Can Indirect Tests Detect a Known Recombination Event in Human mtDNA?

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Whether human mitochondrial DNA (mtDNA) recombines sufficiently to influence its evolution, evolutionary analysis, and disease etiology, remains equivocal. Overall, evidence from indirect studies of population genetic data suggests that recombination is not occurring at detectable levels. This may be explained by no, or low, recombination or, alternatively, current indirect tests may be incapable of detecting recombination in human mtDNA. To investigate the latter, we have tested whether six well-established indirect tests of recombination could detect recombination in a human mtDNA data set, in which its occurrence had been empirically confirmed. Three showed statistical evidence for recombination (\( r^2 \) vs. distance, the Homoplasy test, Neighborhood Similarity Score), and three did not (\( D^2 \) vs. distance, Max Chi Squared, Pairwise Homoplasy Index). Possible reasons for detection failure are discussed. Further, evidence from earlier studies suggesting a lack of recombination in mtDNA in humans is reconsidered, taking into account the appropriateness of the tests used, based on our new findings.

The power of many of these tests has been assessed previously using sequence data, simulated under various parameters chosen for the purpose of the study (Posada and Crandall 2001). However, mtDNA evolves under a unique set of parameters, and it remains unclear how effective the available indirect tests are at detecting recombination in mitochondrial sequence. For example, mtDNA is circular and its mutation rate heterogeneously distributed across the genome (Yang 1996), both of which may strongly influence correlation measures of detecting recombination in mtDNA (Wiuf et al. 2001). In addition, when compared with nuclear DNA, mtDNA mutation rates are higher (Ingman et al. 2000; Mishmar et al. 2003) and can be correlated (Nielsen 1997). Further, relative to animals, human mtDNA sequence diversity is low (Jorde et al. 1998). Thus, it is entirely possible that even if recombination in mtDNA occurs naturally in humans, indirect tests currently available will be unable to detect it.

In the only empirically confirmed occurrence of mtDNA recombination in humans, Kraysberg et al. (2004) recovered 33 recombinant maternal molecules from 450 single-molecule polymerase chain reaction clones, derived from the muscle tissue of an individual known to possess a 10:1 excess of paternal-to-maternal mtDNA. The availability of these sequence data has enabled us, for the first time, to assess empirically the effectiveness of indirect tests at detecting recombination in human mtDNA. The recombination tests were selected for evaluation based on previous inclusion in both successful, and unsuccessful, studies of recombination detection. They include three population based tests; the correlation between physical distance and linkage disequilibrium (LD) using both the \( D^2 \) and \( r^2 \) measures of LD (Awadalla et al. 1999) and the Homoplasy test (Smith and Smith 1998). Three general methods were also assessed: Max Chi Squared (Smith 1992), Neighborhood Similarity Score (NSS, Jakobsen and Easteal 1996), and the more recently developed Pairwise Homoplasy Index (PHI, Bruen et al. 2006).

Of these six tests of recombination, three were not able to detect recombination when we know it happened: the Max Chi Squared, PHI, and LD using \( D^2 \) tests. Results from our correlations between LD and physical distance were mixed however as LD versus \( r^2 \) did show a significant negative correlation, indicative of recombination. Recombination was also detected by the NSS and Homoplasy tests. As

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these results come from one sample, it is possible they are not the most statistically probable, assuming $P$ values for each test are normally distributed for this type of data set but rather represent less likely outcomes due to sampling (Innan and Nordborg 2002). To control for this, all six data sets were reevaluated using 100 samples of simulated sequence, generated using parameters that re-created the level of recombination and sequence length seen in the real sequences. From these simulations, the success of the Homoplasy, NSS, and LD versus distance using $r^2$ tests is confirmed, as is the poorer performance of the Max Chi Squared and LD versus distance using $D'$ (table 1). The PHI test shows the greatest divergence in recombination detection ability between the real and simulated data and appears to detect recombination events routinely when applied to the simulated data. This divergence in recombination detection is potentially an artifact of the higher diversity seen in the simulated sequence (average nucleotide diversity, $\pi$, over 10 randomly selected simulated samples $= 2.80 \times 10^{-3}$, compared with $1.25 \times 10^{-3}$ in the Kraytsberg data set), Table 1 summarizes our findings.

The failure of the Max Chi Squared method to detect recombination is initially surprising, as this method was previously found to be a reliable and powerful method for detecting recombination, both in simulated sequences (Posada and Crandall 2001) and real sequences in which recombination had been inferred (Posada 2002). However, a more recent survey shows this test is susceptible to generating false positives when mutation rates are auto-correlated or nonuniformly distributed across the genome (Bruen et al. 2006), and performs less well under a scenario of population growth (Wiuf et al. 2001), factors that might preclude Max Chi Squared from being effective at detecting recombination in human mtDNA data (Cohen 1995; Yang 1995). Similarly, the PHI test has recently been shown to be a powerful test, even with population growth, generating few false positives (Bruen et al. 2006). Thus, its failure to detect recombination in the Kraytsberg data set is also, at first glance, a surprise. However, the prior evaluation of the PHI test’s performance (Bruen et al. 2006), and indeed that of the Max Chi Squared test (Posada and Crandall 2001; Wiuf et al. 2001), focused on simulated, non-mtDNA sequence. Thus, just as a consequence of mtDNA’s unique properties, for example, high auto-correlated mutation rates (Yang 1995; Nielsen 1997), among-site heterogeneity in mutation rates (Yang 1996) and a complicated relationship between physical and genetic distance due to its circular nature (Wiuf 2001), the findings from our study are likely to be different to those previously published. In particular, the low, presumably more realistic (Ingman et al. 2000) nucleotide diversity of the Kraytsberg data set, $\pi = 1.25 \times 10^{-3}$, in comparison with those used in earlier simulation studies, may preclude efficient detection of recombination with these methods. Both methods have been shown to perform less well with low sequence divergence (Posada and Crandall 2001; Wiuf et al. 2001; Bruen et al. 2006), and the Kraytsberg $\pi$ is lower again than the least divergent simulated sequences used in these studies. The Kraytsberg nucleotide divergence at $1.25 \times 10^{-3}$ substitutions per site per generation is, however, within the range of values predicted for human populations ($6.0 \times 10^{-5}$ to $6.8 \times 10^{-3}$, Ingman et al. 2000). Taken together, these findings suggest the diversity of the Kraytsberg data set, and perhaps human mtDNA in general, may be too low for PHI and Max Chi Squared to work effectively.

The failure of the $D'$ method to detect recombination is less surprising, as it is has been shown to be less powerful than $r^2$ at detecting recombination under the finite sites model (McVean et al. 2002), a model that describes well the distribution of polymorphisms at synonymous sites in human mtDNA (Piganeau and Eyre-Walker 2004). As such, the $r^2$ measure has previously been recommended for recombination detection in human mtDNA, using synonymous sites (Piganeau and Eyre-Walker 2004). Our result strongly supports this recommendation.

Recombination in human mtDNA could have substantial impact on mitochondrial disease etiology, transmission, and inheritance. Further, if unaccounted for, mitochondrial recombination may lead to inaccurate inferences drawn from evolutionary analysis (Schierup and Hein 2000a, 2000b; Posada and Crandall 2002). Although there now exists compelling indirect evidence of widespread recombination in animals (Piganeau et al. 2004; Tsoussis et al. 2005), perhaps as a result of greater diversity in animal mtDNA and older mtDNA lineages leading to more opportunities for recombination to occur (Jorde et al. 1998), for humans results thus far are equivocal (table 2).

Results provided here suggest one reason for the apparent lack of indirect evidence of recombination in human mtDNA may derive from an inability of many of the contemporary tests being used to detect naturally occurring recombination in human mtDNA. If we were to revise results of previous indirect studies, based on our findings, the landscape of evidence for recombination in human mtDNA alters. In table 2, we summarize the majority of studies thus far of human mtDNA recombination, using indirect statistical approaches. If we ignore the negative findings from tests that we have shown to be unable to detect recombination in the Kraytsberg mtDNA sequence data, in cases where recombination was detected by another method, the proportion of positive results changes from 20.3% to 23.5%. If we remove these test results from all studies, the proportion of data sets that give a positive result increases from 20.3% to 31.6%. Further development of these
A Summary of Indirect Studies of Recombination Detection in Human mtDNA

<table>
<thead>
<tr>
<th>Study</th>
<th>Data Set</th>
<th>Test/s Used</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Awadalla et al. (1999)</td>
<td>45 mtDNA sequences, global</td>
<td>$D^2$</td>
<td>0.012</td>
</tr>
<tr>
<td>Eye-Walker et al. (1999)</td>
<td>29 mtDNA seqs, global</td>
<td>$H^*$</td>
<td>0 (effectively)</td>
</tr>
<tr>
<td>Ingman et al. (2000)</td>
<td>53 mtDNA seqs from 14 of the major linguistic phyla</td>
<td>$D^4$, $r^2$</td>
<td>ns, ns</td>
</tr>
<tr>
<td>Jorde and Bamshad (2000)</td>
<td>Awadalla data sets plus four</td>
<td>$D^4$, $r^2$</td>
<td>ns</td>
</tr>
<tr>
<td></td>
<td>European data sets</td>
<td></td>
<td>2/8 data sets significant (&lt;0.03 and &lt;0.02)*</td>
</tr>
<tr>
<td>Kumar et al. (2000)</td>
<td>Awadalla data sets</td>
<td>$D^4$, $FET$</td>
<td>ns, ns</td>
</tr>
<tr>
<td>Elson et al. (2001)</td>
<td>64 British mtDNAs and two Africans</td>
<td>$D^4$, $r^2$, $d$</td>
<td>ns, ns</td>
</tr>
<tr>
<td>Herrnstadt et al. (2002)</td>
<td>56 African</td>
<td>$r^2$, $d$</td>
<td>ns, ns</td>
</tr>
<tr>
<td></td>
<td>69 Asian</td>
<td>$r^2$, $d$</td>
<td>sig, sig</td>
</tr>
<tr>
<td></td>
<td>435 European</td>
<td>$r^2$, $d$</td>
<td>ns, ns</td>
</tr>
<tr>
<td></td>
<td>226 Haplogroup H</td>
<td>$r^2$, $d$</td>
<td>ns, ns</td>
</tr>
<tr>
<td>Piganeau and Eyre-Walker (2004)</td>
<td>Awadalla data set</td>
<td>$r^2$, $D^4$, $H$, $GC$, $MS$</td>
<td>ns, ns, 0.0001 ns, ns</td>
</tr>
<tr>
<td></td>
<td>Ingman data set</td>
<td>$r^2$, $D^4$, $H$, $GC$, $MS$</td>
<td>ns, ns, 0.0052 ns, ns</td>
</tr>
<tr>
<td></td>
<td>192 Finnish seqs*</td>
<td>$r^2$, $D^4$, $H$, $GC$, $MS$</td>
<td>&lt;0.05 ns, ns, ns</td>
</tr>
<tr>
<td></td>
<td>Herrnstadt African</td>
<td>$r^2$, $D^4$, $H$, $GC$, $MS$</td>
<td>&lt;0.05 ns, 0.04 ns, ns</td>
</tr>
<tr>
<td></td>
<td>Herrnstadt Asian</td>
<td>$r^2$, $D^4$, $H$, $GC$, $MS$</td>
<td>ns, 0.01 ns, ns</td>
</tr>
<tr>
<td></td>
<td>Herrnstadt European</td>
<td>$r^2$, $D^4$, $H$, $GC$, $MS$</td>
<td>na, na, 0.0001 ns, ns</td>
</tr>
</tbody>
</table>

Global refers to globally distributed.

$*$ Both data sets from Awadalla et al. (1999).

$^a$ These results are for polymorphisms in their data set with no minimum minor allele frequency cutoff.

$^b$ From Finnila et al. (2001).

Tests may be required for optimization in mtDNA, but for now, we have highlighted some tests of choice. Although NSS detected recombination here, it has been suggested that precaution be taken when using this test to detect recombination in mtDNA, especially in divergent sequences, due to an increase in false positive generation as a consequence of substitution rate correlation (Bruen et al. 1999), with the level of recombination set to the recombination parameter of the Kraytsberg data set (rho = 5.492), as estimated in LAMARC (Kuhner 2006), and a mutation rate per site per generation of $5 \times 10^{-7}$.

Indirect Tests of Recombination

Theory predicts that the strength of LD between two alleles should decrease with physical distance in the presence of recombination (Hill and Robertson 1968). Thus, a significant negative correlation between LD and distance could indicate recombination. There are several measures of LD, and two have been used for assessing recombination in mtDNA: $r^2$ (Hill and Robertson 1968) and $D^4$ (Lewontin 1964). Both are assessed here.

The homoplasy test investigates whether more homoplasies (co-occurrence of a polymorphism on separate branches of a phylogenetic tree) occur in the most parsimonious tree, than expected by recurrent mutation under a model of clonal inheritance (Smith and Smith 1998). If an excess of homoplasies is detected, then recombination may be the most likely explanation. The incidence of homoplasy was investigated in the data using the Homoplasy Test, implemented in Linux using a C translation of the original QBASIC version, kindly provided by David Posada (University of Vigo).

The Max Chi Squared method compares the arrangement of segregating sites between two sequences either side of a putative recombination break point, with all other sequences in the alignment (Smith 1992). A sliding window of sequence to analyze was set to the number of polymorphic sites divided by 1.5. Significance was estimated as the proportion of 1,000 permuted test scores, calculated after randomly positioning the informative sites, below the observed test score.

NSS describes the extent of clustering of compatibilities (either compatible or incompatible) of adjacent informative sites in a sequence alignment (Jakobsen and Eastal 1996). Higher NSS values than expected by chance can be explained by recurrent mutation, gene conversion, or recombination. Significance of the observed NSS is achieved by randomly permuting the order of informative sites 1,000 times and determining the fraction of random scores that are at least as high as the observed data.
The PHI measures the mean refined incompatibility score between sites within a window of sequence of preset length and reflects the minimum number of homoplasies on any tree required to describe the genealogical history of a pair of sites (Bruen et al. 2006). If recombination is responsible for homoplasies, PHI scores should be lower than if recurrent mutation is responsible, as recurrent mutation is not correlated with physical distance. An estimate of the statistical significance of the PHI was achieved by randomly permuting site positions in the alignment (simulating no recombination) 1,000 times, and calculating the proportion of times the permuted PHI score is less than or equal to the observed score.

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Literature Cited


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Testing Indirect Detection of mtDNA Recombination 1439