Clinal patterns of human Y chromosomal diversity in continental Italy and Greece are dominated groups (Hg) depending on the type of variation used to define them.

For single nucleotide polymorphism (SNP) variation, the phylogenetic relationships among Hg's can be reconstructed unequivocally, assuming a monophyletic origin of the derived state at each variant position. Experimental data have not contradicted this assumption and a comprehensive tree has been recently presented (YCC, 2002). A notable feature of this tree is the pres-

Table 1
Haplogroup relative frequencies (%), sample size and diversity indexes

	Haplogroup												
	Pop. sample[a] (code)	P* (xR1a)	R1a	DE	G2	I-M170	J2- (DYS413 ⩽ 18)	J2*- (xDYS413 ⩽ 18)	J* (xJ2)	A	Y* (xA, DE, G2, I, J, P)	Sample size (n)	Diversity index ± SE
	Italy												
1	Val di Non (VAL)	**73.3**	6.7				3.3	6.7			10.0	30	
2	Verona[b] (VER)	45.5	9.1	9.1		4.5	22.7	4.5			4.5	22	
3	Garfagnana (GAF)	**76.2**	4.8	2.4	4.8		2.4	7.1			2.4	42	
4	Genoa[b] (GEN)	**48.3**		24.1	10.3	6.9	6.9		3.4			29	
5	L'Aquila[b] (LAQ)	25.7	5.7	11.4	5.7	8.6	25.7	5.7	2.9		8.6	35	
6	Pescara[b] (PES)	45.0		15.0			10.0	5.0	15.0		10.0	20	
7	Avezzano[b] (AVE)	41.4	6.9	3.4	6.9	10.3	13.8	3.4	3.4		10.3	29	
8	Benevento (BEN)	26.1	2.2	17.4	10.9	8.7	19.6		6.5		8.7	46	
9	Cilento (CIL)	29.2	2.1	12.5	14.6	6.3	16.7	4.2	6.3		8.3	48	
10	Foggia[b] (FOG)	11.1		11.1	14.8	**18.5**	**40.7**	3.7				27	
11	North Gargano[b] (GAR)	27.6	3.4	24.1		3.4	10.3	10.3	17.2		3.4	29	
12	Casarano[b] (CAS)	30.0	10.0	20.0	10.0	5.0	20.0	5.0				20	
13	Brindisi (BRI)	18.4	5.3	**26.3**									

In order to assay the gradient of haplogroup di erentiation, we carried out spatial autocorrelation analysis (Sokal and Oden, 1978), using the program AIDA (Bertorelle and Barbujani, 1995). We performed several runs using di erent numbers of distance classes to faithfully represent the geographical distances among samples, yet retaining a meaningful number of comparisons in each class. The option for obtaining distance classes

Among the Italian samples, only three Hg's have frequencies >10%, accounting for more than two thirds of chromosomes. On the other hand, the three most common Hg's found among the Greek samples account for only 55% of chromosomes. Accordingly, Hg diversity is higher in Greece than in Italy (Table 1).

3.2. Patterns of genetic di erentiation among populations

In order to have a synthetic view of gene pool similarities among population samples, we used correspondence analysis (Fig. 2a). The first two dimensions explain 40 and 17% of the total inertia, respectively, summarizing more than half of the total variation. Dimension 1 mainly reflects the frequency of Hg P* (xR1a) (61% of the dimension), whereas dimension 2 reflects mainly the frequency of Hg R1a (47%). Hg's I-M170 and J2-(DYS413 $\leqslant$ 18) contribute almost equally to both dimensions (16 and 15% to dimension 1 and 10 and 18% to dimension 2, respectively).

In the space defined by the first two dimensions, samples from the two countries show little overlap. Two Italian populations (GAF, VAL) are clearly separated from the rest on the first dimension. The Greek samples span the entire range of the second dimension. Within each country, there is no clear correspondence between the positioning of the samples in the first two dimensions

occupy positions at opposite edges of the Italian cluster. The FOG sample, geographically very close to GAR and BRI, maps far apart from the latter ones, closer to two Cretean samples. As to Greece, the two Cretean samples CHA and HER are clearly separated from both RET

frequencies as a function of latitude and longitude. This method was applied only to the most frequent Hg's (DE, I-M170, J2-(DYS413$\leqslant$18) and P* (xR1a) if >10% in each national sample). Among the seven regressions, only P* (xR1a) in Italy shows a significant geographic dependence ($F = 12.1$; $p < 0.001$), with an average increase of 3.1% per degree of latitude and a decrease of 2.8% per degree of longitude. Interestingly, the map of this Hg frequencies (Fig. 1) shows equal-frequency lines crossing the Italian peninsula, with a limited number of outlying locations. Note that the method used here, which preserves the observed data points, also produces a central Italian belt of Hg P* (xR1a) even if none of the three locations sampled within this belt (LAQ, AVE, and PES) fall within this range.

3.3. Molecular diversity within Hg's

Given the highly variable spatial pattern of the overall Y chromosomal diversity, we identified the instances of the largest variation in Hg frequencies in a given location by comparison to the corresponding national average. The dinucleotide STRs associated with each Hg could provide hints on possible recent founder or drift e ects that raised the frequency of the same Hg in certain locations. The criterion used was an increase of more than 10% in the frequency of a Hg (>1 standard error in all cases) in a local sample compared to the frequency of the same Hg in the corresponding overall national sample

systematic change of Hg frequencies among sampling locations spanning a drastic change in the altitudinal features of the environment, from the Carpathians mountains to the steppic plains of eastern Europe in Romania and Moldova. Similarly, six of our Greek samples are island populations. These are likely to have experienced some degree of reproductive isolation, possibly leading to random Hg frequencies fluctuations rather than clinal variations.

Major peopling events may also leave their signature. Only Hg P* (xR1a) in Italy displays a significant decrease in frequencies, from the north-west to the south-east. Many authors agree in considering this Hg as the signature of the Paleolithic inhabitants of the entire European continent. Wilson et al. (2001) have identified a particular STR haplotype within this Hg as the characteristic shared by Celtic-speaking populations and the Basques by common descent from a relatively homogeneous pre-agricultural gene pool. In this context, the most frequent YCAII and DYS413 STR alleles observed

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