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Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells

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1–41 [Author affiliations appear at end of paper.]

Mitochondrial genomes are separated from the nuclear genome for most of the cell cycle by the nuclear double membrane, intervening cytoplasm, and the mitochondrial double membrane. Despite these physical barriers, we show that somatically acquired mitochondrial-nuclear genome fusion sequences are present in cancer cells. Most occur in conjunction with intra-nuclear genomic rearrangements, and the features of the fusion fragments indicate that nonhomologous end joining and/or replication-dependent DNA double-strand break repair are the dominant mechanisms involved. Remarkably, mitochondrial-nuclear genome fusions occur at a similar rate per base pair of DNA as interchromosomal nuclear rearrangements, indicating the presence of a high frequency of contact between mitochondrial and nuclear DNA in some somatic cells. Transmission of mitochondrial DNA to the nuclear genome occurs in neoplastically transformed cells, but we do not exclude the possibility that some mitochondrial-nuclear DNA fusions observed in cancer occurred years earlier in normal somatic cells.

[Supplemental material is available for this article.]
Although mtDNA nuclear transfer in a HeLa cell line derivative, and thus occurring in vitro, has been reported (Shay et al. 1991), de novo nuclear transfer of mtDNA in animal somatic tissues has not previously been comprehensively studied to our knowledge. To investigate the possibility of somatic mitochondrial-nuclear DNA fusion, we analyzed next-generation paired-end DNA whole-genome sequencing data from 559 primary cancers, 28 cancer cell lines (referred as S87 cancer whole genome below) and normal DNAs from the same individuals (Supplemental Table 1).

Results

Discovery of somatic mtDNA transfers to cancer nuclear genomes

From the 587 pairs of cancer and normal whole-genome sequencing data, we searched for cancer-specific clusters of discordant paired-end sequence reads in which one member of the read-pair mapped to the nuclear genome and the other to the mitochondrial genome, and then characterized the nuclear-mitochondrial genome junctions to nucleotide resolution using individual sequence reads that bridged the junction (Fig. 1A). In 12 samples (overall positive rate 2.0%, 12 out of 587 samples), we observed 25 cancer-specific mitochondrial-nuclear DNA junctions (Table 1; Supplemental Figs. 1–6). Given that there are two junctions for a single integration event, we conclude that there are most likely 16 independent mtDNA insertions (Table 1). In addition to somatic transfers, we observed several novel rare germline (inherited) events that were shared between cancer and paired normal samples (Supplemental Table 2; Supplemental Material).

Breast cancer PD11372a showed a somatically acquired integration of almost the entire human mtDNA sequence (16,556 bp) into a highly amplified 2.75-Mb-long region of Chromosome 10q22.3. The integration event was strongly supported by both discordant and split read clusters (Fig. 1B–D) and was confirmed by short- and long-range PCR across the nuclear-mitochondrial genome junctions (Supplemental Figs. 7, 8; Supplemental Table 3). It was not found in normal tissue (blood) from the same individual or from all the other cases and did not match any known inherited nuclear mtDNA-like sequences (known as numts) (Gherman et al. 2007; Hazkani-Covo et al. 2010). Consistent with its somatic origin, the mtDNA fused to the nuclear genome harbored sequence polymorphisms identical to those present in the mitochondria of this individual (14,905 G > A; 15,028 C > A; 15,043 G > A; 15,326 A > G; 15,452 C > A, and 15,607 A > G). Fluorescence in situ hybridization (FISH) experiments performed on formalin-fixed paraffin embedded tissue confirmed that the fused DNA segment exists in the nuclei of cancer cells (Fig. 1E).

In total, we found 10 primary cancers (1.8%, 10/559) and two cancer cell lines (7.1%, 2/28) with somatic mtDNA integrations into their nuclear genomes (Table 1; Supplemental Figs. 1–6). Of the 12 cancers, two (primary cancer PD13296a and cancer cell line NCI-H2087) had more than one mitochondrial-nuclear DNA translocation event. All integrations were supported by both discordant and split reads and further confirmed by PCR across the nuclear-mitochondrial genome junctions (Supplemental Fig. 7; Supplemental Table 3). All inherited mtDNA substitution polymorphisms near these breakpoints were detected (Table 1). To further visualize the transfer events, we performed high-resolution FISH on stretched DNA fibers (fiber FISH) from the melanoma cell line, CP66-MEL (Fig. 2A).

Somatic nuclear integration of mtDNA is frequently combined with other rearrangements of the nuclear genome

The rate of somatic nuclear transfer of mtDNA may vary according to tumor type. Triple-negative breast cancer showed a fivefold higher frequency compared to estrogen-receptor (ER) positive breast cancers (6.2% and 1.2%, respectively; Fisher’s exact test \( P = 0.002 \)). Triple-negative breast cancer genomes carry a higher number of chromosomal rearrangements than ER-positive breast average (254 and 94, respectively, in our data set). As a result, there was a suggestive positive correlation between the number of chromosomal rearrangements and mtDNA transfers (Mann-Whitney \( U \) test, one-sided \( P = 0.05 \)) (Fig. 2B).

The length of mtDNA fragments transferred ranged from 148 bp to entire mitochondrial genomes (16.5 kb) (Table 1). Interestingly, breakpoints in mtDNA were enriched near the mitochondrial genome heavy strand origin of replication (\( \chi^2 \) test, \( P = 0.0005 \)) (Fig. 2C). This suggests that the generation of mtDNA segments to be integrated into the nuclear genome is not random and may occur in a mtDNA replication-dependent manner (Lenglez et al. 2010).

Of the 25 mitochondrial-nuclear DNA junctions, at least 17 (68.0%) were clearly associated with other nuclear chromosomal rearrangements (e.g., inversions, translocations, and large deletions) in the vicinity (Table 1; Supplemental Figs. 1–6). For example, with respect to PD11372a described earlier, genomic fragments from Chromosomes 10, 11, and mtDNA generated complex derivative chromosomes (Fig. 3A). In PD6047a, an mtDNA fragment was involved in chains of complex genomic translocations involving Chromosomes 6, 7, 11, 22, and X (Fig. 3B). In PD10014a, a local inversion was combined with the mtDNA integration event (Fig. 3C), and in PD4252a, a 16.5-kb mtDNA integration was found in a position on the X Chromosome from which ~20 kb of nuclear DNA had been somatically deleted (Fig. 3D). Thus, mtDNA is often integrated into nuclear genomes in the vicinity of, or as part of, complex rearrangements. Although germline numts tend to occur near transposable elements such as LINEs and SINEs (Mishmar et al. 2004), we do not observe this association for somatic events (\( \chi^2 \) test, two-sided \( P = 0.33 \)) (Supplemental Table 4).

There was overlapping sequence microhomology (from 1 to 4 bp) in 20/25 breakpoints (80%) (Fig. 4A, B; Table 1; Supplemental Figs. 1–6), substantially more than expected by chance (\( \chi^2 \) test, \( P = 5 \times 10^{-25} \)). Thus, DNA sequence microhomology plays an important role in mitochondrial-nuclear DNA integration events, although blunt-end DNA repair was also observed. In two breakpoints, we also found nontemplated short-nucleotide insertions (1 and 4 bp long) (Fig. 4A; Table 1). Overall, these features are characteristic of DNA double-strand break repair by nonhomologous end joining (NHEJ) (Hastings et al. 2009). However, they do not rule out replication-based mechanisms switching template between nuclear and mtDNA, such as microhomology-mediated break-induced replication (MMBR) (Liu et al. 2011).

We investigated the timing of somatic mtDNA integration into the nuclear genome by assessing cases in which a metastatic sample had been sequenced in addition to the primary tumor. One such case (PD4252a) showed the mitochondrial-nuclear integration event in the primary but not in the metastasis (Fig. 4C), indicating that mtDNA transfer to the nucleus can occur after...
neoplastic transformation and during the course of subclonal evolution of the cancer. The other (PD6728b) showed it in both the primary and metastasis (Fig. 4C), suggesting that this event occurred in the common ancestral cancer clone or in normal somatic cells prior to neoplastic change.

Nuclear transfer of mtDNA is unexpectedly frequent in human somatic cells

To obtain a perspective on the frequency of mitochondrial-nuclear DNA translocation, we compared its rate to that of intranuclear
<table>
<thead>
<tr>
<th>Tissue</th>
<th>Sample</th>
<th>Left junction (Nuclear)</th>
<th>Left junction (MT)</th>
<th>Right junction (MT)</th>
<th>Right junction (Nuclear)</th>
<th>Frag. size (bp)</th>
<th>Micro-homology (bp, bp)</th>
<th>Variants (#D/#P)*</th>
<th>Context of rearrangement</th>
</tr>
</thead>
<tbody>
<tr>
<td>Primary</td>
<td>PD11372a</td>
<td>10+:81,670,932</td>
<td>M−:15,157</td>
<td>M+:15,171</td>
<td>[10+:78,920,385]</td>
<td>16,556</td>
<td>(0,1)</td>
<td>6/6</td>
<td>mtDNA insertion with complex rearrangements</td>
</tr>
<tr>
<td></td>
<td>PD4252a</td>
<td>X+:45,631,665</td>
<td>[M+:14,450]</td>
<td>M+:14,496</td>
<td>X+:45,652,120</td>
<td>16,616</td>
<td>(2,1)</td>
<td>2/2</td>
<td>mtDNA insertion with large chr. deletion</td>
</tr>
<tr>
<td></td>
<td>PD6047a</td>
<td>X+:14,944,764</td>
<td>[M−:12,735]</td>
<td>M−:16,128</td>
<td>[7+:96,923,229]</td>
<td>13,177</td>
<td>(1,1)</td>
<td>6/6</td>
<td>Multiple interchromosomal translocations</td>
</tr>
<tr>
<td></td>
<td>PD10014a</td>
<td>17−:75,618,348</td>
<td>[M−:13,365]</td>
<td>M−:9055</td>
<td>[17+:75,688,733]</td>
<td>4311</td>
<td>(2,3)</td>
<td>0/0</td>
<td>mtDNA insertion with large chr. deletion</td>
</tr>
<tr>
<td></td>
<td>PD13296a</td>
<td>4+:102,463,870</td>
<td>[M−:14,705]</td>
<td>M−:13,235</td>
<td>[4+:102,464,084]</td>
<td>1471</td>
<td>(4,0)</td>
<td>0/0</td>
<td>mtDNA insertion with large chr. deletion</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>148</td>
<td>(4,2)</td>
<td></td>
<td>mtDNA insertion with complex rearrangements</td>
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<tr>
<td></td>
<td>PD11397a</td>
<td>19−:12,650,382</td>
<td>[M+:16,233]</td>
<td>M+:96</td>
<td>[17+:40,005,738]</td>
<td>433</td>
<td>(0,2)</td>
<td>1/1</td>
<td>Multiple interchromosomal translocations</td>
</tr>
<tr>
<td></td>
<td>PD7404a</td>
<td>1+:44,914,376</td>
<td>[M+:3732]</td>
<td>––</td>
<td>&gt;200</td>
<td>(1,2)</td>
<td>0/0</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>PD6733b</td>
<td>6−:45,823,498</td>
<td>[M+:16,107]</td>
<td>––</td>
<td>&gt;200</td>
<td>(0,–)</td>
<td>1/1</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>PD11768a</td>
<td>1−:144,944,326</td>
<td>[M+:16,104]</td>
<td>––</td>
<td>&gt;200</td>
<td>(4,–)</td>
<td>1/1</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Cell line</td>
<td>CP66-MEL</td>
<td>3+ :51,419,506</td>
<td>[M+:204]</td>
<td>[M+:16,193]</td>
<td>[3+:47,419,447]</td>
<td>7425</td>
<td>(1,1)</td>
<td>1/1</td>
<td>mtDNA insertion</td>
</tr>
<tr>
<td></td>
<td>NCI-H2087</td>
<td>10+:26,775,605</td>
<td>[M+:1690]</td>
<td>––</td>
<td>&gt;200</td>
<td>(1,–)</td>
<td>1/1</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td></td>
<td>20−:33,836,717</td>
<td>[M−:5666]</td>
<td>––</td>
<td>&gt;200</td>
<td>(1,–)</td>
<td>1/1</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td></td>
<td>17−:7,481,787</td>
<td>T [M+:3452]</td>
<td>––</td>
<td>&gt;200</td>
<td>(1,–)</td>
<td>1/1b</td>
<td>Multiple interchromosomal translocations</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>17−:31,744,235</td>
<td>[M+:4346]</td>
<td>––</td>
<td>&gt;200</td>
<td>(3,–)</td>
<td>1/1</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

*aInherited mtDNA polymorphisms in the vicinity of breakpoints. (#D) Number of detected, (#P) number of present.

* A somatically acquired heteroplasmic mutation in mitochondria.
interchromosomal translocation, taking into account the sizes and copy numbers of the mitochondrial and nuclear genomes. Our sequencing data suggest that each cancer cell carries ~500 copies of circular mtDNA (median value 495) (Fig. 5A), amounting in aggregate to ~8 million base pairs (bp) of mtDNA (500 copies × 16.5 kb) enclosed by the mitochondrial double membrane in the cytoplasm of each cancer cell. The average frequency in the cancers analyzed of mitochondrial-nuclear DNA fusion was 8 million base pairs (bp) containing ~16.5 kb incorporated into micronuclei (Liu et al. 2012). Thus, mtDNA fragments incorporated into micronuclei could end up fused to shattered nuclear chromosomes. It is worthy of note that mtDNA escaping to the nucleus can be actively used for DNA repair in Saccharomyces cerevisiae (Ricchetti et al. 1999; Yu and Gabriel 1999), particularly when error-free DSB DNA repair is not possible. Whether this applies in mammalian cells is unknown.

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Some of the somatic nuclear mtDNA integrations we identified are directly adjacent to nuclear genes. For example, nuclear-mtDNA fusion in JD11372a occurred in the fifth intron of the KCNMA1 gene, a potassium channel frequently amplified in prostate and breast cancers (Oeggerli et al. 2012). However, we do not find obvious enrichment of the nuclear-mtDNA fusion breakpoints near human nuclear genes. RNA-seq from the NCI-H2087 cell-line indicates that mtDNA fragments in the nucleus of the cell line are not expressed as parts of mitochondrial-nuclear fusion transcripts. Thus, the majority of the nuclear mtDNA translocation events are likely to be passenger events, similar to mutations of all other types in most cancer genomes. However, we do not exclude the possibility that some of these events may have functional consequences in human cancer by generating fusion mRNA transcripts (Shay et al. 1991) and/or truncating cancer genes by mtDNA insertion within exons.
Nuclear integration of mitochondrial DNA in cancer

This study has shown that fusion of mtDNA to nuclear DNA occurs in human somatic cells at a rate similar to that of translocation between nuclear chromosomes. Physical migration of mtDNA into the nucleus may be much more frequent in stem cells than in a terminally differentiated stage (Schneider et al. 2014). Further studies will need to address the mechanisms by which the apparent physical barriers to contact between mitochondrial and nuclear DNA are so effectively overcome.

Methods

Samples and sequencing data

We analyzed 559 primary tumors and 28 cancer cell-lines in this study. Paired-normal samples for all the cancers were also included in this study in parallel. Whole-genome sequences used in this study were generated by Illumina platforms (either Genome Analyzer or HiSeq 2000). Cancer genomes were sequenced to at least 25× coverage. With respect to TCGA data, we downloaded aligned BAM files through UCSC CIGAR (http://cghub.ucsc.edu). Sequencing reads were aligned on the human reference genome build 37 (GRCh37) and human reference mtDNA sequence (revised Cambridge reference sequence, rCRS) (Andrews et al. 1999), mainly by the BWA alignment tool (Li and Durbin 2009). SAMtools (Li et al. 2009) was used for manipulating sequence reads.

Calling mitochondrial-nuclear DNA fusion events

We employed a pipeline for identification of putative mtDNA translocation to chromosomal DNA (Fig. 1A). From paired-end whole-genome sequencing data of tumors, we extracted discordant reads (DRs), where one end aligned uniquely to mtDNA and the other end to nuclear DNA. In all cases, both ends must have a mapping quality greater than zero. Those discordant reads are clustered together using the following criteria: reads sharing (1) close alignment positions (<500 nucleotides) for both ends on nuclear and mtDNA, and (2) the same orientations. In order to remove false positives, we removed clusters supported by less than five discordant reads.

In order to remove potential germline calls, several filters are applied to the tumor candidate cluster. The clusters from tumor cells were removed if they overlap with clusters identified from matched and/or unmatched normal tissues by more tolerable criteria (supported by more than one discordant read) from (1) its paired-normal tissue, and (2) from the other 586 unmatched normals.

Filtered clusters were further refined with known germline human numbers, a combined set from the human reference genome (hg19) detected by BLAT (Kent 2002) (n = 123) and from Simone et al. (2011) (n = 766). Finally, 25 clusters were selected as somatic candidates.

Nucleotide-resolution breakpoints for the translocation junctions

To obtain nucleotide-resolution breakpoints, we searched for split-reads (SRs) with one of the ends spanning the junction of the translocation. We extracted “orphan” or “mate-unmapped” reads (one end of a read is unmapped by the BWA aligner) in the vicinity (<1000 bp) of discordant-read clusters on nuclear and mitochondrial genome sequences. Sequences from the unmapped end are then re-aligned by BLAT (Kent 2002), which enables split-read mapping.
Figure 4. Nucleotide-resolution breakpoint sequences and the timing of somatic mtDNA nuclear integration. (A) Breakpoint sequences of nuclear-mtDNA fusions in PD13296a. Red rectangles highlight sequence microhomology and non-template nucleotides insertion. (B) Breakpoint sequences of nuclear-mtDNA fusions in PD6728b. Red rectangles highlight sequence microhomology. (C) Phylogenetic trees showing the timing of somatic mtDNA nuclear transfers in PD4252 and PD6728 samples. (MRCA) Most recent common ancestor cell.

Validation by PCR

A PCR validation assay of the somatic mtDNA transfer was performed using genomic DNA from both cancer and paired-normal tissues. Primers were designed to amplify all the breakpoints (Supplemental Table 3). The short-fragment PCR reactions were performed as previously described (Tubio et al. 2014). With respect to long-range PCR, elongation time was increased 1 min per kb.

Generation of FISH probes

Human bacterial artificial chromosomes (BAC) and fosmid clones used in this study were obtained from the clone archive team of the Wellcome Trust Sanger Institute. Plasmid DNA was prepared using the PhasePrep BAC DNA kit (Sigma-Aldrich). Human mtDNA was isolated from lymphoblastoid cells using a Mitochondrial DNA Isolation kit (Abcam).

Probes for use in FISH were made as described before (Gribble et al. 2013). Purified mtDNA and plasmid DNA were first amplified using a GenomePlex Whole Genome Amplification (WGA) kit (Sigma-Aldrich) following the manufacturer’s protocols, then labeled using a WGA reamplification kit (Sigma-Aldrich) with a custom-made dNTP mix. Probes for interphase FISH were labeled directly with Aminoallyl-dUTPs - ATTO-488, -Cy3, -Texas Red, and -Cy5 (Jena Bioscience); probes for fiber-FISH were labeled with Biotin-16-dUTP, Digoxigenin-11-dUTP (Roche), and DNP-11-dUTP (PerkinElmer).

Validation by fiber-FISH with single-molecule DNA fibers generated by molecular combing

Single-molecule DNA fibers from the cancer cell line, CP66-MEL, were prepared by molecular combing (Michalet et al. 1997) following the manufacturer’s instructions (Genomic Vision). Briefly, the cells were embedded in a low-melt-point agarose plug (1 million cells per plug), followed by proteinase K digestion, washing in 1 × TE (10 mM Tris, 1 mM EDTA, pH 8.0) and beta-agarose digestion steps. The DNA fibers were mechanically stretched onto saline-coated coverslips using a Molecular Combing System (Genomic Vision).

For fiber-FISH, ~500 ng of labeled DNA from each probe and 4 μg of human Cot-1 DNA (Invitrogen) were precipitated using ethanol, then resuspended in a mix (1:1) of hybridization buffer (containing 2 × SSC, 10% sarkosyl, 2 M NaCl, 10% SDS, and blocking aid [Invitrogen]) and deionized formamide (final concentration 50%). Coverslips coated with combed DNA fibers were dehydrated through a 70%, 90%, and 100% ethanol series and aged at 65°C for 30 sec; followed by denaturation in an alkaline denature solution (0.5 M NaOH, 1.5 M NaCl) for 1–3 min, three washes with 1×PBS (Invitrogen), and dehydration through a 70%, 90%, and 100% ethanol series. The probe mix was denatured at 65°C for 10 min before being applied onto the coverslips, and the hybridization was carried out in a 37°C C incubator overnight. The post-hybridization washes consisted of two rounds of washes in 50% formamide/2× SSC (v/v), followed by two additional washes in 2× SSC. All post-hybridization washes were done at 25°C, 5 min each time. Digoxigenin-11-dUTP (Roche) labeled probes were detected using a 1:100 dilution of monoclonal
mouse anti-dig antibody (Sigma-Aldrich) and a 1:100 of Texas Red-X-conjugated goat anti-mouse IgG (Molecular Probes/Invitrogen); DNP-11-dUTP (PerkinElmer) labeled probes were detected using a 1:100 dilution of Alexa 488-conjugated rabbit anti-DNP IgG and 1:100 Alexa 488-conjugated donkey anti-rabbit IgG (Molecular Probes/Invitrogen); biotin-16-dUTP (Roche) labeled probes were detected with one layer 1:100 of Cy3-avidin (Sigma-Aldrich). After detection, slides were mounted with SlowFade Gold mounting solution containing 4′,6-diamidino-2-phenylindole (Molecular Probes/Invitrogen). Images were captured and processed as described above.

Correlation between somatic mtDNA integration site and transposable elements

We performed a study similar to the previous report (Mishmar et al. 2004). We calculated the distance between each mtDNA-insertion site (breakpoint) and its nearest transposable elements (either of SINE, LINE, LTR, simple repeat, or DNA transposon by RepeatMasker, downloaded from the UCSC Genome Browser, June 6, 2013). Then, each mtDNA-insertion site was categorized into one of four groups: (A) breakpoint within a transposable element; (B) breakpoint within 15 bp from a transposable element; (C) within 15–150 bp; and (D), >150 bp. In order to understand the positional enrichment of breakpoints from transposable elements, we randomly generated in silico breakpoint positions 40 times as many (total \( n = 1000 \)) as we observed from each chromosome in the real data set. In silico breakpoints located within gaps of the human reference genome were removed and replaced by newly generated insertions. For these in silico-generated breakpoints, the distances from the nearest transposable elements were calculated and then categorized into one of the four groups (A, B, C, and D). Finally, the difference in the frequency of breakpoints in each group between the observed and in silico-generated data set was compared using a \( \chi^2 \) test.

Assessment of mtDNA copy numbers

To understand mtDNA copy numbers in a cancer cell, we compared average read depth of coverage between 22 autosomes and mtDNA. With respect to the tumor sequences by whole-genome sequencing, average haploid autosomal coverage (RD_{autosome}) was obtained from the read depth of 2.685-Gb-long autosomal regions (excluding chromosomal gaps). Likewise, average mtDNA coverage (RD_{mtDNA}) was obtained from the read depth of the

**Figure 5.** Frequency and potential mechanisms of somatic mtDNA nuclear transfer in human cancer. (A) Estimated circular mtDNA copy numbers (in the cytoplasm) per cancer cell from 587 cancer tissues sequenced. The ratio of read depths between autosomes and mtDNA was used (see Methods). (B) Similar frequency of somatic nuclear mtDNA integrations compared to the frequency between autosomes (chromosomal translocation). (C) A model of somatic mtDNA transfer to the nuclear genomes.
16.5-kb mitochondrial genome. Finally, mtDNA copy number in a diploid cell \( (C_{mt}) \) is calculated as shown below:

\[
C_{mt} = 2 \times \frac{R_{mtDNA}}{R_{autosome}}.
\]

**Assessment of translocation rate for autosomes and mitochondria**

We identified structural variations among nuclear chromosomes (large deletions, tandem duplications, inversions, and interchromosomal translocations) using the BRASS II algorithm (Nik-Zainal et al. 2012), which identifies rearrangements by clustering discordant read pairs that point to the same junction and confirms breakpoints by local assembly of unmapped reads. The sensitivity and specificity of the BRASS II algorithm is equivalent to those values of the algorithm used for mitochondrial-nuclear DNA fusions (data not shown). We extracted interchromosomal translocations to calculate the rate of such events. The rate of each haploid autosome \( (R_{tr,ch}) \) is calculated as shown below:

\[
R_{tr,ch} = \frac{N_{tr,ch}}{(2 \times L_{ch}) / N_{sam}}.
\]

where \( N_{tr,ch} \) is the total number of somatic interchromosomal translocation junctions involving a specific chromosome, \( L_{ch} \) is the length of the nonredundant region of the chromosome in megabases, and \( N_{sam} \) is the total number of samples analyzed. To obtain the unique region length \( L_{ch} \), we excluded redundant (or highly repetitive) sequence lengths from the ungapped length of each chromosome. Genomic regions classified in one or more of the three criteria shown below were defined as redundant, where translocation events could not be easily detected due to ambiguous read alignment: (1) simple repeats, located by Tandem Repeats Finder (Benson 1999); (2) segmental duplications with moderate to high sequence similarity \( (>95\%) \) (Bailey et al. 2002), or (3) repetitive sequences including up to 10 different classes of repeats (such as SINE, LINE, LTR, DNA transposons, and microsatellites), located by the RepeatMasker program (http://www.repeatmasker.org), with a low divergence level \( (\text{divergence} < 5\%) \). These nonredundant sequence regions were downloaded from the UCSC Genome Browser (http://genome.ucsc.edu).

Similarly, the rate of mitochondrial-nuclear DNA translocations \( (R_{tr,mt}) \) was calculated as below:

\[
R_{tr,mt} = \frac{N_{tr,mt}}{(C_{mt} \times L_{mtDNA}) / N_{sam}}.
\]

where \( N_{tr,mt} \) is the total number of junctions of somatic mitochondrial-nuclear DNA fusions identified, \( C_{mt} \) is the median value of mitochondrial genome copy numbers in a diploid cancer cell calculated above (495 copies), and \( L_{mtDNA} \) is the length of the mitochondrial genome in megabases (0.016569 Mb).

**Assessment of the rates of nuclear mtDNA fusion and mtDNA escape to the nucleus**

Fusion of mtDNA to the nuclear genome requires at least two events, each of which could influence the rate of mitochondrial-nuclear DNA fusion. These include escape of mtDNA to the nucleus and integration to nuclear DNA. According to this model, the overall number of such fusion events can be calculated using the rates for these processes \( (\rho_{escape} \times \rho_{integration}) \), respectively:

\[
N_{tr} = N_{sam} \times N_{gen} \times \rho_{escape} \times \rho_{integration}.
\]

where \( N_{tr} \) is the number of total somatic mitochondrial-nuclear DNA fusion events \( (n = 12) \), \( N_{sam} \) is the total number of cancer tissues \( (n = 587) \), and \( N_{gen} \) is the number of average cell generations from the fertilized egg. Using a reasonable assumption that \( N_{gen} = 1000 \), we obtain the rate of somatic mtDNA fusion to the nuclear genome \( (\rho_{escape} \times \rho_{integration}) \) to be \( 2 \times 10^{-5} \) per cell per cell generation \((\text{pcpg})\). With one more very conservative assumption that \( \rho_{integration} \) is 0.1, we obtain \( \rho_{escape} \) to be \( 2 \times 10^{-4} \) pcpg, or at least one escape event per 5000 cell generations. We hypothesize that the real \( \rho_{integration} \) value is thought to be much lower than 0.1, which results in a higher \( \rho_{escape} \). For example, during the generation of knockout mice, homologous recombination allows one fixation event per 1000–10,000 microinjected DNA copies (Brinster et al. 1985). The integration rate may, however, be higher than the rate in cancer cells with defective homologous recombination-based repair and increased availability of nuclear double-strand breaks, which can be joined to by NHEJ or MMBIR.

The mtDNA fusion to the nuclear genome in the germline (the rate of nemacs insertion) is around \( 5 \times 10^{-6} \) per germ cell per individual generation in previous phylogenetic studies (Hazkani-Covo et al. 2010). The rate is equivalent to \( ~5 \times 10^{-6} \) pcpg, given that the number of germ cell divisions per human generation is \( \sim 100 \) (401 in males and 31 in females [Drost and Lee 1995]).

**Data access**

Sequence data for sample pairs with positive mtDNA nuclear transfer have been submitted to the European Genome-phenome Archive (EGA; https://www.ebi.ac.uk/ega/home). The study accession number is EGAS00001001234. Sample accession numbers are available in Supplemental Table 1.

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