Mitochondrial Damage in the Trabecular Meshwork of Patients With Glaucoma

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Objectives: To analyze the frequency of mitochondrial DNA (mtDNA) damage in patients with primary open-angle glaucoma. Oxidative damage plays a major role in glaucoma pathogenesis. Since no environmental risk factor for glaucoma is recognized, we focused our attention on mitochondria, the main endogenous source of reactive oxygen species.

Methods: Mitochondrial damage was evaluated analyzing a common mtDNA deletion by real-time polymerase chain reaction in trabecular meshwork collected at surgery from 79 patients with primary open-angle glaucoma and 156 unaffected matched controls. In the same samples, polymorphisms of genes encoding for antioxidant defenses (GSTM1), repair of oxidative DNA damage (OGG1), and apoptosis (FAS) were tested.

Results: Mitochondrial DNA deletion was dramatically increased (5.32-fold; P = .01) in trabecular meshwork of patients with glaucoma vs controls. This finding was paralleled by a decrease in the number of mitochondria per cell (4.83-fold; P < .001) and by cell loss (16.36-fold; P < .01). Patients with glaucoma bearing the GSTM1-null genotype showed increased amounts of mtDNA deletion and a decreased number of mitochondria per cell as compared with GSTM1-positive subjects. Patients bearing a FAS homozygous mutation showed only a decreased number of mitochondria per cell.

Conclusions: Obtained results indicate that mitochondrial damage is targeted by the glaucomatosus pathogenic processes. Some subjects bearing adverse genetic assets are more susceptible to this event.

Clinical Relevance: Oxidative damage to the trabecular meshwork exerts a pathogenic role in glaucoma inducing mitochondrial damage and triggering apoptosis and cell loss. This issue may be useful to develop new glaucoma molecular biomarkers and to identify high-risk subjects.
The aim of our study was to analyze the frequency of mtDNA\(^{4977}\) in patients with POAG vs controls to evaluate the role of mitochondrial dysfunction in the glaucomatous TM. This end point was analyzed in the iris of the same patients to evaluate the peculiar susceptibility of TM to oxidative stress as compared with other anterior chamber tissues. This issue is relevant because we recently demonstrated that TM is the most sensitive tissue to in vitro oxidative stress in the anterior chamber.\(^{13}\)

The quantification of mtDNA\(^{4977}\) was carried out by quantitative polymerase chain reaction (QPCR), which is highly sensitive and reliable as confirmed by the increasing number of articles using this method.\(^{14,15}\)

Insofar, evidence demonstrating the purported role of mitochondrial damage in POAG pathogenesis is overwhelming, but most results were not obtained using POAG target tissue, ie, the TM. Our study provides for the first time, to our knowledge, evidence that mitochondrial damage really occurs in the TM of patients with glaucoma, thus providing evidence for its pathogenic role in glaucoma.

Genetic factors predispose to POAG development. However, glaucomas caused by single gene mutations are extremely rare. The most relevant POAG-related mutations are those occurring in MYOC and OPTN, which occur in less than 3% of POAG.\(^{16}\) MYOC was demonstrated to be a structural component of the mitochondrial wall, further suggesting an important role of mitochondrial damage in POAG-related TM degeneration.\(^{17}\)

Accordingly, the analysis of genetic risk factors should be also focused on genetic polymorphisms conferring a moderate risk but widely spread in the population. On this basis, we decided to analyze the role of frequent genetic polymorphisms as possible contributors to the mtDNA damage occurring in glaucomatous TM. Selected genes included (1) glutathione-S-transferase 1 (GSTM1), coding a protein involved in the scavenging of reactive oxygen radicals;\(^{18}\) (2) 8-oxo-guanine glycosylase 1 (OGG1), coding a protein repairing 8-oxo-2'-deoxyguanosine, the main oxidative DNA lesions increased in the TM of patients with POAG;\(^{19}\) and (3) FAS, coding a protein involved in the activation of the apoptotic cascade.\(^{20}\)

GSTM1 represents a pivotal intracellular defense against oxidative stress and its homozygous deletion has been associated with an increased level of oxidative DNA damage in TM.\(^{19}\) Accordingly, a GSTM1 polymorphism has been proposed as a possible risk factor for glaucoma, although other studies did not confirm this finding.\(^{21,22}\) OGG1 adverse polymorphisms inducing failure in its repairing ability have been related to increased sensitivity to oxidative damage, resulting in cell death.\(^{23}\) FAS polymorphisms modulate cell attitude to undergo apoptosis as a consequence of oxidative stress.\(^{20}\)

The goal of our study was to analyze the interaction between mtDNA damage, genetic polymorphisms, and POAG.

### METHODS

#### SUBJECT RECRUITMENT AND SAMPLE COLLECTION

The study had a case-control design. Recruited cases had POAG requiring surgical intervention. Inclusion criteria for cases was the presence of POAG with no tonometric evidence of any glaucoma types other than POAG. The TM samples were collected by standard surgical trabeculectomy, as previously reported.\(^{2,19}\) All the enrolled patients furnished an informed, written consent and were treated in accordance with the Declaration of Helsinki.

Trabeculectomy specimens were collected from 79 patients with glaucoma, including 49 women and 30 men, mean (SE) age, 66.4 (2.19) years. All patients had elevated IOP (minimum, 23 mm Hg; maximum, 36 mm Hg; mean ± SE, 27.8 ± 3.69 mm Hg). Specificity of TM alterations was examined by analyzing the iris in a subgroup of 19 patients.

For control samples, we used trabeculectomy specimens collected from 156 subjects, mean (SE) age, 65.1 (1.17) years and sex matched with cases. Samples were collected from glaucoma-free cornea donors by the Melvin Jones Eye Bank, as previously reported.\(^{19}\)

Sample collection from controls was performed no later than 1 hour after death, thus ensuring cell viability, as necessary for the corneal transplant. Samples were immersed in stabilizing buffers containing antioxidants and stored in a deep freezer (−80°C). DNA purification was performed by incubating samples with proteinase K followed by solvent extraction in an oxygen-free atmosphere.\(^{19}\)

#### DETECTION OF mtDNA\(^{4977}\) DELETION AND mtDNA COPY NUMBER

Quantification of mtDNA\(^{4977}\) deletion and total mtDNA were performed by real-time PCR (QPCR) using fluorescent probes (Figure 1). Two QPCR reactions were performed in parallel for each sample, the first to detect the amount of total mtDNA, the second to quantify mtDNA\(^{4977}\) deletion. The total mtDNA reaction was carried out using 2 primers (total mtDNA sense: CGCATCTCAACTGCCTGCTATG and CGCATCCATGATCGCG-BHQ1-3' and total mtDNA antisense: ATCCACCTCACTTGCCCTGCTATG) flanking a sequence of mtDNA (474 bp) known not to be susceptible to the deletion\(^{2}\) and an ad hoc–designed FAM-labeled molecular beacon (total mtDNA: 5'-FAM-CGGACATCAGGCAACGAGCACGCGATCCATGATCGCG-BHQ1-3') (the mtDNA\(^{4977}\) deletion reaction was performed using 2 primers (deleted mtDNA sense: GCCGGCTATTTACCTCATAAG and deleted mtDNA antisense: GTTGGAGAAGAATTPCAGGTTC) recognizing mtDNA regions flanking the deletion site plus a molecular FAM-labeled beacon (deleted mtDNA: 5'-FAM-CGGACATCAGGCAACGAGCACGCGATCCATGATCGCG-BHQ1-3') targeting a DNA sequence between the 2 primers and ahead of the deletion site. Because of the short elongation time, only deleted mtDNA can efficiently produce amplicons (ie, double-strand DNA 400 bp) containing the target sequence for the deleted mtDNA molecular beacon.

A Basic Local Alignment Search Tool search for the deleted mtDNA amplicon and probe were performed with high specificity. The stringent conditions of the reaction are a further warrant for specificity. The incidental cross-reaction of the probe with genomic DNA was further assumed as negligible because mtDNA presents in each cell in multiple copy as compared with nuclear DNA (mDNA).

The reaction conditions were 5 µL of 10× PCR buffer, 0.4 µL of 100mM dNTP mix, 2 µL of 50mM magnesium chloride, 0.5 µL of platinum Taq polymerase (Invitrogen Corp, Carls-
bad, California), 37.1 µL of sterile water, 1 µL of 10µM sense primer, 1 µL of 10µM antisense primer, 2 µL of molecular beacon, and 1 µL of DNA (25 ng).

The QPCR reactions were performed in a rotating real-time thermocycler (Rotorgene3000; Corbett Life Science, Sydney, Australia), using the following temperature ramp: 94°C for 2 minutes followed by 45 cycles at 94°C for 30 seconds, annealing temperature of 54°C for total mtDNA and 51°C for deleted mtDNA for 30 seconds, and 72°C for 30 seconds. Fluorescence was acquired at the end of each annealing step. Each sample was tested in duplicate.

The reaction efficacies for the total mtDNA and mtDNA4977 deletion quantifications were assayed and the results were 0.73 and 0.78, respectively. An internal control was tested in each reaction and the results were expressed as relative quantity (sample/internal control). The specificity of the amplification product and the results were confirmed by capillary electrophoresis using the Agilent 2100 Bioanalyzer with a DNA 1000 Series II kit (Agilent Technologies, Waldbronn, Germany), thereby confirming QPCR results by capillary electrophoresis of amplified mtDNA sequences.

The relative ratio of deleted mtDNA to total mtDNA was assessed for each sample and normalized for cell number as assayed quantifying by QPCR the housekeeping gene GAPDH.

The amount of mtDNA4977 deletion was expressed as percent of total mtDNA.

EVALUATION OF THE nDNA:mtDNA RATIO

The relative amount of total nDNA in each sample was evaluated by quantifying the copies of GAPDH by QPCR. This parameter was related both to mtDNA copy number (nDNA:mtDNA ratio) and to the amount of wet tissue processed (DNA per milligram of wet tissue). This last parameter was assumed as an indicator of cell number in TM.

GENETIC POLYMORPHISM ANALYSES

Genetic polymorphisms were analyzed in an aliquot (0.1 µg) of nDNA as purified from TM samples. The OGG1 Ser326Cys polymorphism, resulting from a C->G transversion in exon 7, was evaluated as previously described by QPCR using a pair of gene-specific molecular beacons to discriminate between the occurrence of this genetic variant on both alleles (homozygous mutant), 1 allele only (heterozygous), or no allele (wild type).25 The FAS promoter 670 polymorphism, resulting from an A/G substitution at the 670 nucleotide position in the enhancer region of the gene, was evaluated by QPCR using a set of gene-specific molecular beacons to distinguish the occurrence of this genetic variant on both alleles (homozygous mutant), 1 allele only (heterozygous), or no allele (wild type).
Table 1. mtDNA Damage in TM as Detected in 79 Patients With POAG and 156 Controls

<table>
<thead>
<tr>
<th>Disease Status</th>
<th>mtDNA$^{4977}$ Deletion:mtDNA Ratio, %&lt;sup&gt;a&lt;/sup&gt;</th>
<th>Total mtDNA&lt;sup&gt;b&lt;/sup&gt;</th>
<th>mtDNA:nDNA Ratio&lt;sup&gt;c&lt;/sup&gt;</th>
<th>Total nDNA per Milligram of Wet Tissue Ratio&lt;sup&gt;d&lt;/sup&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>Controls</td>
<td>6.52 (2.31)</td>
<td>17.96 (1.63)</td>
<td>8.47 (1.00)</td>
<td>9.49 (1.69)</td>
</tr>
<tr>
<td>POAG</td>
<td>34.68 (23.57)&lt;sup&gt;f&lt;/sup&gt;</td>
<td>3.72 (1.29)&lt;sup&gt;f&lt;/sup&gt;</td>
<td>51.6 (0.48)&lt;sup&gt;g&lt;/sup&gt;</td>
<td>0.58 (0.14)&lt;sup&gt;h&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

Abbreviations: mtDNA, mitochondrial DNA; mtDNA$^{4977}$, 4977–base pair mtDNA; nDNA, nuclear DNA; POAG, primary open-angle glaucoma; TM, trabecular meshwork.

<sup>a</sup>This molecular end point reflects the amount of mtDNA$^{4977}$ deletion as an indicator of mitochondrial damage.
<sup>b</sup>This molecular end point reflects the total mtDNA copy number, its decrease expressing the mitochondrial loss in the examined tissue (TM).
<sup>c</sup>This molecular end point reflects the total mtDNA copy number per cell; its decrease is expression of mitochondrial loss normalized for the number of cells composing the examined tissue (TM).
<sup>d</sup>This molecular end point reflects the number of cells composing the examined tissue (TM), its decrease expressing the occurrence of cell loss.

<sup>f</sup>Significantly higher than controls at $P<.05$.
<sup>g</sup>Significantly lower than controls at $P<.05$.
<sup>h</sup>Significantly lower than controls at $P<.01$.

Molecular beacon sequences were human FAS wild type: 5’-FAS-CCGGAATCTGTACTTCCACTCAAGAAAGCT-3’ and human FAS mtDNA: 5’-HEX-CCGGAATCTGTACTTCCACTCAAGAAAGCT-3’. The PCR primer sequences were human FAS sense: 5’-CCCTTTTCAGAGCCCTATGG-3’ and human FAS antisense: 5’-TGCTGGAGTCACTCAGAGAAAG-3’. The reaction was performed at 94°C for 2 minutes, followed by 45 cycles at 94°C for 30 seconds, 66°C for 15 seconds, 64°C for 15 seconds, 53°C for 30 seconds, and 72°C for 30 seconds. The HEX signal was acquired at the end of the 66°C step and FAM signal, at the end of the 64°C step.

The GSTM1 polymorphism, including the gene presence on 1 or both alleles (positive) or its homozygous deletion (null), was investigated by QPCR as previously described. All primer sequences and PCR conditions were determined using Beacon Designer software (Premier Biosoft International, Palo Alto, California) purchased from TIB Molbiol (Berlin, Germany).

**STATISTICAL ANALYSES**

Comparisons among quantitative variables in different groups of patients were executed by analysis of variance and Student’s $t$ test for unpaired data after checking the normality of the distribution by skew kurtosis analysis. The accepted level of significance in all cases was $P<.05$. In situations without a normal distribution of data, a nonparametric test was used (Mann-Whitney test and Kruskal-Wallis test). Correlations between continuous variables were tested by linear regression analysis. Differences of frequency distributions among nominal variables were tested by $χ^2$ test. All statistical analyses were performed using Statview software (Abacus Concept, Berkeley, California).

**RESULTS**

**mtDNA COPY NUMBER AND mtDNA$^{4977}$ DELETION IN TM OF PATIENTS WITH POAG VS CONTROLS**

A remarkably high level of molecular damage was detected in mtDNA in the TM of patients with POAG as compared with unaffected controls. In particular, there was a statistically significant 3.32-fold increase in the level of mtDNA$^{4977}$ deletion in the TM of patients with glaucoma as compared with controls (Table 1). These data were confirmed by capillary electrophoresis, resulting in a 1.7-fold in-
Mitochondrial loss and damage observed in patients with open-angle glaucoma. This decrease of the nDNA per milligram of wet tissue (16.36-fold) and the nDNA per milligram of wet tissue ratio indicates the occurrence of a dramatic drop in cell number in the TM. This finding was paralleled by a remarkable and statistically significant (P < .05) decrease of the nDNA per milligram of wet tissue (Table 3). The variability of the results obtained in cases was remarkable and cannot be attributed to interexperimental variability, which fell lower than 30% when replicate samples were analyzed. Nevertheless, the difference in mtDNA levels as detected in controls and cases was remarkable and statistically significant (P = .01).

Furthermore, both the amount of mtDNA (4.83-fold) and the nDNA per milligram of wet tissue ratio (16.36-fold) were reduced in glaucomatous TM (Table 1). This decrease of the nDNA per milligram of wet tissue ratio indicates the occurrence of a dramatic drop in cell number in the TM. This finding was paralleled by a rising incidence of mtDNA damage, as indicated by the increase in mtDNA deletion and the decrease in mtDNA copy number per cell.

A negative correlation between age and mtDNA: nDNA ratio was observed in controls (r = −0.192; P < .05) but not in patients with POAG (r = −0.069; P = .27).

Table 2. mtDNA Damage as Evaluated in Parallel in the TM and Iris of the Same 19 Patients With POAG

<table>
<thead>
<tr>
<th>Disease Status</th>
<th>mtDNA(^{4977}) Deletion:mtDNA Ratio, %</th>
<th>Total mtDNA</th>
<th>mtDNA:nDNA Ratio</th>
<th>Total nDNA per Milligram of Wet Tissue Ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>TM</td>
<td>49.23 (18.10)(^e)</td>
<td>1.09 (0.34)(^f)</td>
<td>3.81 (0.36)(^f)</td>
<td>0.38 (0.08)(^e)</td>
</tr>
<tr>
<td>Iris</td>
<td>15.28 (10.04)</td>
<td>2.17 (0.37)</td>
<td>7.68 (1.51)</td>
<td>0.12 (0.01)</td>
</tr>
</tbody>
</table>

Abbreviations: mtDNA, mitochondrial DNA; mtDNA\(^{4977}\), 4977-base pair mtDNA; nDNA, nuclear DNA; POAG, primary open-angle glaucoma; TM, trabecular meshwork.

\(^a\)This molecular end point reflects the amount of mtDNA\(^{4977}\) deletion as an indicator of mitochondrial damage.

\(^b\)This molecular end point reflects the total mtDNA copy number, its decrease expressing the mitochondrial loss in the examined tissue (TM).

\(^c\)This molecular end point reflects the total mtDNA copy number per cell; its decrease is expression of mitochondrial loss normalized for the number of cells composing the examined tissue (TM).

\(^d\)This molecular end point reflects the number of cells composing the examined tissue (TM), its decrease expressing the occurrence of cell loss.

\(^e\)Significantly higher than the iris at P < .05.

\(^f\)Significantly lower than the iris at P < .21.

The correlation between the mtDNA deletion and the mtDNA:nDNA ratio was not significant in controls (r = 0.090; P = .25) but was of borderline statistical significance in patients with glaucoma (r = −0.277; P = .06). These results indicate that mtDNA deletion is inversely related to the decrease of mtDNA copy number in patients with glaucoma but not in controls. No correlation

Table 3. Frequency of Analyzed Genetic Polymorphisms in Patients With Glaucoma, Controls, and the General Population as Inferred From Available Literature

<table>
<thead>
<tr>
<th>Gene</th>
<th>Genotypes</th>
<th>Patients With POAG</th>
<th>Controls</th>
<th>General Population</th>
<th>OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Wild type</td>
<td>50</td>
<td>50</td>
<td>60(^{15})</td>
<td>0.83 (0.49-1.54)</td>
</tr>
<tr>
<td></td>
<td>Null polymorphism</td>
<td>50</td>
<td>40</td>
<td>60(^{15})</td>
<td>0.84 (0.43-1.67)</td>
</tr>
<tr>
<td></td>
<td>Wild type</td>
<td>39</td>
<td>50</td>
<td>51(^{12})</td>
<td>0.74 (0.39-1.44)</td>
</tr>
<tr>
<td></td>
<td>Heterozygous mutant</td>
<td>49</td>
<td>50</td>
<td>60(^{15})</td>
<td>0.83 (0.38-1.86)</td>
</tr>
<tr>
<td></td>
<td>Homozygous mutant</td>
<td>39</td>
<td>50</td>
<td>60(^{15})</td>
<td>0.74 (0.19-2.83)</td>
</tr>
</tbody>
</table>

Abbreviations: CI, confidence interval; OR, odds ratio; POAG, primary open-angle glaucoma.

\(^a\)Statistically significant difference in patients with POAG vs controls (P < .05).

FREQUENCIES OF GENETIC POLYMORPHISMS

The percentages of various polymorphisms as analyzed in patients with POAG and controls are reported in Table 3. None of these differences was statistically significant except an increased frequency of the GSTM1-null genotype in patients with POAG as compared with controls. By comparison, the frequency of the various genotypes as detected for each gene in the general population is reported (Table 3).

INFLUENCES OF GENETIC POLYMORPHISMS ON MITOCHONDRIAL DAMAGE

OGG1 polymorphisms did not exert any significant influence on any of the molecular end points tested (Table 3). The GSTM1 homozygous deletion was associated with an increased level of mtDNA deletion (1.7-fold) and a decreased amount of total mtDNA (2.5-fold) and mtDNA:nDNA ratio (2.3-fold). Conversely, the amount of nDNA per milligram of wet tissue was not affected (Table 3). The FAS homozygous mutation was significantly correlated both with a decreased amount of mtDNA (2.3-fold) and mtDNA:nDNA ratio (3.2-fold). Conversely, no effect of this mutation was detected on the amounts of deleted mtDNA and nDNA per milligram of wet tissue (Table 3).

RELATIONSHIPS AMONG MOLECULAR END POINTS

The correlation between the mtDNA deletion and the mtDNA:nDNA ratio was not significant in controls (r = 0.090; P = .25) but was of borderline statistical significance in patients with glaucoma (r = −0.277; P = .06). These results indicate that mtDNA deletion is inversely related to the decrease of mtDNA copy number in patients with glaucoma but not in controls. No correlation
was observed among the other molecular end points tested in controls or patients with glaucoma.

**COMMENT**

Though many studies in the literature analyze mitochondrial dysfunction in POAG, most of them were carried out on surrogate tissue (Table 4). To the best of our knowledge, this is the largest study performed analyzing genetic polymorphisms and molecular alterations directly in TM.

Our study provides evidence that mtDNA damage occurs in the target tissue of POAG, the TM. Such damage is detectable only in the TM and not in other anterior chamber districts, eg, the iris. Genetic polymorphisms affect the amount of mtDNA damage in TM.

The level of mtDNA detected in glaucomatous TM is remarkably high. By comparison, the level of mtDNA as detected by our group using the herein-reported QPCR method in stemlike mammary cells spanned from 0.9% to 2.1% only. Markaryan et al detected a similar range of molecular lesions in different tissues of cochlear structures using the same method.

The high interindividual variation in the level of mtDNA, especially in patients with POAG, could be due to some still unidentified genetic polymorphisms or to the variability in the dietary intake of antioxidants. It is unlikely that such variability could be due to differences in diseases status because all patients were carriers of advanced unbalanced POAG requiring surgical trabeculectomy. Other variables possibly contributing to this variability might be related to mitochondrial haplotypes, which are characterized by different sensitivity to oxidative damage and undergo interindividual variations. However, to our knowledge, no direct relationship between mtDNA haplotypes and POAG prevalence has been reported.

A further explanation for the high variability of mtDNA deletion observed in POAG may be due to the low amount of mtDNA detected that affects PCR amplification conditions requiring many amplification cycles.

Our findings shed light on mechanisms contributing to TM degeneration in POAG. In cases of oxidative stress, mitochondrial damage triggers apoptosis. These mechanisms result in degenerative phenomena in tissues composed of perennial cells, such as TM.

Our results are in agreement with previous studies performed in vitro in TM primary cultures collected from patients with POAG and donor eyes, indicating that in POAG mitochondrial dysfunction results in intracellular calcium and oxidative overload. Primary open-angle glaucoma–related mitochondrial alterations detected in vitro include lower adenosine triphosphate production and decreased transmembrane potential resulting in mitochondrial complex I defect associated with the degeneration of TM cells. The occurrence of mitochondrial functional defects in glaucomatous TM cells resulting in abnormal vulnerability to intracellular calcium increase has been reported.

Mitochondrial haplogroups have been examined as a possible genetic factor for glaucoma. No association between mitochondrial haplogroups and POAG has been reported, although a possible association with primary angle-closure glaucoma has been reported in a small study.

Mitochondrial damage and loss occurring in TM trigger both degenerative and apoptotic phenomena resulting in cell loss. This cell loss clinically manifests as IOP increase. Decrease of TM cellularity during glaucoma course has been previously reported, although to a lesser extent than those indicated by our results. Changes in TM composition during glaucoma course could contribute to the detected decrease of the DNA per milligram of wet tissue ratio.

The TM specificity of mtDNA damage in POAG is supported by the comparison with the iris of the same patients with POAG in whom such damage was not detected. This comparison was performed between 2 neighbor tissues of the anterior chamber, thus being highly specific. The lack of mtDNA damage in tissues different from TM is in agreement with the negative findings reported by other studies in blood lymphocytes of patients with POAG.

A comparison of mitochondrial damage and genetic polymorphisms does not support a major role for OGG1 in POAG. Conversely, both GSTM1 and FAS appear to affect molecular damage occurring in TM of patients with POAG. Patients devoid of GSTM1 activity have increased mtDNA deletion. This finding may be interpreted as resulting from the decreased antioxidant defenses observed in subjects with GSTM1 deletion, demonstrated by the increased TM oxidative DNA damage in the GSTM1-null vs GSTM1–positive patients with POAG.

FAS homozygous mutations did not exert an influence on the level of mtDNA deletion while decreasing the mtDNA copy number and the mtDNA:nDNA ratio. In the anterior chamber of the eye, FAS has been demonstrated to provoke apoptosis increasing myocilin release from mitochondria to cytosolic compartments of TM cells. Further studies are required to clarify in which glaucoma types, other than POAG, high levels of mtDNA deletion occur in TM.

### Table 4. Mitochondrial Dysfunction in TM and Surrogate Tissues of Patients With Glaucoma

<table>
<thead>
<tr>
<th>Substrates</th>
<th>Mitochondrial Defect</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>Human TM cultures</td>
<td>Pro370Lue mutant myocilin</td>
<td>26,27</td>
</tr>
<tr>
<td></td>
<td>Truncated myocilin</td>
<td>28</td>
</tr>
<tr>
<td>TM of the adult rhesus monkey</td>
<td>Swollen mitochondria in endothelial cells</td>
<td>29</td>
</tr>
<tr>
<td>Primary cultures of TM cells</td>
<td>Dysfunction in calcium regulation</td>
<td>30</td>
</tr>
<tr>
<td></td>
<td>Myocilin partially released from</td>
<td></td>
</tr>
<tr>
<td></td>
<td>mitochondrial compartments</td>
<td></td>
</tr>
<tr>
<td>TM tissue</td>
<td>Defect in the mitochondrial complex I</td>
<td>11</td>
</tr>
<tr>
<td>Porcine TM cells</td>
<td>Increase in iROS and expression of</td>
<td></td>
</tr>
<tr>
<td></td>
<td>inflammatory mediators</td>
<td></td>
</tr>
<tr>
<td>Blood samples</td>
<td>CYP1B1 mutations</td>
<td>33</td>
</tr>
<tr>
<td></td>
<td>mtDNA changes</td>
<td>10</td>
</tr>
<tr>
<td>Human corneal fibroblasts</td>
<td>Myocilin mutations in human TM cells</td>
<td>24</td>
</tr>
<tr>
<td>Human TM biopsies</td>
<td>mtDNA deletion</td>
<td>Current study</td>
</tr>
</tbody>
</table>

**Abbreviations:** iROS, intracellular reactive oxygen species; mtDNA, mitochondrial DNA; TM, trabecular meshwork.

*All cultured cells, nontarget; only 1 on TM from living patients.*
In conclusion, our results indicate that patients with POAG bear genetic predisposition to oxidative stress contributing to mtDNA damage and apoptosis. Mitochondrial DNA deletion is a severe damage transmitted during mitochondrial mitosis to new mitochondrial progeny. Accordingly, mitochondrial damage progressively increases with age. On this basis, POAG may be interpreted as a mitochondrialopathy affecting TM cells, thus hampering aqueous humor outflow.

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Author Contributions: Dr Izzotti had full access to all the data in the study and takes responsibility for the integrity of the data and the accuracy of the data analysis.

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REFERENCES


