Human mtDNA and Y-chromosome variation is correlated with matrilocal versus patrilocal residence

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Genetic differences among human populations are usually larger for the Y chromosome than for mtDNA[1–3]. One possible explanation is the higher rate of female versus male migration due to the widespread phenomenon of patrilocality, in which the woman moves to her mate's residence after marriage. To test this hypothesis, we compare mtDNA and Y-chromosome variation in three matrilocal (in which the man moves to his mate's residence after marriage) and three patrilocal groups among the hill tribes of northern Thailand. Genetic diversity in these groups shows a striking correlation with residence pattern, supporting the role of sex-specific migration in influencing human genetic variation.

Patrilocality, in which men stay in their birthplace and women move, occurs in about 70% of human societies[4]. Patrilocality has been invoked to explain the usual patterns observed in human populations: high mtDNA and low Y-chromosome diversity within groups, large between-group differences for the Y chromosome, and small between-group differences for mtDNA. If patrilocality is responsible for these patterns, then matrilocal groups (in which the women stay in their birthplace and the men move) might show the opposite patterns: high Y-chromosome and low mtDNA diversity within groups, large between-group differences for mtDNA, and small between-group differences for the Y chromosome. Here we compare Y-chromosome and mtDNA diversity in three matrilocal groups (Lahu, Red Karen and White Karen; the two Karen groups were sampled from multiple villages that were 5–25 km apart) and three patrilocal groups (Akha and two groups of Lisu, one sampled near Chiang Rai and one sampled about 220 km away, near Mae Hong Son) from northern Thailand.

We obtained blood samples between 1996 and 1998, with informed consent. From these we prepared transformed cell lines from which we subsequently extracted DNA[5]. We analyzed 360 bp of the first hypervariable segment (HV1) of the mtDNA control region, corresponding to positions 16024–16383 (ref. 6), using standard methods (Oota, unpublished data). To assess Y-chromosome variation, we carried out multiplex typing of nine short tandem repeat (STR) loci (*DYS385a/b*, *DYS389I*, *DYS389II*, *DYS390*, *DYS391*, *DYS392*, *DYS393* and *DYS394*) as previously described (http://www.ystr.org/usa). The HV1 sequences have been submitted to the HVRbase database[7] and are also available from the authors, as are the Y-STR haplotypes. We estimated haplotype diversity within groups[8] for the HV1 sequences and the Y-STR haplotypes, and calculated the genetic distances between groups based on d_A values[8] for the HV1 sequences and R_{st} values[9] for the Y-STR haplotypes.

The haplotype diversity for mtDNA was higher in all of the patrilocal groups than in any of the matrilocal groups (Fig. 1). The mean mtDNA diversity in the patrilocal groups was 0.937, which is significantly greater than the mean mtDNA diversity of 0.860 in the matrilocal groups (Mann-Whitney U-test, $P<0.05$). Conversely, the Y-STR haplotype diversity was higher in all of the matrilocal groups than in any of the patrilocal groups (Fig. 1). The mean Y-STR diversity was 0.965 in the matrilocal groups, significantly greater than the mean Y-STR diversity of 0.863 in the patrilocal groups (Mann-Whitney U-test, $P<0.05$). In addition, the average genetic distance based on mtDNA HV1 sequences was significantly higher among the matrilocal groups than among the patrilocal groups, while the average genetic distance based on Y-STR haplotypes was significantly higher among the patrilocal groups than among the matrilocal groups (Table 1).

Genetic variation in the north Thailand hill tribes thus shows a striking correlation with residence pattern. Matrilocal groups have high within-group diversity for the Y chromosome and large between-group distances for mtDNA, whereas patrilocal groups have high within-group diversity for mtDNA and large between-group distances for the Y chromosome. All of the groups studied come from the same geographic region, speak related Sino-Tibetan lan-

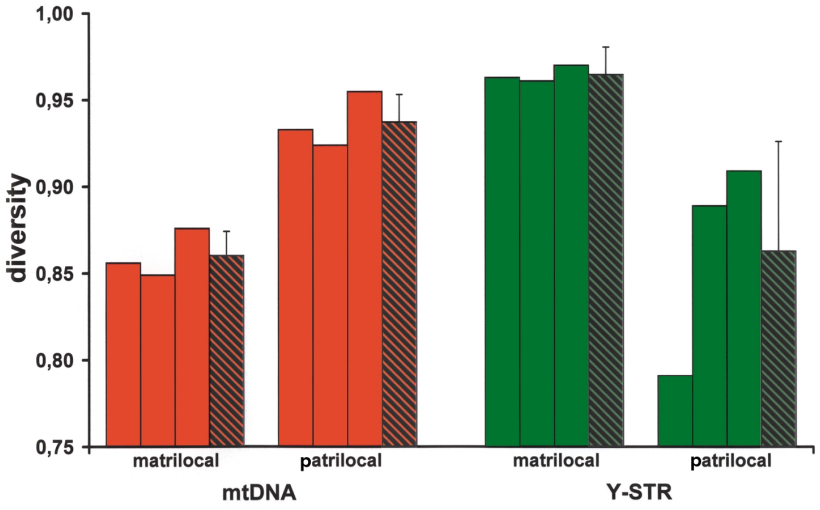

Fig. 1 Diversity in mtDNA (red) and Y-STR (green) haplotypes in three matrilocal and three patrilocal groups from northern Thailand. From left to right, the matrilocal groups (mtDNA sample size, Y-STR sample size) are Lahu (39, 17), Red Karen (39, 30), and White Karen (40, 20); the patrilocal groups are Akha (91, 21), Lisu from near Chiang Rai (53, 9), and Lisu from near Mae Hong Son (42, 22). The fourth (shaded) bar in each group indicates the mean diversity (and standard error) for the group.

Table 1 • Average genetic distances and standard errors based on mtDNA HV1 sequences and Y-STR haplotypes among matrilocal and patrilocal groups

	d_A (×100) mtDNA	R_{st} Y-STR
Matrilocal	0.290 ± 0.086	0.131 ± 0.006
Patrilocal	0.118 ± 0.028	0.451 ± 0.007

Genetic distances (d_A and R_{st}) and standard errors (based on 1,000 bootstrap replicates) were calculated using SENDBS (http//www.cib.nig.ac.jp/dda/ntakezak.html#sendbs) for the mtDNA sequences and RSTCALC (http://helios.bto.ed.ac.uk/evolgen/rst/rst.html) for the Y-STR haplotypes. The genetic distances are significantly different between matrilocal and patrilocal groups for both the mtDNA ($P=0.03$) and the Y-STR ($P<0.001$) comparisons, with P values based on the overlap in the distributions of the bootstrap replicates.

guages and practice similar subsistence modes of agriculture. These shared attributes make it unlikely that the correlation is accounted for by some other factor that differs between the matrilocal and patrilocal groups, such as reproductive success. Moreover, although our results do not rule out a role for variance in male reproductive success in influencing patterns of genetic variation, theoretical considerations suggest at best a minor effect of such variance[1]. We conclude that patrilocality does appear to be primarily responsible for the higher between-population genetic differences consistently observed for the Y chromosome as opposed to mtDNA or autosomal loci. Our results also provide evidence for the importance of social structure in influencing human genetic diversity[10–12].

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