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Pathway-Focused Arrays Reveal Increased Matrix Metalloproteinase-7 (Matrilysin) Transcription in Trachomatous Trichiasis

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Purposes. Several genes that are associated with protection from or susceptibility to trachomatous trichiasis (TT) have been identified through genetic association studies. Yet there have been few studies in which gene expression profiles were assessed in TT cases and disease-free controls. The purpose was to identify genes that are differentially expressed in the upper tarsal conjunctiva of subjects with TT.

Method. Pathway-focused gene arrays were used to screen conjunctival RNA expression of 226 gene transcripts of interest. The screening was followed by validation of differentially expressed genes by qRT-PCR on an independent set of samples. Three different techniques were then used to test for quantitative differences in the recovered conjunctival protein fraction.

Results. Focused arrays identified a set of 13 differentially expressed genes. Validation by qRT-PCR confirmed differential expression in four of these genes (COL1A1, COL7A1, MMP7, and TLR6). Increased expression of MMP7 was the only consistent differentially regulated gene in the conjunctival samples of trichiasis subjects. MMP7 was present in isolated conjunctival proteins and in the tissue culture supernatants of peripheral blood lymphocytes after stimulation.

Conclusions. There is an imbalance in extracellular matrix turnover with minimal contribution of adaptive immune responses at this stage of trichiasis. There was little evidence of broad differential expression in genes characteristic of polar responses of adaptive T cells or macrophages. The control of the MMP7 response and its activity appears significant in the fibrotic changes observed in TT. (Invest Ophthalmol Vis Sci. 2010;51:3893–3902) DOI:10.1167/iovs.09-5054
were then vortexed vigorously and the swab discarded. The lysate was passed through a column that binds DNA. The column was washed, and the DNA was eluted in 100 μL of RNase-free water. Ethanol was added to the flow-through from the DNA column and added to a minispin column (RNeasy; Qiagen, Ltd.). Total RNA bound to the membrane was subjected to DNase I digestion. The total RNA was eluted in 60 μL of RNase-free water. Proteins were precipitated from the flow-through with buffer APP. The precipitated proteins were collected by centrifugation, and total protein was redissolved in 100 μL of 5% sodium dodecyl sulfate (SDS). DNA and protein samples were stored at −20°C and RNA at −70°C.

**Quantification of Total Amounts of Nucleic Acid and Protein**

Total RNA was quantified in a 2-μL sample by reading the absorbance at 260 nm (NanoDrop model ND-1000; Thermo Scientific). Total DNA was quantified by measuring the amount of mitochondrial DNA present in the sample using SYBRgreen qPCR. Total protein was quantified in 10-μL samples with an enhanced biocinchonic acid (BCA) assay (Pierce Chemical, Rockford, IL) on the spectrophotometer (NanoDrop ND-1000; Thermo Scientific).

**Generation of Labeled aRNA Probes and Gene Array Analyses**

Total RNA was amplified and labeled with biotin-UTP (Message Amp II kit; Ambion Europe Ltd.). Biotin-labeled aRNA was produced after two overnight rounds of in vitro transcription. Labeled aRNA was hybridized overnight to each membrane and two separate membranes (arrays) were used for each subject (with the exception of one sample from an affected case on one Th1/Th2/Th3 array). All arrays, hybridization solutions, wash, and probe detection kits were purchased (SuperArray Bioscience Corp., Frederick, MD). Each array consisted of 115 genes (two blanks, three artificial sequences, one bacterial plasmid sequence (PUC18), two biotin-coupled positive controls, and five reference genes covering seven positions) that were selected for involvement in pathways focused on human extracellular matrix and adhesion molecules (OHS013) or human Th1/Th2/Th3 cells (OHS034). Bound aRNA was detected by the addition of streptavidin-alkaline phosphatase (CDP-Star; Roche Diagnostics, Indianapolis, IN). Images of the membranes were captured with a chemiluminescence detection system (Chemi-Doc; Bio-Rad Laboratories, Ltd., Hemel Hempstead, UK) with a CCD camera after 100 seconds of exposure for ECM arrays and 200 seconds for Th1/Th2/Th3 arrays. Each 16-bit TIFF file was then downloaded into array-analysis software (GEArray Expression Analysis Suite 2.0; SuperArray) for image processing and array analysis. Local background correction for spot intensity was applied to each membrane and the raw spot intensities values were then exported to a spreadsheet along with all array meta-information (Excel; Microsoft, Redmond, WA). The raw spot intensities, images, and array information were then analyzed by using the image-processing and array tool features in commercial software (MatLab; The MathWorks, Natick, MA).

**Array Normalization**

We tested 11 different array normalization strategies, the most appropriate array normalization method was selected by testing each normalization with the technique described by Kroll and Wilt.(2) Normalization of the arrays with the global mean was selected as the best fitting normalization method. The filtered gene list of significantly differentially regulated gene transcripts was then produced based on rank differences in signal intensities. A distribution-free test of significance based on rank difference was used. Genes with rank differences which were significant at the 10% level, without adjustment of P-values for multiple testing, were considered differentially expressed. Only those in which at least five subjects had above-background expression values were selected for further analysis. Since multiple array normalization strategies were tested, only genes that appeared in global mean
normalization and at least one of the other 10 normalization strategies tested were selected. Reproducibility and consistency between arrays was tested with a rank-based ANOVA. Last, a categorical nonquantitative analysis, based on presence or absence scoring, was also performed. These categorical data were analyzed by Fisher’s exact test, and the results used to complement the quantitative analysis of differential gene expression. We calculated the percentage of false-positive, differentially expressed genes at the 10% and 5% level according to the method described by Stekel.25

Quantitative RT-qPCR

The PCR primer sequences used in this study are listed in Supplementary Table S1 (all Supplementary Tables are available at http://www.iovs.org/cgi/content/full/51/8/3893/DC1). qRT-PCR was performed using a two-step protocol previously described.24 Gene expression was quantified in duplicate by real-time qPCR (Quantitect SYBR Green PCR kit; Qiagen, Ltd.) on a real-time thermal cycler (Rotor-Gene 6000; Corbett Research, Cambridge, UK). Standard curves were used to quantify the copy number in unknown or test samples, as described by Burton et al.20

Mitochondrial DNA qPCR

PCR was performed on genomic DNA with primers for human-specific hypervariable 1 (HV1) D-loop region mitochondrial DNA in conditions described by Harding-Esch et al.28 The amount of DNA in the sample was then expressed as follows: The sample with the highest cycle threshold (Ct) was selected as the reference, and all other samples (n) were then estimated relative to this value by multiplying it by two to the power of the difference in the cycle threshold [2(Ct|n| - Ct|ref|)].

Testing for C. trachomatis

A commercial assay (Amplicor CT/NG; Roche Diagnostics) was used for detection of C. trachomatis in cases and controls, as described elsewhere.29 The reaction buffer conditions required were attained by first diluting purified DNA (9 μL) in 94.5 μL of a 50:50 mixture of lysis and diluent buffers; 50 μL was then used in the standard assay. Positive and negative samples were assigned according to the manufacturer’s instructions.

SDS-PAGE, Silver Staining, and Immunoblot Analysis

Total protein was pooled from each of the cases and controls, and 10 μg of protein was denatured by boiling in SDS-PAGE gel-loading buffer and loaded onto 5% to 15% polyacrylamide gradient gels (Bio-Rad Laboratories, Ltd.). Ten microliters of protein-marker IV (peqGOLD; Peqlab, Erlangen, Germany) was loaded as size markers. Total protein in SDS-PAGE gels was visualized by staining (ProteoSilver kit; Sigma-Aldrich, Poole, UK), per the manufacturer’s protocol. Immunoblots were prepared as just described after the transfer of proteins from the SDS-PAGE gel to nitrocellulose membranes. The membranes were then preblocked in a TBS-T (Tris-buffered saline, 0.1% Tween) supplemented with 5% powdered milk solution overnight at 4°C before immunoblot analysis. The membranes were incubated with a primary anti-MMP7 antibody (MAB9071; 1:100; R&D Systems Europe Ltd, Abingdon, UK), followed by a secondary anti-mouse IgG horseradish peroxidase-conjugated antibody. Bound antibodies were detected with enhanced chemiluminescence (ECL Plus; GE Health Care, Amersham, UK), according to the manufacturer’s instructions. Chemiluminescent output was then visualized with a 1-minute exposure using standard x-ray film. The films were photographed and scanned by a gel documentation system and analyzed (GelDoc with Quantity-one software; Bio-Rad Laboratories, Ltd.).

In Vitro Culture and Stimulation of PBMCs

PBMCs were isolated and cultured as described elsewhere.27 The cells were co-incubated with 5 μg/mL of pokeweed mitogen (PWM), sero-
numbers and brief descriptions of gene product function. In total, nine genes were considered significantly upregulated, and three were downregulated in the TT cases compared with the controls. One additional gene (COL1A1) was identified as significantly more frequently expressed in the TT cases than in the controls based on categorical scoring of spot presence or absence (Supplementary Table S2). The signal intensities of these spots are close to background. At $P < 0.1$ or $P < 0.05$, the number of potential false-positive genes with differential gene expression was calculated as 24 and 0.6, respectively. The raw acquired images of the developed arrays are shown in Supplementary Figure S1 http://www.iovs.org/cgi/content/full/51/8/3891/DC1, and tables of the raw and background spot intensity values are given in Supplementary Table S3. There were no significant differences between the cases and controls in the total number of genes expressed on each type of array (reference genes and control sequences were excluded). A simple summary table of the genes expressed in the extracted conjunctival RNA is shown in Supplementary Table S4.

**Validation of Differentially Expressed Genes in Total RNA from Ocular Swabs from an Independent Set of TT Subjects and Controls**

Initially, human ribosomal protein 1 (HuP01), used in several other studies as a housekeeping gene,

<table>
<thead>
<tr>
<th>Gene Array Samples</th>
<th>Cases</th>
<th>Controls</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age (range), y</td>
<td>67 (49–80)</td>
<td>65 (44–80)</td>
</tr>
<tr>
<td>Sex</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>Male</td>
<td>8</td>
<td>8</td>
</tr>
<tr>
<td>Female</td>
<td>18.72 (8.4–65)</td>
<td>15.8 (10.2–64.4)</td>
</tr>
<tr>
<td>Total RNA yield (ng/μL)</td>
<td>NT</td>
<td>NT</td>
</tr>
<tr>
<td>CT/NG Amplicor</td>
<td>ECM</td>
<td>40 (29–64)</td>
</tr>
<tr>
<td>Median number (range) of genes expressed per array type</td>
<td>49 (36–65)</td>
<td></td>
</tr>
<tr>
<td>Th1/Th2/Th3</td>
<td>35 (19–55)</td>
<td>48 (21–65)</td>
</tr>
</tbody>
</table>

**qRT-PCR Samples**

| Age (range), y | 54 (3–76) | 50 (3–75) |
| Sex | 22 | 22 |
| Male | 25 | 25 |
| Female | 13.75 (6.4–29.2) | 13.64 (2.9–22.8) |
| Total DNA* (qPCR) | 3300 (67–13790) | 3536 (27–39840) |
| Total protein (ng/μL) | 509.8 (100–794) | 351.4 (119–791) |
| CT/NG Amplicor (n positive) | 1 | 0 |

$n = 11$ for both cases and controls for Gene Array; $n = 47$ for both groups for qRT-PCR. Data are expressed as median (range). NT, not tested.

* Below measurable range (<2 ng/μL) of the spectrometer (OD 280 nm) and therefore estimated by relative quantification real-time PCR.

**SDS-PAGE Resolution of Isolated Conjunctival Proteins**

Silver staining was used to visualize the total protein content recovered from the conjunctival swabs of the cases and controls in SDS-PAGE gels (Fig. 3). The proteins were pooled from each of the 47 cases and controls, and equivalent amounts of protein were loaded on the gel. No gross differences in the number or the intensity of the protein bands were evident. Overall, the cases and controls appeared to have nine major bands. A dominant, intense band at ~60 kDa was present in both groups. The gels were analyzed (Quantity-one software; Bio-Rad) and produced a density profile that suggested a small change between the cases and controls in abundance of proteins below the major band at ~60 kDa.
Detection of MMP7 in Recovered Conjunctival Proteins by Immunoblot Analysis

The molecular weight of pro-MMP7 is 28 kDa; however, the recombinant hMMP7 (MMP7 Quantikine kit; R&D Systems) is produced in carrier form with a larger molecular weight. Figure 4, lane 2, shows a large band at ~70 kDa when probed with anti-MMP7 that served as a positive control reaction. When probed with secondary antibody alone (lane 3) there was no reactivity. A band of equal intensity was visible in lanes 4 (pooled cases) and 6 (pooled controls) at ~26 kDa, when probed with monoclonal anti-MMP7 antibody. No bands were visible in lanes 5 (pooled cases) and 7 (pooled controls) when probed with secondary antibody alone.

Quantification of MMP7 by Quantikine Capture ELISA

Since quantitative differences between the cases and controls could not be determined with immunoblot analysis, we attempted to measure MMP7 levels in the individual samples of recovered conjunctival proteins and in PBMC tissue culture supernatants. PBMCs were used as a source of cells that express abundant levels of MMP7, to complement the estimates of MMP7 levels directly recovered from the conjunctival proteins. However, the levels of MMP7 could not be measured in recovered total conjunctival protein collected from ocular swabs because of the inhibition of the assay by the samples. MMP7-spiked samples remained inhibited despite dilution of the samples and exchange of sample in appropriate buffers and diluents. MMP7 levels in culture supernatant of PBMCs appear to accumulate over time since at 2 days after culture, levels were not detectable (data not shown). By 6 days of culture spontaneous production of MMP7 in unstimulated cultures was highest in both the cases and controls, although highly variable (Fig. 5). Stimulation with either PWM or EBs inhibited or blocked the spontaneous production of MMP7 by PBMCs. This difference in levels reached borderline significance in response to stimulation with EBs, such that in the cases, stimulation with EBs had a smaller effect on the inhibition of MMP7 production than in the controls. The degree of inhibition or the amount of

![Image](https://example.com/image1.png)

**Figure 1.** Total RNA was isolated from conjunctival swabs of 11 trichiasis cases and 11 age-, sex-, and location-matched controls. mRNA was amplified, biotin labeled, and used as a probe on each array. The array layouts with gene symbols are shown in (a) for ECM and cell adhesion molecules and in (c) for Th1/Th2/Th3. (b, d) Genes in which the rank difference was significant at the 10% level are indicated by their designated gene symbol. (Red) Genes with increasing intensity of expression; (green) decreasing intensity of expression between cases and controls for each array type.
MMP7 production did not correlate (positively or negatively) with either the PBMC proliferative index or production of IFN/H9253 (data not shown).

**DISCUSSION**

We investigated conjunctival gene expression in subjects with TT using low-density, focused gene expression arrays and qRT-PCR, targeting the genes involved in inflammation and ECM composition. Validation of focused array data by RT-PCR confirmed the differential expression of genes involved in ECM regulation (MMP7, COL1, and COL7) and innate immune responses (TLR6), but only MMP7 expression was consistent between results obtained with arrays and qRT-PCR. There was no evidence from qRT-PCR of differential regulation of Th2 transcription factors, NK2 cell markers, or suppression of IFN/H9253 signaling by SOCS1. The addition of CCL18, NOS, and ARG to

**FIGURE 2.** Median difference (with upper or lower quartile range) in relative expression from total RNA conjunctival samples of 47 cases and 47 controls measured by qRT-PCR with primers specific for each gene. Positive differences indicate an upregulation in disease and negative differences indicate a reduction in expression. Unadjusted significant P-values (P < 0.05), shown above each target gene, were calculated with Wilcoxon-signed rank test. Bars indicate significantly downregulated genes. Bonferroni correction for multiple testing estimates significant values needed to reach 0.05/16 (P < 0.003125).

**FIGURE 3.** Conjunctival protein fraction from pooled cases (10 µg) and pooled controls (10 µg) run on 5% and 15% SDS-PAGE silver-stained gels. Density profiles are shown to the right of each lane, indicating a small change in profile shape and height below the major 60-kDa band (arrows).
screen for macrophage polarization found no evidence of polarization.

**MMP7** upregulation is widely found in other fibrotic diseases and tumor metastasis.³³,³⁴ **MMP7** is naturally expressed in epithelia and injured tissues and is increased in alternatively activated (M2) macrophages.³⁶⁻³⁷ **MMP7** has a wider role than ECM regulation, with an increasingly recognized position in innate defense by its action on latent TNF, α-defensins, and FAS ligand.³⁸⁻⁴⁰ Mice deficient in **MMP7** (mmp7⁻/⁻) that lack functional intestinal α-defensins are highly susceptible to infection by enteric pathogens. They also have reduced levels of active FAS ligand and epithelial cell apoptosis. Furthermore, **MMP7** is crucial in establishing chemokine gradients; mmp7⁻/⁻ mice are unable to effectively recruit neutrophils to sites of pathogen entry or tissue damage,⁴¹ suggesting an important role in inflammation. It is also responsible for activation of pro-TNF on macrophages⁴² and has been identified as a biomarker of idiopathic pulmonary fibrosis.⁴³

The role of MMPs in *Oblamymda*-induced diseases has been studied. **MMP9** has received the most attention after reports that indicated increased conjunctival expression²⁰,²⁴ and enzymatic activity²⁸ in trachoma patients. As yet, there are no small rodent models of ocular chlamydial infection that can reproduce the chronic changes observed in the human conjunctiva. Urogenital infection of the mouse offers the next best approximation in small rodents and does induce the expression of MMPs (MMP2, -9, and -12⁴⁴). Administration of chemical inhibitors of MMPs protected mice from ascending infection and hydrosalpinx.⁴⁵ Subsequent experiments in MMP9KO mice demonstrated that the ablation of MMP9 production was sufficient in this model to prevent the pathologic changes associated with ascending genital infection.⁴⁶ Changes in MMP7 levels have not been directly reported in response to chlamydial disease, although the effect of infection in MMP7KO mice has been studied in relation to sequelae and the immune response. Deficiency in MMP7 had little effect on the magnitude or duration of infection, fertility rates, and hydrosalpinx formation,⁴⁷ leading the authors to conclude that MMP7 was not a requirement in the progression or resolution of chlamydial infection in this model. However, the natural history of ocular infection in humans is markedly different from that in murine genital tract models of infection; thus, the contribution of MMP7 to fibrosis in trachoma is likely the result of repeated or prolonged inflammatory insults, which are often associated with colonization with multiple bacterial species.

**MMP7** is one of several genes whose expression is controlled via Wnt (wingless, int) signaling. At least seven recognized terminal target genes of canonical Wnt signaling have been identified in fibrosis (BMP, MYC, CD44, NOS2, **MMP7**, PPAR, and FN1).⁴⁸ Four of these genes (CD44, NOS2, **MMP7**, and FN1) were upregulated in TT cases on the array. A limited number of genes involved in the Wnt signaling pathway were covered on the array, some of which are involved in E-cadherin signaling and the maintenance of the epithelial cell barrier.

Immune-mediated fibrotic diseases, such as schistosomula-induced hepatic fibrosis, are dominated by Th2-cytokine responses where IL13 and the decoy receptor IL13Rα2 are key.⁴⁹ IL-11 and its receptors are also clearly identified as playing a significant role in some immune-mediated fibrotic diseases.⁵⁰ More recently polarized macrophages that favor deposition of collagens and fibrosis have been demonstrated to be important in the development of disease (e.g., pulmonary fibrosis⁴¹ and responses to chronic helminth infection⁵²). There was no evidence of Th1/Th2/Th3 polarization, although altered expression of Nfatc1/4, Socs1, and Tmed1 may suggest some evidence of inhibition of IFNγ signaling and stimulation of Th2, NK2 cells. We did not identify any of the factors found in previous studies on trichiasis patients as having significantly altered expression (IL1B, TNF, MMP1/TIMP1). Nor were genes

![Image](image-url)
that have been identified in other infection or immune-driven fibrotic diseases differentially expressed. This does not rule out the involvement of these genes in the disease process. The small number of subjects studied and the sensitivity of the array could account for the lack of differences. In addition, the simplified WHO grading system used to identify cases and controls, although satisfactory for rapid population screening by national control programs, does not record additional important information for detailed research that may be required. Taken together, these factors may explain why these genes were not identified as differentially expressed. Within these limitations, the results identify the major changes in gene expression in this group of subjects and point to changes in MMP7 as the major gene with altered expression.

Since MMP7 gene expression was upregulated in the TT cases, we investigated whether the change would be reflected in the proteins recovered from the same conjunctival samples. The total protein showed some evidence of changes in the abundance of proteins below 60 kDa. This result warrants further study by two-dimensional SDS-PAGE. Using immunoblot analysis, we demonstrated the presence of MMP7, but attempts to quantify the amount of protein by capture ELISA were inhibited by the sample. The assay used to quantify MMP7 was developed to be performed in the presence of TIMP, the natural inhibitor of MMP7; thus, inhibition was due to an unknown factor. The lack of differences in MMP7 in pooled samples by immunoblot analysis may be masked the natural biological variation of the samples and the semiquantitative nature of immunoblot analysis techniques. Stimulation of PBMCs from cases and controls with C. trachomatis EBs resulted in a reduction in the inhibition of spontaneous production of MMP7 in the cases compared with that in the controls (i.e., higher levels of MMP7 remained in the supernatants of cases after stimulation). This observation is difficult to interpret and relate to the increased MMP7 gene expression observed in the conjunctiva of the TT cases. However, PBMCs are a recognized source of MMP7 in several studies, including the observation of differing levels of spontaneous production between clinical groups.\(^{53,54}\)

RT-PCR in 47 case-control pairs showed that TLR6 expression was reduced in TT cases, suggesting that the host’s recognition of bacterial ligands is affected in TT cases. Alternatively, reduced TLR6 expression could be due to a reduced number of TLR6-expressing cells or changes caused by the disease process that result in the well-described increased susceptibility to other bacterial infections.\(^{55}\) In the mouse, reduced Tlr6 expression has been shown in macrophages on stimulation with TNFα or IFNγ, and a proinflammatory environment has also been shown to reduce TLR6 expression in epithelial cells.\(^{57}\)

Reduced transcripts of two collagen proteins in subjects with scarring trachoma suggest that the composition of the extracellular matrix is altered. Collagen type I (COL1A1) and VII (COL7A1) transcripts were downregulated in individuals with TT. Many factors including cytokines affect expression of COL1A1, TGFβ, IL-1β, TNFα, and IFNγ have all been shown to affect expression of COL1A1.\(^{58}\) COL7A1 gene expression is also regulated by proinflammatory cytokines (TNFα, IL-1β, and TGFβ), expression is up- or downregulated depending on the cell-type and the cytokines present,\(^{59,60}\) indicating a complex biology. Transcription of COL7A1 is important in the formation of anchoring fibrils, and this may play a role in the morphologic changes that take place in the conjunctiva of subjects with trichiasis.

C. trachomatis DNA was detected in only one individual, consistent with the low prevalence of C. trachomatis infection normally seen in subjects with TT in The Gambia and elsewhere.\(^{61}\) We did not collect additional swabs for standard microbial cultures. Publications in the literature suggest that ~40% of subjects with TT are colonized with at least one nonchlamydial bacterial species.\(^{62}\) The contribution of additional species and changes in the ocular microbiome are therefore important, since they directly influence the host’s expression profile and response to further challenge by infection.\(^{63}\) The altered PBMC response levels of MMP7 in trichiasis may be a result of inherited genetic polymorphisms that predisposes the host to inflammation-driven fibrosis. Investigation of the signaling pathways and downstream targets of MMP7, along with MMP7 polymorphisms (some of which have already been identified as risk factors for fibrosis\(^{64,65}\)), may yield important information in the etiology of the scarring process.

We ultimately found four genes with altered expression: MMP7, COL1A1, COL7A1, and TLR6. We accepted a high rate of potential false-positive association when screening genes by the array and subsequently during validation by qRT-PCR, since the normal methods of correcting P-values and the general applicability of adjusting for multiplicity of tests remain matters of contention among biostatisticians.\(^{23,28}\) We therefore leave our colleagues to balance the significance of the findings against the interpretation of the study results. An independent replication study with a larger number of subjects studied by each method is the most appropriate manner of testing these associations. We suggest that in geographic regions where active trachoma and infection are hypoenemic, the C. trachomatis-specific adaptive and regulatory immune responses exert their major effect, if any, during the active stages of the disease when conjunctival scarring is in its early stages. The later stages of disease, such as those seen in adult TT cases, which are characterized by innate proinflammatory and fibrotic responses, continue to progress once the inflammatory environment is established and maintained by other non-chlamydial inflammatory insults. In populations, where rapidly advancing TS and TT can be observed in children and young adults, the role of C. trachomatis-infection and the inflammatory immune response in the acceleration of the disease process requires closer inspection with longitudinal follow-up of participants and repeated measures of gene expression.

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References


