ARVO-INDIA
Indian Eye Research Group

31st Annual Meeting of ARVO-INDIA

ADVANCING INTERDISCIPLINARY VISION RESEARCH

SANKARA NETHRALAYA, CHENNAI

JULY 26TH AND 27TH, 2025

PROGRAM BOOK

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ARVO-INDIA
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Program Schedule – Day 1

ARVO-INDIA 2025 MEETING			
Day 1 - 26th July 2025			
Venue: VD Swami Auditorium			
Time (in hrs)	**Event**	**Speaker**	**Title**
08:00 -08:50	**Registration**		
08:50 -09:00	**Inauguration**		
Session 1: Stem Cells, Development and Regenerative Therapies			
Chair: Dr. Indumathi Mariappan, LVPEI, Hyderabad *Dr. S. Krishnakumar, MRF, Chennai*			
09:00-09:20	**Keynote Lecture 1**	**Dr. Gowri Priya Chidambaranathan** *AMRF, Madurai*	Towards development of a stem cell-based therapy for patients with primary open angle glaucoma
09:20-09:35	**Invited Talk 1**	**Dr. Rajani Battu** *CEGR, Bengaluru*	Early results of Eyecyte RPE™ in the treatment of dry Age-related macular degeneration and Geographic atrophy.
09:35-09:50	**Invited Talk 2**	**Dr. Swaminathan Sethu** *Narayana Nethralaya, Bengaluru*	Immunological barriers and considerations in gene therapy
09:50-10:00	Free paper 1	Ms. Gopika S Kumar *AMRF, Madurai*	Pigmentation loss reflects EMT and Functional decline in iPSC-derived RPE cells
10:00-10:10	Free paper 2	Dr. Aatish Mahajan *LVPEI, Hyderabad*	Effect of maternal diabetes on placental epigenetics and its influence on retinal development in infants
10:10-10:20	Free paper 3	Mr. Namit Dey *Pandorum Technologies, Bengaluru*	3D cell migration model for screening corneal implants for efficient wound healing
10:20-11:00	**Photo session / Tea break/ Stalls**		
Session 2: Genetics, Molecular and Cell Biology			
Chair: Dr. P. Sundaresan, AMRF, Madurai *Dr. S. Sripriya, VRF, Chennai*			
11:00 - 11:15	**Invited Talk 3**	**Dr. Shailja Tibrewal** *SCEH, New Delhi*	Caring for Rare Eye Diseases - building an ecosystem
11:15-11:35	**Keynote Lecture 2**	**Dr. Inderjeet Kaur** *LVPEI, Hyderabad*	Complementing the neurodegeneration, neuroinflammation and neovascularisation in the eye.

11:35-11:45	Free paper 4	Mr. Shubhrajit Barman *CSIR-IICB, Kolkata*	SPARC as a novel driver of gliosis and mitochondrial dysfunction in early diabetic retinopathy
11:45-11:55	Free paper 5	Mr. Dhruv Sharma *LVPEI, Hyderabad*	To investigate the role of intraflagellar transport protein gene IFT88 in Leber Congenital Amaurosis and Retinitis Pigmentosa in Indian Patients
11:55-12:05	Free paper 6	Ms. Erudhayadhas Lavanya *VRF, Chennai*	Evaluation of novel cell penetrating peptides targeting neuronal protein 3.1(P311) in preventing epithelial to mesenchymal transition in ARPE 19 cells
12:05-12:15	Free paper 7	Ms. Syed Ali Fathima Afrin J *VRF, Chennai*	DNA methylation profiling in Bardet-Biedl Syndrome
Session 3: Dr. S. S. Badrinath Oration			
Chair: Dr. Lingam Gopal, MRF, Chennai *Dr. Girish S Rao, MRF, Chennai*			
12:15-13:00	**Dr. Gullapalli N Rao** **LVPEI, Hyderabad**		**Eye Research in India: Current status and Future possibilities**
13:00-14:00	**Lunch/ Quiz (Preliminary round)**		
Session 4: Dr. Bireswar Chakrabarti Oration			
Chair: Dr. Subhabrata Chakrabarti, LVPEI, Hyderabad			
14:00-14:45	**Dr. Ghanshyam Swarup** **CSIR-CCMB, Hyderabad**		**Molecular mechanisms of pathogenesis of glaucoma caused by mutations of Optineurin**
14:45 – 15:45	**Poster/ Tea Break/ Stalls**		
Session 5: Bioinformatics, Computational Biology and Artificial Intelligence			
Chair: Dr. V. Umashankar, NIRT, Chennai *Dr. A. R. Anand, MRF, Chennai*			
15.45 – 16:00	**Invited talk 4**	**Dr. Karthik Raman** *IITM, Chennai*	Computational approaches to understanding microbial eco- systems: Disentangling complexities with metabolic modelling
16:00-16:15	**Invited talk 5**	**Dr. Bharanidharan Devarajan** *AMRF, Madurai*	Enhancing Genomic Discovery with a Novel Computational Framework for Eye Disease-Specific Pathogenic Variants
16:15-16:25	Free paper 8	Dr. Devanjali Relan *BML Munjal University, Gurugram*	Automated HbA1C classification from retinal images using a hybrid deep learning framework
16:25-16:35	Free paper 9	Mr. Sujoy Mukherjee *LVPEI, Hyderabad*	Customized version of vessel density quantification with image processing
16:35-16:45	Free paper 10	Ms. Vennela Vankudoth *University of Hyderabad, Hyderabad*	Age-dependent variations in corneal nerve morphology
16:45-17:45	**Quiz**		
19:00-20:00	**Cultural performance by Mr. Saisharan and his band (Hotel Ambassador Pallava)**		
20:00 onwards	**Banquet dinner (Hotel Ambassador Pallava)**		

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Program Schedule – Day 2

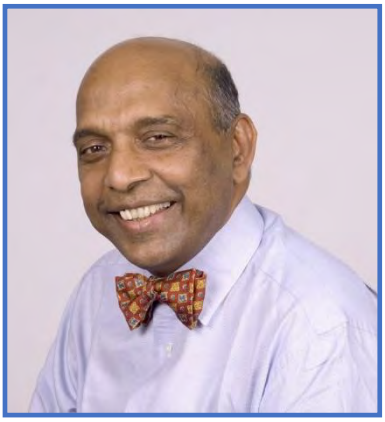
ARVO-INDIA 2025 MEETING			
Day 2 - 27th July 2025			
Venue: VD Swami Auditorium			
Time (in hrs)	**Event**	**Speaker**	**Title**
Session 6: Microbiology and Ocular Infections			
Chair: Dr. Savitri Sharma, LVPEI, Hyderabad *Dr. K. Dharmalingam, AMRF, Madurai*			
09:00-09:20	**Keynote Lecture 3**	**Dr. Ashok Kumar** *Wayne State University,* USA	Targeting cell death pathways in ocular infections
09:20-09:35	**Invited Talk 6**	**Dr. Joveeta Joseph** *LVPEI, Hyderabad*	Tracking Superbugs: Genomic Surveillance of Antimicrobial Resistance in Ocular Infections in Southern India
09:35-09:45	Free paper 11	Ms. Saraswathi B MRF, Chennai	Diagnostic utility of targeted Nanopore sequencing in patients with canaliculitis
09:45-09:55	Free paper 12	Ms. Dharsini Nandhakumar *AMRF, Madurai*	Prospective evaluation of RID-MYC assay for POC diagnosis and clinical management in smear and culture-negative keratitis with IVCM correlation
10:00-10:05	Free paper 13	Dr. Lakshminarayanan Gowtham *LVPEI, Hyderabad*	Novel small molecule inhibitor AXM017 for fungal keratitis treatment: Evaluation of in vitro efficacy and safety
10:05-10:15	Free paper 14	Dr. Bibrita Bhar *LVPEI, Hyderabad*	Self-assembling peptide hydrogels from nature's defenders: Next generation biomaterial engineering against fungal keratitis
Session 7: Clinical Ophthalmology and Optometry			
Chair: Dr. Srikant Bharadwaj, LVPEI, Hyderabad *Dr. Anuradha Narayanan, MRF, Chennai*			
10:15-10:35	**Keynote Lecture 4**	**Dr. Prema Padmanabhan** *MRF, Chennai*	Biomechanics and Mechanobiology: Yin and Yang
10:35-10:50	**Invited Talk 7**	**Dr. Monisha Esther Nongpiur** *SERI, Singapore*	Phenotypic heterogeneity in primary angle closure disease: Insights from anterior segment imaging
10:50-11:05	**Invited Talk 8**	**Dr. Aiswaryah Radhakrishnan** *SRMIST, Chennai*	Emotion, cognition and ocular parameters

11:05-12:00	**Poster/ Tea Break/ Stalls**		
Session 8: Prof. D. Balasubramanian Oration			
Chair: Dr. Nirmala Subramanian, MRF, Chennai *Dr. Joveeta Joseph, LVPEI, Hyderabad*			
12:00-12:45	**Dr. Savitri Sharma** **LVPEI, Hyderabad**		**Diagnostic and Therapeutic challenges of *Pythium insidiosum* keratitis**
12:45-13:45	**Lunch/ Board meeting**		
Session 9: Nanobiotechnology and Ocular Pharmacology			
Chair: Dr. Velpandian, AIIMS, New Delhi *Dr. J. Narayanan, VRF, Chennai*			
13.45 – 14:00	**Invited talk 9**	**Dr. Nirmal Jayabalan,** *BITS – Hyderabad, Hyderabad*	Topical drops to protect the eyes from systemic drug-induced ocular toxicity
14:00-14:10	Free paper 15	Dr. Manisha Malani *BITS – Hyderabad, Hyderabad*	Valproate-associated Dry eye: Interplay between inflammation and oxidative stress
14:10-14:20	Free paper 16	Ms. Shridula Sankar *BITS – Hyderabad, Hyderabad*	Shift from invasive to non-invasive treatment for Keratoconus: Resveratrol-loaded polymeric ocular patch
14:20-14:30	Free paper 17	Mr. Tapas Kumar Roy *AIIMS, New Delhi*	Understanding ocular delivery of biotherapeutics: Insights into peptide transporters and blood-ocular barriers
Session 10: Interdisciplinary insights in Ocular diseases			
Chair: Dr. G. Kumaramanickavel, Narayana Nethralaya, Bengaluru *Dr. N. Angayarkanni , MRF, Chennai*			
14:30-14:40	Free paper 18	Dr. Nirbhai Singh *PGIMER, Chandigarh*	Soluble biomarkers sFLT-1 and sST2 predict outcomes to anti-VEGF therapy in DME: an interdisciplinary approach
14:40-14:50	Free paper 19	Mr. Saurabh Kumar *LVPEI, Hyderabad*	Altered lipid metabolism is a crucial regulator in Retinopathy of prematurity
14:50-15:00	Free paper 20	Mr. Pradeep K *Narayana Nethralaya, Bengaluru*	Untargeted metabolomics and histology of the anterior lens capsule reveal novel metabolites and ECM markers in anterior subcapsular cataract
15:00-15:10	Free paper 21	Mr. Maradani Bhavani Shankar *VRF, Chennai*	Aptamer based detection of Cystatin-C for screening of diabetic retinopathy
15:10-15:20	Free paper 22	Dr. Debasmita Pankaj Alone *NISER, Odisha*	Unlocking the molecular code of pseudoexfoliation glaucoma: Multi-omic signatures of disease progression
15:20-15:40	**Concluding Session and Prize distribution**		
15:40-16:00	**High Tea**		

ORATION AWARD LECTURES

Dr. S. S. Badrinath Oration

Eye Research in India: Current status and Future possibilities



Dr. Gullapalli N Rao, Dip. American Boards, FACS, FRCS, FNAMS, D.Sc., MD
Founder-Chair, L V Prasad Eye Institute
Hyderabad, India

Eye research in India has made a steady progress over the past two decades earning a respectable position on the global stage. However, this activity is limited to a select number of places and people.

Increasing number of clinicians involved in research, greater interest among basic scientists in pursuing eye research as a cause, more public health research programmes and more international collaborations have contributed to this enhanced stature of our country.

The limitations continue. Near zero interest for research in medical collages and residency programmes, limited investment in research activity by institutions, suboptimal allocation of support from governmental funding agencies continues to be barriers for accelerated growth and to find solution to our problems.

Some thoughts about how India can enhance its research productivity will be presented.

Dr. Bireswar Chakrabarti Oration

Molecular mechanisms of pathogenesis of glaucoma caused by mutations of Optineurin

Dr. Ghanshyam Swarup, PhD, FNA, FASc
Former J C Bose Fellow, CSIR-Centre for Cellular and Molecular Biology, Hyderabad, India

Genetic alterations in Optineurin (OPTN) are associated with certain neurodegenerative disorders, including glaucoma, amyotrophic lateral sclerosis (ALS), and frontotemporal lobar dementia (FTLD). Glaucoma-associated mutations of OPTN are generally single copy missense mutations, whereas ALS-associated OPTN mutations include deletions, truncations and missense mutations. OPTN is an adapter protein that plays a crucial role in mediating many cellular functions, including autophagy, vesicle trafficking, and various signalling pathways. Our objective has been to understand the normal cellular functions of OPTN, and also explore the alterations in these functions caused by mutations, which may contribute to retinal ganglion cell death associated with glaucoma. We identified several OPTN-interacting proteins that are involved in regulating or modulating various functions of OPTN. Some of the glaucoma-associated mutants such as E50K, M98K, H486R and 2bpIns show altered interactions with the cellular proteins that leads to defective functions and retinal cell death. We have generated OPTN-deficient mice and cells derived from these mice to understand normal functions of OPTN. Recent work has identified certain cytoprotective functions of OPTN under conditions of cellular stress, including ER stress, oxidative stress, TNF alpha, and protein homeostasis stress. OPTN modulates signalling pathways induced by these stress signals. Some of the glaucoma-associated mutants are altered in stress-induced signalling pathways regulated by OPTN which possibly contribute to retinal cell death. Overall, several mechanisms including impaired autophagy and vesicle trafficking, and altered stress-induced signalling contribute to the retinal cell death caused by glaucoma-associated mutants of OPTN.

Prof. D. Balasubramanian Oration

Diagnostic and therapeutic challenges of *Pythium insidiosum* keratitis

Dr. Savitri Sharma, MD
Director Emeritus, Laboratory Services-LVPEI Network, L.V. Prasad Eye Institute, Hyderabad, India

A large number of fungal species are associated with keratitis and the most frequent species involved worldwide are *Fusarium* and *Aspergillus*. However, almost 10 to 23% of fungal isolates from fungal keratitis patients remain unidentified owing to lack of sporulation in culture. Molecular microbiologists have used ribosomal DNA sequence analysis to determine the species of non-sporulating fungi. At our institute, in 2015, DNA sequencing of such isolates revealed the presence of *Pythium insidiosum,* an oomycete, among them. DNA sequencing from south India earlier listed this organism in 2008 among one of the species of non-sporulating fungi causing keratitis. The class oomycetes is a group of fungus-like (parafungal) microorganisms that are closely related to the green algae in the kingdom Stramenopila. The main feature of oomycetes is the development of sporangia with biflagellate zoospores in aquatic atmosphere. We have now learnt the microscopic features and culture characteristics of this organism and are able to identify by zoospore formation in the laboratory. In last nine years we have diagnosed more than 300 cases and have reported the clinical features and treatment options.

In order to study the condition in greater details we started our journey in the :1. development of an experimental rabbit model for corneal infection by *P. insidiosum,* 2. determination of the efficacy and safety of different antibiotics in the treatment of corneal infection by *P. insidiosum* in rabbit cornea, 3. study of the innate and adaptive immunity expressed by cornea when challenged with *P. insidiosum* in a rabbit model, 4. identification of putative virulence genes using *in silico* bioinformatic tools by comparative genomics and 5. study of the temporal expression of selected virulence genes in the *ex-vivo* culture of human cadaveric cornea infected with *P. insidiosum.*

The experimental rabbit model of *Pythium* keratitis showed that the intracorneal route of inoculation of *P. insidiosum* zoospores was necessary for infection in the cornea while the low dose of zoospore inoculum was sufficient for the infection. There was no need of

immunosuppression to induce *Pythium* keratitis in the rabbits and topical inoculation of *P. insidiosum* zoospores could not induce a successful infection in the animals. The *in-vivo* efficacy of antibacterial antibiotics (azithromycin, linezolid and tigecycline) for the treatment of *P. insidiosum* infection estimated in the rabbit cornea showed higher efficacy of linezolid. No toxicity was seen for any of the drugs on topical application. Thus, use of topical linezolid and azithromycin with oral azithromycin was recommended for the clinical trial of *P. insidiosum* keratitis in humans. Significant reduction in the proportion of patients requiring therapeutic keratoplasty was seen in the arm treated with antibiotics.

The immune response of the rabbit cornea to *P. insidiosum* infection demonstrated strong involvement of the innate immune mediators such as cytokines IL-1β, IL-6, chemokine IL-8 and antimicrobial peptides CAP-18 and LeukoP. The results showed the significant association of immune mediators of the innate immunity with early to mid-stage of keratitis in rabbits. To validate the role of innate immunity in *Pythium* infection in the rabbits, the expression of pathogen recognition receptors (PRRs) was evaluated. The expression profile of PRRs showed the involvement TLR-4 and Dectin-1 of human corneal epithelial cells (hCECs) with recognition of *P. insidiosum*. By contrast, the response of adaptive immunity of the cornea was poor to the infection.

Bioinformatics analysis of the whole genome of a clinical isolate of *P. insidiosum* helped to identify the three crucial virulence genes including aspartate aminotransferase 3 (AAT3), mitogen activated protein kinase 7 (MAPK7) and ADP-ribosylation factor 2 (ARF2) that might have the possible role in the pathogenesis of *Pythium* keratitis. As the genes are necessary for the carbon and nitrogen metabolism (AAT3), cell growth and survival (MAPK7) and microbial infections (ARF2), they could play a significant role in *Pythium* infection. The mRNA expression analysis of these virulence genes (Aspartate aminotransferase 3, ADP-ribosylation factor 2 and stress associated mitogen activated protein kinase 7) in the human cadaveric corneas challenged with *P. insidiosum* (an isolate from severe ocular infection) revealed the association of PsMPK7 gene with infection progression. This gene is important for response to stress, detoxification of reactive oxygen species, germination of cysts and production of zoospores.

With increased awareness about the pathogenic role of *P. insidiosum* and availability of molecular methods for identification, we are witnessing a rise in reports of *Pythium* keratitis. The role of public education to use personal protective equipment while working in fields for the prevention of the disease is required. Our publications on ocular pythiosis have contributed to the understanding of *P. insidiosum* keratitis to a large extent and we hope to continue efforts to better the treatment outcome using adjunctive therapy along with antibiotics.

KEYNOTE LECTURES

Keynote Lecture 1

Towards a stem cell-based therapy for patients with primary open angle glaucoma

Dr. Gowri Priya Chidambaranathan, PhD
Scientist - 4, Aravind Medical Research Foundation,
No.1, Anna Nagar, Madurai

Human trabecular meshwork (TM) is a tiny porous tissue located in the iridocorneal angle of theeye responsible for the drainage of the intraocular fluid – aqueous humor (AH) and hence the intraocular pressure (IOP) homeostasis. Primary open angle glaucoma (POAG), a leading cause of blindness worldwide, is associated with a drastic reduction in TM cellularity, higher extracellular matrix deposition, and increased oxidative stress leading to increased stiffness, elevated IOP and optic nerve damage if untreated. The current therapy for POAG is lifelong use of drugs with side effects or surgical intervention.

Previous reports from our laboratory confirmed that adult tissue resident stem cells of TM to be located in the anterior non-filtering region. Along with the drastic reduction in TM cells in glaucomatous condition, we demonstrated for the first time a significant reduction in the TM stem cells (TMSCs). Further, transplantation of cultured TMSCs in an organ culture model for ocular hypertension reduced the IOP indicating the need for a stem cell-based therapy for POAG. Recent advances in nanotechnology have identified that the exosomes or small extracellular vesicles (sEVs) as an alternate for stem cell therapy. The TMSC-sEVs enhanced wound healing efficacy and the anti-oxidant potential of TM cells compared to TM cell-sEVs indicating the possibility of developing a TMSC-sEV-based therapy for patients with POAG. Mass spectrometry analysis identified 2802 proteins in TMSC-sEVs and 2848 in TM cell-sEVs. Differential expression analysis identified that the TMSC-sEVs to be enriched with proteins associated with wound healing, cell proliferation, migration, anti-oxidant, and anti-apoptotic activities, consistent with the findings in other mesenchymal stem cells. Pathway analysis highlighted the enrichment of proteins associated with PI3K-AKT and MAPK signaling pathways. Further validation by western blotting confirmed that TMSC-sEVs effectively modulated these pathways in TM cells, which are essential for cell proliferation and survival under oxidative stress. Further animal studies are essential to confirm the efficacy of TMSC/TMSC-sEVs in regenerating the TM and in restoring the normal IOP, thus towards establishing a stem cell-based therapy for POAG.

Keynote Lecture 2

Complementing the neurodegeneration, neuroinflammation and neovascularisation in the eye

Dr. Inderjeet Kaur, PhD

Brien Holden Eye Research Centre, L V Prasad Eye Institute (KAR campus), Hyderabad, India.

Chronic inflammation leading to neo-vascularization and neurodegeneration are major causes of irreversible vision loss in retinal vascular diseases like retinopathy of prematurity (ROP), diabetic retinopathy (DR), age-related macular degeneration (AMD) and uveitis. Currently, there is an unmet clinical need for the lack of availability of highly robust diagnostic strategies for the early detection of these conditions. Treatment options are also limited owing to lack of timely diagnosis and appropriate therapeutics. These conditions exhibit increased oxidative stress, complement activation, microglia-mediated release of pro-inflammatory markers, VEGF signaling and abnormal neo-vessel proliferation that eventually result in neuronal death. Complement system composed of classical, lectin and alternate pathways serves the major function of immune surveillance by eliminating immune complexes and apoptotic cells, as well as mediating cross-talk with immune cells for adaptive immune functions thereby modulating immune and inflammatory responses in the eye. Studies by us and others have implicated a dysregulated complement system leading to aberrant immune activation and inflammation in the pathogenesis of AMD, DR, Uveitis and ROP. At the cellular level, immune stimulus activates microglia and astrocytes to proliferate and release cytokines/chemokines causing further inflammation and neo-vascularization. Therefore, it is expected that complement-based therapeutics would help in aggressively targeting immune dysregulation under oxidative stress, reducing the cell death, inflammation and abnormal angiogenesis in the retina for mitigating the disease progression and vision loss.

Keynote Lecture 3

Targeting cell death pathways in ocular infections

Dr. Ashok Kumar, PhD
Associate Professor, Department of Microbiology, Immunology, and Biochemistry, Wayne State University, Detroit, Michigan, USA

Ocular infections such as endophthalmitis can lead to severe inflammation and irreversible vision loss, often exacerbated by host cell death responses. Our laboratory has been investigating the molecular mechanisms underlying retinal cell death during infectious endophthalmitis to identify novel therapeutic targets. Using integrative omics approaches, including metabolomics and transcriptomics, we have uncovered the activation of multiple cell death pathways, including apoptosis, pyroptosis, and ferroptosis. These cell death mechanisms appear to play distinct roles in causing retinal tissue damage and amplifying inflammatory responses. In particular, ferroptosis, an iron-dependent form of oxidative cell death, emerged as a critical contributor to disease pathology. Ongoing studies from our group suggest that pharmacological inhibition of ferroptosis could significantly reduce endophthalmitis severity, highlighting the potential of cell death modulation as a novel adjunctive treatment approach for infectious endophthalmitis.

Keynote Lecture 4

Biomechanics and Mechanobiology:

Yin and Yang

Dr. Prema Padmanabhan, MS

Distinguished Senior Consultant,

Department of Cornea & Refractive Surgery

Medical Research Foundation, Chennai, India

Biomechanics and mechanobiology are two sides of the coin of Ocular Homeostasis. Biomechanics refers to the mechanical properties of various biological structures in the eye and mechanobiology explains the biological response of ocular cells and tissues to those mechanical properties. This interface between structure and function is being increasingly recognized as being pivotal to the constitution and maintenance of ocular homeostasis, the breakdown of which is often the root cause of various ocular pathologies. Understanding this relationship, then, will not only provide useful insights into pathophysiology but will also pave the way to identify potential therapeutic targets and promises to drive future innovation. This is a brief overview of the current understanding of the mediators that forge this relationship, the key roles they play in maintaining homeostasis, the dynamics of their response to physiological and pathological stresses and in wound healing. The possible therapeutic strategies this may lead to will be highlighted with clinical illustrations.

INVITED TALKS

Invited Talk 1

Early results of Eyecyte RPE™ in the treatment of dry Age-related macular degeneration and Geographic atrophy

Dr. Rajani Battu, MS, DNB, FRCS (Edin)
Medical Director, Centre for Eye Genetics and Research, Bengaluru, India

Cell replacement therapy is an attractive therapeutic option for dry Age-Related Macular Degeneration (AMD) & Geographic Atrophy (GA); use of human induced pluripotent stem cell (iPSC)- derived RPE has advanced to clinical trials. Eyestem reports interim safety & efficacy results from our Phase 1/2a clinical study in patients (N=9) with dry AMD & GA (NCT06394232) using an allogeneic suspension of RPE cells (Eyecyte-RPE™).

In a phase 1/2a study, we transplanted a suspension of 100-300k (dose escalation) iPSC- derived RPE (Eyecyte-RPE™) cells subretinally in subjects with dry AMD and GA via a 25G pars plana vitrectomy and subretinal delivery of cells in 9 eyes with concomitant oral immune suppression. Endpoints included systemic & ocular safety, changes in visual function, RPE loss area, retinal sublayer thickness and defect areas on OCT. An automated artificial intelligence (AI)-based segmentation algorithm was used for OCT analyses.

All subjects underwent successful delivery of Eyecyte-RPE™ cells. Subjects have completed a follow up of 1 week- 6 months. Till date, Eyecyte-RPE has been well tolerated in all eyes. The most common ocular AEs were subconjunctival hemorrhage (2/6 eyes), mild preretinal hemorrhage (7/9 eyes), both of which were self-limiting. Improvement of visual acuity (ranging from 5-30 letters) was seen across 6 eyes till date.

Subretinal transplantation of Eyecyte-RPE cells in eyes with dry AMD and GA appears to be well tolerated. The encouraging signals of safety and efficacy will be further explored in a randomized, controlled Phase 2 clinical trial.

Invited Talk 2

Immunological barriers and considerations in gene therapy

Dr. Swaminathan Sethu, PhD

Scientist, Immunology, GROW Research Lab, Narayana Nethralaya Foundation, Bengaluru, India

Gene therapy (GT) is revolutionizing and extending therapeutics options for a variety of conditions ranging from inherited genetic disorders to cancer. The clinical successes of gene therapy are tempered by associated adverse effects (AE). The AE ranges from regional tissue atrophy to systemic toxicity affecting critical organs including liver, heart, lungs, and kidneys. Gene therapy-associated immunotoxicity (GTAIm) remains one of the significant contributors to GT-associated AE with significant impact on treatment outcomes and patient safety. GTAIm is mediated via (i) vector- and transgene-specific immunogenicity, and (ii) non-specific overt immuno-inflammatory reactions. Immunological memory (humoral and cellular) against GT vectors (e.g., adeno associated virus – AAV) either prior to therapeutic administration or after, results in reduced transduction efficiency and has bearing on redosing regimens. Similarly, immunogenicity to the transgene reduces the longevity of therapeutic efficacy. Exaggerated response of the immune system and concomitant capillary-leak syndrome and/or cytokine storm associated with systemic administration of GT products has significantly contributed to the morbidity and mortality in some patients. Immune-modulating drugs are being used in the clinics to manage immune-related AE during GT. However, strategies for screening, monitoring, and mitigating GTAIm are essential for the success of gene therapy in the clinics. Towards this our studies report higher levels of AAV2 and AAV6-specific total antibody, neutralizing antibody, and lymphocytes compared to AAV8 and AAV9 in healthy volunteers and patients with genetic conditions. Our in vivo studies demonstrate that immunogenicity and circulatory immune perturbation following AAV vectors administration are influenced by AAV serotypes, route of administration and background inflammatory state. Further, efforts are being made towards rendering GT products hypoimmunogenic by capsid and cassette engineering as well. Enhanced focus in preventing and mitigating GTAIm will substantially improve clinical safety, efficacy, and longevity of gene therapy.

Invited Talk 3

Caring for Rare Eye Diseases - building an ecosystem

Dr. Shailja Tibrewal, MS

Consultant, Department of Pediatric Ophthalmology,
Dr. Shroff's Charity Eye Hospital, New Delhi, India

Rare eye diseases, though individually uncommon, collectively impact millions worldwide, often leading to severe visual impairment or blindness. These conditions, such as inherited retinal dystrophies, anophthalmia, coloboma, and ocular manifestations of systemic syndromes, are frequently overlooked due to limited awareness, fragmented care pathways, and scarce research investment. This talk, *"Caring for Rare Eye Diseases – Building an Ecosystem"*, focuses on the urgent need to create a comprehensive, collaborative framework to address the unique challenges posed by rare ocular conditions.

The presentation will outline key pillars essential to this ecosystem: early and accurate diagnosis, access to specialized care, genetic counseling, robust patient registries, targeted research, and policy support. It will highlight the importance of multidisciplinary collaboration involving ophthalmologists, geneticists, researchers, patient advocacy groups, and health policymakers. The talk will draw on our real-world experiences and emerging models from India and abroad to demonstrate how integrated networks and centers of excellence can transform the landscape of rare eye disease care.

Additionally, the role of technology, such as artificial intelligence, telemedicine, and next-generation sequencing, in improving access and precision will be discussed. Emphasis will be placed on empowering patients and caregivers through education and advocacy, ensuring that no one is left behind due to the rarity of their condition.

By building an inclusive ecosystem, we can shift from isolated interventions to a sustained, systemic response that brings hope and tangible solutions to those affected by rare eye diseases.

Invited Talk 4

Computational Approaches to Understanding Microbial Eco- systems: Disentangling Complexities with Metabolic Metabolic Modelling

Dr. Karthik Raman, PhD
Professor, Department of Data Science and AI,
IIT Madras, Chennai, India

In this talk, we explore complex microbial communities and the interactions therein using advanced computational methods and mathematical modelling. We focus on scalable algorithms and tools developed, notably the Panera algorithm, which generates Pan Genus Metabolic Models (PGMMs) to surmount uncertainties in the composition of communities. Panera enables us to better understand the metabolic capabilities across genera, by accounting for species variations. The talk will also broadly focus on network-based approaches to capture microbial interactions, illustrating the utility of graph-based approaches to elucidate metabolic exchanges and dependencies within communities. We apply these methodologies to investigate diverse environments, from deep-sea (hydrothermal vents) to outer space (the International Space Station)! The methodologies include genome-scale metabolic modelling, Metabolic Support Index (MSI), and the MetQuest algorithm, which enable us to interrogate complex microbial communities, quantifying interspecies support and metabolic interactions. Overall, our work seeks to build novel methodologies for understanding microbial interactions in microbiomes, leveraging them for clinical, industrial and environmental applications, broadly impacting health and sustainability.

Invited Talk 5

Enhancing Genomic Discovery with a Novel Computational Framework for Eye Disease-Specific Pathogenic Variants

Dr. Bharanidharan Devarajan, PhD Scientist, Microbiology, and Bioinformatics, Aravind Medical Research Foundation, Madurai, India

Recent advances in next-generation sequencing (NGS), particularly Whole-Genome Sequencing (WGS) and Whole-Exome Sequencing (WES), have revolutionised the discovery of disease-causing genetic variants. However, identifying truly pathogenic variants—especially single-nucleotide variants (SNVs) and small insertions/deletions (InDels), which account for approximately 85% of known pathogenic changes—remains a significant bottleneck. Current tools, which rely on genome-wide and pan-disease datasets, often lack disease specificity, potentially compromising variant prioritization due to diverse gene-phenotype relationships and inheritance mechanisms.

To address this limitation, we developed eyeVarP, a machine learning-based framework trained on curated ocular-specific and non-ocular variant data to prioritise pathogenic variants specific to eye diseases. eyeVarP integrates variant- and gene-level features using a random forest model, while the accompanying VarP pipeline enables scalable filtration and annotation of missense and InDel variants from WGS/WES data. Benchmarking against other pan-disease-specific models, eyeVarP demonstrated better performance in predicting eye disease-specific pathogenicity. This computational framework demonstrates the potential to improve variant interpretation and support more accurate genetic diagnoses in future clinical applications.

Invited Talk 6

Tracking Superbugs: Genomic Surveillance of Antimicrobial Resistance in Ocular Infections in Southern India

Dr. Joveeta Joseph, PhD

Head of Microbiology; Research Scientist, Jhaveri Microbiology Centre, L V Prasad Eye Institute, Hyderabad, India

Ocular infections have a substantial impact on global vision health. Despite their association with severe vision impairment, very few studies have invested in monitoring antimicrobial resistance over time using whole genome sequencing approaches. Here, we assembled 291 high fidelity bacterial genomes isolated from a cohort of 349 subjects using long-read sequencing technology. These assemblies were studied to understand the correlation between AMR gene signatures and antibiotic susceptibility and further, the association of AMR genes with mobile genetic elements. *Pseudomonas aeruginosa* (62;21.3%) was the most frequently sequenced pathogen followed by *Staphylococcus aureus* (60;20.6%) and *Staphylococcus epidermidis* (35; 12%). Several emerging sequence types (STs) were identified, including a new S. aureus ST associated with vancomycin and teicoplanin resistance. Antimicrobial resistant gene (ARG) analysis suggested the potential presence of new AMR mechanisms in several antibiotic classes. Shared extended-spectrum beta-lactamase (ESBL) genes in multi drug resistant (MDR) *Escherichia coli* and *Klebsiella pneumoniae* were observed along with high sequence similarity in their plasmid genetic architecture. Genetic determinants of high-risk *K. pneumoniae* and *P. aeruginosa*, and their association with mobile genetic elements was evaluated. In this work, we identified the presence of potential novel AMR mechanisms. This study generated genomic data of several ocular pathogens which is essential for understanding of pathogen evolution and AMR mechanisms. The presence of potential novel AMR mechanisms reiterates the need for genomic surveillance in LMICs.

Invited Talk 7

Phenotypic Heterogeneity in Primary Angle Closure Disease: Insights from Anterior Segment Imaging

Dr. Monisha Esther Nongpiur, MD, PhD

Associate Professor and Clinician Scientist, Singapore Eye Research Institute, Singapore

Primary angle closure disease (PACD) comprises a clinical continuum that begins with primary angle closure suspect (PACS) and may progress to primary angle closure glaucoma (PACG). PACD is characterized by significant genetic and phenotypic heterogeneity. Understanding this variability is essential for accurate risk stratification, prognostication, and personalized management. Advances in anterior segment imaging — including anterior segment optical coherence tomography (AS-OCT), ultrasound biomicroscopy (UBM), and swept-source imaging — have markedly enhanced our ability to characterize anterior segment anatomy with high resolution and reproducibility, revealing distinct anatomical subtypes and underlying mechanisms of angle closure.

This talk will highlight the utility of imaging-derived parameters — such as iris configuration, lens vault, anterior chamber area and width, and plateau iris features — in delineating phenotypic subgroups within PACD. We will also present the application of unsupervised clustering techniques to identify anatomically and mechanistically distinct PACD subtypes. This approach offers a data-driven means of capturing the heterogeneity of PACD and advancing our understanding of disease pathophysiology beyond traditional classification frameworks.

Invited Talk 8

Emotion, Cognition and Ocular Parameters

Dr. Aiswaryah Radhakrishnan, PhD

Associate Professor, Department of Optometry, SRM Medical College Hospital and Research Centre

Chennai, India

Emotion refers to complex psychological states involving feelings, thoughts, and behavioral expressions. Emotions can range intense to fleeting emotions and can be in the positive or negative spectrum. The autonomic nervous system plays an important role in emotional physiology regulating the heart rate, muscle tonicity, hormonal release and perspiration among other physiological responses. In the eye, extreme emotions are found to be associated with changes in pupil size, blink rate, intraocular pressure changes and vascular changes in conjunctiva, choroid and retina. In this ongoing study, we measured changes in ocular parameters such as accommodation, pupil size, tear prism height, blink rate and eye movement behaviour while the subjects viewed short videos eliciting each of the five primary emotions: Happy, Sad, Fear, Anger, Disgust and Surprise, with high and cognitive loads. The videos were projected in a commercial HD display that was viewed through a mirror by the left eye while the above measurements were performed using an open field autorefractor in the right eye. We found that the accommodative amplitude decreased and the pupillary constriction increased for videos eliciting fear and anger, while disgust decreased the accommodation amplitude significantly. Blink rate was significantly higher for disgust and lower for happy videos. Similarly, there were significantly higher number of regressive eye movements with videos eliciting fear, anger and disgust response than for happy response. The tear prism height did not change for these short-term emotional responses elicited. High cognitive demand resulted in increased accommodative amplitude, decreased pupil size and lower blink rates. These results have potential implications in using ocular biometrics as objective diagnostic parameters to understand the emotional state of non-verbal patients and probably as a therapeutic solution for binocular vision problems involving the accommodative apparatus.

Invited Talk 9

Topical drops to Protect the Eyes from Systemic Drug-Induced Ocular Toxicity

Dr. Nirmal Jayabalan, PhD
Translational Pharmaceutics Research Laboratory (TPRL), Department of Pharmacy, Birla Institute of Technology and Science-Pilani, Hyderabad Campus, Hyderabad, India

Medicines used systemically (oral and intravenous) can cause toxicity at off-target sites such as the eye (uveitis, retinopathy, and even vision loss). In India, nearly 20% of the elderly population suffers from chronic diseases, such as asthma, arthritis, and tuberculosis, requiring prolonged treatment. Despite the toxicity, patients often continue the medications due to their benefits or lack of other therapies.

Membrane transporters falsely recognize xenobiotics (drug molecules) as endogenous substrates, leading to accumulation at off-target sites and causing drug-induced toxicity. Our studies have shown that systemic drugs (e.g., cyclophosphamide) enter the eye through membrane transporters in the lacrimal gland through tear secretion and accumulate on the ocular surface. However, the modulation of transporters using therapeutic molecules (transporter inhibitors) could lead to unwanted drug-drug interactions. Therefore, we have developed eye drops containing non-therapeutic inhibitors (excipients) for transporters to prevent the entry of systemic drugs causing ocular toxicity into the eye – A simple solution for complex problems.

Preventing ocular toxicity through simple eye drops promises significant societal benefits by enhancing patients' quality of life and reducing healthcare burdens. The development of excipient-based eye drops could be a safer prophylactic alternative, leading to better adherence to prescribed treatments that improve overall health outcomes.

FREE PAPER ABSTRACTS

ARVO-INDIA
Indian Eye Research Group

31st Annual meeting of ARVO INDIA

Free Papers – 26th July 2025

Free paper ID	Speaker	Title
Free paper 1	Ms. Gopika S Kumar *AMRF, Madurai*	Pigmentation loss reflects EMT and Functional decline in iPSC-derived RPE cells
Free paper 2	Dr. Aatish Mahajan *LVPEI, Hyderabad*	Effect of maternal diabetes on placental epigenetics and its influence on retinal development in infants
Free paper 3	Mr. Namit Dey *Pandorum Technologies, Bengaluru*	3D cell migration model for screening corneal implants for efficient wound healing
Free paper 4	Mr. Shubhrajit Barman *CSIR-IICB, Kolkata*	SPARC as a novel driver of gliosis and mitochondrial dysfunction in early diabetic retinopathy
Free paper 5	Mr. Dhruv Sharma *LVPEI, Hyderabad*	To investigate the role of intraflagellar transport protein gene IFT88 in Leber Congenital Amaurosis and Retinitis Pigmentosa in Indian Patients
Free paper 6	Ms. Erudhayadhas Lavanya *VRF, Chennai*	Evaluation of novel cell penetrating peptides targeting neuronal protein 3.1(P311) in preventing epithelial to mesenchymal transition in ARPE 19 cells
Free paper 7	Ms. Syed Ali Fathima Afrin J *VRF, Chennai*	DNA methylation profiling in Bardet-Biedl Syndrome
Free paper 8	Dr. Devanjali Relan *BML Munjal University, Gurugram*	Automated HbA1C classification from retinal images using a hybrid deep learning framework
Free paper 9	Mr. Sujoy Mukherjee *LVPEI, Hyderabad*	Customized version of vessel density quantification with image processing
Free paper 10	Ms. Vennela Vankudoth *University of Hyderabad, Hyderabad*	Age-dependent variations in corneal nerve morphology

ARVO-INDIA
Indian Eye Research Group

31st Annual meeting of ARVO INDIA

Free Papers – 27th July 2025

Free Paper ID	Speaker	Title
Free paper 11	Ms. Saraswathi B MRF, Chennai	Diagnostic utility of targeted Nanopore sequencing in patients with canaliculitis
Free paper 12	Ms. Dharsini Nandhakumar *AMRF, Madurai*	Prospective evaluation of RID-MYC assay for POC diagnosis and clinical management in smear and culture-negative keratitis with IVCM correlation
Free paper 13	Dr. Lakshminarayanan Gowtham *LVPEI, Hyderabad*	Novel small molecule inhibitor AXM017 for fungal keratitis treatment: Evaluation of in vitro efficacy and safety
Free paper 14	Dr. Bibrita Bhar *LVPEI, Hyderabad*	Self-assembling peptide hydrogels from nature's defenders: Next generation biomaterial engineering against fungal keratitis
Free paper 15	Dr. Manisha Malani *BITS – Hyderabad, Hyderabad*	Valproate-associated Dry eye: Interplay between inflammation and oxidative stress
Free paper 16	Ms. Shridula Sankar *BITS – Hyderabad, Hyderabad*	Shift from invasive to non-invasive treatment for Keratoconus: Resveratrol-loaded polymeric ocular patch
Free paper 17	Mr. Tapas Kumar Roy *AIIMS, New Delhi*	Understanding ocular delivery of biotherapeutics: Insights into peptide transporters and blood-ocular barriers
Free paper 18	Dr. Nirbhai Singh *PGIMER, Chandigarh*	Soluble biomarkers sFLT-1 and sST2 predict outcomes to anti-VEGF therapy in DME: an interdisciplinary approach
Free paper 19	Mr. Saurabh Kumar *LVPEI, Hyderabad*	Altered lipid metabolism is a crucial regulator in Retinopathy of prematurity
Free paper 20	Mr. Pradeep K *Narayana Nethralaya, Bengaluru*	Untargeted metabolomics and histology of the anterior lens capsule reveal novel metabolites and ECM markers in anterior subcapsular cataract
Free paper 21	Mr. Maradani Bhavani Shankar *VRF, Chennai*	Aptamer based detection of Cystatin-C for screening of diabetic retinopathy
Free paper 22	Dr. Debasmita Pankaj Alone *NISER, Odisha*	Unlocking the molecular code of pseudoexfoliation glaucoma: Multi-omic signatures of disease progression

Free paper 1: Pigmentation loss reflects EMT and Functional decline in iPSC derived RPE cells

Gopika S. Kumar[1], Anwar A. Palakkan[1]

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Purpose: There is currently no standardized method for evaluating the functional competence of iPSC-derived RPE (iRPE) cells. This study investigates whether pigmentation levels in iRPE cells correlate with their functional integrity, with the goal of establishing pigmentation as a non-invasive, quantifiable marker of iRPE cell quality. **Methods:** iRPE cells were cultured on various extracellular matrix (ECM) coatings—Collagen, Fibronectin, Geltrex, and Laminin—to identify substrates that best support long-term culture. Cell morphology (via phase-contrast microscopy), melanin pigmentation (based on bright field images), gene expression (qPCR), and protein expression (immunostaining) were evaluated across passages. Cell circularity was assessed using ZO-1 immunostaining. Expression of epithelial-to-mesenchymal transition (EMT) markers, RPE-specific functional genes, and TGF-β pathway genes was analysed and compared to pigmentation levels, which were quantified using a custom ImageJ plugin. To further validate findings, iRPE cells cultured on collagen were treated with the TGF-β inhibitor SB431542, and changes in EMT and functional gene expression were assessed in relation to pigmentation levels. **Results**: Laminin and Geltrex supported better retention of RPE morphology (hexagonal shape), higher expression of functional genes (PAX6, CRALBP, RPE65), and reduced expression of EMT markers (FN1, LUM, ASMA), compared to collagen and fibronectin. A strong correlation was observed between pigmentation loss and functional decline. Treatment with SB431542 led to increased pigmentation and restoration of functional gene expression (RPE65) in collagen-cultured cells, further supporting the link between pigmentation and iRPE cell functionality. **Conclusion:** Pigmentation levels in iRPE cells are strongly associated with their functional status. Loss of pigmentation correlates with EMT and decreased functionality, whereas restored pigmentation is linked to the recovery of RPE-specific features. Pigmentation thus represents a reliable, non-invasive indicator of iRPE cell health and functionality.

Free Paper 2: Effect of maternal diabetes on placental epigenetics and its influence on retinal development in infants

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Purpose: The study is designed to uncover the effect of altered micronutrient status in maternal diabetes, effect on DNA methylation and genomic imprinting, how in-utero transfer of these events to developing fetus could influence retinal development. **Methods:** Maternal and cord blood along with placental samples were collected from nine normotensive women and twelve women with diabetes (Eight gestational diabetes and four with pre-gestational diabetes). Infants born to these mothers were followed up for their retinal evaluation. Biochemical analysis of micronutrients in serum was performed using electrochemiluminescence method. The gene expression of transporters (folate (PCFT, RFC), vitamin B12 (CD320), glucose (GLUT-1), DNA methyltransferase (DNMT1, 3A and 3B), and imprinted genes (H19, IGF2) were assessed in placenta by qRT-PCR. Data analysis was carried out using graph pad prism.

Results: The birth weight of infants born to pre-gestational diabetic mothers was decreased. In maternal and cord serum, significant decrease in vitamin B12 and folate levels ($p<0.01$) was observed in pre-gestational diabetic mothers which resulted in increased expression of B12, folate ($p<0.05$) and glucose transporters (GLUT-1) in placenta. Elevated levels of homocysteine resulted in an increased expression of DNMT 3A,3B ($p<0.05$). The expression of H19 (maternally imprinted) was significantly increased ($p<0.05$) and IGF2 expression (paternally imprinted) decreased in pre-gestational diabetic mothers. Evaluation of independent set of infants born to diabetic mothers (N=22) with clinical signs of ROP suggested a significant association between ROP and pre-gestational diabetes ($p<0.05$). **Conclusion:** Our results suggest that maternal diabetes, particularly pre-gestational diabetes, may confer an increased risk of developing ROP.

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Free Paper 3: 3D cell migration model for screening corneal implants for efficient wound healing

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Purpose: Physiologically relevant in vitro models are vital for studying tissue regeneration and reducing animal use. Existing 2D models emphasize unidirectional migration and fail to mimic centripetal epithelialization with stromal regeneration. This study proposes a 3D cell migration assay to model corneal wound healing as promising alternative to animal testing. **Method:** A 3D corneal wound healing model was developed using human corneal epithelial (HCE) cells on a collagen gel bed mimicking native ECM, the outcome of which was compared to 2D scratch assay. A cylindrical wound was created in the center using a 2 mm trephine, and Kuragel[1], a biopolymeric test formulation was filled in the wound cavity. Cell migration, morphology, and re-epithelialization were monitored to assess wound closure over time. Results: Kuragel-filled cylindrical wounds showed HCE migration and invasion generally by 3-4 days of seeding followed by ~70% closure by 48 h and near-complete epithelialization by 72 h post cell entry into the wound site. Alternatively, 2D scratch assay exhibiting unidirectional cell movement closed within 48 h. The 3D migration assay more closely replicates native human corneal healing kinetics (7–14 days[2]) than 2D models. Confocal microscopy confirmed tight junction formation via ZO-1 staining, indicating barrier restoration. Further, circular wound geometry promoted natural cell migration. Conclusion: The current 3D model enables multidimensional cell-material interactions, better reflecting native corneal physiology, that can be utilised for screening and potency assessments for corneal implants. With increasing restrictions on animal testing[3], these 3D in vitro models offer valuable, ethical alternatives for preclinical research.

References: 1. 2. 3. Agrawal, P. et al. Kuragel: A biomimetic hydrogel scaffold designed to promote corneal regeneration. iScience 27, (2024). Vaidyanathan, U. et al. Persistent corneal epithelial defects: a review article. Medical Hypothesis, Discovery and Innovation in Ophthalmology 8, 163 (2019). US FDA. FDA Announces Plan to Phase Out Animal Testing Requirement for Monoclonal Antibodies and Other Drugs. April 10, 2025. https://www.fda.gov/newsevents/press-announcements/fda-announces-plan-phase-out-animal-testing requirement-monoclonal-antibodies-and-other-drugs (2025).

Free Paper 4: SPARC as a novel driver of gliosis and mitochondrial dysfunction in early diabetic retinopathy

Shubhrajit Barman[1,2,3], Senthil Kumar Ganesan[1,2,3 #]

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Purpose: Diabetic retinopathy (DR) often begins silently, making early intervention a major challenge. In this study, we explore the role of the protein SPARC as a critical regulator of early retinal damage. We investigated on how SPARC triggers harmful glial activation and disrupts mitochondrial health, two critical events in the early stages of DR. **Methods:** Using single-cell RNA-seq data (E-MTAB-9061, PRJNA653629), we found that SPARC is predominantly expressed in Müller glial cells. We modeled early DR using STZ-induced diabetic rats (n=6/group) and high-glucose-treated Müller cells (rMC-1, 25 mM). SPARC was silenced using lentiviral shRNA. We assessed gliosis through GFAP staining, tracked cell proliferation, migration, and cell cycle changes, and evaluated mitochondrial function using membrane potential, ROS levels, TCA cycle activity, and intracellular calcium. Statistical analysis included t-tests and ANOVA ($p<0.05$). **Results:** SPARC knockdown significantly reduced GFAP levels (↓42% in rats, ↓54% in cells), suppressed cell migration (↓45%) and proliferation (↓38%), and G2/M cell cycle arrest. Mechanistically, SPARC interacted with integrin α5β3 to activate FAK and ERK signaling (pFAK ↑2.1-fold, pERK ↑1.8-fold), leading to gliosis and a shift toward a mesenchymal like state (↑α-SMA, Vimentin, N-cadherin). Silencing SPARC also rescued mitochondrial function: ΔΨm increased by 50%, decreased mitoROS, mitochondrial fragmentation and calcium levels, and TCA activity improved. **Conclusions:** Our findings establish SPARC as a central player in early DR, connecting glial activation with mitochondrial dysfunction. Beyond its mechanistic role, SPARC shows strong potential as both a biomarker and a therapeutic target offering a promising new direction for early-stage DR treatment.

Free Paper 5: To investigate the role of intraflagellar transport protein gene IFT88 in Leber Congenital Amaurosis and Retinitis Pigmentosa in Indian Patients

Dhruv Sharma[1,2,7], Deepika C Parameswarappa[3,5], Deepak Kumar Bagga[4], Brijesh Takkar[3,5], Subhadra Jalali [3,5], Indumathi Mariappan [2,6], Chitra Kannabiran[1,2]

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Purpose: 1. Identifying pathogenic mutations in *IFT88* in subjects affected with RP and LCA. 2. Deriving genotype-phenotype associations among patients with mutations. 3. *In vitro* investigation of identified *IFT88* mutants. **Methods:** DNA from 91 probands was screened for variations in the coding regions of *IFT88* by standard methods and sequence data were analyzed by appropriate follow-up as required. Wild type mouse cDNA was obtained in a lentiviral construct expressing a fusion of *Ift88* cDNA with EGFP. Three mutants of IFT88, reported in literature, were selected for cloning and expression. Mutant clones were generated by site-directed mutagenesis with appropriate mutant primers, and the wild type *Ift88* cDNA clone in the lentivirus vector, and confirmed by sequencing. **Results:** Partial screening of the IFT88 gene revealed six changes, all of which were characterized as benign variants on the basis of their presence in normal populations, and on predicted impact on pathogenicity. Twenty patients had three changes that were in the exons, of which all were missense. Three patients had one intronic change each located in three distinct regions of corresponding introns. Frequencies of these changes were assessed from available databases. Expression of WT Ift88-EGFP fusion proteins showed localization to ciliary basal body. **Conclusions:** Data obtained so far upon partial screening of IFT88 indicated the presence of various non-pathogenic alterations. Further work is in progress in order to understand the role of IFT88 in LCA and RP in Indian patients. Studies of mutant constructs of Ift88-EGFP are in progress.

Free Paper 6: Evaluation of novel cell penetrating peptides targeting neuronal protein 3.1(P311) in preventing epithelial to mesenchymal transition in ARPE 19 cells

Lavanya Erudayadhas[1,5], Hemavathy Nagarajan[2], Rajesh Sekar[1], Barath Gajendran[3], Sampathkumar Ranganathan[2]; Umashankar Vetrivel[4], Sharada Ramasubramanyan[1]

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Purpose: TGF-β-induced EMT transformation in retinal pigmented epithelial cells is one of the key pathological processes in vision threatening conditions such as Proliferative Vitreoretinopathy, Age-related Macular Degeneration, Diabetic Retinopathy etc. Recent studies have shown an RNA-binding protein Neuronal Protein 3.1 (P311) bound to eukaryotic initiation factor 3b (eIF3b) binds to the 5'- untranslated region (5'-UTR) of TGFβ1-3 to promote their translation. Thus, the aim of the study was to design and functionally characterize novel cell penetrating peptide inhibitors (P311-CPP) that compete against the endogenous P311-eIF3b binding site thereby halting the EMT transition in ARPE19 cells. **Methods:** P311-derived peptides were computationally designed and cytotoxicity was measured using MTT assay in ARPE-19. The cells were pre-treated with peptide for 1hr prior to induction with pro-inflammatory cytokine TNF α for 48hr. The anti-fibrotic effect of CPPs were confirmed through qPCR and western blotting of EMT markers and functionally validated using cell migration assay, collagen deposition (sirius red), EAFD formation etc. **Results:** The computational analysis yielded a non-toxic CPP, P311-CPP with good physio-chemical and cell penetrating properties. ARPE-19 treated with peptide and TNFα stimulation showed significant reduction of expression of mesenchymal markers such as N-cadherin, ZEB1, etc and decreased expression of extra cellular matrix marker such as COL1A1 which was also verified by collagen assay (Sirius Red). In addition, there was significant inhibition of cell migration, and reduced number of EAFDs upon peptide treatment. **Conclusion**: PEP_E1, a peptide inhibitor shows promising results as therapy in reducing TGFβ1 protein translation and ECM deposition upon pro-fibrotic stimuli substantially increasing the translational potential of this study.

Free paper 7: DNA methylation profiling in Bardet-Biedl Syndrome

Syed Ali Fathima Afrin J[1,2], Megha Thippanna[1], Sripriya S[1]

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Introduction: Bardet-Biedl Syndrome (BBS) is a rare autosomal recessive ciliopathy characterized by features such as retinitis pigmentosa, polydactyly, obesity, renal anomalies, and intellectual disability. Recent advances highlight the diagnostic relevance of episignatures, distinct DNA methylation patterns in various genetic syndromes, especially neurodevelopmental disorders. Given the pleiotropic nature of ciliopathies, this study aimed to identify a unique epigenetic signature associated with BBS. **Methods:** Genome-wide DNA methylation profiling was performed using the Illumina Infinium MethylationEPIC BeadChip on a discovery cohort of N=6 BBS patients and N=7 unrelated controls. Data were processed using the ChAMP pipeline in R to identify differentially methylated positions (DMPs) and regions (DMRs). A support vector machine (SVM) model was applied to evaluate the classification power of the methylation signature, and DMRs were defined using the bumphunter algorithm with ≥10% methylation difference and adjusted $p < 0.05$. Gene prioritization was performed using VarElect, and biological pathway enrichment was assessed through Gene Set Enrichment Analysis (GSEA). The prioritized DMRs were validated using Sanger-based bisulfite sequencing in an independent cohort of N=30 BBS patients and compared against non-syndromic inherited retinal dystrophy (IRD) cases. **Results and conclusion:** The analysis identified 187 DMPs capable of distinguishing BBS patients from controls with high specificity. A refined set of 39 DMRs (190 CpG sites) mapped to genes involved in retinal and kidney development. These findings suggest that BBS exhibits a distinct peripheral blood episignature, potentially aiding in diagnosis and interpretation of uncertain genetic variants.

Free Paper 8: Automated HbA1C classification from retinal images using a hybrid deep learning framework

Dakshi Arora[1], Parag Garg[1], Manisha Saini[1], Deepikasri J S[2], Sathishkumar Sundaramoorthy[3], Dhanashree Ratra[4], **Devanjali Relan**[1]

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Purpose: Motivated by the need for accessible and blood-free diagnostic alternatives in diabetes screening, this study presents a non-invasive deep learning framework for the automated classification of glycated haemoglobin (HbA1c) levels using retinal images . **Methods**: The dataset comprised of 912 retinal images, from diabetic (604) and control subjects (308). Data augmentation gave a total of 5,472 images. The dataset was divided into a training set (70%), a validation set (20%), and a test set (10%), to maintain class distribution across splits. Image preprocessing included grayscale conversion, resizing, Gaussian filtering, normalization, and data augmentation techniques. to enhance model robustness and generalizability. The proposed system consist of transfer learning with multiple pretrained backbones and a hybrid UNet- based attention mechanism to enhance feature extraction, particularly focusing on capturing retinal patterns. **Results:** For binary classification, HbA1c levels were categorized into Optimal (<6.5%) and Not Optimal (≥6.5%) , with the model achieving a test accuracy of 92%. For the *Not Optimal* class, the model recorded a precision of 0.94, recall of 0.89, and F1-score of 0.92, while the *Optimal* class achieved a precision of 0.95, recall of 0.97, and F1-score of 0.96. In the multiclass setting, levels are classified into Optimal (<5.7%), Elevated (5.7%-6.4%), and High (>6.5%), achieving a test accuracy of 89%. The Elevated class recorded the highest precision at 0.92, indicating that 92% of the samples predicted as Elevated were correctly classified, while the High class achieved the highest recall at 0.94, correctly identifying 87% samples. The Optimal class exhibited the highest F1-score of 0.91, reflecting a balanced performance between precision and recall. **Conclusions:** These results demonstrate the model's effectiveness in accurate HbA1c prediction and highlight its clinical potential for diabetes screening. It can eliminate the need for invasive blood tests, reduce operational costs and allow faster diagnostic workflow. Future work will focus on refining the integration model into a user-friendly mobile application for deployment as point-of-care testing.

Free paper 9: Customized version of vessel density quantification with image processing

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Purpose: To establish a customized technique to measure retinal vessel density and compare with existing values provided by the machine. **Methods:** It was a prospective cross-sectional study in one of the tertiary eye care centers. One of the objectives is to have macular vessel density across the eyes for a precise analysis, hence, samples of OCTA data were collected for comparison. Customized scripts were made through programming language (MATLAB) which shall replace in-built vessel density scalar values (Topcon Swept Source OCT- Machine). **Results:** Total 80 samples were selected which includes the image of superficial capillary plexus from OCTA. Descriptive statistics were used for the calculations. Vessel density parameters were analyzed from different quadrants of macular region and fovea where the actual mapping is done by the machine. Agreement plots were made between machine induced data vs customized MATLAB algorithms. The result showed good agreements among the data for macular vessel density. Machine systematically overestimates the foveal avascular region (false positive) than MATLAB. **Conclusions:** Although fundamental extraction of vessel density is a 3-D concept, a proper approach and application of image processing can be applied on 2-D images for the same at ease. **Keywords:** OCTA: Optical Coherence Tomography Angiography, MATLAB: Matrix Laboratory

Note: The work is one of the objectives of PhD thesis titled as “Comparison of visual function abnormalities with visual pathway involvement in glaucoma”.

Free paper 10: Age-dependent variations in corneal nerve morphology

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Purpose: To evaluate age-related changes in corneal nerve morphology using in vivo confocal microscopy (IVCM) in a healthy Indian population. **Methods:** A cross-sectional study was conducted with 42 males and 38 females, aged between 18 and 85 years. Participants were divided into four age groups (<20, 20-40, 40-60, and >60 yrs). IVCM imaging was performed using the Heidelberg Retina Tomograph III (HRT-RCM). Eight central and one inferior whorl (IW) images per subject were analysed for corneal nerve fiber length (CNFL), fiber density (CNFD), branch density (CNBD), total branch density (CTBD), fiber area (CNFA), fiber width (CNFW), and fractal dimension (CNFracDim). **Results:** All central nerve parameters showed a statistically significant difference across age groups for CNFL (p=0.023), CNFD (p=0.037), CNBD (p=0.025), CTBD (p=0.017), CNFA (p=0.002), CNFW (p=0.002), and CNFracDim (p=0.036). In the inferior whorl, all parameters except CNFW (p=0.078) were significantly different across age groups. Correlation analysis with age resulted in a significant low positive correlation with central CNFW (r=0.398, p<0.001), and a significant low negative correlation with central CNFD (r=-0.301, p=0.007). In the inferior region, CNFL, CNFD, CNBD, CTBD, CNFA, and CNFracDim resulted in weak negative correlation (p<0.01). **Conclusions:** Corneal nerve morphology changes with age. These results indicate that the corneal nerve width increases with increasing age. Whereas all other variables showed an inverse correlation with age. Age-related changes in corneal nerve parameters were more pronounced in the inferior whorl. Compared to the central cornea, the inferior whorl may act as a potential biomarker for early detection of age-related changes.

Keywords: CCM, Normative Data, Inferior Whorl, Corneal Nerve Parameters, Age

Free paper 11: Diagnostic utility of targeted Nanopore sequencing in patients with canaliculitis

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Purpose: Identification of causative pathogen is crucial in the management of canaliculitis patients. However, since the infection is often polymicrobial and caused by anaerobic bacteria, conventional techniques lack sensitivity. The purpose of the study was to evaluate the utility of Next-generation metagenomic sequencing (NGS) using the Nanopore sequencing technology to identify potential causative pathogens in canaliculitis. **Methods:** A total of 10 canalicular pus samples were collected from patients presenting with canaliculitis at the Oculoplasty clinic at Sankara Nethralaya. In addition to microscopy and culture, the clinical samples were subjected to 16S rDNA PCR followed by gene sequencing using the nanopore platform. Taxonomic classification using the obtained raw data was performed in real-time using cloud-based EPI2ME software. **Results:** Nanopore sequencing showed the presence of bacteria in all 10 samples. While conventional aerobic and anaerobic culture detected polymicrobial infection only in one sample, NPS detected polymicrobial aetiology was seen in 9/10 samples (90%). Several genera of bacteria (>1% abundance) were identified, including *Fusobacterium spp* and *Prevotella spp* in 7 eyes, *Streptococcus spp* in 5 eyes, *Parvimonas*, *Gemella* and *Campylobacter spp* in 3 eyes, *Porphyromonas, Dialister, Tannerella, Peptostreptococcus, Peptococcus, Mycoplasma, Capnocytophaga* and *Staphylococcus spp* in 2 eyes and *Actinomyces, Bacillus, Escherichia* and *Haemophilus spp* in one eye. **Conclusion:** This study successfully demonstrated the presence of multiple aerobic and anaerobic bacteria in samples from infectious canaliculitis using targeted nanopore sequencing. Nanopore sequencing provides potential for cost-effective point-of-care diagnostics for polymicrobial infections such as canaliculitis, where anaerobes are a major aetiology.

Free paper 12: Prospective evaluation of RID-MYC assay for POC diagnosis and clinical management in smear and culture-negative keratitis with IVCM correlation

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Purpose: To evaluate the diagnostic utility of the RID-MyC assay in smear- and culture-negative suspected fungal keratitis (FK) cases, correlate its results with in vivo confocal microscopy (IVCM), and assess its role in guiding clinical management and outcomes for early point-of-care (POC) detection. **Methods:** This prospective study was conducted over 75 days at Aravind Eye Hospital, Coimbatore, and included 275 corneal scrape samples from patients with suspected FK. Of these, 89 samples were negative by KOH and/or Gram stain and showed no growth in culture. Among them, 41 underwent IVCM to assess fungal presence and were tested using the RID-MyC assay, a rapid nucleic acid-based detection method. Clinical management and outcomes were documented to evaluate the correlation between RID-MyC results, IVCM findings, antifungal therapy, and visual prognosis. **Results:** RID-MyC detected fungal DNA in 23 of the 28 IVCM-positive cases and was negative in eight of the 13 IVCM-negative cases, demonstrating a sensitivity of 82.1% and specificity of 61.5%, with good concordance with clinical imaging. Ten cases showed discordance: five IVCM-negative and RID-MyC-positive (no prior antifungal use; mean ulcer size 3.13 mm; visual acuity declined from 0.17 to 0.06) and five IVCM-positive and RID-MyC-negative (two had prior antifungal use; mean ulcer size 2.88 mm; visual acuity improved from 0.19 to 0.50). **Conclusions:** RID-MyC showed high sensitivity in detecting fungal DNA in smear- and culture negative FK and correlated with IVCM. Its rapid results support its potential as a reliable POC diagnostic tool to enable timely antifungal therapy and better outcomes.

Free paper 13: Novel small molecule inhibitor AXM017 for fungal keratitis treatment: Evaluation of in vitro efficacy and safety

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Purpose: Fungal keratitis (FK) is a severe ocular emergency affecting approximately one million people annually, with *Aspergillus*, *Fusarium*, and *Candida* species responsible for 95% of cases. Currently, Natamycin (5%) is the only FDA-approved treatment for FK. The novel small molecule AXM107 exhibits broad-spectrum antifungal activity against seven distinct fungal species, indicating its potential as a promising antifungal candidate. This study aims to evaluate the *in vitro* efficacy and safety of AXM107 for FK treatment. **Methods:** The minimum inhibitory concentration (MIC) and minimum fungicidal concentration (MFC) of AXM107 were determined against clinical keratitis isolates of *Candida* (n=10), *Fusarium* (n=8), and *Aspergillus* spp. (n=6). The effects of AXM107 on fungal biofilm inhibition, cellular morphology, time-kill kinetics at MICs, and interactions with amphotericin B were assessed. Safety was evaluated using human corneal epithelial cells (HCEs) and the hen's egg chorioallantoic membrane (HET-CAM) test. **Results:** AXM107 demonstrated cidal effects against *Candida* spp. with MIC90 and MFC90 values of 0.0313 and 0.156 µg/mL, respectively. It showed static activity against filamentous fungi, inhibiting *Aspergillus* growth by 80% at 1.25–20 µg/mL and *Fusarium* at 0.019–0.312 µg/mL. AXM107 exhibited concentration-dependent biofilm inhibition, disrupted fungal morphology, and significant growth suppression ($p<0.05$) up to 48 hrs. AXM107 synergized with amphotericin B (FIC <0.5). It was safe for HCEs at concentrations up to 20 µg/mL and showed no vascular defects *in ovo*. **Conclusion:** AXM107 demonstrated effective antifungal activity and safety *in vitro*, suggesting its potential as a promising candidate for FK treatment. **Key words:** Fungal keratitis, AXM107, Ophthalmics, *Fusarium*, *Aspergillus*, *Candida*, efficacy and safety.

Free paper 14: Self-assembling peptide hydrogels from nature's defenders: Next generation biomaterial engineering against fungal keratitis

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Purpose: Fungal keratitis (FK) is a severe and potentially threatening corneal infection, often leading to even permanent vision loss[1]. The causative agents, primarily Fusarium and Candida spp., often exhibit limited responsiveness to current antifungal therapies due to poor ocular penetration and bioavailability[2, 3]. This study aims to design and characterize novel self assembling hydrogels derived from truncated sequences of a host defense peptide (HDP), engineered to exhibit antifungal activity and suitability for in situ ocular delivery.

Methods: Short peptide sequences were derived from the C-terminal region of HDP. Selected peptides were synthesized and subjected to solvent-switch-induced gelation. The resulting hydrogels were characterized via FTIR spectroscopy, SEM, and rheometry. In vitro antifungal efficacy was evaluated against ocular Candida albicans and Fusarium solani isolates using agar-based assays. Biocompatibility was assessed using human corneal epithelial cells (HCECs) through LDH cytotoxicity assay and Live-dead analysis and cytokine profiling.

Results: Two peptides (R7 and rR8) demonstrated rapid in situ gelation in phosphate buffer (pH 7.4). FTIR revealed a shift in amide I band, indicative of β-sheet formation. SEM analysis confirmed a porous, fibrillar network. rR8 displayed potent fungicidal activity, eliminating fungal growth comparably to amphotericin B, while R7 showed limited inhibitory effect. Both hydrogels were stable in PBS for 21 days, with showing no cytotoxicity in HCECs.

Conclusion: This study presents a rational design strategy for developing Fmoc-modified short peptides with self-assembling and antifungal properties. The resulting hydrogels exhibit physicochemical stability, ocular biocompatibility, and antifungal efficacy, offering promise as next-generation biomaterials for localized therapy in FK.

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Free Paper 15: Valproate-associated Dry eye: Interplay between inflammation and oxidative stress

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Purpose: Valproate, an antiepileptic drug, causes carnitine deficiency and dry eye syndrome. However, the underlying ocular toxicity mechanism has not been explored. We hypothesize that Valproate causes modulation of carnitine transporters, Novel Organic Cation Transporters (OCTN), and leads to dysregulation of the immune system and poor homeostasis of reactive oxygen species (ROS) and reactive nitrogen species (RNS). Furthermore, treating with L-carnitine could mitigate the Valproate-associated toxicity. **Methods:** The rabbit corneal epithelial cells were treated either with Valproate (1 mM) only or co-treated with L-Carnitine in the molar ratio of 0.5, 1, and 2 for 48 h. The gene expression of OCTN, inflammatory (Interleukin-IL6, Matrix Metalloproteinase-MMP9), and oxidative stress (Superoxide Dismutase-SOD1) markers were evaluated using polymerase chain reaction and normalized with beta-actin. The generation of ROS and RNS was evaluated using the 2'-7'-dichlorofluorescein-diacetate and Griess assays, respectively. **Results:** The relative OCTN1 (3-fold) and OCTN2 (1.5-fold) expression increased in the Valproate-treated group compared to the control group, with decreased expression when co-treated with L-Carnitine. Similarly, compared to the control group, the IL-6 (2-fold) and SOD1 (3-fold) increased, and MMP-9 decreased (3-fold) in Valproate-treated cells, with a decrease in IL-6 and SOD1 and an increase in MMP-9 in carnitine co-treated cells. The Valproate treatment did not induce ROS but increased RNS with a decrease in carnitine co-treated cells. **Conclusions:** Valproate increased the OCTN expression, further promoting inflammation and nitrative stress. Interestingly, co-administration of L-carnitine with Valproate reduced its associated toxicity. Therefore, L-carnitine-based topical drops can be explored to reduce the dry eye syndrome caused by systemic Valproate.

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Free paper 16: Shift from invasive to non-invasive treatment for Keratoconus: Resveratrol-loaded polymeric ocular patch

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Purpose: Keratoconus is a corneal ectatic disorder where inflammation and oxidative stress lead to loss of biomechanical strength of the cornea. Resveratrol has antioxidant and anti-inflammatory properties that could scavenge the cells from reactive oxygen species (ROS) and prevent collagen breakdown. In our work, resveratrol is formulated as nanomicelles, which were loaded into a polymeric solution and fabricated as a patch (REPAT), which could be a potential alternative therapy for keratoconus. **Methods:** Resveratrol nanomicelles were prepared using thin film hydration. REPAT was fabricated using an extrusion-based 3D printing technique and was characterized for in vitro drug release. The cell viability and antioxidant activity were evaluated in the human corneal epithelial cells (HCECs) against hydrogen peroxide-induced ROS. Ocular pharmacokinetics and in vivo efficacy (collagenase-induced keratoconus) were evaluated in rabbits for their skewed radial axes (SRAX) value, corneal shape, and thickness after topical administration of REPAT. **Results:** The REPAT showed a 100% resveratrol release in five days. The REPAT treatment showed significantly higher cell viability, 61.03 ± 9.98%, and an oxygen scavenging activity of 69.14 ± 6.46% compared to the untreated ROS-induced-HCECs. REPAT sustained tear drug levels for 72 hours (54.11 ± 3.18 μg.h/mL) and improved penetration in the aqueous humor until 12 hours (119.25 ± 7.45 ng.h/mL). When treated with REPAT, the keratoconus-induced rabbit eyes showed an improved SRAX and corneal thickness. **Conclusion:** REPAT could be a potential alternative therapy for treating keratoconus by reducing oxidative stress. Further studies need to be conducted to identify specific oxidative and inflammatory markers.

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Free paper 17: Understanding ocular delivery of biotherapeutics: Insights into peptide transporters and blood-ocular barriers

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Purpose: Increasing number of peptide-based therapies holds potential for developing new drugs for ocular diseases, making it crucial to understand peptide transporters in ocular tissues to optimize PK/PD. **Methods:** To determine the substrate specificity, transcorneal penetration of glycylsarcosine (glysar) was evaluated at different concentrations and pH. Further, rabbits (n=4) were divided into two groups: 1) Glysar (substrate), 2) Glysar with losartan (blocker) pretreatment. The treatment was given via topical, intravenous (IV) and intravitreal (IVT) route. After topical instillation and IV administration of drugs, tear and aqueous humor (AH) were collected. Various ocular fluids and tissues were collected following IVT at 15, 30, 60 and 120 mins. The drug levels were analyzed using LC-MS/MS. **Results:** Topically applied glysar (68.42 µmol/mL) showed a maximum AH concentration of 3 nmol/mL at 30 min. Upon blockage of transcorneal peptide transporters, the conc. of glysar was reduced to 0.3 nmol/mL ($p<0.001$). Tear kinetics of glysar showed a rapid decline at 30 min upto 1 hr followed by a gradual precorneal elimination. After blocker pre-treatment, the precorneal residence of glysar (0.09 nmol/mL) decreased significantly ($p<0.001$). However, after IV administration of glysar, its conc. in AH of blocker pre-treated group was reduced to 0.38 nmol/mL ($p<0.01$) and in tear increased to 2.79 nmol/mL ($p<0.05$). After IVT administration of glysar, its conc. in cornea, lens, iris ciliary body, conjunctiva and plasma of blocker pre-treated group was reduced to 9.6 nmol/mL ($p<0.01$), 1.07 nmol/mL ($p<0.01$), 10 nmol/mL ($p<0.01$), 16.38 nmol/mL ($p<0.05$) and 0.25 nmol/mL ($p<0.001$) respectively. **Conclusion:** This study provides the first insights into the presence, regional variation, and functional role of peptide transporters in ocular uptake, crucial for developing peptide transporter-targeted ocular drug delivery.

Free paper 18: Soluble biomarkers sFLT-1 and sST2 predict outcomes to anti-VEGF therapy in DME: an interdisciplinary approach

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Purpose: Diabetic macular edema (DME) results from retinal vascular leakage and fluid accumulation beneath the retina. Anti-VEGF therapy is standard care for DME, yet many patients respond poorly due to persistent inflammation and retinal barrier dysfunction. This study adopts a multidisciplinary approach by merging clinical phenotypes with systemic immunology and molecular profiling to investigate biomarkers predictive of therapeutic response in DME. **Method:** Serum from 22 DME patients treated with ≥3 anti-VEGFs over ≥6 months was analysed. Patients were stratified as responders or non-responders based on changes in BCVA, and CRT. Bead-based multiplex assays quantified angiogenic, inflammatory, and adhesion molecules. Correlations between cytokines and clinical parameters were assessed using GraphPad Prism. **Results:** Responders demonstrated significant improvements in BCVA ($p<0.05$) and CRT ($p<0.001$), alongside elevated levels of sST2, sFLT-1, and MCP-1. sFLT-1 negatively correlated with BCVA ($r= –0.40$), indicating a protective role. In contrast, non-responders exhibited higher IL-18 ($p<0.05$) and a positive sFLT–1 BCVA correlation ($r = 0.33$). Network analysis showed distinct patterns: responders had inverse Ang-2/sST2 correlation ($r= –0.38$), while non-responders showed pro-inflammatory clustering (Ang-2/sST2: $r=0.46$; PlGF/MCP-1: $r=0.52$). ROC curves confirmed the predictive utility of sFLT-1, sST2, and MCP-1 (AUC≈0.8). **Conclusion:** This study identifies soluble serum markers, sFLT-1 and sST2, predictive of anti-VEGF response in DME patients. Responders had elevated sFLT-1 (a VEGF neutraliser) and sST2 (an IL-33 pathway inhibitor). Non-responders showed higher IL-18 and Ang-2/sST2 ratios, indicating persistent inflammation and angiogenesis. These biomarkers could guide patient stratification, with non-responders potentially requiring adjunctive anti-inflammatory or alternative angiogenic therapies.

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Free paper 19: Altered lipid metabolism is a crucial regulator in Retinopathy of prematurity

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Purpose: Preterm infants are highly susceptible to retinopathy of prematurity (ROP), characterized by abnormal retinal blood vessel growth and inflammation. Clinical evidences suggest that ROP infants are deficient in key lipid metabolites comprising long-chain polyunsaturated fatty acids (PUFAs), such as docosahexaenoic acid (DHA) and arachidonic acid (AA). However, the mechanisms underlying lipid dysregulation in ROP pathogenesis is yet unclear. **Methods:** The lipid metabolites and proteins in the vitreous humor were identified by LC-MS (ROP = 19, control = 19) and retinal gene expression was assessed by microarray (ROP = 3, control = 3). Lipid metabolizing enzymes, angiogenic, and cell death markers were quantified in the blood of ROP babies (n= 70) and controls (n= 56), and validated in human primary retinal cell cultures and ROP retinas by IHC. **Results:** Overall 343 lipids were identified of which, 155 were significantly altered in ROP along with downregulations of fatty acids and phospholipids. Reduced levels of PUFA and sphingosine-1-phosphate (S1P) with increased ceramides, indicated a pro-apoptotic and pro-inflammatory shift. These changes were accompanied by upregulation of ceramide synthase (*CERS1*) and downregulation of *SPHK1*. Additionally, altered expressions of genes involved in lipid metabolism (*ALOX5, COX2, CYP1B1, CYP2C8, EPHX2*), angiogenesis (*VEGF165/189, VEGFR2*), and apoptosis (*CASP3/8, HIF1A*) indicated impaired lipid signaling in ROP. Hypoxia-treated retinal cultures recapitulated the patient lipid alterations, confirming the involvement of AA–ceramide pathway. **Conclusions:** These findings suggested that altered lipid profiles may contribute to abnormal angiogenesis and inflammation and underscored the role of AA and ceramide metabolism in ROP pathogenesis.

Free paper 20: Untargeted metabolomics and histology of the anterior lens capsule reveal novel metabolites and ECM markers in anterior subcapsular cataract

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Purpose: Anterior subcapsular cataract (ASC) presents surgical challenges due to subcapsular fibrotic plaques and poor pseudophakic lens positioning. Early metabolic changes underlying fibrotic transformation remain unclear. We integrated untargeted LC-MS metabolomics with histological and immunofluorescence analysis to identify early fibrotic markers in ASC. **Methods:** Anterior lens capsules were obtained during phacoemulsification and classified as fibrosed or non-fibrosed based on clinical and histological evaluation (H&E staining). ECM markers, including Collagen IV and E-cadherin, were assessed by immunofluorescence. UHPLC-MS–based untargeted metabolomics was performed. Data were analyzed using MetaboAnalyst, with PLS-DA, volcano plots, and pathway enrichment. Metabolites were annotated using OmicsCraft, KEGG, and HMDB. **Results:** Fibrosed capsules showed epithelial thickening and ECM accumulation. Collagen IV expression was elevated and E-cadherin reduced, indicating EMT. Metabolomics revealed several significantly altered features ($p < 0.05$, fold change >1.5 or <1.5), including increased N-acetylneuraminic acid, sphingosine, thiodiglycolic acid, and benzylformic acid. Enriched pathways included the pentose phosphate pathway, lysine degradation, and linoleic acid metabolism. **Conclusions:** We report distinct metabolic and ECM alterations in ASC, with evidence of EMT and novel metabolite biomarkers. These findings support future development of anti-fibrotic strategies to improve cataract surgery outcomes.

Free paper 21: Aptamer based detection of Cystatin-C for screening of diabetic retinopathy

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Purpose: Diabetic retinopathy (DR) is a major microvascular complication of diabetes mellitus (DM), leading to progressive retinal vessel damage and potential vision loss. As the prevalence of DM increases, early and accurate DR diagnosis is critical. Manual examination of retinal changes is laborious and subjective. Cystatin-C (Cys-C), a biomarker unaffected by age, gender, or muscle mass, has shown superior diagnostic potential over serum creatinine and 12 other circulating biomarkers in distinguishing sight-threatening DR (STDR) from no DR in our multicentre studies. National Health and Nutrition Examination Survey (NHANES) data further support Cys-C as a better predictor of DR. While antibodies are common in diagnostics, they pose limitations such as variability and complex production. Aptamers—short, single-stranded nucleic acids selected via the SELEX (Systematic Evolution of Ligands by Exponential Enrichment) process serve as stable, specific, and reproducible alternatives. **Methods:** In this study, aptamers were selected using recombinant Cys-C for positive selection and pooled Cys-C–depleted human serum for negative selection. Iterative SELEX cycles yielded two aptamer pairs suitable for use as capture and detection probes and evaluated using sandwich assays via dot-blot and plate methods. **Results:** The selected aptamer pairs demonstrated high specificity and sensitivity in detecting Cys-C in serum samples. The assay was adaptable to multiple target-based outputs and compatible with ELONA (Enzyme-Linked Oligonucleotide Assay) and dot-blot methods. **Conclusion:** This aptamer-based assay offers a promising, cost-effective alternative to antibody-based diagnostics and holds potential for development into a point-of-care in-vitro diagnostic (IVD) kit for early DR screening and management.

Free paper 22: Unlocking the molecular code of pseudoexfoliation glaucoma: Multi-omic signatures of disease progression

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Purpose: Pseudoexfoliation is a complex, age-related disorder and a leading cause of irreversible blindness, characterized by the pathological accumulation of proteinaceous material that elevates intraocular pressure and causes optic nerve damage. Despite an unclear etiology, accumulating evidence implicates the interplay of genetic and epigenetic factors. This study integrates genetic, epigenetic, and metabolic factors in an Indian cohort to identify candidate biomarkers and therapeutic targets. **Methods:** qRT-PCR, western blotting, immunohistochemistry, ELISA, CRISPR/Cas9-based functional assay, Sanger sequencing, DNA methylation profiling, 3C-based enhancer promoter interaction assays, and LC-MS analysis. **Results:** Our work highlights a significant association of risk variants in *Clusterin (CLU)* and *Fibulin-5 (FBLN5)* risk variants with pseudoexfoliation, influencing gene expression and enhancer activity. Chromatin conformation capture assays revealed regulatory interactions between enhancers and the promoters of CLU. Epigenetic silencing of Heat Shock Protein 70 (HSP70), CLU hypomethylation, and dysregulation of microRNA-223 indicated multilayered control of chaperone expression. Proteostasis disruption was supported by altered expression of unfolded protein response (UPR) genes -Calnexin and Synoviolin-1, with reduced proteasomal activity. Quantitative analysis of vimentin suggested its biomarker potential, while mechanistic studies of Dickkopf-1 (DKK1) and Rho-Associated Protein Kinase 2 (ROCK2) were implicated in protein aggregation. Additionally, metabolomic profiling revealed significant disruptions in amino acid and lipid metabolism. **Conclusions:** Our findings underscore the importance of population-specific risk factors and reinforce the translational potential of multi-omics in stratifying patients and identifying therapeutic entry points. Understanding the interplay among genetic predisposition, epigenetic modifications, and dysregulated cellular-metabolic pathways provides critical insights into the molecular pathogenesis of pseudoexfoliation.

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IN101: Does altered C-peptide levels promote pro-fibrotic effects in diabetic retinopathy?

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Purpose : The role of C-peptide in the development and progression of diabetic retinopathy is incompletely understood. In addition to its role as a marker of beta-cell function, its role as a cellular signaling molecule exhibiting protective role needs more studies. Both deficiency and excess of C-peptide promote diabetic complications. This study evaluated fibrosis markers at the systemic level in diabetic retinopathy cases with and without kidney involvement in terms of chronic kidney disease. **Methods:** As part of hospital based prospective pilot study at Medical Research Foundation Chennai Type 2 Diabetes Mellitus (T2DM) patients were classified as without (n=18) and with Diabetic Retinopathy (DR) (n = 24), and patients with Chronic Kidney Disease (CKD) as without DR (n=11) and with DR (CKD-DR) (n=18). Plasma C-peptide (postprandial) and Plasma levels of TGF-β1 were estimated by ELISA, apart from postprandial blood sugar (PPBS), HbA1c, uric acid, urea & creatinine. **Results:** Plasma C-peptide was significantly reduced in DR compared to CKD-DR ($p= 0.02$). Plasma TGF-β1 was significantly increased in DR compared to CKD-DR ($p = 0.04$). **Conclusion:** Plasma C-peptide levels significantly decreased, and conversely, TGF-β1 levels increased in diabetic retinopathy. Furthermore, a significant negative correlation seen between C-peptide and TGF-β1 levels reveals disease progression and fibrotic stress in diabetic retinopathy patients.

IN102: Endogenous trace amines in the neurodegenerative diseases: potential biomarker and therapeutic target

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Purpose: Trace Amine-Associated Receptors (TAARs), especially TAAR1, are linked to CNS functions and neuropsychiatric disorders. As the retina is a neural extension of the CNS, it offers a non-invasive window into neurodegeneration. For the first time, this study explores the trace amines as plausible ocular biomarkers in neurodegenerative diseases such as glaucoma and age-related macular degeneration. **Methods:** A study was conducted at the Dr. Rajendra Prasad Centre for Ophthalmic Sciences, AIIMS, New Delhi. A total of 80 patients (n=20/each) from Wet Age-related Macular Degeneration (WAMD) and Dry Age-related Macular Degeneration (DAMD), Primary Open Angle Glaucoma (POAG), and Primary Angle Closure Glaucoma (PACG) were recruited. The clinical parameters such as IOP, visual acuity, OCT etc. were obtained. The blood samples were collected and analysed for trace amines and neurofilament light chain (NfL) by LC-MS/MS and ELISA, respectively. **Results:** The mean age of study cohort was 73 + 8.76 years with 45% female population. The synephrine levels were 3 folds higher in POAG group as compared to PACG (p=0.006). Tryptamine and phenylethonalamine levels were 2.9 (p=0.04) and 1.9 folds (p=0.08) higher in the WAMD compared to DAMD. The NfL levels in POAG patients significantly correlated with the total trace amines (p=0.004) and synephrine (0.0003) levels. Other trace amines levels were comparable within the sub-types of glaucoma and AMD. **Conclusion:** Altered trace amine and NfL profiles suggest a potential TAAR-related mechanism in neurodegeneration. These biomarkers may serve as complementary tools for early detection and characterization of neuro-degenerative disorders of eye.

IN103: Resident memory T-cells in the eye: Prognostic biomarkers in sight-threatening uveitis?

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Purpose: Tissue-resident memory (TRM) T cells are site-specific memory T cells implicated in chronic inflammation across various autoimmune and infectious diseases. We sought to investigate the phenotype, distribution, and function of TRM cells in the vitreous fluid of patients with posterior segment uveitis. **Methods:** Immune cells were isolated from vitreous samples obtained during diagnostic or therapeutic vitrectomy. Cells were stimulated with a mycobacterial peptide pool as well as with anti-CD3/anti-CD28 (TCR-mediated stimulation), stained with antibodies, and analyzed using flow cytometry. CD4+ and CD8+ TRMs were identified by manually gating based on negative expression of CD45RA and CD62L, and positive expression of the canonical markers CXCR6, CD69, and CD103. Unsupervised clustering was performed using FlowJo to identify the diversity of TRMs in posterior uveitis. **Results:** CD4 TRMs were primarily CD69+ single-positive, while CD8 TRMs also included significant CD69+CD103+ double-positive and CD103+ single-positive populations. TRM-associated markers CXCR6, CCR5, and CD49a were significantly elevated in CD8 cells, particularly among CD69+CD103+ TRM subpopulation. Functional assays demonstrated stronger IFN-γ, IL-17, and TNF-α production from TRMs compared to non-TRM cells upon anti-CD3/anti-CD28 activation, as well as antigen-specific activation with mycobacterial peptide pool (in tubercular uveitis samples). Unsupervised clustering revealed prominent CD4 and CD8 TRM populations, including unconventional central memory TRM subsets. **Conclusion:** Eye-infiltrating CD4 and CD8 TRMs form phenotypically and functionally distinct, antigen-responsive T cell populations in human uveitis, underscoring their potential as biomarkers and possible therapeutic targets.

IN104: Distinct Tear Fluid Macrophage Migration Inhibitory Factor (MIF) And Inflammatory Mediator Profiles In Uveitis Patients

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Purpose: Uveitis, an ocular inflammatory condition, contributes to 10–25% of blindness worldwide. Irrespective of the etiology intraocular immuno-inflammatory imbalance is central to its pathobiology. Hence, we investigated the status of immune augmenting and dampening factors in relation to Macrophage Migration Inhibitory Factor – MIF (known for its dual role) in the tear fluid (TF) of patients with non-infectious idiopathic uveitis (IU) or Vogt-Koyanagi-Harada (VKH) disease. **Methods:** TF samples were collected from health control subjects (n=20; eyes) and patients with IU (n=28; eyes) or VKH (n=27; eyes). Levels of MIF, IL-1β, IL-2, IL-6, IL-8, IL-10, IL-13, IL-17A, TNF-α, IFN-γ, TGFβ-1, MPO, MMP-9, NGAL and TIMP1 in the TF were measured by bead-based multiplex ELISA. **Results:** Levels of MIF along with IL-2, IL-6, IL-8, IL-10, IL-13, IL-17A, TGF-β1, MMP-9, and NGAL were significantly ($P<0.05$) elevated in uveitis patients (VKH+IU) compared with controls. Significant increase in MIF, IL-6, NGAL and TGF-β1 were observed in VKH and IU compared with controls. However, significantly higher TF levels of IL-2, IL-8, IL-10, IL-13, IL-17A, TNF-α, IFN-γ, and MMP-9 were limited only to VKH patients. Additionally, several factors including IL-8, IL-13, IL-6, IL-10 and IL-17A, showed strong positive associations with MIF, in VKH patients, a pattern absent in IU and controls. In contrast, a moderate positive correlation between MIF and IL-1β was observed only in IU patients but not in VKH or controls. **Conclusions:** Our findings identify distinct TF immuno-inflammatory profiles in VKH and IU, linking MIF-cytokine interactions to disease pathogenesis; and supports non-invasive TF inflammatory factors-based stratification of uveitis subtypes.

IN105: Altered Tear Fluid Immuno-Inflammatory Profiles In Patients With Scleritis

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Purpose: Scleritis, a severe ocular surface inflammatory condition, comprises approximately 5–10% of all ocular inflammatory cases and presents a high recurrence rate of 30–50%. The various immunological and molecular factors contributing to scleral inflammation remains to be understood. Hence, this study aimed to investigating immuno-inflammatory factor alterations in tear fluid (TF) of patients with active scleritis. **Methods:** TF samples were collected from scleritis patients (n=30; eyes) and healthy controls (n=20; eyes) at the time of presentation. Levels of MIF, IL-1β, IL-2, IL-6, IL-8, IL-10, IL-13, IL-17A, TNF-α, IFN-γ, TGFβ-1, MPO, MMP-9, NGAL and TIMP1 in the TF were measured by bead-based multiplex ELISA. **Results:** The TF levels of IL-6, IL-10, IL-13, IL-17A, IFN-γ, TGFβ-1, NGAL, and MMP9/TIMP1 ratio were significantly increased, while the levels of TIMP1 was significantly decreased in scleritis patients' samples compared with healthy controls ($P<0.05$). The increase in MMP9/TIMP1 ratio was due to the decrease in TIMP1, as MMP9 level was not significantly different. Although the levels of MIF (known for its immune activating and dampening roles) did not change in these patients, a distinct positive association of MIF with IL-1β, IL-10, IL-13, IL-17A, IFNγ, and TGFβ-1 was observed in scleritis patients, but not in controls. Conversely, strong correlations of MIF with IL-2, MMP-9, MPO, and TIMP1 was observed in healthy controls but not in scleritis patients. **Conclusion:** Our findings suggest dysregulated ocular surface inflammatory milieu in scleritis. Unique associations between MIF and inflammatory factors can be explored to further the understanding of disease pathogenesis in scleritis.

IN106: Proteomic Analysis Of Plasma Small Extracellular Vesicles (SEVs) In Patients With Diabetic Retinopathy (DR) In The Indian Population

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Purpose: Diabetic retinopathy (DR), a common microvascular complication of diabetes, affects nearly one-third of individuals and poses a major risk of vision loss. This study analyzed the proteomic profile of plasma-derived small extracellular vesicles (SEVs) from proliferative DR (PDR) patients to identify potential biomarkers and support a multi-analyte panel for DR prediction in the Indian population. **Method**: Plasma SEVs were isolated from patients with Type II diabetes mellitus without retinopathy (DM), as well as from patients with non-proliferative diabetic retinopathy (NPDR) and PDR (N=4 in each group) using ultracentrifugation. The isolated SEVs were characterized using immunoblotting, Nanoparticle Tracking Analysis (NTA), and Transmission Electron Microscopy. The plasma SEV protein samples were further processed for mass spectrometry. The raw data were analyzed using Proteome Discoverer software (version 1.4) and MaxQuant (version 2.6.3.0). **Results**: NTA revealed no significant differences in the mean diameter and concentration of plasma small extracellular vesicles (SEVs) among the study groups. SEV identity was validated using established exosomal markers CD63 and TSG101. Principal component analysis (PCA) of MaxQuant-processed data revealed a clear separation between groups, with tight clustering of samples within each group, indicating high intra-group consistency. Proteomic profiling uncovered significant dysregulation of proteins across DM, NPDR, and PDR groups, as visualized in the heatmap. These proteomic alterations in plasma SEVs reflect key gene ontology components relevant to DR pathogenesis, including wound healing, Complement activation, blood coagulation, and plasminogen activation. **Conclusion**: This study has identified several dysregulated plasma SEV proteins in patients with DR compared to DM patients without retinopathy.

IN107: Alterations In Tear Film Parametrs And Proteomics During Menstrual Cycle

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Purpose: The current study assessed the cyclical changes in tear film parameters during menstrual and follicular phases of healthy women. **Methods:** Forty-six eyes of 23 healthy women with regular menstruation had their tear film parameters (Schirmer test, Lipid layer thickness, Tear osmolarity, Tear meniscus height, Non-invasive tear break-up time) assessed along with tear proteomic analysis during D1 (menstruation) and D14 (follicular) of the menstrual cycle for three months. **Results:** During the menstrual phase, NIBUT (P=0.0003) values showed a marked reduction compared to the follicular phase. Schirmer (P=0.22), LLT (P=0.99) and TMH (0.58) values also varied insignificantly during menstrual and follicular phases. The TMH (P=0.07) and LLT (P=0.14) values difference between menstrual and follicular phases at three months were not statistically significant but Schirmer value (P=0.02) was statistically significant. Tear proteomics showed 31 significant proteins were found in the follicular versus menstrual phase. Of these significant proteins, 12 proteins were upregulated and 19 proteins were downregulated, mainly involved with other biological and metabolic processes of protein synthesis. **Conclusions:** Tear film stability is reduced during the menstrual phase compared to the follicular phase with alterations of protein synthesis processes. The impact of sex hormones in healthy women should be considered while collecting tears or testing dry eye parameters.

IN108: Causal Correlations Of Biocides Plasma Levels With Emerging Incidences Of Glaucoma And Myopia

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Purpose: To study circulating biocides levels in patients with neurodegenerative ocular disorders, and their potential association with disease pathology. **Methods:** Glaucoma (n=10) and myopia (n=10) patients were recruited from Dr. Rajendra Prasad Centre for Ophthalmic Sciences, AIIMS, New Delhi. Demographic and clinical data, including intraocular pressure (IOP) for glaucoma and refractive error for myopia, were recorded. Plasma concentrations of common biocides were measured using liquid chromatography-tandem mass spectrometry (LC-MS/MS). In-silico docking studies assessed binding affinity of biocides to cholinergic and adrenergic receptors using Scigress modeling software. **Results:** Mean age of glaucoma (60% males) and myopia (60% males) patients was 63.4 ± 5.6 years and 10.6 ± 3.3 years, respectively. In myopic patients, metribuzin concentration was 0.167 3.5 ng/mL. Dimethoate was mostly undetectable, except in a few cases showing low levels (0.163–0.718 ng/mL) and one high level (~4.7 ng/mL). Binding energies for affinity to muscarinic3 receptors were -81.47 kcal/mol and -63.1kcal/mol respectively. In glaucoma patients, imidacloprid was detected in 90% of samples (0-1.405 ng/mL) and its binding energy for affinity to muscarinic 3 receptors was -107.9 kcal/mol.Moderate correlation was observed between IOP and imidacloprid levels in glaucomatous patients ($r_{spearman}$=0.5183). In myopia patients, weak correlation was observed between refractive index and plasma levels of metribuzin ($r_{spearman}$=-0.2857) and dimethoate ($r_{spearman}$=-0.1881). **Conclusion:** Elevated biocide levels observed in glaucoma and myopia patients, suggest a potential link between biocide exposure and neurodegenerative ocular disorders. Future studies are in progress to elucidate mechanism of biocides in disease progression.

IN109: Comparison Of Folate Transporters, One-Carbon Metabolism Among Decidual Layers Of Pre-Term Placenta: Implications For Risk Of Retinopathy In Infants

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Purpose: Folate (Vitamin B9) is a nutrient important for pregnancy and eye health. The role of folate deficiency is implicated in retinal diseases but the exact mechanism of how it contributes remains unexplored. This study is designed to explore the effect of folate transporters in decidual layer of placenta in-utero as to how transfer of folate to the developing fetus could affect the ROP progression. **Methods:** Placenta samples were collected from controls(n=10) and preterm deliveries; n=12 (seven without ROP and five with ROP). Preterm infants (≤34 weeks, ≤1700g) were classified based on retinal evaluation. Gene expression of folate transporters (PCFT, RFC), metabolic enzymes (MS, MTHFR), angiogenic factor (VEGF), and hypoxia marker (HIF-1α) in decidual layers was analyzed using qRT-PCR and GraphPad Prism. **Results:** The study results demonstrates that the expression of folate transporter namely, proton coupled folate transporter was significantly increased in preterm with ROP ($p < 0.01$) in the decidua basalis and parietalis region with respect to control however, reduced folate carrier showed consistent upregulation across all decidual regions ($p<0.01$). We also observed increase in the expression of methylene tetrahydrofolate reductase and methionine synthase ($p<0.01$) with ROP development in decidua basalis. Hypoxia-inducible factor and VEGF expression was found to be increased in the decidua basalis region of placenta with ROP. **Conclusion:** The study demonstrates deficient folate status as evident from increased expression of folate transporters which could be associated with hypoxic stress in-utero. This might result in fetal growth retardation and confer increased risk of retinopathy.

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IN110: Plasma Inflammatory Markers Association With Macrophage Activation And Gut Dysbiosis In Idiopathic Uveitis: A Pilot Study

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Purpose: To assess plasma inflammatory markers associated with macrophage activation and gut dysbiosis in Idiopathic Uveitis (IU) patients. **Methods:** A cohort of 9 IU patients and age-matched healthy controls not diagnosed with gastrointestinal or autoimmune conditions was recruited. Detailed ocular examination was carried out for IU patients. Plasma samples were analyzed for anti-inflammatory (IL-10), pro inflammatory (IL-6, TNF-α, IL-1β), and macrophage polarization (CXCL-10 for M1 and CCL-2 for M2) markers using ELISA. The plasma was also subjected for circulating short-chain fatty acids levels using LC-MS/MS. The severity of IU was correlated with the pre- and pro inflammatory markers. **Results:** IU and control cohorts had mean age of 36.5±8.6 and 30.5.6±5.7 respectively, and were predominantly male (66.6% in IU; 55.8% in control). Median values for circulating markers were 0.014 (IL-6), 0.010 (TNF-α), 0.705 (IL-1β), 1.076 (CXCL-10), 0.009 (IL-10), and 25.301 (CCL-2) pg/mg in IU group and 0.005 (IL-6), 0.005 (TNF-α), 1.167 (IL-1β), 0.245 (CXCL-10), 0.015 (IL-10), and 27.328 (CCL-2) pg/mg in control group. Significant elevation of IL-6 was observed in IU as compared to control group (p=0.0064). In IU group, moderate correlations were observed between presence of inflammatory cells in ocular anterior chamber and IL-6 (0.46), IL-1β (0.45), CXCL10 (0.45) and TNF-α (0.40). **Conclusions:** This pilot study has demonstrated the involvement of IL-6 and CXCL-10 with occurrence of idiopathic uveitis and their moderate correlation with the disease state. The disturbed gut microflora may be a potential triggering factor for the onset of IU.

IN111: Plasma And Vitreous Extracellular Vesicle-Derived Retinol Binding Protein 3 As A Molecular Signature Of Proliferative Diabetic Retinopathy

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Purpose: Diabetic retinopathy (DR), a leading cause of irreversible blindness, advances silently in its early stages. With diabetes prevalence expected to exceed 643 million by 2030, early prediction of vision-threatening DR (VTDR) is critical. Most reported circulatory biomarkers lack evidence of direct involvement in DR pathogenesis, highlighting the necessity for DR-specific factors reflecting retinal angiogenic pathophysiology. This study investigates extracellular vesicle (EV)-associated proteins, for their potential as reliable biomarkers. **Methods:** Small extracellular vesicles (SEVs) were isolated from vitreous humor (VH) of patients with proliferative DR (PDR) and from macular hole (MH) controls. Shotgun mass spectrometry was employed to characterize altered protein cargo. Immunoblotting and ELISA validated RBP3 levels in VH-SEVs. Plasma SEVs were similarly analyzed from diabetic patients with non-proliferative DR (NPDR), PDR, and diabetes without retinopathy.

Results: Shotgun mass spectrometry identified Retinol Binding Protein 3 (RBP3), a photoreceptor derived retinoid transporter with protective roles in DR, within VH-SEVs. RBP3 levels were significantly reduced in VH-SEVs from PDR patients compared to MH controls. Immunoblotting and ELISA confirmed this finding. In plasma, SEV-associated RBP3 levels demonstrated a decreasing trend from NPDR to PDR stages, with the lowest levels observed in PDR patients. Diabetic patients with PDR had significantly lower plasma SEV-RBP3 levels than those without retinopathy. **Conclusions:** RBP3, a DR-relevant retinal protein, was identified in circulatory SEVs with significant reductions with DR progression, especially in PDR. This highlights RBP3's clinical potential as a non-invasive biomarker for the early prediction and monitoring of VTDR.

GE112: Leber Congenital Amaurosis: Genetic Spectrum And Genotype-Phenotype Correlations For Precise Molecular Diagnosis

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Purpose: Leber congenital amaurosis (LCA) is a severe inherited retinal dystrophy and a major cause of childhood blindness. With the advent of gene therapy as a promising treatment, accurate molecular diagnosis is crucial for effective management and intervention. Therefore, this study aims to identify causative mutations in LCA patients and develop an ethnic specific gene panel for diagnosis. **Methods:** Whole-exome sequencing (WES) was performed in 65 unrelated LCA patients. Detailed ophthalmic evaluations, pedigree charts, and family histories were obtained to enable genotype–phenotype correlation. Peripheral blood DNA samples were used for WES, and pathogenic variants were prioritized and validated through Sanger sequencing. Segregation analysis was performed in available family members to confirm inheritance patterns. **Results:** WES of 65 LCA patients revealed mutations in 14 out of 29 LCA candidate genes in 35 patients. The most frequently mutated genes were CRB1 (n=7), GUCY2D (n=4), LCA5 (n=4), NMNAT1 (n=3), and AIPL1 (n=3). Other mutated genes included RDH12, IFT140, CRX, RPE65, and KCNJ13 (each n=2), as well as ALMS1, TULP1, PRPH2, and RPGRIP1. Fourteen patients carried novel variants in known LCA genes. Additionally, 13 patients (20%) had mutations in genes associated with other IRDs with syndromic conditions. The structural impact of CRB1 variants was analysed through homology modelling using UCSF Chimera. **Conclusion:** This study provides insight into the genetic profile and mutation spectrum of candidate genes of LCA. Deep intronic and regulatory regions may be involved in negative cases, which could be identified by whole-genome sequencing and GWAS. Molecular findings have also helped in accurate diagnosis, better patient management, and genetic counselling.

GE113: Exploring Mitochondrial Genetic Variants In Primary Open-Angle Glaucoma

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Purpose: Primary open-angle glaucoma (POAG) is a major global cause of irreversible blindness, with its incidence steadily increasing in the Indian population. It is characterized by progressive degeneration of retinal ganglion cells (RGCs) and optic nerve damage. While POAG has a multifactorial etiology, recent studies suggest a pivotal role for mitochondrial DNA (mtDNA) mutations, particularly through mechanisms involving oxidative stress and mitochondrial dysfunction. This study aimed to investigate the spectrum of mtDNA variants associated with POAG in a South Indian cohort. **Methods:** We performed a comprehensive analysis of the mitochondrial genome in patients clinically diagnosed with POAG, using peripheral blood-derived DNA. Whole mitochondrial genome sequencing was carried out on unrelated individuals to identify mtDNA variants. Pathogenicity was assessed based on bioinformatic predictions, conservation analysis, and reported clinical significance. Prioritized variants were subsequently validated using Sanger sequencing. Mitochondrial haplogroups were also assigned to evaluate lineage-specific susceptibility. **Results:** We observed a significant enrichment of potentially pathogenic mtDNA variants in POAG patients, notably within genes encoding subunits of mitochondrial Complex I. These variants are predicted to impair oxidative phosphorylation and elevate oxidative stress levels, contributing to RGC degeneration. Additionally, haplogroup analysis revealed associations between specific mitochondrial lineages and increased risk of POAG, suggesting an ancestral genetic predisposition. **Conclusion:** Our findings highlight mitochondrial dysfunction, driven by Complex I-related mtDNA mutations, as a critical factor in the pathogenesis of POAG. The observed haplogroup associations reinforce the role of maternal lineage in disease susceptibility. This study underscores the need for population-specific mitochondrial studies and suggests the potential application of mtDNA variants as biomarkers for risk prediction and prognostic assessment in glaucoma management.

GE114: Multi-SNP Profiling In Age-Related Macular Degeneration: Bridging Genetic Risk, Clinical Phenotypes And Oxidative Stress

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Purpose: AMD causes irreversible vision loss in the elderly, with genetics contributing 46–71% to its susceptibility. While ARMS2 and HTRA1 polymorphisms affect mitochondrial function, CFH variants are the key regulators of the alternative complement pathway in AMD. This study evaluates how the cumulative risk allele burden influences both AMD clinical severity and oxidative stress, highlighting its role in risk assessment and early intervention. **Methods:** AMD (n=113) and control (n=99) participants were genotyped for ARMS2 rs10490924, HTRA1 rs11200638, and CFH rs1061170 SNPs. AMD patients were grouped by risk allele load (high-risk: 4–6 alleles; low-risk: 0–2 alleles). Genotypic data were correlated with clinical phenotypes. Serum SOD activity was assessed in high-risk (n=21), low-risk (n=18) AMD patients, and controls (n=22) was performed. **Results:** High-risk allele load was more frequent in AMD patients (47.8%) than controls (25.3%), while low-risk alleles were less frequent (26.5% vs. 49.5%). High-risk individuals developed AMD 2.3 years earlier (mean age 66.7 vs. 69 years, $p<0.001$ and exhibited more severe phenotypes—large drusen (48% vs. 29.3%, $p<0.01$), pigmentary changes (44.4% vs. 27.8%, $p<0.01$), and CNVM (43.3% vs. 26.9%, $p = 0.02$). Serum SOD activity was significantly lower in high-risk patients compared to low-risk patients and controls($p<0.01$) (AUC~0.7). **Conclusion:** Elevated cumulative risk allele load in ARMS2, HTRA1, and CFH is associated with earlier AMD onset, severe phenotypes and compromised oxidative defense of SOD, linking genetic risk to clinical manifestations. These findings support the integration of genetic screening and oxidative stress markers into AMD risk assessment and management.

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GE115: Integrated Genetic, Molecular, And Clinical Characterization Of Pachychoroid Spectrum Disorders

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Purpose: Pachychoroid spectrum disorders (PSD), including CSC, PNV, and PCV, are characterized by abnormally thickened choroid and overlapping clinical features with neovascular Age-related Macular Degeneration (nAMD), complicating accurate diagnosis and management. Lack of validated molecular biomarkers and limitations in current imaging, lead to misclassification of pachychoroid phenotypes as nAMD, contributing to suboptimal therapeutic decisions. This study integrates genetic, molecular and clinical imaging data to differentiate between PSD phenotypes from nAMD and refine clinical management. **Methods:** Patient cohorts comprised PSD (n=16), AMD (n=54), and controls (n=20). Multimodal imaging done via OCTA. Genetic analysis focused on ARMS2 rs10490924, HTRA1 rs11200638, and CFH rs1061170. Serum cytokines, including angiogenic and inflammatory mediators, were quantified using multiplex bead-based flow cytometry. **Results:** PSD patients exhibited higher frequencies of ARMS2 and HTRA1 risk alleles compared to controls ($p=0.02$), supporting shared genetic susceptibility with AMD. However, PSD patients had significantly fewer large drusen than AMD patients ($p<0.05$), suggesting pathological distinctions. Cytokine profiling revealed significant differences in Ang-2, EGF, EPO, and VEGF levels between PSD (n=12) and controls (n=20). Subtype analysis (PCV vs CSC, n=10 each) identified divergent levels of HGF, EPO, SCF, and G-CSF, underscoring unique molecular patterns between PSD subtypes. **Conclusion:** PSDs share genetic risk factors with AMD, still exhibit distinctive clinical and molecular characteristics like reduced drusen burden and cytokine profile. Differential expression of growth factors, angiogenic and inflammatory mediators, not only differentiate PSDs from nAMD but also PSD phenotypes like PCV and CSC. These findings support multimodal framework for improved diagnosis and targeted therapies.

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GE116: Comparative Analysis Of Transcriptome In Behcets' And Vogt-Koyanagi-Harada Identifies Disease Associated Genes And Pathways: An Explorative Study

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Purpose: VKH and BD are types of non-infectious uveitis that are characterized as chronic inflammatory diseases affecting various parts of the body. In this study we have explored the common and disease specific gene expressions through transcriptomic profiling of the peripheral lymphocytes from these patients. **Methods:** Blood samples from the uveitis patients (VKH and BD) and healthy controls was collected with informed consent after detailed ophthalmic evaluation. Total RNA was extracted (Trizol Chloroform method) from the peripheral blood lymphocytes followed by RNA sequencing in 3 patients per group and compared with the controls. Differential gene expression analysis in R package Deseq2 was performed and genes that showed 10-fold change in the expression were further validated by qPCR in an independent cohort of N=12 each in the BD, VKH and controls. Pathway analysis was performed by Gene ontology and KEGG analysis. **Results:** A total of 209 and 121 differentially expressing genes were identified in BD and VKH respectively when compared to controls. Genes *HLADRB5*, *HLADRB1 HLA-B and TRBV6-1* showed similar expression pattern in both diseases (both in the exploratory and replication cohort. **Conclusions:** This study highlights a similar expression pattern of the genes involved in T cell receptor signalling, Antigen presenting and Nitrogen metabolism pathway in both the diseases, correlating with the disease pathology.

GE117: A Case-Control Study To Elucidate The Association Of Single Nucleotide Polymorphisms In Inflammation And Immune Pathway Genes In Vogt-Koyanagi-Harada Disease

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Purpose: Vogt-Koyanagi-Harada (VKH) disease is an autoimmune, non-infectious panuveitis affecting eye (granulomatous anterior uveitis), meninges (symptoms include: stiffness, headache, meningitis), inner ear (vertigo, tinnitus), skin and hair (alopecia, vitiligo and poliosis). The study aims to analyze the genetic association of candidate genes involved in immune and inflammatory mechanisms which are altered in VKH. **Methods:** Fifty patients diagnosed with VKH syndrome after comprehensive clinical evaluation that includes: Slit Lamp Bio microscope, Fundus Fluorescein Angiography (FFA) and Swept source-Optical Coherence Tomography (OCT) were enrolled in the study. The SNPs in candidate genes MMP9 (rs2250889), IL17F (rs763780), FGFR1OP (rs2301436) and JAK-1 (rs310241) were genotyped by PCR based direct sequencing and analyzed. Genotype and allele frequencies were compared between the cases and unrelated healthy controls by Chi-square test for independence to determine the association between two qualitative variables. All statistical analysis was performed using MedCalc software. **Results & Conclusions:** The wild type genotype of SNP (i) rs2250889 was frequently represented in cases when compared to controls and showed statistical significance ($P<0.05$, $OR>1$) in dominant, co-dominant and over dominant models (ii) rs2301436 showed significant association with the cases in over dominant model with a (P value = 0.04, $OR>1$). Replication of the study findings in a large sample size, possible effect on the structure / function of the protein, comparison with other types of non-infectious uveitis is further warranted to elucidate the specific association of these SNPs with VKH.

MB118: Development Of Ultrasensitive LC-MS/MS Method For The Analysis Of Sphingolipids And Sex Steroid Hormones In Tear Fluid Samples

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Purpose: Studies have reported the alteration in sphingolipids and sex steroid hormones can contribute to the progression of various ocular surface disorders. Therefore, this study aimed to develop ultra-sensitive LC-MS/MS method for detection of these endogenous markers in tear fluid. **Methods:** A rapid and highly sensitive Liquid chromatography-tandem mass spectroscopy (LC-MS/MS) method was developed and validated for the 10 sphingolipids and 3 sex-steroid hormones in the tear fluid as per US-FDA guidelines for bioanalytical method validation. The mass spectrometer was optimised for compound and source dependent parameters. The extraction of these endogenous substance from the schrimers strips were optimised to get the maximum recovery. The developed method extraction and sensitivity was assessed in the tear fluid collected from heathy volunteers. **Results:** The ultrasensitive method could detect (C17 Ceramide (d18:1/17:0), C16 Ceramide (d18:1/16:0), C18 Ceramide (d18:1/18:0), C24 Ceramide (d18:1/24:0), C1P (d18:1/2:0), C2 C1P (D18:1/2:0), S1P (d20:1), S1P (d17:1), C1P (d18:1/8:0), Sphingosine (d17:0), androgen progesterone and estrogen in the extracted schrimers strip. The method exhibited high sensitivity, with a limit of detection (LOD) of (range: 0.77-64.97ng) and a limit of quantification (LOQ) of (range 15.62-500ng). Both the methods showed good linearity (r2>0.992), intra-day and inter-day accuracy (80-120%), and precision (<20% CV). Out of 10 sphingolipids, 9 were detected in the tear samples and out of 3 sex steroid hormones, only and rostenedione was detected in the tear samples.
Conclusions: Our newly developed ultrasensitive LC-MS/MS method can be used as a tool for detecting sphingolipids and sex steroid hormones in human tears.

MB119: Molecular Mechanisms Of EGFR Inhibitor-Induced Ocular Toxicity: Role Of Inflammation

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Purpose: Epidermal Growth Factor Receptor (EGFR) inhibitors administered systemically, including Erlotinib and Afatinib, are potential anticancer agents but are associated with ocular toxicity. EGFR is known to regulate the immune response in the ocular tissues. We hypothesise that EGFR inhibition could dysregulate the inflammatory cytokines and cause ocular toxicity. This study investigates the effects of EGFR inhibitors on inflammation in corneal cells. **Methodology:** Human Corneal Epithelial (HCE) cells were treated with EGFR inhibitors (Erlotinib and Afatinib) for 24 to 72 h. Erlotinib was administered topically in the right eye of Wistar rats, once a day for one and four weeks. Animals were euthanized, and eyes were enucleated, and the cornea was dissected. Total RNA was isolated from HCE cells and rat corneal tissue using TRIZOL reagent, while protein was extracted using RIPA lysis buffer. Polymerase Chain Reaction (PCR) and Western blotting were performed. **Results:** PCR analysis demonstrated a significant upregulation of pro-inflammatory cytokines TNF-α (10 to 50-fold), IL-6 (2 to 8-fold) and the profibrotic marker TGF-β2 (2 to 4-fold) in HCE cells, at 24, 48, and 72 h post-EGFR inhibition. Corneal tissue showed a 2 to 6-fold increase in TNF-α, IL-6 and TGF-β2 at 1 and 4 weeks. Western blot analysis confirmed elevated protein levels of TNF-α and IL-6. **Conclusion:** The observed upregulation of TNF- and IL-6 at both gene and protein levels in vitro and in vivo studies suggests that inflammation is the potential mechanism underlying EGFR inhibitor induced ocular toxicity. These findings emphasise the need for further research to develop strategies for mitigating these side effects.

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MB120: Expression Of Slc Family Transporters In Various Ocular Diseases

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Purpose: Transporters play a functional role in maintaining ocular homeostasis by regulating the transport of endogenous molecules across cellular barriers. Dysregulation of transporters disrupts the intracellular microenvironment, triggers immune cell activation and impairs cytokine production leading to pathogenesis of inflammation. This study aims to investigate the expression of transporters such as solute carrier transporters (SLC) in ocular inflammatory diseases. **Methods:** Anterior and posterior uveitis was developed using intravitreal administration of lipopolysaccharide in rabbits. After 48 h, animals were euthanized, followed by dissection of anterior and posterior eye segment. Anterior and posterior eye segment were homogenized, and RNA was isolated using TRIzol reagent. Polymerase chain reaction was performed to assess the gene expression of various SLC transporters in diseased and control groups. Beta-actin was used as housekeeping gene. **Results:** The gene expression of target gene was normalized with beta-actin expression. The relative expression of SLC22A1 (organic cation transporter 1), SLC22A2 (organic cation transporter 2), SLC22A4 (organic cation/carnitine transporter 1), and SLC22A5 organic cation/carnitine transporter 2) decreased 3-fold in lipopolysaccharide group compared to control group. Whereas SLC22A8 (organic anion transporter 3) decreased by 11-fold and SLC15A2 (Peptide Transporter 2) decreased by 50-fold in lipolysaccharide treated group relative to control group. **Conclusions:** Gene expression analysis showed the downregulation of transporter in anterior and posterior uveitis. These studies indicate that the altered expression of membrane transporters could play a critical role in pathogenesis of ocular diseases. Further mechanistic studies are required to understand the role of transporters in ocular inflammation.

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MB121: Localisation Of Multiple Isoforms Of Human Tear Lysozyme In The Extracellular Vesicle

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Purpose: Lysozyme is a key immune enzyme found in bodily fluids like tears, saliva, and milk, where it provides protection against infections. In ocular health, tear lysozyme levels are an important biomarker, with reductions associated with conditions such as conjunctivitis, dry eye syndrome, and corneal ulcers. This study shows the presence of lysozyme isoforms in human tears and their localization within extracellular vesicles (EVs). **Methodology:** Tear samples from healthy individuals and patients with healed keratitis were analysed. Samples underwent initial centrifugation at 10,000 × g for 30 minutes at 4 °C, followed by ultracentrifugation at 120,000 × g for 70 minutes to isolate extracellular vesicles (EVs). Western blotting was used to detect lysozyme isoforms and assess protein profiles. EV identity was confirmed using the markers CD63 and CD9. Additionally, mass spectrometry was employed for protein identification and isoform characterisation. Lysozyme activity was quantified using a lysozyme assay kit. **Results:** Tear samples from keratitis patients showed increased high molecular weight proteins. Lysozyme isoforms (~14.4 kDa) were present in both groups, with EVs mirroring tear film profiles. Mass spectrometry identified 923 proteins in control EVs and 1081 in infected EVs, including two Lysozyme-C isoforms. Lysozyme activity was higher in control EVs (192 U/ml) than in infected EVs (82 U/ml). **Conclusion:** This study reveals multiple lysozyme isoforms in human tears and their localization within EVs, highlighting a potential role for EVs in lysozyme transport and immune defense in the eye.

MB122: Deciphering The Role Of Alu Complementary DNA In Ocular Angiogenesis

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Purpose: Major causes of ocular blindness in India are neovascular age-related macular degeneration(nAMD), proliferative diabetic retinopathy, retinopathy of prematurity, and ischemic retinal vein occlusion. The common culprit amongst all diseases is angiogenesis. Anti-VEGF therapy is used for management, but sometimes nonresponsive cases may lead to tractional retinal detachment and further blindness. Alu complementary DNA is known to trigger inflammation and degeneration; however, its mechanism of causing angiogenesis remains unclear. Here, we aim to demonstrate the mechanism by which Alu cDNA causes RPE degeneration and mediates angiogenesis via the STING Pathway. **Methods:** To understand the role of alu cDNA, we employed the ARPE19 and HUVEC cell lines and transfected them with alu cDNA exogenously. We then evaluated cytotoxicity using cytotoxic assays, examined the expression of angiogenic markers, and investigated altered pathways, including STING, VEGF, and Retroelements. Furthermore, we analyzed tube formation to demonstrate angiogenesis in a gel matrix and the scratch assay to assess cell migration. **Results:** Transfection of ARPE-19 cells with Alu cDNA resulted in increased cytotoxicity and upregulation of inflammatory and immune genes, including cGAS and STING. Alu cDNA-treated ARPE-19 and HUVECs cells enhanced endothelial cell migration, tube formation, and VEGF expression, indicating a strong proangiogenic effect. Localization can be seen by immunofluorescence. **Conclusions:** These findings identify Alu cDNA as a dual-function driver of degeneration and neovascularization, suggesting that targeting the Alu cDNA–STING–VEGF axis may offer a novel therapeutic strategy for nAMD and related retinal diseases.

MB123: Spatial Transcriptomic Analysis Of Adult Human Retinal Pigment Epithelium

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Purpose: The presence of stem cells (SCs) in the peripheral human retinal pigment epithelium (RPE) has been identified upon culturing. This study aims to identify the location of SCs in native human RPE using spatial transcriptomics. **Methods:** Paraffin sections of human retinal tissue from central to peripheral region of donor eyes were used for spatial transcriptomics with the 10X Genomics Visium v2 CytAssist and Illumina sequencing. Analysis with Spaceranger was carried out to demulitplex the data, and gene expression was visualised using cloupe browser. Seurat was used for cell annotation, clustering, differential gene expression, and pathway analysis to uncover transcriptomic profiles. Genes associated with stemness, which were common in three previously published single-cell RNA sequencing (scRNA-seq) data, were identified by Meta-data analysis. The expression of these genes in different regions (central, equatorial and peripheral) of RPE was confirmed by spatial transcriptomic analysis and validated by quantitative real-time PCR (qRT PCR). **Results:** Six SC associated genes (MET, BMP7, RDH10, WWC1, ARHGAP18 and NEAT1) were identified in all the three scRNA-seq datasets. Analysis of the spatial expression profile identified MET, BMP7, RDH10, and WWC1 to be upregulated in the peripheral region. qRT-PCR analysis confirmed the higher expression of all the four genes in the peripheral RPE compared to central and equatorial RPE. **Conclusion:** This study identified four stemness-related genes involved in regulating the RPESCs to be upregulated in peripheral RPE. Further studies are essential to identify the other genes regulating RPESCs and the associated signalling pathways.

MB124: DPP8 Downregulation And Pyroptosis In Fuchs-Endothelial Corneal Dystrophy

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Purpose: Fuchs Endothelial Corneal Dystrophy (FECD) is a progressive ocular disorder characterized by corneal endothelial cell degeneration, thickening of the Descemet membrane, and formation of guttae. While genome-wide association studies (GWAS) have identified several loci linked to FECD, the functional relevance of many variants remains unclear. This study aimed to evaluate the association between the intronic SNP rs352476 and FECD and investigate the role of its associated gene, DPP8, in disease pathogenesis. **Methods:** Genomic DNA from 140 FECD patients and 420 age- and sex-matched controls was analyzed for rs352476 using Sanger sequencing. A Chi-square test was used to assess genetic association. A dual luciferase reporter assay was performed for both alleles to evaluate regulatory effects. qRT-PCR, western blotting, and immunofluorescence were used to assess DPP8 expression in human corneal tissues. Activation of the pyroptosis marker Caspase-1 was analyzed via western blotting. **Results:** A significant association was observed between rs352476 and FECD ($P = 0.03$). The risk allele 'A' showed reduced luciferase activity compared to the protective 'G' allele. DPP8 was significantly downregulated in FECD samples at both mRNA and protein levels. Correspondingly, active Caspase-1 expression indicated activation of pyroptosis in the FECD corneal endothelium. **Conclusion:** Our findings suggest that the rs352476 risk allele may downregulate DPP8 expression, potentially leading to inflammasome activation and pyroptosis in corneal endothelial cells, contributing to FECD pathogenesis. This highlights DPP8 as a novel potential molecular target for therapeutic intervention.

Keywords: GWAS, SNP, rs352476, DPP8, pyroptosis, Caspase-1, inflammasome.

MB125: Beyond VEGF Inhibition: Revealing Angiopoietins And Inflammatory Pathways Driving DME Through Multi-Omics

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Background: Despite widespread use of anti-VEGF therapy, a substantial proportion of diabetic macular edema (DME) patients exhibit limited anatomical and visual improvement. This study addresses an interdisciplinary challenge: deciphering the complex, multifactorial nature of DME pathophysiology beyond VEGF inhibition by integrating cytokine profiling, serum proteomics, and network-based correlation analysis to identify predictive biomarkers of therapeutic response. **Methods:** Serum samples from 44 DME patients, each treated with ≥3 anti-VEGF injections over ≥6 months, and were classified as responders or non-responders based on BCVA and CRT. Multiplex bead-based assays measured angiogenic, inflammatory, and adhesion molecules. LC-MS/MS-based proteomics identified differentially expressed serum proteins. Statistical analysis was performed using GraphPad Prism, MetaboAnalyst and Reactome analysis. **Results:** Responders demonstrated markedly elevated Ang-1 ratios, showing robust correlations to reduced CRT and improved BCVA (AUC >0.9). Proteomic signatures included vascular-protective proteins like PEDF, clusterin, and complement factor B. Biologically coherent inter-ratio associations were observed in responders (ρ=0.5–0.85), reflecting functionally coordinated interactions between Ang-1 pathways and vascular-protective mediators. In contrast, non-responders exhibited pro-inflammatory mediators (complement C3, angiotensinogen) and amyloidogenic proteins (transthyretin), alongside dysregulated Ang-1 ratio hyper-correlation (ρ >0.95), indicating collapsed regulatory networks and persistent inflammation. **Conclusion:** This multi-omics approach not only identifies Angiopoietin-1 ratios as key biomarkers for predicting anti-VEGF treatment response but also reveals the functional integrity of the vascular network in DME. It differentiates responders from non-responders with high precision, enabling early identification of patients who may benefit from alternative therapies beyond anti-VEGF. These findings highlight the importance of biomarker-guided management of DME patients.

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MB126: Identification Of Dysregulated Gene Clusters And Pathways Driving Ocular Surface Squamous Neoplasia Progression

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Purpose: Ocular Surface Squamous Neoplasia (OSSN) is a sight-threatening malignancy with a clinical spectrum ranging from mild dysplasia to invasive carcinoma. The aim of this study was to characterize molecular signatures associated with OSSN progression using transcriptomic profiling. **Methods:** RNA-sequencing was performed on clinically and histopathologically verified OSSN tissues, including non-invasive and invasive subtypes, alongside healthy conjunctival controls. Differential gene expression and pathway enrichment analyses were carried out to identify key molecular drivers of disease progression. **Results:** The transcriptomic landscape of OSSN revealed significant dysregulation of genes such as *TP53, CXCL9, CXCL11, IL6, TNFα, PRDX1, PRDX4, MMP7, MMP9*, and *KRT4*. These genes were associated with biological processes including inflammation, apoptosis, cell cycle dysregulation, oxidative stress, and extracellular matrix degradation. Notably, distinct gene expression signatures differentiated non-invasive from invasive OSSN, suggesting molecular markers of disease severity. **Conclusions:** Our findings provide novel insights into the molecular mechanisms of OSSN pathogenesis. The identified dysregulated genes and pathways offer potential biomarkers for early diagnosis and stratified therapeutic interventions in OSSN management.

MB127: Differential Expression Of Transcription Factors In Moderate And Severe Fuchs Corneal Endothelial Dystrophy

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Purpose: Fuch's corneal endothelial dystrophy (FECD) results in the death of the non proliferative endothelial cells of the posterior corneal surface leading to corneal swelling, clouding, and potential blindness. Few studies have indicated possible role of transcription factors involved in endothelial to mesenchymal transition (EndMT) in the disease progression. This study aimed to evaluate the expression of targeted transcription factors relevant to EndMT associated with tissue repair, in the corneal endothelium of FECD patients in order to understand their role in disease pathogenesis. **Method:** A prospective, pilot, case control study for studying the gene expression in patients with Fuch's corneal endothelial dystrophy. Transcription factors *Zeb-1, TCF-4, Smad3, Smad4*, Zinc finger proteins *SNAI1, SNAI2,* lymphoid enhancer binding factor 1 (*Lef-1*), N-Cadherin (*CDH2*), Claudin10 (*CLDN10*), Nuclear factor (erythroid-derived 2)-like 2 (*Nrf2/NFE2L2*) that are involved in EndMT were selected for the study. Fourteen FECD endothelium were compared with 15 donor corneal rim endothelium for the gene expression analyses using quantitative real time PCR. The cases were classified as moderate and severe based on their clinical presentation. **Results:** Significant differential expressions were seen in the genes studied. Smad3 expression was increased ($p=0.0251$) in moderate cases compared to control but decreased in severe cases. Further, *TCF4* and *Nrf2* showed significant changes with increase in moderate cases but decreased with severity ($p = 0.0262$ and $p = 0.0350$ respectively) indicating their possible role in disease progression. **Conclusion:** Our pilot study on transcription factor gene expressions in FECD patient's tissue samples suggests *Smad3, Nrf2* and *TCF4* play an important role in the disease pathogenesis and progression by modulating EndMT.

MB128: Potential Role Of Long Noncoding RNAs (lncRNAs) For Predicting The Development And Progression Of Diabetic Retinopathy

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Purpose: Diabetic retinopathy (DR) is a leading cause of vision loss, characterised by the retinal dysfunction under chronic hyperglycaemia. The study was designed to investigate differences in the expression profiles of lncRNAs among different categories of DR, diabetes mellitus (DM) and controls to evaluate their potential role as a predictive marker for DR. **Methods:** Patients with different categories of DR (proliferative DR and nonproliferative DR), diabetic individuals without DR (DM) and normal controls (n=20/category) were enrolled for this study. Bulk transcriptome analysis was performed in blood samples (n=3/category). Data analysis was performed using Partek flow version 12.3.1. and significantly dysregulated lncRNAs were further validated using qRT-PCR. Receiver operating characteristic (ROC) analysis was utilized to evaluate the diagnostic value of lncRNAs for DR. **Results:** 1372 lncRNAs were found to be significantly expressed in DR categories and DM individuals as compared to controls. GO analysis showed that the several metabolic processes were possibly influenced by these dysregulated lncRNAs. Interestingly, in our data *MALAT1* and *DANCR* were found to be downregulated in PDR subjects specifically, whereas *ANRIL, MEG3, GAS5 and NEAT1* were found to be upregulated consistently in PDR, NPDR and DM subject. These lncRNAs correlated with *VEGF* and Wnt signal pathways. ROC curves analysis showed good diagnostic potential for *ANRIL, GAS5* among PDR vs DM and *MEG3*, *DANCR* among NPDR vs DM. **Conclusion:** Our study provides a proof of concept that lncRNAs might serve as novel diagnostic and prognostic biomarker for DR.

MB129: Regulatory Role Of MicroRNAs In Wnt Signaling Pathways Associated With Steroid-Induced Ocular Hypertension -An Insight From Ex Vivo Studies

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Purpose: Among the several signaling pathways, Wnt signaling pathway has been implicated in the pathogenesis of glaucoma including steroid-induced glaucoma (SIG). The aim of the present study was to investigate the regulatory role of miRNAs in Wnt signaling pathway associated with steroid-induced Ocular hypertension (SI-OHT) *ex vivo* model. **Methods:** The steroid responsiveness of the human donor eyes was established in an ex vivo model using human anterior segment perfusion culture (HOCAS) based on intraocular pressure change after steroid treatment for 7 days. Total RNA was extracted from the HTM tissues and miRNA expression was analysed using the NanoString nCounter miRNA expression assay. After quality check and normalization, DEMIRs were analysed and compared among 5 groups (Group#1: GC-R vs. vehicle; Group#2: GC-NR vs. vehicle; Group#3: overlapping DEMIRs between Group#1 and #2; Group#4: unique DEMIRs of GC-R; and Group#5: unique DEMIRs of GC-NR) using Python's automatic analysis algorithm. The miRNAs linked to Wnt pathways were then aligned with the DEMIRs identified in Group #1 and #2 using Python packages. The interactions between the DEMIRs and their respective target mRNAs were visualized using IPA's graphing tools. Additionally, the IPA Overlay-MAP (Molecular Activity Predictor) tool was utilized to illustrate the expression levels of these target mRNAs based on our previously generated mRNA-seq data from GC-R and GC-NR TM cells. **Results:** In the Wnt/β-catenin signaling pathway network, several mRNAs, including Cadherin genes (CDH1 and CDH5), Wnt genes (WNT4, WNT6, WNT7B, WNT10B, and WNT11), SFRP genes (SFRP2 and SFRP4), KREMEN, and MMP7, were found to be down-regulated in Group #1 (GC-R vs. Vehicle) based on previous mRNA-seq data from TM cells (represented as green nodes). A subset of DEMIRs was exclusively up-regulated in Group #1 as identified by Nanostring TM tissue data and was predicted to target specific mRNAs within the pathway. **Conclusion:** This study provide insights into the regulatory network of miRNAs in Wnt signalling pathway which will help developing miR-based therapeutics to mitigate the adverse effects of steroids in the eye.

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CB130: HMGB1 As A Driver Of Inflammation In HIV-1 TAT Activated Retinal Muller Glia

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Background: HIV infection leads to chronic inflammation and activates immune system. High mobility group box 1 (HMGB1) plays important role in gene transcription, DNA repair and maintain chromatin stability in quiescent cells. Studies demonstrate elevated HMGB1 protein levels in serum of PLHIV with progressive infection, which upon antiretroviral therapy reduces. It has been associated with inflammation and contributes to immune activation. In the CNS expression of HMGB1 is found in neurons and astrocytes, but rarely in microglia. **Method:** In our study of transcriptomic data from retinal Muller glia upon HIV- TAT exposure, we found HMGB1 as a key target of controlling inflammation. We used Real time PCR, TEER and Western blot to evaluate HMGB1 levels upon TAT exposure and its association with various signalling pathway. **Results:** Our result shows TAT induced oxidative stress that reflected in MTT assay. Physiological changes lead to compromised permeability barrier in cell monolayer and significant elevation of HMGB1. We find intervention at the PI3K/AKT signalling pathway and release of HMGB1 is impacted during inflammation. HMGB1 could be potential therapeutic target and inhibiting its release by using PI3K inhibitor, LY 29004 for inhibiting HIV infection. **Conclusion:** Our study concludes in depth study of PI3K/AKT signaling pathway and inhibitor of HMGB1 could be new intervention in the field of HIV research.

CB131: Demonstrating The Anti-Fibrotic Property Of Relaxin-2 (RLN2) In TGF-ß2 Induced Fibrosis Model Of Glaucoma Using Human Organ Cultured Anterior Segment

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Purpose: Human relaxin (RLN2), a 6-kDa peptide hormone, possesses anti-inflammatory, anti-fibrotic, vaso-dilatory, anti-angiogenic, and cardio-protective actions. The anti-fibrotic activity of RLN2 has been extensively studied in non-ocular fibrotic diseases and not in ocular fibrosis especially glaucoma fibrosis. Therefore, the aim of the present study is to investigate the anti-fibrotic property of Relaxin-2 (RLN2) in TGF-β2 induced Fibrosis model of glaucoma using Human Organ Cultured Anterior Segment (HOCAS). **Methodology:** In order to establish fibrosis in an *ex vivo* model of glaucoma, HOCAS was established with paired or single eye using human donor eyes. After baseline stabilization, one eye was infused with TGF-β2 in DMEM medium for 7d and the other eye received plain medium as a vehicle control. In another experiment, the effect of RLN2 in mitigating the fibrosis induced by TGF-β2 was investigated. At the conclusion of the experiments, the eyes were processed for the analysis of fibrotic markers by western blot and immunohistochemistry analyses. **Results:** TGF-β2 treatment reduced the outflow facility (OF) by 14%. The reduction in OF was substantiated with the increased expression of fibrotic markers. No significant change in outflow facility was observed with RLN2 treatment. However, the presence of RLN2 alleviated the fibrosis induced by TGF-β2 treatment. **Conclusion:** This is the first study demonstrating the anti-fibrotic property of RLN2 in human trabecular meshwork fibrosis induced by TGF-β2 treatment in human donor eyes. Relaxin-2 may be a promising anti-fibrotic agent in alleviating fibrosis associated with glaucoma.

CB132: Overexpression Of FADS1 In Retinoblastoma: Functional Studies And Its Therapeutic Potential

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Purpose: To investigate the role of fatty acid desaturase 1 (*FADS1*) dysregulation in the tumorigenesis of human retinoblastoma (RB) and its therapeutic potential. **Methods:** The expression of FADS1 protein in RB was determined by immunohistochemistry (IHC) analysis of archived patient tissue samples, and immunoblotting in established RB cell lines. Functional studies upon shRNA-mediated FADS1 silencing were performed to elucidate its role in cell viability, cell cycle progression and cell death regulation. **Results:** Immunoblotting and IHC analysis showed an elevated expression of FADS1 protein in retinoblastoma cell lines and patient tumor specimens compared to uninvolved healthy retina. Further, shRNA-mediated knockdown of FADS1 led to decreased cell viability relative to scrambled/empty vector control cells. The mechanism of cell death is currently being investigated. **Conclusions:** The overexpression of FADS1 in RB suggests its potential involvement in tumor progression and highlights it as a candidate therapeutic target for limiting RB tumor cell growth.

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CB133: Design and Evaluation of LIM Kinase -Specific Peptide Inhibitors as a Novel Therapeutic Strategy for Ocular Cancer

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Background: Intraocular cancers such as retinoblastoma and uveal melanoma are primary tumors that lead to vision loss and in some cases life-threatening. A key player in disease progression is the Rho/ROCK/LIMK signaling pathway, and of particular importance are the LIM kinases (LIMK1 and LIMK2), which strictly regulate cytoskeletal dynamics. The actin and tubulin framework plays a critical role in cancer progression and metastasis by affecting cell movement, division, and the ability to invade surrounding tissues. While existing ROCK inhibitors have shown promise as anti-cancer therapy, they are often associated with significant and detrimental off-target side effects. Hence, there is a need for highly specific inhibitors that target LIM kinases directly, aiming for better safety and effectiveness in treating ocular cancers. **Methods:** Substrate-competitive peptide inhibitors targeting LIMK1/2-cofilin interaction interface were computationally designed and functionally validated as effective inhibitors for LIM kinases using HeLa cells. Their physicochemical properties, predicted cell-penetrating abilities, molecular dynamics (MD) simulations, and binding free energy calculations were assessed to evaluate their stability and binding affinity. **Results:** Among the two peptides, CIPLK1 (active state) and COPLK2 (inactive state) notably reduced pCofilin levels in a dose-dependent manner. Both peptides also increased acetylated α- tubulin expression, with COPLK2 showing a particularly strong effect. These findings position CIPLK1 and COPLK2 as promising lead candidates for further exploration as LIMK-targeting therapeutics. **Conclusion:** LIMK2-specific peptides may represent a target-specific and safer alternative with a low toxicity profile for novel cancer treatments and other LIMK-related pathologies.

CB134: Elucidating The Role Of Zinc-A2-Glycoprotein In The Pathogenesis Of Proliferative Diabetic Retinopathy

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Purpose: To investigate the clinical significance and mechanistic role of Zinc Alpha 2 Glycoprotein (ZAG) in the pathophysiology of diabetic retinopathy (DR) through a case-control prospective study, followed by in vitro cell culture experiments. **Methods:** Human retinal endothelial cells (HRECs) under normal glucose (5.5 mM) and high glucose (25 mM) conditions, were exposed to recombinant ZAG. Cytotoxicity was assessed by MTT. Gene expression of metabolic markers was validated by qPCR. To demonstrate the functional importance of ZAG in-vitro, the tube formation assay was performed. **Result:** We had identified ZAG to be significantly elevated in both the vitreous and aqueous humour of PDR cases compared to Macular Hole controls. It showed a positive correlation with adiponectin, leptin, galectin-3, VEGF, PTX3, and TNF-α. Logistic regression showed ZAG as a risk factor for PDR (Odds Ratio 20.167, 95% CI 3.927–103.576, P=0.001)(i). whereas in the in-vitro experiments, ZAG supplementation led to upregulation of metabolic markers like PPAR γ and adiponectin as well as reduced inflammatory marker TNF α and angiogenic marker VEGF in HREC cells. Tube formation assay demonstrated ZAG's potential to inhibit tube formation, especially under HG conditions, supporting the gene expression results. **Conclusion:** ZAG is elevated in PDR and modulates metabolic, inflammatory, and angiogenic pathways in retinal endothelial cells. Its anti-angiogenic effect, confirmed by tube formation assays and gene expression analysis, highlights ZAG as a potential therapeutic target in diabetic retinopathy. Further studies are warranted to validate these findings and advance their clinical translation.

Reference: (i) Prakash Umapathy, Kishore Arumugam ,Ramya Benita Babu , Ramya R Nadig , Rajiv Raman , Girish Shiva Rao , Muna P Bhende , Viswanathan Natarajan , Ramkumar KM Barathi Devi SR. A case–control prospective study to glycoprotein role in the pathophysiology of diabetic retinopathy. International Ophthalmology. Available from: https://doi.org/10.1007/s10792-025-03482-w

CB135: Mitochondrial Dysfunction And Impaired Autophagy Are Evident In Glaucomatous Tenon's Tissue

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Purpose: Glaucoma is the leading cause of blindness worldwide. TGFβ has been extensively studied in association with glaucoma pathogenesis and assumed to mediate mitochondrial dysfunction and autophagy. In this study, we have evaluated the mitochondrial and autophagy genes in PACG tenon tissue cultures and direct tenon tissues. **Methods:** HTFs were cultured from patients undergoing cataract (control) and Glaucoma trabeculectomy surgery. The cultured PACG HTF were exposed to TGF β and mitochondrial genes (MFN2, OPA1, DRP1 and FIS1), autophagy genes (LC3B, P62 and BEC1) were analysed by qPCR and immunofluorescence. The mitochondrial membrane potential was assessed by JC1 staining. The expression of these genes were also verified in the direct PACG tissue samples. **Results:** In this study, we observed significant increase ($p \leq 0.05$) in transcript levels of mitochondrial fission protein DRP1 and apoptotic gene VDAC1 and decreased levels of fusion genes MFN1, MFN2 in TGF β treated PACG HTF cultures compared to cataract. We observed a significant decrease ($p \leq 0.05$) in the transcript and protein levels of autophagy related genes Beclin-1 and LC3IIB and increased levels of P62 in PACG cultures which was verified in the direct PACG tenon tissues. Mitochondrial morphology was altered to round, punctuate and doughnut shape than highly branched tubular mitochondria, with a decrease in mitochondrial membrane potential in PACG HTFs treated with TGF-β1 compared to cataract. **Conclusion:** Our results confirm that TGF beta induces mitochondrial dyshomeostasis in PACG cultured tenon cultures which was also confirmed in human tenon tissue with increased TGF beta expression.

CB136: A Novel Perspective On Proliferative Diabetic Retinopathy: Compartment-Specific Biochemical Disturbances

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Purpose: To investigate trace element levels, oxidative stress markers, and angiogenic/inflammatory profiles in serum and vitreous samples of patients with proliferative diabetic retinopathy (PDR), and compare them to diabetic (DM), non-proliferative diabetic retinopathy (NPDR), and non-diabetic controls with and without cataract. **Methods:** Trace elements (copper, zinc, iron) in serum and vitreous, oxidative stress markers (SOD, GSH, MDA, ceruloplasmin), and biochemical parameters (urea, creatinine, HbA1c) in serum were assessed. Inflammatory and angiogenic factors (PTX3, VEGF, PDGF-AA, IL-8, HBEGF, PEDF) were quantified in vitreous using Luminex multiplex assay. Correlation and logistic regression analyses were performed to identify disease-specific associations. **Results:** Serum iron was significantly reduced in PDR, while copper and zinc showed no notable serum changes. However, vitreous copper and zinc were markedly elevated in PDR versus macular hole controls ($p < 0.05$). SOD was decreased in PDR, and serum ceruloplasmin was significantly elevated, correlating positively with VEGF and platelet counts. Iron showed a consistent inverse association with disease severity and renal dysfunction (elevated urea and creatinine), while ceruloplasmin emerged as a strong systemic biomarker for PDR ($p < 0.01$). In vitreous, PDR samples showed significant increases in copper, zinc, PDGF-AA, PTX3, and IL-8 (all $p < 0.05$), suggesting their role as localized markers of disease severity. **Conclusion:** PDR exhibits compartment-specific dysregulation of trace elements, systemic oxidative stress, and elevated intraocular inflammatory/angiogenic mediators. The dissociation between serum and vitreous findings underscores the role of local microenvironmental changes in retinal pathology, highlighting potential diagnostic and therapeutic targets including ceruloplasmin, PDGF-AA, and vitreous copper/zinc.

CB137: Targeting Copper To Inhibit High Glucose-Stimulated Migration In Retinal Cells

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Purpose: Retinal microvascular dysfunction is a major complication in diabetic retinopathy. Current treatment regimens have considerable limitation, thereby emphasizing new strategies. The effect of copper chelator on high glucose induced retinal barrier impairment and its migration was studied in Adult retinal pigment epithelial cells (ARPE-19) and human retinal endothelial cells (HRECs). **Methods:** ARPE19 and HREC cells were treated with high glucose (HG - 25 mM) with and without copper (50 μM for ARPE19 and 2.1μM for HREC). Copper chelator penicillamine/Triethylenetetramine and siRNAs for CTR1 (copper transporter 1) were used in these conditions for treatment, respectively. Scratch assay and transwell migration assays were performed to check for the migratory and invasive capacity of the cells under the treatment conditions. All experiments were done in triplicate and statistical analysis was performed using two-way ANOVA. **Results:** High glucose with and without copper treatments induced migration and invasion in the retinal cells. This effect was inhibited by copper chelation. **Conclusion:** Copper chelation inhibited the retinal cell migration and invasion, which could be evaluated as a strategy for retinal microvascular dysfunction.

CB138: Advanced Gylcation Endproduct (AGEs) Induced Epigenetic Changes In Endothelial/Pericytes Co-Culture Model

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Purpose: Diabetic retinopathy is a significant microvascular problem that affects the working population globally. Though hyperglycaemia is the key factor, it has also been shown to generate epigenetic alterations in retinal cells, modulating inflammatory genes and antioxidant enzymes. Further AGEs chronic byproducts from hyperglycaemia have not yet been investigated for their epigenetic modulation. In this study, we have investigated the DNA methylation profile in a co-culture model on exposure to CML a predominant AGE found in retinal tissues of PDR cases. **Methods:** Human Retinal Endothelial Cells(HREC)-Group1 and Human Retinal Pericyte(HRP)-Group2 in a Co-Culture model 6w/p Insert were treated with 3.81nM carboxy methyl lysine in normal glucose (5.5 mM) for 24 h. Methylation profiles were analyzed using Infinium EPIC Array (935K) and validated by qPCR. Serum levels of FBXW7 were measured in PDR patient samples. All experiments were performed in triplicate and analyzed using two-way ANOVA. **Results:** Comparative methylation analysis between two groups of HREC (Group1) & HRP (Group2) identified seven commonly hypermethylated and five commonly hypomethylated genes. FBXW7 was significantly hypermethylated, while SF3B1 and DIXDC1 were markedly hypomethylated. Protein-protein interaction analysis revealed TP53 as a central hub among the hypermethylated genes. CpG island mapping revealed locus-specific methylation heterogeneity. Expression levels of methylated genes were validated by qPCR, confirming methylation-associated changes in retinal cells. Interestingly FBXW7 levels were reduced in serum samples of proliferative diabetic retinopathy (PDR) patients. **Conclusion:** This study has identified a critical marker FBXW7 to be differentialy methylated in co culture model. These findings highlight FBXW7 as a potential epigenetic biomarker and therapeutic target, further validation in site specific biological samples, such as tear fluid could pave way for predicting it as an early biomarker.

CB139: Alteration In The YAP Signaling Pathway In Cataractous Human Lens Epithelium

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Purpose: The loss of $SOX2^{+}GJA1^{-}$ lens epithelial stem cells, along with the decrease in sphere forming ability, was evidenced in the central zone of cataractous lenses. Nuclear localization of Yes-associated protein (YAP) has been linked to stemness in various tissues. This study aims to investigate the expression of YAP signaling genes in the anterior human lens epithelium of normal and cataractous lenses. **Methods:** Whole mounts of human anterior lens epithelium from normal and cataract lenses were immunostained for SOX2, YAP, pYAP, and α-SMA, followed by confocal microscopic analysis. Further, the expression of YAP signaling genes was analyzed by western blot. Results: The nuclear and cytoplasmic expression of YAP as well as the pYAP was identified to be reduced in cataractous lens compared to normal lens. While $SOX2^{+}YAP^{+}$ cells were identified only in normal lens, α-SMA was highly expressed in cataractous lens epithelium. Western blot confirmed the immunostaining data pYAP/total YAP expression was lower in cataractous lens than in normal lens. Additionally, the upstream genes MST2 and LATS were downregulated in cataractous lens. **Conclusion:** The absence of $SOX2^{+}YAP^{+}$ cells in cataractous lens indicates a probable role of stem cells in the development of age-related cataract. Further studies are essential to elucidate the role of YAP signaling in the pathogenesis of cataract.

CB140: Effect Of Methotrexate, Tissue Plasminogen Activator And Anti-VEGF On An In Vitro Model Of Proliferative Vitreoretinopathy

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Purpose: To study the changes seen in the morphology and pro-inflammatory and fibro angiogenic markers concentration in vitreous milieu after treating it with Anti-VEGF, Tissue plasminogen activator (t-PA) and Methotrexate (Mtx). **Method:** Retinal pigment epithelial (RPE) cells were utilized to establish an in vitro disease model. The cells were exposed to cadaveric vitreous, as well as vitreous and subretinal fluid from diseased eyes. Three experimental groups were created: (a) a 1:1 mixture of patient-derived vitreous and subretinal fluid, (b) vitreous from macular hole patients, and (c) cadaveric vitreous. ARPE cells were treated with these different vitreous combinations and anti-VEGF, Methotrexate and t-PA to simulate disease conditions. The expression of pro-inflammatory markers (IL-6, IL-8, TNF-α), fibrogenic factors (collagen, fibronectin), and angiogenic markers (VEGF-A, VEGF-C) was then analyzed and compared with the cadaveric vitreous group (control group). Quantitative PCR (qPCR) was performed to assess the gene expression of these markers. **Result:** Our findings demonstrate that methotrexate treatment significantly modulates fibrosis markers, with elevated levels observed in proliferative vitreoretinopathy (PVR) group. Vascular endothelial growth factor A (VEGFA) exhibited a slight reduction in the PVR group following methotrexate administration. In contrast, VEGFC levels were mildly upregulated post-treatment. Notably, tissue plasminogen activator (t-PA) displayed the most substantial changes, with a marked impact on inflammatory markers compared to its effects on angiogenesis and fibrosis-related factors. These results suggest that methotrexate exerts distinct regulatory effects on fibrotic, angiogenic, and inflammatory pathways in PVR and MH. **Conclusion:** Methotrexate can be used in early stages of PVR where inflammation is the main culprit whereas anti-fibro angiogenetic properties of t-PA supports further study of its therapeutic role in vitreoretinal disorders.

SC141: Modelling Retinal Microvascular pathology using iPSC Derived Human Retinal Pericytes

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Purpose: Retinal pericytes are vital components of the neurovascular unit, playing a central role in maintaining vascular stability and regulating blood-retinal barrier function. Their early loss is a defining feature of diabetic retinopathy (DR), contributing to microvascular dysfunction and disease progression. However, the limited availability and variability of primary human retinal pericytes pose significant challenges for mechanistic studies and drug discovery. Induced pluripotent stem cell (iPSC)-derived retinal pericytes offer a promising and scalable alternative, enabling the development of physiologically relevant in vitro models to better understand retinal vascular pathology. **Methods:** iPSCs were differentiated into retinal pericyte-like cells using a targeted, stepwise protocol. Lineage identity was validated through gene and protein expression analysis. To mimic early DR pathology, cells were exposed to hyperglycaemic and inflammatory conditions. Label-free live-cell imaging was performed using Nanolive holotomography to capture real-time structural and organelle-level changes. In parallel, qPCR analysis was conducted to profile expression of key stress-responsive genes related to oxidative stress, inflammation, and cell survival. **Results:** iPSC-derived retinal pericytes were successfully generated and exhibited robust expression of lineage-specific markers like PDGFR-ß, CSGP4, NGFR. Upon exposure to stress conditions, these cells demonstrated early signatures of dysfunction as revealed by dynamic imaging. Molecular profiling further indicated upregulation of stress-associated transcripts, supporting activation of cellular stress pathways consistent with early diabetic retinopathy. **Conclusion:** This iPSC-based model offers a valuable tool to investigate the early cellular events driving pericyte pathology in diabetic retinopathy. By recapitulating stress-induced dysfunction in vitro, it provides a foundation for identifying disease mechanisms and accelerating the development of targeted therapeutic interventions.

SC142: Bio-Inspired 3D Printed Patterned Patches For Enhanced Ocular Residence

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Purpose: Eye drops remain the first line treatment option for the anterior eye segment diseases. However, high pre-corneal clearance and less drug residence time of topical eye-drops lead to poor bioavailability. Bio-inspired corneal patches could improve the drug residence time, muco-adhesion and bioavailability. Hence, this study aims to fabricate various patterned patches and investigate their role in enhancing ocular residence. **Methods:** Different patterns were designed using Computer Aided Design software and their molds were fabricated using SLA 3D-printing technique. Patterns like Hemispheres(HS), columns(C), pyramids(PY), squares(SQ) and hexagons(HX) were optimized for width, pitch and height. Patterned polymeric patches were prepared by replica moulding technique. The patches were characterized for physico-chemical properties, contact angle and hysteresis, *ex vivo* mucoadhesion and *in vivo* residence time in rabbits. **Result:** The contact angle of all the patterns was observed to be $\theta > 70^{0}$ with higher contact angle hysteresis $\theta > 25^{0}$ stating higher adhesive tendency to the surfaces. The patterned patch showed better ex-vivo mucoadhesion PY(0.07 ± 0.02 N/cm2), CL (0.07± 0.03 N/cm2), HX(0.05 ± 0.02 N/cm2), compared to the plain patch(0.02 ± 0.01 N/cm2). Also, the PY patterned patch showed highest corneal residence time (13h) followed by CL (6h) and HX (5h) in comparison to plain patch (3h). **Conclusion:** The patterned patches showed enhanced mucoadhesion and residence time compared to plain patch, which can be related to the influence of microstructures on the fabricated patches. Further, studies are required to assess the biocompatibility and therapeutic effectiveness of the fabricated patches in pre-clinical models.

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SC143: Impact Of Fabrication Technique On Ocular Patch: Solvent Casting Vs 3D Printing Technique

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Purpose: A polymeric ocular patch offer advantages, including enhanced mucoadhesion and prolonged ocular residence time compared to conventional eye drops. Polymeric patches are prepared using various techniques such as solvent-casting, hot melt extrusion and 3D printing. The current study focuses on the impact of solvent casting and 3D printing technique on characteristics of the patch. **Methods:** Patches were prepared using chitosan (2% w/v), hydroxypropyl methylcellulose K4M (2.5% w/v), gelatin (3% w/v), and kappa carrageenan (1% w/v) and fabricated using solvent casting and an extrusion-based 3D printing method and further dried at 60 °C. The fabricated patches were evaluated for their weight variation, thickness uniformity, swelling index, and in vivo mucoadhesion. **Results:** We have selected chitosan patches prepared using solvent casting and 3D printing technique for comparison, the solvent-casted patch had a weight of 6.70 ± 0.31 mg and thickness of 0.17 ± 0.02 mm, while 3D-printed patch had weight of 3.17 ± 0.01 mg and thickness of 0.07 ± 0.01 mm. The swelling index of the solvent-casted patch was found to be higher 1579.19 ± 51.93% compared to 125.74 ± 64.01% for 3D-printed patch. The in vivo mucoadhesion was found to be higher for 3D-printed patch upto 6 hours as compared to solvent-casted patch upto 4 hours. **Conclusion:** The 3D-printing technique shows a promising result due to its reproducibility and less batch-to-batch variation. Further, evaluation studies are required to understand the impact of various fabrication designs on polymeric arrangement in the patch dynamics of 3D-printed patch.

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SC144: iPSC-Derived Retinal Pigment Epithelium (RPE) Cells (Eyecyte-RPE) Maintain Their Functional Integrity For Extended Periods Post Freeze-Thaw

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Purpose: Cell replacement therapy is rapidly emerging as a promising approach for retinal degenerative diseases like age-related macular degeneration (AMD), where RPE cells are damaged. Most ongoing clinical trials utilize live RPE cell suspensions or patches. Based on the promising data from our Phase 1 clinical trials (NCT06394232), we strongly believe that a cryopreserved allogeneic RPE product would enable large-scale production and easy access, making it affordable. Here we show that Eyecyte-RPE retain their characteristics upon revival and subsequent culturing. **Method:** iPSCs were differentiated into RPE cells through enrichment around day 45, followed by expansion and maturation until day 120. Differentiated RPE cells were authenticated by $TYRP1^{+}$/$PMEL17^{+}$ staining as identity markers and pigment epithelium-derived factor (PEDF) secretion by ELISA, as a measure of potency, before cryopreservation. Post-revival, cell viability, growth kinetics, trans-epithelial electrical resistance (TEER), and PEDF secretion were evaluated at 2, 4, 6, and 8 weeks. Flow cytometry and melanin quantification were also performed to establish purity and functionality. **Result:** RPE cells demonstrated robust survival upon freeze-thaw and could be successfully cultured. At 4-6 weeks, RPE cells acquired hexagonal morphology with intense pigmentation, expressed RPE-specific markers and demonstrated progressive increase in PEDF secretion and barrier function. **Conclusion:** Cryopreserved RPE cells retain viability, identity, purity and potency comparable to live cells. These findings underscore the feasibility of large-scale manufacturing and widespread distribution of cryopreserved, allogeneic RPE cell products for future clinical applications and support the vision improvement observed in our Phase 1 clinical trial, 10-11 months post injection.

SC145: Optimization Of AAV - Mediated Gene Augmentation In Photoreceptor Progenitor Cells Differentiated From Disease-Specific iPSC Line

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Purpose: The visual cycle comprises of a series of enzymatic reactions critical for photoreceptor function. Mutations in *RDH12*, which encodes retinal dehydrogenase 12, an enzyme leads to reduction of all-trans-retinal to all-trans-retinol causing Leber congenital amaurosis 13 (LCA13). Loss of RDH12 activity results in accumulation of toxic waste in the retina and inflicts photoreceptor degeneration. With no available treatment options, gene therapy offers a promising strategy to restore *RDH12* function in LCA13 patients. **Method:** Multiple adeno-associated virus (AAV) serotypes were evaluated for their transduction efficiency in photoreceptor progenitors (PRPs) cells derived from healthy individuals and LCA13 patients. Transduction efficiency was quantified by assessing GFP reporter expression. The most efficient serotypes were identified and subsequently tested both in vitro and in vivo to confirm their transduction potential. Gene augmentation was performed in LCA13-derived PRPs using the selected AAV serotypes, and restoration of *RDH12* expression was validated at the transcript and protein levels via quantitative PCR, immunocytochemistry and western blot analysis. **Result:** Among the AAV serotypes tested, AAV2 and AAV5 demonstrated better transduction efficiency and were therefore selected for subsequent in vitro and in vivo studies. These serotypes effectively augmented *RDH12* expression in both healthy and LCA13-derived photoreceptor progenitor cells. **Conclusion:** In vitro experiments helped to optimize the AAV-mediated gene augmentation strategy in patient specific cells. Ongoing studies in animal models aim to further evaluate its translational potential. These preliminary findings lay the groundwork for the development of a robust gene therapy approach for the treatment of LCA13.

SC146: Unravelling MicroRNA Signatures In Human Trabecular Meshwork Stem Cells: Implications With Ageing And In Glaucoma

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Purpose: The adult human trabecular meshwork stem cells (TMSCs) located in the non-filtering (NF) region were identified to be significantly reduced with ageing and drastically in primary open angle glaucoma (POAG). This study aims to identify the molecular regulators (miRNAs) of TMSCs and to examine how their expression changes with ageing and in glaucoma. **Methods:** MiRNA profiling of the filtering (F) and NF regions of donor TM tissues was carried out with Nanostring nCounter human miRNA assay kit. The differentially expressed miRNAs were confirmed by real time PCR (RT-PCR) using tissues from donors of age: 0-30, 30-60, >60 years, and paraffin sections of known glaucomatous donor tissues. miRTarBase was used to predict the targets for validated miRNAs and ShinyGO 0.82 for functional enrichment. **Results:** Twenty six significantly up-regulated and three down-regulated miRNAs were identified in the NF region compared to F region (fold change >+1.2). RT-PCR analysis confirmed 4/7 upregulated miRNAs - hsa-miR-184, hsa-miR-107, hsa-miR-34a-5p and hsa-miR-24-3p to be highly expressed in NF region and 3/3 downregulated miRNAs - hsa-miR-145-5p, hsa-miR-22-3p and hsa-miR-376a-3p to have reduced expression. An age-related reduction of hsa-miR-107, hsa-miR-184, and hsa-miR-34a-5p was observed in the NF region. In glaucomatous tissues, all three downregulated miRNAs showed increased expression in F and NF region. Target prediction identified these miRNAs to regulate pathways involved in stem cell maintenance, including MAPK, PI3K-AKT, FOXO, and HIF signalling **Conclusion:** MiRNAs highly expressed in the NF of TM were identified, and their dysregulation may contribute to TMSC loss with ageing and in glaucoma.

SC147: Investigating The Therapeutic Potential Of Mesenchymal Stem Cell Derived Exosomes In Corneal Tissue Regeneration

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Corneal blindness is a condition affecting millions of people worldwide and its treatment is impacted by the limited availability and quality of donor cornea tissues. Mesenchymal stem cell (MSC) derived nanosized extracellular vesicles (EVs), known as exosomes, have shown great promise in the treatment of various clinical disorders, and were used in this study to demonstrate their regenerative and therapeutic potential in healing corneal wounds. These exosomes isolated by tangential flow filtration, ultracentrifugation and purified by density gradient separation were evaluated by nanoparticle tracking analysis and electron microscopy for size estimation, and western blot for protein profile as per MISEV2018- guidelines. They showed a narrow size distribution (70-150 nm) and appeared as typical cup-shaped vesicles in transmission electron microscopy. They displayed characteristic MSC-derived EV-markers CD9, CD63, CD81, TSG101, Flotillin, and Alix. Their therapeutic potential was established by *in-vitro* functional assays using human corneal epithelial (HCE) cells and *in vivo* studies performed in New Zealand white rabbits. The exosomes showed significant activity in terms of anti-inflammation, anti-fibrosis, neurogenesis and anti-angiogenesis. Thus, MSCs-derived exosomes stimulate re-epithelization and support transparent regeneration of diseased cornea, observed both *in vitro and in vivo*. They are promising candidates for the clinical translation towards the treatment of various corneal disorders such as neurotropic keratitis, inflammation, and keratoconus to restore vision.

SC148: From Chemistry To Clarity: Influence Of Crosslinker In 3D Bioprinted Corneal Constructs

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Purpose: Corneal blindness affects millions worldwide, creating a critical need for alternative treatment strategies such as bioengineered corneal lenticules. This study introduces a unique take on investigating the effect of various photoinitiators on the fabrication and performance of 3D bioprinted corneal lenticules using Digital Light Processing (DLP) technology. **Methods:** A dual-network bioink composed of methacrylated hyaluronic acid (HA-MA) and methacrylated gelatin (Gel-MA) was developed to mimic native corneal properties1. Two photoinitiator systems were evaluated: type I LAP (lithium phenyl 2,4,6-trimethyl benzoyl phosphinate) and type II Ru/SPS (ruthenium with sodium persulfate). These systems were assessed for crosslinking efficiency, optical clarity, mechanical integrity, and swelling behavior. **Results:** LAP photoinitiator system initiates polymerization through unimolecular bond cleavage and Ru requires a co-initiator (SPS) to initiate the polymerization reaction between HA-MA and Gel-MA. Due to their different mechanism of action, the successful printing with LAP-based bioinks requires higher light intensity and three times longer exposure times during each layer printing compared to Ru/SPS-based bioink. We utilized understanding of the different mechanisms to adjust the printing parameters and successfully printed corneal lenticules with HA-MA/Gel-MA bioink using LAP and Ru/SPS. Ru/SPS-based lenticules exhibited significantly lower swelling than LAP-based lenticules. This is attributed to the higher molar absorptivity2 of Ru/SPS ($\varepsilon \approx 14600\ M^{-1}\ cm^{-1}$) compared to LAP ($\varepsilon \approx 30\ M^{-1}\ cm^{-1}$), enabling more efficient crosslinking. **Conclusion:** While both the photoinitiators successfully printed corneal lenticules however, Ru/SPS-system requires lower light intensity and exposure time over LAP based bioink. Photoinitiator selection critically impacts functional performance of bioprinted constructs which can be utilized for bioinks screening.

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PA149: Using Optomotor Reflex For Longitudinal Monitoring Of Diabetic Retinopathy Progression In Mouse Model

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Purpose: This study aimed to develop an automated optomotor reflex (OMR) quantification system for detecting and tracking progressive contrast sensitivity loss in a mouse model of diabetic retinopathy, providing a robust tool for longitudinal monitoring of disease progression. **Methods:** Diabetes was induced in C57BL/6 mice (n=6) via streptozotocin injections (50 mg/kg/day for five consecutive days). OMR was assessed at 5, 9, and 13 weeks post-induction using a custom-built arena equipped with four monitors displaying moving sine-wave gratings across a range of contrasts (10%, 25%, 50%, and 100%). Mice were placed on a central pedestal with a mirror base, and their head movements were recorded using an overhead infrared camera. DeepLabCut was used to extract the position of different body parts. And the angular displacements of these body parts relative to the body centre were used to evaluate OMR. **Results:** OMR tracking across multiple body parts demonstrated that snout measurements conferred superior sensitivity in detecting the behaviour. Diabetes induction in mouse models was confirmed by 6-hour fasting glucose levels exceeding 250 mg/dl, with approximately 60% of animals developing diabetes. Utilising snout-based OMR, a significant reduction in stimulus tracking ability was observed in diabetic mice compared to controls only after 13 weeks (post-diabetic induction). In particular, diabetic animals exhibited a pronounced impairment in their capacity to track stimuli at lower contrast levels. **Conclusions:** The integrated OMR platform enables sensitive, longitudinal detection of visual behavior in diabetic retinopathy. This approach provides a quantitative, non-invasive method for monitoring disease stages and supports preclinical evaluation of neuroprotective interventions.

PA150: Development Of DNA Aptamers By Hybrid-Selex Targeting B7H3

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Purpose: B7H3 (CD276), a type I transmembrane glycoprotein implicated in tumor immune evasion and therapeutic resistance, is upregulated in primary retinoblastoma. We aimed to engineer high-affinity ssDNA aptamers against B7H3 via a refined hybrid-SELEX platform integrating protein- and cell-based selection pressures to yield conformationally selective ligands suitable for diagnostic and targeted theranostic applications. **Methods:** Iterative SELEX cycles were performed against recombinant human B7H3 protein, followed by live-cell SELEX on RB cell lines overexpressing native B7H3. Library evolution was tracked by qPCR enrichment kinetics, and post-SELEX pools were subjected to Illumina-based next-generation sequencing. Candidate aptamers were ranked via bioinformatic algorithms (FASTAptamer toolkit and MEME-ChIP motif analysis) and chemically synthesized with 5′ fluorophores. Binding kinetics were determined using flow cytometry and surface plasmon resonance (SPR), while functionality was evaluated through dot blot, sandwich dot blot, western blot (denatured antigen), and FFPE-compatible immunohistochemistry. **Results**: Lead aptamers exhibited nanomolar dissociation constants (Kd 19–50 nM) with high target specificity. Aptamer VRF-HS_B7H3-03 uniquely recognized linear epitopes, retaining binding in denatured assays. Sandwich dot blots validated dual non-overlapping epitope recognition. IHC mirrored monoclonal antibody performance but with lower nonspecific binding and superior tissue penetration. **Conclusions:** These structurally optimized ssDNA aptamers demonstrate robust performance across analytical platforms. Their synthetic tractability, thermal stability, and capacity for site-specific modification render them ideal candidates for aptamer-based imaging agents, ADC-mimetics, and multiplexed immunodiagnostic platforms in B7H3-expressing tumors.

PA151: Maternal Riboflavin Deficiency Impairs Offspring's Retinal Function In Rats

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Purpose: The eye and skin are the sites for the first clinical symptoms observed in riboflavin (vitamin B2) deficiency. The retina is highly enriched in riboflavin, yet its role in retinal development remains poorly understood. This study investigates the impact of maternal riboflavin deficiency on retinal function in rat offspring. **Methods:** Female Wistar rats were assigned to three dietary groups: control (AIN93G diet with 5 mg/kg riboflavin), pair-fed (control diet, intake matched to deficient group), and deficient (0.5 mg/kg riboflavin). After establishing a riboflavin deficiency, females underwent mating, gestation, and lactation. Retinal function was assessed in the offspring at postnatal day 30 by electroretinography (ERG). Retinal tissues were collected for molecular analysis and also fixed for histological evaluation. **Results:** Offspring from riboflavin-deficient dams showed significantly reduced a- and b-wave amplitudes and prolonged implicit times in both scotopic and photopic ERG. Flicker ERG responses were diminished, indicating dysfunction in the cone cells. Histological analysis revealed a reduction in cell counts in both the outer and inner nuclear layers. Rhodopsin expression was decreased, while HIF-α levels were elevated in the deficient group. The pair-fed group did not differ from controls. **Conclusions:** Maternal riboflavin deficiency disrupts normal retinal development and function in offspring. These findings highlight the crucial role of riboflavin in promoting healthy retinal maturation and maintaining visual pathway integrity.

PA152: Molecular & Pathological Insights Of Diabetic Retina In Post-Mortem Donor Eyes

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Purpose: Understanding the key molecular events of Diabetic retinopathy (DR), particularly from retina is limited to *in-vitro* cell culture and *in-vivo* animal models, owing to limited availability of clinical tissues from patients. Thus, we have established a protocol to categorize eyes with marked disease pathology for reliable sampling of human cadaveric eyes for research investigations into DR. **Methods:** The posterior segment of human donor eyes were obtained with detailed information on cause of death, presence of any systemic co-morbidities including diabetes history if applicable. The eyes were categorized as diabetic with retinopathy changes based on fundus examination by indirect ophthalmoscopy and histopathological evaluation of the retina. Expression of neurodegenerative markers such as Gfap, Iba1, Synaptophysin and other angiogenic molecules such as *VEGF, VEGFR2* etc were evaluated to establish a panel of markers to categorize diabetic donor eyes as retinopathy samples. **Results:** Retinal tissues obtained within 12 hours post-mortem were included into the study. IDO and histological evaluation were the first screening tool to evidence diabetes related changes in the retina. In the selected DR eyes, there was significant decrease of Synaptophysin compared to non-diabetic retinae. There was also a marked differential expression of genes such as *SNCG, NEFM, GRIK, GRM6* etc, and demarcating retinopathy like changes that also correlated with IDO and histopathology for DR. **Conclusion:** A comprehensive protocol has been established in this study to categorize and identify diabetic eyes with confirmed disease pathology that is crucial for sampling the eyes for DR investigations.

PA153: Deciphering Cross-Regulation Between MYCN Oncogene And TET1 Protein In Human Retinoblastoma

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Purpose: MYCN oncogene plays a pivotal role as a key driver of oncogenesis in retinoblastoma (RB) and may regulate Ten-Eleven Translocation (TET) gene expression, implicating a role for TET proteins in RB. As key DNA demethylases, TET proteins have attracted attention for their dysregulation in MYCN-amplified solid cancers. This study aims to explore the MYCN-TET1 axis to uncover novel epigenetic interventions to suppress tumor growth in RB. **Methods:** TET protein expression was analysed in RB cells and patient tissue specimens using immunoblotting and immunohistochemistry. TET1 was targeted in RB cells by genetic silencing using shRNAs and functional assays were performed.

Promoter analysis of TET1 was performed to identify MYCN binding sites upstream of its transcription start site. Reciprocal regulation between MYCN and TET1 was assessed by evaluating changes in their protein levels following gene-specific knockdown using immunoblotting. **Results:** TET1 was found to be overexpressed in RB. shRNA-mediated silencing of TET1 resulted in hindered RB cell survival. Promoter analysis revealed multiple MYCN binding sites upstream of TET1 transcription start site. Suppression of MYCN expression resulted in a marked downregulation of TET1, while silencing of TET1 similarly led to a decrease in MYCN protein levels, indicating their potential cross regulation. **Conclusions:** TET1 is overexpressed in RB and mediates its cell survival. The interplay between MYCN and TET1 suggests a regulatory loop that may contribute to tumorigenesis, highlighting potential therapeutic targets in RB. Additional validation is needed to comprehensively determine the functional role of TET1 in RB.

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PA154: Effects Of Different Times Of Natural-UV Exposure On Wistar Rats And Their Behaviour - Rodent Study

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Purpose: Dopamine plays a vital role in motor behaviour and maintains the retinal neuronal health. Exposure to ultraviolet (UV) light might influence retinal dopamine levels. This study aims to investigate the effect of short span of UV exposure on retinal dopamine and related behaviour. **Methods:** Three groups of male Wistar rats (n=6 in each group) were divided into normal controls (NC) and two exposure groups: morning (8.15-9.00 AM) and evening (4.15-5.00 PM) for 15 days. Behaviour analysis was performed post exposure. The animals underwent a two-day training session on a rotarod, with the final test conducted on the third day where the time of fall and their acceleration were recorded and compared across the groups. **Results:** The rotarod test did not reveal any noteworthy variance in the time and acceleration across the groups post exposure in all 3 days. ($p>0.05$). **Conclusion:** The behavioural aspect highlights the possible influence of direct sunlight exposure on retinal DA levels and their correlations with the behavioural analysis, despite, no significant difference between the group.

PA155: Chromatin Remodeling In Action: EZH2 And The Invasive Front In Retinoblastoma

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Purpose: Retinoblastoma (RB), the most common pediatric intraocular cancer, poses therapeutic challenges due to chemotherapy-related toxicity and drug resistance. A microarray-based study by Nalini et al. (2013) revealed widespread gene deregulation in post-chemotherapy RB, including upregulation of EZH2, a histone methyltransferase implicated in tumor progression and chemoresistance. This study aims to investigate EZH2 protein expression in RB, particularly in tumors invading the optic nerve (ON), and to correlate expression with histopathological and radiological findings. **Methods:** A retrospective analysis was performed on 21 formalin-fixed paraffin-embedded RB samples from the L & T Ocular Pathology Department. Immunohistochemistry (IHC) for EZH2 was conducted using the D2C9 monoclonal antibody; Weri-Rb-1 served as the positive control. EZH2 expression was analyzed in relation to ON invasion, choroidal invasion, tumor differentiation, and anaplasia. MRI findings were compared with histopathology to assess concordance. Tissue microarray were prepared using WERI-Rb-1 & NCCRbC51 cells treated with vincristine, etoposide, and carboplatin. IHC was carried out using EZH2 antibody. **Results:** EZH2 was strongly expressed in tumor cells invading the ON and choroid, but was absent in adjacent normal retina. Expression intensity varied with histological features. EZH2 expression showed significant correlation with high-risk pathological features ($p = 0.03156$), includes Choroidal invasion more than 3mm, and post-laminar optic nerve invasion. MRI showed moderate agreement with histopathology for choroidal invasion (84.61%, $\kappa = 0.409$), but poor agreement for ON invasion (46.15%, $\kappa = 0.099$). IHC on Tissue Microarray revealed strong expression of EZH2 in both control & chemo-treated WERI-Rb-1 and NCC-Rb C51 cells. **Conclusion:** EZH2 is overexpressed in invasive RB, particularly with ON involvement. Its distinct nuclear staining pattern supports its utility as a biomarker. EZH2-targeted therapies like tazemetostat may offer new avenues for high-risk RB management.

PA156: Molecular And Histopathological Insights From The Lens Capsule Of Iridocorneal Endothelial Syndrome

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Purpose: Iridocorneal endothelial (ICE) syndrome is a rare ocular disorder marked by abnormal proliferation of corneal endothelial cells, progressive iris atrophy, and secondary glaucoma. Although theories such as aberrant membrane formation and neural crest cell migration have been proposed, its exact pathophysiology remains unclear. **Methods:** A 60-year-old female with no history of trauma presented for cataract evaluation. Examination of the right eye revealed an eccentric, irregular pupil displaced superonasally, with iris thinning and stretching. Gonioscopy showed PAS in the superonasal and nasal quadrants; the remaining angles were open. IOP was 14 mmHg with a CDR of 0.65 and no anti-glaucoma medications. Specular microscopy showed an endothelial cell count of 1291/mm² with poor hexagonality. A diagnosis of ICE syndrome was made. During cataract surgery, an abnormal capsular adhesion was noted. The lens capsule was sent for histopathological analysis and molecular testing; blood was sent for whole-exome sequencing (WES). **Results:** The morphology of the patient-derived cells from the lens capsule was differentiated from that of the healthy lens capsule. The molecular profile of these cells showed increased expression of TNF-α and CXCL10, α-SMA, and fibronectin, highlighting fibrosis mediated by integrin β1. The apical and basal polarities were maintained as assessed by the increased expression of PARD3 and ZO-1.WES revealed no pathogenic or likely pathogenic variants. The histological images showed a thickened capsular basement membrane and hyperchromatic nuclei, indicating activated fibroblast cells. **Conclusion:** This case highlights cytokine-mediated fibrosis, likely driven by integrin signaling, suggesting fibrotic remodeling beyond the corneal endothelium in ICE syndrome.

PA157: Mitochondria-Driven Ferroptosis In The Progression Of Primary And Post-Chemotherapy Retinoblastoma

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Purpose: Retinoblastoma is the most common intraocular tumour occurs in children. Mitochondrial dysfunction and increased reactive oxygen species have been found in cancerous cells, including Rb. Mitochondria play a diversified role in the process of ferroptosis, the iron metabolism, OXPHOS pathway, etc. GPX4 is the central mediator of ferroptosis. Therefore, the aim of the study is to investigate the expression of mitochondrial-mediated ferroptosis genes in Rb patients. **Methods:** This prospective study includes 71 Rb cases (50 primary and 21 chemoreduced Rb cases). Real-Time PCR was performed to assess the mRNA expression levels of mitochondrial genes (BAX, ACSF2, LONP1, CISD1, SOD2 & MFRN1/2) along with anti-ferroptosis, GPX4 gene. Immunoexpression of GPX4 was also determined followed by western blotting. The expression levels of these genes were correlated with clinicopathological parameters. **Results:** There was male preponderance in this study. In 50 primary Rb cases, high mRNA expression of Bax was observed followed by LONP1. While MFRN1/2, SOD2 and CISD1 were moderately expressed and ACSF2 was downregulated. GPX4 was upregulated in our cases. Post-laminar optic nerve and optic nerve head invasion were observed in 22% and 40%, respectively. We found similar level of gene expression for MFRN1/2, BAX, CISD1, LONP1 and SOD2, but GPX4 was downregulated and ACSF2 was upregulated in our cases. **Conclusions:** Our findings revealed dysregulation of mitochondrial genes involved in oxidative stress and apoptosis which may have a potential role in tumour-progression of Rb. Further studies could provide a better insight of these genes in prognostication of Rb patients.

PA158: Distinct Tear Cytokine Signatures In Acute And Chronic Steven Johnson Syndrome

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Purpose: To characterize and compare the tear cytokine profiles in acute and chronic phases of Stevens-Johnson Syndrome (SJS) using advanced proteomics, and to identify key inflammatory mediators associated with disease severity and progression. **Methods:** Tear samples from 36 subjects (11 acute SJS, 15 chronic SJS, 10 healthy controls) were analyzed using the OLINK® Target 48 Cytokine Panel based on Proximity Extension Assay technology. Clinical grading, imaging, and statistical analysis were performed alongside bioinformatics assessments including pathway enrichment, protein–protein interaction (PPI) networks, and correlation with clinical severity scores. **Results:** A total of 32 and 20 cytokines were significantly dysregulated in acute and chronic SJS, respectively. Acute SJS showed marked upregulation of CCL7, IL-6, IL-1β, OSM, and MMP1, while chronic SJS exhibited elevated IL-6, IL-1β, and CCL4 along with downregulation of CXCL10, IL-7, and EGF. Distinct cytokine signatures were noted for each disease phase, with a core set of overlapping inflammatory markers. Pathway enrichment highlighted activation of cytokine–cytokine receptor interaction, chemokine signalling, and macrophage-associated processes. **Conclusion:** This study reveals distinct yet overlapping tear cytokine profiles in acute and chronic SJS, with specific cytokines correlating with clinical severity. Findings suggest a central role for cytokine-chemokine inflammation in disease persistence and provide a basis for biomarker-guided monitoring and personalized therapeutic interventions in ocular SJS.

PA159: Tear Cytokine Profiling of VKC Reveals a Shift Toward Chronic Inflammatory Signatures

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Background: Vernal keratoconjunctivitis (VKC) is a chronic allergic eye disease that can progress from seasonal symptoms to persistent inflammation thereby leading to vision threatening complications. While Th2-mediated pathways are established in VKC, the molecular correlates of clinical severity remain poorly understood. This study aimed to profile tear cytokines in VKC patients and evaluate their association with disease phenotypes and clinical features. **Methods:** Tear samples were collected using Schirmer's strips from VKC patients (moderate intermittent and moderate persistent) and healthy controls. Proteins were eluted and quantified. Cytokine profiling was performed using the OLINK® Target 48 Cytokine Panel. Statistical analyses included t-tests, fold-change comparison, heatmaps, volcano plots, and correlation with clinical parameters using Spearman's coefficient. Pathway enrichment was conducted using STRING. **Results:** Cytokines including IL-15, CXCL11, CXCL9, MMP12, and CCL13 were significantly upregulated in VKC compared to controls, with higher expression in the persistent group. These cytokines showed strong correlations with symptom duration, limbal involvement, and papillae size. Pathway analysis revealed activation of IL-17, JAK STAT, and chemokine signaling pathways. **Conclusions:** Tear cytokine profiling revealed distinct immune signatures associated with VKC severity. The moderate persistent phenotype showed a more aggressive inflammatory profile, suggesting a point of transition in disease chronicity. These findings support the use of tear cytokines as potential biomarkers for disease monitoring and targeted therapy.

CL228: Utility Of Ocular Surface Analyzer In SJS And Its Molecular Correlations

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Purpose: Stevens-Johnson Syndrome (SJS) is a severe hypersensitivity reaction often caused by drugs or infections, leading to skin and mucosal damage, including chronic ocular complications like dry eye. Dry Eye Disease (DED) is a multifactorial condition involving tear film instability and inflammation. Both significantly affect quality of life, with SJS requiring specialized ocular management. **Methods:** In this prospective study, 130 eyes of 65 SJS patients and 140 eyes of 70 DED patients underwent Ocular Surface Analysis (OSA), including: a) Lipid Layer Thickness (LLT), b) Non-Invasive Break-Up Time (NIBUT), c) Tear Meniscus Height (TMH), d) Meibography. SJS patients also had conjunctival imprints analyzed via real-time PCR for TLR9, MYD88, TNFSF14, IL-8, and C3a, and neutrophil extracellular traps via MPO-DNA ELISA. Data were compared using unpaired t-tests; correlations were drawn between OSA parameters and molecular markers. **Results:** SJS patients had significantly worse BCVA (1.33 vs. 0.09, $p<0.0001$) and lower TBUT (1.13 vs. 3.88 sec, $p<0.0001$). Despite a slightly higher NIBUT (7.26 vs. 6.18 sec, $p=0.024$), LLT was lower in SJS (22.99 vs. 27.89 nm, $p=0.007$). Meibography scores were also reduced in SJS ($p<0.0001$). High TNFSF14 expression correlated with lower NIBUT ($p=0.0034$). **Conclusion:** OSA provides valuable non-invasive insights into tear film and meibomian gland dysfunction. It outperforms traditional tests like Schirmer's and TBUT, particularly in detecting abnormalities in SJS-related dry eye.

MI201: Microbiological Profile And Antibiotic Susceptibilities In Culture Proven Post-Operative Endophthalmitis At A Tertiary Care Hospital In South India

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Purpose: To determine the microbial spectrum and the susceptibility pattern of bacteria in culture-positive post-operative endophthalmitis referred to a single tertiary care hospital over the last decade. **Methods:** The laboratory records of patients presenting with post-operative endophthalmitis from whom vitreous and/or aqueous aspirates were obtained for microbiological investigations at Sankara Nethralaya from January 2015 to December 2024, were reviewed to investigate microbiological profile and antibiotic sensitivities. **Results:** A total of 165 isolates were identified from 164 patients. Gram positive bacteria, Gram-negative bacteria and fungi accounted for 44.5%, 36% and 20.2 % of all isolates, respectively. Among bacteria, the most prevalent pathogens were coagulase-negative Staphylococcus (32%), followed by Pseudomonas aeruginosa (17.5%) and Staphylococcus aureus (6.8%). Amongst fungi, the predominant organisms were found to be Aspergillus species (30%) and Candida species (27%). Among Gram positive bacteria, vancomycin susceptibility was 96%, while ciprofloxacin susceptibility was 60%. Gram-negative bacteria, showed a susceptibility of 70 % against ceftazidime, 76% against ciprofloxacin, 77% against amikacin and 67% against gentamicin. There was no significant change in the trends of bacteria isolated and antibiotic susceptibilities during the study period. **Conclusion:** Though Gram-positive bacteria were predominant, Gram negative bacteria and fungi continue to be important aetiological agents of post-operative endophthalmitis in our setting. An overall resistance of 30% to ceftazidime, an empirical intravitreal therapy for Gram negative bacteria is concerning. The present large case series would be an important addition to literature on evolving trends in aetiology and antibiotic susceptibilities, providing crucial information for treatment guidelines, especially for empirical therapies.

MI202: Development Of An Integrated RPA-EXO Probe Assay For Low-Complexity And Rapid Detection Of Fungal DNA In Ocular Infections

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Purpose: To develop an integrated recombinase polymerase amplification (RPA) assay using an exo probe for rapid and specific detection of fungal DNA from *Fusarium, Aspergillus*, and *Candida* species—major pathogens in ocular fungal infections. **Methods:** An RPA assay was optimized using an exo probe designed to target conserved fungal DNA regions. The assay combines amplification and real-time fluorescence-based detection in a one-pot, isothermal format. DNA from *Fusarium spp*., *Aspergillus spp*., and *Candida spp*. was used to validate assay performance. Specificity was assessed against non-target bacterial and human DNA, as well as no-template controls. **Results:** The integrated RPA-exo probe assay specifically detected fungal DNA from the three target genera without cross-reactivity to non-fungal DNA. The assay produced consistent and reproducible results, with a total turnaround time of under 25 minutes at a 39^{o}C, and minimal equipment requirements and sample processing. **Conclusion:** This integrated, one-pot RPA-exo probe assay provides a rapid and specific method for detecting fungal DNA in ocular infections. Its simplicity, speed, and high specificity make it a promising tool for early fungal diagnosis and as a point of care diagnostic tool, particularly in resource-constrained settings.

MI203: Isolation And Characterization Of Extracellular Vesicles From *Aspergillus flavus* Cultures Exposed To Stress

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Purpose: The role of extracellular vesicles (EVs) of the fungal pathogen in keratitis remains unclear. This study compares EVs from clinical and environmental *A. flavus* isolates exposed to cell wall and UV stress to identify stress induced alterations in the EV cargo and function. The goal is to understand how the role of EVs in the modulation of stress response. **Methods:** Two A. flavus isolates—ATCC 200026 (saprophyte) and MTCC 13369 (clinical)—were used. EVs were isolated using ultracentrifugation from cultures grown in minimal media with and without Congo red or from spores treated with UV for 60 seconds. Nanoparticle Tracking Analysis was used to determine EV size and concentration, and EV proteome cargo was identified using mass spectrometry. EV mediated transfer of stress response was studied subsequently. **Result:** Both A. flavus isolates showed reduced colony growth with increasing Congo red concentration. Congo red-treated EVs were more spherical and smaller in size. NTA showed similar EV concentrations across strains. Structural proteins were abundant in EVs. ATCC 200026 culture was more UV resistant compared to MTCC 13369. UV-treated EVs promoted colony formation in ATCC 200026 after 90 seconds of UV treatment. **Conclusion:** EVs from UV resistant clinical A. flavus isolates showed distinct proteomic profiles. The UV resistance property is transferred to UV sensitive cells by the extracellular vesicles.

MI204: Host Defense Peptide Exhibits Potent Antifungal Activity Against *Candida albicans*: A Promising Therapeutic For Fungal Keratitis

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Purpose: Fungal keratitis is a leading cause of blindness which is mainly caused by *Candida albicans*. It is included in the high priority pathogen list recently published by WHO and needs immediate intervention considering the currently available therapies are either limited or ineffective. Host Defense Peptides (HDP) are envisaged as potential antimicrobial candidates that can help us to combat drug resistant pathogen. **Methods:** *C. albicans* (ATCC and clinical isolate) was grown in sabouraud dextrose broth (SDB) for overnight. The antifungal activity, biofilm studies, time kill kinetics, binding, and membrane damage by the HDP was ascertained by using previously described methods from our lab (Roy *et al.,*2024). The transcriptome analysis was also done for *Candida* treated with peptide. **Results:** We found HDP was able to inhibit the growth of *C. albicans* by 50% at 6 hr which further increased to 90% inhibition by 24 hr and more than 80% inhibition of biofilm formation. The fungal membrane damage by the peptide was evident from scanning electron microscope images. HDP binds to the membrane and induced membrane damage which resulted in PI uptake and cell cycle arrest. The transcriptome data indicated 1601 upregulated and 741 downregulated genes in Candida treated with the peptide. **Conclusions:** Our study demonstrates that Host Defense Peptides (HDPs) effectively inhibit *Candida albicans* growth and biofilm formation, induce membrane disruption, and alter gene expression. These findings highlight HDPs as promising candidates for combating fungal infections, including those caused by drug-resistant strains.

Reference: Roy, Sanhita, Bharathi Bhogapurapu, Sreyanki Chandra, Karishma Biswas, Priyasha Mishra, Abhijit Ghosh, and Anirban Bhunia. "Host antimicrobial peptide S100A12 disrupts the fungal membrane by direct binding and inhibits growth and biofilm formation of Fusarium species."*Journal of Biological Chemistry*300, no. 3 (2024).

MI205: IGKV1-17: A Novel Diagnostic Biomarker For Tubercular Uveitis Infection

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Purpose: Diagnosing Tubercular Uveitis (TBU) is challenging due to overlapping features with non-infectious uveitis and limited sensitivity of existing diagnostic tools like TST, IGRA, PCR-methods, especially in paucibacillary vitreous samples. Moreover, it remains unclear whether TBU results from active *Mycobacterium tuberculosis* infection or hypersensitivity reaction to dead bacilli. Accurate diagnosis is essential before initiating anti-tubercular therapy, which carries significant risks. Hence, a highly sensitive alternative technique is required. A previous LC-MS-based proteomic study revealed overexpression of Ig kappa chain V–I region Gal (IGKV1-17) protein in vitreous of TBU patients. This study investigates IGKV1-17 protein's expression in vitreous of TBU patients compared to non-infectious uveitis and healthy individuals to evaluate its potential as a novel diagnostic biomarker. **Methods:** Vitreous samples from RT-PCR-confirmed TBU patients, healthy and non-infectious uveitis controls were analysed for IGKV1-17 protein expression using Western blotting and ELISA. Western blots were quantified with ImageJ software, while ELISA results were statistically evaluated using one-way ANOVA and ROC curve in GraphPad Prism software. **Results:** The study included 40 patients (26 males, 14 females; aged 18–79years). Western blotting showed overexpression of IGKV1-17 in TBU patients compared to controls. ELISA OD values ranged from 1.01–1.7 in TBU patients and 0.1–0.8 in healthy and non-infectious uveitis controls. One-way ANOVA revealed significance ($P < 0.0001$), while ROC curve identified OD cut-off of 1.049, with 100% sensitivity and specificity in distinguishing TBU from controls. **Conclusion:** Protein IGKV1-17 emerges as a potential novel diagnostic biomarker for distinguishing TBU from non-infectious uveitis and healthy individuals.

MI206: Peptide-Based Drug Conjugates For Enhanced Natamycin Delivery In The Treatment Of Fungal Keratitis

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Purpose: We aim to develop peptide-based drug delivery systems by conjugating natamycin with synthetic peptides VRF005 and VRF007 using amide bond. The conjugates are characterized and evaluated for cytotoxicity and cellular uptake in human corneal fibroblasts to target fungal keratitis effectively **Methods:** Synthetic peptides VRF005 and VRF007 were conjugated with the antifungal drug natamycin via carbodiimide chemistry using 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide (EDC) and N-hydroxysuccinimide (NHS) as coupling agents. The free peptides and the resulting peptide–natamycin conjugates were characterized using Fourier-transform infrared spectroscopy (FTIR), high-performance liquid chromatography (HPLC), electrospray ionization liquid chromatography–mass spectrometry (ESI-LC-MS), and circular dichroism (CD) spectroscopy to assess chemical integrity, purity, and secondary structure. Cytotoxicity was assessed on human corneal fibroblast cells using the MTT assay. Cellular peptide uptake studies were performed using fluorescent labeling and microscopy. **Results:** Conjugation of natamycin to VRF005 and VRF007 using EDC-NHS chemistry was confirmed by FTIR, HPLC, and ESI-LC-MS. Circular dichroism (CD) spectroscopy indicated that the peptides retained their secondary structure post-conjugation. Cytotoxicity assays demonstrated high biocompatibility, with over 80% cell viability observed for both free peptides and conjugates. Fluorescence microscopy revealed internalization of the peptide–natamycin conjugates and free peptides in corneal fibroblast cells. **Conclusion:** We have synthesized, characterised peptide natamycin drug conjugate for its biophysical and chemical stability. The conjugates were not toxic to stromal fibroblast cells and shown cellular uptake. The conjugates are yet to be tested in in vivo model.

MI207: MiRNA Profiling Reveals Novel Mechanistic Insights On The Role Of Neurotrophin Signaling In *Pseudomonas aeruginosa* Keratitis

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Purpose: Pseudomonas aeruginosa (PA) keratitis results in rapid and severe ulceration of the cornea leading to vision loss if untreated. The pathways associated with excessive inflammation leading to corneal tissue damage are poorly characterized. MicroRNAs may modulate critical pathways involved in inflammation and ulcer healing and thus contributing to disease pathogenesis. In this study, we propose to decipher the signalling pathways associated with poor outcomes of PA keratitis by analysing the miRNA expression profile. **Methods:** Ulcerated (n=3) and healthy corneal buttons were acquired after TPK surgery and from cadavers through Aravind International Eye Bank, Madurai respectively. Total RNA was isolated using Trizol method. Small RNA sequencing was performed by outsourcing and the raw data was analysed with in-house bioinformatics pipeline. Target prediction and pathway analysis were performed with differentially expressed (DE) miRNA. **Results:** Expression profiling identified 122 DE miRNAs in PA keratitis patients. Target prediction yielded 9,862 mRNAs, of which 4,539 were confirmed to be expressed in the cornea using in-house transcriptomic data. These were subsequently used for pathway analysis. Neurotrophin signalling emerged as one of the top significant KEGG pathway. Cytoscape analysis showed miR-181a-5p, miR-21-5p and miR-22 3p to regulate Neurotrophin signalling by targeting the genes CALM1, TRAF6, PRKCE, NTRK2 and MAPK14. Further, the altered expression of miR-22-3p was validated using qRT-PCR. **Conclusion:** Our study highlights Neurotrophin signalling as a key pathway involved in corneal ulcer pathology. Functional studies are warranted to decipher it's anti-inflammatory and cell survival effects in corneal epithelial cells which could be beneficial during ulcer healing.

MI208: A Cluster-Based Case Series Validating The RID-MYC Assay For Rapid Detection Of Fungal Endophthalmitis

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Purpose: To validate the diagnostic accuracy of the CRISPR-Cas12a-based RID-MyC assay for detecting fungal DNA in intraocular samples, using a unique clinical opportunity arising from a cluster outbreak of fungal endophthalmitis (FE) following cataract surgery. **Methods:** A cluster of postoperative FE cases caused by Candida spp. was reported from a private hospital, received at tertiary centers in Coimbatore and Madurai. A total of 17 intraocular samples from 10 patients were collected. All samples underwent culture, PCR, and RID MyC assay. Sanger sequencing was performed for molecular confirmation and species identification. **Results:** Culture and/or intraocular lens (IOL) analysis confirmed fungal growth - *Candida spp* in 12 samples, while five were culture-negative. PCR detected fungal DNA in 16/17 samples. RID-MyC was positive in all 17 samples (100%). Sanger sequencing of five samples confirmed the presence of *Candida spp*., supporting the molecular and clinical findings. RID-MyC showed higher sensitivity than both culture and PCR, detecting fungal DNA even in culture-negative and PCR-negative cases. The time to diagnosis using RID MyC ranged from 6 to 80 minutes, with a mean of 26 minutes, enabling same-day diagnosis. **Conclusion:** This outbreak scenario provided a rare opportunity to clinically validate the RID-MyC assay in the absence of a definitive gold standard. RID-MyC demonstrated high sensitivity and accuracy in detecting fungal pathogens, including in samples where conventional methods yielded negative or inconclusive results. Its rapid turnaround and reliability highlight its strong-potential as a frontline diagnostic tool for FE, particularly in settings with a high prevalence of culture-negative cases.

MI209: Comparative Host Transcriptome Analysis To Identify Core And Pathogen-Specific Immune Response In Fungal Keratitis

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Rationale: Fungal keratitis, mainly caused by *Fusarium* spp. and *Aspergillus flavus*, is a leading cause of corneal blindness in tropical regions. Despite treatments like natamycin and voriconazole, outcomes remain poor. Studies show pathogen-specific differences in host protein expression, such as mBD3, Factor H-like proteins, and zinc alpha-2 glycoprotein, highlighting their role in disease pathogenesis and outcomes. This study analyzes the transcriptomic profiles of *Fusarium* spp. and *A. flavus* keratitis to uncover pathogen-specific immune responses. **Methods:** We profiled mRNA expression of *Fusarium* spp. and *A. flavus-infected* human corneal tissues separately. High-throughput RNA sequencing was performed to examine differential gene expression in infected samples compared to healthy cadaver corneal samples. RNA was extracted and sequenced, to identify differentially expressed genes (DEGs). Validation of selected genes was performed using real-time quantitative PCR (RT-qPCR). **Results:** Differential expression and Venn analyses identified 744 DEGs in *A. flavus* and 645 in *Fusarium* spp.-infected samples, with 393 shared, 246 unique to *A. flavus*, and 250 to *Fusarium* spp. Enrichment of shared DEGs revealed activation of IL-17, TNF, and chemokine signaling pathways. Key IL-17 hub genes—*S100A7*, *S100A8*, *S100A9*, and *CXCL8* were validated by RT-qPCR. *Fusarium* spp.-specific DEGs (*C3*, *IL6*, *IL19*, *LRG1*) were enriched in acute inflammation and leukocyte adhesion pathways, while *A. flavus*-specific DEGs (*TREM2*, *APOE*) were linked to adaptive immunity. RT-qPCR confirmed their pathogen-specific relevance. **Conclusion:** This study reveals distinct transcriptomic profiles and both shared and pathogen-specific immune responses in *Fusarium* spp. and *A. flavus* keratitis. These findings offer insights for developing targeted diagnostics and therapies.

MI210: In-Vitro Study To Understand The Role Of Oxidative Stress In The Pathogenesis Of Mucormycosis

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Purpose: Mucormycosis is an angioinvasive, lethal fungal infection, caused mainly by *Rhizopus spp*. Fungal infection known to induce oxidative stress by activating intrinsic antioxidant signaling, which when goes unchecked can led to cellular damage. In this study, we aim to determine the role of oxidative stress to understand molecular mechanism of disease pathogenesis and host immune response in rhino-orbital-cerebral mucormycosis. **Methods:** Formalin fixed paraffin embedded (FFPE) exenterated tissue sections (5µm) with confirmed cases of mucormycosis were obtained from ophthalmic pathology department, LVPEI and immunostaining were performed by the standard method of immunohistochemistry. For *in-vitro* study, we have established the method of culturing primary human sino-nasal epithelial cells (SNECs). The cells were then grown and infected with *Rhizopus arrhizus* for different time point of infections and immunostaining were performed with antibodies specific for oxidative stress. **Results:** We have studied fourteen infected and eight control tissue and increased expression of several oxidative stress markers were observed in infected patient tissue sections compared to control. We have standardized and established the culture of primary human SNECs and checked the expression of epithelial cell markers. *Rhizopus arrhizus* infection in SNECs induced expression of various oxidative stress markers and helped in the activation of antioxidant signaling pathway. **Conclusions:** This result indicates oxidative stress may play an important role in the disease progression of Mucormycosis. This will help us to understand further molecular mechanism that governs the pathogenesis of this disease.

MI211: Antifungal Susceptibility Profile And Species Diversity Of Dematiaceous Fungi In Ocular Infections At A Tertiary Eye Care Center In Southern India

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Background/purpose: Ocular mycoses cause significant blindness worldwide. Since last decade, dematiaceous molds have become the third most common pathogens associated with ocular infections, with rising incidences of antifungal resistance. Currently, there is no defined breakpoints/cut-offs existing for antifungal susceptibility testing (AFST) of melanized molds. This study aimed to characterize the antifungal susceptibility profile of a large collection of dematiaceous fungi, focusing on rare species causing ocular infections. **Methods:** Antifungal susceptibility testing was performed for 151 melanized filamentous fungi, isolated between January 2022 through March 2025, following CLSI M38 guidelines. Isolates were identified by LPCB mount and ITS region sequencing when needed, and a maximum likelihood phylogenetic tree was constructed for 20 nonsporulating or rare dematiaceous molds. **Results:** Dematiaceous fungi were isolated predominantly from keratitis, and spanned multiple taxonomic orders, with *Pleosporales* (n=65, 43%) being most common. *Curvularia* spp. was the leading genus (n=26), followed by *Lasiodiplodia* spp.(n=18), *Bipolaris* spp.(n=13), *Scedosporium* spp.(n=12), *Colletotrichum* spp.(n=11) and *Exserohilum* spp.(n=9). Natamycin showed the least *in vitro* activity with the highest MIC_{50} / MIC_{90} of 8 µg/ml /32 µg/ml, while voriconazole had the lowest (0.12/4 µg/ml), followed by ketoconazole (0.25/4 µg/ml). Caspofungin also showed high MEC_{90} (16 µg/ml), and posaconazole, amphotericin B, and itraconazole had MIC_{90} values of 8 µg/ml. Notably, 4.6% of isolates were pan-resistant. *Sordariales* were susceptible to all antifungals, except natamycin (MIC_{90} ≥16 µg/mL), whereas *Microascales*, *Glomerellales*, *Botryosphaeriales*, and *Pleosporales* showed higher resistance. Phylogenetic analysis identified nine rare genera including *Podospora, Humicola, Canariomyces, Colletotrichum*, *Cladosporium, Macrophomina, Edenia* and *Corynespora sp.* **Conclusion:** Voriconazole showed the best *in vitro* activity against dematiaceous fungi, while natamycin was least effective. Combination antifungal therapy should be considered for the treatment of these dematiaceous fungi. Analysing AFST profiles from a comprehensive dataset can guide ophthalmologists in selecting the most appropriate antifungal or combination therapeutic strategy for effective management.

MI212: Distinct Corneal Gene Expression Profiles Associate With Differential Disease Trajectories In Fusarium And Aspergillus Keratitis

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Purpose: To test the hypothesis- pathogen specific host-response signatures underlie disease trajectories in fungal keratitis subtypes. **Methods:** Corneal tissue samples were collected from treatment-naïve patients with *Fusarium*, *Aspergillus flavus*, no-growth keratitis, and healthy cadaver donors. Patients were stratified by severity at presentation and treatment outcome into four groups: non severe healed, severe healed, non-severe not-healed, and severe not-healed. Three replicates of pooled RNA samples for each group were used for mRNA sequencing. Unsupervised hierarchical clustering and differential gene expression analyses were conducted relative to healthy controls and non-severe healed groups. Candidate gene panels for healing and non-healing were identified. Several candidates were validated using corneal epithelial cell line infection models with fungal spores or LPS stimulation. **Results:** Our study population revealed differential disease trajectories in fungal keratitis subtypes. Consistent with this, our host-transcriptomic analysis revealed *Fusarium* and *A. flavus* specific signatures of differential gene expression in the patient subgroups. Briefly, in Fusarium keratitis, healed and non-healed subgroups showed unique clusters of differential expression relative to the controls. In contrast, in *Aspergillus flavus* keratitis, common pool of genes were identified in healed and not healed samples, showing differential expression in opposite direction relative to the controls. Several selected candidate genes showed altered expression in corneal epithelial cell lines with Fusarium spore infection or LPS stimulation. **Conclusion:** Our data imply that distinct host-transcriptomic signatures might underlie different fungal keratitis outcomes, uncovering pathogen-specific healing and non-healing gene panels for early prediction of disease course.

PH213: A Quantitative Analysis Of Tensile Strength In Sutures For Ophthalmic Applications

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Purpose: This study investigates the tensile properties and fracture behavior of commonly used ophthalmic sutures, namely 6-0/7-0/8-0 braided Vicryl, 8-0/9-0/10-0 monofilament Nylon, and 9-0/10-0 monofilament Polypropylene, under straight, knotted, and looped configurations. **Methods**: Uniaxial tensile tests of sutures were conducted at a 30 mm/min strain rate with a 120 mm gauge length to study the mechanical properties. Fractography was carried out using SEM to characterize the fracture behavior at the failure surface of sutures. **Results:** The braided absorbable Vicryl sutures showed high stiffness, high break strength, and low elongation at break, whereas monofilament Nylon sutures had the lowest stiffness, low break strength, and high elongation at break in all tested configurations. The monofilament polypropylene suture exhibited moderate stiffness, break strength, and elongation at break. The SEM fractography of sutures revealed that the sutures had gradual fracture initiation followed by catastrophic failure under the uniaxial tensile load. **Conclusion:** The braided absorbable Vicryl sutures are preferred for stiffer tissue surgeries, requiring high stiffness and break strength. Nylon and Polypropylene monofilament sutures are preferred in soft tissue surgeries due to their smooth surface, lower stiffness, and high elongation.

Keywords: Ophthalmic sutures, mechanical testing, sutures, tensile strength, SEM fractography.

PH214: Developing A Nanoparticle Mediated Drug Delivery System To Treat Diabetic Retinopathy

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Purpose: Diabetic retinopathy (DR) affects over 126.6 million globally, with projections rising to 191 million by 2050. Current anti-VEGF therapies require frequent intravitreal injections, risking complications. We developed a liposome-based nanocarrier for sustained aflibercept delivery to reduce injection frequency and improve safety. **Methods:** Liposomes were prepared via lipid thin-film hydration, loaded with aflibercept, and encapsulation efficiency was quantified (Micro BCA Assay), Characterization using size/zeta potential (DLS), morphology (AFM, Cryo-TEM), and cytotoxicity (MTT assay on RPE cells). **Results:** Liposomes exhibited uniform spherical morphology (DLS: ~120 nm; zeta potential: −19 to −27 mV) and retained stability >2 months. Encapsulation efficiency reached 51%, with no cytotoxicity observed in RPE cells (viability >90% at 1000 µg/mL). AFM and Cryo-TEM confirmed structural integrity, correlating with DLS data. **Conclusion:** Our liposomal formulation demonstrates optimal size, stability, and drug loading capacity with excellent biocompatibility. This system holds promise for sustained intravitreal therapy in DR, potentially reducing treatment burden and complications associated with repeated injections.

PH215: Modulation Of Cannabinoid Receptor With Non-Prostaglandin Analogues For Altering Aqueous Humor Dynamics

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Aims / Purpose: Cannabinoid receptors (CB1 and CB2), which are present in the retina, ciliary body, iris, Schlemm's canal, and trabecular meshwork, have been explored for the treatment of glaucoma since 1970. This study explores the agonism of CB1 receptors in the iris-ciliary body via non-prostaglandin molecules to regulate the aqueous humor dynamics. **Methods:** In-silico molecular docking was performed to assess the binding affinity of various prostaglandin and non-prostaglandin analogues, including ricinoleic acid, to CB1 (6n4b) and CB2 (8GUR) receptors using Scigress modeling software version FJ2.6 (EU 3.1.8). The Gene expression for CB1 receptor was analysed in rabbit cornea, ciliary body, and SIRC 1 cell line by conventional PCR. The receptor interaction with ricinoleic acid was assessed in SIRC1 cell lines using the cAMP assay. **Results:** RA showed a stronger interaction with CB1 and CB2, with lower energy (- 66.4443 and -107.394 kcal/mol) compared to its endogenous ligand anandamide (control) (-59.0433 and -70.694 kcal/mol), respectively. The gene expression studies confirmed the presence of the CB1 receptors in the cornea, ciliary body, and SIRC 1 cell line. The interaction studies revealed dose-responsive interaction of non-prostaglandin analogues with the CB1 receptor. **Conclusions:** The modulation of CB1 receptors for regulating the aqueous humor dynamics may present a suitable/safer alternative to the existing prostanoid receptor based prostaglandin analogues therapy.

PH216: Investigating The Degradation Mechanisms Of Ophthalmic Antibiotics

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Purpose: Antibiotics such as Ceftazidime, Vancomycin, Cefazolin, and Colistin are compounded extemporaneously to treat bacterial keratitis. These drugs are prone to instability as they have several functional groups that can undergo hydrolysis, oxidation, or photolytic degradation. Hence, to develop a stable formulation, it is important to identify the degradation pathways of these drugs. Therefore, a stability-indicating analytical method was developed, and forced degradation studies were performed to investigate the degradation mechanism for each of these antibiotics. **Methods:** Stability indicating reverse phase HPLC methods for antibiotics were developed using C18 columns, phosphate or acetate buffer as the aqueous phase, and acetonitrile as the organic phase. The developed methods were validated according to the ICH guidelines Q2(R2) for linearity, accuracy, precision, and system suitability for the drug quantification and degradant products. The drugs were subjected to forced degradation under different conditions (acidic, alkaline, oxidative, thermal, and photodegradation) to evaluate the primary degradation pathways. **Results:** The developed HPLC methods could detect the degradant products and drug molecules. Forced degradation studies showed that all the drugs were highly susceptible to hydrolytic degradation, with primary degradation occurring through alkaline hydrolysis. The percentage of drug degraded in alkaline conditions was 100%, 76.2%, 65.7%, and 95.2% for ceftazidime, vancomycin, cefazolin, and colistin, respectively. **Conclusion:** The developed HPLC methods were validated to characterize the major degradation pathways for the drugs, which occurred primarily through hydrolysis. These studies are essential for formulation development and to provide insights into the chemical stability of the molecules.

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PH217: Preclinical Efficacy Evaluation Of Subconjunctival Corticosteroid-sparing Agent In Lipopolysaccharide-Induced Acute Posterior Segment Inflammation Model

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Purpose: Posterior uveitis is a sight-threatening condition typically treated with corticosteroids, though their use is limited due to their significant side effects. Methotrexate is a commonly used off-label corticosteroid-sparing agent to treat posterior uveitis, but systemic toxicity, invasiveness, and frequent intravitreal injections remain the major drawbacks. To address these limitations, this study aimed to evaluate the safety and efficacy of methotrexate administered via a minimally invasive subconjunctival route in rabbits, offering a potential alternative delivery route. **Methods:** The New Zealand white rabbits were used to assess the safety and efficacy of subconjunctival methotrexate. The safety assessment was done using different doses (400 to 3200 µg), and the injected eyes were thoroughly investigated using imaging techniques and histology. The therapeutic efficacy of subconjunctival methotrexate was evaluated in the lipopolysaccharide (LPS)-induced acute posterior uveitis rabbit model. Vitreous protein estimation and retinal cytokine expression were performed to assess the therapeutic benefits of the subconjunctival route. **Results:** In safety studies, upon imaging and histology examination, no obvious changes were observed in the anterior and posterior segments of the eye. Subconjunctival methotrexate reduced the vitreous protein content by 1.8-fold and retinal cytokine (IL-6) levels by 5.8-folds compared to the diseased group (only LPS). **Conclusions:** Methotrexate injected via the subconjunctival route was found to be safe and efficacious in the present study. However, further investigations are required to assess the therapeutic efficacy in the chronic preclinical posterior uveitis model.

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PH218: Role Of Curcumin On Microglial Modulation And Its Impact On Photoreceptor Cell Death

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Purpose: Retinal diseases involve chronic inflammation and photoreceptor degeneration, driven by overactivated microglia releasing pro-inflammatory and neurotoxic factors. Curcumin has shown anti-inflammatory potential, whereas its impact on microglial activation and photoreceptor damage remains unclear. This study aims to evaluate curcumin's potential to modulate microglial activation and neurotoxicity in photoreceptor cells. **Methods:** The safety of curcumin on N9 microglial cells and 661W photoreceptor cells was assessed using the 3-(4,5 dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay. LPS-stimulated N9 microglial cells were treated with 5 μM curcumin for 24 h. Pro-inflammatory (IL1β, TNF-α, iNOS) and microglial activation (CD86, CSF1, CSF1R) genes expression was determined by RT-qPCR, and nitric oxide (NO) secretion was assessed using the Griess assay. Safety and neurotoxicity were determined in 661W photoreceptor cells cultured with microglia-conditioned medium (MCM) in the absence and presence of curcumin supplementation. **Results:** Treatment of LPS-activated N9 microglia with curcumin significantly decreased the expression of the pro-inflammatory and microglial activation markers, CD86 (9-10 fold), IL1β (2 fold), TNF-α (1-2 folds), CSF1 (7-8 folds), CSF1R (2-3 folds), and iNOS (4-5 folds). Curcumin has also reduced the production of NO and decreased microglia-induced neurotoxicity on 661W photoreceptor cells. **Conclusions:** Curcumin potentially counter-regulated microglial activation and photoreceptor damage, suggesting its therapeutic potential against retinal inflammation and degeneration. Further studies are needed to elucidate the role of curcumin in regulating the complex interplay between the microglia, photoreceptors, and their downstream molecular targets involved in retinal degeneration.

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PH219: Nature-Inspired Surfaces To Disrupt Bacterial Biofilms

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Purpose: Biofilms associated with bacterial infections make it challenging to treat the condition. Natural topographical features on petal and leaves surfaces possess nano and micro-structures demonstrating antibacterial properties. We hypothesize, mimicking these patterns on polymeric patches may disrupt the bacterial biofilms. Therefore, this study focuses on fabricating nature-inspired polymeric patches to evaluate their impact on biofilm disruption, providing a novel strategy for the treatment. **Methods:** Polydimethylsiloxane molds of rose petal (RP), lotus leaf (LL), taro leaf (TL) were used to fabricate patterned polymeric patches with the combination of xanthan-gum, κ-carrageenan and poly-vinyl alcohol. The efficacy of the patterned patch was evaluated on *Staphylococcus aureus* biofilm using crystal-violet and XTT (2, 3-bis-(2-methoxy-4-nitro-5-sulfophenyl)-2H-tetrazolium-5-carboxanilide) assays. The Live/Dead assay and Scanning Electron Microscope (SEM) were performed to understand the impact of nature inspired structures on biofilm disruption. **Results:** Percentage bacterial survival assessed using Crystal violet assay showed decrease in biofilms treated with RP (38.47%), LL (68.04%), TL (60.76%) compared with plain patches (89.03%). XTT assay showed significant reduction in bacterial viability with RP (27.10%), LL (29.76%) and TL (30%) compared to plain patches (62.98%). Decrease in biofilm growth was also observed by Live/Dead assay and SEM after application of patterned patch compared to the plain patches. **Conclusion:** Nature-inspired patches display an enhanced biofilm disruption property compared to plain patches and thus could be a promising drug delivery platform to combat biofilms associated with corneal infections. Further in-vivo studies need to be performed to evaluate the efficacy of patterned patches loaded with antimicrobials in treating corneal infections.

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PH220: Minimally Invasive Subconjunctival Depot For Prolonged Anti-VEGF Therapy To Treat Posterior Segment Diseases

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Purpose: Chronic posterior segment ocular diseases (wet age-related macular degeneration and diabetic retinopathy) often require frequent intravitreal injections of anti-VEGFs. An alternative is a minimally invasive subconjunctival injection, but it faces rapid drug clearance. A light-responsive hydrogel (LRH), UV crosslinked in situ gel, could form a depot in the subconjunctival space, reduces clearance and enabling transscleral permeation of Bevacizumab (BVZ). **Methods:** The light-responsive methacrylated alginate (AlgMA) was synthesized and characterized. BVZ-loaded LRH (BVZ-LRH) was formulated to evaluate in vitro release kinetics, swelling behavior, and permeation across porcine sclera. In vivo residence time was examined using indocyanine green (ICG) in a rat model, and safety was evaluated through histological analysis. **Results:** AlgMA was confirmed by Proton-Nuclear Magnetic Resonance (1H-NMR) and Fourier Transform Infrared spectroscopy (FTIR). UV crosslinking (365 nm) resulted in the prolonged in vitro BVZ release (>7 days) and permeation across the sclera. Release followed Korsmeyer-Peppas kinetics, supported by the swelling behaviour of the hydrogel. The ongoing NIR-imaging showed that the hydrogel depot resides in the subconjunctival space for >7 days. The hydrogel was found to be safe in retinal pigment epithelial cells (>75% viability), and further in vivo safety was confirmed by histology. **Conclusions:** AlgMA-based LRH system shows promise as a minimally invasive platform for prolonged drug delivery via the subconjunctival route. It enhances residence time and biocompatibility, potentially reducing injection frequency for chronic posterior segment diseases. Further, studies are ongoing for in vitro drug release and in vivo residence studies.

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PH221: In Silico Simulation Of Hydrolytic Degradation Mechanisms Using Density Functional Theory And Transition State Theory

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Purpose: Antibiotics like cephalosporins and glycopeptides, are commonly used in off-label preparations to treat ophthalmic infections. However, they are susceptible to degradation, leading to a shorter shelf life. Lack of adequate knowledge formed the basis for this study to delineate the degradation mechanism of these compounds in-silico to enable us to improve their stability. **Methods:** Cefazolin, Ceftazidime, Vancomycin, and Colistin were selected as model drugs to simulate the degradation reaction using the Schrodinger Material Science Suite (2023-24). Our previous studies show alkaline hydrolysis as the primary degradation pathway for these drugs. Multiple hydrolysis reactions were simulated to understand drug interaction with water. The intermediates of the reactions were obtained using transition state theory, and their relative free energies (ΔG) were calculated using density functional theory. **Results:** The energy diagrams of the hydrolysis reactions were obtained and compared. Hydrolysis of the β-lactam ring in Cefazolin (followed by lactone ring formation) (ΔG=6.24 kcal/mol) and Ceftazidime (ΔG=164.97 kcal/mol) was confirmed to have lower ΔG values compared to other reactions. In Vancomycin, succinimide intermediate-mediated hydrolysis had a lower ΔG (ΔG=40.96 kcal/mol) value relative to that with direct hydrolysis. Colistin underwent a side chain cleavage in alkaline conditions, leading to ring opening (ΔG=34.14 kcal/mol). **Conclusion:** Major degradants of the antibiotics were identified by comparing the reaction energy of possible pathways. Further, forced degradation studies are needed to validate the simulated data. These findings provide crucial insights for developing stable formulations for these drugs.

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PH222: Novel Reverse Phase High Performance Liquid Chromatography (RP-HPLC) Method For Simultaneous Estimation Of Ciprofloxacin And Dexamethasone

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Purpose: Ciprofloxacin (CIP) and Dexamethasone (DEX) are frequently co-formulated in ophthalmic preparations for antimicrobial and anti-inflammatory effects. Given the increasing use of combination ophthalmic preparations, a reliable analytical method is necessary for the simultaneous estimation of both drugs enabling development of formulaton. **Method:** An RP-HPLC method was developed using an Inertsil ODS C18 column (5µm, 250 x 4.6mm). The mobile phase was composed of acetonitrile and phosphate buffer (pH 3.05) in a 60:40 ratio with a flow rate of 0.8 mL/min. Detection was carried out using a PDA detector at wavelengths 242 nm (CIP) and 276 nm (DEX). The method was validated in accordance with ICH Q2(R2) guidelines for parameters such as linearity, accuracy, precision, specificity, limit of detection (LOD), and limit of quantitation (LOQ). **Results:** The developed method successfully distinguished CIP and DEX, with retention times of 5.8 minutes and 2.8 minutes, respectively. The calibration curve was plotted in the concentration range of 0.558-75 µg/ml (CIP) and 0.195-25 µg/ml (DEX) with correlation coefficients of R^2>0.999. The method demonstrated acceptable precision, with relative standard deviation (RSD) values less than 2%, in accordance with the limits specified by ICH Q2(R2) guidelines.The method sensitivity was validated through the LOD and LOQ values for CIP and DEX, which were 0.059 and 0.089 µg/ml and 0.156 and 0.271 µg/ml, respectively. **Conclusions:** A sensitive, fast and robust RP-HPLC method was developed and validated for routine analysis of ciprofloxacin and dexamethasone in ophthalmic formulations.

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PH223: Development Of Bilayer Polymeric Patches Loaded With Natamycin And Voriconazole For Effective Treatment Of Fungal Keratitis

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Purpose: Fungal keratitis has increasing antifungal resistance each year against the current treatment. Conventional eye drops face limitations like frequent administration and overexposure of drug, leading to antimicrobial resistance. This study proposes formulating a dual-drug bilayer patch to decrease drug overexposure and harness the synergistic effect by combining Natamycin and Voriconazole (Nat-Vori). **Method:** The bilayer patches were prepared by inclusion complex of Nat-Vori using Hydroxypropyl-β-Cyclodextrins with polymer composition of chitosan, Hydroxypropyl-methyl-cellulose, and sodium carboxymethyl-cellulose. The developed patches were characterized for morphological, wetting, and release properties. **Result:** The drug to Hydroxypropyl-β-Cyclodextrins ratios were optimized by phase solubility study, yielding stability constants 7452.11 M-1 and 272.20 M-1 for Natamycin and Voriconazole, respectively. Atomic force microscopy showed a uniform surface on the chitosan layer and a rough surface in the HPMC layer. Thermal evaluations confirmed the stabilization of drugs in the bilayer patch. The contact angle was lower for the chitosan side (36.31 ± 5.00°) as compared to the HPMC side (44.88 ± 6.48°). Further, the in vitro drug release studies showed more than 90% of Natamycin and 75% of Voriconazole released from the patch within 4 hours. **Conclusion:** The dual-drug bilayer patch could be a potential treatment option for treating fungal keratitis by providing a simultaneous release of Natamycin and Voriconazole. In addition, the decreased overexposure due to improved corneal residence and its synergistic effect can lead to a potential reduction in resistance development. Further studies are required to evaluate the efficacy and potential of the formulation.

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PH224: Topotecan Microneedle Scleral Patch For Retinoblastoma Treatment

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Aim & objective: This study aims to design, fabricate, and evaluate the pharmacokinetic properties of topotecan loaded microneedle scleral patch (MSP) in rabbit ocular model. **Methods:** MSP containing 90 conical microneedles in a 15*6 array format was designed using AutoCAD. The 3D printed master mold was used to prepare polydimethyl siloxane (PDMS) production mold. High molecular weight sodium hyaluronate was used to fabricate MSP. The composition used for casting microneedles includes 3% w/w topotecan and 7% w/w sodium hyaluronate. MSP was characterized by using stereomicroscope and SEM. The compression and insertion force of MSP were determined. The insertion depth of MSP within excised goat sclera was analyzed. *In vitro* dissolution study and drug content analysis of MSP were performed. *Ex vivo* and *in vivo* biodistribution study of topotecan-MSP was performed in goat and rabbit eye models, respectively. **Results:** The microneedle dimensions were found to be 548±3.7, 336±7.5, and 18.48 µm for length, base width, and tip diameter, respectively. The compression and insertion force of the topotecan MSP was found to be 71±5.6 N and 1.7±0.3 N, respectively. The insertion depth of the topotecan-MSP within the excised goat sclera was found to be 225 µm. The amount of topotecan loaded in microneedles and baseplate was found to be 103±9.6 and 17.6±4.0 µg, respectively. The microneedles were found to dissolve within 25 s in PBS. The flux of topotecan delivered using MSP was significantly ($P<0.05$) greater (4.8±0.55 µg/cm2/h) compared with topotecan solution (1.5±0.81 µg/cm2/h). E*x vivo* biodistribution study showed 0.41 µg/g topotecan present in the retina-choroid after 1 h application. The topotecan distribution in the retina-choroid complex was greatest 1 h after application of MSP (2.75±2 µg/g) and intravitreal injection (10.33±5.02 µg/g). The microneedles were completely dissolved within 5-7 min with an unchanged retinal fundus appearance. **Conclusion:** Topotecan-loaded MSP offers a promising minimally invasive alternative drug delivery route for treating retinoblastoma.

Keywords: Microneedle scleral patch, Retinoblastoma, Targeted drug delivery.

PH225: Investigating The Role Of Temperature In The Physicochemical Characterization Of Ocular Films

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Purpose: Polymeric films have been widely used in ocular drug delivery due to their mucoadhesive nature and sustained drug release. The process parameters for film preparation define its physicochemical, mechanical, and release properties, among which the drying process is one of the critical parameters. In the current study, different drying temperatures were used to prepare polymeric films, and their impact on physicochemical and mechanical properties was evaluated. **Methods:** The polymeric films consisting of 2% Chitosan and Amphotericin (Model drug) were developed using the solvent casting method and dried at different temperature conditions (Freeze drying (FD), Room temperature (RT), 37°C, and 60°C). The films were evaluated for their morphology, moisture content, tensile strength, and drug release profile. **Results:** The morphology results show a rough mesh-like surface in FD films, whereas other films show a smooth and uniform surface. The moisture content was higher (29.9 ± 2.05 %) in RT dried films and lower (16.66 ± 4.58 %) in 60°C dried films. Similarly, the films dried at 60°C show higher tensile strength and lower % elongation, whereas those dried at RT show higher % elongation and lower tensile strength. An in vitro drug release study shows that films dried at a higher temperature release the drug faster than films dried at a lower temperature. **Conclusions:** The current work highlights that variations in drying temperature influence moisture retention, tensile properties, and release profiles, ultimately affecting film stability and functionality. However, the film properties vary based on the polymer and drug selection; therefore, they should be studied specifically.

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PH226: Nano Meets Nature: Natural Bioflavonoid Based Eye Drops To Treat Ocular Pain

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Purpose: Ocular pain is the common underlying factor in various conditions like injury, chronic diseases and post-surgical complications. The current therapies for managing ocular pain (non-steroidal anti-inflammatory drugs and corticosteroids) have limited efficacy and unintended adverse effects. Targeting Transient Receptor Potential Vanilloid 1 (TRPV1) expressed on the cornea has been reported to alleviate pain. Our previous work predicted hesperidin as a potential TRPV1 modulating drug using machine learning. In this study, we have developed hesperidin nanomicelles and evaluated its potential as a topical therapy for ocular pain. **Methods:** Computer simulations were performed to understand the interaction of hesperidin with TRPV1. Hesperidin nanomicelles were developed using thin film hydration and characterised for their size, entrapment, osmolality, in vitro release, and stability. Further, the safety, efficacy, and pharmacokinetics of hesperidin nanomicelles were evaluated in pre-clinical models. **Results:** Hesperidin displayed a stronger binding affinity (1.48-fold) to TRPV1 compared to the reported antagonist. The hesperidin nanomicelles had a particle size of 67±1.9 nm, entrapment efficiency of 93.09±0.97% and osmolality of 302 mOsm/kg. The developed formulation exhibited first-order release for 48 hours and was stable up to 60 days. The formulation was biocompatible with human corneal epithelial cells. The in vivo evaluation indicated that the developed formulation was safe, bioavailable and effectively reduced ocular pain. **Conclusions:** Hesperidin was repurposed as a natural TRPV1 modulating drug and was delivered efficiently to the cornea using nanomicelles to treat ocular pain. However, further studies are required to understand the mechanism of action of hesperidin in modulating TRPV1.

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PH227: Assessment Of Dipyridamole Eye Drops For Corneal Neovascularization: Pharmacokinetics And Therapeutic Outcomes

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Purpose: Corneal neovascularization (CNV) compromises corneal transparency and vision, with current treatments limited by cost, invasiveness, and safety concerns. Dipyridamole (DYP), a phosphodiesterase inhibitor with anti-angiogenic and anti fibrotic properties, offers therapeutic potential but suffers from poor solubility and bioavailability. This study aimed to develop and evaluate a novel topical DYP formulation for CNV treatment. **Method:** A topical DYP formulation was prepared using Cremophor EL (2%) as a solubilizer and hydroxypropyl methylcellulose (0.45%) to enhance corneal residence time. Physicochemical properties, pharmacokinetics, therapeutic efficacy, and ocular safety were assessed. Pharmacokinetic profiling was conducted in rabbits, while therapeutic efficacy was evaluated in a rat model of alkali burn-induced CNV. Bevacizumab (BVZ) served as a reference control. **Result:** The high-dose DYP formulation (0.08%) achieved a 2.47-fold higher AUC in aqueous humor compared to the low-dose (0.008%). In the rat CNV model, the high dose DYP reduced neovascularization by 79.15%, closely approximating BVZ (87.8%). Both DYP concentrations significantly reduced corneal scar tissue, indicating anti-fibrotic activity. No ocular irritation or structural abnormalities were observed, confirming the formulation's safety. **Conclusion:** Topical DYP demonstrated robust anti-angiogenic and anti-fibrotic efficacy, comparable to BVZ, while offering a cost-effective and non-invasive alternative. The formulation's favourable pharmacokinetics and safety profile support its potential as a treatment for CNV and other anterior segment pathologies. Further clinical investigations are warranted to establish its translational value in ophthalmic care.

CL229: The Effectiveness Of Active Office Based Anti-Suppression Therapy For Amblyopia Among Adults- A Retrospective Observation

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Purpose: To understand the effectiveness of active office based anti-suppression vision therapy in improving visual functions among young adults with amblyopia. **Methods:** A retrospective data of patients who visited amblyopia clinic in a tertiary eye care center was reviewed from Jan 2019 to Dec 2023. Patient's age ranging from 18 35 years, diagnosed with amblyopia and had undergone ten sessions of active anti suppression therapy at clinic were included. Any previous history of surgical squint correction, retinal surgery, intra ocular lens implantation, retinal pathology or neurological problem were excluded from data. **Results:** A total of 23 adults were included in the study with mean age of 22 (±4) years; out of which 16 (69%) were male. Among 23 participants, anisometropic amblyopia was the most common (14 cases, 60%), followed by strabismic amblyopia (7 cases, 30%). Deprivational and mixed amblyopia were observed in one case each (4%). The mean best-corrected distance visual acuity in the amblyopic eye was 0.66 (±0.25) logMAR pre-therapy and 0.58 (±0.25) logMAR post-therapy. Although the difference was not statistically significant, a clinically meaningful improvement of one line was observed. Low contrast visual acuity and single optotype acuity showed statistically significant improvements. The mean low-contrast acuity improved from 0.69 (±0.21) to 0.62 (±0.22) logMAR, and single optotype acuity improved from 0.52 (±0.24) to 0.43 (±0.21) logMAR (paired t-test, $P < 0.01$). **Conclusion:** Office based active anti-suppression therapy can effectively enhance the visual functions among adults with amblyopia.

CL230: Evaluate The Ocular Surface Health In Patients Using Corneal And Semi Scleral Contact Lenses

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Introduction: Corneal and semi-scleral contact lenses are increasingly been consider as the inceptive correction for the patients with irregular corneal astigmatism especially in cases of keratoconus. In the study, patient report higher level of comfort and visual satisfaction with semi scleral contact lenses. **Objective:** This study aims to compare the ocular surface health in patients using corneal and semi scleral contact lenses. **Methods**: Prospective observational study includes patients with irregular corneal astigmatism starting corneal and semi scleral contact lenses. All these patients had mean corneal curvature between 47D to 55D and ocular surface health assessed before and after wearing contact lenses for 6 months. **Results**: Forty eyes of 33 keratoconus patients were included in the study. Semi scleral lenses dispensed in 20 eyes and rest 20 eyes with corneal lenses. Mean Schirmer'1 value were 7 sec (±1.6 sec) and 10 sec (±1.9 sec), mean LLT 34nm (±7nm) and 55 (±11nm), mean NIBUT 5.5 sec (±1.2 sec) and 8.6sec (±1.5 sec) in corneal and semi scleral contact lenses respectively at 6 month. **Conclusion**: Patients using semi scleral contact lenses were more satisfied in terms of quality of life and overall visual performance as compared corneal contact lenses. The visual acuity achieved from these lenses were comparable but outcomes measures of ocular surface health were better in semi scleral lenses.

CL231: Does Kahook Dual Blade Excisional Goniotectomy Change Environmental Carbon Emission In Glaucoma Patients On Topical Iop Lowering Medications?

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Purpose: To assess the change in carbon footprint due to low-density polyethylene (LDPE) eye drop bottle after Kahook dual blade (KDB) excisional goniotectomy with phacoemulsification surgery in patients with glaucoma. **Methods:** A retrospective study of glaucoma patients >18 years old who underwent KDB with phacoemulsification and had a pre and post follow-up of 1 year were included. Demographic, clinical, surgical data was recorded. Carbon emission attributable to glaucoma medication bottles was estimated by converting the weight of used eye drop bottles to kg CO2eq using a carbon footprint calculator. The change in carbon footprint after surgery was assessed. **Results:** Thirty-five glaucoma patients (63.1±15.4 years) who underwent KDB excisional goniotectomy along with phacoemulsification surgery were included. Mean IOP prior to surgery was 17.8±5.2 mmHg. Mean IOP 1-year pre surgery was 18.8±6.7 mmHg which significantly decreased to 14.7±3.6 mmHg ($p = 0.002$) 1 year post surgery. Mean total number of bottle 1 year preoperatively and postoperatively was 19±8 and 5±7 per person respectively. Total weight of eye drop bottles used decreased from 86.55±38.87 grams preoperatively to 24.33±33.21 grams postoperatively over 1 year with a 71.9% reduction ($p < 0.001$). Carbon footprint due to decrease in LDPE bottle use (estimating a footprint of 5.74 kg CO_2e/kg) changed from 0.496±0.22 kg of CO2e/kg to 0.137±0.19 kg of Co2e/kg with a significant 72 % reduction ($p < 0.001$). **Conclusion:** A significant reduction in carbon footprint was noted after one year due to reduced AGM use post KDB excisional goniotectomy.

CL232: Characterizing The Macrophage Like Cells In Glaucoma Using Optical Coherence Tomography Angiography

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Purpose: Activation and migration of the macrophage-like cells (MLCs) is the earliest sign of neurodegeneration. This study assessed the MLCs on the retinal surface and quantitatively correlated them with other neurodegenerative markers in early and advanced glaucoma. **Methods:** This prospective case-control study enrolled 303 eyes (118 early glaucoma, 85 advanced glaucoma, 100 controls). A 3-µm slab above the vitreoretinal interface was manually segmented in en face 6*6 mm macular scan of optical coherence tomography angiography (OCTA). Using a semiautomated method, binarization and quantification of MLCs were done and compared among groups. Correlation was done with ganglion cell layer (GCC), nerve fiber layer (RNFL), foveal thickness (CSFT), corneal thickness (CCT). **Results:** MLC activation resulting in increased density was seen in early glaucoma with further increase in advanced glaucoma. (Controls 14.12±3.07cells/mm2, early glaucoma 19.35±2.08cells/mm2, advanced glaucoma 29.35±3.33cells/mm2, p=0.000). There was a significant positive correlation between MLC density and GCC, RNFL and CSFT (p=0.000). MLCs were negatively correlated with CCT (p=0.000). **Conclusion:** OCTA is a simple and noninvasive technique to demonstrate MLC activation in early and advanced glaucoma. MLCs show excellent correlation with GCC, RNFL and HVF indicating the potential as a biomarker for glaucomatous progression. Further studies are required to understand the origin, function of theses MLCs in glaucoma.

CL233: Role Of Macular Thickness And Macular Vessel Density And Foveal Avascular Zone In Glaucoma Patients With Focal Disc Damage

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Purpose: To analyze role of OCT angiography-based parameter and macular thickness in glaucoma patients with focal disc damage. **Method:** In this observational study 46 eyes of 27 patients were included. Primary glaucoma with focal disc damage (32 eyes) and 14 eyes with glaucoma suspect were included. The patients were divided into two groups with those with central visual field defect versus (group 1) those without the central field defect (group 2). Both groups were compared for macula-based parameters based on macula thickness measured with the macula OCT and macula OCT angiography 6 mm scan-based vessel density and foveal avascular zone (FAZ) parameters. **Results:** The mean age included was 54 ±1.7 years. In group one 22 eyes and group two 24 eyes were included. Mean vascular density (%) for total macula region (15.49 vs 16.6 p=0.02) and outer macular region (15.54 vs 16.79 p = 0.008) was less in group 1. Mean macula thickness was reduced in patients with group 1(central inferior region <0.001 central temporal region <0.001, inferior region0.003, nasal 0.004 and temporal region 0.002). FAZ did not show any difference between both the groups (Area mm^2. 023 vs 0.24 p=0.79, perimeter mm 2.08 vs.2.04 p=0.8). The area and perimeter of FAZ showed negative correlation with the central macular thickness for both groups (p<0.01) . **Conclusion:** Patients with central visual field loss with focal disc damage showed reduced macular thickness and macular vessel density while FAZ parameters did not show statistically significant difference. Longitudinal prospective analysis may provide the answer.

CL234: Linking Retinal Structure And Visual Function In Glaucoma Using Optical-Coherence Tomography And Eye-Movement Perimetry

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Purpose: To characterize the correlation between structural and reaction-time changes in glaucoma. **Methods:** In this prospective cross-sectional study, participants underwent Cirrus Spectral Domain Optical-Coherence Tomography to measure Ganglion Cell Inner Plexiform Layer (GCIPL) and Retinal Nerve Fiber Layer (RNFL) thickness in both eyes. Functional assessment across the visual field included saccadic reaction time (SRT) using Eye-Movement Perimetry and mean deviation (MD) using Standard Automated Perimetry. Structure–function correlations were analyzed using linear regression and linear mixed effects modelling (LMEM). **Results:** Forty-two participants were categorized as healthy controls (n=16), perimetric glaucoma (n=14), and glaucoma-suspects (n=12); mean age was 51±13 years (79% male). Linear regression of SRT with GCIPL and RNFL thickness, pooled across all participants and eyes, explained 20–30% of the variance, indicating limited predictive power but suggesting faster SRT with thicker GCIPL and RNFL. LMEM showed a significant effect of GCIPL (p=0.008) but not RNFL (p=0.06) on SRT. Regression of MD with GCIPL and RNFL thickness explained 30–40% of the variance, indicating moderate predictive value. Both GCIPL (p=0.0003) and RNFL (p=5×10^{-6}) thickness showed a significant effect on MD according to LMEM. **Conclusions:** Retinal GCIPL and RNFL thickness are modestly to moderately correlated with functional visual outcomes in glaucoma. While structural parameters explain only a limited proportion of the variance in SRT and MD, the significant association between retinal thickness and functional performance highlights its value as a biomarker. The structure-function link based on retinal thickness remains incomplete, necessitating further research to identify additional structural contributors to visual-function decline.

CL235: Zone-Wise Ischemic Profiling In Diabetic Retinopathy Using RVBA And NPI Metrics In UWF-FA With Explainable Deep Learning Classification

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Purpose: This study aimed to explore zone-specific ischemic patterns in diabetic retinopathy (DR) by quantifying Retinal Vascular Bed Area (RVBA) and Non-Perfusion Index (NPI) UWF-FA and to develop an explainable deep learning (DL) model to classify DR severity based on these metrics. **Methods:** A pilot dataset of 45 eyes (15 each with moderate NPDR, severe NPDR, and PDR) was analyzed. RVBA and NPI were quantified globally and within anatomical zones defined by the ETDRS 7-field overlay: the ETDRS-central zone and ETDRS-peripheral zone, using validated ImageJ macros. Statistical comparisons of global and zone-wise metrics across DR severity stages were performed. A feedforward neural network was trained using zone-wise RVBA and NPI values as input features to classify DR stage. SHAP analysis was used to interpret feature importance and model explainability. **Results:** The mean age of participants was 57.2 ± 6.1 years, with 62% being male. Both RVBA and NPI differed significantly across DR stages ($p < 0.0001$). RVBA increased with severity, particularly in the ETDRS- central zone, while NPI was significantly elevated in the ETDRS-peripheral zone in severe NPDR and PDR. The DL model achieved 82.2% of classification accuracy. SHAP analysis revealed NPI in the peripheral zone as the dominant feature especially in PDR, followed by RVBA in the central zone. **Conclusions:** This pilot study suggests that zone-wise ischemic biomarkers from UWF-FA reveal distinct patterns aligned with DR severity. Peripheral ischemia is a dominant feature in advanced disease. An interpretable DL framework using RVBA and NPI may support granular DR staging and tailored clinical decision-making.

CL236: A Deep Learning Approach For Classification Of Systemic And Ocular Diseases Using Auxiliary Classifier Generative Adversarial Networks

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Purpose: This study explores the use of Auxiliary classifier Generative Adversarial Networks (AC-GANs) to develop a single framework capable of effectively classifying various ocular and systemic diseases using retinal images. **Methods:** Five publicly available datasets (High-Resolution Fundus (HRF) dataset, Drishti-GS, Eye Disease Classification, 1000 Fundus Images dataset, and AI- generated dataset) and dataset collected retrospectively from Sankara Nethralaya were used. Datasets were grouped into systemic diseases (diabetes mellitus, hypercholesterolemia, and ischemic heart disease) and ocular diseases (diabetic retinopathy and glaucoma). First image augmentation was performed, then the dataset was systematically partitioned into training (70%), validation (10%), and test (20%) subsets using stratified sampling. Finally utilizing an AC-GAN) for multi-class classification. **Results:** In the 2-class classification, we differentiate between ‘normal’ and ‘glaucoma’, and the classification accuracies achieved were 98.20%, 96.21%, 97.80%, 95.20% and 87.82% on HRF, Drishti-GS, AI generated dataset, 1000 Fundus Image dataset and Eye Diseases Classification dataset In 3-class classification ('normal', 'glaucoma', and 'diabetic retinopathy'), accuracies of 98.02% and 92.90% were obtained. Additionally, proposed model achieves a classification accuracy of 87.50% on a private systemic disease dataset that includes diabetes mellitus, ischemic heart disease, hypercholesterolemia, and normal cases. **Conclusions:** The findings demonstrate the effectiveness of the proposed AC-GAN approach in accurately classifying both ocular and systemic diseases from retinal images using a single framework. This suggests the model's potential as a comprehensive diagnostic tool for rapid, non-invasive and large-scale screening of multiple disease states.

CL237: Profile Of Oculomotor Parameters At Post Cerebrovascular Accident - A Retrospective Observation

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Purpose: This retrospective observational study investigated the clinical profile of oculomotor parameters in patients with a history of cerebrovascular accident (CVA). **Methods:** This retrospective observational study reviewed the medical records of patients diagnosed with CVA who were referred to the neuro-optometry clinic between January 2024 and December 2024. The study included patients with documented oculomotor assessments, including vergence parameters, eye alignment, saccades, pursuit, developmental eye movement ratio, and reading speed. Demographic data, type of CVA, location, and oculomotor parameters were documented and analyzed using Microsoft Excel. **Results:** A total of 34 patient records were analyzed. The mean age of the participants was 56.64 years ±11.87, with a gender distribution of 76.47% males and 23.53% females. The average breakpoint of the near point of convergence was 13.67 cm (±11.52). Furthermore, 52.94% had distance orthophoria, 38.23% exhibited distance exophoria, and 2.94% had distance esophoria. Of these, 50% had near exophoria, and 44.11% were near orthophoria. Orthotropia was observed in 41.17%, and exotropia in 2.94%. The mean distance negative fusional vergence break point was 5.70 (± 4.06) and 9.58 (± 6.24) at near, respectively. The mean distance positive fusional vergence break point was 12.58 (±12.48) and 17.97 (± 13.99) at near. The mean DEM ratio was 1.23 (± 0.60), with a mean horizontal saccade time of 65.27 seconds (±35.55), and an average reading speed of 78.91 wpm (±48.28). **Conclusions:** Oculomotor dysfunction is a common and varied manifestation following CVA. Early identification of these deficits is essential for implementing targeted neurorehabilitative strategies to improve functional vision and quality of life.

Keywords: Cerebrovascular accident, oculomotor parameters, near point of convergence, Saccades-pursuits, Developmental eye movement test, negative fusional vergence, positive fusional vergence, oculomotor dysfunction, and neuro-optometry rehabilitation.

CL238: Ocular Profile Of Individuals With Visual Snow Syndrome

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Purpose: To understand the binocular vision parameters in individuals diagnosed with Visual Snow Syndrome (VSS). **Methods:** This observational study included participants presenting to a binocular vision clinic with symptoms associated with VSS. Individuals with retinal or other ocular comorbidities were excluded. **Results:** Twenty-six participants were included with mean (SD) age of 28 (± 6.5) years, and 17(65%) were male. Mean spherical equivalent refractive error were-1.07 (±1.5) Dioptre, -1.05 (±1.6) Dioptre in right and left eye respectively. Non-strabismic binocular vision anomalies were observed in 24 (92.3%) participants. Reduced accommodative facility was seen in 11 (42.3%), convergence insufficiency, Excess and basic exophoria in 1 (3.84%), convergence insufficiency with reduced accommodative facility in 7 (26.9%), and fusional vergence dysfunction in 3 (11.5%). Distance heterophoria showed exophoria in 7 (26%) and orthophoria in 19 (73%) and near heterophoria were esophoria in 3 (11%), orthophoria in 14(53%), and exophoria in 9(34%) participants. Mean (SD) heterophoria was -0.8 (± 1.5) Prism dioptre (PD) at distance and -1.9 (± 3.8) PD at near. The near point of convergence (break) was 5.5 (± 4.01) cm. Monocular accommodative dynamics were 0.69 (± 0.23) Dioptre in right eye and 0.77 (± 0.24) Dioptre in left eye. Fusional divergence (base-in) break values in PD were 7.15 (± 1.9) at distance and 11.5 (± 3.4) at near, while fusional convergence (base-out) break values were 16.8 (± 9.02) at distance and 26.3 (± 10) at near. **Conclusion:** This observational report describes the fusional vergence and accommodative profile among visual snow syndrome.

CL239: Temporal Shifts In Visual Attention: Gaze Consistency And Saliency Effects During Free-Viewing

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Purpose: This study investigated how visual attention evolves during free-viewing by examining gaze patterns across individuals, including temporal changes in fixation patterns and the influence of visual saliency. **Methods:** Forty-five healthy adults (Median age(IQR):51(14)y) viewed ten static real-world scenes for 15 seconds each while their gaze was simultaneously recorded using a remote eye-tracking system. Fixation heatmaps were generated, and gaze parameters computed. Using a bootstrapping approach, random subsets of gaze data were compared to assess gaze pattern consistency. Heatmap similarity was analyzed across the full viewing period and within early and late time intervals using Jensen–Shannon Divergence (JSD), where JSD=0 indicates identical maps and JSD=1 indicates no similarity. Each scene was processed through a computational saliency model (Itti&Koch,1998). The proportion of gaze fixations overlapping the computed salient regions was calculated to evaluate saliency's influence on gaze. **Results:** Across the full viewing period, the median JSD between participant subgroups was 0.11 (IQR: 0.10–0.12), despite differences in visual content. Gaze consistency declined over time, with median JSD increasing from 0.10 in early viewing to 0.20 in late viewing, reflecting greater individual variability. Visual saliency strongly influenced gaze, with 50–84% of fixations falling on predicted salient areas. **Conclusions:** The data suggest that free-viewing is initially consistent and driven largely by visual saliency but becomes more individualized over time due to top-down influences such as prior knowledge. Free-viewing can hold clinical value in assessing the dynamic interaction between bottom-up saliency and top-down cognitive context in individuals with visual or cognitive impairment.

CL240: Visual Function Deficits In Psychotropic Monotherapy Vs Combination Therapy: Evidence From A Cross-Sectional Pilot

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Purpose: To evaluate the differential impact of psychotropic monotherapy (antipsychotics or antidepressants alone) versus combination therapy (antipsychotics & antidepressants) on visual functions with reference to healthy controls. **Methods:** This study included 35 participants, divided into 4 groups: antipsychotics monotherapy (n = 6), antidepressants monotherapy (n = 4), combination therapy (n = 5), and healthy controls (n = 20). Visual assessments included visual acuity, color vision, contrast sensitivity and stereopsis. Statistical analysis was conducted to compare each treatment group with controls and also with each other. **Results:** No significant differences in visual functions were observed between the psychotropic groups (antipsychotics vs antidepressants, antipsychotics vs combination therapy and antidepressants vs combination therapy); ($p < 0.05$). Combination therapy group exhibited color vision deficits in right, left and both eyes with higher total error scores (Median =16.00, 24.00, 16.00, IQR = 16.50, 13.00, 13.00) and impaired stereopsis (Median = 40 arc secs, IQR = 30 arc secs) compared to controls (Median =11.00, IQR = 0.00); ($p < 0.05$). The antipsychotic (Median = 22.5 arc secs, IQR = 12.50 arc secs); and antidepressant monotherapy group (Median = 40.00 arc secs, IQR = 15.00 arc secs) exhibited a significant reduction in stereopsis compared to controls (Median = 20.00 arc secs, IQR = 0.00 arc secs); ($p < 0.05$). **Conclusion:** Although monotherapy and combination therapy did not differ significantly in their impact on visual functions, both showed deficits when compared to controls. Combination therapy affected both stereopsis and color vision, while monotherapy mainly reduced stereopsis.

CL241: Prediction Error And Visual Outcomes After Retropupillary Iris Claw Lens Implantation In Pediatric Eyes With Insufficient Capsular Support

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Purpose: To study the prediction error, visual outcome, and complications after retropupillary iris claw intraocular lens (ICIOL) implantation in pediatric eyes with incomplete capsular support. **Methods:** This retrospective study included children aged 4-18 years who underwent primary or secondary implantation of ICIOL between September 2021 to July 2024. The indications for surgery, best corrected visual acuity (BCVA), refraction at postoperative 6 weeks, biometric parameters, and intra and post-operative complications were recorded. The IOL power was selected based on the age of the patient and A constant of the ICIOL. The prediction error (PE) was calculated as the difference between the targeted refraction and the spherical equivalent after suture removal. **Results:** 40 eyes of 25 patients were included with a mean age of 10.35 years and a male-to-female ratio of 14:11. Idiopathic ectopia lentis and trauma were the most common indications. Primary ICIOL implantation was performed in 13 eyes and secondary implantation in 27 eyes. The mean BCVA improved from 1.3±0.5 to 0.36±0.32 LogMAR. The mean PE was 1.23±0.99 (+3.38 to -4 D), with a PE >1D observed in 19 eyes (47.5%). Overcorrection was seen in 22 eyes while undercorrection was seen in 16 eyes. The most common intraoperative and postoperative complication was difficult haptic enclavation (3 eyes) and transient rise in IOP (9 eyes). **Conclusion:** ICIOL is a safe and effective procedure in pediatric eyes with insufficient capsular support, however yields a PE of >1D in almost half of the eyes.

CL242: Impact On Contrast Sensitivity Among Asymptomatic And Symptomatic Visual Display Terminal Users

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Purpose: The current study investigated the contrast sensitivity in symptomatic and asymptomatic visual display terminal (VDT) users. **Methods:** VDT users with at least 4 hours of daily exposure to the screen were considered for the present study. VDT users were categorized into symptomatic or asymptomatic based on the following parameters: VDT usage details, blink rate, Ocular Surface Disease Index (OSDI), tear meniscus height (TMH), non-invasive tear break-up time (NIBUT), meibography, tear osmolarity, and Schirmer-I. Further, the contrast sensitivity was investigated for symptomatic and asymptomatic VDT users with the CS gratings of 3, 6, 12, and 18 cycles/degree spatial frequency. **Results:** VDT users with lower OSDI/Schirmer-I/NIBUT values and higher partial gland/corneal strain grade were grouped as symptomatic. While, asymptomatic VDT users have values within the reference range for the respective parameters. A significantly decreased contrast sensitivity was experienced in symptomatic VDT users as compared to asymptomatic VDT users. At the same time, both of the groups exhibited similar corrected visual acuity. **Conclusion:** The contrast sensitivity is highly affected for symptomatic VDT users compared to asymptomatic VDT users.

CL243: Comparison Of Low-Dose Atropine (0.01%) In Retarding Myopia Progression In Fast Progressors Vs Slow Progressors

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Purpose: To evaluate the effect of 0.01% atropine (LDA) on myopia progression in slow vs fast progressors. **Methods:** Retrospective study including children 0.75D/Year). The best corrected visual acuity, cycloplegic refraction, and axial length (AL) were noted at the pre-LDA, LDA, and post-LDA visits. The demographic data, clinical parameters, pre LDA and post-LDA progression rate of SE and AL were compared between the SP and FP. **Results:** The pre-LDA progression rate was slow in 33 (39.8%) and fast in 50 (60.2%) eyes. Parental myopia was more common among FP (74.4% vs. 32.3%, p = 0.003). Myopia progression rate reduced from 0.51±0.22 D/Year to 0.28±0.53 D/Year (p=0.004) in SP, and from 1.39±0.96 to 0.25±0.48 (p<0.001) in the FP. The mean follow-up was 1.9 ± 0.98 years. Myopia progression reduced by 82% in the FP vs 43.1% in the SP. The AL elongation rate was reduced by 77.5% in the FP (0.40±0.39 to 0.09±0.17, p=0.01) with a negligible change in the SP (0.23 ± 0.10 to 0.22 ± 0.18, p=0.742). 14% of eyes continued to progress rapidly despite LDA, with amblyopia being a significant risk factor. **Conclusion:** Response to 0.01% atropine was greater in FP as compared to SP, suggesting a severity-dependent effect.

CL244: Comparative Study Of Axial Length And Refraction: Myopia Master Vs. Argos And Open-Field Auto Refractor

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Purpose: To evaluate the agreement and interchangeability of axial length (AL), axial length to corneal radius ratio, (AL/CR) and spherical equivalent (SE) measurements from Myopia Master versus ARGOS and Open Field Autorefractor. **Methods:** A total of 39 myopic eyes were included with a SE between -0.75 D to -11.87 D of which 20 were classified as low myopes (LM), 8 as high myopes (HM), and 11 as anisomyopes (AM). Ocular biometry and SE were measured with ARGOS Biometer, Myopia Master and Grand Seiko WAM5500 Open field auto refractor. **Results:** Paired t test was used to compare the means of AL and SE, Intraclass Correlation Coefficient (ICC) was performed to check the reliability and reproducibility of the instruments and Bland-Altman plots was used to check the agreement between the instruments. Only, LM had clinical significance ($p<0.01$) in SE and AL mean between the instruments. ICC revealed an excellent correlation between the instruments for all the parameters in all the three groups. SE of LM had ICC of 0.97 (95%CI:0.89-1.00), HM had ICC of 0.97 (95%CI:0.86-1.00). AL of LM had ICC of 1.00 (95%CI:0.98-1.00), HM had ICC of 1.00 (95%CI:1.00-1.00). AL/CR of LM had ICC of 0.99 (95%CI:0.99-1.00), HM had ICC of 1.00 (5%CI:0.98-1.00). Bland-Altman plots showed moderate to good agreement between instruments across all groups in all parameters, supporting their reliability for the clinical use. **Conclusion:** Myopia Master and ARGOS agree on axial length, but SE bias limits interchangeability; larger sample needed for validation.

CL245: The Impact Of Outdoor Exposure, Near Work And Circulating Biomarkers (Vitamin D3, Dopamine) On Myopia Onset And Progression

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Purpose: (i) Investigate the association between myopia and plasma levels of vitamin D3 and dopamine. (ii) Examine the correlation between outdoor activity, focused near work and myopia progression. **Methods:** In this cross-sectional prospective observational study, we enrolled 278 children aged 6–15 years, comprising 105 emmetropic controls and 173 myopic children (58 with stable myopia, 58 with progressive myopia, and 57 progressive myopia on low dose atropine). Detailed history regarding daily duration of outdoor activity and focused near work were collected. Plasma dopamine and vitamin D3 concentrations, were analyzed via blood sampling. **Results:** No statistically significant difference was observed in plasma dopamine levels between the control and myopic groups. Plasma vitamin D3 levels were significantly lower in myopic children compared to controls (P 0.004). Myopic children exhibited significantly reduced outdoor activity (2 hours/day) than controls ($P<0.0001$). **Conclusion:** While conventional myopia management focuses on optical correction, our findings suggest that systemic screening for vitamin D3 deficiency, along with targeted lifestyle modifications to promote outdoor activity and limit prolonged near work, should be integrated into comprehensive myopia control strategies.

CL246: Transforming Vision: Exploring The Efficacy Of Orthokeratology For Mild To Moderate Myopic Refractive Corrections In North-Indian Population

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Aim and Objective: To evaluate the safety and efficacy of overnight Orthokeratology as a treatment for mild myopic refractive correction. **Methods:** This prospective study enrolled 18 patients (36 eyes) at Dr R P Centre for Ophthalmic Sciences, AIIMS, Ansari Nagar, New Delhi. Clinical assessments were performed, including UCVA, BCVA, Cycloplegic refraction, Corneal pachymetry, Axial length and Corneal topography. After assessment, appropriate Ortho K contact lens was chosen, and final evaluation done using fluorescein dye by checking centration, movement, and degree of applanation in treatment zone. Dispensing was done after adjusting final Base curve (BC), Overall Diameter (OD), Return Zone Depth (RZD) and Landing Zone Angle (LZA). **Results:** Thirteen participants with mean age 24.5 years (72% Males) were recruited and followed up after 1 month. Participants had significant improvement in mean UCVA, Right eye 0.658 (SD±0.58) to 0.016 (SD±0.014), Left eye 0.600 (SD±0.56) to 0.025 (SD±0.021) with p- value < 0.0001 and mean Refractive error of Right eye -1.98 DS (SD±1.55) to +0.583 DS (SD± 0.47), Left eye -1.72 DS (SD± 1.63) to +0.50 DS (SD± 0.25) with p-value < 0.0001 at 1 month. Corneal fluorescein staining was noted in some patients, but no corneal infiltrate or ulcer noted in any patient. **Conclusion:** Orthokeratology (Ortho-K) Contact lenses present a compelling option for correcting mild myopic refractive errors. The efficacy of Ortho-K lenses in reshaping the cornea overnight offers a practical and reversible solution. Ortho-K lenses stand as a promising avenue for those seeking an alternative to traditional corrective measures for mild refractive errors.

CL247: Keratitis Associated With Miltefosine Therapy In Post-Kala-Azar Dermal Leishmaniasis: Clinicopathological And Microbiological Insights

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Purpose: To investigate the clinical, pathological, and microbiological features of keratitis in patients receiving miltefosine for post-kala-azar dermal leishmaniasis (PKDL), evaluate potential drug induced ocular toxicity and describe the characteristic clinical presentation and management of keratitis in these cases. **Methods:** A retrospective analysis was conducted on five patients with post-kala-azar dermal leishmaniasis (PKDL) who developed keratitis during miltefosine therapy between April 2018 and December 2019. All patients underwent detailed ophthalmic evaluation, including slit lamp biomicroscopy and corneal imaging. Corneal scrapings were subjected to Gram staining, KOH mount, culture for bacteria, fungi, and Acanthamoeba, as well as pan-fungal PCR, to exclude infectious etiologies. Real-time PCR for *Leishmania donovani* was performed on ocular surface samples to rule out active parasitic infection. To reconfirm the diagnosis of PKDL, rK39 rapid serological testing for anti-rK39 antibodies and repeat skin biopsies for Leishman Donovan (LD) bodies were performed in all cases. Drug causality was assessed using the WHO UMC criteria. **Results:** All patients presented with ocular symptoms such as pain, redness, watering, photophobia, and decreased vision. Slit-lamp examination revealed peripheral, para-limbal, ring-shaped, full-thickness stromal infiltrates characteristic of ulcerative keratitis. Two patients had unilateral involvement, while three exhibited bilateral keratitis. The mean duration of miltefosine therapy before symptom onset was 48 days. Microbiological testing, including PCR for *Leishmania donovani*, was negative in all cases, supporting a diagnosis of sterile, likely immune-mediated keratitis. Causality assessment suggested a 'probable' link to miltefosine. Discontinuation of the drug and initiation of corticosteroid therapy led to clinical resolution in all cases. Visual outcomes were more favourable in unilateral cases compared to bilateral ones. **Conclusions:** These observations indicate that prolonged use of miltefosine might cause keratitis that resembles infectious keratitis. Negative microbial and RT-PCR findings reinforce its non-infective pathogenesis. Early diagnosis, prompt discontinuation of the drug, and timely initiation of corticosteroid therapy are the key to successful management.

CL248: Pre-Operative Conjunctival Flora In Patients Prior To Vitreoretinal Surgery

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Purpose: To evaluate the ocular flora along with antibiotic sensitivity of bilateral Conjunctival swab prior to vitreoretinal surgeries and to determime the fellow eye diagnosis which warrants a bilateral conjunctival swab. **Methods**: Retrospective observational study where bilateral (including eye which was operated and fellow eye) conjunctival swab data which was collected pre-operatively before undergoing vitreoretinal surgery including their antibiotic sensitivity report is collected,classified and analysed. **Results:** Out of 190 eyes of 95 patients,the overall bacterial isolation rate in our study was 33.7% (64 of 190 eyes).Swab culture results in the fellow eye showed a higher percentage of swab positivity compared(27 of 64 eyes,42.2%) to the swab positivity of eyes which were to be operated(37 of 64 eyes,57.8%).The most common organism overall was gram postive bacilli *P.acnes* (47 of 64 eyes,73.4%).The most common fellow eye diagnosis which showed fellow eye swab positivity was Retinal detachment(10 of 37 fellow eyes), followed by diabetic retinopathy complications(9 of 37 eyes) and phthisical eyes(9 of 37 eyes).Out of 37 eyes ,10 were post vitrectomised. **Conclusion:**This study reiterates the need to do bilateral swabs instead of unilateral swabs before any intraocular surgery. . Patients with non-seeing fellow eyes with a diagnosis of either retinal detachment, proliferative diabetic retinopathy complications (especially post vitrectomised eyes) and phthisical eyes have a higher probability of conjunctival swab positivity and such eyes warrant bilateral conjunctival swabs to be taken pre operatively.

CL249: Structural Retinal Changes In Toxoplasmic Retinochoroiditis Assessed By Swept-Source OCT

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Purpose: To present swept-source optical coherence tomography (SS-OCT) findings in eyes with toxoplasmic retinochoroiditis and evaluate retinal and choroidal changes across disease activity phases, correlating these with visual outcomes. **Methods:** This retrospective observational study included 33 patients (39 eyes) diagnosed with toxoplasmic retinochoroiditis. Eyes were categorized into active (n = 5), reactive (n = 13), and inactive (n = 27) phases based on clinical and imaging findings. SS-OCT parameters assessed included retinal and choroidal thickness, retinal layer integrity, and vitreous changes. Best-corrected visual acuity (BCVA) and SS-OCT images were recorded at presentation and at the final follow-up. Disease activity transitions and lesion zones were documented. **Results:** The cohort included 21 males and 12 females with a mean age of 25.39 ± 16.56 years. Bilateral involvement was observed in six patients. BCVA improved from 0.67 ± 0.58 at presentation to 0.47 ± 0.42 at the final visit. Active eyes showed the highest foveal thickness (302 ± 290 µm) and frequently exhibited posterior hyaloid alterations, vitreous hyperreflective dots (80%), and intraretinal/subretinal fluid. Subfoveal choroidal thickness was greatest in active eyes (376.8 ± 68.7 µm). RPE disruption, ellipsoid zone loss, and outer retinal atrophy were more common in reactive and inactive phases. Disease activity converted in 13.3% of episodes. **Conclusions:** SS-OCT reveals distinct structural patterns corresponding to different stages of toxoplasmic retinochoroiditis. Active disease is marked by retinal edema and vitreoretinal interface changes, while chronic phases show retinal thinning and RPE damage. SS-OCT is valuable for monitoring disease progression and guiding treatment. KEYWORDS: Toxoplasma retinochoroiditis, SS-OCT, Activity.

CL250: Validation Of Standardization Of Uveitis Nomenclature (SUN) Classification Criteria For Three Uveitic Entities

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Purpose: To validate the Standardization of Uveitis Nomenclature (SUN) classification criteria proposed by the SUN working group. **Methods:** A retro-prospective case control study examined 240 uveitic patients from a Tertiary eye care centre between 2021 to 2025. The study consisted of three groups in which each had age-matched controls. Predictive values like Sensitivity, Specificity, Negative Predictive Value (NPV), Positive Predictive Value (PPV), Negative Likelihood Ratio (NLR), Positive Likelihood Ratio (PLR) are calculated for the three classification criteria of serpiginous choroiditis (SC), Vogt Koyanagi Harada Disease (VKH), Tubercular uveitis (TB). It assesses whether the expert diagnosis is comparable to the SUN classification criteria. **Results:** A total of 240 participants were included in the study out of which 120 were cases and 120 were controls. The study included three groups with each group comprising 40 cases and 40 controls. For the VKH group, the SUN classification criteria showed a sensitivity of 72%, specificity of 100%. For the SC group, sensitivity was 80%, specificity 100%. However, the classification criteria of TB have showed less sensitivity and a specificity of 100%. The SUN classification criteria of VKH, SC has showed higher correlation of 0.754, 0.816 with expert diagnosis respectively. **Conclusion:** The SUN Classification criteria of VKH and SC have the higher predictive values. These findings suggest that SUN criteria closely align with expert's clinical diagnosis. To further confirm these findings, many prospective multicentre studies should be conducted in the future.

CL251: Long-Term Visual And Clinical Outcomes In Vogt Koyanagi Harada Disease - Insights From 395 Eyes In A Referral Eye Centre In Eastern India

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Purpose: This study aims to evaluate the long-term complications in VKH, to understand the disease progression, and the impact of visual acuity during the follow up period at a tertiary eye care centre in Eastern India. **Methods:** A retrospective cross-sectional observational study of VKH patients diagnosed between 2005 and 2023 was followed up using the electronic medical records (EMR) in a tertiary eye care centre in Eastern India. India. Multiple clinical data points were collected, compiled, and analyzed statistically. The findings were then discussed and compared with the similar studies from other parts of the globe. **Results:** We analyzed 395 eyes of 207 patients. 188 (90.82%) had bilateral involvement, and 19 (9.18%) had unilateral involvement. Patients presented to us in various stages of the disease. In our study, the most common complication is the complicated cataract, 133 eyes (33.67%), followed by Glaucoma, 123 eyes (31.14%), and sunset glow fundus, 95 eyes (16.45%). In this study, 141 (35.70%) eyes showed improvement in vision, 145 (36.71%) showed deterioration, and 107 (27.09%) eyes showed stable vision. **Conclusion:** Our study showed rare extraocular features in VKH patients of Eastern India. Our study also showed that topical steroids, along with intravenous methylprednisolone, followed by oral steroids with immunosuppressive therapy are a first line of treatment is quite effective in salvaging the vision. However, one-third of patients have deterioration of vision in long-term follow-up. Cataract and glaucoma were the most common complications. Newer investigation modalities like swept source optical coherence tomography help in diagnosis and follow-up.

CL252: Histopathology, Immunohistochemistry, And Molecular Biology In Eviscerated And Enucleated Specimens Of End-Stage Uveitis Disease

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Purpose: To study 30 eyes with end stage uveitis requiring enucleation or evisceration. **Methods**: Retrospective study of histopathology (HPE), Immunohistochemistry (IHC), and polymerase chain reaction (PCR) on paraffin embedded tissues. **Results:** Sympathetic ophthalmia (10) showed granulomatous inflammation with CD3+. VKH (1) showed non granulomatous inflammation with CD3+ and CD20+. Tuberculous uveitis; panuveitis (7), anterior uveitis (2), scleritis (1) and sclerouveitis (1) showed caseating granulomatous inflammation, MTB-PCR positive in many and acid-fast bacilli in 3 tissues. Eales disease (3) showed non-granulomatous inflammation, MTB-PCR+ in 2. Rare cases included one each of Pars planitis with CD3+ and CD68+; Acute retinal necrosis with vascular occlusion, herpesinclusions, and PCR positivity; Nocardiosis with necrotizing granulomas and subretinal abscess; Post-dengue endophthalmitis with suppurative necrosis and *Bacillus cereus* isolation; and neovascular glaucoma with uveitis. **Conclusion:** Despite advanced immunosuppression and biologicals, some uveitis reach end stage; HPE, IHC and PCR are helpful to understand the patho-mechanisms of these diseases.

CL253: Bridging Vision And Inclusion: A Multi-Sectoral Study On Low Vision Education, Stakeholder Perceptions Among The Schools For Visually Impaired

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Purpose: The uptake of Low Vision Services (LVS) and Assistive Technology (AT) in India remains inadequate despite increasing awareness. Teachers, Parents, and Children. This study addresses a significant gap in understanding how teachers, parents, and children with visual impairment (VI) perceive, engage with, and implement LVS and AT within educational settings. **Methods:** A cross-sectional study was conducted across institutions for the VI in Chennai and Thiruvallur districts. A validated, stakeholder-specific KAP survey was developed using the Delphi technique and administered to 30 teachers, 45 children with VI, and 45 parents. Data were analysed using SPSS version 20. Bloom's cutoff criteria were used to classify the category of the Knowledge, Attitude, and Practice scores. **Results:** Teachers demonstrated the highest KAP levels, with 23.3% showing good knowledge, 76.7% positive attitudes, but only 30% moderate practice related to low vision and associative factors. Significant knowledge-score associations were found with postgraduate education ($p=0.011$), specialization in visual impairment ($p=0.001$), and Government school affiliation ($p<0.001$). Children exhibited positive attitudes (47% good), moderate practices (20% used devices), but poor knowledge (80%). Parent scores were lowest overall, with 89% showing poor knowledge and 89% poor practice; however, attitudes were generally positive and varied by education level. **Conclusion:** The study underscores the need for structured stakeholder-specific education, training, and policy support to improve the uptake of LVS and AT. Enhanced teacher training, parental awareness programs, and accessible educational environments are critical for inclusive education and rehabilitation of children with visual impairment.

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