

Title: The Greeks in the West: genetic signatures of the Hellenic colonization in southern Italy and Sicily

Tofanelli Sergio^{1*}, Brisighelli Francesca^{2,3*}, Anagnostou Paolo^{4,5}, Busby George BJ^{2,6}, Ferri Gianmarco⁷, Thomas Mark G⁸, Taglioli Luca¹, Rudan Igor⁹, Zemunik Tatijana¹⁰, Hayward Caroline¹¹, Bolnick Deborah¹¹, Romano Valentino^{12,13}, Cali Francesco¹², Luiselli Donata¹⁴, Shepherd Gillian B¹⁵, Tusa Sebastiano¹⁶, Facella Antonino¹⁷, Capelli Cristian²

Affiliations:

1 Dipartimento di Biologia, Università di Pisa, Via Ghini 13, 56126 Pisa, Italy.

2 Department of Zoology, University of Oxford, South Parks Road, OX1 3PS Oxford, UK.

3 Sezione di Medicina Legale-Istituto di Sanità Pubblica, Università Cattolica del Sacro Cuore, Roma, Italia

4 Dipartimento di Biologia Ambientale, Università “La Sapienza”, Piazzale Aldo Moro 5, 00185 Roma, Italy.

5 Istituto Italiano di Antropologia, Piazzale Aldo Moro 5, 00185, Roma, Italy

6 Wellcome Trust Centre for Human Genetics, Roosevelt Drive, Oxford

7 Dipartimento ad Attività Integrata di Laboratori, Anatomia Patologica, Medicina legale; U.O. - Struttura complessa di Medicina legale, Via del Pozzo, 71 – Policlinico, 41124 Modena, Italy.

8 Department of Genetics, Evolution and Environment, University College London, London, UK

9 Centre for Population Health Sciences, The University of Edinburgh Medical School, Teviot Place, Edinburgh EH8 9AG, Scotland, UK

10 Department of Medical Biology, University of Split, School of Medicine, Soltanska 2, 21000 Split Croatia

11 MRC Human Genetics Unit, Institute of Genetics and Molecular Medicine (IGMM), University of Edinburgh, Western General Hospital, Crewe Road, Edinburgh EH4 2XU United Kingdom.

12 Dipartimento di Fisica e Chimica, Università di Palermo, Palermo, Italy

13 Laboratorio di Genetica Molecolare, I.R.C.C.S. Associazione Oasi Maria SS., Troina (EN), Italy

14 Laboratorio di Antropologia Molecolare, Dipartimento di Scienze Biologiche, Geologiche e Ambientali, Università di Bologna, Via Selmi 3, 40126 Bologna, Italy.

15 A.D. Trendall Research Centre for Ancient Mediterranean Studies, La Trobe University, Australia

16 Soprintendenza del mare. Regione Siciliana, Via Lungarini, 9 90133 Palermo, Italy.

17 Soprintendenza per i Beni Archeologici della Calabria, Piazza de Nava 26, 89100 Reggio Calabria, Italy.

* contributed equally to the paper

Corresponding author:

Cristian Capelli

Department of Zoology, South Parks Road, OX1 3PS, University of Oxford, Oxford, UK

cristian.capelli@zoo.ox.ac.uk

ABSTRACT

Greek colonization of South Italy and Sicily (*Magna Graecia*) was a defining event in European cultural history, although the demographic processes and genetic impacts involved have not been systematically investigated. Here, we combine high-resolution surveys of the variability at the uni-parentally inherited Y chromosome and mitochondrial DNA in selected samples of putative source and recipient populations with forward-in-time simulations of alternative demographic models to detect signatures of that impact. Using a subset of haplotypes chosen to represent historical sources, we recover a clear signature of Greek ancestry in East Sicily compatible with the settlement from Euboea during the Archaic Period (8th-5th century BCE). We inferred moderate sex-bias in the numbers of individuals involved in the colonization: a few thousand breeding men and a few hundred breeding women were the estimated number of migrants. Lastly, we demonstrate that studies aimed at quantifying Hellenic genetic flow by the proportion of specific lineages surviving in present-day populations may be misleading.

Running title: Genetic legacy of *Magna Graecia*

Key words: Hellenic colonization; Y chromosome; mtDNA; Sicily; Italy

INTRODUCTION

“...board a fast ship to Sicily, where you could sell them for a profit.” (Homer, *Odyssey* XX 382-383)

From the 8th century BCE, the Western Mediterranean witnessed a settlement process which originated in the Aegean and had its center of gravity in Eastern Sicily and Southern Italy, an area later known as *Magna Graecia*. A substantial agreement on the drivers of this colonization and the geo-historical dynamics of the settlements is present (e.g. Graham 1982, Pugliese Carratelli 1996, Guzzo 2011) but the nature of early settlements, the scale of demographic impact and its genetic legacy are still debated. Archaeologists, historians and demographers have proposed different degrees of Greek contribution, with scenarios ranging from a colonization process based on small groups of males moderately admixing with autochthonous groups (Boardman 1980 p.163, Yntema 2011), “like ants or frogs about a pond” (Plato, *Phaedo* 109a-b), to substantial migrations from Greece and a Hellenic origin for a significant part of the pre-Roman Italian population (Dunbabin 1948, Faure 1978, Scheidel 2003). The pattern of genetic variation observed in Italian populations has been interpreted either as supporting a substantial Greek contribution to the current Sicilian and southern Italian gene pool (Piazza et al. 1988, Cavalli-Sforza et al. 1994), or having being shaped by other demographic processes (Capelli et al. 2007, Brisighelli et al. 2012, Boattini et al. 2013).

When the genetic impact of the Greek Colonization (hereafter GC) has been specifically addressed (Di Gaetano et al. 2009, King et al. 2011) a lineage-based interpretative approach was used, relied upon the frequency of the more frequent haplogroups (E-V13) or STR motifs (Balkan Modal Haplotype) in present-day Greeks. However, these approaches can be strongly misleading. Population patterns might not hold when SNPs defining finer haplogroup assignments are genotyped. Moreover, it is problematic to treat specific lineages or haplotypes as markers of GC, as these studies have done, because (1) the region where a haplotype is most common today is not necessarily the region where it originated (Edmonds et al. 2004, Klopstein et al. 2006), (2) modern population samples from the hypothesized source region may not be a good proxy for

ancestral source populations, and (3) present-day patterns might be related to other events that triggered migration along the same route, most notably the Neolithic agricultural revolution or migratory flows during the Bronze Age, the Classical Era, and the Christian Era. In addition, previous investigations have not formally tested alternative demographic models to clarify the scale of migration associated with the GC, an issue that has been puzzling demographers for long (Beloch 1886, Mc Evedy & Jones 1978; Hansen 2006; Turchin & Scheidel 2009).

In order to search and characterize the genetic echoes of the demographic impact of the colonization process we applied a hypothesis-testing approach consisting of a deep molecular characterization at male specific Y chromosome regions coupled with a dedicated sampling strategy to include relevant source and recipient populations. In addition, extensive simulations aimed at comparing alternative models for the origin and fate of Greek genetic contributions to southern Italy and Sicily were performed. In doing so, we: (a) tested for the presence of specific and robust signatures of Greek contribution to Italy and Sicily; (b) tested alternative models to estimate the most likely scale of the colonization process, with a focus on the relative contribution of males versus females; and (c) evaluated the implications of lineage-based approaches in the characterization of past demographic events.

MATERIALS AND METHODS

Sampling

A total of 811 unrelated individuals native to Greek districts thought to be at the origin of the GC migrations (Euboea island and Corinthia) and of cities placed in close proximity to primary and secondary Greek colonies in southern Italy were recruited through informed consent (Figure 1). The project received ethical approval by the institutions involved in the collection of the samples. Other putative recipient population samples from northern and central Italy were made available (N=201; Brisighelli et al. 2012). In addition, DNA samples from Albania (Ferri et al. 2010), Croatia (Rudan et al. 2009) and West Anatolia (Richards et al. 2000) were obtained as reference populations. To analyse samples of source, recipient and reference populations of comparable

size, Italian populations were clustered into six main groups following geographical and historical criteria (Table S1).

DNA was extracted from whole blood or oral samples (buccal swabs or saliva) through a modified salting out procedure (Walsh et al. 1991) or commercially available extraction kits (Master Pure™ Purification kit, Epicentre, Nucleon BACC, GE Healthcare Life Sciences).

Genotyping

A total of 59 previously published SNPs was analysed following a hierarchical genotyping strategy. Samples were amplified in a standard PCR reaction and the SNaPshot Multiplex System (Life Technologies Corp., Carlsbad, CA, USA) primer extension protocol was used. All samples were first genotyped for markers , E-M35, F-M89, G-M201, H-M282, I-M170, K-M9, J-M172, J-M267, J-M304, R-M173, P-M45, R-M17, R-M269, in order to classify them into major European branches. Samples belonging to haplogroups E-M35, E-M78, J-M172, I-M170 and R-M269 were further analysed by means of haplogroup specific multiplexes (Table S2). Furthermore, samples assigned to haplogroup G-M201 were analysed for markers M406 and P15 through direct sequencing (Table S3). Nomenclature used for haplogroup labelling follows YCC conventions (The Y Chromosome Consortium 2002) and recent updating (ISOGG Y-Tree 2015 <http://www.isogg.org/tree/>).

The entire dataset was also analysed at a total of 26 YSTRs: those included in the AmpFlSTR® Yfiler® PCR Amplification kit (Applied Biosystems, Foster City, CA) and additional 9 YSTRs (DYS460, DYS388, YCA-II a/b, DYS461, DYS445, YGATA-A.10, DYS413 a/b) by suitably designed multiplexed-PCR reactions (Table S4). We finally assembled a haplotype dataset based on 20 of the 26 analysed STR markers by excluding those STRs that in the PCR analysis co-amplify two loci and whose allele assignation to a defined locus was not possible (DYS385 a/b, YCA-II a/b and DYS413 a/b). A subset of samples (N=304) has been analysed for the Hypervariable Region I (HVR-I) of mitochondrial DNA using primers 15997L and 017H.

Data are available at <http://zenodo.org/>: DOI:10.5281/zenodo.15988 (Y markers); DOI:10.5281/zenodo.15987 (mtDNA markers).

Statistical Analyses

An F_{ST} genetic distance matrix (Slatkin 1995) was computed on Y haplogroup frequencies using the Arlequin package (version 3.5.1.2, Excoffier et al. 2010) and graphically represented by a non-metric multidimensional scaling (NM-MDS) (Kruskal 1964). The analysis involved 18 population samples: the six Italian recipient groups, the two source samples from Greece (Euboea, Corinthia), the three reference samples (Turkey, Albania, Croatia) and seven additional samples from Crete (Martinez et al. 2007, King et al. 2008), mainland Greece (King et al. 2008) and Lebanon (Zalloua et al. 2008). To make possible comparison across datasets genotyped with different SNP panels, haplogroups were pooled to the least basal common node on the ISOGG 2015 Y tree (<http://www.isogg.org/tree/>) for a total of 17 groups. Stress value suggests a non-random distribution of population samples in the bi-dimensional plot (0.0758, $p < 0.05$, Sturrock & Rocha 2000).

Inferring pairs of Y haplotypes with GC ancestry

To identify pairs of Y haplotypes in the source and recipient populations with a TMRCA compatible with the migrations from Greece to southern Italy and Sicily in the Archaic Period we used Equation 31 described by Walsh (2001, p.907) as implemented in the software ASHES 1.1 (ashes.codeplex.com; Capelli et al, 2009). Briefly, TMRCA Bayesian posterior distributions were calculated for pairs of chromosomes separated by 0 to 2k mutational steps (where k is equal to the number of loci), assuming haplotypes composed by the set of 20 selected Y-STR loci (see above), a strict stepwise mutational model, a mutation rate of 3.09×10^{-3} per locus per generation (averaged values from Burgarella et al. 2011 and Ballantyne et al. 2010) and a lambda value of 0.0002 ($1/N$, where N =effective population size; here used $N=5,000$ in accordance to Hammer 1995). For each k we explored the likelihood distribution at 102 (Greek Colonization Scenario, GCS; approximately 2,750 years ago using 27 years per generation) and 300 (Neolithic Scenario, NS; approximately 7,500 years ago using 25 years per generation) generations (Table S5). We corrected the male generation intervals calculated upon present-day genealogies (31.9 years, Helgason et al. 2003) according to the generalised reduction of life expectancy in pre-historic

societies and the Y-based estimates calibrated in traslocated historical groups (25-30 years, Bonne-Tamir et al. 2003). To assess which interval of mutational differences between haplotypes is the most suitable to represent the GC contribute to Italy, we normalized each distribution and chose the mutational range within the likelihood inferred for the GCS which minimized the overlapping ($<0.4\%$) with the distribution inferred for the NS. Such a range was 8-12.

To estimate the 95% confidence boundaries, we approximated each distribution to a normal one, centered on the most likely TMRCA value. We then calculated the area below the posterior distribution comprised between the most likely value and the origin of the curve, and equated this value to 50% of the total likelihood curve. The 2.5-97.5% bounds of the distribution were identified as the TMRCA values comprising the 95% of the right and left hand sides likelihood of the curve.

Tracking genetic footprints of the GC legacy in Italy

In order to detect Greece-to-Italy genetic contributions from the Archaic Period (1000-400 BCE), we first performed pairwise comparisons at 20-locus YSTRs haplotypes between either sources (from Euboea, Corinth) or reference populations (from Croatia, Albania, Turkey) and putative recipient populations (20 Italian groups pooled in six geographical districts, Table S1). Then, we calculated, for each population pair and within the same haplogroup, the proportion of haplotypes diverging for 8-12 mutational differences. To assess whether the enrichment in haplotype pairs matching this interval was significantly higher between sources and recipient populations than between sources and reference populations, we performed Fisher exact tests with the Arlequin software v 3.5 (Excoffier et al. 2010). We applied the same procedure to both the whole sample (Not Filtered or NF) and a subset of haplotypes (Filtered or F), the latter obtained by removing all haplotypes from recipient populations with fewer than 7 mutational differences from source population haplotypes, since the effect of more recent demography might overestimate this signal.

Computer simulations

To estimate the contribution of Greek colonizers to present-day southern Italian communities, we applied a hypothesis-testing approach based on the deviation from observed values of the

haplotype divergence expected under different simulated scenarios. As measure of molecular divergence we used DHS, a distance measure that calculates the extent of exactly matching haplotypes between pairs of diverging pools (Tofanelli et al. 2009). The closer the divergence between pools of haplotypes, the lower the value of DHS, ranging from 0 (all haplotypes shared by the two populations) to 1 (no shared haplotypes).

As paternally-inherited molecular markers we used a set of Y-STRs selected upon the number and the type which maximise the duration of DHS linearity with time. Six was the highest number that ensures DHS increases linearly within the last 300 generations (Figure S1). Accordingly, we choose six loci: DYS393, DYS445, DYS456, DYS460, DYS461, GATA-A10. The selected panel included loci characterised by tetrameric regular repeats, high and comparable estimated mutation rates (between 2.5 and 3.3×10^{-3} mut/gen according to Burgarella et al. 2011 and Ballantyne et al. 2010) and no incomplete alleles. As maternally-inherited molecular markers we used 360bp HVR-I sequences, whose divergence, as measured by DHS, increases linearly over 300 generations (Figure S2).

Different sets of parameters (see Table S6) were modelled under a stochastic Markov chain Monte Carlo (MCMC) method as implemented in the software ASHES (<http://ashes.codeplex.com/>). As starting haplotype pools, we used source and recipient meta-populations obtained by reiterating the real data n -times (Euboea and Corinth samples as source, a mix of southern Italian samples as recipient) until a final N_e equal to one-sixth of the current census size estimated according to the two demographic models was reached. For each simulation model we considered two populations coming into contact at time t_0 and exchanging $M=N_e m$ haplotypes from the source to the recipient pool, where N_e is the effective size and m the fraction of migrants. From time t_1 , the two populations were allowed to evolve independently for 102 (Y haplotypes) or 110 (mt haplotypes) generations – that is the time since the migration to Italy of the early colonizers from Greece (~2750 ya assuming respectively 27 and 25 years per generation). For each model 100 iterations were performed and summary statistics of DHS values were calculated. We considered as varying parameters the initial effective size of source and recipient populations, the increment rate (0.00

ind/gen, stationary model; 0.01 ind/gen, growth model), and the number of exchanged haplotypes M (0, 500, 1000, 5000). Invariants were the mutation rate (0.0027 mut/site/gen for Y haplotypes; 0.0000041 mut/site/gen for mt haplotypes), haplotype diversity (0.90 and 0.80 respectively for source and recipient Y haplotypes; 0.96 and 0.92 respectively for source and recipient mt haplotypes), and DHS between source and recipient pools at t_0 (0.7 for Y haplotypes; 0.5 for mt haplotypes). The latter values are those expected between pool of haplotypes coming into contact 2,750 ya after an initial divergence from an ancestral Anatolian pool some 6,250 (150 gen) or 7,500 (200 gen) ya under a model implying germ-line mutation rates as above and no size increment (data not shown).

The distributions of simulated DHS values were compared with empirical values calculated for each source/recipient pair of samples. Euboea and Corinth have been used as source samples, and Italians (pooled into six main geographic areas: West Sicily, East Sicily, Ionian Italy, South Italy, Central Italy, and North Italy) have been used as recipient samples. The data were considered to fit the model when observed DHS values fell within two standard deviations by the mean of the simulated distribution.

RESULTS

Population relationships

Y haplogroup frequencies are reported in Table S7 while the overall pattern of inter-population genetic relationships is shown in Figure 2 and Table S10. Cretan, mainland Greek and Lebanese samples were introduced to widen the spectrum of the historical players acting in south-eastern Mediterranean at the time of the GC, as proxies of non-Corinthian Dorian colonizers of South Sicily (since Crete contributed to the foundation of Gela and, in turn, Akragas), non-Euboean Ionian colonizers of South Italy and East Sicily, and Phoenician settlers in West Sicily, respectively. Looking at the reciprocal positions on the plot, little evidence of these historical events emerges, with the positioning reflecting geography rather than history. Accordingly, we observe higher genetic distance than that expected based on archaeological evidence between

putative descendants of source (Greeks from Ionia, Corinthians, and Cretan) and recipient (Sicilians) groups of the GC, as well as between the putative founders (Lebanese) of the Phoenician colonies in western Sicily (Motya, Panormos, Solus) and the present-day population.

Signatures of the Archaic Hellenic contribution

To detect genetic signatures of Greek migration into southern Italy and Sicily related compatible with the Archaic scenario, we compared fractions of haplotype pairs within the 8-12 mutational range, or “GChp”, with the same fractions obtained by using Albanian, Croatian and Turkish samples as reference sources (Table 1a).

Samples from East Sicily, West Sicily, South and Central Italy showed significant ($P < 0.01$) enrichment of GChps when the Greek sample from the Euboea Island was compared to Corinthia and reference sources. Except in West Sicily and Central Italy, this enrichment remained highly significant even after correcting for multiple tests ($P < 0.05$). Conversely, when considering Corinthia against other reference sources, none of the recipient samples showed a full set of significant values. The comparisons involving recipients versus Albania most commonly showed a lack of significant enrichment in GChps with respect to Euboea and Corinthia. We reasoned that contacts either between sources and recipients or between sources after the GC, i.e during the Classical and Christian periods, might have contributed to increase the GChps rate. Thus, in order to provide more stringent conditions for haplotype identification, we excluded all haplotypes with a molecular distance less than 7 mutational steps. This “filtered” dataset confirmed the pattern observed with the less stringent criteria for the East Sicily/Euboea pair, which showed significant enrichment in GChps in two out of three comparisons even after the Bonferroni correction (Table 1b). The results for West Sicily and South Italy did not hold statistical significance when a Bonferroni correction was applied. None of the other Italian recipients showed a full set of significant enrichment with Euboea or Corinthia.

Estimating Greek contribution

The number of GChps identified using the suggested molecular distance cannot be used either to directly estimate the current Greek legacy in Italian populations, or to provide an indication of the

original demographic contribution. Nevertheless, this approach helped us to identify populations (East Sicily, and, to a lesser degree, West Sicily and South Italy), that are characterized by a significant association with Greek populations derived during the time window of interest.

To quantify the original demographic impact of the Greek settlers inferable from present-day Y chromosome variability, we explored two main census scenarios using a simulation-based approach. In the first scenario, High-count or HC, we based our model on the demographic estimates of Beloch (Beloch 1886, Mc Evedy & Jones 1978), who suggested a census size of 1.35 Million people for Sicily and of 3 Million for Greece at the time of the Hellenic colonization in the Archaic Period. In the second scenario, Low-Count or LC, we modelled population size estimates that were smaller by an order of magnitude (Turchin & Scheidel 2009). Nevertheless, the two scenarios have similar source/recipient effective size ratios (S/R). If we assume that the proportions of past Sicilian, Euboean and Peloponnese census and male (and female) effective population sizes, is one sixth of the current census size, we estimate a S/R of 3.65 for the HC model and a S/R of 3.75 for the LC model. Simulation results are reported on Figure 3 and Table S8. When considering Y-STR haplotypes, the observed DHS value between Euboea and East Sicily (0.5353) is compatible with an effective number of migrants ranging between 500 and 5,000, clearly rejecting larger contributions (10,000), irrespective of the scenario considered. The DHS value obtained for HVR-I haplotypes (0.5995) supports an effective number of migrants between 500 and 1,000, with larger contributions clearly excluded. When the NRY- and mtDNA-based estimates are paired according to the demographic model, the male-to-female migrant ratio ranged between 1:1 and 2:1 under a population growth model and between 2:1 and 10:1 under a constant population size model.

Lineage-based demographic estimates

Previous investigations (Di Gaetano et al. 2009, King et al. 2011) have suggested the Y chromosome lineage E-V13 is a marker of the Hellenic contribution in the Mediterranean. In order to test the validity of this approach we repeated the enrichment test described above by considering only haplotypes belonging to the E-V13 lineage. Given the relatively low frequency

of this haplogroup in areas outside the Balkan peninsula, only the East Sicily sample provided a size of NRY haplotypes (N=20) large enough to perform meaningful comparisons. All the 20 E-V13 haplotypes in the sample from East Sicily had matches in the 8-12 mutational range when compared with GC and reference sources. Accordingly, no enrichment in GChps was found except vs Turkey (Fisher's exact test, $p < 0.01$). When haplotype pairs with mismatches of 0-7 steps were removed (F dataset), both Croatian and Turkish samples showed an increased relative number of GChps (respectively 9 and 7) with respect to the other source samples (2 in Albanian and Corinthian samples, 1 in the Euboean sample).

We further explored the impact of haplotypes belonging to specific lineages by calculating the fraction of GChps belonging to the various SNP-defined lineages contributing to the overall enrichment (Table S9). E-V13 is the major contributor for all the sources excluding Croatia. The contribution of E-V13 in Euboea and Corinthia was much lower than in the three reference sources (range 12.6-17.1% vs 17.5-22.8%). Similarly, we evaluated the contribution of E-V13 GChps in the F dataset (Table S9). As such, E-V13 haplotypes are no longer the major fraction of GChps and were under-represented in Corinthia (3.4%) and Euboea (1.1%). Figure 4 clearly shows that for these two candidate GC sources the largest quote of E-V13 haplotypes pairs did not fall in the 8-12 but in the 1-4 mutational steps interval. Moreover, it demonstrates that only haplotype pairs within the Albania sample reached the highest peak within the 8-12 range.

DISCUSSION

Evidence of Hellenic genetic echoes in Italy

The history of the European continent has been characterised by a large number of migration and admixture events (Hellenthal et al. 2014). The peopling of the Mediterranean is a clear example of this complexity. Here, the use of descriptive approaches aiming at summarising the observed genetic variation can easily miss signatures related to a given event.

Aware of these limitations, we attempted to recover genetic signals related to the Greek colonisation in southern Italy by analysing samples specifically collected to provide information

on the source and recipient populations actually involved. None of the Italian populations showed a closer affinity with Greek and Greek-related sources when Y chromosome data was analysed using MDS analyses (Figure 2). There are many explanations for this: limited historical migration between the two countries; lack of continuity between original and present-day source populations with current samples not being a good proxy of the ancestral populations they come from; the signal of the ancestry could be confounded by more recent or more ancient events. Nevertheless, when we used an approach designed to take into account the mutational process we recovered a signature of the Greek Contribution to Sicily during the Archaic Period. A first-level analysis based on the Bayesian posterior distribution of mutational steps compatible with the former colonization phase (GChps) showed that the most evident signal was in East Sicily, but this was also found to have parallels, or have diffused into neighbouring regions of West Sicily and South Italy. A second-level analysis, performed under more stringent conditions, again detected a signal in East Sicily. The lack of similar signals in other areas known to have been colonised by Greek migrants (e.g. Ionic Italy) can be explained by inadequate source samples (i.e. the Achaia region is not represented in our dataset), as well as by either a lower demographic impact or subsequent population discontinuity. We note that many of the pairwise comparisons were not significant due to high background signals from the Albanian sample, this being particularly noticeable when the Corinthian sample was involved. The easiest explanation for this is the close genetic affinity observed among the two areas (see Figure 2) deriving from direct and/or indirect gene-flow. For example, it is known that Greek colonies in present Albanian territory, such as Apollonia and Epidamnos, were founded by Corinthians (Boardman 1980) and that the area around Korinth was settled by southern Albanian orthodox Christians between the 13th and 16th century, the descendants of whom are identified as Arvanites (Hall 2000). During the sample collection, attention was given to this issue: individuals who self-reported as Arvanite were excluded from the analysis. Nevertheless, some Arvanite ancestry will have been unreported and may have affected the results.

Despite the multiple alternative explanations for historical gene flow, it is relevant to stress here that a signature specifically related to the Euboea island in East Sicily was consistently found at different levels of analysis, in line with the historical and archaeological evidences (Boardman 1980, Pugliese Carratelli 1996, Guzzo 2011), attesting an extended and numerically important Greek presence in this region.

Sex-biased gene flow

The numerical dimensions of the migration from Greece that resulted in the establishment of Hellenic colonies have been debated by scholars for centuries (see Scheidel 2003 among others). The signal from East Sicily points toward the lower end of the size spectrum proposed by historical demographers, with values in the order of thousands breeding men and few hundreds breeding women. From this perspective, our results are then compatible with the hypothesis that the migration and settlement process was driven by males. Interestingly this is one of the few cases of sex-biased gene flow skewed towards an increased male instead of female contribution (Heyer et al, 2012).

It is obvious that such numbers refer to the colonists who arrived in East Sicily as inferred from the descendants still living today. It is also worth stressing here that such estimates should not be taken as absolute but considered as indicative of the scale of the contribution. A possible flaw in these results could be also due to the sex-differential migratory rate after the first settlement. It is known that patrilocality is a commonplace in continental Italy and Sicily. This may have facilitated the diffusion of mtDNA variation at a larger scale than Y chromosome variation, thus lowering the probability of finding local female genetic signatures of the GC (Heyer et al. 2012, but see Marks et al. 2012).

Lineage-based estimations

The genetic contribution of a given source within a defined historical scenario has often been estimated using the number of chromosomes assigned to given haplogroups assumed to have a specific geographic/ethnic origin. In relation to the Greek colonization of the Mediterranean, the lineage defined by the E-V13 marker has been used to estimate the Hellenic contribution to the

Sicilian gene pool (Di Gaetano et al. 2009). By assuming that all E-V13 chromosomes have a Hellenic origin, authors estimated a contribution of approximately 37% to the population in Sicily. The reconstruction of a STR-based network linking the Sicilian modal haplotype and its one-step neighboring haplotypes provided a TMRCA of about 2,380 years before present, with a 95% confidence ranging between 675 and 6,940 years ago. More recent contributions and differential origins are expected to affect such estimates, but attempts to mitigate the impact of these phenomena were not implemented.

In this study we highlighted that, when alternative sources were taken in consideration, E-V13 did not show any specificity as a marker of the Hellenic contribution. The signal that we found using the full set of haplotypes within a limited range of mutational distance disappeared when only E-V13 unbounded haplotypes are considered, becoming even significant for other non-Greek sources when a filter for recent gene-flow was applied. The contribution of E-V13 from Corinthia and Euboea, in fact, reaches its peak well before the 8-12 mutational steps range (Figure 4), while in this range and samples it showed minor relative frequency.

These findings suggest a poor association between the Y haplogroup E-V13 and the East-to-West GC migratory waves. The effects of more recent gene-flow or sampling bias, may have masked the original E-V13 signal from Greece. At any rate, our results caution against the use of specific lineage-based approaches to test for hypothesized population contributions and underline the need for a more targeted approach to explain the occurrence of given haplotypes within a population, providing tests of alternative hypotheses, a wide spectrum of reference samples and mutation-limited inference methodology.

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Conflict of interest

The authors declare no conflict of interest.

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FIGURE CAPTIONS

Figure 1. Map pointing the geographic origin of source, recipient and reference population samples. Primary and secondary colonies founded during the Archaic Age of the Hellenic expansion to South Italy and Sicily are also showed in gray dots.

Figure 2. NM-MDS bi-dimensional plot of F_{ST} pairwise genetic distances among investigated population samples and additional reference samples from the literature (Cretan and Lebanese) based on the frequencies of 17 Y haplogroups.

Figure 3. Plots of observed (lines) and expected (bars) DHS values for each simulated evolutionary scenario. M0, M500, M1,000, M5,000=Number of migrants; k=stationary model, growth=expansion model with increment $I=0.01$ ind/gen. High Count = census sizes as in Beloch 1886; Low Count = census sizes as in Turchin & Scheidel 2009. Blue lines/bars = results involving the Euboean sample as source population; Red lines/bars = results involving the Corinthian sample as source population. A certain parameter set was considered as fitting the model when the observed DHS fell within a two standard deviations interval (bars) of the simulated distribution at time $t=102$ (Y haplotypes) and $t=110$ (mtDNA haplotypes) generations.

Figure 4. Relative percentage of mutational steps between E-V13 haplotypes pairs in source and reference population samples.

SUPPLEMENTARY LEGENDS

Figure S1. Variation through time (in generations) of DHS values (averaged upon 100 iterations) using haplotypes composed by different numbers of Y-STR loci. A starting pool of 1,000 haplotypes, stationarity, and a rate of 0.0027 stepwise mut/site/gen were used as model parameters.

Figure S2. Variation through time (in generations) of DHS values (averaged upon 100 iterations) using haplotypes composed by different lengths of HVR-I sequences. A starting pool of 1,000 haplotypes, stationarity, and a rate of 0.0000041 mut/site/gen were used as model parameters.

Table S1. Subdivision of Italian population samples into geographic groups.

Table S2. Oligonucleotides used for multiplex PCR amplification assays and snapshot multiplex primer extensions.

Table S3. Oligonucleotides used in PCR amplification assays for the direct sequencing of SNPs M406 and P15 within haplogroup G-M201.

Table S4. Oligonucleotides used in PCR amplification assays for allele assignment at 8 Y-STR loci: DYS460, YCAII, DYS388, YGATA-A.10, DYS461, DYS413, DYS385, DYS445.

Table S5. Bayesian posterior distributions for each k mutational step between pairs of chromosomes under the Greek Colonization (GC) and the Neolithic (NS) scenario. p102 - likelihood distribution at 102 generations (GC), p300 likelihood distribution at 300 generations (NS), MAX – highest values for each distribution.

Table S6. Sets of simulated parameters for both stationary and growth models.

Table S7. Y-chromosome haplogroup frequencies.

Table S8. Pairwise DHS distances between Italian and Greek populations for Y chromosome and mtDNA haplotypes. (a) observed values, b) expected intervals under different demographic models.

Table S9. SNP-defined lineages contributing to the overall enrichment of haplotype pairs compatible with the Greek Colonization (GChps).

Table S10. Pairwise F_{ST} genetic distance matrix computed on Y haplogroup frequencies.