Harnessing cell-encapsulated hydrogels to study astrocyte mechanoresponse in 4D

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Keywords: optic nerve head astrocytes, biomechanical strain, glaucoma, mechanobiology, ECM hydrogels, transcriptomics, morphology

Abbreviations

ATP adenosine triphosphate
ATR ataxia telangiectasia and Rad3 related
CNS central nervous system
ECM extracellular matrix
ETC electron transport chain
F-actin filamentous actin
GFAP glial fibrillary acidic protein
HIF-1α hypoxia-inducible factor 1 α
IL6 interleukin 6
IL17 interleukin 17
IOP intraocular pressure
MONHA mouse optic nerve head astrocyte
mTOR mammalian target of rapamycin
ONH optic nerve head
PI3K-Akt phosphoinositide 3-kinase Ak strain transforming
TGFβ2 transforming growth factor beta 2

Abstract

In glaucoma, the optic nerve head (ONH) is exposed to increased biomechanical strain, impacting the resident astrocytes that maintain neural homeostasis. After injury, astrocytes exhibit morphologic and metabolic shifts; however, the specific impact of glaucoma-related biomechanical strains on astrocyte behavior remains poorly understood. To address this, we utilized our previously established 3D cell-encapsulated ECM hydrogel to elucidate ONH astrocyte transcriptomic and cellular responses to varying biomechanical strain levels over time. Murine ONH astrocyte-encapsulated hydrogels were subjected to 0, 3, or 10% cyclic strain for 4h and 24h. Using confocal reflectance microscopy, we observed that hydrogel porosity was adequate for nutrient supplementation, while bulk hydrogel stiffness and cell viability remained unchanged after biomechanical strain. Mechanotranscriptional responses were robustly altered within 4h in a hydrogel region-, strain-, and time-dependent manner. RNA sequencing revealed changes in gene expression related to cell morphology, division, senescence, hypoxia, metabolism, and ECM regulation. Morphometric analyses of strained ONH astrocytes showed reduced F-actin area coverage, increased GFAP, HIF-1α, fibronectin, and collagen fibril reorganization. Our findings demonstrate that ONH astrocyte transcriptional responses are highly dependent on duration/magnitude of biomechanical strain and surrounding ECM density, corresponding with altered cell morphology, hypoxia, and ECM modification. This ONH astrocyte-encapsulated hydrogel provides a valuable platform for nuanced future manipulation of porosity, ECM composition, and cellularity to study the impact of biomechanical strain on ONH pathophysiology.

1. Introduction

Astrocytes are the master glial cells regulating central nervous system (CNS) homeostasis. They provide trophic and matrix support to neurons, contribute to modulating synaptic activity and interact with neighboring glial cells and blood vessels to ensure optimal function and protection of neuronal tissue [1-5]. Astrocytes are highly sensitive to biomechanical stimuli, with their development and heterogeneity influenced by the surrounding biomechanical environment [6-8]. Equally important to healthy physiologic conditions is the response of astrocytes to different biomechanical insults within a diseased CNS. In neuropathies induced acutely by trauma (i.e., traumatic brain or spinal cord injuries) or chronically by neurodegeneration (i.e., glioblastoma or glaucoma), astrocytes are subjected to various degrees of pathological biomechanical stimuli - compression, tension, tissue stiffening/softening - and their mechanoresponse is directed by the magnitude and duration of these cues [9-11].

One of the hallmark features of astrocyte response to pathological biomechanical stimuli is the development of reactive astrogliosis [4, 12-15]. In glaucoma, this phenomenon is most notable within the optic nerve head (ONH), where there is progressive loss of retinal ganglion cells ultimately leading to irreversible blindness [16, 17]. The local astrocytes within this region provide key support to axons and are first responders to acute glaucomatous insult prior to neuronal dysfunction [18, 19]. As part of their early response, astrocytes lose their stellate morphology in favor of a more polarized cell shape; they also drastically alter their actin cytoskeleton architecture, and upregulate intermediate filament proteins associated with reactive gliosis such as glial fibrillary acidic protein (GFAP), vimentin, and nestin [18, 20-23].

As the disease progresses, astrocytes decouple from neighboring cells and remodel the surrounding extracellular matrix (ECM) by significantly increasing production of ECM proteins

(i.e., fibronectin and collagen IV), matrix crosslinking/degrading enzymes (i.e., transglutaminase 2 and matrix metalloproteinases 2/9), and pro-fibrotic cytokines (i.e., transforming growth factor beta 2 (TGFβ2)) [24-26]. These glial cells are also responsible for matching the metabolic demand of neurons under stress. This metabolic interdependence, exemplified by the glutamate-glutamine cycle and astrocyte-mediated vasodilation, is crucial for neuronal health and its disruption contributes to neurodegenerative diseases [5, 27].

Evidence supports that the ONH in glaucoma is subjected to various degrees of compressive and tensile strains that vary by microregion. Specifically, finite element modeling studies predict between 3-10% compressive and 2-5% tensile biomechanical strain on the ONH with intraocular pressure (IOP) elevation [28-30]. While many studies have used such modeling approaches to understand the biomechanical strains within the glaucomatous ONH, there are limited reports on the direct transcriptional and morphologic response of local astrocytes to isolated biomechanical strains. This is a crucial gap in our understanding of how glaucomatous biomechanical strains can impact astrocyte behavior and, ultimately, disrupt their functional support of neurons. Prior studies have reported on ONH astrocyte cell cultures subjected to mechanical stressors such as hydrostatic pressure and tension in 2D [27, 31, 32]. While not without merit, conventional 2D *in vitro* culture systems are not suitable to analyze 3D astrocyte morphological complexity and coupling under biomechanical forces. Furthermore, it is nearly impossible to subject monolayer astrocyte cultures to compression in 2D.

We previously developed a cell-encapsulated hydrogel system containing murine ONH astrocytes and ECM biopolymers (collagen type I and hyaluronic acid), which permits detailed analysis of cell shape and cell-cell/cell-ECM interactions in 3D [33]. In the present study, we investigated how ONH astrocytes that are encapsulated within this ECM hydrogel respond to

varying degrees of compressive biomechanical strain over time (i.e., in 4D) using a well-established bioreactor [34-36]. We aimed to thoroughly characterize the transcriptional and morphological responses of astrocytes to strain magnitude and duration, and ECM collagen density. To achieve this, we conducted bulk RNA sequencing and morphometric analyses to determine changes in gene expression, cytoskeletal organization, metabolic function and ECM remodeling over time. Ultimately, our study represents a comprehensive investigation of time-dependent ONH astrocyte mechanoresponses to glaucoma-relevant biomechanical strains and seeks to provide mechanistic insights into broader astrocyte mechanodysfunction in neurodegenerative diseases of the CNS.

2. Methods

2.1 Mouse ONH astrocyte isolation and culture

C57BL/6J mice were purchased from the Jackson Laboratory (Bar Harbor, ME) and bred in house according to the institutional guidelines for the humane treatment of animals (IACUC #473) and to the ARVO Statement for the Use of Animals in Ophthalmic and Vision Research. Each harvest used 5-8 mice aged 6-8 weeks. The isolation/culture of primary mouse ONH astrocytes (MONHAs) was performed as previously described [37]. Briefly, optic nerve head tissue was dissected from each eye using a SMZ1270 stereomicroscope at a location proximal to the sclera. The samples then underwent digestion in 0.25% trypsin (Invitrogen, 25200-056, Carlsbad, CA, USA) for 15 minutes at 37 °C. Following digestion, the tissue was resuspended in MONHA growth medium, consisting of Dulbecco's modified Eagle's medium, DMEM/F12 (Invitrogen, 11330-032, Grand Island, NE, USA), supplemented with 10% fetal bovine serum (FBS; Atlanta Biologicals, S11550, Atlanta, GA, USA), 1% penicillin/streptomycin (Corning, 30-

001-CI, Manassas, VA, USA), 1% Glutamax (Invitrogen, 35050-061, Grand Island, NY, USA),

and 25 ng/ml epidermal growth factor (EGF; Sigma, E4127-5X, St. Louis, MO, USA). The

digested ONH tissue was then plated onto T75 cell culture flasks coated with 0.2% gelatin and

incubated at 37 °C in a humidified atmosphere with 5% CO2. MONHAs migrated from the ONH

tissue over a period of 10-14 days before the first passage. All subsequent experiments included

MONHAs at passage 3.

2.2 Preparation of PDMS molds

A polydimethylsiloxane (PDMS) mixture was used at a 10:1 ratio of elastomer to curing

agent as per the manufacturer's instructions (PDMS; Sylgard 184, Dow Corning, Midland, MI,

USA). This mixture was poured into custom 3D printed ABS-M30 filament negative molds (F170;

Stratasys, Eden Prairie, MN, USA), measuring either 10 mm diameter x 6 mm depth or 8 mm

diameter x 4 mm depth, cured at 60°C, and autoclaved prior to use.

2.3 Preparation of MONHA-encapsulated hydrogels

MONHA-encapsulated hydrogels were prepared as previously described [33]. Briefly,

MONHAs (2.5×10^6 cells/ml) in media were mixed with 3.1 mg/ml methacrylate-conjugated

bovine collagen type I (MA-COL; molecular weight: ~300 kDa, degree of methacrylation: ~60–

70%; Advanced BioMatrix, Carlsbad, CA, USA), 1 mg/ml thiol-conjugated hyaluronic acid (SH-

HA; Glycosil®; molecular weight: ~300 kDa, degree of thiolation: ~20–30%; Advanced

BioMatrix), and 0.025% (w/v) riboflavin (Sigma-Aldrich, R7774, Darmstadt, Germany)

(photoinitiator) on ice. The chilled MONHA hydrogel precursor solution was pipetted as 250 µl

into 8 x 4 mm PDMS molds or 500 µl into 10 x 6 mm PDMS molds. Constructs were then

crosslinked by exposure to low intensity blue light (405-500 nm) (OmniCure S1500 UV Spot

Curing System; Excelitas Technologies, Mississauga, Ontario, Canada) at 10.3 mW/cm² intensity

for 5 minutes. Following hydrogel crosslinking, each MONHA-encapsulated hydrogel was

carefully removed from its respective PDMS mold and left in MONHA growth medium [33, 37].

MONHA-hydrogels were cultured for 14 days prior to any experiments, and media was

replenished every 2-3 days.

2.4 MONHA-encapsulated hydrogel pore size analysis

The collagen network of acellular and MONHA-encapsulated hydrogels was imaged with

confocal reflectance microscopy on a Zeiss LSM980 scanning confocal microscope (Carl Zeiss

Microscopy, Jena, Germany) using a 40x water immersion objective (LD LCI Plan-Apochromat

40x/1.2 Imm Corr DIC M27, Zeiss). The excitation wavelength was set to 488 nm and backscatter

signal was collected via a beam splitter BC80/20. Pore size within the collagen gel was calculated

using an algorithm as previously described [38]. In brief, 6-9 fields of view were obtained from

the core and periphery of MONHA-encapsulated hydrogels for each magnitude of strain (i.e., 0%,

3%, or 10%) at each timepoint (i.e., 4 hours, 24 hours). The image size was set to 1024 x 1024

pixels in x/y and the z-step interval set to 0.5 μm collecting a total of 50 μm in the z-axis direction.

The confocal z-stack images of the collagen gel were input to FIbeR Extraction MATLAB code

[39] to extract the Euclidean distance map. The pore size was then extracted using the bubble

analysis algorithm in MATLAB [40].

2.5 MONHA-encapsulated hydrogel permeability analysis

To determine the permeability of MONHA-encapsulated hydrogels, acellular and

MONHA-encapsulated hydrogels were crosslinked on top of 3 μm pore size transwell inserts in

12-well plates (Thermo Fisher, 141080, Kennebunk, Maine, USA). Before initiating the

permeabilization assay, gels were equilibrated in DMEM/F12 for 24h. The assay was initiated by

adding 200 μl of a 1000 μg/ml FITC-labelled dextran (70 kDa) tracer solution (FITC-DEAE-

Dextran; Sigma, 54702-1G) into the top chamber above each hydrogel. In the bottom chamber,

1000 μl Dulbecco's Phosphate Buffered Saline 1X (DPBS; Invitrogen, 14190-44) was added

which served as receiving medium. The tracer molecule leakage into the bottom well was

quantified (i.e., after permeating through the hydrogel). A volume of 600 μl from the bottom well

was withdrawn at each time point (5, 10, 15, 30, 45 min – 1, 2 h), and each time it was replenished

by an equal volume of fresh DPBS. For quantification, a standard curve was generated using

graded dilutions of FITC-labelled dextran (1 to 1000 μg/ml). A volume of 200 μL for each

supernatant sample and standard were transferred into a 96-well plate and absorbance was

measured at 490 nm using a BioTek Gen5 microplate reader (version 3.16; Agilent Technologies,

Palo Alto, CA, United States). The concentration of "leaked" FITC-labelled dextran in the

collected samples was determined using a standard curve equation and as previously described

[41, 42]. Cumulative FITC-labelled dextran at each time point was calculated by using:

Total FITC-labelled dextran in the bottom chamber before removal at time point t:$\text{Total}_t = C_t$

$\times 1000 \mu L$;where C_t is concentration FITC-DEX at time point t.

Total FITC-DEX removed at time point t:$\text{Removed}_t(\mu g) = C_t \times 600 \mu L$; where $600\ \mu L =$ volume

removed.

Remaining FITC-DEX in the bottom well after removal at time point t:$\text{Remaining}_t\ (\mu g) = \text{Total}_t$

$(\mu g) - \text{Removed}_t\ (\mu g)$.

The cumulative leaked FITC-labelled dextran up to time point t :

$$\text{Cumulative}_t = \sum_{t=0}^{t} Removed_t\ (\mu g)$$

2.6 MONHA-encapsulated hydrogel collagen fiber signal intensity, compaction and cell

alignment analysis

For collagen signal intensity and compaction analyses, MONHA-encapsulated hydrogels

were imaged using confocal reflectance microscopy (see Methods 2.4). Fold-change collagen

signal intensity in MONHA-encapsulated hydrogels was quantified with background subtraction

from an acellular hydrogel using Z-project Maximum Intensity Projection in FIJI and further

normalized to number of nuclei. Collagen compaction was determined as previously described

[43]. In brief, the mean intensity of collagen fibrils in the fixed area around the astrocytes was

computed and then normalized against the mean intensity of the collagen fibrils as deduced from

acellular collagen images. The cropped area was found with binarized fluorescent images of the

astrocytes with pretrained denoising convolutional neural network (dsCNN)/median filter and

adaptive threshold functions in MATLAB. Moreover, due to the large sample size (number of

pixel intensity N > 10000), we used Cohen's effect size d to compare the relative difference

between the mean value of different groups (i.e., substantive significance), which scales with

sample size unlike p-value (i.e., statistical significance) [44]. Cohen's d = 0.20, 0.50, and 0.80 was

used to indicate the effect size as small, medium, or large, respectively.

2.7 Mechanical loading of MONHA-encapsulated hydrogels

Using a custom bioreactor system [34-36], unconfined MONHA-encapsulated hydrogels

were cultured for 14 days, then subjected to either 0%, 3% or 10% cyclic compressive strain at

1Hz for 4 hours and 24 hours. These biomechanical strain intensities have been previously

correlated with strains within the glaucomatous ONH [28-30]. Hydrogels were placed on PDMS-

coated glass containers and maintained in 40 ml of astrocyte media for the duration of

biomechanical strain. A thermoplastic polyester platen attached to a linear actuator (Zaber Inc.,

NA08A30-T4), with 5 mm clearance from the glass wall and 10 perforations (5 mm in

diameter/perforation) cyclically compressed the hydrogels to 3 or 10% of their height. 0% static

controls were maintained in similar conditions with the platen immediately above the hydrogels,

but not actively compressing them. For post-strain analysis, the top 1 mm (adjacent to the

compressive platen) and bottom 1 mm (adjacent to the glass container) were discarded as to avoid

any biased effects caused by contact with the platen or glass container, and the 3 mm core was

further separated from the periphery of the hydrogel to allow for systematic comparisons between

different regions, magnitudes and durations of biomechanical strain.

2.8 MONHA-encapsulated hydrogel cell viability analyses

Cell viability within the hydrogel was determined using a CellTiter 96® Aqueous Non-

Radioactive Cell Proliferation Assay (MTS; Promega, Madison, WI, USA) as per the

manufacturer's instructions. Following 24 hours of cyclic strain, MONHA-encapsulated hydrogels

were incubated with the staining solution (114 μl MTS, 6 μl PMS solution, 600 μl media) at 37 °C

for 4h, and absorbance at 490 nm was assessed with a spectrophotometer plate reader (BioTEK,

Winooski, VT, USA). Fold-change over time of blank-corrected absorbance values was analyzed

to quantify cell viability in hydrogels.

2.9 RNA sequencing and data sharing

The 3 mm core and the remaining periphery of MONHA-encapsulated hydrogels were

isolated after biomechanical strain for bulk RNA-sequencing. Three samples per strain group (i.e.,

0%, 3%, 10%) at each time point (i.e., 4h, 24h) were used. Briefly, each sample was homogenized

for 2 minutes using a Fisherbrand™ 150 Handheld Homogenizer. Total RNA was extracted using

Trizol reagent (Invitrogen, 15596026, Carlsbad, CA, United States) according to the

manufacturer's protocol. 250 ng of extracted RNA was used as input to the Illumina Stranded

mRNA Library prep kit as per the manufacturer's instructions. Library quality and quantity was

assessed with Agilent 2100 Bioanalyzer (Agilent Technologies, Palo Alto, CA, United States). 36

libraries were pooled together for sequencing on an Illumina NextSeq 2000 next-generation

sequencing instrument with paired end 2x100bp. High-quality clean reads were filtered into

FASTQ format. RNA sequencing data is deposited and accessible through NIH Gene Expression

Omnibus (GEO) DataSets GSE300233.

2.10 Bioinformatic data analysis

RNA-seq data were analysed using the online platform Illumina Partek-Flow (version

12.6.1) (Chesterfield, Missouri, USA). Briefly, FASTQ files were subjected to sequence quality

checks using "QC for Sequencing Reads" tool. Using the STAR 2.7.8a tool the reads were mapped

against the mouse reference genome mm39. Aligned reads were then quantified to annotation

model of mouse genome. Principal component analysis (PCA) of the top 2000 genes with greatest

variance in expression was applied to all samples to delineate clustered groups between

biomechanical strain durations and intensities. Differentially expressed genes (DEGs) across time

(i.e., 24h vs 4h) and biomechanical strain magnitude (i.e., 0% vs 3% vs 10%) as cofactors were

determined using ANOVA. Separately, pairwise comparisons between biomechanical strain

intensities (i.e., 3% vs 0%, and 10% vs 0%) at each timepoint (i.e., 4h or 24h) within each hydrogel

region (i.e., core or periphery) were identified using DESeq2 tool. For both analyses, the genes

and transcripts with FDR corrected p-value ≤ 0.05 and |Log2 fold change| ≥ 1.50 were considered

differentially expressed. Gene ontology (GO) pertaining to biological process, cellular component,

and molecular function for each individual comparison was determined based on the over

representation analysis (ORA) using the publicly available enrichment tool WEB-based GEne SeT

AnaLysis Toolkit (https://www.webgestalt.org) [45, 46] with FDR corrected p-value ≤ 0.05. Gene

Set Enrichment Analysis (GSEA) against KEGG/Reactome databases was used to delineate altered

molecular pathways across time amongst all groups and significance was set to FDR corrected p-

value $\leq$ 0.05 and |Log2 fold change| $\geq$ 1.50.

2.11 Encapsulated MONHA morphological analysis

Following application of biomechanical strain, MONHA-encapsulated hydrogels were

fixed with 4% PFA at 4 °C overnight, permeabilized with 0.5% Triton™ X-100 (Thermo Fisher

Scientific) and stained for filamentous actin (F-actin; Alexa Fluor® 488- or 594- conjugated

Phalloidin (1:200, Abcam, Ab176757 or Ab176753); nuclei were counterstained with DAPI.

Fluorescent z-stack images were captured using an air 20x objective (Plan-Apochromat 20x/0.8

M27, Zeiss) and a Zeiss LSM780 scanning confocal microscope (Carl Zeiss Microscopy, Jena,

Germany). The image size was set to 1024 x 1024 pixels or 512 x 512 in x/y, and six titled z-stack

images consisting of 100 μm in z-axis direction with the z-step interval set to 1.3 μm were obtained.

Assessment of cell morphology was conducted using Z-project Maximum Intensity Projection in

FIJI (NIH, Bethesda, MD) across individual z-stacks. F-actin masks were then generated and

binarized in FIJI, and the area of F-actin coverage was calculated by the ratio of percentage of

pixels with non-zero pixels [47].

2.12 MONHA-encapsulated hydrogel sectioning and immunohistochemical analysis

MONHA-encapsulated hydrogels were cultured for 14 days prior to biomechanical loading

for 4h and 24h and then fixed with 1% Pagano fixative solution (i.e., 4% PFA, 50 mM Sucrose,

25 mM MgCl2, 2.5 mM KCl, HEPES 7.4) [48] at 4°C overnight. Samples were then washed with

DPBS and embedded in 10% bovine gelatin (Sigma-Aldrich, G9382-500G). Subsequently,

gelatin-embedded MONHA-encapsulated hydrogels were fixed again with 1% Pagano fixative

solution at 4°C overnight and then washed with DBPS. Using the Leica VT1000 S vibratome, 150

μm sections were cut and collected in cold PBS. Sections were then permeabilized with 0.5%

Triton™ X-100 for 15 min, blocked in 7% normal goat serum (Abcam, Ab7481) for 1h and

immunostained in 1% normal goat serum (Abcam, Ab7481) for either GFAP (Anti-GFAP

Antibody Cy3 Conjugate, 1:100, Millipore, MAB3402C3), fibronectin (rabbit anti-fibronectin

antibody, 1:100, Abcam, Ab2413) or hypoxia-inducible factor 1α (HIF-1α; rabbit anti-HIF-1

alpha antibody, 1:200, Abcam, Ab228649) overnight, followed by stain with Alexa Fluor® 488-

conjugated secondary antibody (goat polyclonal antibody to rabbit IgG, 1:500, Abcam, Ab150077)

for 1 h; nuclei were counterstained with DAPI (Abcam, Ab228549). Sections were mounted with

ProLong™ Gold Antifade (Thermo Fisher Scientific, P36930, Waltham, MA, USA) on

Superfrost™ Plus microscope slides (Fisher Scientific, 1255015). 3-4 fields of view per core or

periphery of the hydrogel were acquired using an air 40x objective (S Plan Fluor 40x/0.6, Nikon)

and an Andor BC43 SR spinning-disk confocal microscope (Oxford Instruments, Belfast, Northern

Ireland). The image size was set to 2040 x 2040 pixels in x/y and the z-step interval set to 1 μm

collecting a total of 40 μm in the z-axis direction. Fold-changes in normalized signal intensity were

quantified with background subtraction using Z-project Maximum Intensity Projection in FIJI and

further normalized to number of nuclei for GFAP and HIF-1α analyses.

2.13 MONHA-encapsulated hydrogel rheology analysis

MONHA-encapsulated hydrogels, fabricated using the 10 x 6 mm PDMS molds, were

cultured for 14 days prior to application of biomechanical strain. Immediately following 24 hours

of mechanical loading, viscoelasticity of MONHA-encapsulated hydrogels (N = 6 per group) was

measured using a Kinexus rheometer (Malvern Panalytical, Westborough, MA, USA) with an 8

mm diameter parallel plate. Rheometry measurements were performed as previously described

[33, 49]. Briefly, an 8 mm geometry was lowered onto the hydrogels to establish a calibration

normal force of 0.02 N. Subsequently, an oscillatory shear-strain sweep (0.1–60%, 1.0 Hz, 25 °C)

was performed to determine storage modulus (G') and loss modulus (G") values within the linear

viscoelastic region. The storage modulus for each sample was then converted to elastic modulus

(E) using the equation $E = 2 * (1 + v) * G'$, assuming a Poisson's ratio (v) of 0.5 for the ECM

hydrogels.

2.14 Statistical analyses

Statistical analyses were performed using GraphPad Prism software v10.0.2 (GraphPad

Software, La Jolla, CA, USA). Experiments were conducted at least in triplicate. Individual sample

sizes are specified in each figure caption. Group comparisons were determined by one-way

(ANOVA) with Tukey's multiple comparisons *post hoc* as appropriate and Cohen's effect size d

as described in Methods 2.6 [44]. All data are shown with mean ± SD. The level of significance

was set to $p < 0.05$.

3. Results

3.1 Characterization of MONHA-encapsulated hydrogel pore size, permeability, and regional

differences.

Under healthy conditions, local astrocytes create a honeycomb network spanning the

diameter of the rodent ONH [50]. Their processes can measure a thickness of 1.3 ± 0.04 μm with

elongations of up to 30 μm [51]. To determine whether our previously developed hydrogel system

was adequately porous to allow for astrocyte process elongation and coupling through the collagen

network, we first quantified the pore size of acellular hydrogels in the absence of biomechanical

strain. Using confocal reflectance microscopy to directly visualize collagen fibers within acellular

hydrogels, we observed that the collagen fibrils displayed a homogeneous network with pore sizes

ranging from 2-7 μm (Suppl. Fig. 1A-B).

Next, we quantified hydrogel permeability over time (Suppl. Fig. 1C). Since our MONHA

growth media contains primarily FBS proteins ranging $< 60 - 70$ kDa (with albumin being the

most abundant) [52, 53], and growth factor EGF of ~ 6 kDa [54], we chose to use a 70 kDa FITC-

labelled dextran tracer solution as an indicator for permeability. Both the acellular and MONHA-

encapsulated hydrogels showed robust permeability, as seen by the rapid detection of increased

fluorescence below the hydrogel within 5 minutes of adding FITC-labelled dextran solution to the

top of the hydrogels (Suppl. Fig. 1C). Thus, these results support that MONHA-encapsulated

hydrogels allow for efficient and adequate nutrient distribution.

To characterize the architecture of the ECM network within our MONHA-encapsulated

hydrogels, we evaluated the compaction of collagen fibrils. We observed regional differences

within our constructs such that samples at baseline (under no biomechanical strain) displayed

increased collagen compaction in the periphery of the hydrogel as compared to the core (Suppl.

Fig 2A-B). Moreover, the collagen compaction appeared greater immediately adjacent to astrocyte

cell bodies/processes (Suppl. Fig. 2A). Collectively, these data support that encapsulated ONH

astrocytes differentially remodel and contract their surrounding collagen fibers in the core as

compared to the unbound periphery of the hydrogel. Because of this heterogeneity in collagen

compaction, we artificially delineated the core from the periphery of MONHA-encapsulated

hydrogels for subsequent experiments and comparisons (Suppl. Fig. 2C).

3.2 Quantification of astrocyte cell viability within MONHA-encapsulated hydrogels after cyclic

biomechanical strain.

After characterizing the hydrogel system, we then applied compressive biomechanical

strains to MONHA-encapsulate hydrogels using a custom bioreactor [34-36]. We applied 3% and

10% compressive strains, which have been reported in ONH tissues during glaucomatous insult

[28-30]. After 24h of biomechanical strain, we quantified astrocyte cell viability in MONHA-

encapsulated hydrogels (Suppl. Fig. 3). We found no detectable difference in total viability by

MTS assay after biomechanical strain for 24h (Suppl. Fig. 3).

3.3 Biomechanical strain regulates global transcriptomic response of MONHAs across strain

level and time

Astrocytes within the ONH are transcriptionally responsive to alterations in IOP. Several

murine experimental glaucoma studies have investigated the effects of elevated IOP on ONH

astrocyte gene expression and downstream responses [19, 55, 56]. However, it is not clear how

glaucoma-associated *biomechanical strains* directly affect ONH astrocyte gene expression and

molecular pathways. Here, we investigated the transcriptional response of ONH astrocytes to

biomechanical strain across strain intensities and durations. Overall, all the RNA samples showed

high quality indicated by an RNA integrity number (RIN) ≥ 8.

To assess the global transcriptional effects of biomechanical strain on astrocytes, we

performed principal component analysis (PCA) on bulk RNA sequencing data from MONHA-

encapsulated hydrogels subjected to 0%, 3%, or 10% static compression for either 4 hours or 24

hours per hydrogel region (i.e., core or periphery). Within the core of the hydrogel, the first three

principal components (PC1, PC2, and PC3) accounted for a cumulative 84.5% of the total variance

in the dataset, with PC1(i.e., time) alone explaining 63.07% (Suppl. Fig. 4A). Within the periphery

of the hydrogel, the top three principal components accounted for 84.4% of total variance (PC1:

57.58%, PC2: 17.46%, PC3: 9.36%) (Suppl. Fig. 4B). PCA revealed that the duration of

biomechanical strain primarily drove transcriptional variation, with samples separating along PC1.

Strain dynamics in both regions were most observed with 10% strain revealing an initial significant

shift along PC2 and PC3 in the 4h groups and maintained in 24h groups. Overall, the PCA results

of both the core and periphery demonstrate that the responses of encapsulated MONHAs to

biomechanical stress are modulated in a time- and strain- dependent manner, with more

pronounced transcriptional changes observed under higher and prolonged strain compared to 0%

controls.

3.4 Pairwise analysis reveals distinct transcriptional responses dependent on magnitude of

biomechanical strain and hydrogel region.

Our initial investigation into the impact of biomechanical strain on MONHA-encapsulated

hydrogels focused on how different strain intensities (i.e., 3% or 10%) affect gene expression at

different timepoints (i.e., 4h or 24h). DESeq2 analysis identified 19,163 genes after 4h

biomechanical strain and 18,376 genes after 24h biomechanical strain. We applied a cutoff of FDR

≤ 0.05 and fold change $|FC| \geq 1.5$. DEGs from the core of the hydrogel are depicted in Table 1 and

in Fig. 1 A, B and Fig. 2 A, B. To simplify the discussion, we have annotated groups by "magnitude

of strain" followed by "hydrogel region"; thus, the hydrogel core that underwent 3%

biomechanical strain is denoted as *3c*, while the hydrogel periphery is denoted as *3p*. In response

to both intensities of biomechanical strain, we observed fewer DEGs in the 24h group vs the 4h

group, supporting that encapsulated MONHAs adapt to biomechanical strain with increasing

durations (Table 1).

	4h	24h
3% vs 0%	**1,368 total DEGs** 686 upregulated, 682 downregulated	**377 total DEGs** 104 upregulated; 273 downregulated
10% vs 0%	**1,968 total DEGs** 880 upregulated; 1088 downregulated	**413 total DEGs** 147 upregulated; 266 downregulated

452   **Table 1.** DEGs with FDR ≤ 0.05 and fold change $|FC| \geq 1.5$, core of the hydrogel.

453  For all groups, to identify the functional categories the DEGs were enriched in, the list of

454 DEGs per comparison were uploaded to the publicly available WEB-based GEne SeT AnaLysis

455 platform. In the *3c* group after 4h biomechanical strain, over representation analysis (ORA)

456 revealed enrichment of GOs involved in cell-cell junction, collagen-containing ECM,

457 laminin/fibronectin binding, and cell proliferation and migration (Fig. 1C). With increased

458 magnitude of strain, the *10c* group after 4h biomechanical strain showed enriched pathways in the

459 regulation of immune/defense response, response to cytokine, mitochondrion, adenosine

460 triphosphate (ATP)/nucleotide binding, and regulation of programmed cell death (Fig. 1D). These

461 findings suggest that, with short duration of strain (4h), increased magnitude of biomechanical

462 strain induced a shift in DEGs enriched in morphology, ECM regulation, and cell proliferation

463 (3%) to enrichment in inflammation regulating and cell cycle/division-related pathways (10%)

464 (Fig. 1C, D).

Fig. 1. Pairwise transcriptional mechanoresponse of MONHAs encapsulated within the hydrogel core to 4h of biomechanical strain. (A-B) Volcano plots representing the number of DEGs with FDR ≤ 0.05 and |FC| ≥ 1.5 in response to 3% and 10% biomechanical strain for 4h. **(C-D)** Listed are five representative gene ontology (GO) pathways per functional group of the top 30 most significant GOs at each timepoint.

Similar analyses were done for MONHAs undergoing biomechanical strain for 24h. For

the *3c* group after 24h biomechanical strain, GOs showed genes enriched in cell cycle, DNA

replication, organelle fission, condensed chromosome, microtubule associated complex, DNA

helicase activity and ATP binding (Fig. 2C). In contrast, in the *10c* group after 24h biomechanical

strain, GOs showed enriched genes in pathways of carbohydrate/AMP binding, response to

hormone, cell-substrate junction, response to hypoxia, and oxidoreductase activity (Fig. 2D).

These findings suggest that application of biomechanical strain for longer durations (24h) induces

a shift in DEGs enriched cell cycle and division pathways (3%) to enrichment in metabolism and

ECM regulatory pathways (10%) (Fig. 2C, D).

Fig. 2. Pairwise transcriptional mechanoresponse of MONHAs encapsulated within the hydrogel core to 24h of biomechanical strain. (A-B) Volcano plots representing the number of DEGs with FDR ≤ 0.05 and |FC| ≥ 1.5 in response to 3% and 10% biomechanical strain for 24h. **(C-D)** Listed are five representative gene ontology (GO) pathways per functional group of the top 30 most significant GOs at each timepoint.

491   We then analyzed the periphery of the hydrogel, where cells were surrounded by more

492   densely packed ECM (Suppl. Fig. 2). Again, we applied a cutoff of FDR ≤ 0.05 and fold change

493 |FC| ≥ 1.5; DEGs from the periphery of the hydrogel are depicted in Table 2 and in Suppl. Fig. 5

494   A, B and Suppl. Fig. 6 A, B.

	4h	24h
3% vs 0%	**688 total DEGs** 336 upregulated, 352 downregulated	**13 total DEGs** 6 upregulated; 7 downregulated
10% vs 0%	**801 total DEGs** 322 upregulated; 479 downregulated	**445 total DEGs** 112 upregulated; 333 downregulated

Table 2. DEGs with FDR ≤ 0.05 and fold change |FC| ≥ 1.5, periphery of the hydrogel.

In this peripheral region, for relatively short duration biomechanical strain (4h), we

similarly observed that MONHAs displayed a shift in DEGs enriched in cellular signaling

regulation (*3p*) to inflammation and metabolism pathways (*10p*) (Suppl. Fig. 5C, D). Interestingly,

analysis of the *3p* group after 24h biomechanical strain identified few DEGs with no significant

GOs by our FDR cutoff values. The *10p* group after 24h biomechanical strain showed GOs

primarily enriched in ECM regulation and adhesion (Suppl. Fig. 6C).

Taken together, these transcriptomic and functional analyses provide new insights into

astrocyte responses to isolated biomechanical stimulation.

3.5 Hydrogel region and duration of biomechanical strain modulate key astrocytic molecular

and metabolic pathways

To investigate the contribution of increasing magnitude and duration of biomechanical

strain to MONHA transcriptional response, we performed ANOVA of biomechanical strain groups

across timepoints followed by GSEA against both KEGG and Reactome databases. In the hydrogel

core, encapsulated astrocytes downregulated pathways related to focal adhesions *(Col6a6; Flnc;*

Flt1; Hgf; Itga10), integrin cell surface interactions *(Itga5; Itga7; Itgb3; Itgb8; Lama2)*, and ECM

interactions *(Col6a5; Col6a6; Itga10; Tnxb)* (Fig. 3A, B, D). These altered pathways corroborate

our findings on genes enriched in GOs associated with cell morphology and ECM reorganization.

Biomechanical strain on encapsulated astrocytes also led to the downregulation of key signaling

pathways regulating astrocyte quiescence, including those regulating stem cell pluripotency *(Rest;*

Tbx3; Wnt11), calcium signaling *(Camk2a; Fzd3; Fzd4),* interleukin-6 (IL6) *(Clcf1; Cntfr; Il6ra;*

Lif; Lifr; Osmr), phosphoinositide 3-kinase Ak strain transforming (PI3K-Akt) *(Bcl2l11; Chuk;*

Vegfa; Flt3l; Gdnf; Hgf; Il6ra), and Wnt signaling *(Wnt11; Wnt5a)* (Fig. 3A, B, D).

Additionally, MONHAs encapsulated within the core of the hydrogel showed significant

changes in metabolism with increasing time and magnitude of strain. Specifically, we observed

upregulated pathways related to metabolic and respiratory electron transport chain (ETC) (Fig. 3A,

B, C). As a part of the mitochondrial oxidative phosphorylation, the ETC is crucial for ATP

production. These upregulations corresponded with gene enrichment in metabolism/ETC

complexes and in thermogenesis (*Acot2, Aldh1a1, Acy1, Adh7, Atp6v0d2, Cox6b1, Cox7a2,*

Cox7b, Cox7c, Cox8a, Ndufa1, Ndufa11, Ndufa12, and *Ndufb8)* (Fig. 6A-C*).* Interestingly,

pathways for both cell cycle/repair *(Ccnb1; Ccnb2; Ccne1; Cdc20; Cdc45; Cdk1; Cdk18; Chek2)*

and cellular senescence *(Ccna2; Ccne2; Foxm1; Map2k6; Rbl1; Rras)* were also upregulated (Fig

3A-C), potentially indicating a cytoprotective stress response to increasing biomechanical strain

over time.

We then investigated the <u>hydrogel periphery</u>, where astrocytes were surrounded by a denser

ECM at baseline. Here, we found that peripheral MONHAs also downregulated pathways related

to cell cycle, mitosis, DNA synthesis, replication, and repair, ATP activation in response to

replication stress, and chromosome maintenance, but observed a lack of IL6/Wnt signaling

pathways (Suppl. Fig. 7A-D).

Collectively, these findings reveal that biomechanical strain plays a crucial role in

modulating astrocyte mechano-transcriptional response. Specifically, increased strain over time

induces downregulation of pathways related to cell structure and signaling while upregulating

metabolic and stress response pathways, possibly indicating an attempt at maintaining cellular

function and survival. Conversely, a denser ECM in the hydrogel periphery may provide a level

of protection to increasing compressive strain over time and, as such, it may dampen the pro-

inflammatory reactive astrocyte phenotype and modulate cell cycle, suggesting a link between

ECM composition and astrocyte-mediated inflammation. These astrocyte transcriptional profiles

elucidate the complex changes over time interlinking biomechanical forces, ECM density, and

cellular mechanoresponse.

Fig. 3. Transcriptional mechanoresponse of MONHAs encapsulated within the hydrogel core over time with increasing strain. (A-B) Listed here are 20 up and down most significant pathways against KEGG and Reactome databases with representative 35 DEGs for the **(C)**

548   upregulated and **(D)** downregulated pathways (FDR ≤ 0.05 and |FC| ≥ 1.5) based on ANOVA

549   analysis of MONHAs mechanoresponse over time (i.e., 24h vs 4h) with increasing strain.

3.6 Increased compressive strain alters MONHA cytoskeletal architecture.

Immediately following glaucomatous insult, ONH astrocytes respond by reorienting their

cell bodies and remodeling their F-actin cytoskeleton architecture [18, 20-23, 51]. Given that

transcriptomic analyses showed an enrichment in genes regulating cell process and cytoskeletal

organization, we asked whether isolated biomechanical strains would alter MONHA morphology

and cytoskeletal architecture in absence of other key *in vivo* microenvironmental cues. To do so,

we quantified F-actin area coverage and levels of GFAP expression in MONHA-encapsulated

hydrogels after biomechanical strain application for 4h and 24h, respectively.

After 4h cyclic biomechanical strain, MONHAs showed no significant changes in F-actin

area coverage in either the core or periphery of the hydrogels (Fig. 4A-C). In contrast, after 24h of

cyclic biomechanical strain, there was a significant drop in F-actin area coverage within the core

of the hydrogel in a strain-dependent manner (Fig. 4A-C). Both *3c* and *10c* groups showed ~50%

decrease in F-actin area coverage compared to control (0%) (Fig. 4C). Interestingly, application of

biomechanical strain did not alter the F-actin area coverage in the periphery of the hydrogel in

either strain group (Fig. 4C). Consistent with the observed F-actin remodeling, encapsulated

MONHAs showed varied cell alignment in response to duration and magnitude of strain (Suppl.

Fig. 8). While both 4h groups and periphery groups had no effect on cell alignment, the *10c* group

demonstrated a significant increase in astrocyte alignment in response to biomechanical strain

(Suppl. Fig. 8B). Overall, these data demonstrate that encapsulated MONHAs are robustly

mechanoresponsive, altering cellular morphology in response to biomechanical stimuli.

Fig. 4. Regional differences in MONHA morphology in response to duration and magnitude of biomechanical strain. (A) Representative fluorescence images of astrocyte F-actin staining (A) and cytoskeletal binarized masks (B). Scale bar: 100 μm. **(C)** Quantitative analyses of F-actin mask area (N = 6 fields of view/group). Statistical significance was determined using one-way ANOVA (*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, **** $p < 0.0001$) for F-actin area fraction analyses.

Astrocytes respond to glaucomatous insults within the ONH by undergoing reactive gliosis, in part characterized by an increase in expression of intermediate filaments such as GFAP [4, 57, 58]. We previously showed that both MONHAs in 2D and encapsulated within 3D hydrogels can

be induced to express higher levels of GFAP upon stimulation with a known inducer of astrocyte

reactivity such as exogeneous TGFβ2 [33, 37]. Therefore, we asked whether application of cyclic

biomechanical strain would induce a similar induction in intermediate filaments. Control (0%

compression) MONHA-encapsulated hydrogels showed baseline immunoreactivity of GFAP

throughout the hydrogel. After both 4h and 24h of biomechanical strain, GFAP immunolabeling

increased ~1.5 fold in both the core and periphery of the hydrogel (Fig. 5A-C, Suppl. Fig. 9A-C).

As such, these data support that biomechanical strains directly induce cytoskeletal alterations in

encapsulated astrocytes.

589
590 **Fig. 5. GFAP expression of encapsulated-MONHAs within the hydrogel core in response to**
591 **biomechanical strain. (A)** Representative fluorescence images and quantification of fold change
592 in astrocyte GFAP signal intensity (N = 6 fields of view/group) after 4h **(B)** and 24h **(C)** of
593 increasing strain (i.e., 3% or 10%). Statistical significance was determined using one-way
594 ANOVA (*p < 0.05 , **p < 0.01, ***p < 0.001) for GFAP expression levels. Scale bar: 20 μm.
595
3.7 Biomechanical strain alters HIF-1α levels within MONHA-encapsulated hydrogels.

Glaucomatous insults are associated with hypoxia and metabolic stress within the retina

and ONH since IOP-induced deformations can impact the local vasculature and reduce

oxygenation of the ONH [59-61]. Since our transcriptomic data revealed many altered pathways

pertaining to cellular response to stress and hypoxia, and altered metabolic processes, we asked if

astrocytes within our model could modulate expression of HIF, thereby potentially affecting

downstream metabolic activity. Specifically, to determine whether encapsulated MONHAs

undergo such metabolic stress in response to cyclic biomechanical strain, we examined levels of

HIF-1α after application of biomechanical strain. HIF-1α immunoreactivity was low in control

(0%) samples at both timepoints (i.e., 4h and 24h; Fig. 6, Suppl. Fig. 10) regardless of hydrogel

region (i.e., core vs periphery). Hydrogel-encapsulated MONHAs exhibited significantly

increased HIF-1α levels by ~1.25-fold in the core groups after 4h cyclic biomechanical strain and

by ~2-fold in the periphery (Fig. 6A, B); HIF-1α also increased ~1.5-2-fold after 24h cyclic

biomechanical strain (Fig. 6A, C). Similar trends of HIF-1α elevation were observed in the

periphery of the hydrogel (Suppl. Fig. 10). Taken together, these data support that cyclic

biomechanical strain can directly induce metabolic insufficiency.

Fig. 6. HIF-1α expression of encapsulated-MONHAs within the hydrogel core in response to
biomechanical strain. (A) Representative fluorescence images and quantification of fold change
in astrocyte HIF-1α expression signal intensity (N = 6 fields of view/group) after 4h **(B)** and 24h

of increasing strain (i.e., 3% or 10%). **(C)**. Statistical significance was determined using one-way

ANOVA (*$p < 0.05$, **$p < 0.01$, ***$p < 0.001$) for HIF-1α expression levels. Scale bar: 20 μm.

3.8 Biomechanical strain on MONHA-encapsulated hydrogels induces matrix remodeling via

collagen network remodeling and fibronectin deposition.

Our transcriptomic analyses showed a strong enrichment in genes related to collagen and

ECM modulation. *In situ,* ONH astrocytes can modulate their surrounding ECM via secretion of

crosslinking and/or degrading enzymes [24, 57]. Therefore, we asked how application of cyclic

biomechanical strain would influence astrocyte modulation of the ECM microenvironment. We

first performed confocal reflectance microscopy to directly visualize collagen fibers within

MONHA-encapsulated hydrogels after biomechanical strain. We previously showed that control

constructs (0%) display regional differences in collagen arrangement, with more uniformly

distributed collagen fibers within the core of the hydrogel, and an increased density of collagen

fibers in the periphery of the hydrogel (Suppl. Fig. 2). While 4h of cyclic biomechanical strain did

not induce significant remodeling of the collagen fibrils across groups, after 24h biomechanical

strain, both 3% and 10% showed significant *decrease* of collagen compaction within the core (Fig.

7A, B) and a significant *increase* in collagen compaction in the periphery compared to control

(0%) (Suppl. Fig. 11A, B). Collectively, these data support that application of cyclic

biomechanical strain for 24h significantly alters collagen compaction in a region-dependent

manner.

Fig. 7. ECM collagen fibrils remodeling in the core of MONHA-encapsulated hydrogels in response to biomechanical strain. (A) Representative fluorescence images of collagen fibrils remodeling in response to duration (i.e., 4h or 24h) and magnitude of strain (i.e., 3% or 10%) (N = 6 fields of view/group). Scale bar: 20 μm. **(B)** Quantification of collagen compaction post strain.

641 Cohen's effect size d (Cohen's d = 0.20, 0.50, and 0.80 is used to indicate the effect sizes as small,
642 medium, or large, respectively).
643
Reactive astrocytes increase secretion of key ECM scaffold proteins such as fibronectin.

This glycoprotein can also interact with other ECM proteins (i.e., collagen I and laminin) further

promoting matrix crosslinking and, thus, contribute to the stiffening and fibrosis of the ONH tissue

[24, 57, 62-65]. As such, we investigated how biomechanical strain impacts astrocyte secretion of

fibronectin. Across all groups, biomechanical strain increased fibronectin deposition in MONHA-

encapsulated hydrogels (Fig. 8). After 4h of biomechanical strain, hydrogels showed a ~2.5-3-fold

increase in fibronectin immunolabeling within the core, and a ~1.5-fold increase within the

periphery (Fig. 8 A, B). Similar trends were observed with 24h of biomechanical strain, such that

the core displayed a ~6-fold increase (Fig. 8 A, C), and the periphery of the hydrogels had a less

robust ~2-fold increase in fibronectin immunolabelling (Suppl. Fig. 12).

Fig. 8. ECM fibronectin secretion in the core of MONHA-encapsulated hydrogels in
response to biomechanical strain. (A) Representative fluorescence images of fibronectin in
response to duration (i.e., 4h or 24h) and magnitude of strain (i.e., 3% or 10%) (N = 6 fields of
view/group) and **(B-C)** quantification of fold change in fibronectin signal intensity. Statistical
significance was determined using one-way ANOVA (*$p < 0.05$, **$p < 0.01$, **** $p < 0.0001$)
for fibronectin signal intensity. Scale bar: 20 μm.
661

662   The observed alterations in ECM protein compaction and deposition could potentially

663 impact the global stiffness of MONHA-encapsulated hydrogels. Thus, we analyzed the overall

664 rheological properties of hydrogels after biomechanical strain. After application of 3% or 10%

665 biomechanical strain for 24h, we found no significant differences in hydrogel stiffness compared

666 to their uncompressed (0%) controls (Suppl. Fig. 13).

667   Collectively, these data show that cyclic biomechanical strain significantly alters collagen

668 distribution and astrocyte fibronectin production in MONHA-encapsulated hydrogels, indicating

669 a dynamic interplay between mechanical stimuli, ECM remodeling, and astrocyte

670 mechanoresponse.

672 *4. Discussion*

674   Mechanical injury is a driving factor in the pathogenesis of several CNS disorders,

675 including traumatic brain injury, spinal cord injury, and glioma [7, 66-68]. In glaucoma, increased

676 biomechanical strains on the ONH have long been associated with elevated IOP and disease

677 progression [28-30, 57]; and yet, the mechanoresponse of ONH resident cells remains poorly

678 understood. ONH astrocytes have emerged as key regulators of retinal ganglion cell axonal health.

679 In *in vivo* glaucoma models, these local astrocytes are amongst the first to respond by reorganizing

680 their cytoskeleton architecture and gap junction coupling [18, 20-23, 51]. In the present study, we

681 sought to comprehensively analyze the direct transcriptional and functional responses of astrocytes

682 to glaucomatous biomechanical strains, to better understand the role of these pathologic

683 biomechanical forces on astrocyte behavior.

Dissecting the ONH astrocyte mechanoresponse by modeling glaucomatous biomechanical

strains in a 3D ECM hydrogel system

Prior studies have explored ONH astrocyte mechanoresponse to glaucomatous

biomechanical strains using conventional 2D *in vitro* cultures [27, 69]. However, it is increasingly

recognized that the ECM significantly influences cell behavior, with mechanical, structural, and

compositional cues playing critical roles in modulating cell function [70]. Newer *in vitro* 3D

models, including our own, utilize viscoelastic ECM biopolymer hydrogels such as collagen and

hyaluronic acid to better mimic the 3D architecture and promote a more natural astrocyte

morphology [33, 71, 72]. By encapsulating astrocytes within a collagen/hyaluronic acid network,

one can directly visualize cell-cell and cell-ECM interactions. We previously showed that

encapsulated murine ONH astrocytes extend processes in 3D, couple with astrocyte neighbors,

and bind to and modify their surrounding ECM [33]. In this study we sought to comprehensively

investigate how 3D-encapsulated ONH astrocytes respond to glaucoma-related biomechanical

strains over time. A custom bioreactor has been used on rat cortical astrocytes encapsulated in

collagen to dissect their mechanoresponse to compression [34]. Building on this prior work, we

used a newer version of the same 3D compressive bioreactor to apply increasing intensities of

biomechanical strain over time (i.e., in 4D) to investigate nuanced ONH astrocyte mechano-

transcriptomic and morphometric responses to mechanical stimuli.

Biomechanical strain triggers a multifaceted transcriptomic and functional response in ONH

astrocytes

Five main functional responses were observed in this study. Hydrogel-encapsulated murine

ONH astrocytes demonstrated transcriptomic alterations in (i) proliferation/senescence, (ii)

cytoskeletal architecture, (iii) metabolic function, (iv) inflammation, and (v) ECM remodeling in

response to mechanical strain. Many astrocytic genes revealed enrichment in DNA replication,

mitotic cell cycle and chromosomal dynamics, as well as cellular senescence and p53 signaling.

Early in *in vivo* glaucoma models, ONH astrocytes proliferate, and exhibit increased reactive

gliosis [19, 23, 73]. With prolonged IOP elevation, ONH astrocytes show evidence of cell

senescence and death [74, 75]. Interestingly, in our study, transcriptional alterations did not

correlate with a change in astrocyte viability in response to relatively short durations of

biomechanical strain of 4h and 24h. Future studies will examine astrocyte senescence/death in

response to longer durations of biomechanical strain.

Biomechanical strain induces alterations of astrocyte cytoskeletal architecture and intracellular

signaling pathways

There is *in vivo* evidence that ONH astrocytes undergo a dramatic reorientation of their F-

actin cytoarchitecture within 8 – 72 h of acute IOP elevation [18, 21-23]. In our study, hydrogel-

encapsulated murine ONH astrocytes downregulated pathways of focal adhesion and ECM-

interactions, and genes were enriched in GOs pertaining to morphological changes such as

cytoskeleton, actin-based cell projection, dendrite and cell-cell junction. *In vivo* glaucoma models

also depict a decrease in astrocyte process complexity and coupling [51, 74], potentially reducing

astrocyte-astrocyte connectivity as well as contact with surrounding blood vessels, retinal ganglion

cell axons, and ECM. Similarly, in response to both 3% and 10% biomechanical strain, we showed

a trend in decreased murine ONH astrocyte F-actin coverage after 4h of biomechanical strain that

significantly worsened with increasing magnitude and duration of strain. Thus, the observed

downregulation of focal adhesion and ECM-interaction regulatory pathways, coupled with

decreased F-actin coverage under biomechanical strain suggests a significant compromise in the

structural and functional integrity of the 3D astrocytic network. As such, a lack of adequate

astrocyte-astrocyte communication and interactions with surrounding ECM may further propagate

glaucomatous damage.

A key feature of the glaucomatous ONH is the onset of reactive astrogliosis and the

development of a pro-inflammatory astrocyte phenotype [14, 23, 57, 58, 76]. This is particularly

evidenced by the upregulation of intermediate filaments like GFAP, vimentin, and nestin, along

with the secretion of inflammatory cytokines [4, 12]. Consistent with these observations, our study

found enrichment of genes related to astrocyte reactivity and inflammation. Moreover, cytoskeletal

alterations can disrupt intracellular calcium signaling [57, 77, 78] . In our model, increased

biomechanical strain downregulated pathways like stem cell pluripotency, calcium signaling, IL6,

PI3K-Akt, and Wnt signaling. Consistent with the variability of F-actin cytoskeletal changes we

observed within our system (i.e., decreased F-actin coverage in the core, but not periphery),

hydrogel-encapsulated murine ONH astrocytes also displayed a range of GFAP upregulation.

Notably, the highest GFAP expression was observed in astrocytes located within the core of the

ECM hydrogel after 24h of biomechanical strain. In line with our RNAseq data, this heightened

reactivity may stem from altered calcium signaling as a direct result of strain-induced F-actin

cytoskeletal remodeling [78]. As such, these cellular changes depict the intricate relationship

between biomechanical forces and astrocyte cytoskeletal/signaling dynamics, and its crucial role

in ONH astrocyte pathogenesis.

In glaucoma models, the optic nerve undergoes hypoxia and metabolic insufficiency,

correlating with increased glycolysis and ATP production [15, 60, 61, 79]. In response to

biomechanical strain, we observed altered pathways related to hypoxia and oxygen levels. Within

4h of biomechanical strain, genes were enriched in cell response to hypoxia pathways and

maintained at longer durations (24h). These transcriptional changes correlated with increased HIF-

1α expression, which can trigger transcription of hypoxia-responsive genes, affecting downstream

metabolism [61, 80, 81]. We also observed upregulated metabolic and respiratory electron

transport/ATP synthesis pathways with genes enriched in mitochondrion and ATP binding. Thus,

our data highlight the important role of biomechanical strain in modulating astrocyte metabolic

function. Moreover, metabolic dysfunction, including altered glycolysis and ATP production, is

intertwined with pathways regulating cell survival and death, and can trigger cellular senescence

[60, 82]. These processes are increasingly recognized as key contributors to the pathogenesis of

glaucoma [83]. Further understanding the metabolic-cell senescence interplay in response to

longer durations of biomechanical strain and alterations of oxygen availability is crucial for

elucidating the mechanisms driving ONH astrocyte dysfunction in glaucoma.

ECM Integrity Modulates Astrocyte Response to Biomechanical Strain

In disease, astrocytes modify the ECM extensively, leading to increased ECM protein

production and crosslinking [24, 57, 62, 63]. Here, our transcriptomic analyses revealed a

significant enrichment of genes associated with collagen, fibronectin, and ECM modulation. More

specifically, we denoted downregulated pathways related to ECM-receptor interaction, integrin

cell surface interactions, ECM proteoglycans and ECM organization. Accordingly, we observed

differences in collagen fiber density after biomechanical strain. After 24h of strain, there was a

significant reduction in collagen compaction surrounding the ONH astrocytes in the core of the

hydrogel, suggesting that the observed changes in F-actin area coverage may diminish cell-ECM

interactions, resulting in a decreased ability to remodel surrounding collagen fibrils. Similar to the

glaucomatous ONH [24, 57, 62-65], we also found increased fibronectin levels in hydrogel-

encapsulated murine ONH astrocytes after biomechanical strain. Astrocyte-driven ECM

remodeling, prompted by increased biomechanical strain, may exacerbate glaucomatous injury

[84]. Future studies targeting astrocyte-mediated ECM modulation are warranted to explore the

restoration of ECM homeostasis to prevent further glaucomatous damage.

Interestingly, we found certain divergent ECM phenotypes in the periphery of the hydrogel,

with collagen fibers showing greater compaction with increasing magnitude and duration of

biomechanical strain. While biomechanical strain resulted in gene enrichment in cell cycle and

ECM regulation, and increased expression levels of GFAP, HIF-1α, and fibronectin (similar to the

core astrocytes), there was greater gene enrichment in mitochondrion, small metabolic process,

and ROS. Notably, there were pathways upregulated in cell cycle/stress, oxidative phosphorylation

and organelle protein trafficking (motor proteins, DNA replication, activation of ataxia

telangiectasia and Rad3 related (ATR) in response to replication stress, Golgi to ER transport),

and downregulated reactivity/inflammation (interleukin 17 (IL17), mammalian target of

rapamycin (mTOR), PI3K-Akt, cytokine-cytokine interaction, calcium signaling). Also in this

region, F-actin area coverage and process complexity remained unchanged after biomechanical

strain and showed *increased* collagen compaction (in contrast to the core of the hydrogel). The

difference in transcriptomic and phenotypic response is quite curious and highlights the important

role that surrounding ECM integrity plays in astrocyte response to biomechanical strain.

Limitations and Future Directions

While the current *in vitro* hydrogel model offers a more controllable microenvironment to

study the complex mechanoresponses of ONH astrocytes, it also presents inherent limitations when

used to mimic the intricate *in vivo* biomechanical loading of the optic nerve head in glaucoma [24,

28-30, 57]. Here, we encapsulated murine ONH astrocytes in a fibrillar ECM hydrogel, which does

not precisely recapitulate the complex composition of a primate lamina cribrosa nor a murine

astrocytic lamina [62, 85, 86]. In the future, the hydrogel system could be modified by ECM

patterning, to generate a more representative lamina cribrosa-like structure. Many of our insights

into mechanisms of glaucoma pathophysiology are gained from experimental rodent models [14,

15, 20, 21, 50, 51, 55, 87-89]. To compare/contrast the effects of isolated biomechanical strain on

ONH astrocyte behavior to existing *in vivo* model systems, here, we encapsulated *murine* ONH

astrocytes. Our model system does allow for the incorporation of other resident cells, including

microglia or human ONH cell types, enabling analysis of cell-cell interactions under

biomechanical strain. It is important to note that our study used static 0% strain as controls, while

astrocytes *in vivo* experience constant biomechanical loading as baseline [24, 28-30, 57]. The

benefit of encapsulating cells within 3D ECM biopolymers is the ability of the cells to directly

interact with and modify these polymers [11, 90-92] (as seen in Suppl. Fig. 2). This supports that

encapsulated astrocytes experience a baseline level of biomechanical strain [93]. Consequently,

our study reports on the effects of *superimposed* compressive biomechanical strain on

encapsulated MONHAs.   Future studies can modify superimposed strain and frequency

appropriate for the species of origin (i.e., murine cells vs. human cells). Lastly, our astrocyte-

encapsulated hydrogel model system is compatible with other bioreactors, such as the FlexCell

tension system [94, 95], permitting future live-cell imaging to investigate the mechanisms

governing mechanotransduction of ONH cells in glaucoma.

Conclusions

Taken together, our transcriptomic and morphometric data provide new insights into ONH

astrocyte responses to isolated biomechanical stimulation. As the key mechanosensors of the

ONH, astrocytes are critical for initiating complex molecular cascades that can result in both

protective and detrimental outcomes, underscoring the importance of studying their nuanced

mechanoresponse. These responses are highly dependent upon dynamic astrocyte-ECM

interactions. Thus, our astrocyte-encapsulated ECM hydrogel is ideal for investigating

mechanisms of cellular mechanosensitivity in response to biomechanical strain, and permits

systematic future manipulation of ECM components/structure, oxygen availability, and even

incorporation of additional cell types to further characterize ONH cell mechanobehavior.

Disclosure

The authors report no conflicts of interest.

Funding

This project was supported in part by a National Institutes of Health (NIH) grant

K08EY031755 (to P.S.G.), R01EY036880 (to P.S.G.), R21EY036198 (to P.S.G.), NIH/National

Eye Institute R01EY034096 (to S.H.), R21EY036189 (to S.H.), BrightFocus Foundation

G2024006S (to S.H.), David Epstein Career Advancement Award in Glaucoma Research from

Research to Prevent Blindness (to S.H.), unrestricted grants from Research to Prevent Blindness

and Lions Region 20-Y1 to SUNY Upstate Medical University Department of Ophthalmology and

Visual Sciences, R35GM142963 (to A.E.P.), R01EY023242 (to Y.L.), R01EY023242S (to Y.L.),

R21EY033961 (to Y.L.), R01EY032960 (to Y.L.), R21EY028671 (to Y.L.), and P30EY031631

(to Y.L.), and private foundations, The Glaucoma Foundation, the BrightFocus Foundation, and

the Glaucoma Research Foundation, (to Y.L.), R21NS139236 (to M.V.).

Acknowledgments

We thank the Neuroscience Microscopy Core at Upstate Medical University and the Blatt

BioImaging Center at Syracuse University for imaging support. **Author contributions:** A.N.S.,

S.P, M-T. H. T., A.K., S.G., M.P.G., M.V., Y.L., A.E.P., S.H. and P.S.G. designed all experiments,

collected, analyzed, and interpreted the data. A.N.S and P.S.G. wrote the manuscript. All authors

commented on and approved the final manuscript. S.H. and P.S.G conceived and supervised the

research.

Data and materials availability: All data needed to evaluate the conclusions in the paper

are present in the paper and/or the Supplementary Materials, and RNAsequencing Data available

on NIH GEO DataSets GSE300233.. Additional data related to this paper may be requested from

the authors.

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Supplementary Information

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1160 **Supplemental Fig. 1. Characterization of the MONHA-encapsulated hydrogel model system.**
1161 **(A)** Representative fluorescence image of collagen fibril distribution and quantification of pore
1162 size range **(B)** within acellular hydrogels (N = 5). Scale bar 10 μm. **(C)** Assessment of the
1163 normalized average permeability of acellular and MONHA-encapsulated hydrogels (N = 3/group)
1164 as calculated by FITC-labelled 70kDa dextran as tracer molecule.
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Supplemental Fig. 2. Regional differences in collagen fibril compaction of MONHA-encapsulated hydrogels. (A) Density of collagen fibrils in the core and periphery of the MONHA-encapsulated hydrogels after 2 weeks in culture; scale bar 20 μm. **(B)** Quantitative analysis of normalized collagen compaction within the core and periphery of MONHA-encapsulated hydrogels (N = 3/group). Cohen's d = 0.20, 0.50, and 0.80 is used to indicate the effect sizes as small, medium, or large, respectively. **(C)** Schematic delineating regional segmentation of MONHA-encapsulated hydrogels post biomechanical strain.

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1176 **Supplemental Fig. 3. Cell viability following biomechanical strain.** Normalized MONHA cell
1177 viability after 24h biomechanical strain via MTS assay (N = 6/group). Significance was determined
1178 by one-way ANOVA using multiple comparisons tests.
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Supplemental Fig. 4. Regional principal component analyses of encapsulated MONHAs
transcriptomes in response to biomechanical strain over time. Each point represents an
individual replicate per region (n = 18/core and 18/periphery) subjected to cyclic biomechanical
strain (blue = 0%, red = 3%, orange = 10%) for 4 hours (small spheres) or 24 hours (large spheres).
Duration of strain (i.e., time) is the dominant source of variation, with point separation along PC1,
and magnitudes of strain are observed with PC2 and PC3. **(A)** In the core region, the three principal
components (i.e., PC1: 63.07%, PC2: 13.38%, PC3: 8.05%) collectively explain 84.5% of the total
variance. **(B)** In the periphery, the three principal components (i.e., PC1: 57.58%, PC2: 17.46%,
PC3: 9.36%) account for 84.4% of total variance.
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Supplemental Fig. 5. Pairwise transcriptional mechanoresponse of MONHAs encapsulated within the hydrogel periphery to 4h of biomechanical strain. (A-B) Volcano plots representing the number of DEGs with FDR ≤ 0.05 and |FC| ≥ 1.5 in response to 3% and 10% biomechanical strain for 24h. **(C)** Listed are five representative gene ontology (GO) pathways per functional group of the top 30 most significant GOs after 4h of strain.

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Supplemental Fig. 6. Pairwise transcriptional mechanoresponse of MONHAs encapsulated within the hydrogel periphery to 24h of biomechanical strain. (A-B) Volcano plots representing the number of DEGs for 24h with FDR ≤ 0.05 and |FC| ≥ 1.5 in response to 3% and 10% biomechanical strain for 24h. **(C)** Listed are five representative gene ontology (GO) pathways per functional group of the top 30 most significant GOs at each timepoint.

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Supplemental Fig. 7. Transcriptional mechanoresponse of MONHAs encapsulated within the hydrogel periphery over time with increasing strain. (A-B) Listed here are 20 up and down most significant pathways against KEGG and Reactome databases with representative 35 DEGs for the **(C)** upregulated and **(D)** downregulated pathways (FDR ≤ 0.05 and |FC| ≥ 1.5)

1209   based on ANOVA analysis of MONHAs mechanoresponse over time (i.e., 24h vs 4h) with
1210   increasing strain.

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Supplemental Fig. 8. Regional differences in encapsulated MONHA cell alignment in
response to biomechanical strain. Quantitative analyses of cell alignment based on F-actin mask
area (N = 6 fields of view/group) in response to 4h **(A)** and 24h of increasing biomechanical strain
(i.e., 3% or 10%) **(B)** within the core of the hydrogel, and 4h **(C)** and 24h of biomechanical strain
(D) within the periphery of the hydrogel, Statistical significance was determined using one-way
ANOVA (** $p < 0.01$).
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1221 **Supplemental Fig. 9. GFAP expression of encapsulated-MONHAs within the hydrogel**
1222 **periphery in response to biomechanical strain. (A)** Representative fluorescence images and
1223 quantification of fold change in astrocyte GFAP signal intensity (N = 6 fields of view/group) after
1224 4h **(B)** and 24h **(C)** of increasing strain (i.e., 3% or 10%). Statistical significance was determined
1225 using one-way ANOVA (*p < 0.05 , **p < 0.01) for GFAP expression levels. Scale bar: 20 μm.
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Supplemental Fig. 10. HIF-1α expression of encapsulated-MONHAs within the hydrogel
periphery in response to biomechanical strain. (A) Representative fluorescence images and
quantification of fold change in astrocyte HIF-1α expression signal intensity (N = 6 fields of
view/group) after 4h **(B)** and 24h **(C)** of increasing strain (i.e., 3% or 10%). Statistical significance
was determined using one-way ANOVA (*p < 0.05 , **** p < 0.0001) for HIF-1α expression
levels. Scale bar: 20 μm.
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Supplemental Fig. 11. ECM collagen fibrils remodeling in the periphery of MONHA-encapsulated hydrogels in response to biomechanical strain. (A) Representative fluorescence images of collagen fibrils remodeling in response to duration (i.e., 4h or 24h) and magnitude of strain (i.e., 3% or 10%) (N = 6 fields of view/group). Scale bar: 20 μm. **(B)** Quantification of

1240   collagen compaction post strain. Cohen's effect size d (Cohen's d = 0.20, 0.50, and 0.80 is used
1241   to indicate the effect sizes as small, medium, or large, respectively).
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Supplemental Fig. 12. ECM fibronectin secretion in the periphery of MONHA-encapsulated
hydrogels in response to biomechanical strain. (A) Representative fluorescence images of
fibronectin in response to duration (i.e., 4h or 24h) and magnitude of strain (i.e., 3% or 10%) (N =
6 fields of view/group) and **(B-C)** quantification of fold change in fibronectin signal intensity.
Statistical significance was determined using one-way ANOVA (***$p < 0.001$, **** $p < 0.0001$)
for fibronectin signal intensity. Scale bar: 20 μm.
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1253   **Supplemental Fig. 13. MONHA-encapsulated hydrogel stiffness following biomechanical**
1254   **strain.** Analysis of the elastic modulus (kPa) of MONHA-encapsulated hydrogels (N = 4/group)
1255   following 24h of increasing biomechanical strain (i.e., 3% or 10%). Significance was determined
1256   by one-way ANOVA using multiple comparisons test.