High-Resolution, Three-Dimensional Reconstruction of the Outflow Tract Demonstrates Segmental Differences in Cleared Eyes

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Purpose. The rate of conventional aqueous humor outflow is the highest nasally. We hypothesized that this is reflected in regionally different outflow structures and analyzed the entire limbus by high-resolution, full-thickness ribbon-scanning confocal microscopy (RSCM).

Methods. We perfused pig eyes by anterior chamber cannulation with eight lectin-fluorophore conjugates, followed by optical clearance with benzyl alcohol benzyl benzoate (BABB). RSCM and advanced analysis software (Imaris) were used to reconstruct a three-dimensional (3D), whole-specimen rendering of the perilimbal outflow structures. We performed morphometric analyses of the outflow tract from the level of the trabecular meshwork (TM) to the scleral vascular plexus (SVP).

Results. Except for pigmented structures, BABB cleared the entire eye. Rhodamine-conjugated Glycine max agglutinin (soybean [SBA]) labeled the outflow tract evenly and retained fluorescence for months. RSCM produced terabyte-sized files allowing for in silico dissection of outflow tract vessels at a high resolution and in 3D. Networks of interconnected lumens were traced from the TM to downstream drainage structures. The collector channel (CC) volumes were 10 times smaller than the receiving SVP vessels, the largest of which were in the inferior limbus. Proximal CC diameters were up to four times the size of distal diameters and more elliptical at their proximal ends. The largest CCs were found in the superonasal and inferonasal quadrants where the highest outflow occurs.

Conclusion. RSCM of cleared eyes enabled high-resolution, volumetric analysis of the outflow tract. The proximal structures had greater diameters nasally, whereas the SVP was larger in the inferior limbus.

Keywords: aqueous flow, ribbon-scanning confocal microscopy, tissue clearing, outflow tract, lectins

IOP is the only modifiable factor in glaucoma shown to slow progression of this leading cause of blindness.1,2 In normal eyes, the trabecular meshwork (TM) was found to be a primary location of outflow resistance.3–5 Sites distal to the TM have not been examined fully due to difficulties visualizing small structures within the sclera.6,7 Recent TM bypass8,9 and ablation studies10–13 demonstrate that the outflow resistance downstream of the TM is much higher in eyes with glaucoma. Only a small fraction of patients (~0.3%) achieve the predicted IOP equal to episcleral venous pressure.13 Pre- and postoperative IOP is also correlated, suggesting an increased post-TM outflow resistance in patients with a higher preoperative IOP.10 Unmasking the three-dimensional (3D) architecture of these outflow structures is necessary to understand their anatomy and function. However, eyes that are more similar in size to human eyes require image acquisition at a depth more than 10 times greater compared with the commonly used mouse models with a scleral thickness at approximately 40 μm14–16 (human limbal sclera: 500 μm17). The technology and methods to detect small structures within solid tissues have only become available recently. Confocal microscopy is a powerful and versatile imaging modality providing detection of a range of fluorophores at a high resolution and in the same sample.20,21 Scatter and an absorbance of the exciting and emitted light within a tissue reduces the maximum depth of confocal microscopy to approximately 100 μm.22 Scatter and absorption can be mitigated through tissue-clearing approaches that remove light scattering and absorbing molecules and match the refractive index (RI) of the tissue to the mounting medium.23–25 Clearing can increase the maximum depth of confocal imaging to many millimeters, often limited only by the microscope optics.24 We recently showed in mouse brains that the depth and large area limits of traditional confocal microscopy can be overcome by using a threefold strategy that uses (1) a high numerical aperture long-working distance objective, (2) a tissue clearing technique, and (3) ribbon-scanning to reconstruct large, 2D images from which 3D projections can be rendered.24 There are important differences between the human and the porcine outflow tract, including the lack of a Schlemm’s
canal.26 However, the consistent high tissue quality, absence of naturally occurring glaucoma, short time from enucleation to use, and wealth of functional outflow studies convinced us to leverage our pig eye model.27–32 We applied ribbon-scanning confocal microscopy (RSCM) to image the lectin-labeled outflow tract anatomy throughout the limbal sclera. This approach poses high demands on data acquisition and processing but provides a comprehensive insight into the complex network of small structures that escape recently used spectral-domain optical coherence tomography33,34 and outflow casting.35 We hypothesized that this would allow correlating regional morphologic aspects to the well-established outflow patterns in this species.27–30,32 Lectins are ubiquitous, carbohydrate-binding proteins that have a high specificity for sugar moieties, and have been used to examine the glycosylation of the TM in glaucoma38 but can also be used to study vessels by binding to their glycocalyx.39,40 To overcome the highly disordered alignment of extracellular matrix components in the sclera,41 primarily water, collagen, and elastin, and their variable RIs,41,42 we modified a benzyl alcohol benzyl benzoate (BABB) protocol as a clearing technique of the lectin-labeled anterior segment.25,43 Using RSCM,44 we reconstructed large volumes of the anterior segment and performed volumetric analysis of the outflow tract architecture.

**Materials and Methods**

**Tissue Preparation and Whole Eye Lectin Perfusion**

Twenty-five freshly enucleated porcine eyes were obtained from a local abattoir (Thoma Meat Market, Saxonburg, PA, USA) and processed within 2 hours. Eyes were procured with eyelids, nictitating membranes, and extraocular muscles attached. Based on these anatomical landmarks, the laterality and orientation were determined. After removal of extraocular tissue, 5 of the 25 eyes were used to optimize the clearing protocol. The remaining 20 eyes were positioned facing up with the optic nerve stump secured in low-compression mounts (CryoElite Cryogenic Vial #W985100; Wheaton Scientific Products, Millville, NJ, USA). In these 20 eyes, a perfusion with the pressure set to 15 mm Hg by gravity was performed as previously described.44 Briefly, the anterior chamber was cannulated with a 20-gauge needle positioned temporally and just anterior to the limbus. With the bevel facing up, approximately 100 μL of aqueous humor per eye was drained. Each lectin (Table) was explored twice in separate eyes. An intracameral bolus of 0.2 mg/mL of lectin in PBS was injected followed by an infusion of the same lectin at a concentration of 0.02 mg/mL for 90 minutes. The lectins tested consisted of a Texas red-conjugated lectin, *Lycopersicon esculentum* agglutinin (TL; Texas red-conjugated; #TL-1176; Vector Laboratories, Inc., Burlingame, CA, USA) and a rhodamine-conjugated lectin kit that consisted of *Concanavalin A* (ConA), *Dolichos biflorus* agglutinin (DBA), *Arachis hypogaea* agglutinin (SBA), *Ricinus communis* agglutinin (RCA), *Glycine max* agglutinin (SBA), *Ulex europaeus* agglutinin (UEA), and *Triticum vulgaris* agglutinin (WGA); (Rhodamine Lectin Kit I, #RLK-2200; Vector Laboratories, Inc.). In addition to the lectin-perfused eyes, a control eye was perfused with PBS. An additional control eye was used to adjust and calibrate the infusion method to a physiologic pressure with a pressure transducer (DTX-plus; Argon Medical Devices, Plano, TX, USA; amplifier; ADInstruments, Colorado Springs, CO, USA).

The surface of the eyes kept was moist with PBS at all times. The eyes were perfusion fixed with fresh 4% paraformaldehyde (Catalog No. P6148; Sigma-Aldrich, St. Louis, MO, USA) postfixed overnight, and hemisected equatorially into an anterior and a posterior segment. The sclera and cornea were left intact, whereas the iris, ciliary body, lens, and vitreous were carefully removed as previously described.35 The anterior segment was bisected into inferior and superior halves. The samples were protected from light to prevent photobleaching of fluorophores.

**Tissue Clearing**

Five of the 25 eyes served to develop the tissue-clearing technique. We focused on BABB as a clearing technique when pilot experiments with CUBIC (clear, unobstructed brain imaging cocktails and computational analysis)25,26 caused the sclera to assume a gel-like consistency, expand, and gradually disintegrate. iDISCO (immunolabeling-enabled 3D imaging of solvent-cleared organs)23 was also evaluated but did not impart sufficient transparency. The BABB clearing method was based on a previous method25 with lengthened incubation times to

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**Table.** Abbreviations, Source of Lectins, Carbohydrate Specificities, Staining Intensity, and Location

<table>
<thead>
<tr>
<th>Lectin</th>
<th>Source</th>
<th>Monosaccharide Binding</th>
<th>Location</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tomato lectin (TL)</td>
<td><em>Lycopersicon esculentum</em></td>
<td>β(1,4)-linked N-acetylglucosamine</td>
<td>3 2 3</td>
</tr>
<tr>
<td>Concanavalin A (ConA)</td>
<td><em>Canavalia esculenta var</em></td>
<td>α-man, α-glc</td>
<td>2 2 2</td>
</tr>
<tr>
<td>Dolichos biflorus agglutinin (DBA)</td>
<td><em>Dolichos biflorus</em></td>
<td>α-galNAc (n-acetylgalactosamine)</td>
<td>3 3 3</td>
</tr>
<tr>
<td>Peanut agglutinin (PNA)</td>
<td><em>Arachis hypogaea</em></td>
<td>galβ3GalNAc or gal</td>
<td>0 0 2</td>
</tr>
<tr>
<td>Ricinus communis agglutinin (RCA)</td>
<td><em>Ricinus communis</em></td>
<td>d-galactose (Gal)</td>
<td>3 3 3</td>
</tr>
<tr>
<td>Soybean agglutinin (SBA)</td>
<td><em>Glycine max</em></td>
<td>α&gt;β-galNAc (n-acetylgalactosamine)</td>
<td>3 3 3</td>
</tr>
<tr>
<td>Ulex europaeus agglutinin (UEA)</td>
<td><em>Ulex europaeus</em></td>
<td>α-fucose (L-fucose)</td>
<td>3 1 2</td>
</tr>
<tr>
<td>Wheat germ agglutinin (WGA)</td>
<td><em>Triticum vulgaris</em></td>
<td>GlcNAc = f-acetylgalucosamine or GlcNac</td>
<td>2 0 0</td>
</tr>
</tbody>
</table>

Location: 3 = strong; 2 = medium; 1 = weak; 0 = negative.
ensure that the full thickness of the sample was penetrated by each solution at its corresponding step. Lectin-perfused samples were transferred into borosilicate glass vials (Catalog No. 03-339-21E; Fisher Scientific, Hampton, NH, USA), washed, dehydrated in increasing ethanol concentrations of 50%, 70%, 80%, and 96% in PBS for 90 minutes each, and left in 100% ethanol overnight. The 100% ethanol was replaced daily for 5 days. A 1:2 mixture of benzyl alcohol (Catalog No. 305197; Sigma-Aldrich) and benzyl benzoate (Catalog No. B6630; Sigma-Aldrich) was created. The dehydrated samples were transferred to a solution of BABB diluted 1:1 in ethanol, incubated for 24 hours, and transferred to 100% BABB for 30 minutes or until visibly clear. The high level of transparency that this protocol achieved could be best appreciated in eyes not stained with lectin or bisected (Fig. 1). For all incubations, samples were placed in solutions of at least twice the volume of the tissue and affixed to a vertical stage rotated at 20 revolutions/min.

Confocal Microscopy

Screening With Upright Confocal Microscopy. We screened the signal intensity and regional binding specificity of the different lectins (Table) in cleared samples on a Fluoview FV1200 upright confocal microscope (BX61; Olympus, Tokyo, Japan). Lectin signals were observed through the oculars, captured images, and in 3D reconstructions (Supplementary Video S1). Mounting chambers were cut from vinyl sheet material (Grip Taupe Shell/Drawer Liner, vinyl material, Model # 04F-C6U59-06; Home Depot, Pittsburgh, PA, USA) and affixed to glass slides with cyanoacrylate adhesive which formed a barrier to contain the BABB. The mounts were left to cure for a minimum of 6 hours to ensure the vinyl enclosure was firmly attached to the glass slide. After sample segments were positioned in their mounts, wells were filled with BABB and sealed on top with a coverslip; caution was taken to avoid trapping of air bubbles.

Whole-Specimen Ribbon-Scanning Confocal Microscopy. After selecting SBA as the preferred lectin for our studies, we acquired complete limbal circumference scans of one eye. Following several pilots, one eye was comprehensively assessed. Following several pilots, one eye was comprehensively assessed. We acquired complete limbal circumference scans of one eye. The scans were obtained on an RS-G4 ribbon-scanning confocal microscope (Caliber I.D., Andover, MA, USA) fitted with a Märzhäuser scanning stage (SCANplus IM 120 × 80, #00-24-579-0000; Märzhäuser Wetzlar GmbH & Co. KG, Wetzlar, Germany). An Olympus 25×, 1.05 NA water immersion objective (XPLN25XWMP2; Olympus) was used to acquire volumes with a voxel size of 0.365 × 0.365 × 2.43 μm as previously described. A scan-zoom of 1.5 was used during acquisition to achieve the desired resolution. Images were acquired over a single channel with an excitation wavelength of 561 and an emission filter of 630/60. Laser percentage, high voltage (HV), and offset were held constant throughout the volume at 2, 72, and 19, respectively. Custom-designed mounting chambers (Supplementary Material) consisted of two threaded anodized aluminum rings, two glass coverslips, and a silicone rubber gasket fitted to the thickness of each specimen. The bottom coverslip (40 mm, round) was sealed with vacuum grease, the chamber was filled with BABB, an appropriately sized gasket was inserted, a second cover glass was overlaid, and the top ring was screwed into place. The pressure between the coverslips secured the sample in place, and pressure on the gasket sealed the BABB solution inside the chamber. Due to the prolonged acquisition time, the ring mounts were secured in place in a custom-designed acrylic pool (Supplementary Material) that allowed for a large volume of water to be placed under the objective. This enabled more than 24 hours of acquisition before requiring the addition of water due to evaporation.

Data Processing and Image Analysis

Volumes of the limbus scans were reconstructed with Imaris 9.0 software (BitPlane AG, Zurich, Switzerland) from full-resolution, large-area composite TIFF images generated by the microscope. All data were saved in the Imaris file format (.ims) using a Lempel-Ziv-Welch (LZW) compression algorithm resulting in files of 1.1 and 0.78 terabytes (TB). The data were stored on network file servers and accessed using 10-gigabit/s network infrastructure. The analysis was performed on custom-built workstations running an Intel Core i7 6700K processor, 64 GB RAM, 10-gigabit/s networking, and NVIDIA GeForce GTX 1070 graphics card. In the superior and inferior portions of the scan, 10 contiguous, full-thickness representative surfaces of the limbal region were created using identical parameters. These were a surface grain size of 5.00 μm, background subtraction with diameter of largest sphere, which fits into the object of 300 μm, a background subtraction threshold value of 250, and a filter to remove particles under 500,000 voxels. Surfaces were segmented into TM, collector channels (CC), and scleral vascular plexus (SVP) (Figs. 2A3, 2B3) with the surface scissors function and labelled correspondingly. The TM was identified as a densely stained region of fibrous tissue at the base of each segment. CCs spanned from their site of connection to the TM to the SVP; a network of superficial vasculature that ran largely parallel to the episclera. Corneal endothelium and material outside the bounds of the limbus was excluded in surface creation and volumetric measurement. Volumes of labeled outflow tract structures were derived from the Imaris statistics function (Fig. 3). The CC openings were counted and measured along the xy-plane in Imaris’s slice mode using the line tool along the widest and narrowest lengths drawn through their central axes (Supplementary Material). The orifices were defined by the appearance of a bright wall in contrast to a dark lumen with defined edges, round or oval, and at least one traceable connection to a larger, more superficial, perpendicularly oriented SVP channel. All measurements were taken at the outermost point where parameters were met. Any orifices concealed by pigment, occasionally encountered in the pig, could not be visualized or considered. Quantitative data obtained from scans of the same eye were compared using the unpaired Student’s t-test. P < 0.05 was considered statistically significant.
Tissue Size Preservation Throughout Clearing

Limbal rings from two anterior segments were used to evaluate tissue dimensions at steps throughout the clearing process to determine when and where, if any, tissue shrinkage may occur. Limbal rings were dissected into 12 clock hours. Each of the 24 samples was approximately 5.7 x 2 mm and were given IDs from 1A through 12A and 1B through 12B. The specimens were taken through the clearing protocol in separate borosilicate vials. Using a stereo dissecting microscope (SZX16; Olympus), samples were placed flat against a glass slide with the TM facing away from the objective and the cornea facing away from the operator. Images were captured immediately after dissection, after PFA fixation, after the last EtOH dehydration step, and after clearing in 100% BABB. Measurements were taken in ImageJ (Version 1.50i; National Institutes of Health, Bethesda, MD, USA) of samples along the longest and widest points of the tissue pieces. Sample measurements were compared to fresh tissue baselines after each clearing step with a paired t-test.

RESULTS

Within 20 minutes to 1 hour of the final BABB exposure, limbal tissue became transparent and allowed grid lines to be seen from behind a cleared anterior segment (Fig. 1). During screening with the laser-scanning confocal microscope, fluorescence was absent in cleared control eyes not perfused with lectins. SBA stained the TM intensely except for a few regions with a weak signal that corresponded to pigment. The eyes could be left for up to 2 months in BABB without a notable difference in transparency or fluorescent signal. The lectin-labeled, cleared anterior segments could be imaged via RSCM (Fig. 2). One lectin-labeled, cleared anterior segment, divided into superior and inferior halves, was imaged via RSCM (Fig. 2). RSCM scan acquisition times for the superior and the inferior limbus segments were 53.4 and 35.2 hours, respectively, whereas the time for conversion from TIFF images to Imaris files was 23.8 and 12.2 hours per specimen. A total of 1,734,246 images were assembled. Data processing, segmentation, and analysis with Imaris took approximately 344 hours. The TL binding pattern matched that observed in lectin-stained cryosections made in previous studies. Of all screened lectins, only WGA and PNA discriminated between different outflow structures (Table). TL, RCA, and SBA labeled the outflow tract with the most uniform signal. Each of these lectins bound to the specific structure of the outflow pathway in every clock hour throughout the anterior segment. Individual cells of the corneal endothelium also stained occasionally and were visible as strand-like puncta (Fig. 2A, right). There were no observed regional variations in the binding pattern when the same lectin was tested in porcine eyes from a different donor. RSCM showed dense tubular networks throughout the tissue (Figs. 2A–B, 2B–4, red) and lumens of variable shape and diameter embedded within the TM (Figs. 3A–C, 3A–C, 4A–C).
Tributaries of a low signal within the TM were oriented parallel to the episclera (Figs. 3A2–3C2, white arrows) and culminated into one or more ovoid lumens at the TM inner wall. These channels spanned from the TM to the SVP (Fig. 3A3–3C3, white arrows) and could be traced in Imaris to render surfaces, illustrating variable branching and conjoining of outflow tracts. The hinge-like orientation of these lumens resembled human outflow tract structures seen in electron microscopy cross sections.48 Often, a single lumen structure was seen just distal to the convergence of three adjacent TM inner wall orifices. The superior hemisection fly-through demonstrated 8 superotemporal and 11 superonasal CCs at the TM level that branched into 16 superotemporal and 25 superonasal CCs at the SVP level (Supplementary Video S2). The hemisection fly-through of the inferior limbus showed 10 inferotemporal and 12 inferonasal CCs at the TM level and 16 inferotemporal and 20 inferotemporal CCs at the SVP level (Supplementary Video S3).

Moving from the proximal to the distal portion of the limbus, orifices at the TM inner wall gave rise to channels, analogous in structure to CCs and aqueous veins, that spanned from the TM up to the SVP with highly variable degrees of branching and tortuosity. All channels running vertically from the TM to the SVP were deemed CCs for this study. Lumens of
some CCs could be traced to a single point of connection with the SVP just distal to the channel’s origin at the TM. Other tracts were highly branched and connected to the SVP much farther from their opening at the TM level or in multiple places (Figs. 2, 3). Some filamentous structures in this region were too fine to distinguish a lumen even with an x-y-resolution of 365 nm (Supplementary Videos S1–S3). CCs were connected to a single, branched, and circumferentially spanning outflow channel with luminal widths notably larger than all other drainage structures. This structure was located within the outer third of the sclera, distal to the TM, and ran parallel to the episclera; it contained many valve-like structures (Supplementary Material) that had a high fluorescent signal. Using Imaris as visualization and analysis software for microscopy, automated surface reconstruction of the outflow tract was performed. Surfaces were segmented, in silico, into TM, SVP, and CC regions (Supplementary Video S4). Reconstruction of individual CC units, from their connection site at the TM to their connection site at the SVP, could be performed through manual tracing (Supplementary Video S5). Relative volumes of outflow structures consistently demonstrate densely stained TM, a lower signal density in the region between the TM and SVP, and high signal density in distal, superficial tracts (Fig. 3).

The CC volumes were more than 10 times smaller than the SVP volumes ($P < 0.001$; Fig. 4A). There were no differences between the temporal and nasal CC or SVP volumes. The inferior CC average volume was 1.9 times larger than the superior average CC volume ($P = 0.002$; Fig. 4B). The inferior SVP average volume was 1.4 times larger than the superior average SVP volume ($P < 0.001$; Fig. 4B). The average cross-sectional area (Fig. 5A) of the proximal end of CCs was 1.7 times larger nasally than temporally ($P = 0.035$) and 4.1 times as large as the distal portion of the CCs ($P < 0.001$). The largest proximal cross-sectional areas were seen in the superonasal and inferonasal quadrants (Fig. 5B). Collectors with the most elliptical shape at their proximal end were again found in the superonasal and inferonasal quadrants (Fig. 5D). Samples did not experience any significant shrinkage caused by paraformaldehyde (PFA) fixation (average size of PFA-fixed tissue compared with baseline: $99.5 \pm 2.5\%$, $P = 0.16$), ethanol dehydration (average size of ethanol-dehydrated tissue compared with baseline: $99.5 \pm 2.9\%$, $P = 0.93$), or BABB clearing (average size of BABB tissue compared with baseline: $99.8 \pm 2.5\%$, $P = 0.57$).

**DISCUSSION**

Outflow resistance in healthy eyes has traditionally been ascribed to the TM, but recent laboratory experiments and analysis of historical data show about half to be located further downstream. Contractile elements in the distal outflow tract indicate that the resistance can be altered. Our clinical findings with ab interno trabeculectomy (AIT), a plasma-mediated TM ablation, in up to 1540 patients highlight the importance of post trabecular resistance, as almost no participant achieved the episcleral venous pressure one would have predicted. Pressures lower than 18.6 mm Hg cannot easily be obtained without medications. Several groups have hypothesized that valve-like structures at the collector orifices are the culprit, but these are mostly disrupted in AIT, and in their entirety in sclerothalamotomy that removes the outer wall as well, suggesting an unidentified mechanism further downstream. To address these questions, we established a method to visualize and acquire large, full-thickness sections of the outflow tract that include a volumetric reconstruction of the porcine outflow.

Various chemical clearing techniques have been developed to address similar questions of 3D structure, connectivity, and the resulting organ function. Clearing methods can be grouped into four categories: solvent based (BABB, iDISCO), hydration (Sca/e A2, CUBIC), simple immersion (FocusClear), and hydrogel embedding (CLARITY, PACT, PARS). We chose pig eyes for this study for the abundance of outflow function data and the short time from enucleation to perfusion, helping confine dyes to the intact vascular spaces. We found that a modified CUBIC protocol did not impart the same level of scleral transparency as BABB, a reagent known to be effective in clearing tissues with a large content of extracellular matrix, like skin and gingiva. We selected a BABB based protocol in this study because it empirically yielded the most transparent samples. Also, BABB is relatively easy and quick (days compared with weeks), low cost, and preserved the signal from the lectin-conjugated fluorophore. Lectins have a long history of being used to label the glyocalyx of vascular endothelium, as well as aging. We assayed for a lectin marker to differentially label TM, CC, and more superficial vasculature but did not observe such specificities. Different lectins marked TM, downstream vasculature (Table), and in some instances, corneal endothelium.
while leaving surrounding scleral tissue unstained. Uniform labeling of the outflow tract was achieved by DBA, RCA, TL, and SBA, as observed under an Olympus FluoView upright confocal microscope. Out of these lectins, SBA was found to display the most complete and uniform labeling of the observable outflow tract morphology. Compared with fluorophores with more blue-shifted excitation and emission maxima, the tissue has reduced autofluorescence and light absorption at the excitation and emission maxima of rhodamine.45 For these reasons and due to data storage and processing limitations, we chose to proceed with the SBA-rhodamine sample for RSCM imaging. These features lend themselves well to volumetric, full-thickness acquisition of the outflow tract. The speed and high resolution achieved with confocal ribbon-scanning enabled the characterization of large volumes of the outflow tract that would not have been feasible with traditional confocal or light-sheet imaging modalities.21 This allowed us to readily isolate CCs and vessels of the SVP from within the complex outflow tract network. We found that the nasal CCs had the largest diameters and could be primarily found in the superonasal and inferonasal quadrant (Fig. 5). In addition to this, the proximal openings are more elliptical than the distal ones in these quadrants, possibly indicating an expandable reserve capacity. This matches function studies well27,44 that showed that nasal outflow44) but have Schlemm’s canal-like segments instead of the mostly continuous single lumen of human eyes and a thicker TM.26,58 Regardless, a similar, preferentially nasal and inferior flow can also be observed in human eyes.59,60 The volumes computed here demonstrate that CCs only contribute to a small spatial fraction of the complex outflow tract in porcine eyes and could generate a considerable post trabecular outflow resistance. This resistance may occur close to the region of the CC–TM interface, where vessel diameters are large but collapsible and oval or closer to the SVP junction point where they are four times smaller (Fig. 5A). Serial sections at the level of the TM and CCs showed numerous fine, filamentous structures that appeared to be connected on only one side and might indicate lymphatic sacs or vascular sprouts.61,62 Recent insights into outflow tract development have pointed toward a mixed origin of Schlemm’s canal and downstream vasculature from lymphatic and blood vessels.63–65 Although lectins show selective binding to specific sugar moieties, lectins that allow to reliably differentiate between lymphatic and blood vessels have not yet been identified. However, the role of glycosaminoglycans,66 flow properties, vessel wall adhesion, and mechanosensation67–69 in glaucoma38 can already be investigated using the lectins and techniques described here. Other staining methods to characterize the outflow tract, for instance, toxins70 or antibodies, must be tested for their compatibility with tissue clearing protocols. Our whole-specimen approach of data acquisition and processing to understand the conventional outflow tract is demanding and poses challenges similar to hypothesis-driven omics integration.71,72 The strategy presented here can now be applied to human eyes to identify the anatomic basis that may contribute to the post trabecular outflow resistance in glaucoma. A limitation of our study is that the visualization of

**Figure 5.** Cross-sectional area of CC sections. (A) CC openings at the level of the trabecular meshwork (proximal CC) had a 1.7-fold larger section area nasally than temporally ($P = 0.035$). Both nasally and temporally, the proximal portion of CCs was larger than their distal portion. (B) Frontal view of a right eye. The greatest section areas were found in the superonasal and inferonasal quadrant. (C) Proximal nasal and temporal CCs were more oval compared with their distal ends as expressed by the ratio of the maximal to the minimal cross-sectional width. (D) In the frontal view of this right eye, cross-sectional areas were more elliptical in the superonasal and inferonasal quadrant.
endothelia-binding dyes aids only to quantify the volume and length of outflow structures but does not allow a direct investigation of outflow or outflow resistance itself. To do so, the structures described here need to be matched to function by using, for instance, canalograms that allow to quantify regionally discrete aqueous humor outflow. This is possible only to a certain depth using noncleared eyes with the dyes used here but might be improved by using fluorophores excited with longer wavelengths that do not require clearing.

Deep tissue analysis of the live aqueous humor outflow tract excited with longer wavelengths that do not require clearing. used here but might be improved by using fluorophores only to a certain depth using noncleared eyes with the dyes

References

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References


**SUPPLEMENTARY MATERIAL**

**SUPPLEMENTARY VIDEO S1.** Small caliber branches of the outflow vasculature.

**SUPPLEMENTARY VIDEO S2.** Superior limbus fly-through.

**SUPPLEMENTARY VIDEO S3.** Inferior limbus fly-through.

**SUPPLEMENTARY VIDEO S4.** Large collector channel unit.

**SUPPLEMENTARY VIDEO S5.** Automated surface reconstruction.