EPFL, Lausanne, June 9th, 2026

18th Annual Swiss Zebrafish Meeting

Book of Abstracts

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9. **Leveraging zebrafish as an in vivo Model for Advancing Cell Therapy in Neurodegenerative Disorders**
   Dr. Zang Jingjing, Department of Molecular Life Science, UZH

Poster number 1

Name: Prof. Jazwinska Anna
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Affiliation: University of Fribourg

Title of abstract:

Cellular and molecular mechanisms of whole-muscle regeneration in zebrafish

Authors' names and affiliations:

Hendrik Oudhoff, University of Fribourg; Florian Baumgartner; University of Fribou; Anna Jazwinska, University of Fribourg

Abstract:

Unlike the fibrotic scarring observed in humans following volumetric muscle loss, zebrafish are capable of fully regenerating 3–4 damaged myomeres within 30 days after cryoinjury. To elucidate the underlying mechanisms, we investigated vascularization and myofiber diversity. Using the regeneration reporter careg — previously characterized in fin blastema, cardiac tissue, and dedifferentiated Müller glia — we identified its expression within regenerating myomeres, suggesting that conserved molecular mechanisms govern tissue restoration across organs. Notably, careg is also expressed in a specialized inner layer of the slow muscle compartment, revealing previously uncharacterized heterogeneity within zebrafish myofiber populations that will be further dissected using transgenic tools. Vascular network analysis with tie2:EGFP transgenic lines indicates that vascularization plays an essential role in this process, and its functional contribution will be assessed using PTK787, a VEGF receptor tyrosine kinase inhibitor. Together, these findings suggest that zebrafish whole-muscle regeneration is orchestrated by an interplay of tissue-intrinsic and systemic regulatory mechanisms.

Poster number 2

Name: Ms. Loureiro Casalderrey Cristina
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Affiliation: UPOATES, EPFL

Title of abstract:

Unwinding the segmentation clock using single-cell multiomics

Authors' names and affiliations:

Cristina Loureiro, EPFL; Chloé Jollivet, EPFL; Laurel Rohde, EPFL; Clement Helsens, EPFL; Andy Oates, EPFL

Abstract:

In vertebrate embryos, a posterior unsegmented tissue called the presomitic mesoderm (PSM) is rhythmically segmented into transient multicellular blocks known somites. A population of cellular oscillators, locally coupled by Notch signalling, generates waves of gene expression that propagate along the PSM. An opposing moving wavefront captures these temporal oscillations and converts them into stable spatial patterns. Signalling gradients regulate the position of this wavefront and thereby somite size. However, how these processes interact at the molecular level to drive boundary formation and cell specification remains incompletely understood. Here, we use single-cell genomics to characterize the gene regulatory dynamics underlying somite formation in zebrafish and discover a continuous and modular landscape of regulatory changes across the PSM, rather than discrete cell states. In addtion, we investigated the transcriptional control of a wavefront gene, showing how enhancer modularity integrates oscillatory and spatial inputs to ensure robust boundary formation. Together, our results provide new insights into the spatiotemporal regulation of somitogenesis.

Poster number 3

Name: Dr. Navajas Acedo Joaquin
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Affiliation: Biozentrum, Basel

Title of abstract:

Spatiotemporal emergence of somatosensory neuron diversity in zebrafish

Authors' names and affiliations:

Joaquín Navajas Acedo, Biozentrum, Switzerland, Allen Discovery Center for Lineage Tracing, WA, USA ; Alex Schier, Biozentrum, Switzerland, Allen Discovery Center for Lineage Tracing, WA, USA

Abstract:

How cellular factors combine in space and time to generate the diverse neuron types of a functional circuit in a robust way remains unclear. The fish primary somatosensory system of Rohon-Beard (RB) neurons develops first and is thought to undergo programmed cell death and be then replaced by the DRG. Our live imaging and deep single-cell transcriptomics across development show that contrary to a ~150-year-old assumption, RB neurons do not disappear. and are heterogeneous at 3 levels: their transcriptome, their axial distribution, and interindividual pattern. Spatiotemporal analysis of RB subtype emergence reveals that it follows a staggered-layer logic, with a ‘pan-RB program’ preceding a stochastic ‘hybrid neurotrophin receptor’ state that resolves into mutually-exclusive subclasses, followed by specialized functional subtypes. Combining in toto cell lineage reconstruction and a custom whole-mount spatial transcriptomics —in the same animal- we show RB neurons possess extremely simple cell lineages and link them to dozens of TFs and somatosensory genes. We also define the regulatory mechanism by TFs underlying the robust emergence of the observed neuronal subtypes across time.

Poster number 4

Name: Dr. Anneser Lukas
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Affiliation: Friedrich Miescher Institute for Biomedical Research

Title of abstract:

Semantic segmentation of space in the adult zebrafish pallium

Authors' names and affiliations:

Lukas Anneser, Friedrich Miescher Institute for Biomedical Research; Sriram Narayanan, Friedrich Miescher Institute for Biomedical Research; Jaap van Krugten, Friedrich Miescher Institute for Biomedical Research; Rainer Friedrich, Friedrich Miescher Institute for Biomedical Research

Abstract:

Across species, navigation involves cognitive representations of the environment. Such representations should combine spatial information with contextual content such as information about landmarks or distinct sections of the environment. Here, we studied the neuronal representation of different 1D corridors in the pallium of adult zebrafish behaving in a closed-loop virtual reality. Activity was measured under head-fixation by non-invasive calcium imaging. We observed the formation of a population code representing both the corridor and the position of the fish within each corridor with high accuracy. Each environment recruited a subset of spatially tuned neurons that collectively established near-orthogonal representations of each corridor. Additionaly, neurons in a lateral domain represented large segments of corridors that were separated by salient landmarks, resulting in coarse-grained representation of the environment, conveying contextual information about corridors and sectors. These findings suggest that the adult zebrafish brain constructs cognitive representations of environments by integrating representations of spatial location and higher-order, hierarchical structure.

Poster number 5

Name: Dr. Mayseless Oded
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Title of abstract:

A multimodal atlas of the zebrafish olfactory bulb links transcriptional identity to odor valence

Authors' names and affiliations:

Oded, Mayseless, Biozentrum, Universität Basel, Basel, Switzerland; Rainer, W. Friedrich, Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland; Alex, F. Schier, Biozentrum, Universität Basel, Basel, Switzerland

Abstract:

Animals classify novel sensory stimuli as attractive or aversive, yet how valence attribution is implemented by defined neuronal populations remains unclear. We integrated single-cell RNA sequencing, whole-mount spatial transcriptomics, neuronal activity mapping, and quantitative behavior to construct a multimodal atlas of the larval zebrafish olfactory bulb. Transcriptionally defined projection neuron and interneuron subtypes formed cohesive spatial domains. Chemically diverse odors evoke stereotyped, valence-specific navigation strategies. Distinct olfactory bulb activity patterns associated with attractive versus aversive odors. Sequencing of odor-activated neurons (CaMPARI-seq), together with spatial mapping of activity onto gene expression, linked positive valence to a short-axon–like interneuron module. Targeted ablation of TH^+ interneurons selectively impaired attraction while sparing aversion. Together, these results identify a transcriptionally defined interneuron module necessary for positive odor valence attribution, linking molecular identity, spatial organization, population activity, and behavior.

Poster number 6

Name: Mr. Julmi Jérôme
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Affiliation: University of Zurich

Title of abstract:

Optogenetic epidermal tightening regulates sensory organ patterning in vivo

Authors' names and affiliations:

Jérôme Julmi, UZH; Robert Bill, UZH and ETH; Jana Wittmann, UZH; Darren Gilmour, UZH

Abstract:

Morphogenesis — the process by which cell collectives are shaped into functional organs — relies on coordinated behaviours such as division, migration, and differentiation. Because organs develop within complex tissue environments, their final form is often influenced by mechanical and developmental feedback from surrounding structures.
Using zebrafish as a model system, we examine how the epidermis and skin mechanosensory organs of the lateral line (LL) develop together. Live imaging shows that the epidermal basal layer transiently “fracks” above the migrating LL primordium, indicating that active skin compliance is required for migration. To test this, we generated optogenetic RhoGEF (optoRho) zebrafish lines enabling light-controlled epidermal contractility. Acute tightening of the skin disrupted LL primordium migration and altered organ patterning, either blocking passage or prematurely “pinching off” organs.
These findings provide an in vivo example of an organ pattern that emerges from a dynamic interplay between a migrating tissue and its local tissue environment.

Poster number 7

Name: Dr. Shamipour Shayan
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Affiliation: University of Zurich

Title of abstract:

Multiplexed embryo profiling links cellular state to zygotic genome activation in single cells

Authors' names and affiliations:

Max Hess, University of Zurich; Marvin F. Wyss, University of Zurich; Edlyn Wu, University of Lausanne; Joel Lüthi, University of Zurich; Chiara Rebagliati, University of Zurich; Nadine L. Vastenhouw, University of Lausanne; Darren Gilmour, University of Zurich; Shayan Shamipour, University of Zurich; Lucas Pelkmans, University of Zurich

Abstract:

Multicellular self-organization emerges from interactions across multiple length scales that shape genome activity and the molecular phenotype of individual cells. Although spatial transcriptomics has advanced rapidly, mapping protein states at high spatial resolution across whole-mount structures remains difficult. Here, we introduce high-throughput 3D iterative indirect immunofluorescence imaging (3D-4i), enabling simultaneous detection of multiple proteins and protein states across the entire zebrafish blastoderm, together with a 3D computer vision pipeline that quantifies morphological and molecular properties from sub-cellular to whole-embryo scales in hundreds of embryos. Using these approaches, we assign cell cycle phase to every cell during the zebrafish mid-blastula transition and uncover the shift from global meta-synchronous mitotic waves to cell cycle desynchronization. We further show that cell cycle phase is the main source of transcriptional variability within a division cycle and, combined with transcription factors and chromatin markers, predicts transcriptional output during zygotic genome activation in single cells.

Poster number 8

Name: Dr. Wan Yinan
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Affiliation: University of Basel

Title of abstract:

Whole-embryo spatial transcriptomics at subcellular resolution

Authors' names and affiliations:

Yinan Wan, University of Basel; Jakob El Kholtei, University of Basel; Ignatius Jenie, UCSD; Bogdan Bintu, UCSD; Alex Schier, University of Basel

Abstract:

Spatiotemporal patterns of gene expression underlie embryogenesis, yet mapping gene expression across whole embryos with both high resolution and comprehensive coverage remains a major challenge. Here, I present a whole-embryo imaging approach based on multiplexed error-robust fluorescent in situ hybridization (weMERFISH), which enables subcellular-resolution profiling of gene expression in intact zebrafish embryos. By integrating these data with single-cell multiomics, we generated a spatial atlas of gene expression and chromatin accessibility across the entire embryo. This framework reveals how complex expression patterns arise from combinations of tissue-specific regulatory elements, how global transcriptional changes align with cellular maturation and morphogenesis, and how sharp tissue boundaries form through changes in gene expression rather than cell sorting. Together, this work provides a scalable approach for whole-organism spatial transcriptomics and new insights into the regulation and dynamics of embryonic development.

Poster number 9

Name: Dr. Zang Jingjing
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Affiliation: Department of Molecular Life Science, UZH

Title of abstract:

Leveraging zebrafish as an in vivo Model for Advancing Cell Therapy in Neurodegenerative Disorders

Authors' names and affiliations:

Hao Ye1, Jingjing Zang2*°, Jiawei Zhu1, Denis von Arx1, Vitaly Pustovalov1, Minmin Mao1, Qiao Tang1, Andrea Veciana1, Harun Torlakcik1, Elric Zhang1, Semih Sevim1, Roger Sanchis-Gual1, Xiang-Zhong Chen1, Daniel Ahmed3, Maria V. Sanchez-Vives4,5, Josep Puigmartí-Luis6.7, Bradley J. Nelson1*, Stephan C. F. Neuhauss2*, Salvador Pané1*
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Abstract:

Neurodegenerative disorders are marked by progressive, region-specific loss of neurons and synaptic connections within the nervous system. Although cell-based therapies are promising, their translation is limited by challenges in precise in vivo targeting and controlled differentiation. Here, we present a magnetically navigable and magnetoelectrically active platform consisting of $CoFe_2O_4$–$BaTiO_3$ nanoparticle-coated neural progenitor cell microrobots (NPCbots), tested in a zebrafish spinal cord injury model. Following intravascular delivery, NPCbots were guided against blood flow in the larval dorsal aorta using a rotating magnetic field, enabling precise in vivo positioning. In the injured spinal cord, alternating magnetic field stimulation induced rapid NPCbot differentiation and integration at the lesion site, enhancing neural regeneration. Functionally, treated zebrafish showed pronounced recovery of swimming and exploratory behavior within three days. Together, these results establish zebrafish as a powerful in vivo platform for magnetically guided cell therapies and highlight NPCbots as a promising strategy for targeted neural regeneration.

Flash presentations & Posters in SV Hall in SV1717

10. **Protein kinase inhibition of medulloblastoma dissemination revealed by in vivo zebrafish xenografts**
    Dr. Veronica Akle, University of Zurich

11. **Beyond the average: Variability in maternally inherited RNAs in response to environmental stress**
    Ms. Anastasiia Berezenko, University of Bern

12. **Reconstructing the synaptic wiring logic for spatial computations in the larval zebrafish telencephalon**
    Dr. Johannes Kappel, FMI, Basel

Poster number 10

Name: Dr. Akle Veronica
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Affiliation: University of Zurich

Title of abstract:

Protein kinase inhibition of medulloblastoma dissemination revealed by in vivo zebrafish xenografts

Authors' names and affiliations:

Veronica Akle1, Beyza Kilic1, Amin Allalou2, Marc Thomas Schönholzer3, Martin Baumgartner3, Stephan Neuhauss1

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2SciLifeLab BioImage Informatics Facility, Uppsala University, Uppsala, Sweden.
3Pediatric Molecular Neuro-Oncology Research, Children's Research Center, University Children's Hospital Zürich, Zürich, Switzerland

Abstract:

Medulloblastoma (MB) dissemination drives recurrence and poor outcome, yet therapies to suppress invasion with low toxicity remain limited. Protein kinases regulate tumor biology, making them attractive targets. We developed a high-throughput zebrafish larval brain xenograft platform for quantitative in vivo assessment of drug efficacy and toxicity.

Fluorescent MB cell lines (ONS-76, D425, HD-MB03) were transplanted into zebrafish brains and maintained in 96-well plates for longitudinal imaging. Larvae were imaged at 0 and 4 dpi using confocal microscopy. Automated analysis quantified tumor growth (area, perimeter) and invasion (fractal dimension, convex hull, complexity). Toxicity was assessed by morphometric profiling on the VAST BioImager to define maximal tolerated doses.

We tested famasertib (MAP4K4), barasertib (AURKB), and dasatinib. Famasertib reduced dissemination in ONS-76. Barasertib was ineffective in ONS-76/D425 but inhibited HD-MB03. Dasatinib showed activity in HD-MB03 with limited effects in ONS-76, revealing subtype-specific responses.

This platform enables scalable in vivo screening and identifies MAP4K4 inhibition as a promising anti-dissemination strategy.

Poster number 11

Name: Ms. Berezenko Anastasiia
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Affiliation: University of Bern

Title of abstract:

Beyond the average: Variability in maternally inherited RNAs in response to environmental stress

Authors' names and affiliations:

Anastasiia Berezenko1,2; Dragan Stajic1,4; Simone Oberhaensli1,3; Irene Adrian-Kalchhauser1;
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2 Graduate School for Cellular and Biomedical Sciences, University of Bern, Switzerland
3 Next Generation Sequencing Platform, University of Bern, Switzerland
4 Centre for Ecology, Evolution and Environmental Changes, University of Lisbon, Portugal

Abstract:

Epigenetic inheritance - the inheritance of genome activity states without DNA sequence changes - contributes to population survival and adaptation to environmental change. We study maternally deposited RNAs, protein-coding and repressed transcripts in oocytes, which provide the intergenerational information during early offspring development and reflect maternal environmental experience.
We hypothesize that environmental stress alters both the composition, driving clutch-level adaptation, and variability of these RNAs, promoting within-clutch diversification (molecular bet-hedging). To test this, we performed single-oocyte RNA-sequencing on oocytes from control and heat-stressed zebrafish mothers across recovery time points. We developed methods to quantify within-clutch, between-mother variability and treatment effects across time and two generations, complemented by behavioral and physiological analyses in offspring.
We find a heritable, multi-layered stress response involving directional changes, mother-specific effects, and variability shifts, highlighting the importance of accounting for both mean expression and variability in understanding adaptation to environmental stress.

Poster number 12

Name: Dr. Kappel Johannes
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Affiliation: Friedrich Miescher Institute for Biomedical Research - FMI

Title of abstract:

Reconstructing the synaptic wiring logic for spatial computations in the larval zebrafish telencephalon

Authors' names and affiliations:

Johannes Kappel, FMI; Chuyu Yang, Max Planck Institute for Biological Cybernetics; Tomáš Gancarčik, FMI; Alessandro Motta, FMI; Michal Januszewski, Google Research; Alexandra Graff-Meyer, FMI; Nila Moenig, FMI; Drew Robson, Max Planck Institute for Biological Cybernetics; Jennifer Li, Max Planck Institute for Biological Cybernetics; Rainer Friedrich, FMI;

Abstract:

Spatial representations are ubiquitous across most animal brains and have been studied extensively in the context of navigation, most notably in grid cells and place cells. A major step towards a mechanistic understanding of their underlying network computations would be a dense, synapse-level circuit reconstruction in conjunction with activity measurements. Recently, place cells were discovered in the telencephalon of larval zebrafish, providing a unique opportunity to discover the rules by which place cells are connected. Using serial block-face scanning electron microscopy (SBEM) we acquired multiple EM volumes of larval zebrafish forebrains after whole-brain imaging in freely swimming animals. We functionally identified hundreds of place cells per brain, mapped them to the corresponding EM volumes, and reconstructed >300 place cells in one sample. We discovered that connected place cell pairs exhibited significantly higher spatial activity map correlations than baseline, suggesting that recurrent connectivity between place cells shapes spatial tuning and population dynamics.

Posters in SV Hall

13. ~~**Cytoplasmic flow is a cell size sensor that scales anaphase**~~
~~Dr. Olga Afonso,University of Geneva~~

14. **The vascular niche as a driver of satellite cell activation after muscle cryoinjury in zebrafish**
Ms. Alessia Ambrosioni, Université de Fribourg

15. **Mechanical Regulation of the** Segmentation Clock
Dr. Feyza Nur Arslan, EPFL

16. **The Experimental and Transgenesis Unit Fish - An open platform for turquoise killifish research**
Dr. Mario Baumgart, Leibniz Institute on Aging (FLI)

17. **Hspb8 as a common marker of primordial and regenerating cardiomyocytes at the myocardium–connective tissue interface**
Mr. Joël Becker Department of Biology, University of Fribourg

18. **Social regulation of fear in zebrafish: Behavior and neural circuits**
Mr. Lukas Breitzler, University of Lausanne, Center for Integrative Genomics

19. **Abolishing mafa activity in neural crests leads impaired HSC emergence**
Ms. Sarah Brivio, Université de Genève

20. **Markers of vulnerable intracranial aneurysm using models of primary cilia deficient zebrafish**
Dr. Anne Cayron, University of Geneva, Department of Pathology and Immunology

21. **Monitoring platelet activation: studying cytosolic calcium signals in zebrafish thrombocytes**
Dr. Paulina Ciepla, Université de Genève

22. **Mapping social cell types**
Mr. Danin Dharmaperwira, University of Lausanne

23. **From darkness to vision: models of laser-induced retinal injury to study regeneration**
Ms. Sara Dori, University of Bern

24. **m6A safeguards rb1 to orchestrate vertebrate eye development**
Dr. Ahmed Elhelbawi, University of Bern

25. **The role of tRNA modifications in developmental tRNA dynamics**
Mr. Raphael Aiki Gerber, University of Bern

26. I**ntegrating live cell dynamics with high-dimensional multiplexed image data of developing zebrafish embryos**
Mr. Daniel Hannuschke, University of Zurich

27. **The role of wobble uridine modifications during zebrafish development**
    Ms. Mayuko Harada, University of Bern

28. **Beyond zebrafish: cardiac regeneration in Puntius titteya**
    Mr. Vincent Hisler, University of Fribourg

29. **EAAT2 deficiency triggers staged transcriptional responses in a zebrafish epilepsy model**
    Ms. Jacqueline Kientsch, University of Zurich

30. ~~**Elucidating neural circuit dynamics in a larval zebrafish model of varying traumatic brain injury severities**~~
    ~~Ms. Laura Köcher, University of Zurich~~

31. **Cebpb and c-Myc are the Primary Signals leading to sparing of Zebrafish Embryos after FLASH Radiotherapy**
    Mr. Louis Kunz, Université de Genève

32. **Novel zebrafish model for Lowe syndrome**
    Ms. Han Lai, University of Zurich

33. **Decoding skeletal muscle diversity in adult zebrafish: Myofiber subpopulations and regeneration at single-nucleus resolution**
    Dr. Rebecca Leech, Université de Fribourg

34. **Cox7a1 Mediated CIV Homodimerization Impacts the Cardiac Injury Response in Zebrafish**
    Ms. Carla Lembke, Universität Bern, Institut für Anatomie

35. **PACE: Integrating Human Genetics and Multimodal Charecterisation for Precision Medicine in Long-QT Syndrome**
    Ms. Ayisha Marwa Mangattu Parambil, University of Bern

36. **Understanding CHT vascular niche and the role of zeb2a in its establishment**
    Mr. Maxim Marfin, University of Geneva

37. **Activation of mfap5 in cardiac fibroblasts is essential for heart regeneration**
    Dr. Ines Marques, University of Bern

38. **3D Organization of Guanine Crystal Stacks in Zebrafish Iridophores**
    Dr. Oleg Mikhajlov, University of Geneva

39. **Integrated Aquaculture and Research Support Services at the Champalimaud Fish Platform**
    Dr. Joana Monteiro, Champalimaud Foundation

40. **Impact of neuroactive chemicals on vertical positioning and swimbladder size in zebrafish larvae**
    Ms. Bente Nissen, Eawag

41. **Investigating the role of lactate dehydrogenase A in neuronal activity and seizure susceptibility**
    Ms. Nicole Odermatt, Department of Molecular Life Sciences, University of Zurich

42. **Dissecting the roles of bmal1 paralogs in the zebrafish circadian system**
    Mr. Michael Ottiger, University of Zürich

43. **Feeling the stretch: uncovering primitive proprioceptors in zebrafish and their role in movement coordination**
    Ms. Delphine Parel, University of Fribourg

44. **Modelling telomere biology disorders in zebrafish impairs developmental hematopoiesis.**
    Ms. Joana Pereira Couto, University of Geneva, department of pathology and immunology

45. **Visual perception of social groups in zebrafish**
    Ms., Matilde Perrino, University of Lausanne

46. **Engineering zebrafish models of myopathic Ehlers-Danlos Syndrome to decode COL12A1 pathogenesis and accelerate targeted therapies**
    Mr. Minh Khoa Yves Pham, Department of Biology, University of Fribourg

47. **Image-Based Analysis of Cell Fate Specification in Embryonic Development**
    Ms. Chiara Rebagliati, University of Zurich

48. **Genetic basis of shoaling behaviour evolution in zebrafish**
    Dr. Carlos Rodriguez-Ramirez, Center for Integrative Genomics, University of Lausanne

49. **Exploring the role of lactate dehydrogenase in regulating neuronal excitability in zebrafish**
    Ms. Milena Ronchetti, Department of Molecular Life Sciences, University of Zurich

50. **Investigating retinal metabolism in Leber Congenital Amaurosis using Zebrafish models**
    Ms. Abhinaya Swaminathan, University of Zurich

51. **Investigating Microglial Lipid Dysregulation Using Zebrafish and Human-like Xenotransplantation Models**
    Ms. Nathalie Tichy, University of Zurich

52. **Understanding the Effects of Heat Shock on Zebrafish Somitogenesis**
    Mr. Emanuel Vasquez, Oates Lab, EPFL

53. **Investigating the Role of Cell Network Architecture in Coupling Fibroblasts In Vivo**
    Ms. Jana Wittmann, University of Zurich

54. **User-Defined FGF Signalling Activation via Optogenetics**
    Mr. Yixin Zhang, University of Zurich

Poster number 14

Name: Ms. Ambrosioni Alessia
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Title of abstract:

The vascular niche as a driver of satellite cell activation after muscle cryoinjury in zebrafish

Authors' names and affiliations:

Alessia Ambrosioni, UNIFR; Florian Baugartner, UNIFR; Anna Jazwinska, UNIFR

Abstract:

We developed a zebrafish cryoinjury model in which 3–4 adjacent myomeres of the caudal peduncle undergo complete regeneration within 30 days post-cryoinjury. Whole muscle restoration demands precise coordination of cellular microenvironments and molecular signalling cascades. Yet the role of vascularization in this process remains largely unexplored. Our preliminary data establish vascularization as modulators of muscle regeneration. Using the transgenic lines tie2:EGFP, we will map the vascular network in real time following cryoinjury. Functional assessment of angiogenesis within the injured zone will be performed using PTK787, a validated VEGF receptor tyrosine kinase inhibitor that blocks blood vessel sprouting. Like mammals, zebrafish harbor satellite cells that drive myofiber repair, but the signals governing their activation remain poorly understood. We hypothesize that endothelial cells and Shh signaling are the key components of the satellite cell niche, providing paracrine cues that license whole muscle regeneration. This project will define the vascular-satellite cell axis in muscle regeneration, with possible implications for treating volumetric muscle loss in humans.

Poster number 15

Name: Dr. Arslan Feyza Nur
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Affiliation: Oates lab, EPFL

Title of abstract:

Mechanical Regulation of the Segmentation Clock

Authors' names and affiliations:

Feyza Nur Arslan, EPFL; Andrew Charles Oates, EPFL

Abstract:

In vertebrate segmentation, expression waves of the segmentation clock sweep across the presomitic mesoderm (PSM), governing periodic segment formation, yet how PSM's mechanical properties influence its oscillatory signaling remains unknown. To address this, we combined live imaging, immunostainings, and single-cell morphometrics, revealing a cell shape and contractility gradient across the PSM that coincides with the slowing of clock oscillations. Consistent with a functional link, chemical perturbation of contractility not only altered cell shape and motility but also impacted clock periodicity. Supporting a cell-autonomous relationship, contractility markers changed during the oscillatory phase of single cells in primary PSM cultures, and cytoskeletal disruption slowed clock dynamics, mirroring in vivo observations. Beyond the cytoskeleton, knockdown of Hyaluronic acid synthase Has2 disrupted clock synchrony, implicating extracellular matrix composition in cell-cell signaling. Together, our findings reveal a coupling between segmentation clock dynamics and cellular/extracellular mechanics, suggesting a more direct interplay between oscillatory signaling and morphogenesis.

Poster number 16

Name: Dr. Baumgart Mario
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Affiliation: Leibniz Institute on Aging (FLI)

Title of abstract:

The Experimental and Transgenesis Unit Fish - An open platform for turquoise killifish research

Authors' names and affiliations:

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[1]Leibniz Institute on Aging – Fritz Lipmann Institute (FLI), Beutenbergstr. 11, Jena, Germany

Abstract:

The Experimental and Transgenesis Unit Fish (ETUF) at the Leibniz Institute on Aging – Fritz Lipmann Institute (FLI) provides a centralized platform for FLI-internal and external researchers to use the short-lived African turquoise killifish (Nothobranchius furzeri) as a vertebrate model for aging research. N. furzeri captures multiple hallmarks of human aging, including age-associated changes in immune function, brain physiology, reproduction, organ function, and behavior, while its short lifespan enables rapid studies of lifespan, healthspan, and intervention strategies.
ETUF supports genetic and non-genetic approaches, combining transgenesis and genome editing with pharmacological and dietary manipulations, behavioral phenotyping, and endpoint analyses at molecular, cellular, and organismal levels. Umbrella licenses are in place to enable the generation and maintenance of genetically modified fish lines and the controlled application of compounds to assess effects on survival, fitness, and behavior. ETUF provides consultation on experimental design, animal experimentation and licensing, readout selection, and endpoint definition. We support compound delivery via food, water, or injection, including guidance on in vivo dosing and concentration finding. ETUF also offers standardized access to tissues and biospecimens and hands-on training in core workflows such as animal handling, dissections, and microinjection techniques.
Killifish research at the FLI has a >15-year track record and has contributed to foundational resources and methodological advances, including genomic tool development, pharmacological paradigms relevant to vertebrate aging, and the generation of genetically modified lines such as the transparent “klara” strain. ETUF builds on this expertise, the FLI’s established fish facility infrastructure, and the experience of killifish experts Annekatrin Richter and Mario Baumgart to provide reliable husbandry, experimental support, and project-specific guidance for researchers entering or expanding their work with N. furzeri.
By opening ETUF to the broader scientific community in March 2025, we aim to make established killifish workflows accessible beyond the FLI, lowering barriers to entry, fostering external collaborations, and accelerating discovery in aging biology. To further expand capacity, we will actively pursue third-party funding to support ETUF-associated R&D projects, priority equipment investments, and additional personnel. To date, ETUF has received six expressions of interest from internal and external groups, with projects at different implementation stages.

Poster number 17

Name: Mr. Becker Joël
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Affiliation: Department of Biology, University of Fribourg

Title of abstract:

Hspb8 as a common marker of primordial and regenerating cardiomyocytes at the myocardium–connective tissue interface

Authors' names and affiliations:

Joel Becker, University of Fribourg; Rebecca Leech, University of Fribourg; Catherine Pfefferli, University of Fribourg; Dogan Grepper, University of Fribourg; Anna Jazwinska, University of Fribourg

Abstract:

The zebrafish heart regenerates efficiently after injury, making it a powerful model for cardiac repair. The careg:EGFP regeneration reporter marks dedifferentiated cardiomyocytes (CMs) in regenerating myocardium, but is also expressed in the primordial layer of the intact ventricle. Notably, both populations occupy a junctional position at the interface between contractile myocardium and connective tissue. We hypothesize that these CMs share conserved molecular programs adapted to the mechanical demands of this border environment. RNA-sequencing of both populations identified Heat-shock protein B8 (Hspb8) as a candidate involved in stress-response. Our custom antibody confirms its selective enrichment in the primordial layer and cardiac border zone after injury. A hspb8:EGFP BAC transgenic reporter faithfully recapitulates this pattern. CRISPR/Cas9 loss-of-function mutants regenerate normally under standard conditions, likely reflecting compensation among heat-shock family members, and we are now challenging this resilience through combined heat-stress exposure. These studies reveal new molecular underpinnings of cytoprotection in border CMs during homeostasis and regeneration.

Poster number 18

Name: Mr. Breitzler Lukas
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Title of abstract:

Social regulation of fear in zebrafish: Behavior and neural circuits

Authors' names and affiliations:

Lukas Breitzler, University of Lausanne - CIG; Alejandro Uribe Arias, University of Lausanne - CIG; Danin Dharmaperwira, University of Lausanne - CIG; Johannes Larsch, University of Lausanne – CIG

Abstract:

Fear-related behaviors are shaped by both external threats and social context. Conspecifics can suppress or amplify defensive responses, yet the mechanisms that integrate social cues into fear circuits remain unclear.

To address this, we established a virtual reality paradigm that delivers controlled threat and social stimuli to freely swimming juvenile zebrafish. We found that social cues from real conspecifics modulate fear in a bi-directional manner—rapid contagion or persistent buffering—depending on context. To isolate the visual component of these interactions, we presented virtual social cues and found they were sufficient to induce sustained buffering. Using whole-brain cfos activity mapping, we identified 13 candidate hotspots across the brain associated with fear and its suppression by social cues. We are now using 2-photon GCaMP imaging and in situ hybridization techniques to classify functional and molecular cell types and map how they integrate social and threat-related information.

These findings show that social motion cues buffer fear via conserved subcortical circuits, establishing zebrafish as a model to dissect the sensory and neural basis of social buffering.

Poster number 19

Name: Ms. Brivio Sarah
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Affiliation: Université de Genève

Title of abstract:

Abolishing mafa activity in neural crests leads impaired HSC emergence

Authors' names and affiliations:

Sarah Brivio, University of Geneva; Chris Mahony, University of Birmingham; Meghna Shankar, IRIBHM Université Libre de Bruxelles; Sabine Costagliola, IRIBHM Université Libre de Bruxelles; Rui Monteiro University of Birmingham; Julien Y. Bertrand, University of Geneva

Abstract:

Hematopoietic stem cells (HSCs) originate from the aortic floor through endothelial-to-hematopoietic transition (EHT), a fundamental process of haematopoiesis. Our previous work identified mafa, as an important regulator of HSC expansion in the caudal hematopoietic tissue (CHT) through endothelial-dependent mechanisms acting on tfec, which we have shown is an important regulator of the CHT niche. We demonstrate that loss of mafa results in defective HSC specification from the aorta, associated with dysregulation of gata2b expression. We show that these mafa-dependent defects can be rescued by osm overexpression. To understand the molecular mechanisms, we generated a UAS:DN-mafa transgenic line to abolish mafa activity in a tissue-specific manner. We tested expression in HSCs, macrophages, endothelial cells or neural crest cells. We show that the latter are responsible for the EHT phenotype observed in mafa-deficient embryos. Our findings suggest that mafa contributes to both HSC emergence and expansion through distinct mechanisms: in neural crests EHT, while in CHT ECs it controls HSC expansion. Ultimately, we aim to fully extricate the effects of mafa on these two mechanisms.

Poster number 20

Name: Dr. Cayron Anne
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Affiliation: University of Geneva, Department of Pathology and Immunology

Title of abstract:

Markers of vulnerable intracranial aneurysm using models of primary cilia deficient zebrafish

Authors' names and affiliations:

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Abstract:

Intracranial aneurysms (IAs) affect 2–5% of the population and can cause life-threatening subarachnoid hemorrhage upon rupture. As criteria to predict rupture risk are insufficient, identifying markers of vulnerable IAs is crucial. Polycystic kidney disease (PKD), linked with primary cilia defects, is associated with high IA incidence and rupture risk. While endothelial alterations have been reported in PKD, specific markers of pathological vasculature remain unidentified.

We used zebrafish with impaired primary cilia. ift88 mutants lacking primary cilia and pkd1a/b morphants with non-functional primary cilia both developed brain hemorrhages, suggesting fragility of brain endothelial cells (ECs) resulting from primary cilia dysfunction. We generated ift88ko;flk1:eGFP zebrafish and produced pkd1a/b flk1:eGFP morphants. Unbiased single-cell RNA sequencing of brain ECs revealed dysregulation of numerous genes in both models. Notably, thrombospondin-type1-domain-containing 1 (thsd1), a gene associated to human IAs, was consistently upregulated.

We identified thsd1 as a potential biomarker of pathological brain vasculature, which may be help predict IA vulnerability in clinics.

Poster number 21

Name: Dr. Ciepla Paulina
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Affiliation: Université de Genève

Title of abstract:

Monitoring platelet activation: studying cytosolic calcium signals in zebrafish thrombocytes

Authors' names and affiliations:

Paulina Ciepla, Geneva Platelet Group, University of Geneva; Richard J. Fish, Department of Genetic Medicine and Development, University of Geneva; Jean-Luc Reny, Geneva Platelet Group, University of Geneva, Division of General Internal Medicine, Geneva University Hospitals; Marguerite Neerman-Arbez, Department of Genetic Medicine and Development, University of Geneva; Pierre Fontana, Geneva Platelet Group, University of Geneva, Division of Angiology and Haemostasis, Geneva University Hospitals.

Abstract:

Thrombocyte activation is critical for hemostasis maintenance. One of the first cellular processes altered during their stimulation is a change in the cytosolic calcium (Ca) concentration. However, studies of Ca signalling in zebrafish thrombocytes are limited.
To study thrombocyte Ca dynamics in vitro, whole zebrafish blood was treated with a range of known human platelet agonists. These compounds were tested to determine their ability to increase the Ca concentration in zebrafish thrombocytes. Next, using these modulators, we also treated the samples with Ca channel inhibitors/agonists to establish the influence of different Ca stores on these responses. A transgenic zebrafish line expressing a GFP-based transgenic Ca indicator in thrombocytes was thus generated (Tg(itga2b:GCaMP6s)) for in vivo study. At 5 days post-fertilization larvae underwent laser-induced injury to initiate clotting in the caudal vein. This enabled us to determine the Ca signal kinetics across the whole population of thrombocytes found in thrombi and measure their intercellular variabilities.
These novel assays expand on the existing panel of tests available for studying of the thrombosis in zebrafish.

Poster number 22

Name: Mr. Dharmaperwira Danin
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Affiliation: University of Lausanne

Title of abstract:

Mapping social cell types

Authors' names and affiliations:

Danin Dharmaperwira, University of Lausanne; Matilde Perrino, University of Trento; Alejandro Uribe-Arias, University of Lausanne; Johannes Larsch, University of Lausanne

Abstract:

Through exchanging and observing 'social cues', animals coordinate behaviour, such as collective movement in herds or swarms. What defines a social cue and how they are processed by neural circuits remain major open questions. Zebrafish emerge as a powerful model system in this domain. Beginning at about 10 days post fertilisation, zebrafish initiate shoaling behaviour, a spontaneous affiliative drive to swim near conspecifics. Previous work identified visual cues that can trigger shoaling, such as simple black dots that move in a fish-like fashion. Brain-wide mapping of neuronal activity in response to such stimuli has revealed distributed contributing brain areas, of which we know most about the thalamus: A dorsal nucleus (DT) is highly enriched for neurons functionally tuned to conspecific motion and is required for shoaling. The genetic identities of the relevant neurons in DT or other brain areas are still unknown. In this project I define the contribution of specific cell types to shoaling as a model for the neuronal control of social affiliation. Cell types processing social signals may be conserved across vertebrates.

Poster number 23

Name: Ms. Dori Sara
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Affiliation: University of Bern

Title of abstract:

From darkness to vision: models of laser-induced retinal injury to study regeneration

Authors' names and affiliations:

Sara Dori, University of Bern; Vittoria Spero, Augenklink Inselspital; Volker Enzmann, University of Bern

Abstract:

Retinal degenerative diseases are complex diseases in which the progressive death of retinal pigment epithelium and/or photoreceptors results in irreversible vision loss due to cell death and the formation of a glial scar in humans. In contrast, in organisms with high regenerative potential like zebrafish, regeneration of functional tissue is achieved through dedifferentiation and proliferation of Müller cells (MC). With our study we aim at uncovering differentially activated pathways that lead to either regeneration or glial scar formation upon injury. For this we set up two models of laser induced retinal degeneration (zebrafish and mouse) using a 532 nm laser system (Micron 5). We optimized laser power and pulse duration to induce replicable damages. We monitored the kinetics of the induced damages using optical coherence tomography imaging and performing immunohistological analyses. We showed early activation and proliferation of MC upon injury induction though expression of PCNA and GFAP and complete retinal regeneration in zebrafish at day 28 post injury. Omics technologies will be implemented in the future to characterize differences in gene expression upon damage.

Poster number 24

Name: Dr. Elhelbawi Ahmed
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Title of abstract:

m6A safeguards rb1 to orchestrate vertebrate eye development

Authors' names and affiliations:

Ahmed Elhelbawi, Department of Chemistry Biochemistry and Pharmaceutical Sciences University of Bern; Antonio Biundo, Max Planck Institute for Molecular Biomedicine Münster; Volker Enzmann, Department of Ophthalmology University Hospital of Bern; Stephan C.F. Neuhauss, Institute of Molecular Life Sciences University of Zurich; Sebastian A. Leidel, Department of Chemistry Biochemistry and Pharmaceutical Sciences University of Bern

Abstract:

N6-methyladenosine (m6A) is the most abundant internal modification of mRNA. Central to controlling gene expression, m6A is associated with various developmental and pathological processes. This dynamic modification is synthesized by Mettl3-Mettl14-Wtap. However, its role and dynamics in vertebrate development, as well as the mechanisms by which intracellular m6A levels are regulated, remain elusive. Here, we profiled the developmental dynamics of m6A in zebrafish and found that m6A dynamically decorates a specific set of signaling transcripts. Mettl3 deficiency leads to the dysregulation of genes related to eye disease and an underrepresentation of eye-specific cell types. These defects manifest as severe visual, histological, and behavioral abnormalities that lead to early lethality within one month post-fertilization. Mechanistically, we discovered that m6A regulates vertebrate organogenesis and eye formation through retinoblastoma 1 (rb1). The rb1 transcript is differentially stabilized in an m6A-dependent manner. Finally, we demonstrate that intracellular m6A levels are tuned by m6A-dependent differential splicing of Wtap, an evolutionarily conserved autoregulatory mechanism.

Poster number 25

Name: Mr. Gerber Raphael Aiki
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Title of abstract:

The role of tRNA modifications in developmental tRNA dynamics

Authors' names and affiliations:

Raphael Aiki Gerber, DCBP University of Bern, Mayuko Harada, DCBP University of Bern, Sebastian Andreas Leidel, DCBP University of Bern

Abstract:

tRNAs are essential adapter molecules required for the translation of mRNA. Importantly, tRNAs undergo post-transcriptional modification. These modifications tune tRNA structure and translation fidelity, and their absence causes human diseases. Although tRNA modification pathways have been extensively studied in yeast and human cells, little is known about tRNA biology during zebrafish development.
The wobble position of tRNA is a hotspot for modifications. Here, we focus on 5-methoxycarbonylmethyl-2-thiouridine (mcm5s2U), which is synthesized by the Elongator complex and Urm1 pathway. We observed a critical role of mcm5s2U in early zebrafish development. Therefore, we performed modification-aware tRNA sequencing to analyze tRNA dynamics during larval development. Furthermore, we are generating CRISPR–Cas9 mutants lacking Nsun2. This enzyme modifies tRNAs at variable-loop cytidines. Loss of NSUN2 function leads to neurodevelopmental disorders in humans.
Therefore, our project will provide new insights into the significance of tRNAs in vertebrate development.

Poster number 26

Name: Mr. Hannuschke Daniel
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Title of abstract:

Integrating live cell dynamics with high-dimensional multiplexed image data of developing zebrafish embryos

Authors' names and affiliations:

Daniel Hannuschke, DMLS - University of Zurich; Shayan Shamipour, DMLS - University of Zurich; Lucas Pelkmans, DMLS - University of Zurich

Abstract:

In developing organisms, cells make fate decisions by sensing morphogen gradients and subsequently upregulating lineage specific transcription factors mediating cell differentiation. Multiplex immunofluorescence approaches have allowed us to further investigate cell fate emergence in the context of cellular state features, such as the cytoskeleton and cell signaling, but are inherently limited in temporal resolution. In my project I aim to address this issue by acquiring single cell tracks from live data of developing zebrafish embryos from 512-cell stage to doming onset. I will establish a pipeline to integrate this live dataset with multiplexed immunofluorescence data, acquired with the whole-mount iterative IF pipeline in our lab. The goal is to map individual cell tracks onto single cells in the fixed data, allowing us to link single cells over time to investigate which signaling environments cells have experienced and how this “memory” might affect cell fate decisions. I hope to provide an end-to-end analysis pipeline that allows leveraging the strength of fixed, multiplex imaging methods to obtain a high-dimensional feature space without sacrificing temporal resolution.

Poster number 27

Name: Ms. Harada Mayuko
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Title of abstract:

The role of wobble uridine modifications during zebrafish development

Authors' names and affiliations:

Mayuko Harada, DCBP University of Bern; Anna Kusnierczyk, DCBP University of Bern; David Haberthür, Institute for Anatomy, University of Bern; Ruslan Hlushchuk, Institute for Anatomy, University of Bern; Möckli, Céline Melanie, VETSUISSE; Sebastian A. Leidel, DCBP University of Bern

Abstract:

Chemical modifications of tRNAs are critical for accurate and efficient translation. Wobble uridines (U34) at the anticodon are modified in all species. In eukaryotes, 5-methoxycarbonylmethyl-2-thiouridine (mcm5s2U) is synthesized at this position. Although U34-modification defects are associated with human neurodegenerative diseases consequent to codon-specific translation defects, their role in vertebrate development remains enigmatic. To better understand the role of U34 in zebrafish, we used CRISPR-Cas9 to inactivate U34-modifying enzymes and analyzed the mutant phenotypes. First, U34 mutants are significantly smaller than the wild type, have lower survival rates, and exhibit increased anxiety. Second, they exhibit reduced reproductive rates and severe developmental defects in their offspring. Third, we observed activation of immune pathways in mutants, consistent with the inflammation observed by histological analysis. Finally, deep sequencing revealed suppression of neuronal genes and impaired muscle organization in mutants, which may contribute to the observed behavioral abnormalities. Our results demonstrate that zebrafish depend on U34 modifications throughout their lives.

Poster number 28

Name: Mr. Hisler Vincent
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Affiliation: University of Fribourg

Title of abstract:

Beyond zebrafish: cardiac regeneration in Puntius titteya

Authors' names and affiliations:

Vincent Hisler, UniFr; Lana Rees, UniFr; Simon Blanchoud, UniFr; Anna Jazwinska, UniFr

Abstract:

Why can some organisms regenerate while others cannot? This question has been investigated for over a hundred years, but mostly in a limited number of model species, making it difficult to draw general conclusions. For instance, teleost fish were long considered to have an exceptional capacity for cardiac regeneration based on studies in zebrafish, until recent discoveries revealed important differences in other species. In this study, we examined myocardial regeneration in Puntius titteya, a freshwater fish from the Cyprinidae family, like the zebrafish. Following ventricular cryoinjury, we analyzed scar formation and resorption, myocardial neoformation, immune activation, and cardiomyocyte cell-cycle reentry and dedifferentiation. This study is in line with efforts to understand cardiac regeneration from a broader evolutionary perspective, which is essential for identifying the factors that promote or limit regenerative capacity.

Poster number 29

Name: Ms. Kientsch Jacqueline
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Affiliation: University of Zurich

Title of abstract:

EAAT2 deficiency triggers staged transcriptional responses in a zebrafish epilepsy model

Authors' names and affiliations:

Jacqueline G. Kientsch, DMLS/LSZGS; Milena Ronchetti DMLS/LSZGS; Stephan C. F. Neuhauss DMLS,UZH

Abstract:

Epilepsy is a common neurological disorder defined by recurrent seizures driven by dysregulated neuronal network excitability. Deficient clearance of extracellular glutamate is a strong trigger of hyperexcitability. Zebrafish lacking the glial glutamate transporter eaat2a develop spontaneous seizures and provide a tractable model of epileptogenesis. We performed bulk RNA-seq on dissected brains from eaat2a-/- and wild-type larvae at 3, 5, and 7 days post-fertilization (dpf). Differential expression analysis identified 899 dysregulated genes at 3 dpf and 2,103 at 5 dpf, with progressively larger effect sizes at later stages. Enrichment analyses indicated induction of motile cilia-associated and neuromodulatory programs, alongside suppression of genome maintenance and translation pathways, revealing a staged transcriptional response that intensifies with seizure progression.

Poster number 31

Name: Mr. Kunz Louis
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Title of abstract:

Cebpb and c-Myc are the Primary Signals leading to sparing of Zebrafish Embryos after FLASH Radiotherapy

Authors' names and affiliations:

Louis Kunz, UNIGE/HUG; Jonathan Ollivier, UNIGE/HUG; Veljko Grilij, CHUV; Pelagia Tsoutsou, UNIGE/HUG; Pierre Montay-Gruel, UZH; Marie-Catherine Vozenin UNIGE/HUG.

Abstract:

FLASH radiotherapy is a promising new treatment modality, allowing to reduce side effects while maintaining equivalent tumor control to conventional treatment, by moving from conventional time of delivery (minutes) to ultra-short delivery (< milliseconds). We recently obtained data suggesting that an active transcription is needed for the FLASH sparing. Molecular investigation should thus allow to identify primary signals leading to this effect.
We performed RNA sequencing 2 hours post irradiation of 1.5hpf and 4hpf ZFE irradiated with 8Gy using electron accelerators (eRT6: 5.5MeV; ELF: 7 or 9MeV, 0.1 - 6×10^6 Gy/s). Differentially expressed genes were identified using DESeq2, pathways using clusterProfiler and TFs using ChEA3. Dynamic of expression of the identify primary signal was then explored by qPCR.
Analysis revealed that the TFs cebpb and c-myc are uniquely activated after FLASH radiotherapy. Fam3a, a target of Cebpb was also found upregulated. Overall, our data indicates that cell proliferation and metabolism are uniquely activated after FLASH. Whether this unique activation is part of a resistance or regenerative program in the ZFE is under investigation.

Poster number 32

Name: Ms. Lai Han
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Title of abstract:

Novel zebrafish model for Lowe syndrome

Authors' names and affiliations:

Han Lai, Jingjing Zang, Monica Goldade, Stephan Neuhauss, Olivier Devuyst & Zhiyong Chen;
Institute of Physiology, Department of Molecular Life Sciences, University of Zurich

Abstract:

The proximal tubule (PT) cells of the kidney reabsorb a large amount of filtered low-molecular-weight proteins and solutes including glucose, phosphate and vitamins etc. Lowe syndrome is endolysosomal disorders causing dysfunction of proximal tubule, which is caused by mutations of OCRL gene, encoding for an inositol polyphosphate 5-phosphatase. Lowe syndrome manifests as PT dysfunction, congenital cataracts, and central nervous system. Almost all frameshift and nonsense mutations causing Lowe syndrome are located between exon 8 and exon 24.The loss of OCRL is compensated by its closest paralog INPP5B in both mouse and zebrafish, but not in human. In order to create genetic models for Lowe syndrome, we generated defective zebrafish model by targeting the exon 9 (ocrl-ex9) of ocrl gene and an inpp5b mutant zebrafish using CRISPR-Cas9 genome editing technology. Frameshift mutations causing premature stop codon were selected for ocrl-ex9 and inpp5b mutant lines. Phenotypic studies showed that 5 days-old ocrl-ex9 / inpp5b double knockout larvae exhibited proximal tubule dysfunction, developmental abnormalities, locomotor impairments, eye defects as well as hyperexcitability in brain. In conclusion, ocrl inactivation in exon 9 cause severe developmental defects, kidney proximal tubule dysfunction, eye defects and neuronal hyperexcitability, associated with mTORC1 hyperactivity. In future studies, we will perform both pharmacological and genetic rescue experiments targeting mTOR to further validate the underlying mechanisms and explore potential therapeutic strategies.

Poster number 33

Name: Dr. Leech Rebecca
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Affiliation: Université de Fribourg

Title of abstract:

Decoding skeletal muscle diversity in adult zebrafish: Myofiber subpopulations and regeneration at single-nucleus resolution

Authors' names and affiliations:

Rebecca Leech, University of Fribourg; Anna Jazwinska, University of Fribourg

Abstract:

Skeletal muscle is one of the body's largest and metabolically active tissues, yet the cellular diversity underlying its function and regenerative capacity remains incompletely understood. Zebrafish are a powerful model for dissecting muscle biology, owing to their conservation of cellular and genetic features with mammals. Their lateral musculature comprises distinct fiber populations: fast- and intermediate-twitch fibers capable of rapid, forceful contractions, superficial slow-twitch fibers specialized for sustained activity, and a rare tonic population with uniquely fatigue-resistant contractile properties. Intriguingly, careg:GFP and smyhc1:LY-Tomato reporters reveal non-overlapping expression within the slow-twitch compartment, exposing unexpected heterogeneity within a previously considered homogeneous population. To resolve this complexity, we will deploy single-nucleus RNA sequencing to define slow myofiber subpopulations and identify novel markers for diverse fibers. Using a zebrafish cryoinjury model, we will determine whether tonic fibers retain regenerative potential. This project will reconstruct transcriptional trajectories governing myofiber differentiation.

Poster number 34

Name: Ms. Lembke Carla
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Affiliation: Universität Bern, Institut für Anatomie

Title of abstract:

Cox7a1 Mediated CIV Homodimerization Impacts the Cardiac Injury Response in Zebrafish

Authors' names and affiliations:

Carla Lembke, Insitute of Anatomy, University of Bern; Nadia Mercader, Insitute of Anatomy, University of Bern

Abstract:

Respiratory complexes dynamically form supercomplexes to adapt to metabolic demands. The zebrafish heart undergoes a major metabolic shift after an injury, which is pivotal for its regenerative capacity. How supercomplex assembly impacts this process is unknown.
Here, we studied the role of supercomplex assembly factor cox7a1 using knockout (KO) and cardiomyocyte-specific overexpression (OE) zebrafish models. KOs lacked Complex IV homodimers (CIV2) and showed accelerated cardiac scar resolution with increased and prolonged cardiomyocyte proliferation. Multi-omics analysis revealed that KO hearts undergo metabolic rewiring and transcriptomic shifts related to muscle differentiation and oxidative stress. Adult OE fish showed no changes in scar resolution at 14 days post-cryoinjury. However, OE larvae displayed altered ventricular volumes following laser ablation, suggesting changes in cardiac stiffness.
Our results demonstrate that cox7a1 KO reduces CIV2 formation and primes the cardiac environment for regeneration through metabolic and transcriptional shifts. This highlights the role of respiratory supercomplex assembly as a regulator of zebrafish heart regeneration.

Poster number 35

Name: Ms. Mangattu Parambil Ayisha Marwa
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Title of abstract:

PACE: Integrating Human Genetics and Multimodal Charecterisation for Precision Medicine in Long-QT Syndrome

Authors' names and affiliations:

Ayisha Marwa Mangattu Parambil, University of Bern; Joana Rechsteiner, University of Bern; Varjany Vashanthakumar, University of Bern; Ekapaksi Wisnumurti, University of Bern; Dr. Marco Osterwalder, University of Bern; Dr. Christiane Zweier, University of Bern; Dr. Katja Odening; University of Bern; Dr. Nadia Mercader,University of Bern

Abstract:

Sudden cardiac death (SCD) accounts for ~15% of mortality, with long-QT syndrome (LQTS) a leading cause in the young. Current risk stratification remains disease-centric and fails to capture gene, variant, and modifier-specific effects. The Precision Diagnosis and Therapy in Cardiac Channelopathies (PACE) framework integrates clinical phenotyping with genetic analysis to enable genotype-resolved insights. In 60 LQTS patients, variants in KCNQ1, KCNH2, and SCN5A were identified in over half of cases, with ~20% carrying multiple variants. To functionally resolve these genotypes, we establish a multimodal pipeline linking human genetics to model systems. In zebrafish, KCNQ1-Arg231Cys variant induces atrioventricular block and reduced survival, consistent with clinical observations, and ongoing work extends this to additional variants. Parallel Drosophila studies reveal synergistic channel interactions, supporting non-additive effects. Human cardioids are being established as a novel platform for LQTS characterization. By coupling patient-specific variants to functional phenotypes, this framework enables gene and variant-specific risk stratification toward precision medicine in LQTS.

Poster number 36

Name: Mr. Marfin Maxim
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Title of abstract:

Understanding CHT vascular niche and the role of zeb2a in its establishment

Authors' names and affiliations:

Maxim Marfin, PATIM UNIGE; Julien Y. Bertrand, PATIM UNIGE

Abstract:

During embryogenesis, Hematopoietic Stem Cells (HSCs) are produced as a rare subset along the aorta, before they extravasate in the Caudal Hematopoietic Tissue (CHT), which creates a vascular niche to promote their expansion. Our goal is to identify transcription regulators required for the vascular niche fate establishment in the ECs. We performed scRNA-seq on sorted endothelial cells of 48 hpf embryos and leveraged SCENIC pipeline to predict TFs active in CHT-ECs. zeb2a, which appeared as a potential candidate, is indeed expressed in the anatomical region of the vascular niche before its establishment. zeb2a-morphants showed a complete absence of the vascular plexus that constitutes the CHT. zeb2a depletion also induced a significant increase in HSC expansion, which was documented via cmyb expression and using gata2b reported line. Migration impairment was ruled out as HSPCs migration to subsequent niches was equally increased. These opposing phenotypes raise the question of whether zeb2a exerts distinct, cell-autonomous roles in CHT-ECs and HSCs. These will be addressed using tissue-specific rescue and KO experiments, followed by transcriptomics analysis using zeb2a KO lines.

Poster number 37

Name: Dr. Marques Ines
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Title of abstract:

Activation of mfap5 in cardiac fibroblasts is essential for heart regeneration

Authors' names and affiliations:

Inês J. Marques, University of Bern; João AS Carvalho, University of Bern; Prateek Arora, University of Bern; Asma Laleh, University of Bern; Nadia Mercader, University of Bern

Abstract:

Zebrafish regenerate the heart in a process involving an early inflammatory phase followed by fibroblast activation, revascularization and replacement of the lost myocardium with new cardiomyocytes (CM). A transient “scarring-like” response, including shedding of extracellular matrix (ECM) does not inhibit regeneration, but might aid to generate a scaffold necessary for its correct progression. We studied the role of mfap5, a gene shown to be involved in skin wound repair and upregulated in human failing hearts, in zebrafish heart regeneration. We found mfap5 is expressed in a subset of fibroblasts in the heart. To study mfap5 in heart regeneration we created a loss of function (LOF) model. Downregulation of mfap5 led to increased CM proliferation at 7 dpi, concurrent with changes in pathways linked to muscle cell differentiation and metabolism. This did not lead to precocious regeneration, and at 30 dpi, we noted impaired scar resolution that allied with upregulation of ECM pathways. scRNAseq data indicated that mfap5 LOF led to a compensatory shift in fibroblast populations which might impact ECM resolution. Our data highlights the importance of mfap5 in heart regeneration.

Poster number 38

Name: Dr. Mikhajlov Oleg
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Title of abstract:

3D Organization of Guanine Crystal Stacks in Zebrafish Iridophores

Authors' names and affiliations:

Oleg Mikhajlov, University of Geneva; Konrad Hedderick, University of Geneva; Frederic Catala, ICFO – The Institute of Photonic Sciences, Barcelona, Spain; Michael Krieg, ICFO – The Institute of Photonic Sciences, Barcelona, Spain; Takuji Adachi, University of Geneva; Frank Julicher, Max Planck Institute for the Physics of Complex Systems, Dresden, Germany; Marcos Gonzalez-Gaitan, University of Geneva

Abstract:

Structural colors in zebrafish arise from iridophores, specialized skin cells containing membrane-bound guanine crystals arranged in parallel stacks. These multilayers act as Bragg reflectors, producing metallic blue coloration and angle-dependent iridescence through light interference. Although the optical principles are well understood, the mechanisms controlling stack formation, spacing, and stability remain unclear.

We combine mechanical measurements with quantitative reflection microscopy to investigate the physical basis of iridophore organization. Using optical tweezers and atomic force microscopy, we measure attractive and repulsive interactions between guanine crystals. In parallel, high-resolution reflectance microscopy captures interferometric patterns from isolated stacks, allowing us to infer crystal thickness, orientation, and intercrystal spacing. Integrating these data enables reconstruction of stack geometry at submicron resolution.

We test whether van der Waals attraction, balanced by repulsive forces from confined materials within membrane chambers, defines equilibrium spacing and stabilizes the multilayer architecture that generates structural color.

Poster number 39

Name: Dr. Monteiro Joana
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Title of abstract:

Integrated Aquaculture and Research Support Services at the Champalimaud Fish Platform

Authors' names and affiliations:

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Pedro Seco, Champalimaud Foundation, Lisbon, Portugal;
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Vanessa Pinto, Champalimaud Foundation, Lisbon, Portugal;
Mariana Salvador, Champalimaud Foundation, Lisbon, Portugal;
Ana Catarina Certal, Champalimaud Foundation, Lisbon, Portugal;

Abstract:

The Champalimaud Fish Platform integrates high-standard aquaculture with comprehensive research support services for aquatic vertebrate models. The facility maintains zebrafish and other teleosts under optimized health and husbandry conditions that ensure animal welfare and genetic integrity.
Services include colony management, controlled breeding, embryo care, genotyping, microscopy-based screening, and cryopreservation. We also offer the generation of genetically modified lines using Tol2-mediated transgenesis and CRISPR/Cas9 genome editing, implemented through adaptable workflows tailored to diverse research needs in close collaboration with the Molecular Tools and Transgenics Platform.
In parallel, species-specific methodologies are developed for emerging fish models, expanding their applicability.
Operating within a collaborative and flexible framework, the platform works closely with researchers to design customized services aligned with experimental goals and welfare standards. Collaborative projects with academic and industry partners further drive innovation.
With this strategy, we aim to promote high-quality, reproducible data and accelerate scientific findings.

Poster number 40

Name: Ms. Nissen Bente
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Title of abstract:

Impact of neuroactive chemicals on vertical positioning and swimbladder size in zebrafish larvae

Authors' names and affiliations:

Bente Nissen, Swiss Federal Institute of Aquatic Science and Technology (Eawag); Alexis Buatois, Eawag; Colette vom Berg, Eawag

Abstract:

Neuroactive chemicals are frequently detected in European waterbodies and may pose a risk to non-target species like fish by altering nervous system function and behavior. Substances with anxiolytic-like properties have shown to increase surface-oriented behavior in zebrafish larvae, a response that similarly occurs under hypoxia. Vertical positioning and buoyancy control rely on proper swim bladder (SB) regulation, which is essential for finding resources, mating, and predator avoidance. In this study, we tested eight chemicals with different mode of action and found that six of them induced SB hyperinflation (SBHI) after 16 h of exposure, and a significant change in vertical positioning over 4 h of behavioral tracking. Four of these chemicals showed SBHI at the end of the behavioral assay, indicating that the increased surfacing preceded SBHI, but the mechanistic connection between these effects remains unclear. Overall, this work investigates whether chemically induced surfacing represents a hypoxia-like response driven by chemical interference with the oxygen-sensing pathways and aims to clarify the mechanisms underlying the altered vertical positioning and SBHI.

Poster number 41

Name: Ms. Odermatt Nicole
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Affiliation: Department of Molecular Life Sciences, University of Zurich

Title of abstract:

Investigating the role of lactate dehydrogenase A in neuronal activity and seizure susceptibility

Authors' names and affiliations:

Milena Ronchetti, DMLS University of Zurich; Nicole Odermatt, DMLS University of Zurich; Stephan C. F. Neuhauss, DMLS University of Zurich

Abstract:

Epilepsy is a neurological disease characterized by excessive neuronal activity and aberrant brain energy metabolism. The brain with its high energy demand requires continuous energy input to maintain its function. The astrocyte-neuron lactate shuttle (ANLS) hypothesis suggests that astrocytes support neurons by converting glucose to pyruvate which is subsequently converted to lactate by the lactate dehydrogenase (LDH). However, the ANLS model has recently been challenged. Our study examines whether the loss of LDHA, the subunit expressed in astroglia, and the resulting lack of lactate affects basal brain activity and modulates seizure susceptibility and characteristics. In our studies we analysed calcium imaging data from our ldha mutant zebrafish line. The mutant zebrafish had a decreased area under the curve, while event amplitude, duration and count remained unchanged. However, exposed to epileptic seizures, the mutant's seizure susceptibility and patterns remained unaltered compared with wildtypes. These findings run against the expectations derived from the ANLS and therefore challenge the current model.

Poster number 42

Name: Mr. Ottiger Michael
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Affiliation: University of Zürich

Title of abstract:

Dissecting the roles of bmal1 paralogs in the zebrafish circadian system

Authors' names and affiliations:

Michael Ottiger, Jingjing Zang, Laura Köcher, Stephan CF Neuhauss; University of Zürich, Department of Molecular Life Sciences

Abstract:

The circadian clock coordinates physiological and behavioral processes in alignment with environmental light–dark cycles. In zebrafish (Danio rerio), genome duplication has generated paralogous clock genes, including bmal1a and bmal1b, whose specific functions remain unclear. Here, we investigate the roles of bmal1 paralogs using CRISPR/Cas9-generated single (bmal1a KO, bmal1b KO) and double (bmal1a/bmal1b KO) mutant lines. Morphological analyses were performed to assess developmental consequences of gene loss. No severe defects were observed and overall morphology appeared normal.
To explore compensatory mechanisms within the circadian network, we analyze the expression of bmal genes (bmal1a, bmal1b, bmal2) across different mutant lines.
Furthermore, locomotor activity is assessed under varying light conditions and light cycles to determine whether and how circadian rhythmicity is disrupted at the behavior level.
This work aims to elucidate how bmal1 paralogs contribute to circadian regulation, functional redundancy, and network robustness in vertebrate systems.

Poster number 43

Name: Ms. Parel Delphine
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Affiliation: Université de Fribourg

Title of abstract:

Feeling the stretch: uncovering primitive proprioceptors in zebrafish and their role in movement coordination

Authors' names and affiliations:

Delphine Parel, UNIFR; Rebecca Leech, UNIFR; Sylvain Bertho, UNIFR; Anna Jazwinska, UNIFR

Abstract:

Muscle spindles are stretch-sensitive proprioceptors that are considered as a tetrapod innovation, with no equivalent reported in fish. We have identified zebrafish cells that are morphologically reminiscent of muscle spindles, challenging this assumption and opening new questions about the evolution of proprioception. Using enhancer screening, we isolated a tnnt1 regulatory element that drives EGFP expression in these putative spindle-like fibers, enabling us to track their formation across ontogenesis with the tnnt1:EGFP transgenic line. To probe their regenerative capacity, we are deploying both classical (NTR1/MTZ) and optimized (NTR2/MTZ) nitroreductase-based ablation systems. The latter will require 100-fold lower MTZ concentrations, making long-term ablation studies feasible. We will assess locomotor performance of fish missing muscle spindles using video tracking to determine whether these fibers play a functional role in coordinated movement. Together, this work will clarify whether zebrafish harbor a primitive or convergent form of proprioceptive sensory structure, with broad implications for understanding the evolutionary origins of the vertebrate sensorimotor system.

Poster number 44

Name: Ms. Joana Pereira Couto
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Affiliation: University of Geneva, department of pathology and immunology

Title of abstract:

Modelling telomere biology disorders in zebrafish impairs developmental hematopoiesis.

Authors' names and affiliations:

Joana Pereira Couto, University of Geneva; Julien Y. Bertrand, University of Geneva

Abstract:

Telomere Biology Disorders (TBDs) are rare diseases caused by pathogenic variants in telomere maintenance genes, leading to genomic instability, premature age-related diseases, and hematological deficiencies. Mutations in ZCCHC8, involved in non-coding RNAs degradation and telomere homeostasis, have been identified in TBD patients. However, their functional consequences remain unclear. Preliminary data suggest that these mutations disrupt the interaction between the nuclear exosome targeting (NEXT) and the human silencing hub (HUSH) complexes, both involved in genome stability. The zebrafish is a relevant model to study the consequences of ZCCHC8 mutations on telomere maintenance, genome stability, and hematopoiesis. We found that zcchc8-morphants show profound defects in HSC emergence, due to hyper-inflammation in the hemogenic endothelium, leading to apoptosis. In parallel, we are establishing zcchc8-deficient zebrafish models, using CRISPR-Cas9 for gene deletion, prime editing to mimic the G184R mutation, and a ubiquitous promoter-driven zcchc8G174R for overexpression. Altogether, these combined approaches should allow us to model these complex diseases in the zebrafish.

Poster number 45

Name: Ms. Perrino Matilde
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Title of abstract:

Visual perception of social groups in zebrafish

Authors' names and affiliations:

Matilde Perrino, University Trento & University of Lausanne; Alejandro Uribe Arias, University of Lausanne; Giorgio Vallortigara, University of Trento; Johannes Larsch, University of Lausanne

Abstract:

Many animals live in groups and make decisions based on others, integrating information from multiple social partners. The number of conspecifics performing an action is a key determinant of behaviour, requiring the nervous system to extract features that scale with group size. Despite extensive work on group behaviour, the mechanisms allowing individuals to integrate multiple social signals and assess their quantity remain unclear.We address this in zebrafish using behavioural assays and two-photon calcium imaging. We investigate how visual features -number of elements and speed- shape shoaling and their integration in the dorsal thalamus. We show that motion cues alone elicit attraction and preference for larger groups, with choices shaped by number and speed in a weighted manner. Dorsal thalamic neurons form two populations responding to bout-like and continuous motion, segregated along the anterior–posterior axis with contralateral tuning. Activity scales with group size via increased recruitment and graded magnitude, while individual neurons integrate element number and speed.These findings show how visual cues from social groups are integrated in a neural circuit for shoaling.

Poster number 46

Name: Mr. Pham Minh Khoa Yves
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Affiliation: Department of Biology, University of Fribourg

Title of abstract:

Engineering zebrafish models of myopathic Ehlers-Danlos Syndrome to decode COL12A1 pathogenesis and accelerate targeted therapies

Authors' names and affiliations:

Minh Khoa Y. Pham, Department of Biology, University of Fribourg; Rebecca Leech, Department of Biology, University of Fribourg ; Anna Jazwinska, Department of Biology, University of Fribourg

Abstract:

Myopathic Ehlers-Danlos Syndrome (mEDS) is an inherited disorder affecting ~1 in 5,000 individuals, characterized by muscle weakness, joint instability, and chronic pain, with symptoms worsening throughout life. Despite its prevalence, mEDS remains incurable and its disease mechanisms are poorly understood. The condition arises from mutations in col12a1, encoding collagen type XII, a structural protein bridging muscle fibers to the extracellular matrix. Current models are limited to the recessive form, leaving a critical gap, as most patients carry heterozygous dominant mutations that remain unmodeled. Determining whether these act through gain-of-function or dominant-negative mechanisms is essential, as this directly informs therapeutic strategy. We propose generating zebrafish mutant lines via CRISPR/Cas9 and base/prime editing to model both recessive and dominant mEDS variants. Multilevel characterization of these lines will elucidate underlying disease mechanisms, while mutation-specific drug screening will identify therapeutics amenable to clinical translation and precision medicine.

Poster number 47

Name: Ms. Rebagliati Chiara
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Affiliation: University of Zurich

Title of abstract:

Image-Based Analysis of Cell Fate Specification in Embryonic Development

Authors' names and affiliations:

Chiara Rebagliati, University of Zurich; Gian-Marco Schaniel, University of Zurich; Shayan Shamipour, University of Zurich; Lucas Pelkmans, University of Zurich

Abstract:

During gastrulation in the zebrafish embryo, cell fate specification is coordinated by physical and chemical cues including the Nodal, FGF, BMP, and Wnt morphogen gradients. While these signals result in robustly patterned structures, distinct cellular fates can emerge even in neighboring cells in similar signaling contexts. In vitro studies suggest that that variability in signaling responses can arise from heterogeneity in physicochemical cellular state or combinatorial ligand-receptor interactions, but how these features fine-tune signaling responses to ensure robust cell fate specification in development has yet to be fully explored. To address this question, an imaging-based method integrating multiplexed RNA FISH and iterative indirect immunofluorescence (4i) in whole-mount zebrafish embryos in high-throughput has been established. This approach will be used to obtain a multimodal dataset that captures expression of signaling network components, downstream signaling effectors, and cellular state properties in embryos during gastrulation, so as to explore which single-cell features contribute to the establishment of signaling and cell fate patterns.

Poster number 48

Name: Dr. Rodriguez-Ramirez Carlos
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Affiliation: Center for Integrative Genomics, University of Lausanne

Title of abstract:

Genetic basis of shoaling behaviour evolution in zebrafish

Authors' names and affiliations:

Carlos Rodriguez-Ramirez, Center for Integrative Genomics; Yann Emmenegger, Center for Integrative Genomics; Johannes Larsch, Center for Integrative Genomics;

Abstract:

Understanding the genetic basis of phenotypes is a key goal of biology. Group swimming (shoaling) in zebrafish (Danio rerio) is a good system to study the genetic basis of social behaviour. A recent breakthrough in the field is that visual cues are sufficient to trigger shoaling behaviour in Danio rerio. Zebrafish have been shown to engage in shoaling with projected dots that moved in a fish-like burst and glide fashion (Larsch and Baier, 2018, Current Biology). Using this reproducible and scalable system, we conducted an artificial selection experiment. We selected individuals for 8-10 generations for either higher or lower shoaling tendency. We find that selection leads to a profound shift in shoaling tendency between the two lines. Now, we are mapping the genetic basis of shoaling evolution in these lines through a QTL mapping experiment, complemented with transcriptomic analysis of brain tissue. With this study we hope to generate insights on how behavioural evolution can occur over a few generations, and also on the genetic and neurobiological basis of social behaviours.

Poster number 49

Name: Ms. Ronchetti Milena
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Affiliation: Department of Molecular Life Sciences, University of Zurich

Title of abstract:

Exploring the role of lactate dehydrogenase in regulating neuronal excitability in zebrafish

Authors' names and affiliations:

Milena Ronchetti, Department of Molecular Life Sciences University of Zurich, Nicole Odermatt, Department of Molecular Life Sciences University of Zurich ,Stephan C. F. Neuhauss, Department of Molecular Life Sciences University of Zurich

Abstract:

Neurons need a constant energy supply for normal function. The astrocyte–neuron lactate shuttle (ANLS) is the prevailing model in which astrocyte-derived lactate generated by lactate dehydrogenase (LDH) fuels neuronal oxidative metabolism. While this metabolic coupling is well described in physiological conditions, its role during epilepsy remains unclear. Epilepsy is characterized by excessive neuronal activity and aberrant energy metabolism. Although metabolic therapies show antiepileptic properties, the underlying mechanisms are not fully understood. Here, we investigate how LDH regulates neuronal activity using cell-type specific knockouts of ldh genes to dissect astrocytic and neuronal contributions. Brain activity is assessed via calcium imaging under baseline and seizure conditions. Global knockout of ldhba shows no difference in basal brain activity. In parallel, the metabolic sensors LiLac and SweetieTS enable in vivo measurement of lactate and glucose dynamics alongside single-cell transcriptome and qPCR analysis. Together, these studies aim to build a comprehensive metabolic profile of the epileptic brain and unravel the mechanisms underlying seizure activity.

Poster number 50

Name: Ms. Swaminathan Abhinaya
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Affiliation: University of Zurich

Title of abstract:

Investigating retinal metabolism in Leber Congenital Amaurosis using Zebrafish models

Authors' names and affiliations:

Abhinaya Swaminathan, Department of Molecular Life Sciences, University of Zurich, Life Science Zurich Graduate School, Ph.D. Program in Molecular Life Sciences, Zurich, Switzerland; Jacqueline Kientsch,Department of Molecular Life Sciences, University of Zurich, Life Science Zurich Graduate School, Ph.D. Program in Molecular Life Sciences, Zurich, Switzerland; Stephan C.F. Neuhauss, Department of Molecular Life Sciences, University of Zurich.

Abstract:

The retina is an energy-intensive tissue and disruptions in metabolic pathways have been associated with retinal dystrophies. Leber Congenital Amaurosis (LCA), is an inherited retinal disorder causing early-onset blindness, linked to mutations in over 29 distinct genes. We propose that metabolic dysfunction could be involved in the pathogenesis of LCA. We focused first on LCA1 or retinal variant guanylyl cyclase 2d (gucy2d), using a gucy2e knockout zebrafish model that we generated and analyzed the phenotype at an early larval stage (5dpf) to characterize the onset of disease. We assessed retinal integrity by immunostaining for proteins expressed in the retina which were comparable to wildtype. Bioenergetics was assayed using the Seahorse XF Analyzer® on whole eye explants where in GlycoStress measurement ECAR (mpH/min) for the parameter Glycolysis was reduced in gucy2e -/- compared to wildtype, conversely glycolytic reserve was increased in gucy2e -/-. Visual function will be evaluated by Electroretinography (ERG). Our results indicate that there is an early onset metabolic dysfunction that predates degeneration in gucy2e -/-. We will extend this analysis to other LCA genes.

Poster number 51

Name: Ms. Tichy Nathalie
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Title of abstract:

Investigating Microglial Lipid Dysregulation Using Zebrafish and Human-like Xenotransplantation Models

Authors' names and affiliations:

Nathalie Tichy, University of Zurich; Francesca Peri, University of Zurich

Abstract:

Microglia play a crucial role in clearing neuronal debris, which requires efficient degradation, recycling, and cargo sorting. These processes are critical during neurodegeneration, as many risk genes encode proteins involved in microglial phagocytosis. Disease-associated microglia accumulate lipids impairing function and homeostasis, yet how lipid pathways shape phagocytic processing in vivo remains unclear. The zebrafish is a powerful model to study neuron–microglia interactions. Our recent work identified the gastrosome, a conserved vesicular compartment in the phagocytic pathway that expands with increased cell death. In NPC1-deficient microglia, cholesterol accumulation enlarges the gastrosome driving a disease-associated morphology. Similarly, ABC transporters are regulators of cholesterol efflux and amyloid-beta handling during AD. Using a CRISPR–Cas9 zebrafish screen, we identified ABCA1 and ABCG1, whose loss causes lipid accumulation and gastrosome enlargement. Combining imaging with genetic and pharmacological perturbations in zebrafish and HuZIBRA, a human–zebrafish platform with transplanted iPSC-derived microglia-like cells, reveals conserved lipid handling mechanisms.

Poster number 52

Name: Mr. Vasquez Emanuel
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Affiliation: EPFL, Oates lab

Title of abstract:

Understanding the Effects of Heat Shock on Zebrafish Somitogenesis

Authors' names and affiliations:

Emanuel Vasquez, EPFL

Abstract:

Somitogenesis relies on the precise synchronization of molecular oscillations and physical tissue remodeling. We use live microscopy to investigate the robustness of the developmental clock by subjecting zebrafish embryos to a 30-minute heat shock (39–40°C) between the 6–15 somite stage. Our data reveal that this acute thermal stress induces a consistent 5-somite developmental delay, related to the disruption of clock oscillations. The presomitic mesoderm (PSM) retains a physiological "memory" of the perturbation; although segment boundary formation eventually resumes, stochastic defects emerge post-recovery. These findings suggest that while the segmentation machinery possesses a degree of resilience, acute thermal stress introduces latent instabilities in the PSM that compromise long-term patterning accuracy. By identifying the mechanical and temporal sources of these defects, we highlight the vulnerability of the zebrafish body plan to rapid environmental shifts during critical windows of morphogenesis.

Poster number 53

Name: Ms. Wittmann Jana
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Title of abstract:

Investigating the Role of Cell Network Architecture in Coupling Fibroblasts In Vivo

Authors' names and affiliations:

Jana Wittmann, DMLS (UZH), Kai Hofmänner, DMLS (UZH) & IRCAN (Nice, France), Darren Gilmour, DMLS (UZH)

Abstract:

Fibroblasts are the predominant cells of the connective tissue. Once considered a homogeneous population mainly maintaining the extracellular matrix, they are now recognised as highly heterogeneous, also functionally, with roles in tissue maintenance, repair, and disease. Recent studies highlight their dynamic behaviour, including transient phenotype changes and roles in stem cell niches and regeneration.
We investigate to which extent fibroblasts organise as interconnected tissue-like structures, aiming to better understand their collective behaviour and adaptive differentiation. For this zebrafish larvae are an ideal model, as fibroblasts emerge early as a diverse population that remains in close spatial proximity.
Through quantitative analysis of in toto imaging data, we were able to show that fibroblast in this system form an interconnected network spanning all sub-types. The use of novel cell adhesion reporters supports the conclusion that these are functional cell-cell contact points. To probe how these contacts are used in cell-cell communication, we are now combining live imaging for calcium, a prevalent secondary messenger, with a pharmacological interference approach.

Poster number 54

Name: Mr. Zhang Yixin
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Title of abstract:

User-Defined FGF Signalling Activation via Optogenetics

Authors' names and affiliations:

Yixin Zhang, University of Zurich; Robert Bill, University of Zurich; Jérôme Julmi, University of Zurich; Darren Gilmour, University of Zurich

Abstract:

Gain of function mutations in FGF receptors (FGFR) are known drivers for developmental abnormalities and cancers. Impacts of such hyperactivation of signalling vary significantly in different tissue contexts, possibly due to the selection of downstream signalling pathways. This project utilises an optogenetic approach to gain control over FGF signalling pathway at different levels. First, opto-FGFRs are constructed and expressed in the zebrafish basal epidermis, which induces a rapid epithelial to mesenchymal transition and increases the fluidity of monolayer. Next, we aim to combine our tool with real-time downstream reporters, to examine if specific pathway is selected and quantify the downstream activation during opto-FGFR activation. Lastly, we aim to activate FGF signalling axis at different level by developing light-controlled Ras and Rac1, whose mutation has been detected in many cancerous tissues. By comparing signalling pathway selection and fate changes with different inputs, and later in other contexts, we hope to shed light on how local tissue environments influence the interpretation of such pathways.