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Chromosome Y microsatellites: population genetic and evolutionary aspects

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Abstract By means of a multicenter study, a large number of males have been characterized for Y-chromosome specific short tandem repeats (STRs) or microsatellites. A complete summary of the allele frequency distributions for these Y-STRs is presented in the Appendix. This manuscript describes in more detail some of the population genetic and evolutionary aspects for a restricted set of seven chromosome Y STRs in a selected number of population samples. For all the chromosome Y STRs markedly different region-specific allele frequency distributions were observed, also when closely related populations were compared. Haplotype analyses using AMOVA showed that when four different European male groups (Germans, Dutch, Swiss, Italians) were compared, less than 10% of the total genetic variability was due to differences between these populations. Nevertheless, these pairwise comparisons revealed significant differences between most population pairs. Assuming a step-wise mutation model and a mutation frequency of 0.21%, it was estimated that chromosome Y STR-based evolutionary lines of descent can be reliably inferred over a time-span of only 1950 generations (or about 49000 years). This reduces the reliability of the inference of population affinities to a historical, rather than evolutionary time scale. This is best illustrated by the construction of a human evolutionary tree based on chromosome Y STRs in which most of the branches connect in a markedly different way compared with trees based on classical protein polymorphisms and/or mtDNA sequence variation. Thus, the chromosome Y STRs seem to be very useful in comparing closely related populations which cannot probably be separated by e.g. autosomal STRs. However, in order to be used in an evolutionary context they need to be combined with more stable Y-polymorphisms e.g. base-substitutions.

Key words Y chromosome · Haplotypes · Evolution · Population studies · Genetic affinities · STR

Introduction

Microsatellite or short-tandem-repeat (STR) loci are not only a very useful tool for mapping disease-associated genes [1], but also turned out to be suitable to infer phylogenetic relationships between human populations [2]. Evolutionary trees based upon autosomal microsatellite haplotype frequencies closely resemble their mtDNA based counterparts [3], although there has been at least one report of only marginal overlap [4]. What is still missing is a human evolutionary tree based on highly polymorphic chromosome Y loci. Until recently this has been hampered by the lack of informative markers on the Y chromosome. Only a small number of Y-chromosomal variations have been reported so far [5–9]. Most of these markers showed genetic diversity between populations but not between individuals in a single population. This limits their usefulness in some, but not all aspects of evolutionary population genetic research [6]. Recently, a series of highly polymorphic Y-specific microsatellites have been developed and tested on different population samples [10–14]. These markers show high levels of Y-chromosomal heterogeneity within and between populations and thus seem to be very useful for population genetic, evolutionary and forensic applications.

However, before such markers can be used widely with a certain reliability, the various aspects of application have to be tested in more than just the few population samples described so far [12, 13]. It was therefore decided at the first Y-user workshop (Berlin, May 1996) that as many male population samples as possible should be typed for at least a set of seven well established chromosome Y STRs: DYS19, DYS389 I+II, DYS390, DYS391, DYS392 and DYS393. For these loci allelic ladders enabling the finetuning of nomenclature were made available for all those interested. Over the course of 1996 genotype data were collected at a central place. Details of the various population samples, loci, protocols and allele frequency distributions from all centres are described in full in this same issue by Kayser et al. [15]. This manuscript describes in more detail some of the results of a comparative analysis on part of the total data set. This analysis shows that the chromosome Y STRs seem to be very useful in comparing closely related populations which, probably, cannot be separated by e.g. autosomal STRs. However, as is also illustrated by Jobling et al. in this issue [16], in an evolutionary context, Y-STRs seem to have a mutation rate which is too high to be of use in itself, and we recommend the use of more stable Y-polymorphisms, e.g. base-substitutions, in combination with the Y-STRs for this purpose.

Materials and methods

Population samples

For the population survey 3825 male DNA samples from 48 different subpopulation groups from Europe, America, Asia, Africa, and Oceania were analysed for one or several loci (see Kayser et al. [15] and Appendix Table 2). For DYS19, we added the information of a recently published global screening [17]. For the purpose of this manuscript only results for the following STRs were considered: the tetranucleotide loci DYS19, DYS389 I/II, DYS390, DYS391, DYS393, and the trinucleotide locus DYS392. For the other loci too few individuals or population samples were screened to allow a meaningful analysis. In order to allow comparison with previously published evolutionary studies, the population samples were pooled, according to Cavalli-Sforza et al. [18], in the following nine distinct geographical regions: (1) Papua New Guinea + Australia (NGA), (2) the Pacific (PAC), (3) South-East Asia (SEA), (4) North-East Asia (NEA), (5) the Arctic (ARC), (6) Amerindians (AMR), (7) Europe (EUR), (8) India (IND), and (9) Africa (AFR). Table 1 summarizes which population samples listed in the Appendix, have been pooled in which geographical region. A few populations, which could not be allocated to any of the nine regions, were excluded from this analysis and are also indicated in Table 1. Because of the extreme small sample size (n = 10), the Pacific region (PAC) was excluded from all further analyses.

Table 1 Allocation of population samples to geographical regions

New Guinea/Australia (NAG):	*Europe (EUR):*
Trobiands	Basque 1
Papua New Guinea 1	Basque 2
Papua New Guinea 2	Berlin 1
	Berlin 2
Pacific (PAC):	Bern
West-Samoa	Brandenberg
	Bremen
South-Eas Asia (SEA):	British
Ami	Catalan
S-Borneo	Hannover
Cambodja	Heidelberg
Chinese	Iceland
Korea	Insbruck
New York Asian	Jena
NO-Thai	Leicester
SO-Thai	Leiden
Taiwan	Magdeburg
	Milano
North-East Asia (NEA):	München 1
Japan 1	München 2
Japan 2	Münster
Japan 3	Roma
Mongolians	Roumenian
Osaka	Trieste
	Udine
Arctic (ARC):	Verona
Inuit	
	India (IND):
Amerinindian (AMR):	Ahom
Mapuches	India 1
Surinam	India 2
Tehuelches	Kachari
Wichis	Pakistan
Yanonami	
	Not included,
Africa (AFR):	*but listed in Appendix:*
New York Black	Belo Horizonte
Ovambo	Buenos Aires
Pygmy	Maroc
	New York Hispanics

In order to compare a set of closely related populations, we used the individual genotypic data from four centres: (1) Leiden, representing the Dutch population, (2) Berlin 1, representing a German population, (3) Bern, representing the Swiss population, and (4) Roma, representing the Italian population.

Experimental details

For a detailed description of all experimental conditions see Kayser et al. [15].

Nomenclature

According to the recommendations of the International Society of Forensic Haemogenetics [19], the number of variable repeats has been used to designate the various Y-STR alleles. Consistent allele designation for all loci involved was ensured by the distribution of sequenced allelic ladders or typed standard DNA samples to all laboratories involved in this study. For those interested, please contact the corresponding author of this manuscript (Peter de Knijff, Leiden University, The Netherlands).

Statistical analyses

For each population sample the allele frequencies for each locus were calculated by simple gene counting procedures. Subsequently, for each of the eight geographical regions a weighted allele frequency was calculated for each of the Y microsatellites. Based on these weighted allele frequencies five different genetic distance measures were computed: Fst [20], Ds [21], Dc [22], Dsw [23] and Ddm or $(\delta\mu)^2$ [24]. The latter two distances were specifically developed to accommodate the increase or decrease in the number of repeats of a microsatellite locus assuming a step-wise mutation model. It was recently shown [25] that of these five distances Dc was superior in obtaining a correct tree topology and only Ds and Ddm rendered correct branch lengths. We therefore continued our calculations with three of the five distance measures: Dc, Ds and Ddm.

Neighbour-joining trees [26] were built for the three remaining distances by means of the PHYLIP 3.5c package [27] for Dc, Ds, and Ddm. Tree robustness was assessed by 1000 bootstrap iterations and the percentage of trees with a given node present in the bootstrapped tree is shown in the figures.

For the comparison of the four European populations, haplotypes were constructed for each individual on the basis of the individual genotypes. These haplotypes were used for the AMOVA analyses as previously described [12] following the recommendations of Michalakis and Excoffier [28]. These analyses result in an estimate of the genetic distance Φ st, which represents the percentage of the total genotypic variance explained by the between population variability. The significance of the various pairwise Φ st values was estimated by 1000 random simulations. The program WIN-AMOVA was used for all these calculations. In addition, the total number of haplotypes shared between two populations was calculated by a simple counting procedure. Haplotype diversity and the probability of identity between two populations was calculated as described by Melton et al. [29]. Comparisons of allele frequency distributions between regions were performed by non-parametric exact-test procedures embedded in the program StatXact (Cytel-Software, Cambridge, Ma.). Details where to obtain the public-domain software DSW, MICROSAT, PHYLIP and WIN-AMOVA are available from the corresponding author.

Results and discussion

Loci, populations and allele frequencies

Table 2 summarizes the number of individuals screened for each of the seven Y-STRs, according to the nine geographical regions. Locus DYS19 is the most often used Y-STR at present, with more than 4500 males screened worldwide [this study and ref. 17]. For the other loci close to a 1000 or more males have been screened for the purpose of this study. Evidently, the Pacific region is very under represented with only 10 Samoan males screened, therefore this region (PAC) was excluded from further analyses. Other under represented regions are the Arctic (with only one Inuit population sample included) and India (with only 25 males screened for most of the loci). Nevertheless, most major geographical regions are represented in this first global survey using Y-STRs.

Table 2 Summary of number of individuals screened for seven chromosome Y STR in nine geographical regions

Geographical region		Chromosome Y STR						
		DYS19	DYS389-1	DYS389-2	DYS390	DYS391	DYS392	DYS393
New Guinea/Australia	(NGA)	135	139	139	134	86	86	86
Pacific	(PAC)	10	10	10	10	10	10	10
South-East Asia	(SEA)	195	81	81	81	56	58	56
North-East Asia	(NEA)	793	190	191	189	40	40	40
Arctic	(ARC)	62	62	62	62	62	62	62
Amerindian	(AMR)	115	100	100	101	101	65	67
Europe	(EUR)	2957	538	537	1046	561	594	608
India	(IND)	144	25	25	25	25	25	25
Africa	(AFR)	147	136	135	147	31	61	31
Combined		4558	1281	1280	1795	972	1001	985

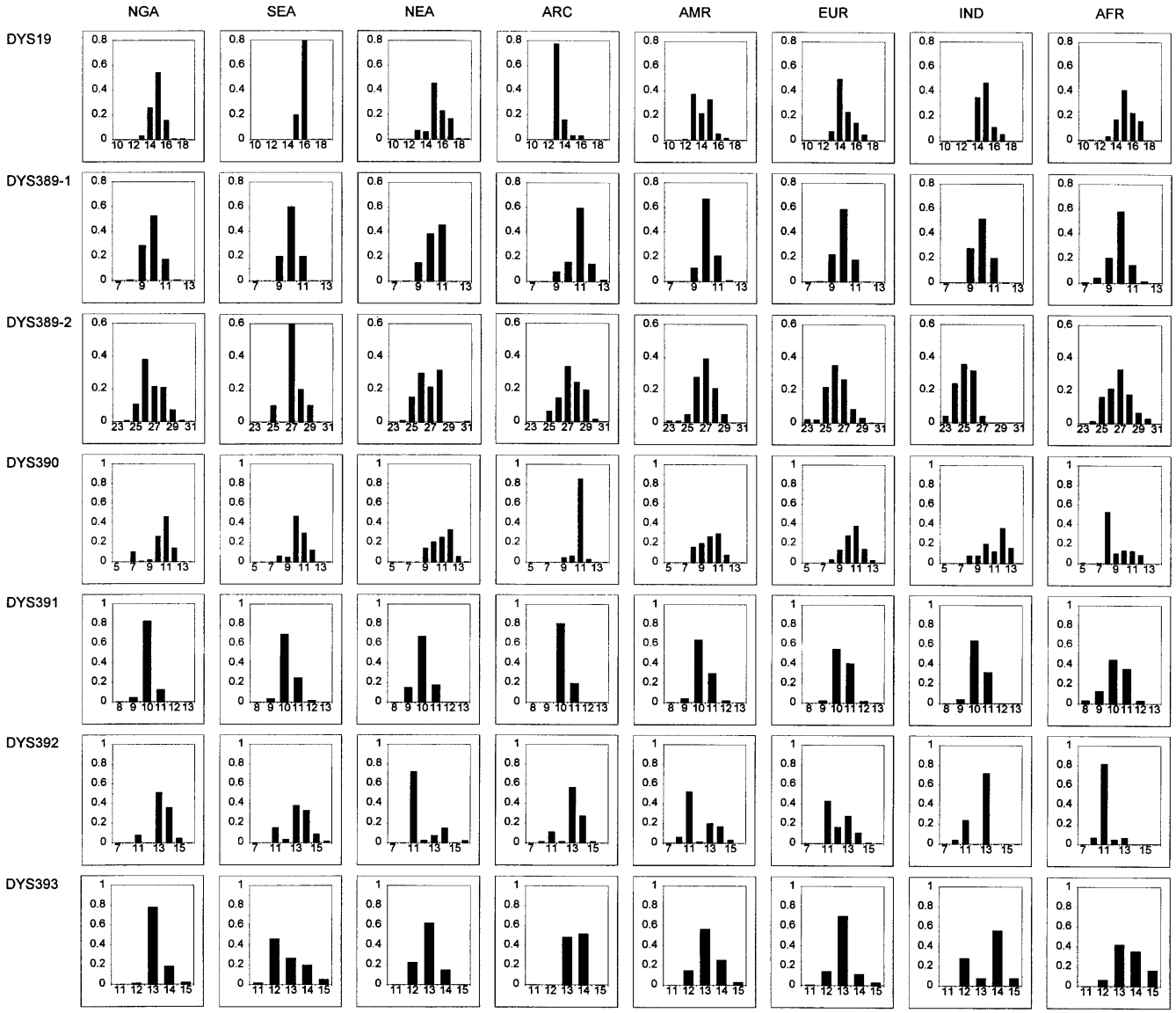

Fig. 1 Distribution of allele frequencies of seven chromosome Y STRs in eight geographical regions. All Y-axes show the allele frequency. All X-axes show the number of variable repeats. On the left of each row of figures the chromosome Y STR locus is indicated. Above each column the geographical region is indicated. For an explanation of the abbreviations see material and methods

Figure 1 illustrates the allele frequency distribution of all seven loci across the eight remaining geographical regions. With the exception of DYS392, all Y-STR loci show a unimodal distribution with one frequent allele and with less frequent neighbouring alleles, differing by one

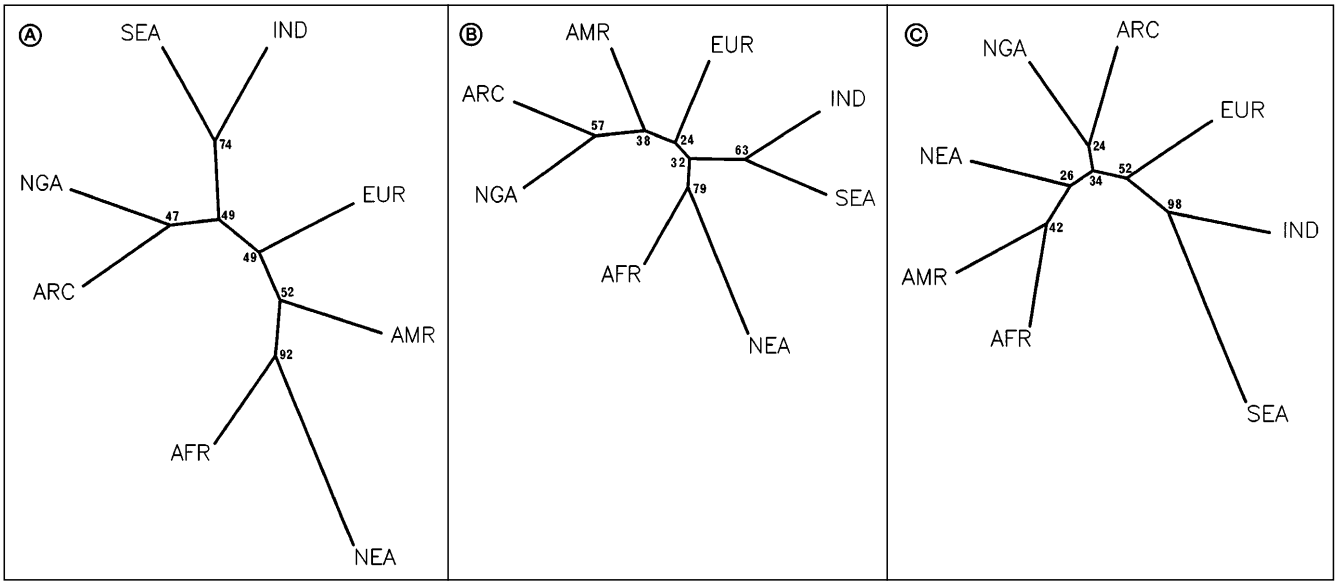

Fig. 2A–C Unrooted Neighbour-Joining trees showing phylogenetic affinities between eight geographical regions based on the genetic distances Ds (**A**), Dc (**B**) and Ddm (**C**). On the end of each branch the geographical region is indicated. For an explanation of the abbreviations see material and methods. The numbers at each node indicate the percentage of trees (out of 1000 bootstrapped replicates) with such a node

repeat unit from the most frequent allele. Thus, the distribution of chromosome Y STR alleles seems to be compatible with the often suggested step-wise mutation model whereby new alleles of a STR-locus descend from the ancestral allele by deletions or expansions of one repeat unit. Across the regions, the most frequent allele differs for virtually all loci. For example, for DYS19 allele 13 is most frequent among the Inuit (77.5%) whereas allele 16 is most frequent among the Samoans (80%). Allele 14 is predominantly a Caucasian allele with high frequencies among Europeans (49.9%) and Indians (35.4%). Allele 15 is the most frequent allele in all remaining populations. Similar trends can be observed for the other Y-STR loci.

DYS392 clearly shows a bimodal allele frequency distribution. In all regions allele 12 is less frequent or even absent when compared with the more frequently occurring alleles 11 and 13/14. When analysed per locus, virtually all pairwise regional comparisons of the allele frequency distributions revealed significant differences (results not shown).

Phylogenetic tree construction

Since there were marked differences in allele frequency distributions, Y-STR loci looked promising for the construction of a phylogenetic tree based on Y-STRs. Based on the regional allele frequencies, three genetic distance measures were calculated: Nei's standard genetic distance Ds [21], Cavalli-Sforza and Edward's chord distance Dc [22] and a distance specifically developed for microsatellite loci Ddm or $(\delta\mu)^2$ [24]. The three unrooted Neighbour-joining consensus trees resulting from 1000 bootstrapped iterations are shown in Fig. 2. As can be seen, the three trees have some characteristics in common, e.g. the combined NGA + ARC and IND + SEA nodes. However there are also some differences, e.g. the Ddm based tree is the only one with an AFR + AMR node. The Ds and Dc based trees look remarkably similar. The most important shared characteristic of all three trees is the relative short African branch length which is not a common feature in both mtDNA sequence based trees and trees based on autosomal loci [18, 30–32]. Also the separation between Europeans and Indians, and between South-East Asians and North-East Asians contrasts strongly with most of the published human evolutionary trees [18]. This can be due to various reasons, but the most likely one could be recurrent mutations. As a consequence of this, similar Y-chromosome haplotypes can occur in widely separated populations without any direct ancestral connection, but simply due to independently occurring mutation events.

Time-depth of Y-lineages, mutation frequencies

We therefore tried to estimate the time span during which the descent of chromosome Y haplotypes could be reliably estimated, assuming a stepwise mutation model. For this, we used the genetic distance measure Ddm, as proposed by Goldstein et al. [24]. Table 3 shows that, assuming a chromosome Y microsatellite mutation frequency of 0.21% (see below), Ddm remains linear over a period of about 1950 generations, or 49000 years (assuming 25 years for one generation). However, there are marked differences between the various loci: DYS393 expands and decreases in a linear fashion in size during only about 600 generations, whereas DYS19 and DYS390 remain linear over a theoretical period of close to 3200 generations. From this it is clear that Y-STR loci are not suitable for any evolutionary inference dating back more than about

Table 3 Estimates of linearity of Ddm of seven chromosome Y STR's

Locus	Number of Repeats			Ddm Linearity	
	Minimum	Maximum	Range	Generations	Years
DYS19	10	19	9	3175	79000
DYS389-I	7	13	6	1389	35000
DYS389-II	23	31	8	2500	62000
DYS390	5	14	9	3175	79000
DYS391	8	13	5	952	24000
DYS392	9	16	7	1905	48000
DYS393	11	15	4	595	15000
Average				1956	49000

40000 to 50000 years ago. Hence, most likely, the positioning of the Africans in the phylogenetic trees (Fig. 2). These results contrast sharply with those based on autosomal STRs which in theory remain linear over 500000–600000 years [24]. This could be entirely due to a markedly different Y-STR mutation rate when compared with autosomal STRs. Goldstein et al. [24] assumed an autosomal STR mutation frequency of 0.015%. We used a mutation frequency of 0.21% for our Y-STRs, which is 14 times faster. This estimate was based on two independently performed studies. Kayser et al. [15] estimated, for DYS19 only, a mutation frequency of 0.32% by comparing 626 father-son pairs. Heyer et al. [33] used deep-rooting paternal pedigrees and found a most conservative mutation frequency, based on nine Y-STRs, of 0.21%. However, less conservative estimates could be as high as 0.46%. Restricting their analyses to only tetranucleotide repeats, Heyer et al. [33] derived a conservative mutation frequency of 0.20%. In addition, no relation between the chromosome Y-STR mutation frequency, the number of repeats, and the complexity of the entire repeat block could be detected. It thus seems justified to use their conservative estimate of 0.21% as the average chromosome Y microsatellite mutation frequency until other studies have proven otherwise. As a consequence of this, populations will share much more Y-haplotypes due to mutation processes than autosomal-STR-based haplotypes.

Comparing closely related populations

Another appealing application of Y-STRs was suggested to be the comparison of closely related populations which can not be separated otherwise [12]. In order to confirm these results, we therefore collected full haplotype data from males from four distinct European male groups: Dutch, Germans, Swiss and Italian males. Tables 4–6 show the results of all statistical comparisons between these four closely related groups of males. Among the total number of 322 males, 211 different 7-locus Y-STR haplotypes were observed (Table 4). For all four populations the haplotype diversity was close to 99% indicating

Table 4 General chromosome Y halotype characteristics in four European populations

	Populations			
	Dutch	German	Swiss	Italian
Number of individuals	88	70	64	100
Number of haplotypes	65	63	51	82
Haplotype diversity	0.983	0.996	0.992	0.994

Table 5 Halotype sharing information

	Dutch	German	Swiss	Italian
	(number of haplotypes shared)			
Dutch	–	12	14	7
German	0.0088	–	12	9
Swiss	0.0096	0.0042	–	8
Italian	0.0048	0.0031	0.0056	–
	(probability of identity)			

Table 6 Results of AMOVA analyses

	Dutch	German	Swiss	Italian
	(significance of Φ st)			
Dutch	–	< 0.0001	0.1768	0.0080
German	0.0812	–	0.0050	< 0.0001
Swiss	0.0070	0.0404	–	0.1259
Italian	0.0236	0.0468	0.0084	–
	(Φ st)			

that most haplotypes were only found in a single male. As shown in Table 5, most shared haplotypes (n = 14) were found between Swiss and Dutch males, closely followed by 12 haplotypes shared between Dutch/German and German/Swiss males. This relative low degree of haplotype sharing is also reflected by the low probability of identity between the populations. To further support this, we estimated the distance Φst, reflecting the between-population genetic variability, by means of AMOVA analyses. On average 3.5% of the total genetic variability between the four population samples was due to variability between populations, with the highest variability (8.12%) between Dutch and German males and virtually no variability between Dutch/Swiss (0.7%) or Italian/Swiss (0.84%) males. Nevertheless, despite these low levels of between- population genetic variability, only two of the six pairwise comparisons (Dutch/Swiss and Swiss/Italian) were not significant, indicating that the Y-chromosomes occurring in these populations are rather similar (Table 6). Thus, based on Y-STR haplotypes, closely related populations can be separated at a significant level. This confirms our previously published results [12] and that of others [13].

From the above, we can conclude that Y-STR loci are extremely useful for the purpose of comparing closely related populations which have diverged during the past

40000–50000 years. This observation is supported by two independent mutation frequency estimates of about 0.21 and 0.32% for Y-STR loci, which is rather high when compared with the mutation frequency estimate of 0.015% for autosomal STRs. As a consequence of this, populations which have diverged long ago, share Y-haplotypes just by recurrent mutation processes and not by descent.

For forensic purposes e.g. disputed paternities and rape cases this will, most likely, cause no problems since Y-chromosome haplotypes will still remain fairly stable during a large enough number of generations. Exclusions, based on Y-STR haplotypes only, can be found and reported with a high degree of accuracy. However, also because of this, non-exclusions cannot be supported by any statistical calculation since even distantly related individuals, as long as they are paternally connected, will reveal identical haplotypes.

As has been described in detail by Jobling et al. [16] and Jobling and Tyler-Smith [6], the evolutionary application of Y-STRs alone will probably not lead to a reliable phylogenetic tree connecting present-day living human populations. For this purpose, they have to be combined with the more stable base-pair-substitution-based haplotypes.

References

1. Weber JL (1990) Informativeness of human (dC-dA)n.(dG-dT)n polymorphisms. Genomics 7:524–530
2. Di Rienzo A, Peterson AC, Garza JC, Valdes AM, Slatkin M, Freimer NB (1994) Mutational processes of simple-sequence repeat loci in human populations. Proc Natl Acad Sci USA 91: 3166–3170
3. Bowcock AM, Ruiz-Linares A, Tomfohrde J, Minch E, Kidd JR, Cavalli-Sforza LL (1994) High resolution of human evolutionary trees with polymorphic microsatellites. Nature 368:455–457
4. Jorde LB, Bamshad MJ, Watkins WS, Zenger R, Fraley AE, Krakowiak PA, Carpenter KD, Soodyall H, Jenkins T, Rogers AR (1995) Origins and affinities of modern humans: a comparison of mitochondrial and nuclear genetic data. Am J Hum Genet 57:523–538
5. Underhill PA, Jin L, Zemans R, Oefner PJ, Cavalli-Sforza LL (1996) A pre-Columbian Y chromosome-specific transition and its implications for human evolutionary history. Proc Natl Acad Sci USA 93:196–200
6. Jobling MA, Tyler-Smith C (1995) Father and sons – the Y chromosome and human evolution. Trends Genet 11:449–456
7. Dorit RL, Akashi H, Gilbert W (1995) Absence of polymorphism at the ZFY locus on the human Y chromosome. Science 268:1183–1185
8. Hammer MF (1995) A recent common ancestry for human Y chromosomes. Nature 378:376–378
9. Whitfield LS, Sulston JE, Goodfellow PN (1995) Sequence variation of the human Y chromosome. Nature 378:379–380
10. Mathias N, Bayes M, Tyler-Smith C (1994) Highly informative compound haplotypes for the human Y chromosome. Hum Mol Genet 3:115–123
11. Roewer L, Arnemann J, Spurr NK, Grzeschik K-H, Epplen JT (1992) Simple repeat sequences on the human Y chromosome are equally polymorphic as their autosomal counterparts. Hum Genet 89:389–394
12. Roewer L, Kayser M, Dieltjes P, Nagy M, Bakker E, Krawczak M, de Knijff P (1996) Analysis of molecular variance (AMOVA) of Y-chromosome-specific microsatellites in two closely related human populations. Hum Mol Genet 5:1029–1033
13. Cooper G, Amos W, Hoffman D, Rubinsztein DC (1996) Network analysis of human Y microsatellite haplotypes. Hum Mol Genet 5:1759–1766
14. Jobling MA, Samara V, Pandya A, Fretwell N, Bernasconi B, Mitchell RJ, Gerelsaikhan T, Dashnyam B, Sajantila A, Salo PJ, Nakahori Y, Disteche CM, Thangaraj K, Singh L, Crawford MH, Tyler-Smith C (1996) Recurrent duplication and deletion polymorphisms on the long arm of the Y chromosome in normal males. Hum Mol Genet 5:1767–1775
15. Kayser M, Caglià A, Corach D, Fretwell N, Gehrig C, Graziosi G, Heidorn F, Herrmann S, Herzog B, Hidding M, Honda K, Jobling M, Krawczak M, Leim K, Meyer E, Oesterreich W, Pandya A, Parson W, Piccinini A, Perez-Lezaun A, Prinz M, Schmitt C (1997) Evaluation of Y chromosomal STRs: a multicenter study. Int J Legal Med 110 : 125–133
16. Jobling M, Pandya A, Tyler-Smith C (1997) The Y chromosome in forensic analysis and paternity testing. Int J Legal Med 110 : 118–124
17. Santos FR, Gerelsaikhan T, Munkhtuja B, Oyunsuren T, Epplen J, Pena SDJ (1996) Geographic differences in the allele frequencies of the human Y-linked tetranucleotide polymorphism DYS19. Hum Genet 97:309–313
18. Cavalli-Sforza LL, Menozzi P, Piazza A (1994) The history and geography of human genes. Princeton University Press, Princeton NJ
19. DNA Commission of the ISFH (1994) Report concerning further recommendations of the DNA Commission of the ISFH regarding PCR-based polymorphisms in STR (short tandem repeats). Int J Legal Med 107:159–160
20. Reynolds J, Weir BS, Cockerham CC (1983) Estimation of the coancestry coefficient: basis for short term genetic distance. Genetics 105:767–779
21. Nei M (1972) Genetic distance between populations. Amer Nat 106:283–291
22. Cavalli-Sforza LL, Edwards AWF (1967) Phylogenetic analysis: models and estimation procedures. Am J Hum Genet 19: 233–257
23. Shriver MD, Jin L, Boerwinkle E, Deka R, Ferrel RE, Chakraborty R (1995) A novel measure of genetic distance for highly polymorphic tandem repeat loci. Mol Biol Evol 12:914–920
24. Goldstein DB, Ruiz Linares A, Cavalli-Sforza LL, Feldman MW (1995) Genetic absolute dating based on microsatellites and the origin of modern humans. Proc Natl Acad Sci USA 92: 6723–6727
25. Takezaki N, Nei M (1996) Genetic distances and reconstruction of phylogenetic trees from microsatellite DNA. Genetics 144:389–399
26. Saitou N, Nei M (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol 4: 406–425
27. Felsenstein J (1989) Phylip-phylogeny inference package (version 3.2). Cladistics 5:164–166
28. Michalakis Y, Excoffier L (1996) A generic estimation of population subdivision using distances between alleles with special reference for microsatellite loci. Genetics 142:1061–1064
29. Melton T, Peterson R, Redd AJ, Saha N, Sofro ASM, Martinson J, Stoneking M (1995) Polynesian genetic affinities with Southeast Asian populations as identified by mtDNA analysis. Am J Hum Genet 57:403–414
30. Vigilant L, Stoneking M, Harpending H, Hawkes K, Wilson AC (1991) African populations and the evolution of human mitochondrial DNA. Science 253:1503–1507
31. Jorde LB, Bamshad MJ, Watkins WS, Zenger R, Fraley AE, Krakowiak PA, Carpenter KD, Soodyall H, Jenkins T, Rogers AR (1995) Origins and affinities of modern humans: a comparison of mitochondrial and nuclear genetic data. Am J Hum Genet 57:523–538
32. Pérez-Lezaun A, Calafell F, Mateu E, Comas D, Ruiz-Pacheco R, Bertranpetit J (1997) Microsatellite variation and the differentiation of modern humans. Hum Genet 99:1–7
33. Heyer E, Puymirat J, Dieltjes P, Bakker E, de Knijff P (1997) Estimating Y-chromosome-specific microsatellite mutation frequencies using deep rooting pedigrees. Hum Mol Genet 6 (in press)