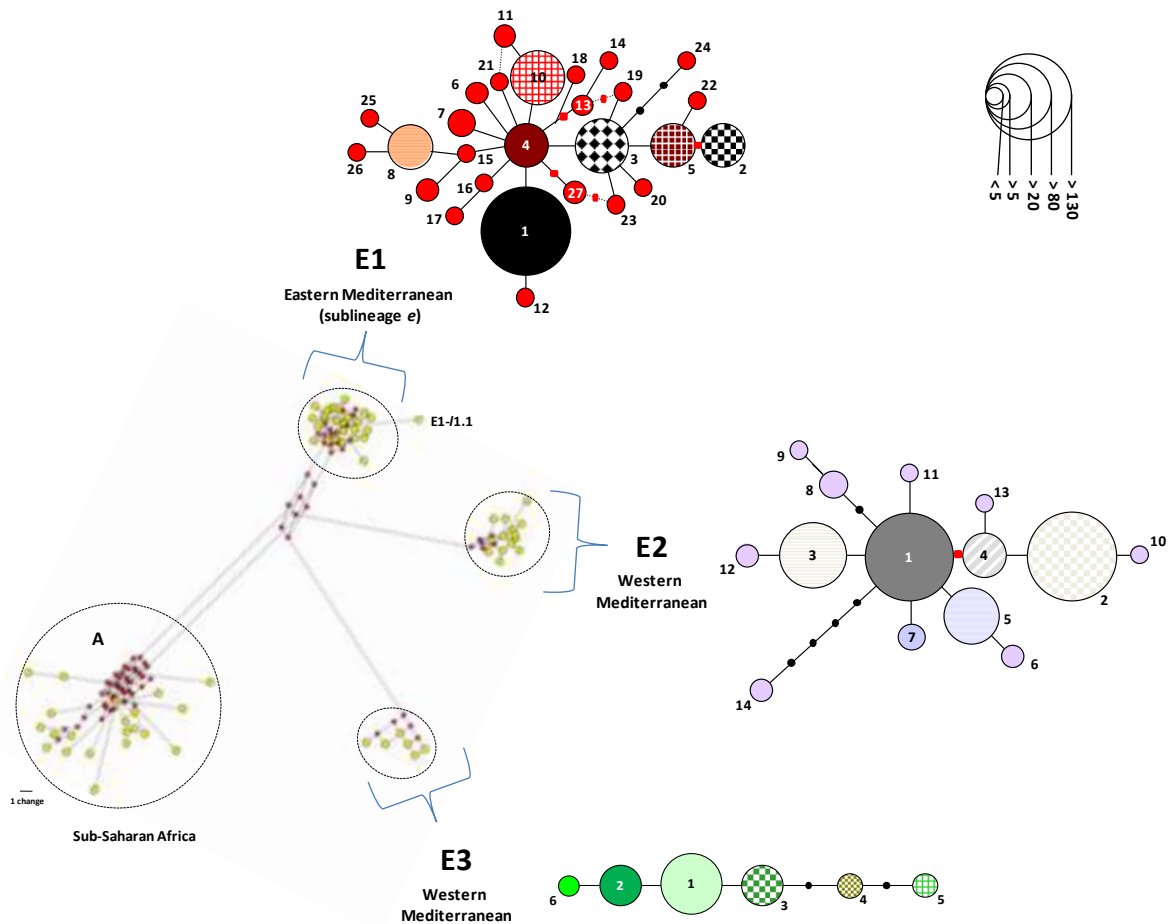


FIG. S1. Reduced median networks [12] of Mediterranean Olive plastid DNA haplotypes (data from 1,797 individuals of cultivated and wild accessions [31]). The bottom left network represents the relationships between 69 chlorotypes detected in the Mediterranean basin (48 haplotypes) and Sub-Saharan Africa (21 haplotypes, here used as an outgroup). All haplotypes detected in the Mediterranean basin were observed in Oleaster, except E1-1.1 (formerly L1.1 [28,31]) that represents the major haplotype of the Laperrine's Olive (from Hoggar, Algeria). Each chlorotype is represented by a yellow circle while the putative intermediate nodes are indicated by small red circles. Four groups of chlorotypes were revealed: lineages E1, E2 and E3 in the Mediterranean area, and lineage A in Sub-Saharan Africa. Detailed relationships between chlorotypes within each Mediterranean lineage are also shown. Each chlorotype is numbered and represented by a symbol with a given color and/or motif. For each chlorotype, symbol diameter is proportional to the number of observations. The missing, intermediate nodes are indicated by small black points. The geographic distribution of chlorotypes is given in Fig. 1.

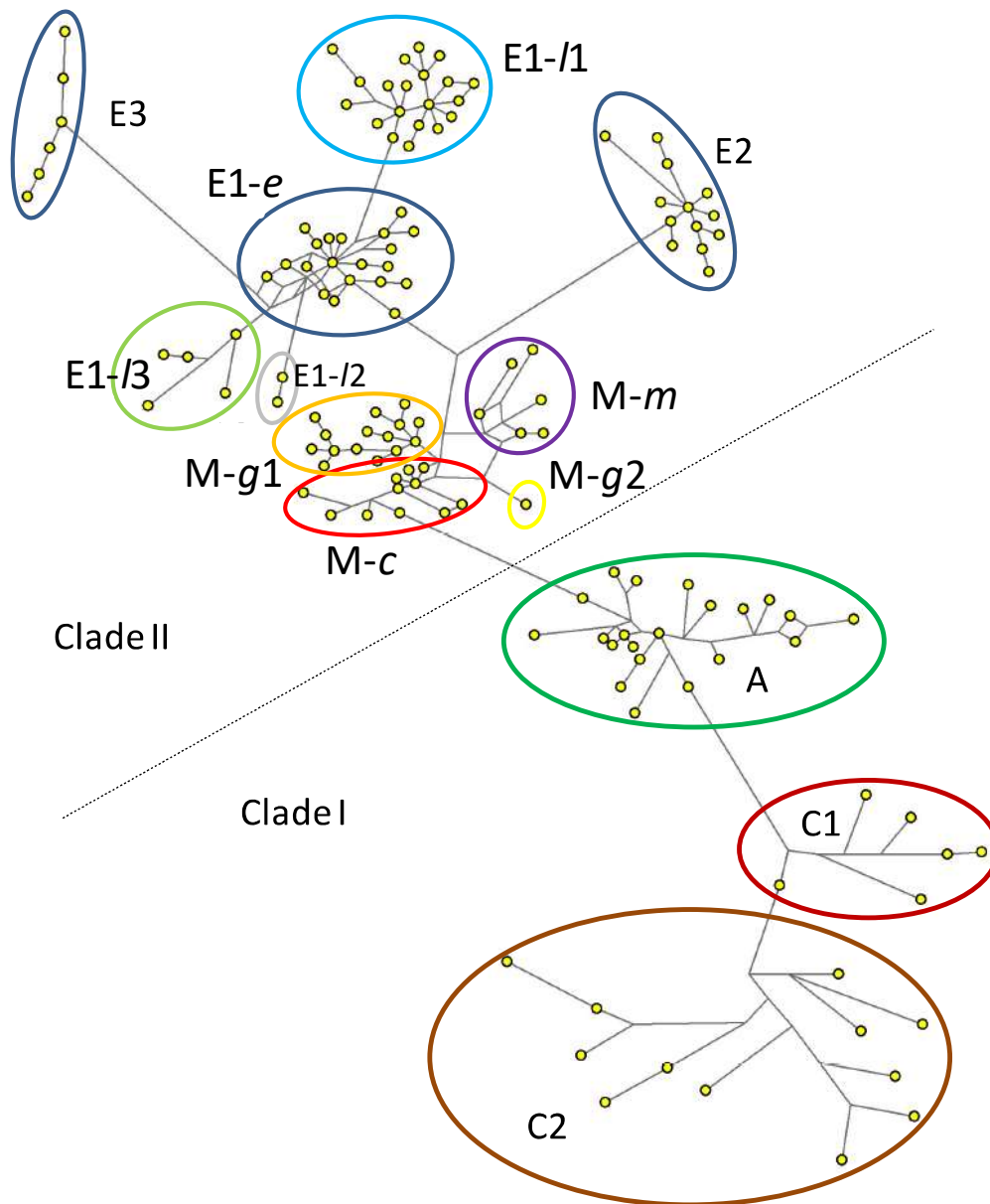


FIG. S2. Median joining network of olive chlorotypes reconstructed with NETWORK [12]. This analysis is based on data given in Table S2. This analysis revealed 13 clusters of haplotypes, hereafter named lineages and sublineages, and identified with a specific code following Besnard *et al.* [34]. Two main clades are distinguished as revealed by Besnard *et al.* [34]. Each plastid lineage/sublineage shows a delimited geographic distribution (see Box 1), except in the central and western Mediterranean regions where lineages E1 (sublineage *e*), E2 and E3 are generally mixed in Oleaster populations [30,31].

REFERENCES

1. **Alagna F, D'Agostino N, Torchia L et al. 2009.** Comparative 454 pyrosequencing of transcripts from two olive genotypes during fruit development. *BMC Genomics* **10**: 399.
2. **Alagna F, Cirilli M, Galla G et al. 2016.** Transcript analysis and regulative events during flower development in olive (*Olea europaea* L.). *PLoS ONE* **11**: e0152943.
3. **Alagna F, Mariotti R, Panara F et al. 2012.** Olive phenolic compounds: metabolic and transcriptional profiling during fruit development. *BMC Plant Biology* **12**: 162.
4. **Albertini E, Torricelli R, Bitocchi E et al. 2011.** Structure of genetic diversity in *Olea europaea* L. cultivars from central Italy. *Molecular Breeding* **27**: 533–547.
5. **Alexander DH, Novembre J, Lange K. 2009.** Fast model-based estimation of ancestry in unrelated individuals. *Genome Research* **19**: 1655–1664.
6. **Angiolillo A, Mencuccini M, Baldoni L. 1999.** Olive genetic diversity assessed using amplified polymorphic fragment length polymorphisms. *Theoretical and Applied Genetics* **98**: 411–421.
7. **Atienza SG, de la Rosa R, León L, Martín A, Belaj A. 2014.** Identification of QTL for agronomic traits of importance for olive breeding. *Molecular Breeding* **34**: 725–737.
8. **Baali-Cherif D, Besnard G. 2005.** High genetic diversity and clonal growth in relict populations of *Olea europaea* subsp. *laperrinei* (Oleaceae) from Hoggar, Algeria. *Annals of Botany* **96**: 823–830.
9. **Baldoni L, Cultrera NG, Mariotti R et al. 2009.** A consensus list of microsatellite markers for olive genotyping. *Molecular Breeding* **24**: 213–231.
10. **Baldoni L, Tosti N, Ricciolini C et al. 2006.** Genetic structure of wild and cultivated olives in the Central Mediterranean Basin. *Annals of Botany* **98**: 935–942.
11. **Ballard JW, Whitlock MC. 2004.** The incomplete natural history of mitochondria. *Molecular Ecology* **13**: 729–744.
12. **Bandelt HJ, Forster P, Röhl A. 1999.** Median-joining networks for inferring intraspecific phylogenies. *Molecular Biology and Evolution* **16**: 37–48.
13. **Banilas G, Hatzopoulos P. 2013.** Genetics and molecular biology of olives. In: *Handbook of Olive Oil: Analysis and Properties*, Aparicio R & Harwood J (Eds). Chap. 5, pp. 129–161, Springer, New York.
14. **Barazani O, Westberg E, Hanin N et al. 2014.** A comparative analysis of genetic variation in rootstocks and scions of old olive trees – a window into the history of olive cultivation practices and past genetic variation. *BMC Plant Biology* **14**: 146.
15. **Barghini E, Natali L, Cossu RM et al. 2014.** The peculiar landscape of repetitive sequences in the olive (*Olea europaea* L.) genome. *Genome Biology and Evolution* **6**: 776–791.
16. **Barghini E, Natali L, Giordani T et al. 2015.** LTR retrotransposon dynamics in the evolution of the olive (*Olea europaea*) genome. *DNA Research* **22**: 91–100.
17. **Bazakos C, Manioudaki ME, Sarropoulou E, Spano T, Kalaitzis P. 2015.** 454 pyrosequencing of olive (*Olea europaea* L.) transcriptome in response to salinity. *PLoS ONE* **10**: e0143000.
18. **Beaumont MA. 2010.** Approximate Bayesian Computation in evolution and ecology. *Annual Review of Ecology, Evolution, and Systematics* **41**: 379–406.
19. **Belaj A, del Carmen Dominguez-García M, Atienza SG et al. 2012.** Developing a core collection of olive (*Olea europaea* L.) based on molecular markers (DARs, SSRs, SNPs) and agronomic traits. *Tree Genetics & Genomes* **8**: 365–378.
20. **Belaj A, Muñoz-Diez C, Baldoni L et al. 2007.** Genetic diversity and population structure of wild olives from the north-western Mediterranean assessed by SSR markers. *Annals of Botany* **100**: 449–458.
21. **Belaj A, Muñoz-Diez C, Baldoni L, Satovic Z, Barranco D. 2010.** Genetic diversity and relationships of wild and cultivated olives at regional level in Spain. *Scientia Horticulturae (Amsterdam)* **124**: 323–330.
22. **Belaj A, Trujillo I, de la Rosa R, Rallo L. 2001.** Polymorphism and discrimination capacity of randomly amplified polymorphic markers in an olive germplasm bank. *Journal of the American Society for Horticultural Science* **126**: 64–71.
23. **Ben Sadok I, Moutier N, Garcia G et al. 2013.** Genetic determinism of the vegetative and reproductive traits in an F1 olive tree progeny. *Tree Genetics & Genomes* **9**: 205–221.
24. **Besnard G, Baradat P, Bervillé A. 2001a.** Genetic relationships in the olive (*Olea europaea* L.) reflect multilocal selection of cultivars. *Theoretical and Applied Genetics* **102**: 251–258.
25. **Besnard G, Baradat P, Breton C, Khadari B, Bervillé A. 2001b.** Olive domestication from structure of Oleasters and cultivars using nuclear RAPDs and mitochondrial RFLPs. *Genetics, Selection, Evolution* **33**: S251–S268.
26. **Besnard G, Dupuy J, Larter M et al. 2014.** History of the invasive African olive tree in Australia and Hawaii: evidence for sequential bottlenecks and hybridizations with the Mediterranean olive. *Evolutionary Applications* **7**: 195–211.

27. **Besnard G, El Bakkali A. 2014.** Sequence analysis of single-copy genes in two wild olive subspecies (*Olea europaea* L.): nucleotide diversity and potential use for testing admixture. *Genome* **57**: 145–153.
28. **Besnard G, El Bakkali A, Haouane H et al. 2013a.** Population genetics of Mediterranean and Saharan olives: geographic patterns of differentiation and evidence for early-generations of admixture. *Annals of Botany* **112**: 1293–1302.
29. **Besnard G, García-Verdugo C, Rubio de Casas R et al. 2008.** Polyploidy in the olive complex (*Olea europaea* L.): evidence from flow cytometry and nuclear microsatellite analyses. *Annals of Botany* **101**: 25–30.
30. **Besnard G, Hernández P, Khadari B, Dorado G, Savolainen V. 2011.** Genomic profiling of plastid DNA variation in the Mediterranean olive tree. *BMC Plant Biology* **11**: 80.
31. **Besnard G, Khadari B, Navascués M et al. 2013b.** The complex history of the olive tree: from Late Quaternary diversification of Mediterranean lineages to primary domestication in the northern Levant. *Proceedings of the Royal Society of London, Series B* **280**: 20122833.
32. **Besnard G, Khadari B, Villemur P, Bervillé A. 2000.** Cytoplasmic male sterility in the Olive (*Olea europaea* L.). *Theoretical and Applied Genetics* **100**: 1018–1024.
33. **Besnard G, Rubio de Casas R, Christin PA, Vargas P. 2009.** Phylogenetics of *Olea* (Oleaceae) based on plastid and nuclear ribosomal DNA sequences: Tertiary climatic shifts and lineage differentiation times. *Annals of Botany* **104**: 143–160.
34. **Besnard G, Rubio de Casas R, Vargas P. 2007.** Plastid and nuclear DNA polymorphism reveals historical processes of isolation and reticulation in the olive tree complex (*Olea europaea*). *Journal of Biogeography* **34**: 736–752.
35. **Biton I, Doron-Faigenboim A, Jamwal M et al. 2015.** Development of a large set of SNP markers for assessing phylogenetic relationships between the olive cultivars composing the Israeli olive germplasm collection. *Molecular Breeding* **35**: 107.
36. **Biton I, Shevtsov S, Ostersetzer O et al. 2012.** Genetic relationships and hybrid vigour in olive (*Olea europaea* L.) by microsatellites. *Plant Breeding* **131**: 767–774.
37. **Bradbury PJ, Zhang Z, Kroon DE, Casstevens TM, Ramdoss Y, Buckler ES. 2007.** TASSEL: Software for association mapping of complex traits in diverse samples. *Bioinformatics* **23**: 2633–2635.
38. **Breton C, Terral JF, Pinatel C, Médail F, Bonhomme F, Bervillé A. 2008.** The origins of the domestication of the olive tree. *Comptes Rendus Biologies* **332**: 1059–1064.
39. **Brito G, Loureiro J, Lopes T, Rodriguez E, Santos C. 2008.** Genetic characterization of olive trees from Madeira Archipelago using flow cytometry and microsatellite markers. *Genetic Resources and Crop Evolution* **55**: 657–664.
40. **Carmona R, Zafra A, Seoane P et al. 2015.** ReprOlive: a database with linked data for the olive tree (*Olea europaea* L.) reproductive transcriptome. *Frontiers in Plant Science* **6**: 625.
41. **Chalak L, Haouane H, Essalouh L et al. 2015.** Extent of the genetic diversity in Lebanese olives: a mixture of an ancient germplasm with recently introduced varieties. *Genetic Resources and Crop Evolution* **62**: 621–633.
42. **Claros MG, Crespillo R, Aguilar ML, Canovas FM. 2000.** DNA fingerprinting and classification of geographically related genotypes of olive tree (*Olea europaea* L.). *Euphytica* **116**: 131–142.
43. **Contento A, Ceccarelli M, Gelati MT et al. 2002.** Diversity of *Olea* genotypes and the origin of cultivated olives. *Theoretical and Applied Genetics* **104**: 1229–1238.
44. **Corander J, Marttinen P, Sirén J, Tang J. 2008.** Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. *BMC Bioinformatics* **9**: 539.
45. **Cruz F, Julca I, Gómez-Garrido J et al. 2016.** Genome sequence of the olive tree, *Olea europaea*. *GigaScience* **5**: 29.
46. **da Fonseca RR, Smith BD, Wales N et al. 2015.** The origin and evolution of maize in the Southwestern United States. *Nature Plants* **1**: art. 14003.
47. **Davey JW, Cezard T, Fuentes-Utrilla P, Eland C, Gharbi K, Blaxter ML. 2013.** Special features of RAD Sequencing data: implications for genotyping. *Molecular Ecology* **22**: 3151–3164.
48. **Davey JW, Hohenlohe PA, Etter PD, Boone JQ, Catchen JM, Blaxter ML. 2011.** Genome-wide genetic marker discovery and genotyping using next-generation sequencing. *Nature Reviews Genetics* **12**: 499–510.
49. **De la Rosa R, Angiolillo A, Guerrero C et al. 2003.** A first linkage map of olive (*Olea europaea* L.) cultivars using RAPD, AFLP, RFLP and SSR markers. *Theoretical and Applied Genetics* **106**: 1273–1282.
50. **Díez CM, Imperato A, Rallo L, Baranco D, Trujillo I. 2012.** Worldwide core collection of olive cultivars based on simple sequence repeat and morphological markers. *Crop Science* **52**: 211–221.
51. **Díez CM, Trujillo I, Barrio E et al. 2011.** Centennial olive trees as a reservoir of genetic diversity. *Annals of Botany* **108**: 797–807.
52. **Díez CM, Roessler K, Gaut BS. 2014.** Epigenetics and plant genome evolution. *Current Opinion in Plant Biology* **18**: 1–8.

53. Díez CM, Trujillo I, Martínez-Uriroz N *et al.* 2015. Olive domestication and diversification in the Mediterranean basin. *New Phytologist* **206**: 436–447.
54. Domínguez-García MC, Belaj A, De la Rosa R *et al.* 2012. Development of DArT markers in olive (*Olea europaea* L.) and usefulness in variability studies and genome mapping. *Scientia Horticulturae* **136**: 50–60.
55. Donaire L, Pedrola L, de la Rosa R, Llave C. 2011. High-throughput sequencing of RNA silencing-associated small RNAs in olive (*Olea europaea* L.). *PLoS ONE* **6**: e27916.
56. Drummond AJ, Suchard MA, Xie D, Rambaut A. 2012. Bayesian phylogenetics with BEAUti and the BEAST 1.7 *Molecular Biology And Evolution* **29**: 1969–1973.
57. El Bakkali A, Haouane H, Hadiddou A *et al.* 2013a. Genetic diversity of on-farm selected olive trees in Moroccan traditional olive orchards. *Plant Genetic Resources-Characterization and Utilization* **11**: 97–105.
58. El Bakkali A, Haouane H, Moukhli A *et al.* 2013b. Construction of core collections suitable for association mapping to optimize use of Mediterranean olive (*Olea europaea* L.) genetic resources. *PLoS ONE* **8**: e61265.
59. Elbaum R, Melamed-Bessudo C, Boaretto E *et al.* 2006. Ancient olive DNA in pits: preservation, amplification and sequence analysis. *Journal of Archaeological Science* **33**: 77–88.
60. Excoffier L, Dupanloup I, Huerta-Sánchez E, Sousa VC, Foll M. 2013. Robust demographic inference from genomic and SNP data. *PLoS Genetics* **9**: e1003905.
61. Excoffier L, Smouse PE, Quattro JM. 1992. Analysis of molecular variance inferred from metric distances among DNA haplotypes: application to human mitochondrial DNA restriction data. *Genetics* **131**: 479–491.
62. Foll M, OE Gaggiotti. 2008. A genome scan method to identify selected loci appropriate for both dominant and codominant markers: A Bayesian perspective. *Genetics* **180**: 977–993.
63. Galla G, Barcaccia G, Ramina A *et al.* 2009. Computational annotation of genes differentially expressed along olive fruit development. *BMC Plant Biology* **9**: 128.
64. García-Verdugo C, Fay MF, Granado-Yela C *et al.* 2009. Genetic diversity and differentiation processes in the ploidy series of *Olea europaea* L.: a multiscale approach from subspecies to insular populations. *Molecular Ecology* **18**: 454–467.
65. García-Verdugo C, Forest AD, Fay MF, Vargas P. 2010. The relevance of gene flow in metapopulation dynamics of an oceanic island endemic, *Olea europaea* subsp. *guanchica*. *Evolution* **64**: 3525–3536.
66. Gutenkunst RN, Hernandez RD, Williamson SH, Bustamante CD. 2009. Inferring the joint demographic history of multiple populations from multidimensional SNP frequency data. *PLoS Genetics* **5**: e1000695.
67. Hamman-Khalifa AM, Navajas-Pérez R, de la Herrán R *et al.* 2007. Establishing the genetic relationships between the wild and cultivated olives using a nuclear intron from nitrate reductase (*nia-i3*). *Plant Systematics and Evolution* **269**: 63–73.
68. Haouane H, El Bakkali A, Moukhli A *et al.* 2011. Genetic structure and core collection of the World Olive Germplasm Bank of Marrakech: towards the optimised management and use of Mediterranean olive genetic resources. *Genetica* **139**: 1083–1094.
69. Hernández P, de la Rosa R, Rallo L, Martín A, Dorado G. 2001. First evidence of a retrotransposon-like element in olive (*Olea europaea*): implications in plant variety identification by SCAR-marker development. *Theoretical and Applied Genetics* **102**: 1082–1087.
70. Hess J, Kadereit JW, Vargas P. 2000. The colonization history of *Olea europaea* L. in Macaronesia based on internal transcribed spacer 1 (ITS-1) sequences, randomly amplified polymorphic DNAs (RAPD), and intersimple sequence repeats (ISSR). *Molecular Ecology* **9**: 857–868.
71. Hosseini-Mazinani M, Mariotti R, Torkzaban B *et al.* 2014. High genetic diversity detected in olives beyond the boundaries of the Mediterranean Sea. *PLoS ONE* **9**: e93146.
72. Joost S, Bonin A, Bruford MW *et al.* 2007. A spatial analysis method (SAM) to detect candidate loci for selection: towards a landscape genomics approach to adaptation. *Molecular Ecology* **16**: 3955–3969.
73. Kaya HB, Cetin O, Kaya H *et al.* 2013. SNP discovery by Illumina-based transcriptome sequencing of the olive and the genetic characterization of Turkish olive genotypes revealed by AFLP, SSR and SNP markers. *PLoS ONE* **8**: e73674.
74. Kaya HB, Cetin O, Kaya HS, Sahin M, Sefer F Tanyolac B. 2016. Association mapping in Turkish olive cultivars revealed significant markers related to some important agronomic traits. *Biochemical Genetics* **54**: 506–533.
75. Khadari B, Breton C, Moutier N *et al.* 2003. The use of molecular markers for germplasm management in a French olive collection. *Theoretical and Applied Genetics* **106**: 521–529.
76. Khadari B, Charafi J, Moukhli A, Ater M. 2008. Substantial genetic diversity in cultivated Moroccan olive despite a single major cultivar: a paradoxical situation evidenced by the use of SSR loci. *Tree Genetics & Genomes* **4**: 213–221.

77. Koudounas K, Manioudaki ME, Kourti A, Banilas G, Hatzopoulos P. 2015. Transcriptional profiling unravels potential metabolic activities of the olive leaf non-glandular trichome. *Frontiers in Plant Science* **6**: 633.
78. Lawson DJ, Hellenthal G, Myers S, Falush D. 2012. Inference of population structure using dense haplotype data. *PLoS Genetics* **8**: e1002453.
79. Liu X, Fu YX. 2015. Exploring population size changes using SNP frequency spectra. *Nature Genetics* **47**: 555–559.
80. Lopes MS, Mendonça D, Sefc KM, Gil FS, da Câmara Machado A. 2004. Genetic evidence of intra-cultivar variability within Iberian cultivars. *HortScience* **39**: 1562–1565.
81. Lumaret R, Ouazzani N. 2000. Ancient wild olives in Mediterranean forests. *Nature* **413**: 700.
82. Lumaret R, Ouazzani N, Michaud H *et al.* 2004. Allozyme variation of Oleaster populations (wild olive tree) (*Olea europaea* L.) in the Mediterranean basin. *Heredity* **92**: 343–351.
83. Manel S, Perrier C, Pralong M *et al.* 2016. Genomic resources and their influence on the detection of the signal of positive selection in genome scans. *Molecular Ecology* **25**: 170–184.
84. Mariotti R, Cultrera NGM, Muñoz-Díez C, Baldoni L, Rubini A. 2010. Identification of new polymorphic regions and differentiation of cultivated olives (*Olea europaea* L.) through plastome sequence comparison. *BMC Plant Biology* **10**: 211.
85. Marra FP, Caruso T, Costa F *et al.* 2013. Genetic relationships, structure and parentage simulation among the olive tree (*Olea europaea* L. subsp. *europaea*) cultivated in Southern Italy revealed by SSR markers. *Tree Genetics & Genomes* **9**: 961–973.
86. Martins-Lopes P, Lima-Brito J, Gomes S, Meirinhos J, Santos L, Guedes-Pinto H. 2007. RAPD and ISSR molecular markers in *Olea europaea* L.: Genetic variability and molecular cultivar identification. *Genetic Resources and Crop Evolution* **54**: 117–128.
87. Muleo R, Colao MC, Miano D *et al.* 2009. Mutation scanning and genotyping by high-resolution DNA melting analysis in olive germplasm. *Genome* **52**: 252–260.
88. Muñoz-Mérida A, González-Plaza JJ, Cañada A *et al.* 2013. De novo assembly and functional annotation of the olive (*Olea europaea*) transcriptome. *DNA Research* **20**: 93–108.
89. Owen CA, Bitá EC, Banilas G *et al.* 2005. AFLP reveals structural details of genetic diversity within cultivated olive germplasm from the Eastern Mediterranean. *Theoretical and Applied Genetics* **110**: 1169–1176.
90. Parra R, Paredes MA, Sanchez-Calle IM, Gomez-Jimenez MC. 2013. Comparative transcriptional profiling analysis of olive ripe-fruit pericarp and abscission zone tissues shows expression differences and distinct patterns of transcriptional regulation. *BMC Genomics* **14**: 866.
91. Platt A, Gugger PF, Pellegrini M, Sork VL. 2015. Genome wide signature of local adaptation linked to variable CpG methylation in oak population. *Molecular Ecology* **15**: 3823–3830.
92. Pritchard JK, Stephens M, Donnelly P. 2000. Inference of population structure from multilocus genotype data. *Genetics* **155**: 945–959.
93. Raj A, Stephens M, Pritchard JK. 2014. fastSTRUCTURE: Variational Inference of Population Structure in Large SNP Data Sets. *Genetics* **197**: 573–589.
94. Reale S, Doveri S, Díaz A *et al.* 2006. SNP-based markers for discriminating olive (*Olea europaea* L.) cultivars. *Genome* **49**: 1193–1205.
95. Ronquist F, Teslenko M, van der Mark P *et al.* 2012. MrBayes 3.2: Efficient Bayesian Phylogenetic Inference and Model Choice across a Large Model Space. *Systematic Biology* **61**: 539–542.
96. Rubio de Casas R, Besnard G, Schönswetter P, Balaguer L, Vargas P. 2006. Extensive gene flow blurs phylogeographic but not phylogenetic signal in *Olea europaea* L. *Theoretical and Applied Genetics* **113**: 575–583.
97. Sarri V, Baldoni L, Porceddu A *et al.* 2006. Microsatellite markers are suitable tools for discriminating among olive cultivars and assigning them to geographically defined populations. *Genome* **49**: 1606–1615.
98. Segura V, Vilhjálmsson BJ, Platt A, Korte A, Seren Ü, Long Q, Nordborg M. 2012. An efficient multi-locus mixed-model approach for genome-wide association studies in structured populations. *Nature Genetics* **44**: 825–830.
99. Vargas P, Kadereit JW. 2001. Molecular fingerprinting evidence (ISSR, inter-simple sequence repeats) for a wild status of *Olea europaea* L. (Oleaceae) in the Eurosiberian North of the Iberian Peninsula. *Flora* **196**: 142–152.
100. Wiesman Z, Avidan N, Lavee S, Quebedeaux B. 1998. Molecular characterization of common olive varieties in Israel and the West Bank using randomly amplified polymorphic DNA (RAPD) markers. *Journal of the American Society for Horticultural Sciences* **123**: 837–841.
101. Wilson I, Weale M, Balding D. 2003. Inferences from DNA data: population histories, evolutionary processes and forensic match probabilities. *Journal of the Royal Statistical Society: Series A (Statistics in Society)* **166**: 155–188.

- 102. Wu SB, Collins G, Sedgley M. 2004.** A molecular linkage map of olive (*Olea europaea* L.) based on RAPD, microsatellite, and SCAR markers. *Genome* **47**: 26–35.
- 103. Yanik H, Turktas M, Dundar E, Hernandez P, Dorado G, Unver T. 2013.** Genome-wide identification of alternate bearing-associated microRNAs (miRNAs) in olive (*Olea europaea* L.). *BMC Plant Biology* **13**: 10.
- 104. Yao JL, Xu J, Cornille A et al. 2015.** A *microRNA* allele that emerged prior to apple domestication may underlie fruit size evolution. *The Plant Journal* **84**: 417–427.
- 105. Yoruk B, Taskin V. 2014.** Genetic diversity and relationships of wild and cultivated olives in Turkey. *Plant Systematics and Evolution* **300**: 1247–1258.