

Women on the move

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When I was a student, anthropology was a largely male-dominated discipline and the role of females was given short shrift. We learned all about 'Man the Hunter'—although an emphasis on 'Woman the Gatherer' would more accurately indicate who really brings home the bacon in most traditional hunting-gathering societies¹—and about alpha males in non-human primates, although females also have a say in who fathers their offspring². Even the titles of the books we read, such as *Mankind Evolving*, *Mankind in the Making*, *Men of the Earth* and *The Ascent of Man*, emphasize the male sex, a trend which has not completely disappeared³, more's the pity.

Our view of migrations in human history is similarly male-dominated; an image that often comes to mind is that of the intrepid explorer leading the way into the unknown, or the conquering hero subjugating the denizens of distant lands (think Marco Polo, Alexander the Great, Genghis Khan or Attila the Hun and you get the idea). A comparison of genetic data by Mark Seielstad and colleagues on page 278 (ref. 4), however, suggests that, as in other spheres, the role of males in migration has been greatly exaggerated; when it comes to exchanging genes among populations, women's movements have been much more important than prevailing 'wisdom' might suggest.

What is the genetic evidence that Seielstad and colleagues marshal in support of this contention? First, a comparison of published data on variation in the maternally inherited mitochondrial DNA (mtDNA), the paternally-inherited Y chromosome and biparentally inherited autosomal loci indicates that differences between populations are much bigger for the Y chromosome than for mtDNA or autosomal loci. The usual measure of population differentiation, F_{ST} , is about 19% for mtDNA, 14% for autosomal loci, and a whopping 64% for the Y chromosome. For those not familiar with the concept of F_{ST} , one way of thinking about these numbers is that if we were to take a sample of popula-

tions from around the world and measure the total genetic variance, and then take just one population from anywhere in the world, on average that one population would have about 81% of the total variance for mtDNA and 86% of the total variance for autosomal loci, but only 36% of the total variance for the Y chromosome. Mito-

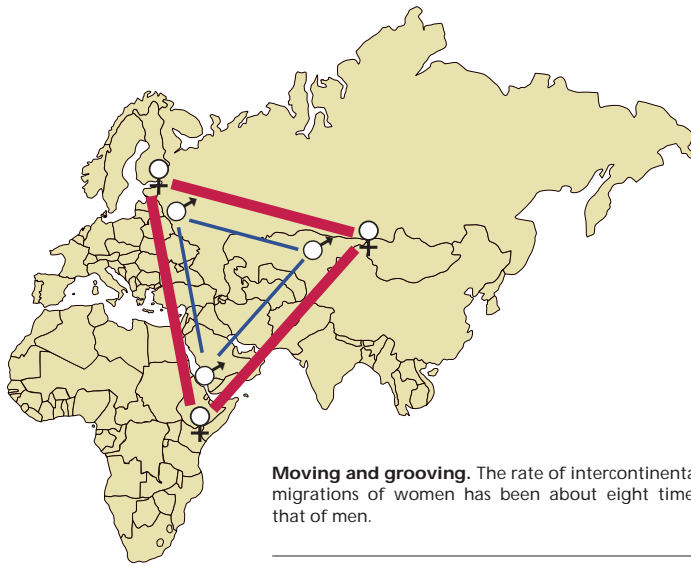
chondrial DNA genetic distances, in remarkably good agreement with the estimated migration rates from the F_{ST} analysis.

Those in the know will find much in the details of these analyses to quibble about. The mtDNA, autosomal loci and Y chromosome studies that were used for the worldwide F_{ST} analysis vary considerably in terms of sample sizes, populations represented and method used to assay genetic variation, which makes a strict comparison of F_{ST} values problematic⁵. For example, the mtDNA data⁶ come from Europe, West Africa, Israel, Asia and North America (two populations from each region), with an average of 67.2 individuals per population, while the Y chromosome data come from 54 populations from Africa, Oceania, Asia, East Asia, Central Asia, India and Pakistan, Europe and the Americas, with an average of just 13.3

males per population⁷. It is not clear which populations were used for the autosomal loci analysis, as the source cited for the F_{ST} values summarizes results from several studies⁸, and the F_{ST} values quoted by Seielstad and colleagues do not appear therein. Moreover, there can be considerable variation among F_{ST} values for a particular class of loci; for example, worldwide F_{ST} estimates based on mtDNA vary from 0.01 to 0.13, depending on which populations are sampled and whether mtDNA variation is assayed by RFLP or sequencing methodologies⁵. The other analyses carried out by Seielstad and colleagues are restricted to particular geographic regions (Africa or Europe) and hence may not be representative of the world, and with respect to the analysis of geographic *versus* genetic distance in Europe there is again the problem of different types of molecular data from different populations. In other words, the authors may be comparing apples and oranges.

What is sorely needed to address this issue is an extensive and intensive survey of mtDNA, Y-chromosome and autosomal variation in the same populations,

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Moving and grooving. The rate of intercontinental migrations of women has been about eight times that of men.

tion rate generally thought that patrilocality was a ready explanation: women move much more frequently between groups than do men, leading to greater between-population differences for the Y chromosome. Those who were surprised wondered if patrilocality, which operates on a local scale, could explain the continental or even global patterns observed by Seielstad and colleagues; such long-distance migrations are still considered to be the male's domain. But the media-savvy Genghis Khans and Attila the Huns of this world may be a relatively recent phenomenon of the past few thousand years or so, and distract from the underlying message of Seielstad's study: if we really want to understand human migrations, we must pay more attention to women's ways. □

sampled comprehensively from around the world (the astute reader will recognize this as a plug for the moribund Human Genome Diversity Project). Nevertheless, these are details, and while the magnitude of the difference between male and female migration rates might shift with further study, the authors have probably got it right in concluding that there is indeed a higher rate of female migration; this conclusion is presaged by previous observations of a greater geographic specificity of Y chromosome polymorphisms compared with mtDNA or autosomal loci^{9–12}.

Is it surprising that the female migration rate is higher than that for males? In order to address this question as scientifi-

cally as possible, I undertook an informal poll of my anthropological colleagues: half said yes, half said no. While various reasons were given for being surprised or not, all of those questioned pointed to the well-known phenomenon of patrilocality in human populations. That is, when males seek a mate, they frequently venture beyond their village, obtain one or more women (by arrangement, trade or force), and bring them back to reside in the male's village. While there are the inevitable exceptions, the majority of human societies around the world practice some form of patrilocality, and this is especially true of hunting-gathering societies¹³. Those of my colleagues who were not surprised by a higher female migra-

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Life, death and nuclear spots

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In addition to nucleoli, eukaryotic nuclei contain a number of subnuclear structures which have a speckled distribution. These include sites of DNA replication, RNA synthesis, spliceosomes, coiled bodies and nuclear bodies^{1,2}. Nuclear bodies, also known as PML-oncogenic domains (PODs), are enigmatic structures identified by immunostaining with antisera from patients with primary biliary cirrhosis, an autoimmune disease which results in the

destruction of bile ducts^{3,4}. Subsequent immunofluorescent studies showed that PML, encoded by a gene mutated in acute promyelocytic leukaemia (APL), localizes to these nuclear spots. Despite a flurry of papers devoted to PML and the identification of nearly 20 POD-associated proteins, the precise role of PODs remains murky. Two studies in this issue^{5,6} go some way to slicing through the murk by providing compelling evidence that PML plays a cen-

tral role in the regulation of programmed cell death (apoptosis).

PML, the eponymous member of the POD, decorates the periphery of the nuclear bodies. In contrast, the PML-RAR α oncoprotein, which results from the aberrant juxtaposition of *PML* and *RARA* in patients with APL, is delocalized from PODs along with PML into smaller microparticulate structures (known as 'microspeckles'; refs 7,8). Disruption of