Low-Pass DNA Sequencing of 1200 Sardinians Reconstructs European Y-Chromosome Phylogeny

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mtDNA coalescence times are not significantly different. This conclusion would hold whether or not an alternative approach would yield more definitive T_{MRCA} estimates.

Our observation that the T_{MRCA} of the Y chromosome is similar to that of the mtDNA does not imply that the effective population sizes (N_e) of males and females are similar. In fact, we observe a larger N_e in females than in males (Table 1). Although, due to its larger N_e, the distribution from which the mitochondrial T_{MRCA} has been drawn is right-shifted with respect to that of the Y-chromosome T_{MRCA}, the two distributions have large variances and overlap (Fig. 3).

Dogma has held that the common ancestor of human patrilineal lineages, popularly referred to as the Y-chromosome "Adam," lived considerably more recently than the common ancestor of female lineages, the so-called mitochondrial "Eve." However, we conclude that the mitochondrial coalescence time is not substantially greater than that of the Y chromosome. Indeed, due to our moderate-coverage sequencing and the existence of additional rare divergent haplogroups, our analysis may yet underestimate the true Y-chromosome T_{MRCA}.

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Supplementary Materials

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Low-Pass DNA Sequencing of 1200 Sardinians Reconstructs European Y-Chromosome Phylogeny

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Genetic variation within the male-specific portion of the Y chromosome (MSY) can clarify the origins of contemporary populations, but previous studies were hampered by partial genetic information. Population sequencing of 1204 Sardinian males identified 11,763 MSY single-nucleotide polymorphisms, 6751 of which have not previously been observed. We constructed a MSY phylogenetic tree containing all main haplogroups found in Europe, along with many Sardinian-specific lineage clusters within each haplogroup. The tree was calibrated with archaeological data from the initial expansion of the Sardinian population ~7700 years ago. The ages of nodes highlight different genetic strata in Sardinia and reveal the presumptive timing of coalescence with other human populations. We calculate a putative age for coalescence of ~180,000 to 200,000 years ago, which is consistent with previous mitochondrial DNA–based estimates.

New sequencing technologies have provided genomic data sets that can reconstruct past events in human evolution more accurately (*1*). Sequencing data from the male-specific portion of the Y chromosome (MSY) (*2*), because of its lack of recombination and low mutation, reversion, and recurrence rates, can be particularly informative for these evolutionary analyses (*3*, *4*). Recently, high-coverage Y chromosome sequencing data from 36 males from different worldwide populations (*5*) assessed 6662 phylogenetically informative variants and estimated the timing of past events, including a putative coalescence time for modern humans of ~101,000 to 115,000 years ago.

MSY sequencing data reported to date still represent a relatively small number of individuals from a few populations. Furthermore, dating estimates are also affected by the calibration of the

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†Laura Morelli prematurely passed away on 20 February 2013. This work is dedicated to her memory.

phylogenetic tree used to establish the rate of molecular change over time. This calibration can either correlate the number of nucleotide substitutions with dates from paleontological/archaeological records (phylogenetic rate) or can use directly observed de novo mutations in present-day families (mutation rate). However, both approaches are complicated by several variables (*6*, *7*).

Some of these problems can be resolved by the analysis of MSY sequencing data from many individuals from a genetically informative population, regarding which archaeological data are available to provide suitable calibration points. This prompted us to use large-scale MSY sequencing data from the island population of Sardinia for phylogenetic analysis. We generated a high-resolution analysis of the MSY from population sequencing of 1204 Sardinian males (*8*). We used a hierarchical approach and, to be consistent with previous work (*5*), focused on approximately 8.97 mega–base pairs (Mbp) from the Y chromosome in the X-degenerated region. We inferred 11,763 MSY phylogenetically informative single-nucleotide polymorphisms (SNPs), detected in at least two individuals and unequivocally associated with specific haplogroups and sub-haplogroups; 6751 of these SNPs had not thus far been reported in public databases.

The informative SNPs were used to construct a parsimony-based phylogenetic tree. To root the tree, we used the chimpanzee genome reference as an outgroup and inferred the ancestral status at all SNP sites except for 26 that were discarded in further analysis. The first bifurcation point, and thus the most recent common ancestor, separates samples 1 to 7 from the rest of the samples (samples 8 to 1204) (Table 1). The average number of derived alleles in the 1204 males is 1002.6 (±21.2 SD) which, consistent with a neutral evolution of these Y polymorphisms, shows a remarkable uniformity of the branch length.

The Sardinian sequences show a very high degree of inter-individual variation. As shown in a schematic tree (Fig. 1), all of the most common Y-chromosome haplogroups previously detected in Europe are present in our sample (Table 1), with the sole exception of the northernmost Uralic haplogroup N. The first bifurcation separates the mostly sub-Saharan haplogroup A (7 individuals, 0.6% in our sample) from the others. Haplogroup E (132, 11.0%) is present with its European clade, characterized by the presence of the M35 marker, together with a small number of individuals belonging to the mainly African clade E1a. The rare haplogroup F (7, 0.6%) is related to haplogroup G (131, 10.9%), which shows a private Sardinian-Corsican clade whose ancient roots have been found in an Eneolithic sample from the Italian Alps (*9*). Haplogroup I (490, 40.7%) is of special interest because it is mostly represented by the I2a1a clade, identified by the M26 marker, which is at high frequencies in Sardinia (*10*) but is rare or absent elsewhere (*11*). Haplogroup J (161, 13.4%) is observed with its main subgroups; and the super-haplogroup K is present with the related L and T branches (36, 3.0%), with a single individual of haplogroup Q (1, 0.08%) and with the more common haplogroup R (239, 19.9%) occurring mostly as the western European M173-M269 branch.

Almost half of the discovered SNPs (4872) make up the skeleton of the phylogenetic tree and constitute the root of the main clades. The skeleton includes lineages that are unbranched for most of their length, with ramifications only in the terminal portion. This indicates an early separation of the clades, followed by new variability generated during subsequent expansion events.

To estimate points of divergence between Sardinian and continental clades, we sequenced two samples from the Basque Country and northern Italy, belonging to haplogroup I, and two, from Tuscany and Corsica, belonging to haplogroup G. We also analyzed the sequence of the so-called Iceman Ötzi (*9*), together with 133 publicly available European sequences from the 1000 Genomes Project database and those SNPs from the International Society of Genetic Genealogy (ISOGG) database detected outside Sardinia.

The Basque individual separates from the basal position of the I2a1a branch that encompasses

Table 1. Super-haplogroups, haplogroups, sub-haplogroups, and private Sardinian-Corsican clades. Here the average number of SNPs defining each class is shown in our 1209 samples. The asterisk (*) denotes that the average number of SNPs for haplogroups A and E cannot be determined with precision because of the lack in our sample of individuals belonging to haplogroups B, C, and D. Consequently, the number reported here is an overestimate. The Sardinian samples are progressively numbered from 1 to 1204, and the non-Sardinian samples are labeled as follows: O, Ötzi; T, Tuscan; B, Basque; C, Corsican; I, northern Italian. The clades containing only private Sardinian SNPs are indicated in Greek letters (progressively from α to δ within each haplogroup).

Super-haplogroup (individual no.)	Mean SNPs	Haplogroup (individual no.)	Mean SNPs	Sub-haplogroup (individual no.)	Mean SNPs	Private Sardinian clade (individual no.)	Mean SNPs
A-R (1–1204; OTCBI)	1002.6	A (1–7)	879.9*	A1b1b2b (1–7)	11.9	α (1–7)	11.9
				E1a1 (8–13)	7.0	α (8–13)	7.0
				E1b1b1a1 (14–45)	87.4		
E-R (8–1204; OTCBI)		E (8–139)	541.8*	E1b1b1b1 (46–115)	96.1	β (49–115)	15.6
				E1b1b1b2 (116–139)	114.9	γ (116–131)	25.8
		F (140–146)	299.0	F3 (140–146)	79.3		
				G2a2b (147–186; OTC)	109.5	α (C; 155–162)	42.8
F-R (140–1204; OTCBI)	534.8	G (147–277; OTC)	373.8			β (163–186)	29.4
				G2a3 (187–277)	120.3	γ (247–277)	25.0
				I1a3a2 (278–279)	0.0		
						α (280–285)	36.0
				I2a1a (280–744; BI)	106.2	β (286–296)	39.1
						γ (297–314)	34.1
		I (278–767; BI)	353.5			δ (315–744)	37.3
I-J (278–928; BI)	387.0			I2a1b (745–746)	0.0		
				I2a2a (747–756)	38.1		
				I2c (757–767)	72.2		
				J1c (768–830)	112.7	α (816–830)	11.0
		J (768–928)	334.3	J2a (831–905)	125.1		
				J2b (906–928)	91.9		
K-R (929–1204)	375.3	K (929–964)	324.9	L (929–936)	123.7		
				T (937–964)	101.3		
		P (965–1204)	359.1	Q1a3c (965)	0.0		
				R1a1a1 (966–980)	13.8		
				R1b1a2 (981–1165)	37.2	α (981–989)	23.0
		R (966–1204)	241.2			β (991–1165)	29.4
				R1b1c (1166–1194)	75.7	γ (1177–1194)	36.2
				R2a1 (1195–1204)	8.5	δ (1195–1204)	8.5

11 Sardinian individuals. The northern Italian sample, instead, most likely reflecting the last step of I2a1 lineages before their arrival in Sardinia, is at the basal point of most of the remaining I2a1a samples (Fig. 2). Considering two other basal lineages encompassing only Sardinian samples, we can infer that when the I2a1a sub-haplogroup entered Sardinia, it had already differentiated into four founder lineages that then accumulated private Sardinian variability. Two other founder clades show similar divergence after entry into the island: one belonging to haplogroup R1b1c (xV35) (whose differentiation is identified contrasting the Sardinian data with the ISOGG and 1000 Genome data), and the other to haplogroup G2a2b-L166 (identified by divergence from a sequenced Corsican sample).

The branch length uniformity observed in our phylogeny is consistent (Fig. 1) with a relatively constant accumulation of SNPs in different lineages over time. Hence, this accumulation can be effectively used as a molecular clock for the dating of branch points. We calibrated the accumulation of Sardinian-specific genetic variation against established Sardinian archaeological records indicating a putative age of initial demographic expansion ~7700 years ago [reviewed in figs. S7 and S8 and the supplementary text (*8*, *12*)] that is also supported by mitochondrial DNA (mtDNA) analyses (*13*). Comparison of Sardinian genetic variation with that found elsewhere helped us to establish the amount of variability produced during and after this expansion, resulting in sublineages that appear to be unique to the island.

We focused our calibration analyses on the individuals belonging to the I2a1a-δ clade, which is shared by 435 individuals and is best suited to assess the Sardinian specific variability. Taking into account the average variation of all Sardinian individuals in the common I2a1a-δ clade of 37.3 (±7.8) SNPs, a calibration point of 7700 years ago results in a phylogenetic rate of one new mutation every 205 (±50) years. Considering that our analysis focused on approximately 8.97 Mbp of sequence from the Y chromosome X-degenerated region, this rate is equivalent to 0.53×10^{-9} bp^{-1} year^{-1}. This phylogenetic rate is consistent with the value of 0.617 (0.439 to 0.707) $\times 10^{-9}$ bp^{-1} year^{-1} from the genome-wide mutation rate observed from de novo mutations adjusted for Y chromosome–specific variables (*14*). Our mutation rate is instead lower than the value of 1.0×10^{-9} bp^{-1} year^{-1} obtained from de novo MSY mutations in a single deep-rooted

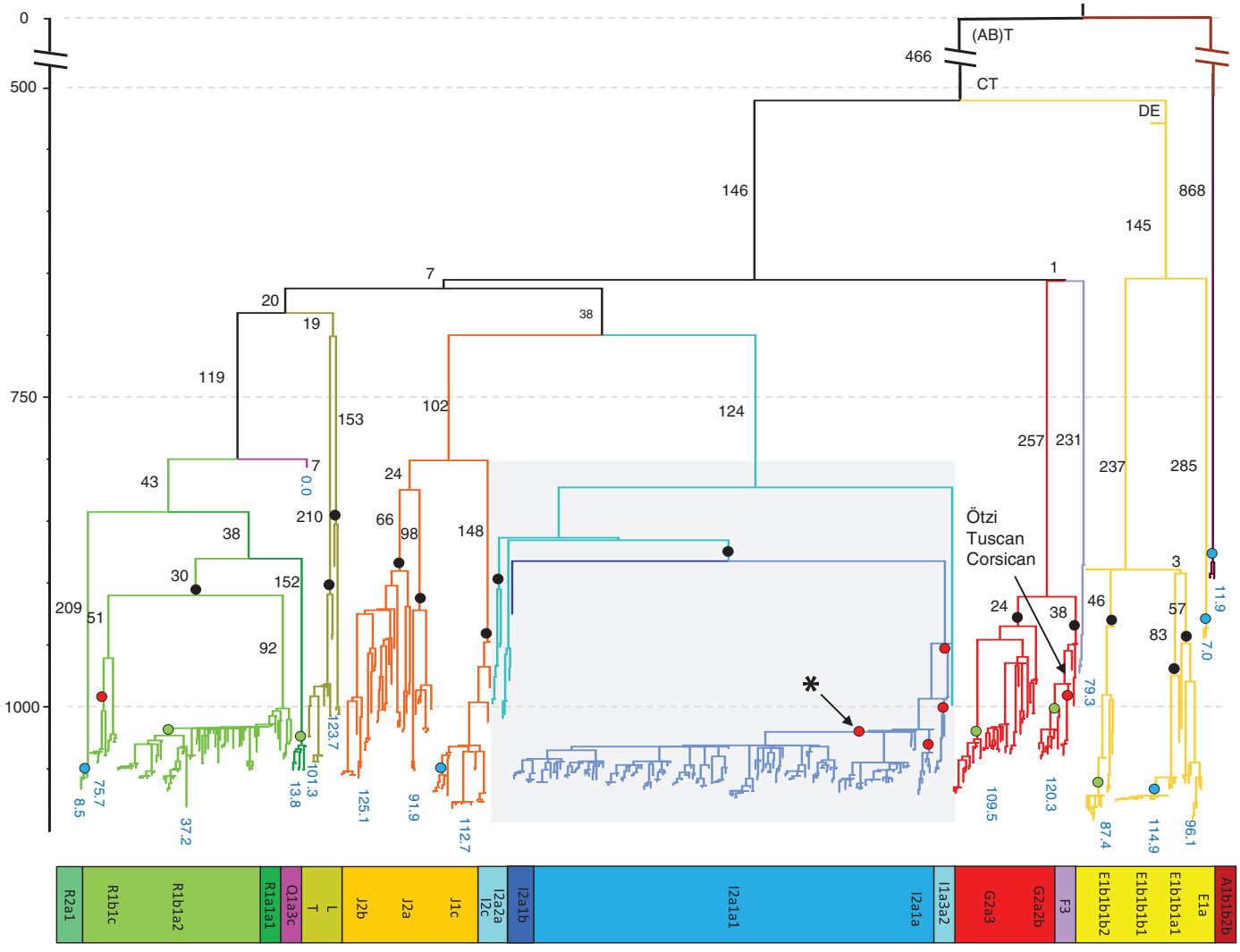

Fig. 1. Phylogenetic tree of the 1209 (1204 Sardinians and 5 non-Sardinians) Y-chromosome sequences. The bifurcations AT, BT, CT, and DE have been inferred because of the absence of individuals belonging to haplogroups B, C, and D in our sample. Colored branches represent different Y-chromosome haplotypes. The number of polymorphisms for the main branches is shown in black; the average number of SNPs of sub-haplogroups is given in blue. The sub-haplogroups are named according to ISOGG nomenclature. The left axis indicates the number of SNPs from the root. The asterisk indicates the calibration point. The colored dots indicate private Sardinian clusters with an average number of SNPs in the range of 35 to 40 in red, 25 to 30 in green, and 7 to 12 in blue. The black dots indicate clusters with an average number of SNPs in the range of 70 to 120. The arrow indicates the position on the tree of the Ötzi, Tuscan, and Corsican samples. The gray box is enlarged in Fig. 2.

family (*5*), which also coincides with that traditionally deduced from the *Homo-Pongo* divergence (*15*).

Using our phylogenetic rate of 0.53×10^{-9} bp^{-1} year^{-1}, we estimated the time to the most recent common ancestor (MRCA) of all samples, whose average variability is 1002.6 (±21.2) SNPs, at ~200,000 years ago. This is older than previously proposed (*16*) for the Y chromosome but is in agreement with estimates from a de novo mutation rate in an African Y-chromosome lineage (*14*) and with the revised molecular clock for humans (*7*) and the TMRCA estimated from analyses of maternally inherited mtDNA (*13*, *17*).

The main non-African super-haplogroup F-R shows an average variation of 534.8 (±28.7) SNPs, corresponding to a MRCA of ~110,000 years ago, in agreement with fossil remains of archaic *Homo sapiens* out of Africa (*7*, *18*) though not with mtDNA, whose M and N super-haplogroups coalesce at a younger age (*13*). The main European subclades show a differentiation predating the peopling of Sardinia, with an average variation ranging from 70 to 120 SNPs (Table 1), corresponding to a coalescent age between 14,000 and 24,000 years ago, which is compatible with the postglacial peopling of Europe.

However, the inferred phylogenetic rate and dating estimates presented here remain tentative, because the calibration date was deduced from archaeological data, which may be incomplete and typically covers a relatively large temporal interval. In the future, a more precise calibration point might be obtained by sequencing ancient DNAs from prehistoric Sardinian remains dated by radiocarbon methods. Further limitations derive from the scarcity of related samples for rare lineages, coupled with the low-pass sequencing approach we used (*8*). Low-pass sequencing is expected to detect nearly all common variants (frequency >1%) but to miss rare variants. Missed variants have competing effects on estimates of ancestral coalescent times: When they lead to missed differences among haplotypes that diverged after the founding of Sardinia, they lower our calibrated estimates of mutation rate and increase coalescent time estimates; when they lead to missed differences among ancestral clades, they lower these time estimates. In fact, despite the overall homogeneity of the length of the branches from the MRCA (Fig. 1), those represented by fewer individuals are generally shorter (*8*). To estimate the effect of missed variants on the age estimates, we sequenced with deep coverage 7 selected individuals, 4 of them belonging to the I2a1a-δ clade, used for calibration, and 3 to the I2a1a-β, J2b2f and A1b1b2b clades. The deep sequencing of the I2a1a-δ samples yielded an average of 45.7 (±2.2) Sardinian-specific SNPs among these haplotypes [versus 37.3 (±7.8) in low-coverage data], corresponding to a phylogenetic rate of 0.65×10^{-9} bp^{-1} year^{-1}. Overall, this reanalysis suggested a slightly more recent MRCA (~8% lower), still in substantial agreement with the antiquity of the main Y-chromosome haplogroups (*8*).

Hence, despite current limitations, the calibration used from common haplogroups in over

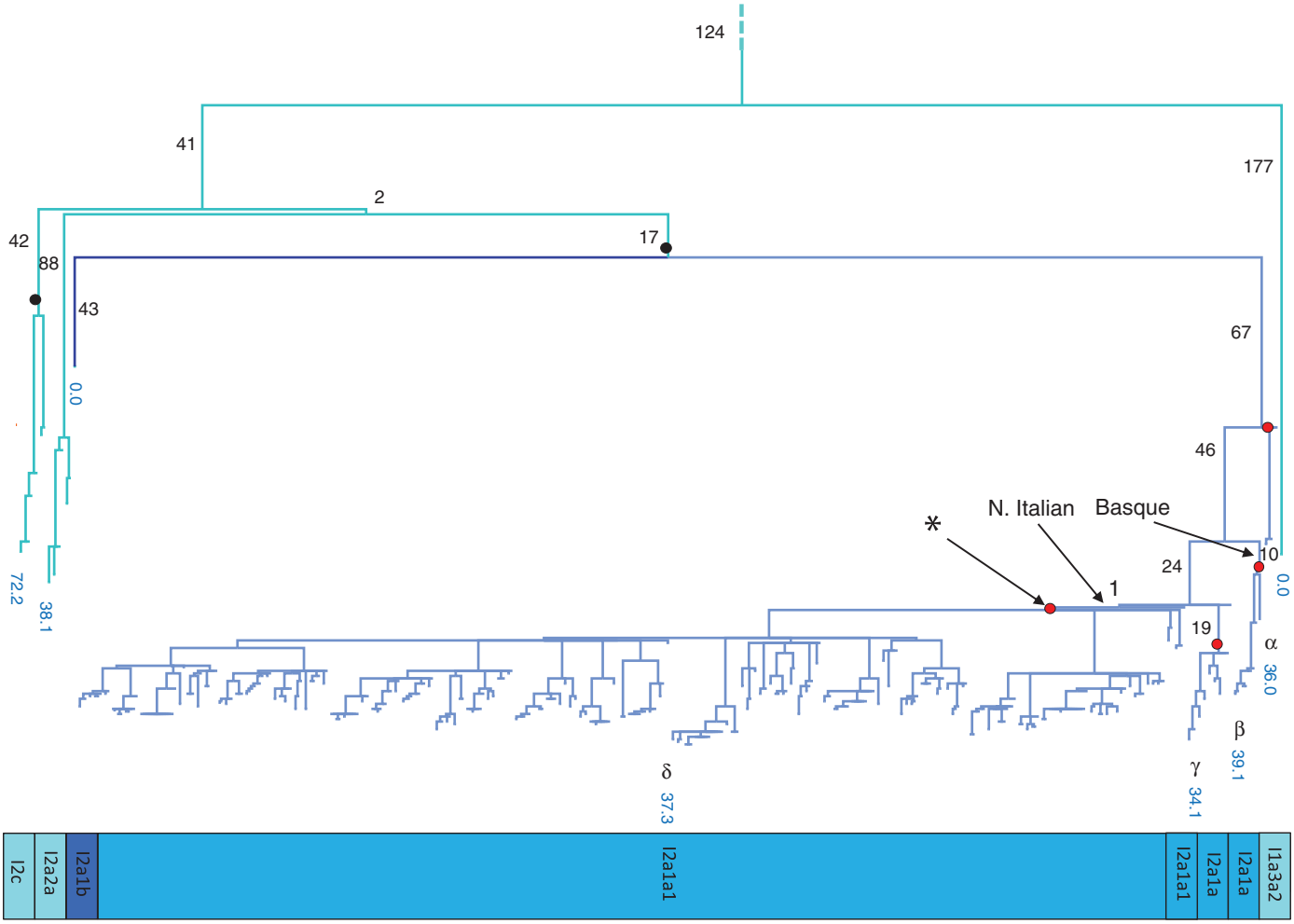

Fig. 2. Phylogenetic tree of the 492 (490 Sardinians and 2 non-Sardinians) Y-chromosome sequences belonging to haplogroup I. The number of polymorphisms for the main branches is shown in black; the average number of SNPs of sub-haplogroups is shown in blue. The sub-haplogroups are named according to ISOGG nomenclature. The red dots indicate Sardinian private clades, labeled in Greek letters as in Table 1. The black dots indicate clusters with an average number of SNPs in the range of 70 to 120. The arrows indicate the position of the northern Italian and Basque samples on the tree. The asterisk indicates the calibration point.

1000 people from this isolated population, including many island-specific SNPs, permits an estimate of main demographic events during the peopling of Sardinia that is concordant with the archaeological/historical record and ancient DNA analysis (*8*). The initial expansion of the Sardinian population, used for calibration, is marked by six clades belonging to three different haplogroups, with an average variation of around 35 to 40 SNPs, representing the ancient founder core of modern Sardinians.

Our data further suggest a more intricate scenario of Sardinian demographic history. Specifically, clades of E, R, and G that show Sardinian-specific variability of 25 to 30 SNPs are consistent with further expansion in the Late Neolithic (~5500 to 6000 years ago) (Table 1). Additional variation putatively arrived with groups of individuals carrying other haplogroups (namely the I clades different from I2a1, J, and T). Taken together, the genetic data and demographic expansions are consistent with classical archaeological data indicating that Sardinia reached a considerable population size in prehistoric times; the estimated population during the Nuragic Period (~2500 to 3700 years ago) was >300,000 inhabitants (*19*). Finally, the rare, mostly African A1b-M13 and E1a-M44 clades could have come to Sardinia in more recent times, up to the historic period corresponding to the Roman and Vandalic dominations, suggested by a private Sardinian variability of 7 to 10 SNPs.

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Supplementary Materials

www.sciencemag.org/cgi/content/full/341/6145/565/DC1
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The Microbial Metabolites, Short-Chain Fatty Acids, Regulate Colonic T_{reg} Cell Homeostasis

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Regulatory T cells (T_{regs}) that express the transcription factor Foxp3 are critical for regulating intestinal inflammation. Candidate microbe approaches have identified bacterial species and strain-specific molecules that can affect intestinal immune responses, including species that modulate T_{reg} responses. Because neither all humans nor mice harbor the same bacterial strains, we posited that more prevalent factors exist that regulate the number and function of colonic T_{regs}. We determined that short-chain fatty acids, gut microbiota–derived bacterial fermentation products, regulate the size and function of the colonic T_{reg} pool and protect against colitis in a *Ffar2*-dependent manner in mice. Our study reveals that a class of abundant microbial metabolites underlies adaptive immune microbiota coadaptation and promotes colonic homeostasis and health.

The intestinal immune system has coevolved with the gut microbiota for the maintenance of intestinal health (*1*). Disruption of this homeostasis leads to intestinal inflammation and disease (*2*, *3*). Colonic regulatory T cells (cT_{regs}) expressing the transcription factor Foxp3 are critical for limiting intestinal inflammation and depend on microbiota-derived signals for proper development and function (*4*–*7*). *Bacteroides fragilis* and clostridial species induce T_{reg} responses (*6*, *7*); however, how the gut microbiota affect cT_{reg} responses across mammalian hosts remains unclear. Although polysaccharide A from *B. fragilis* modulates T_{reg} responses (*6*), such effects are also likely mediated through more common factor(s) produced by many bacterial genera.

Humans and mice rely on bacteria to break down undigestible dietary components, such as fibers (*8*). Short-chain fatty acids (SCFAs) are bacterial fermentation products and range in concentration from 50 to 100 mM in the colonic lumen (*9*). We examined SCFA concentrations in specific pathogen–free (SPF) mice, gnotobiotic altered Schaedler flora (ASF)–colonized mice, and germ-free (GF) mice and found that GF mice had reduced concentrations of the three most abundant luminal SCFAs—acetic acid, propionic acid, and butyric acid (table S1)—as previously reported (*10*) (see also supplementary materials and methods). The decrease of these SCFAs in GF mice suggests that SCFAs may contribute to their immune defects, specifically reduced cT_{reg} numbers. We provided SCFAs in the drinking water (150 mM) to GF mice for 3 weeks and found that SCFAs individually or in combination (SCFA mix) increased cT_{reg} frequency and number (Fig. 1A) but did not increase the number or frequency of splenic, mesenteric lymph node (MLN) cells or thymic T_{regs} (fig. S1). These effects coincided with increased luminal SCFAs (table S1). SCFAs increased $CD4^+$ T cell frequency and number (fig. S2) but did not alter colonic T helper 1 (T_H1) or T_H17 cell numbers significantly (fig. S3).

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