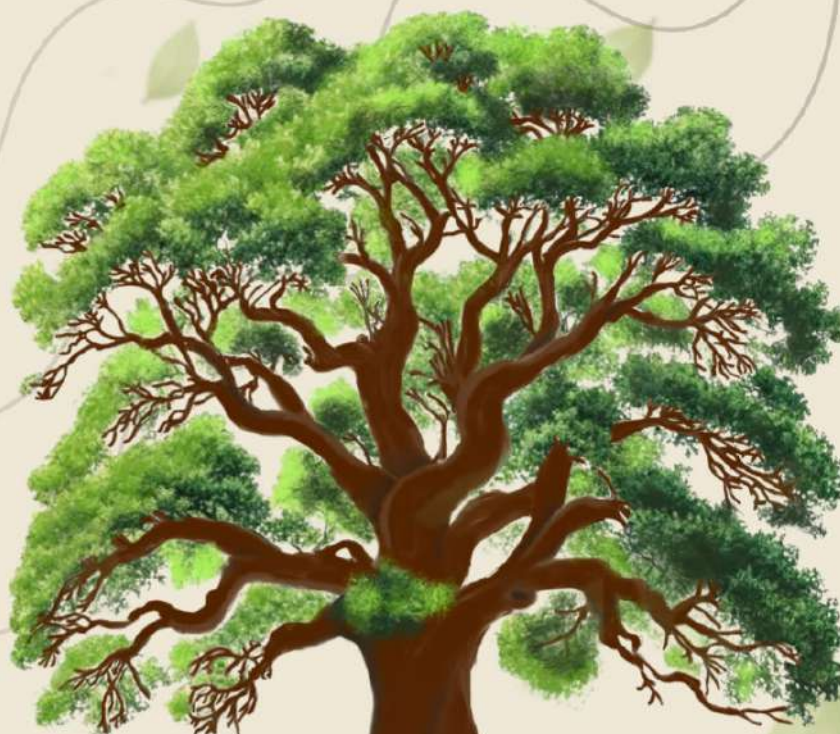




St. Xavier's College (Autonomous), Kolkata
POSTGRADUATE & RESEARCH DEPARTMENT OF BIOTECHNOLOGY

CHIASMA 2026

A CROSSOVER OF MINDS



ENVO-BIO

EXPLORING THE WEB OF LIFE

EDITION XVI

ENVO-BIO

EXPLORING THE WEB OF LIFE



St. Xavier's College (Autonomous), Kolkata

POSTGRADUATE & RESEARCH DEPARTMENT OF BIOTECHNOLOGY

CHIASMA 2026

A CROSSOVER OF MINDS



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EDITORIAL BOARD

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PHOTOGRAPH & ARTWORK

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ATREYEI BANERJEE
DEBARPITA DAS
MADHUJA BHATTACHARYA



MESSAGES

MESSAGE FROM THE RECTOR



Perhaps the most profound discovery of modern biology is also its most elementary: life never exists in solitude.

From genes and cells to organisms and ecosystems, life unfolds through connection, exchange, and profound interdependence. A microorganism in the soil, a pollinating insect, an ancient forest, a winding river, and the human body may seem to inhabit separate worlds. Yet, each is woven into an intricate web of relationships that sustains life itself. The deeper science probes the mysteries of life, the more clearly it reveals that relationship lies at its very heart. It is this profound interconnectedness that the 16th edition of *Chiasma* illuminates through its theme, “Envo-Bio: Exploring the Web of Life.” The name *Chiasma* itself evokes an encounter — a point of crossing where distinct paths meet, exchange, and open new possibilities. In this spirit, *Envo-Bio* unites what can never truly be separated: biology and the environment, the organism and the ecosystem, scientific discovery and human stewardship.

To understand a living system is to understand the web that sustains it; to alter a single strand is to send ripples across the whole. Here lies the quiet gravity of science: as our power to understand and intervene in life grows, so too must our conscience. As the Xaverian scientific community asks, “What can we achieve?” it must also ask, “What ought we to nurture, and who benefits from our choices?” For a scientist, true wisdom lies in peering through the microscope without ever losing sight of the horizon. In the Ignatian tradition, knowledge finds its fullest meaning when it becomes service — when discovery contributes to the common good and to the care of our common home.

Today’s environmental crises lend urgency to this vision. Climate disruption, pollution, habitat destruction, and biodiversity loss serve as stark reminders that when one strand of the web is strained, the effects reverberate across the whole. We are neither masters above this living network nor spectators outside it; we are woven into its fabric. Humanity cannot flourish on a wounded planet. To care for our common home is, ultimately, to care for one another and for the generations yet to come.

May this edition of *Chiasma* stir wonder at the intricate dance of life, kindle a passion for responsible scientific inquiry, and affirm that life flourishes through relationship. As you journey through these pages, may you discover your place within the web — not as distant observers, but as responsible participants entrusted with its care.

My warmest congratulations to the Department of Biotechnology, the editorial team, and every contributor who has brought this 16th edition to fruition. May *Chiasma* inspire us all to explore deeply, question courageously, discover responsibly, and serve life with wisdom and grace.

Rev. Dr. Sacaria Joseph, SJ

Rector

St. Xavier’s College (Autonomous), Kolkata

MESSAGE FROM THE PRINCIPAL



I am delighted to share that the Postgraduate and Research Department of Biotechnology, St. Xavier's College (Autonomous), Kolkata, is launching the sixteenth edition of its departmental magazine, "Chiasma 2026– A Crossover of Minds". This year's theme is "Envo-Bio: Exploring the Web of Life" which aptly depicts the intricate network connecting living organisms on this earth with their surrounding environment. The inherent interdisciplinary nature of biotechnology provides a beautiful platform to appreciate such interconnectedness of diverse life forms with their environment. The applications of biotechnology play a crucial role in the current global scenario by improving human health and societal well-being, enhancing future food security through sustainable agricultural practices and environmental conservation.

This magazine is a culmination of months of tireless effort on the part of the students and faculty members of the Postgraduate and Research Department of Biotechnology. This annual magazine provides a platform for the young aspiring biologists to express their innovative and critical ideas on the aforementioned theme. The department is productively engaged high end research which is reflected in the broad areas covered in this edition of the magazine on the part of the faculty members and students of the department. Since its inception in 2006, the Department has continually strived toward excellence in teaching and research, fostering an environment that encourages inquiry, collaboration and innovation. The recognition earned by its members at national and international levels stands as a testament to their dedication and competence. I extend my warm congratulations to the faculty members, research scholars and students of the Postgraduate and Research Department of Biotechnology for their hard work and collective effort in bringing out this edition of Chiasma 2026. May this spirit of academic pursuit and innovation continue to inspire greater accomplishments in the years ahead.

God bless you all. Nihil Ultra!

A handwritten signature in black ink, reading "D. Savio SJ".

Rev. Dr. Dominic Savio, SJ

Principal

St. Xavier's College (Autonomous), Kolkata

MESSAGE FROM THE VICE-PRINCIPAL (ARTS AND SCIENCE)



“Chiasma 2026– A Crossover of Minds”, the annual publication of the Postgraduate Department of Biotechnology, is now in its sixteenth year. This continuity stands as a remarkable testament to the department’s unwavering commitment to academic excellence, advanced research, and the dissemination of knowledge. This year’s theme, “Envo-Bio: Exploring the Web of Life” reflects the interconnectedness between diverse living forms on the Earth with their surrounding environment. In the current situation of global climate change, biotechnology can provide an interdisciplinary platform for transforming biological resources into sustainable approaches to restore the ecosystem. The magazine provides an engaging platform for the students and research scholars to showcase their scientific insights, creativity, and intellectual curiosity. Along with its scientific contributions, it also serves as a niche for literary and artistic expression, encouraging a holistic growth that nurtures both analytical and creative minds. Congratulations to the Department of Biotechnology on this outstanding achievement. May Chiasma 2026 ignite a lasting spirit of discovery, creativity, and achievement in every learner and researcher.

Prof. Bertram Da'Silva

Vice - Principal (Arts and Science)
St. Xavier's College (Autonomous), Kolkata

MESSAGE FROM THE DEAN OF SCIENCE



It gives me immense pleasure to extend my warmest congratulations to the Department of Biotechnology on the release of the sixteenth edition of their annual magazine, “Chiasma 2026- A Crossover of Minds”. Over the years, Chiasma has evolved into an exemplary platform that not only celebrates scientific inquiry but also fosters collaboration and intellectual growth within our academic community. This year’s theme, “Envo-Bio: Exploring the Web of Life”, highlights the interdependence of biological and environmental systems. The diverse range of articles featured in this edition reflects the department’s unwavering commitment to interdisciplinary research, creativity, and scholarly excellence. I extend my heartfelt appreciation to the editorial team and all contributors of Chiasma 2026 for their dedicated work and enthusiasm which brings this edition to life. I am confident that this publication will continue to inspire students, researchers, and readers alike while further strengthening the Department’s significant contributions to the ever-evolving field of biotechnology.



Dr. Indranath Chaudhuri

Dean of Science

St. Xavier’s College (Autonomous), Kolkata

MESSAGE FROM THE DEAN OF ARTS



It gives me immense pleasure that the Postgraduate and Research Department of Biotechnology, St. Xavier's College (Autonomous), Kolkata, is launching the sixteenth edition of its departmental magazine, "Chiasma 2026 - A Crossover of Minds". The theme for the 2026 issue, "Envo-Bio: Exploring the Web of Life" highlights the dynamic interplay between living organisms and their surroundings. This theme reminds us of the profound applications of biotechnology on human health and societal well-being, enhancing future food security through sustainable agricultural practices and environmental conservation. As we explore these frontiers, we recognize that advances in biotechnology not only deepen our understanding of life, but also empower us to address global challenges responsibly and creatively. This shared pursuit of knowledge encourages collaboration, innovation, and thoughtful action, fostering a generation of scholars who are prepared to contribute meaningfully to the world around them. I congratulate the Department of Biotechnology, all contributors, editors, and readers for their dedication and commitment to this endeavor.

Dr. Farhat Bano

Dean of Arts

St. Xavier's College (Autonomous), Kolkata

MESSAGE FROM THE HEAD OF THE DEPARTMENT



It gives me immense pleasure to introduce the 16th edition of our departmental magazine “Chiasma”. As the department completes 20 years of its glorious journey since its inception, and embarks onto the next venture with new dreams and vision, “Chiasma” has been the platform that mirrors its mission. A department that is truly interdisciplinary in nature, through Chiasma encourages crosstalk between minds that apparently comes from different scientific genre, but mingles at the end to celebrate science in its purest form. The magazine tends to ignite scientific minds by encouraging contributions from the students, research scholars and faculties, giving space for meaningful curiosity and the courage to ask questions be it on the boundless realms of science or on the philosophy of life.

We, as a department are deeply grateful to Rev. Dr. Dominic Savio, SJ, our respected Principal, for his inspiration and guidance. His vision have continually encouraged us to push our boundaries to reach greater heights. Our sincere thanks to Prof. Bertram Da’ Silva, Vice Principal; Dr. Indranath Chaudhuri, Dean of Science; and Dr. Farhat Bano, Dean of Arts, for their unwavering support and hand-holding, at all times.

My heartfelt gratitude and sincere appreciation for Dr. Priyanka De and Dr. Parinita Majumdar, for shouldering this herculean responsibility that has breathed life into “Chiasma”. My biggest round of applause to the editorial team, whose tireless efforts and steadfast dedication over the last few months have made timely publication of this magazine possible.

My warm regards and appreciation for the entire fraternity of the Post-Graduate and Research Department of Biotechnology for their valuable contributions and enthusiastic support. May we continue to dream, appreciate our scientific “unity in diversity” and unravel the true meaning of science.

Dr. Ronita Nag Chaudhuri

Associate Professor and Head of the Department
Postgraduate & Research Department of Biotechnology
St. Xavier’s College (Autonomous), Kolkata

FROM THE EDITOR'S DESK



The departmental magazine “Chiasma - A crossover of minds” is in its sixteenth year and truly reflects the enduring spirit of curiosity, creativity, and academic excellence, since the time of the release of the inaugural issue in 2010. The theme of “Chiasma 2026” is “Envo-Bio: Exploring the Web of Life,” highlighting the interdependence of living organisms and their dynamic relationship with the environment. Every organism is an indispensable part of the ecosystem, intricately connected to the biotic and abiotic components of its surroundings. As an inherently interdisciplinary field, biotechnology bridges diverse areas of science to unravel these complex interactions and deepen our understanding of the interconnected web of life. The annual magazine offers a creative and thought-provoking platform for the young minds to share their innovative perspectives, ideas, and insights under its current theme. The entire Magazine Committee has worked tirelessly, without whose hard toil, the publication of the present volume would have been next to impossible. In spite of having a packed class schedule, the members worked in unison, editing articles, designing the layouts and contents.

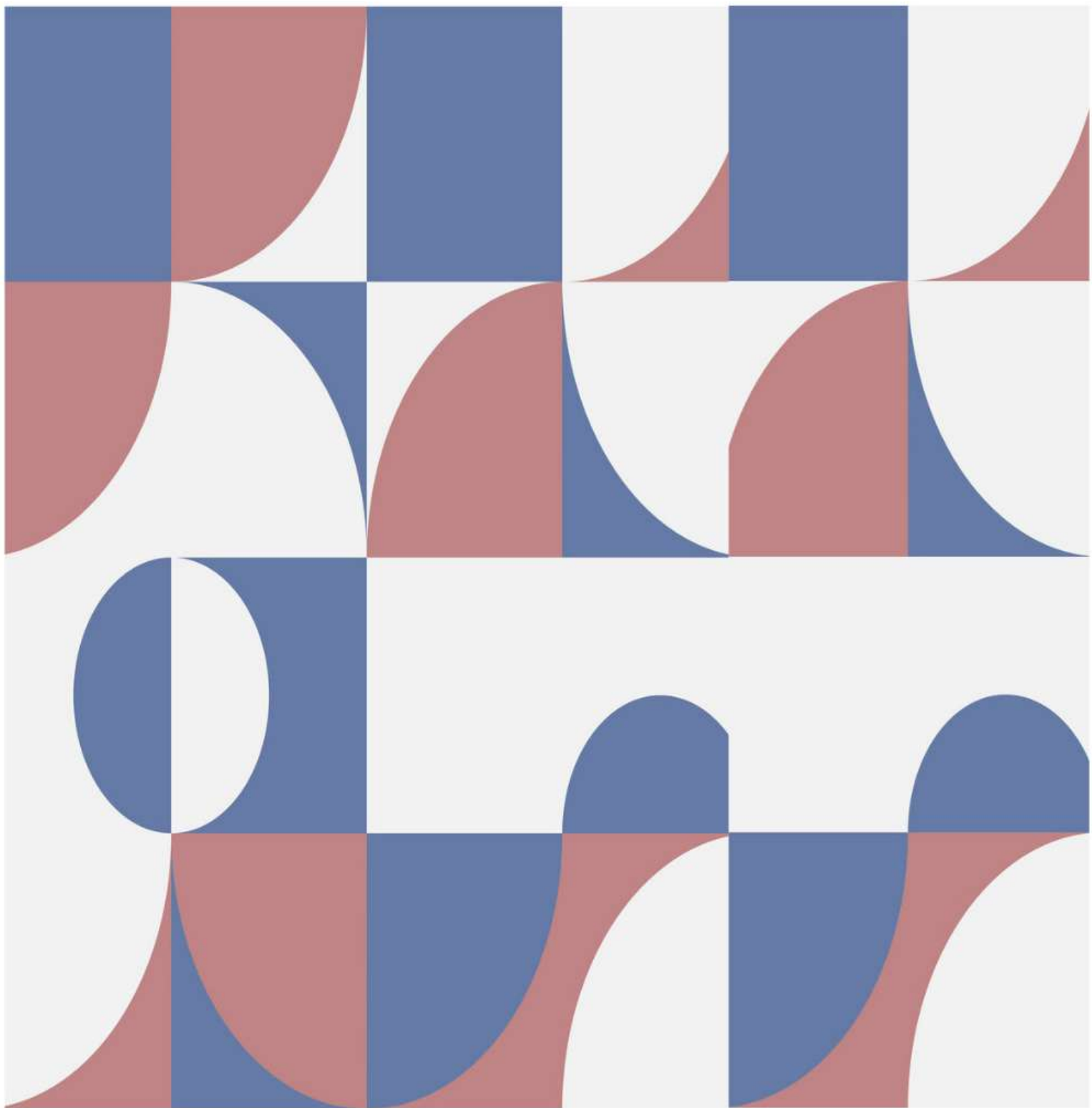
We express our heartfelt gratitude to our respected Father Principal, Rev. Dr. Dominic Savio, SJ, for his continuous motivation and encouragement. We also wish to thank Prof. Bertram Da Silva, our Vice Principal, Dr. Indranath Chaudhuri, our Dean of Science and Dr. Farhat Bano, our Dean of Arts, for rendering their valuable advice. We take this opportunity to thank Dr. Ronita Nag Chaudhuri, our Head of Department and all faculty members and support staff of the Department for their constant cooperation and support in this journey. A special note of thanks to the eminent scientists and all our contributors, whose insights and creativity breathe life into this magazine.

Dr. Priyanka De

Associate Professor,
Postgraduate & Research
Department of Biotechnology
St. Xavier's College (Autonomous), Kolkata

Dr. Parinita Majumdar

Assistant Professor,
Postgraduate & Research
Department of Biotechnology
St. Xavier's College (Autonomous), Kolkata



FACULTY PROFILES



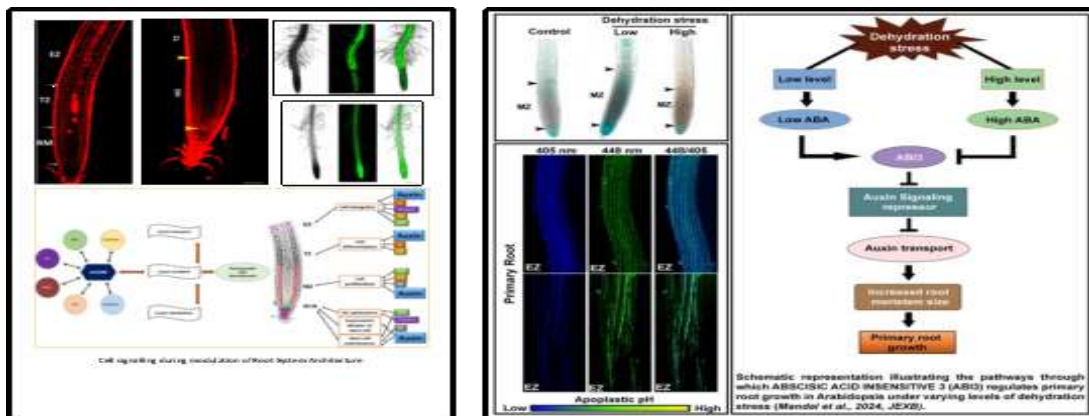
Dr. Ronita Nag Chaudhuri
M.Sc., Ph.D.

Elected Fellow of West Bengal Academy of Science and Technology (FAScT, 2024).

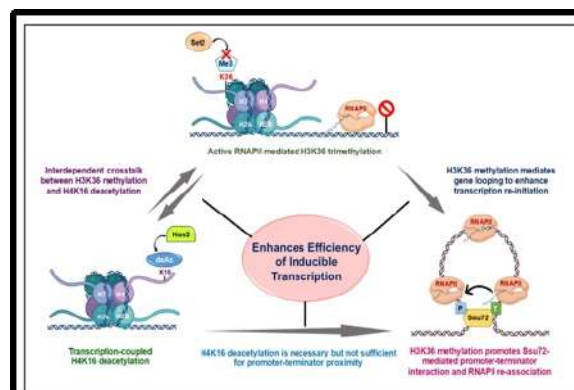
Associate Editor, international peer-reviewed journal "The Nucleus" (Springer-Nature Publication).

RESEARCH INTERESTS

- Investigating the genetic and epigenetic mechanisms involved in regulating developmental and environmental signaling.



- Auxin modulates ABI3 expression as part of a negative feedback loop during lateral root development in *Arabidopsis*. Swarnavo Chakraborty, Sicon Mitra, Saptarshi Datta, Drishti Mandal and **Ronita Nag Chaudhuri***. New Phytologist (2026), DOI: 10.1111/nph.71548
 - Cytokinin response factor 1 acts as a negative regulator of cytokinin-mediated developmental pathways in *Arabidopsis*. Drishti Mandal, Swarnavo Chakraborty and **Ronita Nag Chaudhuri***. Planta (2026) DOI: <https://doi.org/10.1007/s00425-026-04974-4>
 - To grow or not to grow: the enigma of plant root growth dynamism. Drishti Mandal, Saptarshi Datta, Sicon Mitra, Swarnavo Chakraborty and **Ronita Nag Chaudhuri***. Plant Molecular Biology (2025) doi.org/10.1007/s11103-025-01631-4
 - ABI3 regulates ABI1 function to control cell length in primary root elongation zone. Saptarshi Datta, Drishti Mandal, Sicon Mitra, Swarnavo Chakraborty and **Ronita Nag Chaudhuri***. The Plant Journal (2024) DOI: 10.1111/tj.17121.
 - ABI3 promotes auxin signaling by regulating SHY2 expression to control primary root growth in response to dehydration stress. Drishti Mandal, Saptarshi Datta, Sicon Mitra and **Ronita Nag Chaudhuri***. Journal of Experimental Botany (2024) doi: 10.1093/jxb/erae237.
- Investigating chromatin landscape regulation during gene expression and DNA damage repair pathways.



- H3K36 Methylation is Essential for Promoter-terminator Interaction and Re-association of RNAPII to Gene Promoter During Inducible Transcription in Yeast. Priyabrata Singha and **Ronita Nag Chaudhuri***. Journal of Molecular Biology (2026), DOI: <https://doi.org/10.1016/j.jmb.2026.169861>.



Dr. Uma Siddhanta
M.Sc., Ph.D.

FIELDS OF RESEARCH EXPERIENCE	OTHER FIELDS OF INTEREST
1. Enzymology 2. Protein Structure-Function 3. Cell Signaling	1. Immunology 2. Virology



Dr. Sudipa Saha
M.Sc., Ph.D.

AREA OF RESEARCH

Structure function studies of Proteins

RECENT PUBLICATIONS

1. Aparajita Chakraborty, Priyanka De and **Sudipa Saha**. "Structure-function relationship of α -crystallin in the context of vertebrate lens evolution and its role in eye disorders". Journal of Proteins and Proteomics, 2022. <https://doi.org/10.1007/s42485-022-00101-5>
2. Aparajita Chakraborty, Sayak Ganguli, Priyanka De and **Sudipa Saha**. "An insight into the structural analysis of α -crystallin of habitat-specific fish: a computational approach". Journal of Proteins and Proteomics, 2023. <https://doi.org/10.1007/s42485-023-00107-7>
3. Aparajita Chakraborty, Sushmita Nandy, **Sudipa Saha** and Priyanka De. "An Insight on α -crystallin Interactions with Various Proteins in Systemic Disorders". Journal of Stress Physiology & Biochemistry, Vol. 19, No. 3, (2023), 35-46. ISSN 1997-0838.
4. Aparajita Chakraborty, Priyanka De and **Sudipa Saha**. "Elucidating the mechanism of anti-apoptotic activity of α -crystallin and its therapeutic potential". Journal of Stress Physiology & Biochemistry, Vol. 21, No. 1, (2025), 182-189. ISSN 1997-0838.
5. Sutrish Kundu, Vivek Raychaudhuri and **Sudipa Saha**. "GroEL/GroES Mechanism of Action and Formation of Complexes During Reaction Cycle: A Matter of Debate". Journal of Stress Physiology & Biochemistry, Vol. 21, No. 3, (2025), 143 - 160. ISSN 1997-0838.



Dr. Aniruddha Banerji
M.Sc., Ph.D.

PRIMARY AREA OF RESEARCH INTEREST

Cancer Biology

ADDITIONAL AREAS OF RESEARCH INTEREST

Wildlife biology, Evolutionary biology, Environmental biology, Ecology and Epidemiology

RESEARCH ACTIVITIES (2024-26)

PUBLICATIONS

1. I. Chakraborty, A. Roy, **A. Banerji**. The Role of All-trans Retinoic Acid (ATRA) As A Potential Downregulator of Integrin $\alpha 5\beta 1$ Mediated Signalling in Melanomas. *South Asian Journal of Experimental Biology* (2024) vol. 14(6) pp. 282-293. ISSN:2230-9799.
2. A. Roy, **A. Banerji**. Comparative Study of Curcumin, All-Trans Retinoic Acid and Resveratrol: Therapeutic Targeting of Breast Cancer Signalling. *Annual Research & Review in Biology* (2025) vol. 40 (4) pp. 154-164. ISSN: 2347-565X.
3. I. Chakraborty, **A. Banerji**. Signalling Cascades in Melanoma: Understanding the Potential of Phytochemicals as Inhibitors. *Research Perspectives of Microbiology and Biotechnology Vol. 1*, Ed. E. Magiorkinis, Pub: Book Publisher International (2024) pp. 19-31. Print ISBN: 978-81-971580-1-8.
4. A. Roy, **A. Banerji**. Natural Compounds as Promising Modulators of Breast Cancer Signalling: The Significant Role of Tea Polyphenols. *Medical Science: Trends and Innovations Vol. 5*. Ed. M. Refaat, Pub: Book Publisher International (2025) pp. 88-103. Print ISBN: 978-93-49238-11-4.

PLENARY LECTURES

1. **A. Banerji**. "Exploring the potential of some natural phytochemicals for targeting epidermal growth factor receptor (EGFR) in breast cancers", at International Conference on Chemistry for Human Development (ICCHD-2025) organized by University of Calcutta, Biswa Bangla Biswabidyalay, Professor Asima Chatterjee Foundation Kolkata and Luminescent Organic Consortium of India, Jan 2025.
2. **A. Banerji**. "All-trans Retinoic Acid (ATRA): A Potent Inhibitor of Matrix Metalloproteinases and Cellular Signalling Cascades in Cervical Cancer Cells", at International Conference on Chemistry for Human Development (ICCHD-2026) organized by University of Calcutta, Biswa Bangla Biswabidyalay and Professor Asima Chatterjee Foundation Kolkata, Jan 10th-11th 2026.
3. **AWARD**: Awarded Ganatantra Divas Puraskar for Inspiring Contribution to Life Sciences, by International Multidisciplinary Research Foundation (IMRF), India, January 2025.

Ph. D. AWARDED (RESEARCH SCHOLARS)

1. Dr. Anirban Roy (April 2026)
2. Dr. Indira Chakraborty (July 2026)

SELECTED PRESENTATIONS/ ACHIEVEMENTS FROM AB LAB

1. A. Roy, **A. Banerji**. "Curcumin and All-trans Retinoic Acid (ATRA) As Inhibitors of Matrix Metalloproteinase Expression and Activity in Breast Cancer Cells" at Bio Colloq: One Day Conference on Inter-Disciplinary Biological Sciences (National Conference) organized by Ramakrishna Mission Vivekananda Centenary College (Autonomous), Rahara & Academy of Biodiversity Conservation, Jan 2024. Awarded 1st prize for poster presentation.
2. I. Chakraborty, **A. Banerji**. "Potential of All-trans Retinoic Acid (ATRA) For Inhibiting Cellular Signalling Pathways in Melanoma Cells" at Bio Colloq: One Day Conference on Inter-Disciplinary Biological Sciences (National Conference) organized by Ramakrishna Mission Vivekananda Centenary College (Autonomous), Rahara & Academy of Biodiversity Conservation, Jan 2024. (Poster Presentation)
3. I. Chakraborty, **A. Banerji**. "The Role of All-trans Retinoic Acid (ATRA) as a Potential Inhibitor of Signalling Pathways in Cervical Cancers" at 8th World Cancer Congress-2024 (International Conference) organized at JNU Convention Centre, New Delhi, March 2024. (Poster Presentation)
4. A. Roy, **A. Banerji**. "Synergistic Treatment with Curcumin and All-trans Retinoic Acid: Effects on Matrix Metalloproteinases (MMPs) in Metastatic Breast Cancer Cells" at 8th World Cancer Congress-2024 (International Conference) organized at JNU Convention Centre, New Delhi, March 2024. (Oral Presentation)
5. I. Chakraborty, **A. Banerji**. "Targeting Signalling Pathways in Cervical Cancers by All-trans Retinoic Acid (ATRA)" at 7th Regional Science & Technology Congress, West Bengal, 2024-25 organized by Presidency University, Kolkata & DSTBT, Govt. of West Bengal, Jan 2025. (Oral Presentation)
6. A. Roy, **A. Banerji**. "Synergistic Treatment with Curcumin and All-trans Retinoic Acid (ATRA) as Promising Modulator of Signaling Pathways in Breast Cancer" at 9th World Cancer Congress-2026, organized at JNU Convention Centre, New Delhi, March 2026. (Oral Presentation)



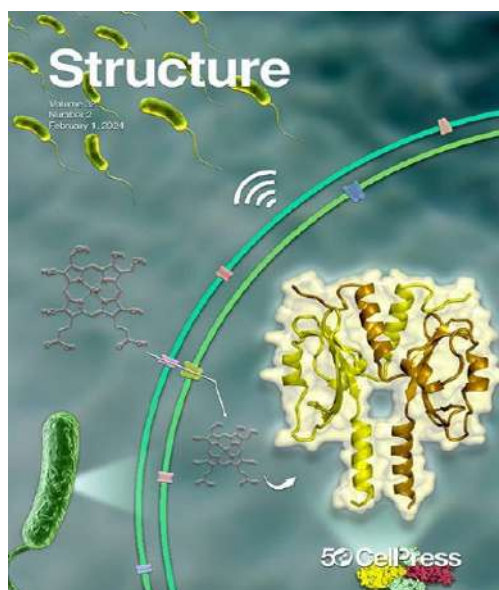
Dr. Jhimli Dasgupta
M.Sc., Ph.D.

RESEARCH INTEREST AND THE PROJECTS RUNNING IN THE LAB

1. Structural aspects of the molecular motors, such as σ^{54} -dependent transcription activators, involved in flagellar gene transcription:
 - Structural and functional aspects of the AAA⁺ ATPase FlrC that controls flagellar synthesis and biofilm formation in motile bacteria.
 - FlrA, the master transcription regulator of flagellar synthesis in motile bacteria: Structural insights, oligomerisation, functional implications, and regulation by the second messenger c-di-GMP.
2. Revelation of the sensory signal and mechanism of FlrB, a unique cytosolic sensor Histidine kinase playing a pivotal role in flagellar synthesis and motility of *V. cholerae*.
3. Understanding the mechanism of nutrient uptake by pathogenic bacteria using ABC transporters to target 'Trojan horse mechanism' of drug delivery.

RECENT PUBLICATIONS

1. Peeali Mukherjee, Wrick Chakraborty, Subhayu Chowdhury, Sayak Ganguli, **Jhimli Dasgupta**. Bioinformatic and genomic analyses on FlrB-FlrC-type TCS orthologs involved in flagellar synthesis of monotrichous Gram-negative bacteria. *Journal of Proteins and Proteomics*, 18 March 2025, 161 – 176.
2. Indrila Saha, Biplab Ghosh, **Jhimli Dasgupta**. Structural insights in to the atypical type-I ABC Glucose-6-phosphate importer VCA0625-27 of *Vibrio cholerae*. *Biochem Biophys Res Commun*. 2024 Jul 5;716: 150030. doi: 10.1016/j.bbrc.2024.150030. Epub 2024 May 1.
3. Peeali Mukherjee, Shubhangi Agarwal, Sritapa Basu Mallick, **Jhimli Dasgupta**. PAS domain of flagellar histidine kinase FlrB has a unique architecture and binds heme as a sensory ligand in an unconventional fashion. *Structure*. 2024 Feb 1;32(2):200-216.e5. doi: 10.1016/j.str.2023.11.014. Epub 2023 Dec 28. (COVER ARTICLE of February 2024 issue)



4. Shrestha Chakraborty, Shubhangi Agarwal, Arindam Bakshi, Sanjay Dey, Maitree Biswas, Biplab Ghosh, **Jhimli Dasgupta**. The N-terminal FleQ domain of the *Vibrio cholerae* flagellar master regulator FlrA plays pivotal structural roles in stabilizing its active state. *FEBS Lett*. 2023 Sep;597(17):2161-2177. doi: 10.1002/1873-3468.14693. Epub 2023 Jul 10.



Dr. Priyanka De
M.Sc., Ph.D.

AREA OF EXPERTISE

Zoology, Physiology, Metabolism, Ecology, Ethology.

BOOK PUBLICATION

1. 'The Ultimate Query', A translation work based on Sarat Chandra Chattopaddhya's Sesh Prasna (ISBN: 978-93-83548-89-7). January 2016.
2. 'Dodo Kothai Tui', a bengali storybook for children (ISBN: 978-93-84184-41-4). December 2016.
3. 'The Enigma of Human Existence: An Odyssey of Survival' (ISBN 978-81-940456-4-9). April 2019.
4. 'Bigyaaner Antoraale', A collection of bengali scientific articles (ISBN: 978-93-84184-87-2). August 2021.
5. 'Enigma of life: An Odyssey of Poetry' (ISBN: 978-93-94035-83-6). January 2024.

JOURNAL PUBLICATION

1. Excess of glucocorticoid induces myocardial remodeling and alteration of calcium signaling in cardiomyocytes. **De P**, Roy SG, Kar D, Bandyopadhyay A. Journal of Endocrinology, 209: 105-114. 2011.
2. Enigma of Slumber. **De P**. Austin Journal of Biotechnology & Bioengineering [ISSN 2378-3036], 1(5): 4. 2014.
3. Diverse Facets of Lipid Metabolism in Cardiac Pathology. **De P**. Journal of Enzymology and Metabolism [ISSN: 2455-4774], 1(1): 105. 2015.
4. Structure–function relationship of α -crystallin in the context of vertebrate lens evolution and its role in eye disorders. Chakraborty A, **De P**, Saha S. Journal of Proteins and Proteomics [eISSN 2524-4663], 14, 25-41. 2022.
5. Global warming and neuromarketing: An opinion-based neurocognitive analysis of associated lifestyle modifications. Sarangi N and **De P**. Journal of Environment and Sociobiology [ISSN: 0973-0834], 19(2), 257-270. 2022.
6. Structure–function relationship of α -crystallin in the context of vertebrate lens evolution and its role in eye disorders. Chakraborty A, **De P**, Saha S. Journal of Proteins and Proteomics [eISSN 2524-4663], 14, 25-41, 2023.
7. An insight into the structural analysis of α -crystallin of habitat- specific fish – A Computational Approach. Chakraborty A, Ganguli S, **De P**, Saha S. Journal of Proteins and Proteomics [eISSN 2524-4663], 14, 111–127, 2023.
8. An Insight on α -crystallin Interactions with Various Proteins in Systemic Disorders. Chakraborty A, Nandy S, Saha S, **De P**. Journal of Stress Physiology & Biochemistry [ISSN 1997-0838], 19(3), 35-46, 2023.
9. Elucidating the mechanism of anti-apoptotic activity of α -crystallin and its therapeutic potential. Chakraborty A, **De P**, Saha S. Journal of Stress Physiology & Biochemistry [ISSN 1997-0838], 21(1), 182-189, 2025.
10. Fentanyl abuse and its implication on health and society. **De P**, Mondal A, Bhattacharya A, Pal N. Journal of Mental Health Issues and Behavior [ISSN: 2799-1261], 5(1), 12-22, 2025.



Dr. Souvik Roy
M.Sc., M. Phil., Ph.D.

AWARDS & RECOGNITIONS

1. B. Sc. [1st Class 1st, Gold-Medalist]
2. M. Sc. [1st Class 1st, Gold-Medalist]
3. 'Microbiologist Society Best Teacher' & 'Bharat Jyoti Puraskar' Awardee [National-Level Awards]

RESEARCH PROFILE AND ITS SOCIAL IMPACT

Research Project (Completed):

Project title: In vitro phytochemical screening of Antioxidant and Antibacterial activities of Leaf Extracts of Pine, Fir and Chinar, and Virtual Screening to identify potential Lead Compounds as Antibacterial Agents; Granting Agency: St. Xavier's College (Autonomous), Kolkata [Intramural Research Grant (Sanction No: IMSXC2023-24/05; dated 18th August 2023)] Period of Sanction: 2023-2025



PUBLICATION PROFILE (2025-26)

PAPERS IN WoS/SCOPUS/UGC-CARE APPROVED JOURNALS

1. Chattopadhyay, D., Saha, A., Tendulkar, D., Banerjee, T., Roy, S., Choudhury, L., Rajendran, R.L., Gangadaran, P., Ahn, B.C. (2026). Targeting tumor metabolism through precision nutrition: A therapeutic strategy to improve cancer outcomes. *World Journal of Clinical Oncology* (WoS-indexed). [ISSN (Online): 2218- 4333; Impact Factor = 3.6] [INVITED ARTICLE] (In Press).
2. Roy, S., Mukherjee, S., Banerjee, A. and Choudhury, L. (2026). Investigating the Role of Bioactive Compounds from *Artemisia annua* in restoring functionality of p53 in cases of Oral Squamous Cell Carcinoma triggered by R280K mutation. *International Journal of Biology, Pharmacy and Allied Sciences* (UGC approved). [ISSN (Online): 2277- 4998; Impact Factor = 2.921] (In Press).
3. Roy, S., Roy, S., Pramanik, S., Chattopadhyay, S., and Choudhury, L. (2026). Unveiling the Pathogen Load and their Multi Drug Resistance in street-vended Coconut Water in Kolkata, India: A Pioneering Insight. *Acta Scientific Microbiology* (Scopus-indexed). [ISSN (Online): 2581-3226; Impact Factor = 1.416] (In Press).
4. Sarkar, S., Roy, S. & Choudhury, L. (2026). Future perspectives for potential therapeutic targeting of liquid liquid phase separation in pathological immunologic condensate signalling ensembles. *Discover Chemistry* (WoS-indexed), 3, 396 [ISSN (Online): 3005-1193].
5. Sarkar, S., Roy, S. & Choudhury, L. (2026). Leveraging engineered small EVs to mitigate cancer pain: a new paradigm. *Journal of Microencapsulation* (WoS-indexed), 1-21. [ISSN (Online): 1464-5246; Impact Factor = 3.2].
6. Sarkar, S., Roy, S., and Choudhury, L. (2026). Importance of the inflammasome in gut-brain axis: from pathological driver to therapeutic target. *Inflammopharmacology* (WoS-indexed). [ISSN (Online): 1568-5608; Impact Factor = 6.3].
7. Banerjee, M., Dey, A., Roy, S., Banik, S.P., & Sarkar, D. (2026). Exploring the functional evolution of Intrinsically Disordered protein regions in p53. *Journal of Experimental Zoology, India* (Scopus-indexed). 29:2, 1209-1218. [ISSN (Online): 0976-1780].
8. Sarkar, S., Roy, S., and Choudhury, L. (2026). Exosomes-mediated intercellular communication and their theragnostic potential against cancer and related disorders: a comprehensive review. *Biotechnology Letters* (WoS-indexed). 48:67 [ISSN (Online): 1573-6776; Impact Factor = 2.1].
9. Roy, S., Bhattacharjee, D., Gupta, H., Choudhury, L., and Sarkar, S. (2026). Microbial Characterization of Chocolates of Three Popular Commercial Brands: A Complete Profiling of Notorious Bacterial and Fungal Contaminants. *Acta Scientific Microbiology* (Scopus-indexed). 9.5:3-19. [ISSN (Online): 2581-3226; Impact Factor = 1.416]
10. Roy, S., Chattopadhyay, D., Choudhury, L., Ghosh, S. and Mahajan, A.A. (2025). Harnessing the power of faecal microbiota transplantation: optimizing neuroimmune function for improved treatment of Parkinson's, Alzheimer's, and multiple sclerosis. *Discover Neuroscience* (UGC approved). 20, 21. [ISSN (Online): 3005-1827; Impact Factor = 4.0].
11. Roy, S., Banerjee, D., Banerjee, A. and Choudhury, L. (2025). Sex hormones and gender differences in immune responses and anticancer immunity: A comprehensive review. *Biologia Futura* (UGC approved). 77(1):1-27. [ISSN (Print): 2676-8615; ISSN (Online): 2676-8607; Impact Factor = 1.5]
12. Sarkar, S., Roy, S. and Choudhury, L. (2025). Arbuscular mycorrhiza symbiosis—from molecular dialogues to biotechnological applications. *Mycological Progress* (UGC approved). 24:67. [ISSN (Online): 1861-8952; Impact Factor = 3.0].
13. Roy, S., Sarkar, S., and Choudhury, L. (2025). Microbial Compounds in Cosmetic Formulations: A Comprehensive Review. *International Journal of Biology, Pharmacy and Allied Sciences* (UGC approved). 14(8): 4638-4661 [ISSN (Online): 2277-4998; Impact Factor = 2.659].
14. Roy, S., Sarkar, S., Paul, U., Biswas, A., Bera, A. and Choudhury, L. (2025). Quinones and their pharmaco-physiological roles in Prokaryotes and Eukaryotes: A Comprehensive Review. *Applied Biochemistry and Microbiology* (UGC approved). [ISSN (Print): 0003-6838; ISSN (Online): 1608-3024; Impact Factor = 1.1].



Dr. Sayak Ganguli
M.Sc., Ph.D.

COURSES TAUGHT

- Plant Diversity and Systematics (Semester II)
- Bioinformatics (Semester V)
- Plant Developmental Anatomy (Semester VI)
- Ethnomedicine, CADD, Plants for Climate action and Sustainable Agriculture (Semester VII)
- Genomics (Semester VIII)
- Intellectual Property Rights, Plant Breeding and Plant Tissue Culture (Semester IX)

CURRENT RESEARCH AREAS

Sundarban Metagenomics	Focus is on the study of rhizospheric and endophytic microflora of true mangroves and crop plants to support habitat restoration efforts and yield enhancement.
Tribal Gut Microbiome	We investigate the gut microbiome of indigenous tribes in West Bengal to gain insights into their dietary habits and nutritional status. This enables us to provide insights into the gut bacteriome – metabolome axis.
AMR in Wastewater and COPD microbiomes	Focus is on the development of methods for pathogen surveillance in urban and rural wastewater and nasal microbiome of COPD patients. This work is crucial for predicting future pandemics and monitoring public health.
Genomics Guided Drug Discovery	Focus is on in-silico methods to analyze the pangenome of different bacterial strains identified from the other research areas, aiming to identify therapeutic targets.

RESEARCH TEAM

1. Dr. Meesha Singh, awarded in 2023 [Wastewater Surveillance and AMR; Currently: Science Communicator, CACTUS Communications]
2. Dr. Sarmishta Mukhopadhyay, awarded in 2024 [Comparative Genomics and Drug Discovery, Currently: DBT BIOCARE FELLOW, CCMB, Hyderabad]
3. Dr. Souradip Basu, awarded in 2024 [Tribal Gut Microbiome; Currently: AICTE PDF at UEM Kolkata]
4. Dr. Rupsha Karmakar, awarded in 2025 [Wastewater Surveillance; Currently: Faculty at VCW, Kolkata]
5. Mr. Wrick Chakraborty – IPCR Fellow in COPD Microbiome
6. Mr. Debava Chaudhuri – UGC – JRF – Sundarban Metagenome Project
7. Ms, Nikkita Das – UGC JRF – Sundarban Metagenome Project

COLLABORATIONS AND FUNDING

1. Postgraduate and Research Department of Microbiology, St. Xavier's College, Kolkata
2. B.R. Ambedkar Chair, Department of Anthropology, University of Calcutta, Kolkata
3. Department of Biotechnology, University of Calcutta, Kolkata
4. Laboratório de Bioinformática e Química Medicinal – LABIOQUIM; Center for Studies of Biomolecules Applied to Health – CEBio, Brazil
5. Integrated Environmental Solutions, India

ADDITIONAL INFORMATION



PUBLICATIONS



DATABASE ACCESSIONS



LINKEDIN



VIDWAN

LAB MOTTO

"If you want to walk fast walk alone, but if you want to walk far walk together"



Dr. Ditipriya Hazra
M.Tech., Ph.D.

AREA OF RESEARCH

1. Studying bacterial chromosome segregation using protein chemistry, structural biology and MD simulation
2. Deciphering molecular mechanism of methyl transferases in antimicrobial resistance

PUBLICATIONS (2025)

1. Ganguly, M., Maitra, H., Roychowdhury, A. and **Hazra, D.**, 2025. Drug designing against PfHT1 coupled with molecular dynamics in plasma membrane environment reveals, ligand-induced conformational change from open to closed state. *IEEE Transactions on Computational Biology and Bioinformatics*.
2. Gupta, R., Ganguly, M., Jana, P., Roychowdhury, A. and **Hazra, D.**, 2025. Two Birds with One Stone: Targeting Wild Type and Drug Resistant Mutant ALK Using Brute Force Screening, MD Simulation and NCI. *IEEE Transactions on Computational Biology and Bioinformatics*.
3. Ganguly, M., Gupta, R., Roychowdhury, A. and **Hazra, D.**, 2025. De novo drug designing coupled with brute force screening and structure guided lead optimization gives highly specific inhibitor of METTL3: a potential cure for Acute Myeloid Leukaemia. *Journal of Biomolecular Structure and Dynamics*, 43(2), pp.1038-1051.
4. Bhattacharya, D., Chakraborty, S., **Hazra, D.**, Roychowdhury, A., Karmakar, A. and Chattopadhyay, S., 2025. Molecular-level analysis of alkyl chain dependent voltage-induced microfluidic alcohol droplet actuation on Teflon/Pt/glass substrate: Revealing the unconventional directional movement. *Journal of Molecular Liquids*, 417, p.126576.
5. Rahman, S., Bhattacharya, A., Jana, P., Ganguly, M., Das, A.K., **Hazra, D.** and Roychowdhury, A., 2025. Subtractive proteomics unravel the potency of D-Alanine-D-Alanine Ligase as the drug target for *Burkholderia pseudomallei*. *International Journal of Biological Macromolecules*, p.144106.
6. **Hazra, D.**, Rahman, S., Ganguly, M., Das, A.K. and Roychowdhury, A., 2025. Molecular dynamics simulation shows enhanced stability in scaffold-based macromolecule, designed by protein engineering: a novel methodology adapted for converting Mtb Ag85A to a multi-epitope vaccine *Journal of Molecular Modeling*, 31(3), p.84.

PROJECT

1. WB-DST sponsored project: "Targeting chromosome segregation system of *Mycobacterium tuberculosis* to design structure-based inhibitors" (2025-2027)
2. Intramural project: "Developing new generation therapeutics against *Mycobacterium tuberculosis* using integrative structural biology and computer aided drug design coupled to DFT"



Dr. Parinita Majumdar
M.Sc., Ph.D.

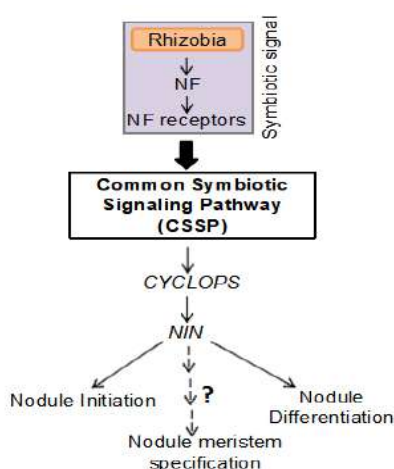
RESEARCH INTEREST

Understanding the molecular mechanisms of nodule organogenesis in model and crop legumes *Medicago truncatula* and *Arachis hypogaea*.

1. Molecular, genetic and biochemical approaches towards characterization of transcriptional regulatory modules involved in nodule development.
2. Identification of genetic predisposition factors in conserved transcriptional modules involved in nodule organogenesis.
3. Unravelling the mechanism of nodule meristem establishment and maintenance in determinate and indeterminate nodules.



Medicago truncatula
(indeterminate nodule)



Arachis hypogaea
(Determinate nodule)

AWARDS AND HONOURS

1. Awarded 1st class first in M.Sc. Microbiology (2013) by the University of Calcutta.
2. Awarded GARP travel grant in 2018 by IISc, Bangalore.
3. Awarded for best poster presentation in IPG symposium, 2023 at Missouri, USA.

PUBLICATIONS

1. **Majumdar P.** and Nath U. (2020) De-ubiquitinases on the move: an emerging field in plant biology. *Plant Biology* 22 (4), 563-572. DOI:10.1111/plb.13118.
2. **Majumdar P.**, Karidas P., Siddiqi I. and Nath U. (2020) The ubiquitin-specific protease TNI/UBP14 functions in ubiquitin recycling and affects auxin response. *Plant Physiology* 184, 1-15. DOI:10.1104/pp.20.00689.
3. **Majumdar P.**, Karidas P., Nath U. (2020) The TARANI/ UBIQUITIN PROTEASE14 protein is required for lateral root development in *Arabidopsis*. *Plant Signaling and Behavior*, DOI:10.1080/15592324.2020.1860386.
4. Smythers, A.L., Bhatnagar, N., Ha, C., **Majumdar, P.**, McConnell, E.W., Mohanasundaram, B., Hicks, L.M. and Pandey, S., 2022. Absciscic acid-controlled redox proteome of *Arabidopsis* and its regulation by heterotrimeric Gβ protein. *New Phytologist*, 236(2), pp.447-463. DOI: 10.1111/nph.18348
5. **Majumdar P.**, Torres Rodríguez M.D., Pandey S. (2023) Role of heterotrimeric G-proteins in improving abiotic stress tolerance of crop plants. *Journal of Plant Growth Regulation* DOI: 10.1007/s00344-023-10965-6.
6. **Majumdar P.**, Molla F., DasGupta M. (2025) From Inception to Maturation: Recent Insights in Nodule Organogenesis. *Physiologia Plantarum* 177 issue3, DOI: 10.1111/ppl.70277.
7. **Majumdar P.**, and DasGupta M. (2026) Molecular cartography of root nodule organogenesis: insights into the role of transcription factors. *Plant Molecular Biology* DOI: 10.1007/s11103-026-01754-2. (In Press).



Dr. Rohit Kunar
M.Sc., Ph.D.

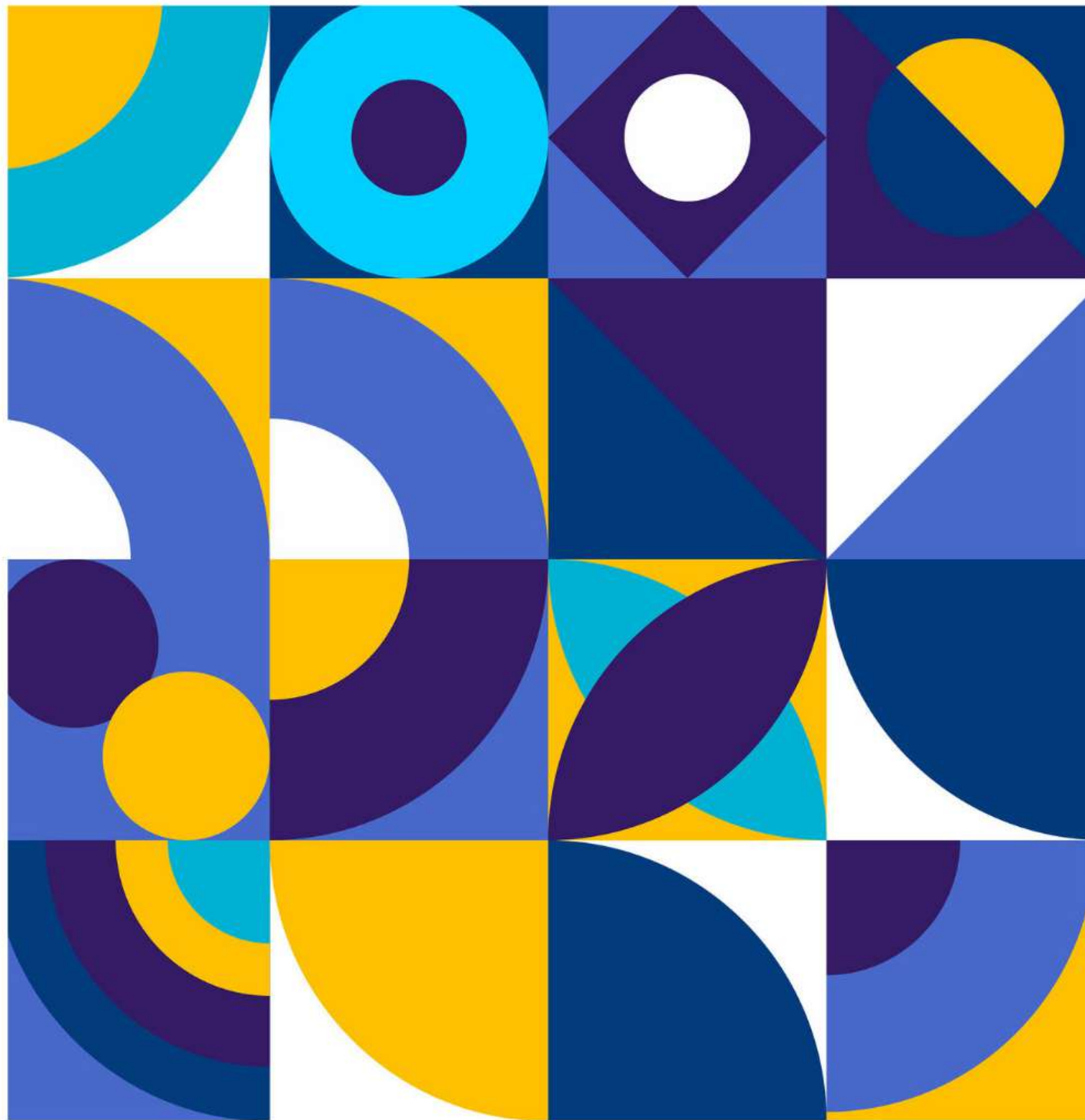
Dr. Rohit Kunar completed his Master's in Biophysics and Molecular Biology from the University of Calcutta, graduating first in order of merit. He earned his Ph.D. from Banaras Hindu University, Varanasi, where he investigated the molecular and developmental genetics of *Drosophila melanogaster*, with a focus on the regulation and developmental expression of the mRNA decapping protein DCP2. Following a brief postdoctoral stint at BHU, he pursued postdoctoral research at the University of North Carolina, Chapel Hill, exploring epigenetic regulation in X-chromosomal dosage compensation in *Drosophila*. His teaching interests include Molecular and Developmental Biology, Chromatin Biology and Molecular Physiology. Finding beauty in the fine details of molecular mechanisms and developmental patterns, his research interests lie at the intersection of molecular developmental genetics and protein biochemistry. A passionate molecular biologist and an ardent lover of microscopy, he believes that science is not only about discovery but also about visual storytelling.

RESEARCH INTERESTS

1. Molecular biology of Development
2. Gene Regulation and Developmental Epigenetics

PUBLICATIONS (2024 – 26)

1. Sultana H., **Kunar R.**, Matera AG. (2025) Chromatin insulators in gene regulation and 3D genome organization. *Biochem Soc Trans* (2025) 53 (05): 1387–1399. (IF: 4.2)



DEPARTMENTAL DIARIES



TEACHING FACULTY



SUPPORT STAFF



CHIASMA COMMITTEE
2026



FIRST YEAR
(Batch of 2026 - 2031)



SECOND YEAR
(Batch of 2025 - 2030)



THIRD YEAR
(Batch of 2024 - 2029)



FOURTH YEAR
(Batch of 2023 - 2028)



FIFTH YEAR
(Batch of 2022 - 2027)



Saptarshi Datta

PI: Dr. Ronita Nag Chaudhuri



Ruchira Das

PI: Dr. Jhimli Dasgupta



Priyabrata Singha

PI: Dr. Ronita Nag Chaudhuri



Swarnavo Chakraborty

PI: Dr. Ronita Nag Chaudhuri



Sicon Mitra

PI: Dr. Ronita Nag Chaudhuri



Sushmita Nandy

PI: Dr. Sudipa Saha
Co-PI: Dr. Priyanka De



Arnab Pal

PI: Dr. Jhimli Dasgupta



Aparajita Chakraborty

PI: Dr. Sudipa Saha
Co-PI: Dr. Priyanka De



Wrick Chakraborty

PI: Dr. Sayak Ganguli
Co-PI: Dr. Partha Sarathi Bhattacharya



Debava Chaudhuri

PI: Dr. Sayak Ganguli



Adrija Chakraborty

PI: Dr. Ronita Nag Chaudhuri



Sanchayita Roy

PI: Dr. Ditipriya Hazra



Nikkita Das

PI: Dr. Sayak Ganguli



Ankita Nanda

PI: Dr. Jhimli Dasgupta



Dr. Preeti Khan
PI: Dr. Ronita Nag Chaudhuri
Ph. D. Awarded: 2024
Currently pursuing post-doctoral research in UTSW, Texas, USA



Drishti Mandal
PI: Dr. Ronita Nag Chaudhuri
Ph. D. Awarded: 2026
Currently pursuing post-doctoral research in CNRS, Montpellier, France



Anirban Roy
PI: Dr. Aniruddha Banerji
Ph. D. Awarded: 2026



Indira Chakraborty
PI: Dr. Aniruddha Banerji
Ph. D. Awarded: 2026



Dr. Indrila Saha
PI: Dr. Jhimli Dasgupta
Ph. D. Awarded: 2024
Currently pursuing post-doctoral research in UBC, Canada



Dr. Peeali Mukherjee
PI: Dr. Jhimli Dasgupta
Ph. D. Awarded: 2025
Currently pursuing post-doctoral research in IIT, Roorkee



Dr. Souradip Basu
Joint PI: Dr. Sayak Ganguli, Dr. Mahashweta Mitra Ghosh
Ph. D. Awarded: 2024
Currently serving as AICTE Postdoctoral Fellow at UEM, Kolkata



Dr. Sarmishta Mukhopadhyay
PI: Dr. Sayak Ganguli
Co-PI: Dr. Santanu Chakrabarti
Ph. D. Awarded: 2024
Currently serving as DBT – BIO CARE Fellow at CCMB, Hyderabad



Dr. Rupsha Karmakar
Joint PI: Dr. Sayak Ganguli, Dr. Mahashweta Mitra Ghosh
Ph. D. Awarded: 2025
Currently employed as Faculty of Zoology at Vivekananda College for Women, Kolkata



Biotech Industry - Academia Conclave (BTIAC 2025)

Convener: Dr. Jhimli Dasgupta

Co-Convener: Dr. Arindam Bakshi

The Postgraduate and Research Department of Biotechnology at St. Xavier's College (Autonomous), Kolkata, successfully organized the Biotech: Industry – Academia Conclave (BTIAC 2025) on 20th November 2025. Dr. Jhimli Dasgupta, Head of the Department & Convener, and Dr. Arindam Bakshi, Assistant Professor & Co-Convener, coordinated the event, under the guidance of Rev. Dr. Dominic Savio, SJ, Principal. Dr. Dibyendu Das of IISER, Kolkata (recipient of the Shantiswarup Bhatnagar Award) and Dr. Amit Ghosh, from IIT Kharagpur, delivered invited lectures. The Panel Discussion brought together distinguished experts from academia, industry, and innovation ecosystems to deliberate on industry-academia collaboration, translational research, entrepreneurship, and policy-driven biotechnology growth. The panel

comprised Dr. Jugnu Jain, Sapien Biosciences; Dr. Sangita Sen Majee, IKP Knowledge Park, Hyderabad; Dr. Barun Kanta Bhattacharyya, East India Pharmaceutical Works Limited; Mr. Probhas Bondhu Chakraborty, Mendine Pharmaceuticals and Dr. Saptarshi Chatterjee, Adamas University & BIRAC E-YUVA Centre. The panel discussion was moderated by Dr. Sayak Ganguli, facilitating engaging discussions and offering valuable insights into research-to-industry pathways. The 15th edition of the departmental magazine Chiasma was also launched on the occasion edited by Dr. Aniruddha Banerji and Dr. Priyanka De. The conclave provided a platform for strengthening industry – academia interaction through expert lectures and panel discussions on innovation, translational research, and emerging trends in biotechnology.



Figure: Few Glimpses of The Event

Field Trip to the Indian Museum, Kolkata

Semester 9

Coordinator: Dr. Aniruddha Banerji

Compilation: Shehala Dhar

On September 19th, 2026, the students of Semester 9, supervised by Dr. Aniruddha Banerji, visited the Indian Museum, Kolkata for an educational field trip as a part of the curriculum for Animal Biotechnology Practical. The Indian Museum is one of the grandest institutions of its kind in India and houses a noteworthy collection divided in various sections of interest. The trip unraveled many sections such as zoology, anthropology, evolution, ecology and biotechnology. We were overjoyed to visualize and experience every aspect of our knowledge with real specimens, intricately maintained in the museum. Our experience was further enriched by the wonderful insights provided by our professor during the field trip.

The museum contains multiple galleries dedicated to specific categories which offered understanding beyond the confinement of a classroom. The Reptile and Bird Gallery contained many specimens from the avian and reptilian kingdoms. We also saw the cast of a fossil specimen of *Archeopteryx lithographica*.

The Fish Gallery had specimens of different fish and marine organisms, providing glimpses into the incredible biodiversity under the ocean. A striking specimen was a piece of wood from a ship which had been pierced by the sword of a sword-fish.

Next, our quest continued to the Mammal Gallery which had a large collection of preserved mammalian specimens and skeletons. The most fascinating exhibits were the enormous skeletal parts of a blue whale, the largest living animal on Earth. The Ecological Gallery showcases animal specimens in their unique ecosystems and biomes. Lastly, we visited the Invertebrate Fossil Gallery which includes a stromatolite fossil from 3,200 million years ago, which is the earliest record of life in India.

Our educational field trip, along with the interpretations of the specimens, enriched our understanding of the biological world and enabled us to appreciate the biodiversity present on Earth.



Industrial Visit to East India Pharmaceutical Works Ltd.

Semester 6

Coordinators: Dr. Souvik Roy & Dr. Ditipriya Hazra

Compilation: Rittika Dhar **Editing:** Pramita Chatterjee & Dr. Souvik Roy

A major objective of the Industrial Visit to East India Pharmaceutical Works Ltd. on 10th & 11th April, 2026, as a compulsory Part of the NEP Bioprocess Technology curriculum, was to understand how concepts of biotechnology such as Synthetic Biology, targeted drug delivery, therapeutic innovations and Bioinformatics are translated into pharmaceutical applications.

East India Pharmaceutical Works Ltd., located at 119, Biran Roy Road West, Sarsuna, Kolkata - 700061, West Bengal, India, was established in 1936, and since then, bears a long history of pharmaceutical research, formulation, and production. The organization focuses on developing quality and affordable medicines, and has undertaken cutting-edge research in areas including Organic synthesis, Biotechnology, Microbiology, Herbal products, and analytical techniques. It follows recognized quality standards such as GMP, GLP, WHO-GMP and ISO 9001:2015.

The product portfolio of East India Pharmaceutical Works Ltd. includes allopathic, ayurvedic/herbal, and personal-care products, covering analgesics, antibiotics, antivirals, antifungals, antiprotozoals, probiotics, vitamins, injectables and other therapeutic drugs. The Research and Development (R&D) Division of the Industry carries out active and innovative research in advanced drug-delivery systems, recombinant DNA technology, economical API synthesis, generics, biomolecules and biological systems. Its Analytical Development Division performs method development and stability testing before products are transferred to the Quality Control (QC) Division and Microbiological Testing. The QC Division verifies raw materials, intermediates and finished products, and en-

sures that manufacturing processes comply with standard specifications. Bioavailability and bioequivalence are considered important regulatory considerations, while product pricing is influenced by pilot-scale formulation, competition, capital investment, labour, raw materials and retail-level costs.

Overall, the Visit provided students with first-hand exposure to Pharmaceutical manufacturing, R&D, Microbiological testing, Analytical instrumentation, Biotechnology, Quality Assurance, regulatory requirements and market considerations. It strengthened the connection between classroom concepts and industrial practices, while providing insights into professional roles and career opportunities in the flourishing Pharmaceutical Sector.

Key Outcomes of the Visit

1. Students were divided into two groups for the Visit, and each group gained first-hand understanding of how concepts of Biotechnology, Microbiology, Analytical Techniques and Pharmaceutical Technology are implemented in an industrial setting.
2. Students learnt the importance of stringent Quality Control, aseptic practices, calibration and stability testing, in compliance with pharmacopeial and regulatory standards.
3. Interaction with industry professionals helped students understand different career paths, job roles, required laboratory skills, internship opportunities and professional expectations in the Pharmaceutical Sector.



Workshop - Nurturing the RNA

Semester 4

Coordinators: Dr. Ronita Nag Chaudhuri & Dr. Sayak Ganguli

A sixteen hour program was conducted by the Postgraduate and Research Department of Biotechnology, St. Xavier's College (Autonomous) Kolkata in collaboration with Andragogy Life Sciences Pvt. Ltd, titled "Nurturing the RNA" on the 15th of May 2026. This comprehensive hands-on practical program was specially designed for students of Semester IV of the Department and aimed to provide them with valuable practical experience in the field. Since RNA isolation and analyses is currently not part of the practical curriculum, this workshop was beneficial for the students to get an exposure to cutting edge research technique which is of international importance.

Learning Outcome

1. RNA isolation from Bacteria, quantification and visualization
2. Preparation of RNA for cDNA synthesis
3. Synthesis of cDNA
4. cDNA amplification by Thermal Cycler
5. Visualization of amplified cDNA by Agarose Gel Electrophoresis

Upon successful completion of the program, each participant was evaluated and received a certificate with grades recognizing their achievement. The collaborating organization also distributed a few prizes for students who executed the training well.



Student Achievements

SEMESTER 9

1. Sukanya Banerjee

- Qualified CSIR NET JUNE 2026 for Junior Research Fellowship with All India Rank 24
- Qualified GATE-XL 2026 with All India Rank 333

2. Sreetama Ghosh

- Qualified GATE-BT 2026 with All India Rank 2
- Qualified GATE-XL 2026 with All India Rank 75
- Awarded the IASc-INSa-NASi Summer Research Fellowship 2026

3. Srabonti Chattopadhyay

- Awarded the IASc-INSa-NASi Summer Research Fellowship 2026
- Published research article in Acta Scientific Microbiology Journal

4. Pramita Dan

- Awarded the IASc-INSa-NASi Summer Research Fellowship 2026

5. Sritama Pramanik

- Awarded the IASc-INSa-NASi Summer Research Fellowship 2026
- Published research article in Acta Scientific Microbiology Journal

6. Salangkrita Roy

- Published research article in Acta Scientific Microbiology Journal

7. Aahelee Ghosh

- Published a review article entitled “Long non-coding RNAs: a new hope for the cervical cancer staging”, in Molecular Biology Reports (Springer Nature)

8. Sanga Chatterjee

- Qualified GATE-XL 2026 with All India Rank 17

9. Sohini Das

- Selected for GRISHMA- Summer Internship Programme, KRITI 2026, IIT Kharagpur

10. Spandan Dutta

- Coauthored book chapter “Using Chitosan Nanoparticles in the Alleviation of Drought Stress in Plants”. Chitosan Nanoparticles for Plant Resilience Under Abiotic and Biotic Stressors (Springer Nature)
- Awarded the IASc-INSa-NASi Summer Research Fellowship 2026

11. Aishani Bhattacharya

- Coauthored book chapter “Using Chitosan Nanoparticles in the Alleviation of Drought Stress in Plants”. Chitosan Nanoparticles for Plant Resilience Under Abiotic and Biotic Stressors (Springer Nature)

SEMESTER 7

1. Adri Garai

- Secured 3rd position in Eureka '26 of Sigma '26, organized by St. Xavier's College Science Association.

2. Ritoja Paria

- Awarded the IASc-INSa-NASI Summer Research Fellowship 2026

3. Rittika Dhar

- Secured 2nd position in Poster Pedia'26, organized by St. Xavier's College Science Association.

4. Samadrita Shaw

- Secured 2nd position in table tennis (women's doubles) and 2nd position in throwball in Xavier's Premier League (XPL).

5. Shreshtha Biswas

- Secured 3rd position in Group dance competition in SpringFest 2026 organized by IIT Kharagpur

6. Simran Alam

- Secured 3rd position in Eureka '26 of Sigma '26, organized by St. Xavier's College Science Association.

SEMESTER 5**1. Abhishikta Gupta**

- Secured 1st position in Eastern dance solo in Xavotsav 2026
- Rank holder in SXCNC (Junior Under Officer)
- Secured 2nd position in firing competition at Combined Annual training camp (NCC)
- Secured 2nd position in Inter College Eastern solo dance competition in Spring Fest organized by IIT Kharagpur

2. Rupayan Mukhopadhyay

- Secured 1st position in Indian College Chess Championship in division 19, 2026 Spring Edition representing St. Xavier's College.

3. Tusaradri Bhattacharjee

- Secured Highest Rank holder in SXCNC (Senior Under Officer)
- Secured 1st position in relay race in NCC Khel 9
- Secured 3rd position in 100m race in NCC Khel 9

SEMESTER 3**1. Arna Mitra**

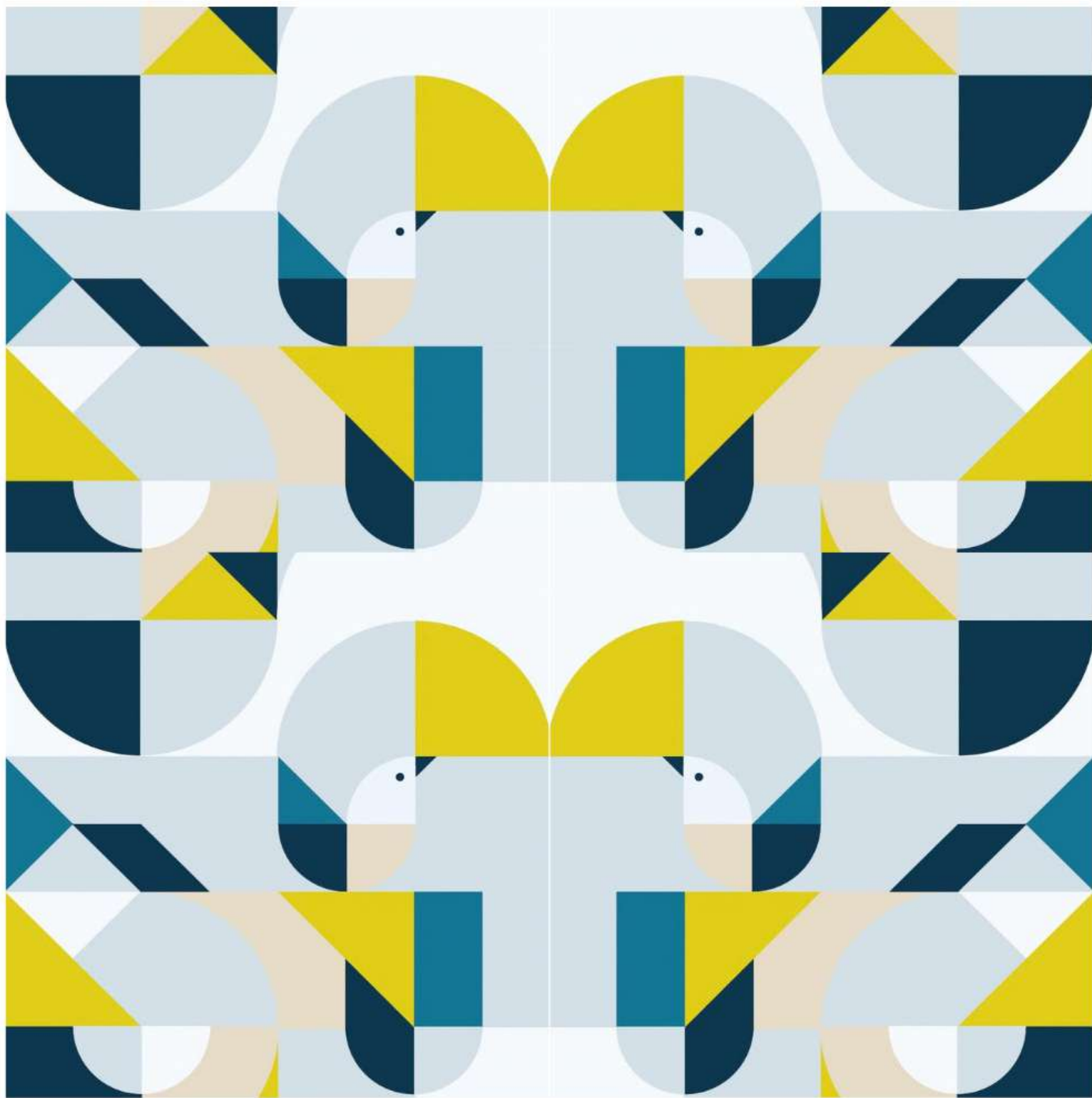
- Secured 2nd Position in "Have a minute", Xavotsav 2026
- Secured 2nd Position in Xavullash Debate
- Secured 2nd Position in Boiragi Debate

2. Tathagata Banerjee

- Secured 1st Position in "Chhonde golpo", Theaxav 2026

3. Priyadarshini Mukherjee

- Silver medalist in Kyokushin Karate National Championship 2025



INVITED
ARTICLES

When Chronic Pancreatitis Mimics Pancreatic Cancer: Resolving the Diagnostic Dilemma through Molecular Precision Medicine

Dr. Srikanta Goswami

Associate Professor

Molecular Gastroenterology Laboratory

BRIC-National Institute of Biomedical Genomics

Kalyani, West Bengal

The clinical dilemma: one pancreatic head mass, two very different diseases

A mass arising in the head of the pancreas represents one of the most challenging diagnostic situations in pancreatic disease. On one side is chronic pancreatitis (CP), a chronic inflammatory and fibrotic disorder that can produce a focal inflammatory mass, often termed a mass-forming chronic pancreatitis. The other condition is pancreatic ductal adenocarcinoma (PDAC), an aggressive malignancy in which early diagnosis is critically important because potentially curative surgery is possible only in a minority of patients. The difficulty is that these two biologically distinct conditions can converge remarkably in their clinical, radiological and even histopathological presentations.

This creates a fundamental dilemma for clinicians: Is the pancreatic head mass an inflammatory consequence of chronic pancreatitis, or is it an underlying malignancy developing within an already chronically inflamed pancreas? The distinction is particularly difficult because chronic pancreatitis itself increases the risk of PDAC, meaning that the presence of chronic inflammation does not provide reassurance against malignancy. Furthermore, the consequences of getting this distinction wrong are substantial. A diagnosis of benign inflammatory mass as malignant one may expose a patient to major pancreatic surgery, such as pancreaticoduodenectomy, with considerable perioper-

ative morbidity and long-term consequences. Conversely, interpreting a malignant mass as inflammatory can result in delayed diagnosis, progression beyond surgical resectability and loss of the opportunity for potentially curative treatment. This is therefore, not merely a diagnostic academic problem—it is a major determinant of patient outcome.

Why conventional diagnosis remains difficult?

Clinical symptoms provide limited discrimination. Patients with either CP or PDAC may present with abdominal pain, weight loss, anorexia, obstructive jaundice, ductal dilatation or new-onset diabetes. In a patient with established CP, symptoms that might otherwise raise suspicion for cancer can easily be attributed to progression of the underlying inflammatory disease.

Imaging presents a similar challenge. Both inflammatory and malignant lesions can appear as poorly defined hypovascular masses in the pancreatic head, associated with pancreatic ductal obstruction, biliary obstruction and surrounding fibrosis. Although modern multidetector CT, MRI and endoscopic ultrasound have substantially improved diagnostic assessment, inflammatory fibrosis and malignant desmoplasia can remain difficult to distinguish. Endoscopic ultrasound-guided tissue acquisition improves diagnostic accuracy, but sampling error remains an important concern, particularly in a fibrotic pancreas where malignant cells

may be sparse.

The commonly used serum biomarker CA19-9 also has important limitations. It may increase in PDAC but can also be elevated in CP, biliary obstruction and cholangitis. Its discriminatory value becomes particularly problematic when CP and obstructive jaundice coexist. Recent evidence continues to show that CA19-9 alone has only moderate ability to distinguish pancreatic cancer from chronic pancreatitis, particularly in early-stage disease.

Thus, the current diagnostic pathway frequently represents an integration of imperfect evidence rather than a definitive molecular diagnosis.

Why an accurate distinction is urgently needed?

The need for improved discrimination extends beyond deciding whether surgery should be performed. CP and PDAC require fundamentally different therapeutic strategies. CP is managed principally through control of inflammation and pain, nutritional support, treatment of exocrine and endocrine insufficiency, and selected surgical or endoscopic interventions. PDAC, in contrast, requires oncological staging and, depending on resectability, combinations of surgery, chemotherapy, radiotherapy and systemic treatment.

The problem becomes even more important because PDAC can develop on a background of chronic inflammation. In such patients, the inflammatory microenvironment may obscure the malignant component both radiologically and histologically. Consequently, the clinically relevant question is not simply whether a mass is present, but whether the molecular architecture of that mass has crossed from chronic inflammatory remodeling toward malignant transformation.

An accurate diagnosis could therefore, prevent unnecessary major surgery in patients with benign inflammatory disease while simultaneously accelerating cancer treatment in patients with occult PDAC.

The opportunity offered by molecular profiling

The limitations of conventional diagnosis provide a strong rationale for developing molecular approaches capable of distinguishing inflammatory pancreatic masses from malignant lesions.

PDAC is characterized by recurrent molecular alterations, most prominently involving mutations in KRAS, TP53, CDKN2A and SMAD4. Activating KRAS alterations occur in the vast majority of PDACs, while TP53, CDKN2A and SMAD4 abnormalities contribute to malignant progression and biological heterogeneity. Importantly, molecular alterations can potentially provide information that is independent of the morphological appearance of the lesion.

A particularly attractive strategy would therefore, be to develop a multi-dimensional molecular signature distinguishing CP from PDAC, rather than searching for a single universal biomarker.

1. Genomic and epigenomic signatures

Targeted sequencing or next-generation sequencing of pancreatic tissue, fine-needle biopsy material or circulating DNA could identify malignant-associated alterations. Detection of canonical PDAC alterations such as mutant KRAS, TP53 or SMAD4 in a suspicious pancreatic mass could provide additional evidence supporting malignancy.

However, genomic mutations alone may not always be sufficient because some oncogenic alterations can occur in precursor lesions or non-invasive pancreatic abnormalities. Therefore, genomic information should ideally be integrated with DNA methylation, chromatin accessibility and other epigenetic signatures. Epigenomic profiling is particularly attractive in CP because chronic inflammation can produce extensive transcriptional and epigenetic remodeling. Identifying methylation patterns that are characteristic of malignant transformation rather than inflammation could potentially provide a molecular boundary between CP and PDAC.

2. Transcriptomic and non-coding RNA signatures

RNA-based approaches provide another powerful opportunity. Bulk RNA sequencing, small-RNA sequencing and analysis of circulating microRNAs could identify transcriptional programs associated with malignant transformation.

Rather than relying on a single differentially expressed gene, a multigene classifier could integrate pathways related to proliferation, epithelial–mesenchymal transition, KRAS signaling, DNA damage, metabolism, extracellular matrix remodeling and inflammatory responses. This is particularly relevant because CP and PDAC share many inflammatory pathways. A useful classifier must therefore distinguish inflammation-associated signals from malignancy-associated signals. Machine-learning approaches could be used to identify combinations of transcripts or microRNAs that maximize discrimination between CP and PDAC.

3. Liquid biopsy and circulating biomarkers

The most clinically attractive strategy may ultimately be a minimally invasive blood-based test. Plasma or serum can provide access to cell-free DNA, circulating tumor DNA (ctDNA), circulating RNA, extracellular vesicles, proteins and metabolites.

ctDNA carrying PDAC-associated mutations could provide evidence of an occult malignant clone, while extracellular vesicles may contain tumor-derived RNAs, proteins and lipids that reflect the molecular state of the pancreatic lesion. Importantly, recent systematic evidence suggests that multi-marker blood-based approaches may outperform CA19-9 alone in distinguishing pancreatic cancer from chronic pancreatitis.

4. Proteomics and metabolomics

Proteomic profiling may capture biological changes that are not apparent at the DNA or RNA level. Mass-spectrometry based approaches can identify proteins associated with tumor-associated inflammation, extracellu-

lar matrix remodeling, metabolic reprogramming and pancreatic cancer progression. Such approaches have already been explored for identifying analytically validated protein biomarkers capable of differentiating CP and pancreatic cancer.

Metabolomics offers a complementary perspective. PDAC and CP differ substantially in cellular metabolism, nutrient utilization, redox balance and lipid metabolism. A combined metabolite signature could therefore, provide an additional layer of discrimination.

Precision medicine: beyond diagnosis

Molecular characterization could also transform management after PDAC is diagnosed. Precision oncology approaches increasingly use tumor and germline profiling to identify patients with potentially actionable alterations. DNA-repair defects, including BRCA1/2-associated abnormalities, may influence sensitivity to platinum-based chemotherapy and PARP inhibition, while rare actionable fusions and selected KRAS alterations can provide opportunities for molecularly matched therapies.

Nevertheless, precision medicine in PDAC remains challenging because most tumors are driven by KRAS alterations that are difficult to therapeutically target, and profound tumor heterogeneity and the stromal microenvironment contributing to treatment resistance.

This makes the CP-versus-PDAC diagnostic problem an especially important area for precision-medicine research. The first precision intervention may not necessarily be a drug; it may be precision diagnosis: determining which inflammatory masses can safely be observed and which harbor malignant biology requiring urgent intervention.

Conclusion

The inflammatory head mass of chronic pancreatitis and pancreatic ductal adenocarcinoma represent a particularly important diagnostic crossroads. Their overlapping clinical and radiological characteristics, together with the limitations of CA19-9 and sampling-based pa-

thology, can create uncertainty precisely when timely decision-making is most important.

Molecular research offers an opportunity to resolve this dilemma by interrogating the biological differences between chronic inflammation and malignant transformation. Genomics, epigenomics, transcriptomics, extracellular-vesicle biology, proteomics and metabolomics, particularly when integrated through computational and machine-learning approaches, could generate a clinically useful molecular classifier.

The ultimate goal should be not simply to discover another biomarker, but to establish a validated precision-diagnostic framework that tells the clinician whether a pancreatic head mass represents inflammation or cancer and, once cancer is confirmed, which molecular vulnerabilities can guide therapy. Such an approach could reduce unnecessary surgery, minimize diagnostic delay and move pancreatic disease management toward genuinely individualized care.

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How does Sex Reversal in Fish become an Integral Part of The Blue Revolution: A New Horizon In Tilapia Culture In India

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Sex ratio in fish

Sexual systems in animals are extremely diverse and vary from gonochorism (separate fixed sexes) to simultaneous hermaphroditism (each individual producing both male and female gametes at the same time) as the extremes in a sexually plastic gradient of intermediate systems (sequential hermaphroditism) and mixed systems (coexistence of males and/or females with hermaphrodites) (Pla et al 2022). These profoundly influence individu-

als' mating success and fitness (Goldberg et al 2017), population sex ratios and effective sizes (Waples 2018), thereby affecting the population dynamics and resilience to environmental and anthropogenic stressors of ecologically and commercially important species that are often endangered or overexploited (Mariani et al 2013).

The sex ratio (the proportion of males to females) in fish is a vital metric that influences reproductive success, population stability,

aquaculture yields, and ecosystem health (Dienye et al 2024). It is a key constraint on reproduction rate in a population, and skewed sex ratios can have major consequences for the population dynamics of a fish species. Fisheries typically have size-selective harvest, and in sexually size-dimorphic species this selectivity skews the adult sex ratio, thus impacting population age structure, fisheries productivity, and yield. The sex ratio can also be skewed during early life stages in fish species with sex determination mechanisms that are sensitive to environmental conditions, which can contribute to population declines when stressful environmental conditions persist (Geffroy and Wedekind 2020).

Tilapia culture in India

Nile tilapia, *Oreochromis niloticus* (Linnaeus, 1758), is presently the third most widely cultivated finfish species globally. Farming of this fish has grown rapidly on a global scale over the last three decades compared with the aquaculture of other species (De and Chakraborty 2025). Global tilapia aquaculture production has grown 11% annually from 0.3 million tons in 1987 to 5.9 million tons in 2017 (Barroso et al., 2019). Tilapia is the only Cichlid (Order: Perciformes) with consistent market values worldwide. It has the potential to fight against malnutrition and food poverty (Wang and Lu 2016, FAO 2017, El-Kassas et al 2020). The fish has become a popular aquaculture species because of its wide tolerance for environmental fluctuations, flexible habitat requirements, rapid growth, and aggressive omnivorous feeding habits (De et al 2022). Total tilapia production in India has reached a level of 3,401 metric tons in recent years, while the government aims to scale tilapia production to 0.766 million metric tons by 2026–2027 and 2.155 million metric tons by 2032.

Sex reversal in Nile tilapia

Sex determination in fish is a flexible process, and individuals are subject to modification by external factors (Chakraborty et al 2011). The Nile tilapia is a gonochoristic teleost with a

stable XX/XY sex-determination system. However, it can exhibit environment-dependent sex determination, where different environmental modulators to which an embryo is exposed during incubation may influence that individual's sex (El-Zaeem et al 2024). Here, estrogens and androgens play a critical role in gonadal sex differentiation, and exogenous sex steroids administered at the time of sex determination can strongly influence the course of sex differentiation (Chakraborty et al 2011).

In general, maturation, natural mortality, and vulnerability to fishing will differ between males and females in sexually dimorphic species, especially if there is spatial segregation by sex. Sex reversal is the biological process where an organism changes its functional biological sex from male to female or female to male, driven by natural social cues, temperature shifts, or chemical exposures (Weber and Capel 2018). Commercial tilapia production generally requires the use of male mono-sex populations because the males grow more rapidly (Chakraborty et al., 2011). All-male Nile tilapia culture is obtained through sex sorting by hand, hormonal sex reversal, maneuvering the temperature, and chromosomal/genetic manipulation (Dauda et al 2014, Olufeagba and Okomoda 2015, Abaho et al 2022). Among all of these techniques, hormonal sex reversal with exogenous steroids, primarily 17 α -methyltestosterone (MT), produces the best masculinization results (Abaho et al 2022, Hassan et al 2025). Numerous studies on tilapia have shown that treatment of XX larvae with MT can induce sex reversal toward testicular development (Chakraborty et al 2011). Average sex-reversal efficacy ranges from 95 to 100%, depending on the management intensity (Silva et al 2023).

Environment-friendly production of monosex all-male tilapia in India

While offering benefits to society, chemicals may be released during their lifecycles and possibly cause harm to humans and ecosystems (Yang et al 2026). Many different natural and synthetic steroid hormones, including MT, have been identified and quantified as wide-

spread aquatic contaminants (Ojogboro et al 2021). It is therefore, desirable to improve techniques with the minimal release of chemicals into the ecosystem so that no harm is caused to the environment.

India aims to foster sustainable growth in the aquaculture sector while minimizing the environmental impact. Different innovations such as recirculating aquaculture systems, biofloc technology, integrated multi-trophic aquaculture, biosecurity and natural treatments are adopted to increase fish production through eco-friendly technological advancements (Arumugam et al 2023). Emphasis has been given to responsible farming practices of Nile tilapia in the country. Phytochemicals with androgenic, growth-promoting, and immunostimulating potential can be a safe, environment-friendly alternative to the synthetic hormone MT. Herbal plants such as *Basella alba* (Family: Basellaceae), *Tribulus terrestris* (Family: Zygophyllaceae), *Asparagus racemosus* (Family: Asparagaceae), *Mucuna pruriens* (Family: Fabaceae), *Withania somnifera* (Family: Solanaceae) and *Chlorophytum borivilianum* (Family: Asparagaceae) are mentioned in the Indian traditional system of medicine, Ayurveda, to possess androgenic activity and increase male virility (Chakraborty et al 2014). The androgenic and anabolic efficacy of these plants [Basella leaves, Tribulus and Mucuna seeds, Asparagus, Withania, Chlorophytum roots] was explored to induce sex reversal, growth and immunity in Nile tilapia. 3-day-old juvenile Nile tilapia (mean weight 0.025 ± 0.009 g, mean length 1.25 ± 0.012 cm) were fed diets containing powdered plant materials, immersed in aqueous extracts of the plants and fed diets containing different solvent extracts of the plant materials at different concentrations. All plant materials produced sex-reversed male fish (> 70%), albeit to different extents. Fish fed diets fortified with plant extracts showed a higher male percentage than direct feeding of feed mixed with plant powder and immersion using aqueous extract. The percentage of males also varied with extracting solvent and concentration for respective plants. Fish fed plant extract-for-

tified diets showed significantly ($p < 0.05$) higher 11-ketotestosterone levels than control males and lower estradiol levels than control females. Aromatase mRNA expression was significantly ($p < 0.05$) down-regulated by all plant extracts with respect to control females. During grow-out pond culture, Nile tilapia fed plant extract-fortified diets showed better growth (achieving a weight of around 500 g in four months), immunity, health and resistance against bacterial infection compared to fish fed a control diet (Ghosal et al 2021, De et al 2022, Mukherjee et al 2022, Mukherjee et al 2023).

In conclusion, this approach provides an avenue to eco-friendly, large-scale production of monosex tilapia and may proceed towards achieving the mandates of the 'United Nations Sustainable Development Goals'. By driving high-yield farming and maximizing resource efficiency, sex-reversed tilapia culture using plant extracts stands out as a pivotal technology powering India's Blue Revolution and securing sustainable aquatic protein for the future.

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Redox Biology of Reactive Nitrogen Species: Signaling and Stress

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Introduction

Nitric oxide (NO) was considered as a toxic atmospheric pollutant for a long period of time. In the 1980s, the discovery of Endothelial Derived Relaxing Factor (EDRF), which is Nitric Oxide (NO) actually transformed our understanding and created the field of redox biology of nitric oxide. In 1992, NO was the molecule of the year published in the journal Science. For the discovery of EDRF or NO as a signal molecule in the cardiovascular system, Robert Furchgott, Ferid Murad and Louis Ignarro won the Nobel Prize in Physiology or Medicine in the year 1998. Like reactive oxygen species (ROS), reactive nitrogen species are also considered as essential physiological mediators at a very low concentration as signal molecule to stressors at a very high concentration. The redox biology of RNS is centered on its dichotomous role in biology and medicine, as its function depends on its concentration, location, duration and the source (1-6).

The Chemical Biology of RNS

RNSs are produced from the reaction of NO with oxygen, superoxide, cellular thiols and metals.

Nitric Oxide (NO): NO is a free radical gaseous lipophilic molecule with a very short half life 0.1-5 seconds in vivo, it is quickly oxidized to nitrite (NO₂), nitrate (NO₃), dinitrogen trioxide (N₂O₃), dinitrosyl iron complexes (DNIC), S-nitrosothiols (RSNO), peroxynitrite (ONOO-) etc. (5).

i. NO is the parent molecule of the RNSs. It has a strong affinity for heme iron and oth-

er metalloproteins, and for other radicals.

- ii. N₂O₃ is a potent nitrosating agent in cells. NO₂ and NO₃ are now recognized as major reservoir of NO in cells under hypoxia via nitrite reductases like deoxyhemoglobin and xanthine oxidoreductase.
- iii. Peroxynitrite (ONOO-) is produced under diffusion controlled reaction between NO and superoxide (O₂⁻). The rate of peroxynitrite formation is faster than the scavenging of superoxide by the superoxide dismutase. It is not a radical but acts as a powerful oxidizing agent and nitrating agent.
- iv. S-Nitrosothiols (RSNOs) and Metal-Nitrosyls as for e.g., S-nitrosoglutathione (GSNO), S-nitrosoalbumin serve as potential NO donors and carriers in cells.

Endogenous NO sources

NO is synthesized by three isoforms of NO synthase (EC 1.14.13.39), which convert L-arginine + O₂ + NADPH to L-citrulline + NO•. These enzymes require molecular oxygen as co-substrates and use cofactors such as (6R-) 5,6,7,8-tetrahydrobiopterin (BH₄), reduced nicotinamide-adenine dinucleotide phosphate (NADPH), flavin adenine dinucleotide (FAD), and flavin mononucleotide (FMN) (6).

- i. eNOS (NOS₃) and nNOS (NOS₁) are constitutive, Ca²⁺/calmodulin-dependent and produce low (nM) concentrations of NO• for signaling. In the vascular environment, endothelium NOS regulates vasodilation and vascular tone. Neuronal NOS (nNOS) mediates synaptic plasticity and neurovascular

coupling.

- ii. Inducible NOS (iNOS) (NOS_2) are expressed in macrophages, neutrophils, and hepatocytes upon cytokine stimulation. It is Ca^{2+} -independent and produces high turnover of $\text{NO}^\bullet$ (μM) for host defense. This isoform is the classic bridge between signaling and stress.

Non-enzymatic sources include nitrate-nitrite-NO pathway and decomposition of RSNOs.

Redox Signaling by RNS: The Physiological Face

RNS signaling complies with the criteria of redox signaling in terms of reaction specificity, target selectivity, favorable kinetics, reversibility, concentration thresholds, spatial and temporal compartmentalization.

i. The Classical NO mediated Cyclic GMP (cGMP)-Dependent Pathway

$\text{NO}^\bullet$ binds to the ferrous heme of soluble guanylyl cyclase (sGC), with picomolar affinity which induces a 200-fold activation. Soluble guanylyl cyclase (sGC) converts GTP to cGMP, which activates Protein Kinase G (PKG), phosphodiesterases, and cyclic nucleotide gated (CNG) channels. This axis mediates vasodilation, platelet inhibition, and smooth muscle relaxation. It is the most sensitive and specific $\text{NO}^\bullet$ signaling pathway (7).

ii. S-nitrosylation mediated Signaling

S-nitrosylation is a reversible post-translational modification in which a NO group is covalently attached to the thiol ($-\text{SH}$) of a cysteine residue and forms S-nitrosothiol (SNO). This reaction happens when excessive NO generates nitrosative stress and follows well-defined chemical pathways. Transnitrosylation is a primary process in which a NO group is transferred from a low-molecular-weight S-nitrosothiol, such as S-nitrosoglutathione (GSNO), to a protein cysteine using thiol-disulfide exchange. Another mechanism is metal-to-cysteine nitrosyl transfer, in which NO coupled to heme or non-heme iron centers combines with adjacent thiols to produce SNO, especially in metalloproteins. Under oxidative or partially oxidizing

circumstances, cysteine residues may generate thiolate anions (S^-), which are more nucleophilic and easily react with $\text{NO}^\bullet$ and equivalent species such as N_2O_3 , producing persistent S-nitrosothiols. Functionally, S-nitrosylation modulates enzyme catalysis, receptor activation, activity of the transcription factor and mitochondrial function. As it is reversible through denitrosylating systems such as thioredoxin or GSNO-reductase, it serves as a redox-based signalling mechanism that couples NO bioactivity to cellular regulation (8).

From Signaling to Stress: Nitrosative Stress

Reactive nitrogen species (RNS) such as peroxynitrite, nitrogen dioxide, and S-nitrosating agents when produced excessively it exceeds the cell's antioxidant and repair capacity leading to the formation of nitrosative stress. In normal physiological conditions, NO signalling takes place through reversible mechanisms like S-nitrosylation but in chronic inflammation or oxidative stress condition elevated RNS levels overwhelm denitrosylation systems and nitrosative stress is generated. Nitrosative stress has been associated with numerous human pathologies, including cardiometabolic disorders, neurodegenerative diseases where post-translational modifications of proteins like S-nitrosylation and nitration play an important role. Altogether, nitrosative stress induces DNA strand breaks, lipid peroxidation and post-translational modification of protein like protein nitration and nitrosylation (9).

a. Peroxynitrite-mediated Damage

ii. Protein Tyrosine Nitration

Peroxynitrite introduces a nitro group to the 3-position of tyrosine to form 3-nitrotyrosine. Unlike S-nitrosylation, this is largely considered as irreversible and protein tyrosine nitration (PTN) is a footprint of pathology. PTN can show either activation/inactivation of enzymes or unaltered protein function. As for e.g. Mn-SOD nitration at Tyr34 leads to inactivation of it, creating a vicious cycle which produces more superoxide. Sarcoplasmic reticulum Ca^{2+} -ATPase and prostacyclin synthase are also found

to be inactivated. In some cases it may create neo-epitopes triggering autoimmunity (5).

iii. Oxidation of DNA, Lipids, and Thiols

Peroxynitrite leads to DNA strand breaks, activating PARP-1, which eventually depletes NAD⁺ and ATP generating cell death. Being a strong oxidant, peroxynitrite oxidizes lipids, initiating chain reaction of lipid peroxidation (5).

iv. Disruption of Fe-S clusters

Peroxynitrite disrupts iron-sulfur clusters in Complex I, II, III and aconitase, blocking mitochondrial respiration irreversibly – contrasting with the reversible regulation by S-nitrosylation of the respiratory chain complexes (5).

b. NOS Uncoupling

Under depleted conditions of substrate (L-arginine) or cofactor (tetrahydrobiopterin, BH₄), NOS itself produces superoxide instead of NO[•], and thus amplifying stress. Tetrahydrobiopterin (BH₄), an important cofactor of NOS, gets oxidized by peroxynitrite, which is a key amplification loop in endothelial dysfunction, diabetes, and hypertension (6).

The Antioxidant and Denitrosylase Defense

Cells try to maintain the following dedicated system to keep RNS signaling compartmentalized:

i. Glutathione/GSNOR system

Reduced Glutathione (GSH) is the first line of defense against any kind of stress including nitrosative stress. Cells maintain a very high concentration of intracellular glutathione where GSNO is in equilibrium with intracellular SNOs. GSNOR actually reduces GSNO to oxidized glutathione and ammonia, thus governing total S-nitrosylation load. GSNOR knockout mice display hyper-S-nitrosylation, which helps in protection against myocardial infarction but susceptible to asthma (10).

ii. Thioredoxin System

Thioredoxin (Trx) is a highly conserved redox-active protein that regulates the redox state of cellular cysteine residues and help to detoxi-

fy nitrosative stress. During nitrosative stress, reactive nitrogen species (RNS) such as nitric oxide (NO) and S-nitrosothiols modify protein thiols through S-nitrosylation, which impairs enzymatic function and signaling. The Trx system, which includes thioredoxin (Trx), thioredoxin reductase (TrxR), and NADPH, functions as a major protein denitrosylase by directly reducing S-nitrosylated cysteines and restoring proteins to their functional thiol state. Trx catalyzes the selective denitrosylation of S-nitrosylated caspase-3, reversing NO-mediated inhibition and regulating apoptosis. The Trx/TrxR system efficiently removes NO adducts from a various cellular protein, confirming its role as a key enzymatic mechanism controlling intracellular S-nitrosylation levels (11).

iii. Peroxiredoxins and Glutathione Peroxidases

Peroxiredoxins (Prxs) are a widespread family of thiol-dependent antioxidant enzymes that act as a first line of defense against both reactive oxygen species (ROS) and reactive nitrogen species (RNS) in cells. Prxs play a crucial role in detoxifying nitrosative stress by neutralizing highly reactive nitrogen-derived oxidants, such as Peroxynitrite (ONOO⁻), in addition to their traditional role of reducing peroxides like H₂O₂ and organic hydroperoxides. Peroxiredoxins are acting as peroxynitrite oxidoreductases; they catalyze a two-electron reduction of peroxynitrite into less reactive species, such as nitrite (NO₂⁻), thus detoxifying peroxynitrite before it can induce irreversible damage. Different members of the Prx family such as “2-Cys” Prxs operate through a conserved catalytic mechanism: a peroxidatic cysteine in the enzyme active site is oxidized by the peroxynitrite, forming a sulfenic acid intermediate, which is then resolved by disulfide bond formation and finally reduced back to the active thiol form by cellular reductants (such as thioredoxin or glutathione) (12).

Glutathione peroxidase (GPx) protects the cells against nitrosative stress by detoxifying reactive nitrogen species (RNS) and minimizing the cellular damage produced by ni-

tric oxide-derived oxidants (NOx). Nitrosative stress is caused by high levels of peroxynitrite (ONOO⁻) and other reactive nitrogen species (RNS), which can nitrate proteins, oxidize lipids, and disturb mitochondrial function and redox balance (13).

Conclusion

The redox biology of reactive nitrogen species illustrate its dose dependence, local concentrations, reaction with NO and RNS. At a low concentrations of NO generation by NOSs, or by non enzymatic reactions, RNS functions through a coordinated manner which is highly specific, reversible modifications, principally by sGC activation and S-nitrosylation, to regulate cardiovascular, neuronal, and metabolic homeostasis. When generated in excess either by iNOS, or when the redox milieu shifts toward oxidation, irreversible tyrosine nitration occur by peroxynitrite.

Modern redox biology therefore not only focuses on RNS simply as damaging agents, but also as a fundamental code which utilizes nitrogen oxides for regulation of cellular functions. Therefore, modern therapeutic strategies are shifting from simple NO donors or NOS inhibitors to modifiers of denitrosylases (GSNOR inhibitors), aiming to restore signaling while preventing stress (14).

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False Nests, Real Benefits: Evolutionary Role of Dummy Nesting in Birds

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Introduction

Nest formation is a crucial task in ensuring critical fitness not only within the avian community, but also in different taxa, as it provides stability to the process of offspring production and nurturing. Over the years of scientific research, it has been observed that the passerine community showcases spectacular variations in the structure of nests. The structural complexity of the nests varies enormously across species, from roughly constructed stick platforms to neatly woven cups, domes and even cavity nests. Physical factors including geographic, spatiotemporal, temperature, climatic and latitudinal differences inevitably contribute to the nesting decisions of birds. Several ecological factors including intraspecies competition, predator availability, vegetation, availability of nesting materials, egg size and eco-geolocation impact the type shape and overall structure of nests. Nests are particularly built to ensure the survival of juveniles at vulnerable stages and for prolonged mono or biparental incubation or simply a reflection of the evolutionary history of an avian lineage.

Understanding the potential factors leading to nest formation leads to the potential challenges that the bird community faces in light of climatic and evolutionary changes. Climate change indicated a prominent change in the nesting behavior due to the adaptive nature of certain birds. Nests provide the basic security net for nestling and also ensure a safe microenvironment free from life-threatening parasites. However, nests also demarcate a prominent location within the breeding territory, which can be exploited by potential nest enemies. These

highly defended localized resources are often targeted by merciless predators from time to time. Nests have also served as the key criterion in reproductive fitness and mate selection.

The term 'dummy nest' holistically translates to an abandoned and loosely constructed secondary nest. While several passerine species have constructed dummy nests for improving reproductive success rates, dummy models have also been tested by the researchers as a decoy for checking out their effects on nesting patterns and behaviors within birds. A common notion is that dummy nests are built to evade attacks from sneaky predators, suggesting the term 'dummy' for the nesting pattern. Certain species of birds resort to nest abandonment before breeding season, thus leading to dummy nest formation. This multi-nesting behaviour might result from external triggers. Vulnerability of the nesting place to events of storm and protection of unhatched eggs and nestlings from predators might be the most justifiable events in dummy nest formation.

Opposing hypotheses

At the onset, let us consider two complementary hypotheses which explain the evolutionary background of dummy nest construction. It would be either; H_0 : predator interference, nesting complexity and reproductive competition do not impact dummy nest decisions or H_1 : predator interference, nesting complexity and reproductive competition impact dummy nest decisions in most birds. Here we look into various published literature on nesting biology, particularly those associated with anti-predator strategies to increase reproductive suc-

cess, design, time and energetics behind nest construction and foraging provisions.

Probing down the evolutionary role

Reproductive insurance

Nesting patterns and designing for avian species substantially determine their reproductive success. Bird species rely on various methods of reducing predation pressure, and improving reproductive success and offspring survival. Dummy nests are one such strategy opted by a large number of birds to ensure maximum survival of nestlings. Biologists studied nest defense behaviour and reproductive success in the form of non-breeding dummy nesting among Northern Hobbies (*Falco subbuteo*), Grass Wrens (*Cistothorus platensis*). Traditionally it was observed that dummy nests substantially reduced the frequency and intensity of predation in the post-egg laying period for the bird species. On the contrary, certain birds like Australian Reed Warbler (*Acrocephalus australis*) build distinct nest structures, termed Type I and II. Type II nests serve as the dummy nests with the sole purpose of providing momentary security to fledglings. In this regard, the hypothesized purpose of dummy nests in reproductive success and diminishing predation pressure does not hold for all bird species. Globally, the dummy nest behaviour was hypothesized to be associated with four key factors: decoys to check predation, advertisement of sexual selection, shelter for fledglings and reduction in intraspecific competition. In case of different birds, dummy nests were observed to be associated with sexual selection. The dummy nests were also used by paired individuals to showcase their parental abilities and influence their partner's investment on reproductive success.

Energetics, survival instincts with dummy nest construction

Dummy nest building might be an energy-intensive process for dummy birds. Grass Wrens (*Cistothorus platensis*) usually build a platform and dummy nest. Here the dummy nests more closely resemble the breeding structures of birds; but the nests are less dense and lack sev-

eral necessary layering, especially those that are imperative in later building stages. Dummy nests may be abandoned during the building process, probably in case of low-cost benefit.

Resource availability and dummy nest formation

Availability of resources during the nesting season and their quality have been examined for many birds. Nest predation behaviour in Ural Owl (*Strix uralensis*) pointed towards significant differences in the proportion of dummies predicted by predators in various food conditions. In intermediate food conditions, distance from owl nests affected predation rates in dummy nests. In other words, prey-predator interaction in areas with dummy nests depends upon fluctuating food availability. A similar study on Australian Reed Warbler (*Acrocephalus australis*) showed whenever birds were relieved from the energetic and temporal constraints through experimental supplementation of foraging resources in their territories, they seemed to invest more in dummy nest construction. Reproductive insurance is one such remarkable aspect that justifies dummy nesting behaviors of birds. Here comes the cost-benefit aspect of dummy nests in a highly predated niche. Alternatively, the success of dummy nests to conceal and maintain the seclusion of nestlings from predation reduces the cost of nest formation and energy investment. Many birds use differentiated nests to improve reproductive success. While traditionally dummy nests were associated with post-egg-laying shelter for passerines, recent studies have provided a different outlook. Evolution in prey-predator interaction strategies has altered the use of spare nests by some bird species. These dummy nests also act as decoys to increase manipulative reproductive behaviour. Having multiple nests increases mating suitability and chances of the male passerine otherwise considered weak in the pact. Another key aspect of dummy nests associated with reproductive strategy and success is reduced intraspecific competition and avoids potential predators. In this case, dummy nests act as an advanta-

geous factor in mate selection and reproductive security.

Post-reproductive refuge for fledglings

Another interesting fact about dummy nest decisions is the post-reproductive success. Dummy nests have been identified to be a great refuge for fledglings of certain bird species. Young nestlings take refuge in dummy nests in absence of parents or sudden attack from apex predators. This increases their chances of survival to a substantial extent. However, several studies observed differences in nest composition of dummy nests. Birds invest resources and time on dummy nests based on certain prerequisites and benefits. In certain birds like Herons, delayed dummy nest building resulted in higher predation. In case of low-cost benefit due to high competition, low resource availability, proximity to the breeding nest, unsuitable nesting conditions or predators, these dummy nests are abandoned at early developmental stage. Hence, all dummy nests may not serve the purpose of reproduction or shelter from predation.

High resource availability

High resource availability implies low intra-specific competition, but not necessarily low prominence of predators. On the other hand, nesting resource availability reduces the cost of dummy nest-building behavior, increasing the benefit of the process. Food resource availability increases the reproductive and post-reproductive sustenance of passerine species. On the contrary, intermediate food resource availability might increase the risk of predation and intraspecific competition. Hence, decisions of dummy nest formation can be considered to be a meticulous process of trial and error within the avian community.

Current trend of research on dummy nesting

Artificial dummy nest introduction

Behavioral strategies associated with bird reproduction with special reference to nesting are the most intriguing aspect of most passerine bird research. Studies based on the

sole purpose of artificial nesting behaviour are not quite abundant. However, artificial model nests made of synthetic materials such as ceramic, and plastic wood that closely replicate the original nests have been a subject of experiment for understanding the predation pattern of birds. Depredation rates of the artificial and natural nests in Red-backed Shrike (*Lanius collurio*) might be associated with certain limitations. Disadvantages over natural nests might include differences in colour, size, microenvironment, egg type and appearance. These anomalies promote depredation activities. Furthermore, artificial nests are deprived of parental vigilance, which might result in a higher prevalence of predators and depredation.

Urbanization and predation rates

The degree of urbanization specifically reduced the predation pressure on either artificial or natural nests, thus reducing the evolutionary fitness behind dummy nesting in urban settings compared to the rest. The artificial dummy nests thus operate as an insurance factor in reproductive success in passerine species in semi-urban or nonurban settings.

Tendency of dummy nesting decision across diverse nesting strategies

Nesting strategy differs depending on different ecological conditions such as nest distribution (solitary or clustered), positioning and nest shape depending on substratum, construction time and complexity of design, whether predators are close or not, nesting species maintaining their own territory or not. Based on the availability of nesting materials, forage stuffs etc. the usage of nests were determined. Dummy nests were constructed more by the solitary nesters compared to species building nests in cluster since close nests provides mutual defenses to each other from potential predators. Short constructed nests are simple in structure and less energetics were linked, thus birds built additional nests within a very short period to decoy predators. Figure 1 shows the propensities of different nesting strategies

to involve dummy nest decision in the nesting ecology.

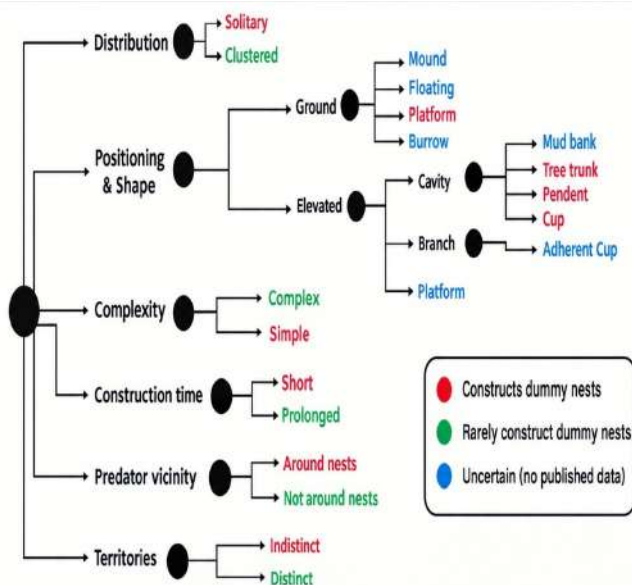


Figure: Propensity of dummy nesting behaviour across diverse nesting strategies in birds

Concluding remarks

Anti-predator behaviour has a direct evolutionary connection with the survival of a species and it is applied at various stages of species' foraging, nesting and territoriality. Initially two opposing hypotheses (H_0 & H_1) were proposed to validate whether the dummy nesting decision impacted by predator interference, nesting complexity and reproductive competition. Birds seem to follow the H_1 i.e., construction of dummy nests have provided birds profound evolutionary advantages and most of them can be categorized as anti-predator strategies to minimize nest predation and increase reproductive success. Dummy nests have inspired researchers to install artificial nests to validate

additional nest construction decision in natural nesting territories. Moreover, species that form simple or short-built nests were found to be the most likely dummy nester, while areas with higher biotic homogenization such as cities, lowered predation risk along with occurrence of dummy nests. Dummy nesting phenomena represent one of the many inherent ways chosen by the birds to maximize their fitness. However, more research is required to determine the actual usage of this strategy and its impact on reproductive success beyond the passerine group.

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FACULTY CORNER

Therapeutic Landscapes and Healing Vibes

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Introduction

The serene lush greenery and natural landscapes, teeming with biodiversity, have a positive impact on our mental framework, whereas continuous bustles of urban life have a profound negative impact on our body and mind. Various studies have shown that nature is a vital positive 'place-factor' in terms of mental health, biophilia being the driving force of well-being. According to E.O. Wilson, who introduced this term '*biophilia*', "*Nature holds the key to our aesthetic, intellectual, cognitive and even spiritual satisfaction.*" The reformed geography of health focusses on the concept of 'therapeutic landscape', the concept developed by Wilbert Gesler in 1992 to examine the physical, mental, and spiritual healing aspects of specific places. In terms of nature, the effects of greenery on overt health and well-being is emphasized with the term '*Vitamin G*', where G stands for the green space around us. In terms of health geography, healthy green space signifies healthy areas of forests and greenery while healthy blue space signifies health-rendering sites, where water lies at the center of promotion of physical and mental well-being.

Neurobiological Perspectives

Therapeutic landscapes, whether extraordinary healing sites or everyday surroundings, support mental health through mechanisms including amygdala deactivation, prefrontal cortex modulation, cortisol reduction, enhancement of parasympathetic nervous system activity, dopaminergic and serotonergic enhancement, elevated brain-derived neurotrophic factor (BDNF), attentional restoration, and neuroplasticity.

Amygdala, Cortisol and Neurotransmitters

A robust body of neuroimaging research

demonstrates that exposure to natural and therapeutic environments reduces activity in the amygdala, the brain alarm centre responsible for threat detection and fight-or-flight responses. A mere walk in nature can do wonders decreasing amygdala activity and that is why, proximity to urban forests correlates with greater amygdala structural integrity. The amygdala's stress-related functions involve signalling to the hypothalamus, which initiates the hormonal stress cascade through hypothalamic-pituitary-adrenal axis (HPA axis), ultimately activating adrenal cortisol production. Our exposure to therapeutic landscapes may block this stress cascade, generating downstream impacts encompassing decreased cortisol levels, blood pressure, and heart rate. The healthy circadian rhythm of cortisol secretion helps to prevent the accumulation of allostatic load and other stress-related ailments, while endorsing attention restoration and relieving mental fatigue. A relaxing walk along sea beach or forest floor and observing picturesque natural blossom or wildlife at play can result in augmented levels of serotonin, a neurotransmitter vital for mood regulation and feelings of happiness and can activate the mesolimbic pathway, the brain's reward circuit, increasing dopamine transmission. Such dopamine release is associated with emotional resilience and achievement, observed when we are in the lap of nature.

Prefrontal Cortex Modulation

Our exposure to therapeutic landscape has profound impact on proper functionality of prefrontal cortex (PFC), the seat of our meta-cognition, involving executive and emotional regulation. Various neuroimaging studies

have shown that rural natural views decreases oxyhemoglobin concentrations in the right PFC compared to urban sights, signifying decreased metacognitive load. On the other hand, urban sights affect the specific areas of brain associated with visual processing and threat monitoring, including hippocampus, amygdala, parahippocampal gyrus, middle and inferior occipital gyrus, and inferior frontal gyrus. Nature exposure leads to increased PFC activation and more engrossment of the regions supporting memory, emotional coordination, and metacognitive flexibility. Researchers have shown that exposure to therapeutic landscapes lead to reduced activity in the subgenual PFC, involved in repetitive negative thinking and rumination, characteristic of clinical depression.

Attention Restoration

According to attention restoration theory, natural surroundings aid to restore our depleted attentional abilities allowing directed attention systems to recover from mental exhaustion. Neurophysiological studies on brain oscillatory patterns have shown that alpha waves (8-13 Hz) predominate during relaxed conditions, while beta waves (14-30 Hz) signify attentional processing and task engagement. Research on contemplative landscapes with great aesthetic and ecological significance reveals distinct brain oscillatory patterns linked to attention restoration. Exposure to natural milieu is connected with quicker recovery rates from surgery as well as making life's demands seem manageable in terms of economic distress.

Neuroplasticity Related Modifications

Neuroplasticity refers to the ability of brain to change and adapt in response to intrinsic and extrinsic stimuli over time. Chronic exposure to therapeutic environments may induce neuroplastic changes affecting brain structure and function over time. Urban living has been connected with increased amygdala activity during stress and increased activity in pregenual anterior cingulate cortex, the brain areas implicated in emotional processing and stress management. Conversely, proximity to greens-

pace correlates with larger total brain volumes, greater gray and white matter, and enhanced amygdala integrity. Neurobiological models propose that chronic stress from our surrounding alters neuroplasticity and neurogenesis in critical areas of hippocampus, PFC, anterior cingulate cortex, and amygdala, thus affecting metacognitive control and mental well-being. Visual stressors in our environment may trigger neurophysiological stress responses, mediated through hypothalamic-pituitary-adrenal (HPA) and sympathetic-adrenal-medullary (SAM) systems, contributing to allostatic load and structural brain alterations. Green spaces counteract these effects by engaging neuroendocrine mechanisms that shift the body toward relaxed states, lowering cortisol, raising serotonin, easing blood pressure, and promoting neuroendocrine equilibrium. Nature exposure also elevates brain-derived neurotrophic factor (BDNF), a biomarker promoting hippocampal neurogenesis and synaptic plasticity and playing a key role in alleviating negative emotions. Forest therapy (*Shinrin-yoku*) elevates BDNF through integrated mechanisms involving stress hormone reduction, growth factor signaling, exercise-induced exerkines, phytochemical exposure, and enhanced cerebral blood flow.

Our brain includes specific structures to observe, assess, memorize, and utilise spatial information. Hippocampus, entorhinal cortex, parahippocampal cortex, and parietal cortex, along with the parahippocampal place area and lingual landmark area, have been identified as vital areas for space perception and navigation. Recent research has demonstrated that the complexity of a geographic background has a direct impact on cortical thickness in the spatial navigation system of brain, signifying the possibility of landscape-induced neural plasticity.

Socio-biological implications

Religious and cultural heritage places including rehabilitation gardens, protected areas, coastal zones, pilgrimage destinations, and indigenous sacred sites, create therapeutic

and peaceful environments, supporting mental well-being through sensory stimulation and aesthetic appreciation. Even urban cultural heritage, encompassing historical buildings and waterbodies, boosts mental health by providing restorative ambience that facilitate relaxation, positivity, and attentional recovery. Walking in urban heritage surroundings supports attentional recovery and positive emotional states. Even, people possessing the habit of visiting urban parks report fewer visits to doctors, while those who engage in exercise in the midst of nature report better improvements in self-esteem and confidence than those who exercise in artificial surroundings.

Karolina Doughty and Anthony Gatrell developed notions of therapeutic mobilities, health benefits arising from movement through landscapes rather than static presence in them. For example, walking together produces therapeutic landscape based impact through mobile engagement with places, combining physical activity, social interaction, and spatial context. Actor-network theory (ANT) and non-representational theory reconceptualised therapeutic landscapes as dynamic assemblages emerging from interactions between human and non-human actors, rather than fixed locations with inherent properties. Drawing on theory of mind and the social biofeedback model, Gilbert Rose suggested that landscapes can function as empathic mirrors, enabling individuals to recognize and process emotional states through engagement with place. This conceptualization connects therapeutic landscapes to neuroscientific findings on place cells, mirror neurons, and the limbic system's role in spatial-emotional processing.

Geographic Information Systems (GIS) help to analyze spatial patterns of mental health and brain data in environmental context. GIS can map mood disorder distributions, identify spatial clusters associated with environmental stressors and target therapeutic interventions to the regions of utmost need. Integrating neuroimaging data with GIS enables spatially ex-

plicit analysis of environment-brain-ethological relationships, informing precision public health approaches to mental health promotion.

Inference

The therapeutic landscapes are healing gardens and the 'world of yoga', rendering the magical power of physical and mental healing. These natural surroundings are not passive backdrops, but active ingredients of welfare, engaging specialized neural circuits for spatial processing, emotional regulation, and stress physiology. Urban planning and design should prioritize the creation and preservation of therapeutic landscapes, recognizing that natural topographies have direct effects on brain structure and function. Geopsychiatry, an emerging transdisciplinary field integrating geography, psychiatry, and neuroscience, offers frameworks for understanding mind-place-planet connections in mental health and ailments. Clinical practice should integrate nature-based interventions alongside conventional treatments, recognizing therapeutic landscapes as viable adjunctive therapies. Joseph Campbell, the famous American mythologist, rightly said, "*The goal of life is to make your heartbeat match the beat of the universe, to match your nature with nature.*"

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One Health 2.0: Bridging Systems Ecology, Genomics, and Climate Change

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Introduction

The Anthropocene is marked by environmental changes that are occurring at a speed and on a scale rarely experienced in human history. Population growth, the continuing loss of biodiversity, increasingly frequent climate extremes, fragmentation of natural habitats, and the emergence of new infectious diseases are not independent problems. They are closely connected and often reinforce one another. As these pressures accumulate, societies are reaching a point where conventional, sector-specific approaches to environmental and health problems are becoming increasingly inadequate. It is now becoming imperative to treat the key stakeholders of the environment as a single unit and from this stems the concept of One Health and Systems Science. Together, this framework provides indications towards detecting, understanding and solving complex health problems.

From One Health to One Health 2.0

The modern One Health concept developed from the recognition that human and animal health cannot be considered independently. Its historical roots can be traced to Calvin Schwabe's idea of "one medicine" in 1976, followed by the Manhattan Principles in 2004. In its early form, One Health was particularly concerned with diseases that moved between wildlife, livestock and humans. The Tripartite Agreement involving WHO, FAO and WOA in 2010 further strengthened the institutional basis of this approach. Despite these developments, health-related activities have often continued to be organized within separate professional and institutional boundaries. The

usual approach of Physicians focusing on clinical health outcomes remains important, but problems arise when these activities are carried out with limited communication between sectors. Such fragmentation can undermine disease surveillance and more importantly conceal the environmental and ecological processes that create or amplify health risks. One Health 2.0 is an attempt to transcend these limitations. It integrates the framework of One Health with the principles of Systems Science, especially Systems Thinking, Systems Dynamics and Systems Design. The conceptual basis can be traced back to Ludwig von Bertalanffy's General Systems Theory that emphasized that biological and social systems are made of interacting and interdependent components.

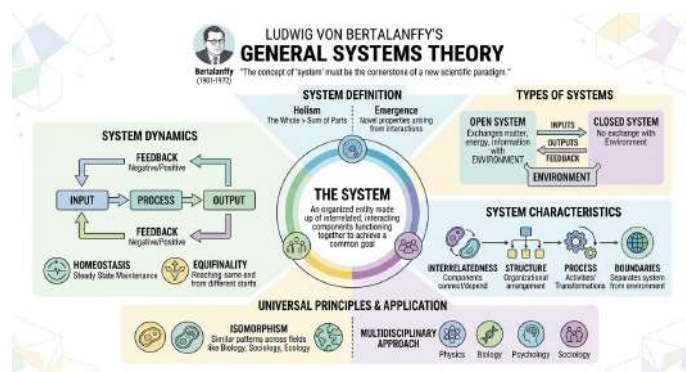


Figure 1: A summary of the General Systems theory [Generated using Open AI – 27th August 2026]

Health as a condition can now be evaluated using two contrasting lenses – one which deals with personalized health and the other which integrates information of interactions among different systems such as human communities, animal populations, climate processes, microorganisms, and socioeconomic structures which interact and influence each other continuously. Thus the current understanding of

diseases not only requires focus on the host and the pathogen but also on the environmental and social factors that regulate the transmission and distribution of the pathogens (public health). A systems-based, One Health approach therefore encourages the integration of different forms of biological and environmental information. Such integration can reveal feedback mechanisms, cumulative impacts and circular relationships that may remain invisible when each sector is examined independently. Disease transmission, for example, may be influenced simultaneously by changes in land use, host population density, climate, human behaviour, pathogen evolution and environmental contamination.

Systems Ecology: The Environmental Foundation of One Health

Ecosystems do not merely provide a passive background in which disease occurs. They actively influence pathogen survival, transmission, host susceptibility and the evolution of infectious agents. A systems-ecology perspective therefore places ecological integrity at the centre of health protection. Healthy ecosystems can act as important buffers against environmental and biological disturbances, whereas degraded ecosystems may increase vulnerability among humans and animals. The environment performs at least three important functions in relation to disease and health – it acts as a reservoir, as a process substrate and as a mediator of health.

The environment as a reservoir and process substrate

Various environment components accumulate, transport and disseminate biological and chemical agents which may be laden with resistance genes, heavy metals, toxic agrochemicals and other runoffs. These have diverse retention time frames and thus serve as sources for redistribution with every associated activity from animals and humans as well as diverse ecological phenomenon. Chemical transformations within ecosystems can further alter the behaviour and toxicity of pollutants. For example, microorganisms can transform inorgan-

ic mercury into methylmercury, a highly toxic form that can accumulate through food webs. Thus, environmental processes can determine whether a contaminant remains relatively inaccessible or becomes biologically available and capable of entering organisms and food chains.

The Environment as a Mediator of Health

Environmental quality also affects the physiological condition of organisms. Animals living under prolonged nutritional, climatic or ecological stress may experience reduced immune competence. Such stress can increase pathogen shedding and potentially facilitate transmission between wildlife, domestic animals and humans. This relationship becomes particularly important when ecosystems are degraded. Habitat loss and habitat fragmentation have been identified to be the two most important drivers of zoonotic spillover in recent years which not only affect agricultural productivity but also impacts wildlife, livestock and human health.

Real-Time Metagenomics and the Changing Landscape of One Health Surveillance

Emerging infectious diseases and antimicrobial resistance create a strong demand for rapid diagnostic and surveillance systems. Conventional approaches that depend on transporting samples to distant laboratories can delay decision-making, particularly during rapidly developing outbreaks. In such situations, obtaining useful information within hours rather than weeks can make a substantial difference. The development of next-generation sequencing and bioinformatics has transformed the possibilities for One Health surveillance. Portable sequencing platforms, particularly nanopore technologies such as the Oxford Nanopore MinION, have made it possible to undertake genomic investigations much closer to the site where samples are collected. Nanopore sequencing works by passing native DNA or RNA molecules through microscopic pores and measuring changes in electrical current as the nucleic acid moves through the pore. These electrical signals can then be converted computational-

ly into nucleotide sequence information. One of the important advantages of this approach is that sequencing and analysis can occur in real time. This opens several possibilities for field-based One Health surveillance. Adaptive sampling allows sequencing software to make decisions about incoming DNA molecules while sequencing is taking place. Sequences of interest can be retained, whereas unwanted sequences can be rejected. This provides a way of enriching specific genomic regions, pathogens or host-associated sequences without necessarily requiring extensive additional laboratory processing. For field investigations, this can make targeted genomic surveillance more practical and potentially reduce the amount of sequencing required to answer a specific question.

Ultra-long reads and direct RNA sequencing

Nanopore platforms can generate very long sequencing reads, in some cases extending over hundreds of kilobases. Such reads can assist in the assembly of complex genomes, including those of polyploid plants and wildlife species with complicated genomic structures. Direct RNA sequencing has revolutionized the transcriptome and spatial transcriptome landscape by preserving information on transcript isoforms and epitranscriptomic modifications in sequencing data. The “Lab-in-a-suitcase” approaches can bring sequencing capacity to

locations where conventional laboratory infrastructure is limited. Instead of requiring all samples to be transported to centralized facilities, genomic analysis can increasingly be performed close to the point of collection.

This decentralization has scientific as well as social implications. Such an approach is also consistent with the principles of access and benefit sharing reflected in the Nagoya Protocol.

One Sample, Many Analyses

The concept of “one sample, many analyses” (OSMA) provides another useful extension of this integrated approach. One of the most prominent examples is in Wastewater based epidemiology, where a single sample is investigated using metagenomic, metabolomic, and analytical chemistry methods as well as high resolution microscopy to identify microplastics. The value of OSMA lies in the ability to extract multiple layers of information from a single environmental sample. Rather than treating each environmental problem as a separate surveillance exercise, an integrated sampling strategy can provide a much broader picture of community and ecosystem health.

Climate Change as a Threat Multiplier

Climate change complicates the One Health paradigm through interconnected environmental pathways. Rising temperatures and altered rainfall shift vector and host ranges while accelerating pathogen replication, intensifying vector-borne (malaria, dengue) and foodborne (salmonellosis) risks. Extreme weather further escalates hazards: flooding destroys sanitation systems to spread waterborne pathogens like *E. coli* and *Leptospira*, whereas droughts cause stagnant, contaminated water resulting in harmful algal blooms, and wildlife immune stress. Beyond infectious diseases, extreme conditions mobilize heavy metals and persistent pollutants into food webs, causing bioaccumulation. These cascading biological and toxicological threats underscore the necessity of integrating environmental pollution and climate dynamics into unified One Health strategies.

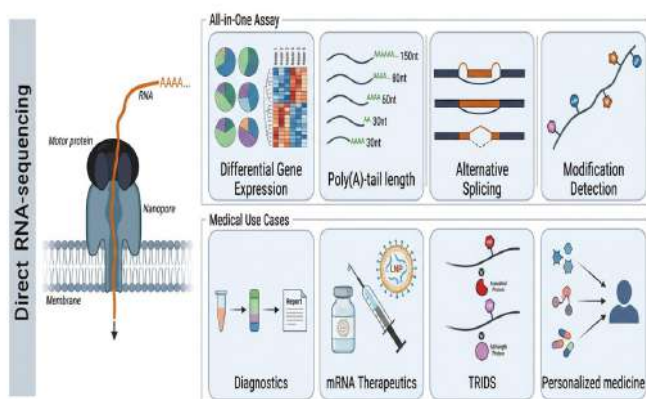


Figure 2: Summary of Direct RNA sequencing and its applications [Modified from: <https://doi.org/10.1093/nar/gkaf1314>]

Climate-Smart One Health: Moving from Concept to Action

The first step is to understand the linkages that exist between climate – ecosystems – agriculture and health. The next challenge is to translate these ideas into practical interventions. Climate-Smart One Health (CS-OH) and Climate-Smart Integrated Pest Management (CS-IPM) provide potential frameworks for doing this. Building on the broader principles of Climate-Smart Agriculture, these approaches aim to achieve several objectives simultaneously: maintaining food production, strengthening agricultural resilience, reducing greenhouse gas emissions and protecting the health of soil, water, plants, animals and people. Several interventions illustrate how these objectives can be brought together.

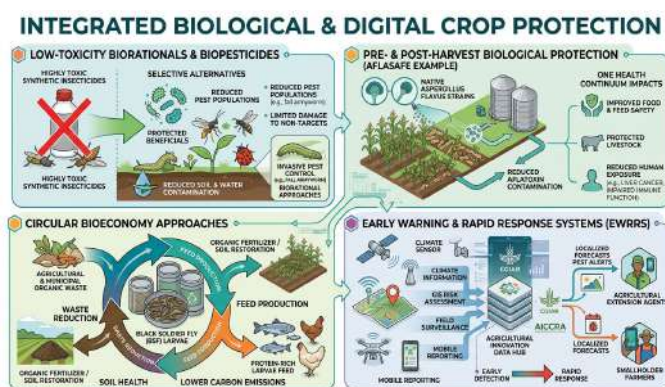


Figure 3: A summary of various Climate Smart One Health Approaches that are being implemented across the world. [Generated using Open AI – 27th August 2026]

Policy Synthesis and Intersectoral Governance

The long-term success of One Health 2.0 will depend on whether institutions can move beyond disciplinary and administrative boundaries. Environmental scientists, ecologists and evolutionary biologists need to work alongside physicians, veterinarians, toxicologists and data scientists. No single discipline has access to all the information required to understand complex health threats.

This also means that national health and environmental policies need to become more preventive. Instead of responding primarily after an outbreak or environmental crisis has occurred, policies should place greater emphasis

on ecosystem restoration, biodiversity conservation, climate adaptation and environmental monitoring.



Figure 4: Image summarizing the institutional and policy reforms that are needed to implement the One Health approach [Generated using Open AI – 27th August 2026]

Concluding Perspective

One Health 2.0 provides a way of responding to this complexity by combining the established principles of One Health with Systems Science and Systems Ecology. Within this framework, the environment is not merely one of three sectors but an active component of the system that influences pathogen transmission, host health, ecological resilience and human well-being. The transition from reactive disease control to resilient health systems therefore requires a broader conception of health—one that recognizes the links among people, animals, microorganisms, ecosystems and climate. St. Xavier's College (Autonomous), Kolkata has initiated a Workshop series on One Health, the first edition of which was held at the Indian Sundarbans on the 20th and 21st of June 2026 and future editions of the same are being planned.

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The Harmony of Epigenetic Regulation: Exploring Cancer through the Lens of Insect Sex Chromosomes

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Introduction

The orchestration of gene expression is essential for physiological homeostasis, development, and cellular identity. Genes express through the RNA, which either codes for the proteins (mRNA), or constitutes non-coding RNAs (ncRNAs) performing diverse functions. Any DNA sequence alteration perturbs the RNAs, leading to alterations of gene expression patterns, affecting cellular *vis-à-vis* histological homeostasis. However, a still finer layer of regulatory module exists beyond the cascade

of gene expression, which, operating through a plethora of mechanisms barring alterations in DNA sequences, such as DNA methylation, modifications of histone proteins bound to DNA and remodelling of chromatin, with or without the aid of ncRNAs. These mechanisms collectively constitute "epigenetics."

One of the instrumental modes of epigenetic regulation is the post-translational modification of the histones around which DNA is wrapped to achieve the compact chromatin that exists in the nucleus of eucaryotic cells.

These modifications, written by a set of proteins, the “writers”, require the “readers,” that, depending on the modification, summon other proteins to either initiate, heighten or inhibit gene expression. Examples include H3K4me3 and H4K16ac, linked to active transcription, and H3K27me3, associated with repression. The “erasers” remove the existing modifications for creation of new ones. Together, these constitute a dynamic ‘histone code’ determining transcriptional competence and orchestrate gene expression, the disruption of which leads to severe consequences, despite the genes bearing no mutations in their coding sequence.

Cancer, although primarily understood as a genetic disorder, is being increasingly recognised as a consequence of epigenetic dysregulation. Reports from diverse tumours show aberrant histone modification patterns associated with malignancy, along with perturbed expression of histone modifying enzymes. These subtle alterations can silence tumour suppressors or activate oncogenes, driving tumour initiation and progression. Hence, understanding the initiation, propagation, and fine-tuning of epigenetic cascades is imperative to discerning the nuances of both physiological and pathological states. The mechanism of X-chromosome dosage compensation in male *Drosophila*, which employs a conserved H3K36 methylation – H4K16 acetylation cascade to cause transcriptional upsurge, offers a genetically tractable platform for dissecting the nuances of analogous cascades operative in mammalian cancers.

The Epigenetic Symphony in Dosage Compensation in *Drosophila*

In *Drosophila*, males carry one X chromosome while females carry two, creating a potential imbalance in X-linked gene expression. To equalise dosage, males upregulate their single X chromosome approximately twofold. This process, dosage compensation, is mediated by the male-specific lethal (MSL) complex, a group of proteins (MSL1-3, MLE and MOF), that specifically target and activates the male X chromosome, aided by the *roX* ncRNAs.

The MSL complex operates through a sequential cascade of histone modifications. The male X-chromosome is first marked by H3K36me3, “written” by Set2. The MSL3 protein recognises and binds this modification, anchoring the complex to the chromatin. Within the complex, MOF, a histone acetyltransferase (HAT), acetylates histone H4 at lysine 16 (H4K16ac). This modification decondenses chromatin, enhancing RNA Polymerase II recruitment and drives transcription. During transcription, Set2 associates with the RNA Polymerase and “writes” the H3K36me3 mark at the 3’ end of the genes. This creates a self-reinforcing loop, where transcription promotes H3K36me3 establishment, which recruits MSL, further boosting transcription.

Beyond H3K36me3, additional histone modifications like H3K4me and H4K20me1 may operate to recruit the MSL complex while yet other marks, may be established in response to H3K36me3, cooperating with H4K16ac to augment transcription. This synchrony of multiple marks working in concert exemplifies the precision of epigenetic regulation.

The Epigenetic Discord in Cancer

The epigenetic harmony so evident in *Drosophila* dosage compensation, is often rendered discordant in human cancers. The same molecular players are involved. In humans as well, SETD2 (the human homologue of *Drosophila* Set2), “writes” the H3K36me3 mark co-transcriptionally which in turn, leads to the establishment of the H4K16ac mark. Depending on the context, the precise readers differ, viz., during DNA double strand break repair, the methylated mark is recognised by LEDGF, which recruits the acetyltransferase KAT8 (hMOF), whereas during transcriptional activation, the mark is read by KAT5 (Tip60) itself. Thus, the cascade *per se* is conserved, but the downstream consequences vary. In malignancies, this axis is frequently dysregulated. In clear cell renal carcinoma and acute leukaemia, SETD2 mutations rank among the most common alterations. Similarly, H3K36me2 and H4K16ac represent epigenetic signatures in diffuse

intrinsic pontine glioma, with H4K16ac being the most acetylated residue. In tumours driven by aberrant Notch signalling, like hepatocellular carcinoma, the MDM2-hMOF-H4K16ac axis is perturbed, depleting H4K16ac and altering the expression of numerous downstream genes, leading to tumour cell proliferation and migration. The broad consequence of perturbation of this axis is transcriptional upheaval, i.e., genes that should remain silent are switched on, while tightly controlled genes are overexpressed. It is this state of epigenetic discordance that characterises the malignant cell.

The Dosage Compensation Lens: A Genetically Tractable Platform for Exploring Cancer Epigenetics

Drosophila has long served as a model organism for studying developmental programs, genetic interactions and modelling of human diseases, owing to its well characterised development, robust genetics, ease of genetic manipulation and feasibility of live imaging. The conservation of core epigenetic machinery between flies and humans, combined with the tractability of modulating chromatin regulators, renders the fly particularly suited, for dissecting the epigenetics of gene regulatory pathways.

In the two seemingly distinct events outlined above, viz., dosage compensation in *Drosophila* and oncogenesis in humans, the same epigenetic cascade operates – the methylation at lysine 36 of H3 leads to the acetylation at lysine 16 of H4, which drives transcription. The striking congruency between these processes suggests that the fly dosage compensation pathway is not merely a developmental curiosity, but a molecular analogue of the pathway to tumorigenesis. In both contexts, this axis culminates in transcriptional output that maintains the physiological state, and any perturbation can lead to pathological or developmental consequences.

Viewing the tumourigenic pathway through the lens of dosage compensation, the yet undiscovered epigenetic cross-talk or transient regula-

tory states could be interrogated to illuminate the (earliest?) events in malignant transformation. Harnessed as a “mini-laboratory,” the fly dosage compensation pathway could be *deliberately* manipulated to identify vulnerable nodes in the establishment and sustenance of the “methylated H3K36 – acetylated H4K16 – transcription” axis. With transcriptional output of genes on the male X chromosome as a simple readout, this pathway could serve as a cost effective, live screening platform for assessing therapeutic efficacy of small molecules, prior to testing in human cell lines and mammalian tumour models.

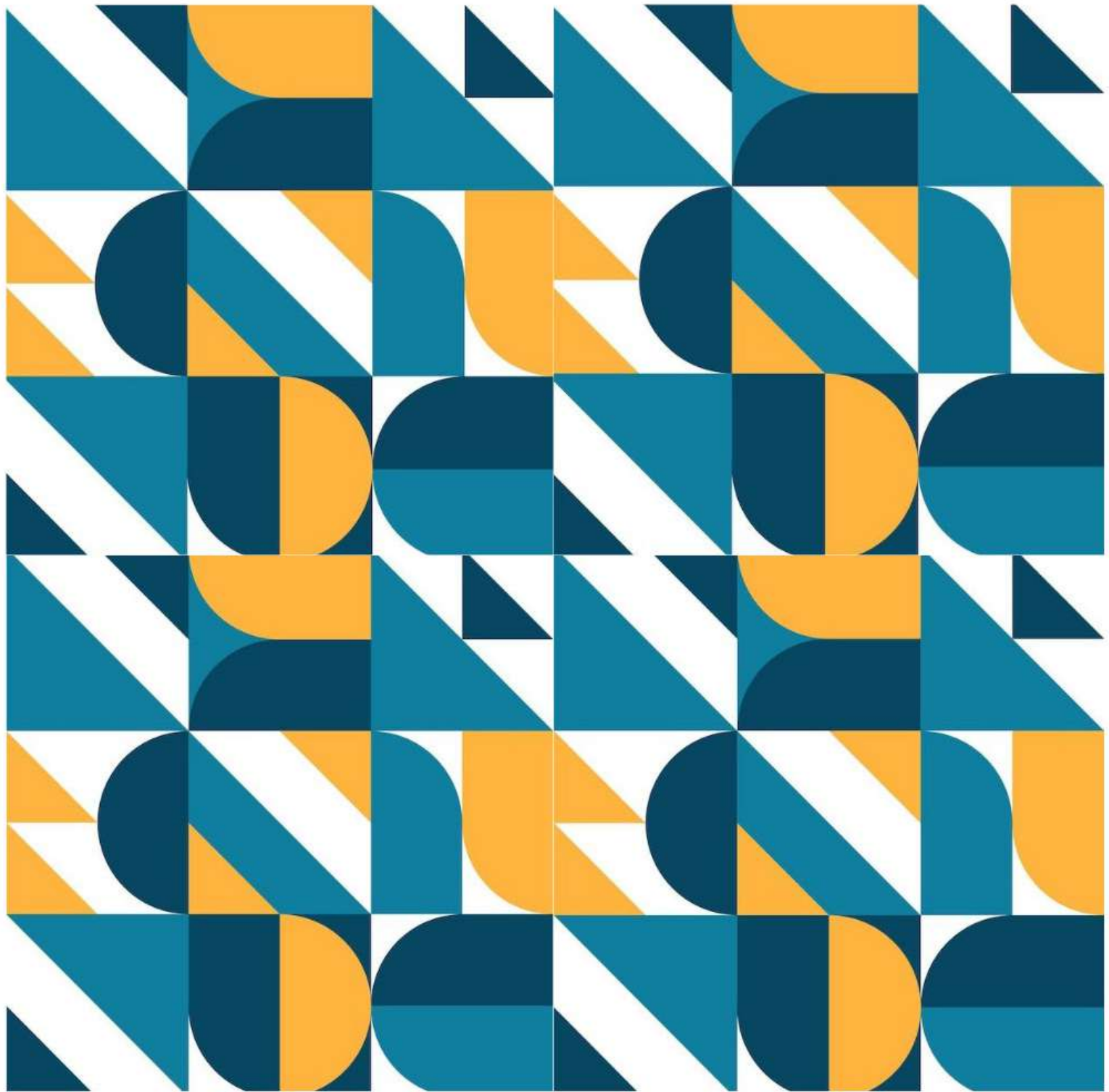
Conclusion

The harmony of epigenetic regulation, as exemplified by *Drosophila* dosage compensation, offers a powerful conceptual and experimental framework for understanding the discord that characterises cancer epigenetics. The sequential, cooperative action of H3K36me3 and H4K16ac on the male X chromosome mirrors the aberrant chromatin modifications observed in diverse malignancies, where perturbation of this conserved axis drives transcriptional upheaval. By exploiting the genetic tractability of the fly dosage compensation pathway, it could be plausible for researchers to dissect the nuances of this cascade, identify vulnerable nodes, and screen for molecules that selectively disrupt the methylated H3K36 – acetylated H4K16 – transcription axis. With the ultimate goal of tumour studies being restoration of physiological homeostasis, such approaches hold promise for developing epigenetic therapies that could correct the aberrant landscape of cancer cells.

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STUDENT CORNER

Mystery of the Hidden Twin

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Keywords: Fetus in fetu, Teratoma, Organogenesis, Monozygotic twins, Radiology

Introduction

Human embryological development is an extremely coordinated, regulated, and complicated process starting right at the moment of fertilization of sperm and ovum at the ampulla of the fallopian tube, followed by a number of cleavage divisions—cellular proliferation, migration, and differentiation—leading to the formation of tissues and organs. Although all these processes are precisely regulated, under certain exceptional circumstances, disturbances during embryogenesis and subsequent organogenesis can lead to developmental abnormalities. Medical science has witnessed many mysterious anomalies—like a baby carrying another tiny fetus within it. These are documented under the name of “Fetus in Fetu” or FIF. Fetus in Fetu is an extremely rare developmental error where a ‘diamniotic monozygotic’ twin (also known as a parasitic twin) gets enclosed within the surviving host twin early in development. In other words, a twin gets absorbed by another twin—yet the fetus keeps on growing! As unusual as it sounds, fewer than 200 cases are reported in medical history till date.

Embryological basis and Pathogenesis

We know that monozygotic twins form when a single fertilized egg splits into two independent embryonic developmental units and start developing into two separate embryos. If the zygote splits approximately 4-8 days post fertilization; i.e., after the Inner Cell Mass has formed but before formation of the amnion, a diamniotic monozygotic twin forms. As they originate from the same zygote, the twins are genetically very similar and hence called as identical twins. According to the Parasitic Twin hypothesis, when the two separate embryos

start growing at different rates, one embryo, the larger one becomes the host twin and the other, the smaller malformed embryo gets engulfed into the body of the host embryo. This engulfed twin cannot survive on its own, forms vascular connections with the host twin due to anastomoses of vitelline circulation and obtains nourishment, hence grows. 80% of Fetus in Fetu cases are found in the retroperitoneum. Development of parasite fetus can also occur in critical places of the body like the stomach, heart, brain, mediastinum or scrotum. Clinical symptoms may range from abnormal swelling of abdomen, vomiting, jaundice to urine retention, respiratory problems etc. It can vary depending upon the size and location of the fetal mass inside the body. In certain cases, this can stay silent during the early years of life, however may become apparent, with symptoms appearing at a later age.

Fetus in Fetu vs. Teratoma

But does that mean all such tissue masses resemble truly a fetus in fetu? Not necessarily. Although similar in apparent appearance, a fetus in fetu condition can often be confused to a Teratoma. A Teratoma is a germ cell tumor composed of derivatives from all three germ layers – ectoderm, mesoderm and endoderm. These arise from pluripotent germ cells that are usually benign and contains skin, hair, teeth within the tumor. Under certain circumstances, the tumor or the teratoma gets so organized that it takes the shape of a fetus. This is called a ‘Fetiform Teratoma’. Usually these are found in ovaries and can be homozygous in some loci but heterozygous to its host. But FIF is typically retroperitoneal, has a vertebral axis about which organogenesis can occur, contains spine and other organs, has a genetic makeup

identical to the host twin. Willis' theory states that FIF is a highly differentiated form of the teratoma, where the encapsulated mass contains a vertebral axis with distribution of certain organs about the axis. Identification of a Fetus in fetu and a Teratoma can be confusing. Both are encapsulated, both are attached to the surrounding tissue and capable of independent growth. Teratoma has neither organogenesis nor vertebral segmentation. This giant retroperitoneal encapsulated mass has fat tissue, teeth, vertebrae, ribs, soft tissues, long bones and limb-like structures. Almost all fetus in fetu cases are anencephalic, i.e, the malformed fetus lacks a brain, skull bones and the head. A true placenta is absent.



Fig: (A) The arrow indicates an axial section of a CT scan with a long bone structure. (B) The arrow points to a sagittal section showing a structure resembling vertebra. (C) The arrow highlights an MRI Scan showing a lesion in the left lumbar region containing both fatty and soft tissue components. Adapted from Sahoo et al. (2024), licensed under Creative Common Attribution License CC-BY 4.0.

Case Reports

There was a recent case report of China where a one-year-old girl was presented to her doctor with motor delay. Her head circumference was very large. Radiological examination of her brain revealed the presence of a huge approximately 13cm large mass that was obstructing the spinal flow leading to hydrocephalus. The downstream increase in pressure led to consequent increase circumference and her motor delays. There was marked presence of vertebrae and other bones

of the limbs. Craniotomy was performed on the FIF. An immature embryo was removed with visible organs like mouth, eye, hair, forearm and hands. Another case report of India where a 17-year-old girl was presented with bulge in the abdomen that has been increasing since the last 5 years – with slight pain and early satiety. No significant weight loss, no issues with bowel movements and normal menstrual history were recorded. Upon carrying out several laboratory blood investigations, the levels of alpha-fetoprotein and β -hCG were found normal. When CT scan was performed, a large, approximately 25 cm mass was observed which had fat, bones, teeth, vertebrae etc. This is the first reported case of adult female Fetus in fetu worldwide. Exploratory laparotomy was performed to surgically removed the huge mass.

Diagnosis

Imaging techniques like CT scan (Computed Tomography) can be used to study complex anatomy or calcification of structures may not be clearly understood through USG (Ultrasonography). CT scan is the best imaging modality for FIF over USG to have high resolution images about the mass which reveals the presence of calcified structures. Sometimes MRI (Magnetic Resonance Imaging) can be performed for pre-operative planning as it provides detailed images to identify vascular connections in and around the mass. Surgical excision or Laparotomy is carried out to carefully excise the malformed fetus from the patient. After surgery, the tissue should be sent for histopathological examination or biopsy to test for presence of biomarkers like alpha-fetoprotein and β -hCG so that chances of teratoma can be ruled out. Low levels of these biomarkers indicate a FIF condition and eliminate the chances of the surgically operated tissue to be a teratoma. Fetus in fetu can also be detected in a pre-natal USG often in the third trimester of pregnancy to understand the presence of any organized fetus-like structure within the original growing fetus.

Conclusion

In conclusion, we can say Fetus in fetu is absolutely remarkable and rare developmental anomaly observed 1 in 5 lakhs of live births. Beyond the clinical perspectives of the disorder, fetus in fetu is a beautiful culmination of developmental biology, radiology and pathology. Studying these bizarre conditions improves diagnosis and management. Parents should remain aware about the condition, so that early detection of such a condition may facilitate timely examination and cure. Biology teaches us that life is not merely created, it is intricately controlled and regulated – but sometimes can make wonderful mysteries by itself!

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Rewiring the Plastisphere: in situ Genomic Editing via CRISPR-Associated Transposases (CAST) System

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Keywords: Plastisphere, CRISPR-associated transposases (CAST), In situ genome editing, Microbial community engineering, Environmental biotechnology

Introduction: The Hidden World of the Plastisphere

Plastic debris in the environment does not remain sterile. Within days, dense microbial biofilms known as the plastisphere colonize it. These communities frequently include organisms adapted to hydrophobic surfaces and, in some cases, limited enzymatic capacity to degrade synthetic polymers. Natural

degradation, however, works too slowly to offset the scale of pollution. A practical doubt for environmental biotechnology is whether we can selectively improve the degradative efficiency of microbes already living on the plastic, without isolating them in pure culture. CRISPR-associated transposase (CAST) system represents one of the most promising tools for such in situ genomic editing.

CAST: From Genome Editing to Community Engineering

Classical CRISPR-Cas nucleases generate double-strand breaks and depend on the host cell's DNA repair machinery. Homology-directed repair, required for insertion of large genetic cargoes precisely, is largely restricted to actively dividing cells and inefficient in most bacteria. Off-target activity and uncontrolled repair outcomes further limit reliability. CAST systems evolved through the natural recruitment of nuclease-deficient CRISPR effectors by Tn7 like transposons. The resulting RNA-guided integrases insert multi-kilobase long DNA payloads at defined genomic sites without requiring homologous recombination or incorporating DNA double-strand breaks.

Two principal classes have been developed into working tools. Type I-F systems, exemplified by the *Vibrio cholerae* CAST, use a Cascade effector complex (multi-subunit nucleoprotein assembly) to target and achieve high on-target specificity. Type V-K CAST systems, built around Cas12k (single-protein Cas effector), are more compact. Both support payload sizes from under 1 kb to more than 10 kb and can be programmed with multiple guide RNAs for simultaneous, multiplexed insertions. In optimised *E. coli* experiments, insertion efficiencies can approach 100%, and the systems function robustly across diverse Gram-negative species. Delivery is not limited to transformation; conjugative helper-independent vectors enable the CAST machinery and mini-transposon cargo to move from a donor strain into recipient cells already present in mixed, living communities.

The transition from engineering a single bacterial genome to manipulating an entire plastisphere represents a complex challenge. The plastisphere is not a collection of isolated microorganisms, but a dynamic and spatially organised community in which microbes compete for resources, cooperate through metabolic interactions, and exchange genetic material. Consequently, altering the genome

of one member could potentially influence the behavioural and metabolic fate of the other. In this context, CAST-based genome editing could mark a revolution in synthetic ecology, moving beyond the modification of individual microorganisms to the alteration of selected members within a functioning microbial community. The outcome, however, depends on how the introduced gene interacts with the existing ecological network.

These features project well onto the requirements of plastisphere engineering. Microbial biofilms on plastic surfaces are spatially structured communities in which horizontal gene transfer occurs at elevated rates. A conjugative CAST vector could deliver, for example, an improved PETase or cutinase cassette under a strong, plastic-responsive promoter into selected members of the mixed community. Because this chromosomal insertion is stable, the new function can persist even after the delivery plasmid is lost. Recent advancement of a rhamnose-inducible ShCAST (*Synechocystis hofmannii* CRISPR-associated transposase) system (RhaCAST) has shown that the technology can be transferred successfully into environmentally relevant non-model genera such as *Burkholderia cenocepacia* and *Burkholderia multivorans*. The platform incorporates both loss- and gain-of-function edits, allows excision and reuse of the selection marker, enabling iterative genome modification without radical accumulation of antibiotic-resistance genes. The broader research landscape continues to expand. The European CASTedit project is systematically engineering CAST systems for more complex cellular contexts, including mammalian cells. Although its primary focus lies outside environmental microbiology, they incorporate RNA-guided transposases as large-payload genome-editing tools, showing independence from cellular division. Parallel advances in ecological community-based editing further support the feasibility of targeting specific taxa within complex microbial assemblages.

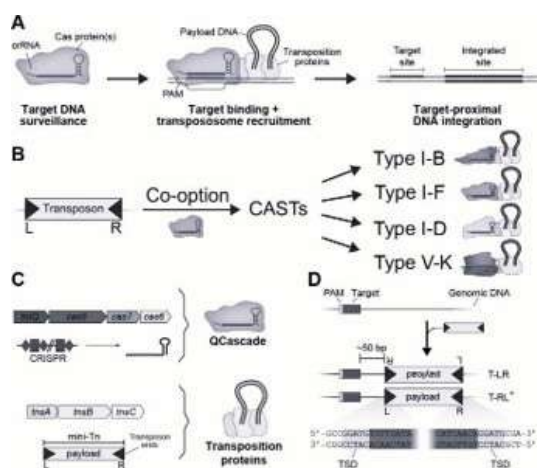


Figure: Overview of CAST system (Gelsinger et al., 2023).
[Under Creative Common License]

Major Challenges: Plastisphere Resistome

An important concern is the plastisphere resistome, the collection of antimicrobial-resistance genes carried by its microbial inhabitants. Recent evidence suggests that plastic-associated biofilms can enrich antibiotic-resistance genes and mobile genetic elements, enabling conditions that favour horizontal gene transfer between microorganisms. This raises a major biosafety doubt for CAST-based engineering, as introducing a new gene function into such a highly connected community would require stringent assessment of how that alteration might interact with the existing resistome. The genetic map of the plastisphere is further complicated by bacteriophages, which interact extensively with bacterial populations and can influence gene movement within microbial communities. Recent research has identified phage-associated metabolic genes in plastisphere communities, depicting the need to consider viruses when predicting the ecological consequences of genetic engineering (Xia et al., 2026). Delivery efficiency still varies among taxa and the taxonomic diversity of natural plastisphere communities has not yet been systematically evaluated. Off-target integration (low with carefully designed Type I-F CAST) must be quantified effectively.

Precision Rewiring: Targeting the right organism

The central challenge in in situ plastisphere engineering is not simply delivering a CAST

system into a complex microbial community, but ensuring that it targets the organism of interest. A plastic-associated biofilm may contain hundreds of bacterial and fungal taxa, each occupying different ecological niche. Editing the wrong niche could produce negligible benefit or negatively impact ecosystem health. Advances in species specific and site-specific genome editing within complex bacterial communities demonstrate that genetic manipulation can be directed towards selected microbial populations without getting isolated. This principle could eventually allow CAST systems to target organisms owning particular metabolic pathways while leaving neighbouring community members unaltered. Achieving such precision would be crucial for transforming CAST from a laboratory genome editing technology into a reliable tool for community-level genetic rewiring.

Nevertheless, the core technical advantages, such as recombination independence, large cargo capacity, and compatibility with conjugative deliveries, position CAST systems as a realistic method for selective rewiring of plastic-associated microbiomes.

Conclusion

Nature has already solved the problem of targeted, large-scale DNA insertion without double-strand breaks. The remaining task is to adapt that solution to the ecological niches associated with anthropogenic plastic pollution. Controlled studies that combine CAST editing with metagenomic monitoring of plastisphere communities represent a logical next step. If successful, they could move the field from descriptive surveys of plastic-associated microbes toward more explicit, community-level metabolic enhancement. The future may not be a single super-degrader, but a microbial workforce where every member has designated role to perform.

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The Language of the Ocean: an Attempt to Understand Communication in Whales

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Keywords: Communication, Vocalization, Codas, Inter-click intervals

Introduction

Communication between organisms is an integral component of survival, encompassing various forms. Although the mention of communication immediately springs forth the idea of human language, in reality it includes all organisms from single-celled bacteria to giant vertebrates like elephants. Despite the mode of communication differing significantly amongst the various species, all organisms communicate in some form or the other. In unicellular organisms like bacteria, communication is via simple chemical signals. An example of this is quorum sensing, which involves production and secretion of autoinducers in the external environment, accumulation of which triggers density-dependent cellular modifications, gene expression and nutrient acquisition. Communication amongst multicellular organisms is more complex, especially in the

Kingdom Animalia. It can range from complex hormonal signalling amongst eusocial organisms for collective societal benefit to communication involving sounds and visual inputs. Various kinds of signs and signals, along with vocal noises, are used for the establishment of territory, in search of mates or just as a signal to warn others of incoming danger. Humans show a much more complex method of communication involving a multitude of languages. Of particular interest is the marine world, which has always been a little obscure to us since the beginning of time. Sound travels in a different manner through water compared to air with the water particles being closely spaced together. However, marine animals still have been found to communicate with each other through a variety of signals, including visual, auditory and chemical signals. A fascinating example of communication in marine animals

is vocalisations produced by whales.

Vocalizations of Odontocete

Sounds produced differ between two suborders of whales, the Odontocete and Mysticete of which the more prominent members have been highlighted. Sperm Whales (*Physeter macrocephalus* of Odontocete) communicate with each other by means of a series of clicks, repeated several times, which are referred to as codas. First coined in 1977 by William A. Watkins and William E. Schevill, these define themselves against the usual click sounds of whales. Communication in sperm whales features a characteristic sequence of Inter-click Intervals (ICIs). Click groups comprising the codas are generally less than two seconds in duration. However, observations indicate that codas, instead of being produced in isolation, are actually part of interactive exchange between two or more chorusing whales, where individual whales chorusing produce a sequence of codas with periodicity of approximately 4 seconds. Communications using codas show amazing levels of complexity, which include a smooth variation in their duration over the course of an exchange as well as the appearance of extra clicks at the end of codas, which indicate discernible features of codas with the capacity to be controlled, hinting at a complex communication system. Efficiency of the vocalization system is denoted by the observation that coda durations (sum of their inter-click intervals) can be regulated by individual whales smoothly over the course of multi-coda exchanges with no obligation towards maintaining the number of clicks or inter-click intervals. This phenomenon has been referred to as rubato. Substantial continuous variations are present here. Also noteworthy is the presence of extra clicks in certain codas appearing at distinct positions in longer exchanges, with most being present at the beginning of call exchanges. This is referred to as ornamentation. This is followed by “change in chorusing behaviour”. Scientists have theorized a Sperm Whale Phonetic Alphabet using whale vocalizations made up of various feasible combinations of rhythm,

tempo, rubato and ornamentation, thereby alluding to something equivalent to the International Phonetic Alphabet for human languages.

Vocalizations of Mysticetes

While sperm whale codas have been shown as analogous to a human Phonetic alphabet language, Baleen whales of suborder Mysticeti, like humpback whale (*Megaptera novaeangliae*) songs, conversely, are not yet suggestive of a structured language with meaningful combinations. However, they still show some semblance of a pattern and seem to follow Zipf's law (how common and rare words appear in a conversation, their frequency, duration, etc.), indicating how the song structure corresponds to human language. The songs are repetitive, complex and structured in a nested hierarchy. A song session consists of multiple songs which can be decomposed into several ‘themes’. Themes, in turn, are a repeated consolidation of ‘phrases’ (made up of individual sound elements). Baleen whales have a unique larynx that produces super low frequency sounds (as low as 12.5Hz) which have the capacity to travel huge distances. Humpback whale song and human speech showcase several structural parallels, including use of similar frequency bands, consisting of both tonal (voiced) and broadband (unvoiced) elements and vocalisations of variable durations punctuated by silence. An experiment was performed by McCowan et al. where they were able to communicate with a Humpback whale, Twain, using a contact call, ‘whup’. The call used was recorded previously from Twain's family group. This demonstrates some form of recognition with the possibility of self-recognition. Twain displayed active engagement in the vocal coordination, modifying her vocalization rates based on broadcast of the ‘whup’ call and also showed capacity to coordinate in an anti-synchronous counter calling framework.

Behavioural Responses to Whale Acoustics

Interesting behavioural responses in whales have been detected upon exposure to calls of other whales. Avoidance response is the predominant behaviour demonstrated by most

cetaceans when exposed to playback sounds of killer whales (*Orcinus orca*), the ocean's apex predator. Some whales, however, are attracted to killer whales' calls. Humpback whales engage in a mixed-species association with herring-eating killer whales. They approach such killer whales and avoid unfamiliar mammal-eating killer whales, which demonstrates their ability to differentiate between different ecotypes of killer whales. On the other hand, pilot whales approach both fish- and mammal-eating killer whales but show differences in behavioural patterns in their approach depending on the ecotype. In the case of fish-eating killer whales, they confront them in huge numbers, manifesting a mobbing-like behaviour, while for mammal-eating killer whales, a cryptic strategy is implemented wherein they stop foraging, form tight groups and spend less time near the surface, all the while approaching the source for inspection and evaluation of threat levels. Killer whales alternatively show avoidance response to the sound of pilot whales, as observed in a study conducted by Selbmann et al. They adjusted group behaviour to facilitate cohesion and aligned themselves side by side to coordinate their travel in the same direction, showing a switch to 'travel behaviour'. There was an increase in call frequency, variable and aberrant calls, which have been hypothesized to indicate excitement or coordinate group behaviour. Stronger responses were shown to be induced by larger group sizes of pilot whales. It is still unclear as to whether they perceive pilot whales as a threat or respond in such a manner due to low costs of avoidance.

Conclusion

It is safe to say that humans are not the only organisms with complex communication systems. Even at the depths of the ocean, conversation goes on amongst the life forms present. Just like humans, whales also indulge in vocalizations which are quite complex in nature. However, noise pollution from large ships, industrial activity and recreational purposes have shown to cause disruption in perceiving vocalizations leading to altered foraging behaviours,

changing of call frequencies, impacting migration as well as increased levels of stress and health impacts. Efforts must be made to preserve the acoustic habitat of such wonderful marine mammals by investing in resources to reduce noise pollution and create safe corridors for migration. Further research into the intricacies of communication in whales will give us insight into the complex behavioural patterns observed in whales.

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Don't Judge An Egg By Its Cover: The Enigmatic Genetics Behind Egg Mimicry in Cuckoos

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Keywords: Cuckoo, Brood Parasitism, Mimicry, Maternal Inheritance, Evolution

Introduction

"Thou mordrer of the heysugge on the braunche that broghte thee forth"

-Parliament of Foules, 1392, Geoffrey Chaucer

Cuckoo is that ungrateful intruder no bird ever wants to find in its nest. Yet its voice has captured the minds of poets and musicians alike. The iconic two syllable onomatopoeic call of the male cuckoo from which it derives its name, is often the harbinger of ushering in of spring. Behind this dichotomous creature, lies a fascinating story of evolutionary genetics that has shaped the survival story of the bird.

The Art of Deception

It is a baffling sight for birdwatchers and field ecologists as a reed warbler meticulously feeds a chick that will grow up to 5 times its own size. Cuckoos are brood parasites. They trick birds of other species into raising their offsprings. And their sophistication in this regard has made them the model organism of brood parasitism. There are queen cuckoo bumblebees that hijack the nest of an alien colony and cuckoo catfish (*Synodontis multipunctatus*) which parasitize the mouth-breeding thick lipped cichlids inhabiting Lake Tanganyika in East Africa. Within birds, cowbirds (Icteridae), honeyguides (Indicatoridae), African finches (Viduidae) and the Black Headed Duck (*Heteronetta atricapilla*) of South America are some of the other known brood parasites.

Parasitic Behaviour of Cuckoos

A molecular phylogeny shows that brood para-

sitism has evolved independently three times within the cuckoo family (Cuculidae). The cuckoo has evolved various adaptations tailored for parasitism. The most elegant trick of these is perhaps the way in which cuckoo eggs often strongly mimic those of the host bird. In response, the hosts themselves have coevolved a diverse repertoire of defensive behaviour to ensure succession of their own progeny. Parasitized hosts display heightened egg rejection behaviour for non-mimetic eggs and lower egg retrieval behaviour compared to birds that are not parasitized. This evolutionary pressure has driven evolution of cuckoo eggs to strongly resemble both the colour and patterning (maculation) of the eggs of the hosts they parasitize.

Same Species, Different Looking Eggs?

For the wide diversity of hosts cuckoos are known to parasitize, their eggs match this diversity with a different appearance of eggs for a different host. Now it would be logical to assume that the phenotype of eggs is specific to a given species of cuckoo which parasitizes a particular host. But as a fact of the matter that is not the case. The common cuckoo (*Cuculus canorus*) parasitizes the nest of both brambling and meadow pipit who have vastly different looking eggs (Figure 1). Thus, the same species of cuckoos is known to parasitize different hosts and hence lays different looking eggs as per the host. Further, there is no assortative breeding by male cuckoos, and they breed indiscriminately with females reared by different foster species. Hence there is a constant gene

flow at the nuclear level that prevents speciation. So what explains this enigmatic phenomenon of intraspecific variation of cuckoo egg appearance?

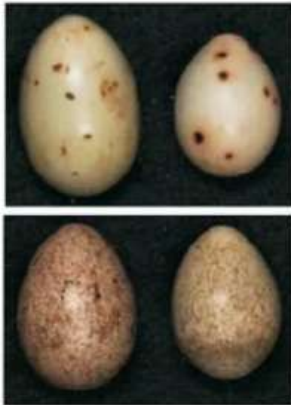


Figure 1 : Photographs of eggs of brambling (top) and meadow pipit (bottom) along with the host specific cuckoo egg [Source: Stevens, M. (2011). Avian vision and egg colouration: Concepts and measurements. In Avian Biology Research (Vol. 4, Issue 4). <https://doi.org/10.3184/175815511X13207790177958>]

Maternal Inheritance of Cuckoo Egg Colouration

The genes for egg colouration would have to be inherited in a manner that would differ according to host species, yet be persistent within the tribe of cuckoos parasitizing a particular host. The most plausible explanation for this phenomenon lies hidden in bird genetics. Birds have a ZW system of sex determination system where the male is homogametic (ZZ) while females are heterogametic (ZW). The W chromosome is passed down matrilineally through generations and is not subject to recombination. From the perspective of the W chromosome, it has only ever been in the female body. It can be said that this chromosome has evolved under a selection of “genetic memory” of the host that the female bird parasitized. Strongly mimetic eggs were accepted by the host and gave rise to cuckoos that survived, and were able to pass on the respective genes to their female offsprings, who in turn would have a better chance to continue their line of succession. On the other hand, eggs that differed in appearance from host eggs faced rejection and those genes were eliminated from the survival race.

This gave rise to matrilineal host specific egg monomorphic tribes within a species referred to as gentes (singular: gens). In random breeding, while the nuclear genome is thoroughly mixed up, the gens specific mitochondrial and W genes of the female remain preserved. Females can thereby mate freely with any male without losing the specific gens-specific adaptation to the host. To complement this, the female chicks are ‘imprinted’ to their foster parent species. When these chicks grow up, they remember the host that reared them and thus choose the same foster nest as their female forebearers.

Modern genetic studies have traced genes responsible for egg colouration to be linked to maternally inherited mitochondrial genes and the W chromosome. In a study, it was found that cuckoos (*Cuculus canorus*) having immaculate blue eggs were distinguishable from other cuckoos in the same area having brown spotted eggs only by their mitochondrial and W-linked DNA while having no significant differences in the autosomal and Z-linked DNA. By their mitochondrial phylogeny, the females were inferred to belong to an ancient maternal lineage dating to around 2.6 Mya. Further studies have identified single nucleotide polymorphisms within several key candidate mitochondrial and W-linked genes that contribute to the divergence of egg colouration. Recently a W-chromosome linked translocation of an autosomal component of the respiratory I complex NDUFAF4 was found, that elucidated a possible link between oxidative phosphorylation and heme-associated pigment synthesis pathway. However, given the architecture of W chromosome and its size it is unlikely that all genes responsible for egg colouration are found on the W chromosome. A more plausible explanation would be that genes contributing to egg colouration are also autosomal, but their expression is regulated by maternally inherited genes. Current analyses confirm that the base colour of cuckoo eggs is controlled by maternal inheritance, while the maculation pattern is controlled by bi-parentally inherited autosomal loci.

Cuckoo egg mimicry being driven by evolutionary pressures is strongly subject to host behaviour. That is why while some have achieved remarkable mimicry to their host eggs, others that parasitize on hosts that have poorly evolved egg discrimination often lay eggs that vastly differ from host eggs. This is especially true of host species that have been newly exposed to parasitism by cuckoos and are still nascent in the coevolutionary arms race. Despite strong preference for their foster nest type, female cuckoos may sometimes, by mistake, or due to lack of proper host nest, lay in a non-foster nest. There may also be translocation of maternally inherited genes under poor selection pressures. These factors over time, give rise to new gentes that help cuckoos expand their host range and diversify.

Conclusion

The cuckoo is a remarkable creature shaped by selection dynamics between parasitic adaptations and host defence function, that captured the attention of Aristotle and continues to riddle us to this day. Maternal inheritance explains the paradox of contrasting egg phenotype within the same species that allows the bird to successfully exploit a plethora of hosts. Cuckoo egg mimicry has thus emerged as the result of an evolutionary tug of war over a sex-limited trait. However, the exact molecular mechanisms contributing to the trait still remain elusive.

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Imitation Games: Turing Patterns In Nature

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Keywords: Evolution, Turing instability, Pattern Formation, Morphogenesis

Introduction

Many of us know of Alan Turing from the 2014 Benedict Cumberbatch film “The Imitation Game”. He was indeed an ‘enigmatic’ code breaker and his Test for Artificial Intelligence is extremely relevant in the ever nearing prospect of a sentient computer. However he also made lasting contributions to the biological sciences. His pioneering research in the mathematical basis of pattern formation is much less publicized, and begets more attention.

Basis of Patterns

This model was based on diffusion dynamics. Usually diffusion is considered to induce stability in systems. However if the diffusion coefficients of two interacting substances vary, then diffusion can also destabilize systems. In his 1952 paper “The Chemical Basis of Morphogenesis”, Turing hypothesized that such interactions can generate periodic patterns even if the initial state of the system is stable and uniform. These are called Turing instabilities, and they in turn generate what are known as Turing patterns. In this mechanism, a substance A (the activator) activates production of itself as well as another substance I (the inhibitor). The inhibitor in turn prevents formation of activator. When A is active at specific positions on the body, I is produced, inhibiting A. However if the diffusion coefficient of I is much higher than A, it can rapidly diffuse away, leaving patches of A which I has not been able to degrade. This gives rise to spots. In a more rectangular area, like the tail of an organism, these spots appear as stripes.

One of the first successes of this theory was by Bernard Richards, who was one of Alan Turing’s last students. In 1953, he set out to solve how diffusion operates in spherical organisms. He

solved certain differential equations and then used Scheme A (a primitive version of an operating system designed by Turing) to plot what these spherical organisms would look like. Despite having no previous biological knowledge of these organisms, the species which he plotted surprisingly corresponded directly to Radiolarians discovered during the 19th century voyage of HMS Challenger. The species discovered during the voyage were later observed and recorded by the great evolutionary biologist Ernst Haeckel, whose sketches (Figure A) are shown. There were 8 variations in growth patterns- the unique feature was the growth of spines from the spherical surface at regular intervals. These corresponded to the spherical models plotted by Richards. Each spine pattern on the radiolarian shells actually represented a family of solutions corresponding to a parameter n , taking values of 2, 4 and 6. In the natural world, 2, 6, 12 and 20 spine variations are found. These variations can be plotted by superimposing some of the differential solutions.

Later such Turing Patterns began to show up everywhere in the animal world and are now known to play important roles in how they develop and function. Prominent processes involving patterns include camouflage and mimicry. The blue-ringed octopus (*Hapalochlaena fasciata*) on feeling endangered produces a blue ring-shaped pattern on its body to warn predators. In some other octopi, such epidermal patterns are implicated both in communication and protection from prey by camouflage. They change their patterning in both colour and texture in response to certain stresses, which helps them mimic their surroundings. It is possible that the Octopus learns to reprogram its Turing patterning dynamics in some way- ex-

tracting information from existing patterns to create new patterns. This is the mechanistic basis of many mimicry models in the animal world.

When it comes to the underlying genetic and molecular mechanism of these pattern formation, much is unknown. However, there are exciting prospects. Lizards and many other reptiles exhibit a plethora of patterns and colours, many of which are important in sexual selection and thus can have evolutionary implications. In Brown Anolis Lizards of the Caribbean (*Anolis sagrei*), the females are polymorphic. They show diamond like or chevron-like patterns on their dorsal surface. Only the chevron morph is found in males. Allelic Variation at the CCDC 170 locus was found to be responsible for the differential migration pattern giving rise to these patterns. CCDC170, a cytoskeletal protein, is known to affect cell migration by acting as an organizer of the Golgi network. Thus migratory capacity of individual cells may change cellular behaviour at the collective level. Again, simple computer models were found to imitate this natural patterning almost perfectly. CCDC170 is also crucial in human health. Usually co-expressed with the Oestrogen Receptor genes, mutations in the gene were found to be associated with progression of Breast Cancer. In another study in African striped mice (*Rhabdomys pumilio*), the Wnt modular *Srpf 2* was found to regulate hair follicle patterning. Thus there are certainly many more fascinating discoveries to be made in the genetics of animal patterning.

On a farewell note

In our journey through the animal world, modelling has been invoked on many occasions. There are a plethora of simulators online where we can experiment with patterns with no prior knowledge. A simple one can be found at - <https://jons.website/projects/reaction-diffusion/>. Some patterns obtained from this simulator have been shown in Figures B and C. It is indeed amazing how the patterns one can generate with the click of a mouse may exist on some creature or the other in the animal world,

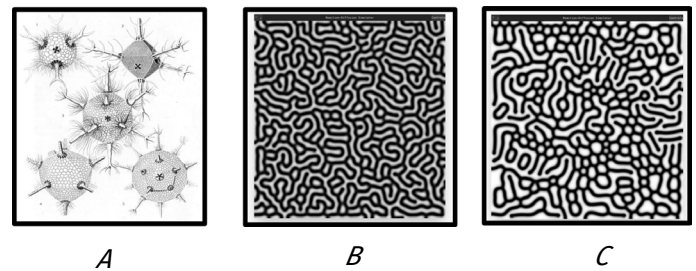


Figure A: From a webified version of “Reticulated Geodesic Constructions” Computers and Graphics, Vol 24, #6, Dec, 2000, pp. 907-910 . Figures B and C: Obtained from the simulator <https://jons.website/projects/reaction-diffusion>

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Breaking Bad: Chromothripsis and Its Role In Cancer

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Keywords: Cancer biology, Genomic instability, Punctuated genome evolution

Introduction

In 1902, Theodor Boveri proposed that improper chromosome segregation during mitosis, resulting in abnormal chromosome numbers (aneuploidy), could contribute to cancer development. Despite stringent cell cycle checkpoints, such aberrant segregation can occur in both normal and malignant cells. Over a century after Boveri's postulation, it has now been established that aneuploidy haunts most human cancer genomes.

More recently, pan-cancer genome analyses have shown that complex chromosomal rearrangements could lead to chromosomal abnormalities by a catastrophic process termed "*chromothripsis*", which in Greek translates to "*shattering of chromosomes*". Chromothripsis is driven by mitotic errors that lead to atypical nuclear structures, which in turn trigger "*localised, but extensive shattering*" of the mis-segregated chromosomes. In various tumour types, especially liposarcoma, osteosarcoma and glioblastoma, chromothripsis signatures are highly frequent.

Mitotic errors result in abnormal nuclear structures

Improper segregation during mitosis leads to atypical nuclear structures such as micronuclei and chromatin bridges. During segregation, it may so occur that the lagging chromosome fails to reach the daughter nucleus, and remains in the 'spindle midzone.' This is frequently caused by merotelic kinetochore attachment. When such cells exit mitosis, these mis-segregated chromosomes get enclosed within miniature

compartments called micronuclei.

Micronuclei are quite similar to the nucleus, but their nuclear envelope is fragile. Chromosomes trapped within the spindle midzone encounter microtubules that can interfere with the recruitment of nuclear-envelope components such as the Lamin B receptor, nuclear pore complexes and Lamin B. As a result, the micronuclear envelope becomes discontinuous and is susceptible to rupture.

When the nuclear membrane is damaged, typically components of the ESCRT-III pathway, including CHMP7 and CHMP4B are involved in repair. However, in micronuclei, there is excessive and aberrant accumulation of these proteins and repair is inefficient. Consequently, the membrane is breached, and the separation (membrane) between the chromosomes and cytoplasm is lost. This disrupts transcription, and the DNA becomes susceptible to cytoplasmic factors and improper replication conditions.

In such micronuclei, DNA replication factors like MCM helicase and Cdt1 cannot be retained, causing micronuclear DNA replication to become incomplete or asynchronous with respect to the nucleus. When such a cell with incompletely replicated micronuclear DNA proceeds into mitosis, chromosome condensation can occur prematurely. This results in replisome disassembly, replication fork collapse, and extensive DNA fragmentation. This process is called "DNA pulverisation", and it provides the mechanistic route towards chromothripsis. When the nuclear envelope is disrupted, the DNA is also exposed to cytosolic exonucleases,

such as TREX1, which degrade the DNA into single-stranded fragments.

Therefore, multiple forms of stress such as incomplete replication, replication fork collapse, nuclease mediated DNA degradation and DNA breakage converge at the micronucleus.

Chromatin bridges can also cause catastrophic rearrangements. They can be formed when chromosomes fail to segregate properly, often because of unresolved replication intermediates or chromosome fusions. These bridges are physically stretched between daughter nuclei, thereby experiencing mechanical tension. At the same time, TREX1 can localise to the chromatin bridges and cause further DNA degradation.

The shattered chromosomes are restitched by NHEJ

After the catastrophic shattering of the chromosomes, they now need to be re-stitched, albeit randomly.

The chromosome fragments should remain physically close to one another to be reassembled. Live cell imaging has shown that fragmented chromosomes (from micronuclei), remain spatially clustered and do not scatter randomly. The CIP2A- TOPBP1 complex has been implicated in tethering the fragments.

The broken ends of the DNA segments are joined by Non-homologous end joining (NHEJ), without requiring a homologous template, during interphase.

Disruption of the NHEJ pathway in *Arabidopsis* mutants lacking DNA Ligase 4 has been shown to block chromosomal re-joining and prevent structural rearrangements in the characteristic pattern of chromothripsis. NHEJ-mediated repair results in incorrect end-to-end joining that generates *deletions, inversions, translocations* and other complex rearrangements. *Microhomology-mediated end joining* (MMEJ) may also lead to this error-prone reconstruction, but only in a small proportion.

The cancerous consequence

The pathological consequence of chromothripsis lies, ultimately in what survives this catastrophe. The cancerous repercussions of chromothripsis are as follows-

1. *Tumour suppressor loss*: In clear cell renal cell carcinoma, chromothripsis could result in a significant loss of the short arm of chromosome 3, which contains four important tumour-suppressor genes (TSGs): VHL, SETD2, BAP1 and PBRM. Consequently, one copy of the different TSGs could be removed in one go. The second copy could be affected by additional mutations, or the individual could already be carrying a germline mutation for the specific TSG. (vis-à-vis Knudson's Two-hit Hypothesis). Chromothripsis can thus remove *multiple genomic brakes in a single event* rather than through a series of independent mutations or deletions. (Fig. 1A)
2. *Oncogenic fusions*: Oncogenic gene fusions may also be mediated by chromothripsis. Chromothripsis in chromosome 2, could lead to the EML4-ALK fusion in *lung adenocarcinoma*. The resulting fusion protein is constitutively active, inducing proliferative signalling. This could in turn result in therapeutic resistance, due to the formation of new genetic configurations. (Fig. 1B)
3. *Oncogene amplification by ecDNA*: Chromothripsis generates extrachromosomal DNA, or ecDNA. After fragmentation, DNA segments carrying oncogenes can circularize to become ecDNA. Subsequently, the amplification of the ecDNA could result in increased oncogene dosage, conferring a selective advantage to the tumor cells. In treatment-resistant melanoma, chromothripsis involving chromosomes containing genes such as BRAF and NRAS can generate fragments that circularise and amplify as ecDNAs. The resulting increase in oncogene copy number can contribute to resistance to MAPK-targeted therapy. (Fig. 1C)

The Epigenetic and Immunological Effect

Micronuclear chromatin acquires repressive histone modifications such as increased $H3K9me3$ and $H3K27me3$ and reduced $H3K27ac$, which may impact transcription on a potentially chromosome-wide scale. However, how these alterations arise is yet to be worked out.

The cGAS-STING pathway gets activated when the DNA is exposed to the cytosol due to the disruption of the micronuclear membrane. Chronic activation of this pathway shifts the tumour microenvironment to a more immune-suppressive state, allowing cancer cells to possibly escape immune surveillance.

Conclusion

Structural variations rearranging sequences were previously thought to accumulate gradually. This dogma was overturned in 2011 with the discovery of chromothripsis, in cancer genomes characterised by the shattering and random restitching of chromosomes. Chromothripsis is an example of punctuated genome evolution acquiring genetic alterations during a single rapid catastrophic event.

Although most chromothripsis events prove lethal or selectively neutral, rare instances could trigger a “perfect storm” of genetic alterations that could drive cancer progression.

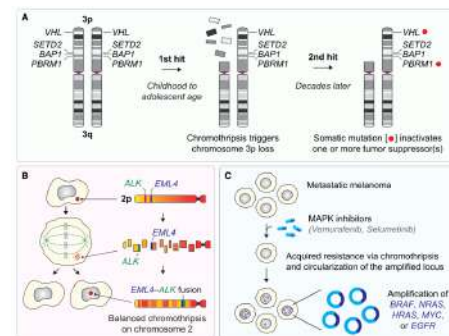


Figure : Cancerous consequences of Chromothripsis
Source: Mazzagatti, A., Engel, J. L., & Ly, P. (2024) Boveri and beyond: Chromothripsis and genomic instability from mitotic errors. *Molecular Cell*

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Has the Immune Address been found in the Directory of the Brain

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Keywords: Cancer biology, Genomic instability, Punctuated genome evolution

Introduction

For the mind does not inhabit the body like a pilot in a ship, but is so closely conjoined and intermingled with it that it forms a single compound.

—René Descartes, *Meditations on First Philosophy*

The brain centrally controls all operations throughout the human body, the main character of all human stories. It receives feedback from all the systems it controls, and a physical manifestation of this, a representation of sorts, develops. By extension, there is likely a representation of the immune system as well. Evidence is present to support the concept of

the brain regulating immune responses, such as:

1. The brain receives immunologic information from peripheral immune organs - like the blurred edges of a painting- the brain and immune system have a diffuse chemosensory connection via cytokines that activate the afferent neurons of the Vagus nerve. This initiates local (cardiovascular, GI tract) immune responses in the host, a major neural pathway identified to date.
2. fMRI experiments on patients who were inflammation-challenged with vaccines (causing peripheral inflammation) and placebo: the former induced altered reactivity in InsCtx (Insular cortex - hidden behind the frontal, parietal, and temporal lobes), causing fatigue. Activity was also seen in the hypothalamus and amygdala. Increased activity of vagus nerve afferents (from 20% to 85%) after a second re-exposure to pathogen antigens has been noted. This information is then relayed to the nucleus of Solitary tract (NTS), and a cascade of responses, known as sickness behaviours, occurs: fever, fatigue, social isolation, and reduced food and water intake.
3. In Wistar rats, association of a taste with an immunosuppressive drug (conditioning to an external cue) and further re-exposure exhibited a repressed immune response. Insular cortex-lesioned rats did not show the conditioned immunosuppression as well, suggesting its importance in this conditioning. Yet how the brain physically represents this state is unknown. InsCtx is the primary site of viscerosensory-cortical interoception. It integrates visceral information processing and bodily sensations like hunger, pain, etc. The study performed by Koren et al. used brain activity-dependent fluorescent cell labelling in TRAP transgenic mice to capture neuron groupings in the InsCtx under two different inflammatory conditions:

In the 1st condition, which brain regions showed

increased activity due to Dextran sulfate sodium (DSS) - induced colitis?

In the experimental set, the TRAP mice were injected with DSS that induced IBS (inflammatory bowel syndrome). After 48 hrs, Tamoxifen (TM) was injected, causing Cre-dependent recombination of the reporter gene to permanently fluorescently tag the neurons (TRAPing), especially in the InsCtx (Fig a and b), during their window of firing. To reduce noise from labelling other populations, Right posterior InsCtx neurons were locally targeted by stereotactically injecting (Fig c) a virus containing a reporter gene.

Both indicated, especially by the insular cortical neurons ($p < 0.0001$), that increased fluorescence referred to increased neuronal activity. However, such results were not enough to prove that these neurons encode immune info.

To answer the above question, the InsCtx neuron groupings, captured during the inflammation challenges, need to be reactivated at will to observe the chance of recapitulation of the inflammatory state.

Let's understand certain terms like DREADDS. This term looks a bit dreadful, but is rather understandable. This is a mutated GPCR (a receptor) that binds to CNO (ligand). This causes reactivation of the target neurons at will. This was co-expressed with a Cre-dependent reporter gene. In the control set, the mice were transfected with a virus containing the reporter gene without DREADD. Hence, CNO failed to bind, ensuring that any changes arose from the reactivation. In the experimental sets, the InsCtx neurons were captured, and after 4 weeks of recovery, CNO was injected (to check whether reactivation alone caused an inflammatory state?). The timing of the TM injection was varied: before DSS; during DSS; after DSS (TRAPing). After capturing and reactivating these 3 populations, the inflammatory state was assessed (to check whether any neuron group after reactivation leads to a colitis-like state? DREADDS were expressed Cre-independently, and twice the neurons were activated (seen in

mice with prior DSS history as well).

Reactivation alone reproduced much of the colitis state in the colon, even without any immune challenge. These effects were confined to the GI tract, such as intraepithelial lymphocytes (IELs), lamina propria leucocytes, T cells, TNF- α , IL-6, IL-17 and IL-10, consistent with a pro-inflammatory shift. No significant immune changes appeared in peripheral blood or mesenteric lymph nodes, suggesting the brain acts directly on gut immunity (local) rather than causing systemic inflammation. Only in InsCtx neurons captured during the original inflammation, i.e during DSS-TM injection, significant increase in colon inflammation was recorded. The non-specific InsCtx neuron reactivation did not detect any significant immune effect in the colon. Under the 2nd condition, zymosan-induced peritonitis (ZIP) model was used (another visceral area-peritoneum) to prove whether the initial findings suggested a generic scenario or an anatomical and immune challenge specificity was present.

Similarly, 2 neuron groups were captured: TM injected before ZIP and during ZIP. The same number of InsCtx neurons, specific for peritoneum, were captured, and like the DSS paradigm, recapitulation of peritonitis occurred. A local response was observed groups and cytokines. Also, 2 consecutive zymosan exposures were done with a 14-day interval, and 2 different neuron ensembles were captured. It showed that unique neuron groups encoded each immune experience.

Koren et al. studied whether InsCtx neurons

could physically talk to the inflamed organ during an immune experience. This was answered using polysynaptic retrograde tracing in TRAP mice, where circuits are traced and labelled backwards using a GFP-labelled PRV- a neurotropic herpes virus that replicates intracellularly from the target tissue via synapses back to the brain. After TRAPing and capturing neurons during colitis, PRV was injected into the colon. It was indeed TRAPed neuronal ensembles expressing GFP, suggesting direct message delivery to inflamed peripheral sites and mediated via autonomic nervous system.

Later, performing DREADD-induced inhibition of InsCtx activity revealed certain immune and clinical parameters being attenuated. The authors conclude that InsCtx neurons can acquire and retrieve specific immune-related information, functioning much like the memory traces classically described for fear learning in the hippocampus, since reactivating neurons captured during an inflammatory episode was enough to re-induce inflammation. Anatomically, these ensembles communicate with peripheral organs through both arms of the autonomic nervous system (the vagal DMV and the sympathetic RVLM). Key questions remain about how context and organ specificity are encoded and which peripheral cells receive the signals. They propose this system evolved to generate anticipatory immune responses to recurring stimuli, but it can also misfire, as in psychosomatic allergies and gut disorders; since InsCtx activity can drive peripheral inflammation, inhibiting the InsCtx may offer a therapeutic route for such conditions.

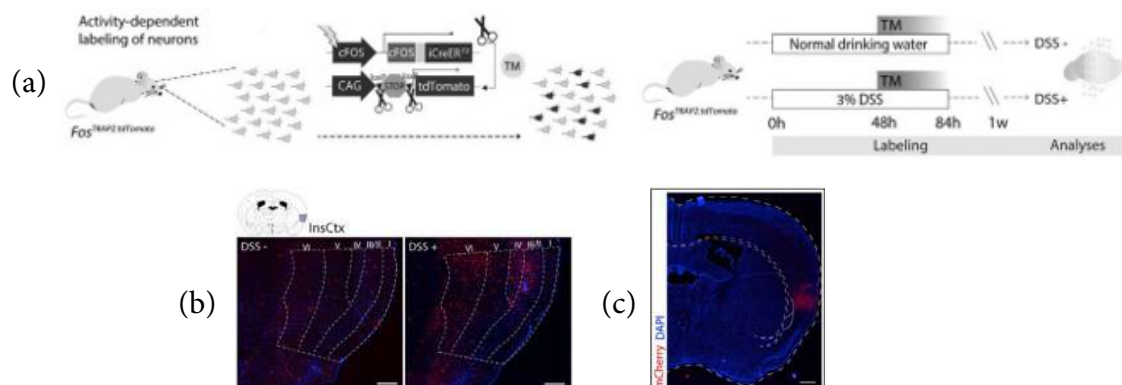


Figure: (a) TRAP-ing method, (b) and (c) Neuroimages of Insular Cortex, Source: Koren et al., 2021

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When “Non-Coding” RNA Makes Proteins: The Case of TERRA

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Keywords: TERRA, Telomeres, RAN translation, Dipeptide repeat proteins, Non-coding RNA

Introduction

Can RNA that scientists have studied for years as “non-coding” RNA produce proteins?

Mammalian telomeres contain a repeated sequence of (TTAGGG)_n, known to protect the chromosome ends. The transcription of the C-rich repeat sequence produces a G-rich long non-coding RNA known as Telomeric Repeat-containing RNA (TERRA), which is involved in telomere maintenance and regulation. This repeat sequence is G-rich and thus can form structures such as G-quadruplexes (G4s) and DNA hybrids, called R-loops. However, the discovery of repeat-associated non-AUG (RAN) translation questions the possibility of repetitive non-coding RNA lacking the AUG start codon being translated into proteins. Recent experiments have shown that TERRA can produce valine–arginine (VR)_n and glycine–leucine (GL)_n dipeptide repeat proteins. This discovery raises an intriguing question about what we truly mean by non-coding RNA and whether some of them have the ability to produce proteins.

Eukaryotes have linear chromosomes with repeated DNA sequences at their chromosome ends called telomeres. In humans, TTAGGG re-

peats are arranged tandemly at the chromosome ends and interact with the shelterin complex, which provides protection to the telomere ends. The primary function of the complex is to prevent the recognition of chromosome ends as double-strand breaks, inappropriate DNA repair, and end-to-end fusion. As the ends of linear DNA cannot be completely replicated due to the end-replication problem, telomeres progressively get shorter with successive rounds of cell divisions. Maintaining telomere length and structure is important, as excessive shortening can compromise chromosome-end protection and contribute to genomic instability.

TERRA: Structure and Regulation

TERRA, an important component of the regulatory system, is actually transcribed from the sub-telomeric regions at the chromosome ends. It is recognised as a long non-coding RNA containing telomeric repeats of the sequence UUAGGG. It is a guanine-rich molecule, can be heterogeneous in length, and can be associated with several telomere-associated proteins.

Expression of TERRA is not always constant; it changes depending on cell type and the conditions a cell is exposed to. A cell can experience

different cellular stresses at different times, which include DNA damage, heat shock, oxidative stress, etc. Studies show that etoposide treatment and serum starvation can increase TERRA levels through p53-responsive promoters. During heat shock, TERRA transcription is induced by HSF1, and NRF1 reportedly regulates TERRA during oxidative stress. Researchers studied telomeric DNA damage, DNA damage response, and replication defects by experimentally increasing or decreasing TERRA levels using approaches such as antisense oligonucleotides, promoter-targeting TALEs, and depletion of TERRA-regulating proteins. The results showed that too little or too much TERRA compromises DNA stability; thus, it needs to be tightly regulated.

TERRA can form R-loops at the telomere when it anneals to the complementary DNA strand, giving rise to a DNA: RNA hybrid, leaving the other strand displaced. These R-loops contribute to telomere maintenance and recombination, particularly in cells using the ALT pathway, but excessive accumulation of R-loops has adverse effects, as it can cause replication stress and telomere instability.

The telomeric repeats in TERRA can fold into RNA-quadruplex (rG4) structures, stabilised by cations such as K⁺ and Na⁺. These structures protect the RNA from RNase degradation and influence its stability and function. The shelterin complex has telomere-associated proteins such as TRF1 and TRF2, with which the TERRA rG4 interacts, aiding telomere regulation. TRF2 simultaneously binds the telomeric DNA and TERRA-rG4. TERRA and TRF2 also bind to the origin recognition complex (ORC), forming a ternary complex that promotes heterochromatin formation at telomeres and may support DNA replication. Disrupting the TRF2-TERRA rG4 interaction can lead to reduced TERRA transcription, telomere shortening, DNA damage, and telomere fragility.

Beyond transcriptional regulation, the activity of m6A modification provides another level of regulation by controlling TERRA stability. The experimental results showed that removing

METTL3 or targeted withdrawal of m6A increased degradation of TERRA; in another case, YTHDC1 depletion reduced its half-life, and tethering YTHDC1 to TERRA prevented this decrease.

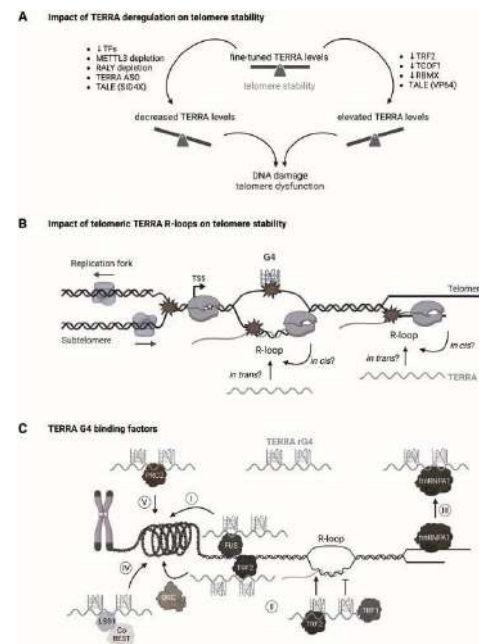


Figure: Regulation and Roles of TERRA at telomeres (Source: <https://doi.org/10.1016/j.semcd.2023.11.001>)

TERRA: from RNA to Protein

As we know, in mammalian TERRA, the repeated run of three Gs in the telomeric sequence can fold into a quadruplex structure. These structures can provide potential loading sites for ribosomes during the repeat-associated non-AUG (RAN) model of translation. RAN translation is a non-canonical form of translation that does not require an AUG initiator codon to initiate translation, bypassing the conventional method of translation. According to a study, it was proposed that stable TERRA secondary structures, such as hairpins or G-quadruplexes, may facilitate structural loading sites for ribosomes. Because there is no canonical AUG codon or start signal, the translation machinery cannot lock into a specific reading frame. Ribosome translation thus, can initiate at any non-canonical nucleotide within the repeat sequence; this allows different reading frames to produce distinct dipeptide repeats. Across the six prospective reading frames, 2 reading frames encounter an immediate stop codon, while the remaining reading frames yield

repeating glycine-leucine (GL), a hydrophobic repeat, and a highly charged valine-arginine (VR) dipeptide. TERRA is primarily sequestered in the nucleus and is bound to telomeres, but under certain cellular conditions, such as starvation, diauxic shift, and telomeric dysfunction, it can trigger its export into the cytoplasm, where the translation machinery is present. TERRA also accumulates in high amounts in the cytoplasm when telomere protection is impaired, following knockdown of the shelterin protein TRF2. The TERRA molecule can exceed ~9000 nucleotides, but some portion of it is 3' polyadenylated, giving the transcripts a longer half-life than non-polyadenylated TERRA. The presence of TERRA in the cytoplasm brings it into proximity with ribosomes, facilitating RAN translation and the subsequent formation of dipeptide repeats.

Experimental evidence for TERRA-Derived Dipeptide Repeats

Filament and amyloid assembly: TEM and cryo-Em revealed that synthetic (GL)₉ and (VR)₁₀ readily self-assemble into uniform 7.5 and 7.9 nm filaments and dense amyloid-like networks.

Correlation with TERRA levels: high-TERRA cell lines (U2OS and ICF syndrome fibroblasts) displayed a threefold higher frequency of cells with ≥ 5 nuclear VR foci compared to primary fibroblasts.

Antibody specificity: Polyclonal antibodies purified via affinity chromatography were raised against (VR)₄, specifically detecting VR repeats without cross-reacting with (GL)₉ (raising an antibody for (GL)_n was not successful) on dot blots, and they yielded SDS-insoluble aggregates at the stacking gel boundary on Western blots. Confocal microscopy of U2OS cells expressing 3X Flag-VR60 confirmed high target colocalization (98%).

These experiments do not give us direct evidence from peptide sequencing and mass spectrometry to confirm that the detected cellular levels are true VR and GL chains directly synthesised from TERRA transcripts. This is a limitation, and it is due to the insolubility of

these peptides and their resistance to trypsin digestion.

Conclusion

Evidence suggests TERRA can undergo RAN translation to produce the dipeptides: VR and GL repeats, suggesting its role may extend beyond previously believed telomere regulation. Such findings connect telomere biology with protein production, ageing, and potentially important cellular processes. Recent discoveries show that VR can interact with ribosomes and influence translation, suggesting these proteins might have varied regulatory roles. TERRA challenges the traditional boundary between coding and non-coding RNA. It also represents a previously overlooked source of biologically active proteins in cells.

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From Microbial Interactions to Ecosystem Engineering: Designing Synthetic Communities For Bioremediation Of BPA

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Keywords: Microbial communities, Epistasis, Microbial consortia, Bisphenol A (BPA), Bioremediation

Introduction

The metabolism of microbial communities have a significant role in sustaining the health of both living microorganisms and environment. Rather than functioning as isolated individuals, the microorganisms interact with each other and these interactions can strongly influence what an entire microbial community is capable of doing. This raises an exciting possibility: can we deliberately design microbial communities with targeted functions, such as the ability to remove environmental pollutants or simply bioremediation?

Designing such communities, however, is not at all straightforward. Microbial species can cooperate, compete, or influence one another in unexpected ways, while environmental conditions can further alter these interactions. To address this problem, inspired from the concept of fitness landscapes, researchers have developed community–function landscapes—a framework that helps us predict how the presence or absence of particular microbial species affects the overall function of a community. These landscapes not only consider the individual contributions of different species but the effects of their interactions in a community as well, known as Epistasis.

The researchers have applied this approach to an important environmental problem: the removal of bisphenol A (BPA), a toxic industrial contaminant. They constructed synthetic microbial communities containing 10 BPA-degrading bacterial species and examined how these performed under increasing concentrations

of BPA where increasing concentration meant higher toxicity. Interestingly, stronger epistatic interactions were observed at higher BPA toxicity, suggesting that interactions between community members become very important for efficient degradation.

Building a Microbial Toolbox

The first need of the researchers was a collection of bacteria from which they could build communities. They sampled soils from five sites with potential BPA contamination and enriched the samples under conditions capable of degrading BPA or capable of surviving alongside BPA degraders. From these, they identified and isolated 16 bacterial strains, out of which 10 were capable of degrading BPA from 30 ppm monoculture while the remaining six showed no degradation activity, but were retained because they had been isolated together with the degraders. Aerobic respiration was confirmed by measuring CO₂ production from individual isolate. Pure cultures could not be isolated; there was contamination in four out of sixteen samples. Then they grew each of the individual isolate in 60ppm BPA, and it was seen that they were capable of degrading BPA individually. However at 150 ppm, neither of the isolates could degrade BPA successfully. This suggested that at higher toxicity, degradation might require cooperation or at least microbial interactions between members of a microbial community. Thus, here came the need of microbial communities. Using their collection of 16 isolates the researchers assembled 70 different synthetic microbial communities of

richness levels 2 to 16. Each community was exposed to five starting concentrations of BPA: 60 ppm, 80 ppm, 100 ppm, 125 ppm, 150 ppm, where an increased concentration indicated increased toxic challenge. The BPA degradation process was followed for 72 hours, allowing the researchers to compare how efficiently the microbial communities removed the contaminant. To quantify degradation, they calculated the Area Under the BPA concentration vs time curve (AUC). Lower AUC corresponds to more rapid and extensive BPA removal, while higher value shows slower degradation. However it was not the number of microbes that mattered, but the microbes present and how they interacted that was important. It was observed that the community containing all the 16 strains did not exhibit faster degradation at any of the five BPA concentrations.

From Microbial Community To Mathematical Landscape

The researchers used an approach called community-function landscape, similar to fitness landscape used in evolutionary biology. Just like a fitness landscape describes how genetic combinations influence the fitness of an organism, similarly the community landscape describes how different combinations of microbial species influence the function of a community. Here, every possible community is imagined as a point on a giant landscape. Some points represent communities that degrade BPA poorly while others represent points that degrade BPA rapidly. The objective here was to find the communities with the desired function without having to test all the combinations experimentally. However the complication was the fact that the whole is not always sum of its parts in biological systems. Suppose bacterium A degrades BPA moderately well and so does bacterium B. One might expect A + B to produce approximately the sum of their individual effects, but that is not the case. Perhaps A produces a metabolite that B needs or maybe B removes a toxic intermediate produced by A. Alternatively, A and B might also compete for the same resource and inhibit each other.

When the combined effects of organisms differ from their expected individual effects, the researchers describe this as epistasis. Since here epistasis dominates, the best community depends on the combination of microbes and their interactions rather than individual performance.

Toxicity Drives Epistasis

The most striking findings emerged when the researchers studied the microbial landscapes at different BPA concentrations. At lower BPA concentrations, individual strain effects were relatively important. However, as BPA concentrations and toxicity increased, these additive effects became less important, while the distribution of epistatic interactions became significant. The researchers quantified this change using the F_1 statistic, which measures the relative contribution of additive effects compared with epistatic effects. A lower F_1 indicates a greater contribution from epistasis.

The F_1 values showed a general decline as BPA concentration increased, particularly at 125 ppm, supporting the conclusion that toxicity indeed drives epistasis. Besides this, it provides a strong ecological insight: “Environmental stress changes not only how organisms perform, but also how strongly they interact.”

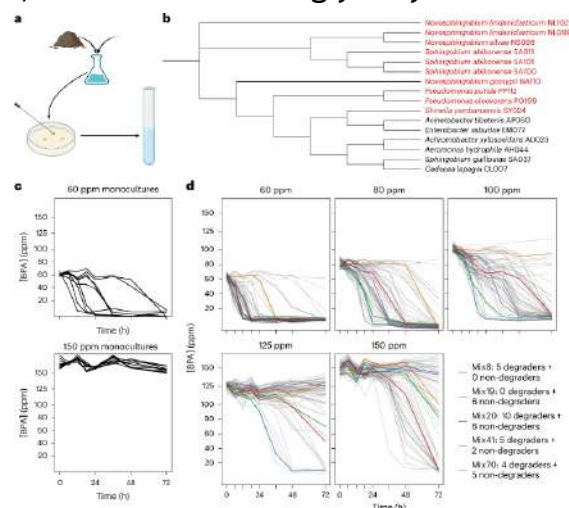


Figure: Experimental workflow and BPA degradation behaviour of the bacterial isolates and synthetic communities. Five communities are highlighted: Mix8 (blue), Mix19 (yellow), Mix20 (green), Mix41 (red) and Mix70 (purple). Panel a created with BioRender.com. Adapted from Yousef et al. (2026).

Can Mathematics Design a Microbial Community?

The community–function models were subsequently used to computationally identify the bacterial combinations that had not been tested experimentally previously. These predicted consortia were assembled in the laboratory and their performance was measured. For the 10 newly assembled communities tested at 100 ppm BPA, the measured and predicted performances showed a significant positive correlation. This represented an important shift in strategy. Rather than isolating, testing and selecting the best bacterium, they now approached it in the way to measure the community interactions and build a mathematical landscape for prediction followed by testing.

From Laboratory to Contaminated Soil

The selected microbial community that performs well in a flask was then tested on field. They introduced ten designed synthetic communities into slurries generated from two BPA contaminated soil types, using initial BPA concentrations of 100 and 125 ppm. The results showed that adding synthetic communities increased BPA removal and in some cases the indigenous microbial community showed limited BPA removal in the absence of the introduced consortium. Importantly, the degradation performance varied as per the synthetic consortium introduced, demonstrating that the identity of the introduced community was important despite the presence of a complex native microbiome. Moreover, the communities showing higher degradation under laboratory conditions generally showed better performance in soil, indicating that the landscapes learned under controlled conditions contained useful information about their behaviour in a more realistic environment. 70 such communities out of nearly 65,000 were tested.

Despite such promising results, laboratory designed consortia represent only a simplified version of natural microbial ecosystems. However, in a natural soil environment, the introduced microorganisms need to interact with a

highly diverse resident microbiome and compete for nutrients and available ecological niches. These variations in nutrient availability and pH shall further modify microbial interactions and activity. Thus the performance observed in synthetic communities under controlled laboratory conditions, may not be always reproducible in every contaminated environment.

The results can be considered consistent with the idea of niche specialization, in which different microorganisms were seen occupying complementary ecological roles. However, extending this approach to complex polluted environments does present us with several challenges. Real contamination sites may contain different pollutants together, and these compounds may affect microbial metabolism and their degradation pathways. Thus, to conclude, successful bioremediation may require both experimental characterization of microbial communities as well as computational approaches accounting for environmental complexities.

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The Trojan Horse: A Link Between Iliad and Biochemistry!

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Semester 5

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Keywords: Siderophores, *P. aeruginosa*, trypanosomes, *C. neoformans*, blood-brain barrier, nanoparticles

Introduction

"We'll play a subtle trick that shall destroy them once and for all. A curse upon Troy but in disguise of a gift!"...that was thousands of years ago, when the foulest war-plan was executed by the Greeks against the Trojans. The Trojan Horse in Homer's 'Iliad' still stands as the symbol of betrayal and false-show to this day. This age-old trick of 'fooling' the receiver is now greatly exploited in Biochemistry to fight against drug-resistant bacteria and also in targeted cancer and cell therapy.

The biochemical 'Trojan horse' refers to a therapeutic drug or toxin that is presented into the host as a harmless or essential molecule (like a nutrient or Fe^{3+} - carrying siderophore) such that it tricks the host's biological and immunity barriers to allow the incorporation of the potent chemical against the host. The following key steps are involved:- (i) Disguise (the drug is chemically bound or conjugated to a carrier that is favoured by the host to absorb), (ii) Smuggling in (the host's own transport system pulls the complex inside bypassing the natural defense and drug-resistance mechanisms), (iii) Release (after the successful entry, the underlying drug is released or activated to work against the host).

The primary medical applications of the 'Trojan Horse' include overcoming drug-resistance by bacteria, brain drug delivery across the blood-brain barrier and uses in cancer and cell therapy.

Defeating Bacterial Drug-Resistance by Antibiotic-Siderophore Conjugates

Pseudomonas aeruginosa, a key pathogen

in human opportunistic infections is a highly evolved gram-negative bacteria that has attained multi-drug resistance over the years. Therefore, it had become necessary to devise new ways to beat them. Aerobic bacteria (such as *P. aeruginosa*) use extracellular Fe^{3+} -chelating ligands (called siderophores) to extract environmental iron for their metabolic use. Siderophores maybe self-generated or obtained from other microbes. *P. aeruginosa* synthesizes its own high-affinity siderophores, namely Pyoverdine (PVD) and Pyochelin (PCH). The antibiotic-siderophore coupling is best done by mixed-type siderophores, which have multiple functional groups integrated in a single molecule. Both PVD and PCH are such kinds of siderophores and therefore, can easily be used as Trojan horses to transfer drug inside the host, who will naturally allow them entry for the obtaining the bound iron. By understanding and exploiting the chemistry of such carrier molecules and chelating ligands, it has been possible to couple various antibacterial drugs with siderophores to develop lethal yet seemingly harmless complexes. We now have Penicillin, Cephalosporin, Quinolone, etc. antibiotics conjugated with PVD and PCH siderophorines that cause significant harm to pathogens like *P. aeruginosa* without even giving prior signals to them!

Curing African Sleeping Sickness with a Biochemical 'Trojan Horse'

African sleeping sickness (or Trypanosomiasis) is caused by protists called trypanosomes, which are skilled parasites and have developed a novel mechanism for evading the human

host system. The cell-coats of infecting trypanosomes have a single protein, recognized by the host immune system. However, by means of a genetic recombination, some cells in the population may develop a new protein coat that is unknown to the host. This repetitive process of changing coats results in a chronic cyclic infection, where a second infection takes over immediately after the previous one is overcome, causing recurring fevers and ultimately killing the host with a weakened immune system. Certain enzyme inactivators can be used to block important metabolic pathways and thereby cause the infectious agent to perish. Polyamine biosynthesis is an essential process in rapidly dividing trypanosome cells that involves the enzyme, ornithine decarboxylase in its first step. An inhibitor of this enzyme, that binds permanently, can therefore adversely affect the parasite. Difluoromethylornithine (DFMO) is such an inhibitor. DFMO interacts with pyridoxal phosphate (PLP), that is the substrate and forms a substrate-inhibitor adduct. The enzyme then forms a stable covalent complex with this adduct and therefore, undergoes an irreversible change.

Evasion of the Blood-Brain Barrier (BBB) using the 'Trojan Horse' Concept

The blood-brain barrier is a highly selective, semi-permeable border of cell-lining around the CNS. Consisting of endothelial cells, astrocytes and strong protein seals; it prevents harmful toxins, pathogens and large molecules in blood from entering the brain. Proteins like neurotrophins, enzymes and monoclonal antibodies cannot be directly incorporated as drugs into the brain as these large molecules are restricted by the brain capillary wall. A breakthrough in the field of brain drug delivery was achieved with the engineering of recombinant fusion proteins ('Trojan horses'), that can bind to specific receptors on the BBB and facilitate the receptor-mediated infusion of the therapeutic drug. Certain yeast like *Cryptococcus neoformans* (a basidiomycete) also use 'Trojan Horse' mechanism to evade the BBB and cause fungal infection. This

theory that an eukaryotic pathogen can exploit host phagocytes as Trojan horses to evade the BBB as a 'passenger' was recently established experimentally. A mixture of fungi and macrophages was incubated for 24 hours in presence of a BBB model. Techniques like flow-cytometry, fluorescent and live-cell microscopy besides multiple BBB models were simultaneously used to demonstrate the Trojan Horse transit in-vitro. Results showed the presence of fungi-loaded macrophages traversing the BBB, thereby suggesting the use of host macrophage by fungal agent as a carrier. Studies further illustrated that in presence of serum (that contains carrier particles), *C.neoformans* better traversed the BBB in comparison to its free state, whereas for *Saccharomyces cerevisiae*, the presence or absence of serum had no influence. This shows that efficient BBB evasion depends greatly on the pathogen's capacity to exploit carrier molecules and therefore, not all pathogens can use the Trojan Horse transit to cross barriers.

Trojan Horse and Cancer Therapy

A 'Trojan Horse' approach in cell therapy involves specialized biological or synthetic vehicles (such as nanoparticles) to directly sneak in cancer-killing drugs while hiding from the body's immune system. Human Papilloma Virus (HPV) is one of the most prominent viral pathogens involved in cancers (especially cervical cancers). Despite having HPV vaccines, the high-cost and inadequate healthcare cause availability issues in economically-lagging nations where the record of such sexually-transmitted infections is disproportionately high. Gene-targeted HPV therapy provides a promising future in the field of cancer therapy. It utilizes CRISPR/Cas and siRNA systems that specifically target and disrupt HPV oncogenes. Nanoparticles (NPs) are small carrier particles (1-100 nm in size) that can potentially traverse through minute gaps in membranes and therefore, used as 'Trojan horses' in gene-targeted HPV therapy. They encapsulate and carry therapeutic nucleic acids (like CRISPR and siRNA), that are specifically functionalized

to target HPV-infected cells, thereby optimizing biodistribution and reducing systemic toxicity. By using receptor-mediated transcytosis, NPs can effectively traverse physiological barriers, ensuring that therapeutic agents accurately reach their intended targets.

Conclusion

With further developments to come, we expect that our biochemical 'Trojan horses' will only get stronger and will soon take over the world of medicine and also extend its conquests in the areas of plant biology and pest control.

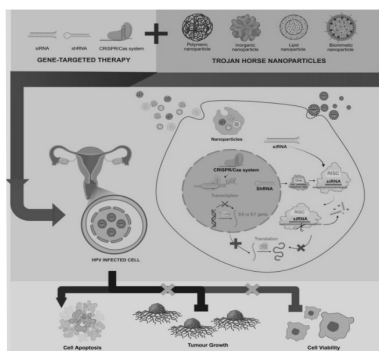


Figure 1: Action of gene targeted nanoparticles

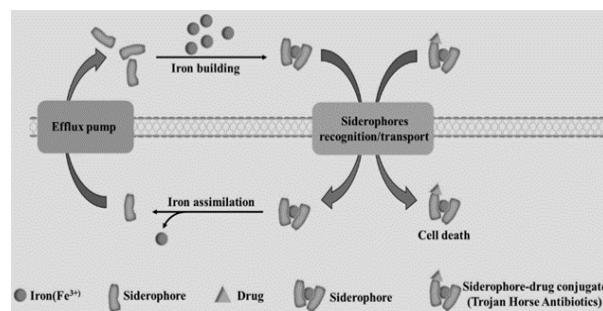


Figure 2: Mechanism of action of Siderophore-drug conjugate

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The Mystery of the Thanato-Code: Decoding Biological Dark Matter to rewrite life

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Keywords: Thanatobiome, Necro-metabolism, Auxiliary Metabolic Genes, Chemical semiotics, Synthetic Microbial Communities

Introduction

The word 'life' paints a picture of a profound network of megafauna and flora painted by a stroke of sunlight. A shift from this luminous surface to the sediments of soil and oceans reveal a community that remains unnamed and uncultured. Scientists call this vast, uncharted territory, biological dark matter—an informal yet evocative term for the microbial and viral DNA and RNA that eludes traditional classification.

Like the cosmological dark matter that solely shapes galaxies, biological dark matter shapes the living world through metabolic force, gene transfer and chemical signalling.

This article sets out to reframe thanatobiome as the planet's central engine of renewal, exploring how viral genes edit metabolism after death, illuminating the coordinating chemical signals and enabling synthetic ecosystems for ecological restoration.

The Universal Translation

The microbes constituting the Biological Dark Matter remain invisible to traditional microbiology and are only detectable through techniques like metagenomics, single-cell genomics and amplicon sequencing. These organisms, such as the enigmatic TM7 lineage and Patescibacteria, possess minimal genomes and often reside as epibionts, relying on complex interactions with members of other communities.

With advancements in artificial intelligence, it became possible to get a glimpse into these proteins: their translation process, clustering of their sequences, their folds and inferring their functions from genetic and ecological contexts. Some uncultured taxa exhibit metabolic streamlining, which means having shed genes for essential nutrients provided by their neighbours, thus creating an intricate web of cross-feeding and co-dependency.

Biological Dark Matter is the planet's genomic 'dark energy', which provides for the metabolic flexibility required for ecosystem resilience. With the help of training models based upon massive metagenomic datasets, researchers can predict the metabolic functions of these microbes, revealing hidden pathways for carbon fixation, nitrogen transformation and pollutant degradation.

The Necro-Metabolism: Death as the Planet's Primary Engine

Often, it is assumed that a piece of life comes to an end with its decay. The cessation of an organism's life signals the activation of a highly coordinated system of metabolic succession known as necro-metabolism—which unlocks the door for specialized microbial communities to dismantle complex biomolecules into their elemental components. The thanatomicrobiome—the community of microbes that colonize internal organs after death, rises first from the body's own reservoirs. With the death of the host, the microbes associated do not die off. Rather they persist in the soil for months and cooperate with native

soil communities to accelerate decomposition and enhance nitrogen cycling. Thus, the thanatomicrobiome acts as a bridge between generations by returning back the nutrients a body once drew from the Earth, ensuring that the elements are never lost but are continuously reinvested into the ecosystem.

Thus, the term “necrobiome” encompasses both internal thanatomicrobiomes and external epinecrotic communities. It is worthy to appreciate the collective efforts of the insects and the decomposers for playing the role of the process' metabolic engine. As a result, the web of life is woven from the threads of death.

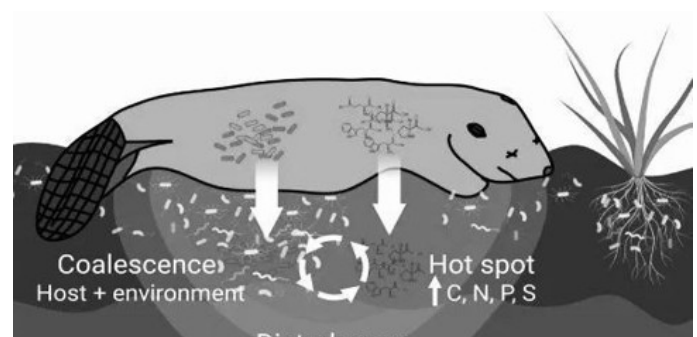


Figure 1: Carcass decomposition results in a flush of nutrient dense decomposition products and microbes to the environment.

Source: DeBruyn, J. M., Keenan, S. W., & Taylor, L. S. (2024). From carrion to soil: microbial recycling of animal carcasses. *Trends in Microbiology*, 33(2), 194–207. <https://doi.org/10.1016/j.tim.2024.09.003>

The Viral Veil

Viruses are known to be one of the most abundant biological entities on Earth. Yet, it is surprising to know that 40-90% of their genetic material remains to be uncharacterized—known as the Viral Dark Matter, the most mysterious component of the Thanato-Code.

These viral entities are not just merely pathogenic but have a huge role as genetic carriers. While infecting a host, they can reprogram the host's genetic code to enhance carbon fixation, stress tolerance and nutrient uptake through specialized components known as 'Auxiliary Metabolic Genes' (AMGs). After the death of the host, these viral particles are

released into the surroundings, thus forming a genetic library which is accessible to newer microbes. Thus, in the context of a necrobiome, viruses act as the regulators of microbial succession through selective predation and horizontal gene transfer. Therefore, this viral veil ensures that the Thanato-Code remains dynamic by allowing rapid adaptation and efficient flow of genetic information across the boundaries of species and kingdoms.

Semiotics- Chemical Syntax of the Grave

This enormously coordinated system does not happen in isolation but is rather driven by 'Chemical Semiotics', which is a highly structured process of molecular signals and gradients. These complex microbial activities are organised through quorum sensing and thus detects population density and triggers synchronized genetic programs.

These communication networks involve complex feedback loops where the products of one organism's metabolism act as the signalling molecules for another. For example, anaerobic species sense the depletion of oxygen in a decaying body and activate the pathways for fermentation and putrefaction. A cascade of volatile organic compounds and secondary metabolites is known to trigger these transitions. Hence, microbial necromass is indeed the chemical engine which shapes the survival of subsequent communities.

Engineering Rebirth through the Thanato-Code

After decoding the metabolic engine of death, the next goal becomes to redesign it. This is achieved by the emerging field of synthetic ecology which aims to design 'Synthetic Microbial Communities' (SynComs) that can mimic the regenerative functions of the natural dark cycle. 'Synthetic Gaia'- a suite of biological tools which is engineered for the bioeconomy and for the restoration of degraded environments, in turn harnesses the metabolic pathways discovered in the uncultured taxa for bioremediation. Furthermore, the study of thanatomicrobiome also provides valuable insights for 'terraformation' strategies, where

synthetic ecosystems are designed to make barren or extreme environments habitable. Thus, by utilising the planet's regenerative capacity, the Thanato- code shows a kind of existence where the vitality of the new is fuelled by the legacy of the old.

Conclusion

The exploration of biological dark matter through the lens of the Thanato-Code paints a coherent and transformative picture: what was once long dismissed as a source of genetic noise or residual decay is now revealed as a highly ordered system, the planet's primary metabolic engine, a library of genetic upgrades released from the grave and a chemical symphony that precisely orchestrates the return of nutrients from dead biomass to living systems. The study on thanatomicrobiome demonstrates decomposition as a highly ordered metabolic engine which connects generations. Viral auxiliary genes suggest the persistence of genetic editing beyond the host, while chemical signalling demonstrates the coordinated 'symphony' which governs the nutrient transfer.

Understanding the Thanato-Code provides an insight into the machinery that turns death into the raw material for a new life. In terms of practical implications, it has the ability to design synthetic ecosystems that can heal degraded soils, revive dying wildlands and restore the disrupted nutrient cycles.

After deciphering the dark matter of biology, mankind steps out of the role of passive observer and begins to participate in the ancient art of renewal itself, making an effort to heal the planet. Beyond this, the same silent code of death might one day provide the instincts of new forms of life in unknown pieces of land.

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Bioelectric Echoes: the Hidden Pulse of Forests

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Keywords: Action potential, Variation potential, Sensor network, Electro-crypsis

Introduction

When we delve deep into the world of nature, it is quite interesting to note that life is fundamentally galvanic. While electrical systems rely on the principle of electrons moving through copper wires, biological systems rely on ions (like sodium, potassium, and calcium) moving through cellular membranes. The currents and interactions observed among living organisms weave together the invisible canvas of nature which forms the “Bioelectric Landscape”.

The topic of Bioelectric Landscape has piqued the interest of scientists from ancient times:

Luigi Galvani (1780s): “Animal electricity,” was discovered by him which proved that electrical currents animate living tissue.

Jagadish Chandra Bose (1900s): Pioneered the study of plant responsiveness, proving that flora exhibit electrical responses to external stimuli (like light, touch, and harsh chemicals) remarkably similar to animal tissues.

Michael Levin (Modern Era): Contemporary research in developmental bioelectricity shows that voltage gradients act as a “morphogenetic blueprint,” instructing cells how to grow, regenerate, and map out biological structures.

Nature serves as an interactive interface. In comparison to traditional interfaces which are anthropocentric (human-centered), designed to translate human intent into machine action, a bioelectric interface is bio-centric (life-centered); it translates the environment’s internal

state into human comprehension.

Mapping the invisible threads of life changes the timeline of conservation. It allows us to listen to the pre-symptomatic whispers of the environment. It moves us away from an era of exploiting nature and toward an era of technological symbiosis.

The Silent Symphony Written in Millivolts

Plants have a unique way of communicating with Bio-electric signals which are measured in millivolts. The membranes of each living cell maintain a voltage difference ranging from -40 to -90 mV, which is generated by the uneven distribution of ions across the plasma membrane. These potentials are not mere by-products of metabolism, rather they help in controlling growth and regulating behaviour. Changes in the environment caused by touch, injury, rapid changes in light conditions or attacks by pathogens can coordinate and cause the rapid opening of both voltage and ligand controlled ion channels. Ions like calcium, potassium and chloride produce two kinds of signals- a rapid action potential and a lower variation potential, which can propagate through the phloem and adjacent tissues with velocities ranging from millimeters to several centimeters per second.

These electrical signals travel faster than many diffusible chemical messengers, forging out the way for stomatal adjustment, the activation of defence- genes and for resource reallocation. In the rhizosphere, root exudates and microbial communities generate local electric fields that influence ion availability and guide mycorrhizal hyphal exploration. Additionally, nerves and muscles in animals amplify signals by the means of spikes and pulses by using the same voltage as the source of information. These millivolt-scale patterns are the invisible threads which bind organisms to their environment, thus translating physical strain, chemical gradients and ecological interactions into a shared electrical code.

Forest as a Living Sensor Network

A forest is not just a collection of trees but is

a biologically powered sensor network. An individual leaf carries surface and extracellular potentials which are sensitive to humidity, atmospheric ions, electromagnetic fluctuations and the electrostatic signatures of the insects approaching them. When part of a leaf gets damaged, the local depolarization emits volatile organic compounds and electric waves that propagate through the vascular system and by the means of root grafts or mycorrhizal networks and can reach surrounding trees. The hovering of a bee near a flower is responsible for inducing a measurable shift in the plant's stem potential, before the contact occurs. In addition, the electrical signal emitted by a single flower can spread to neighbouring flowers through the soil and be detected by them, thus creating a network of electrically interconnected root systems.

Across a large area, mechanical stress on trunks and branches generates piezoelectric-like potentials in cell walls, while wound sites produce steady direct-current fields that induce cell migration and tissue repair. In addition to this, fungi and bacteria in the rhizosphere generate ion fluxes and membrane voltages. Utilizing these signals, forests can monitor weather, track pollinator traffic, allocate resources after damage and to report microclimatic shifts, pollution pulses and biotic threats. As a result, this phenomenon is based upon measurable biophysics consisting of ion fluxes, membrane depolarization and extracellular field changes.

When Flowers, Predators and Prey share an Electric secret

1. Flowers and Bees:

For a long time, scientists tried to solve the mystery of how bumblebees could accurately choose flowers that were bursting with nectar while avoiding those that had just been depleted. The secret is an electrostatic feedback loop. When a positively charged bee (bee acquires a positive charge after flying through the atmosphere) approaches a negatively charged flower (flowers passively conduct the natural negative charge of the Earth), a micro-electrostatic pull occurs. The bee's hairs erect, letting

the bee “feel” the flower’s altered electric field which acts as a real-time status update and informs the bee about the amount of flower’s nectar.

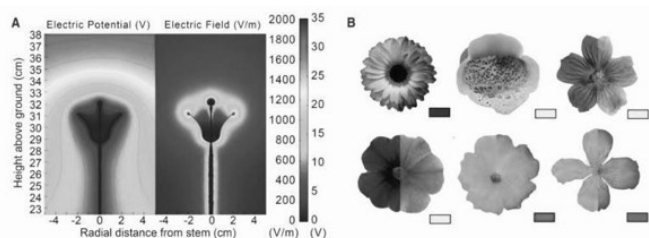


Figure 1: A) Simulation of the electric potential (left) and magnitude of the electric field (right) around a flower in the presence of the average atmospheric electrical gradient of 100 V/m. B) Daniel Robert and his colleagues sprayed different flowers with electrostatic colored powder, showing the parts of the flower where the electric field is stronger. Source: Clarke, D., Whitney, H., Sutton, G., & Robert, D. (2013). Detection and learning of floral electric fields by Bumblebees. *Science*, 340(6128), 66–69. <https://doi.org/10.1126/science.1230883>

2. Predators and Prey:

Predators have evolved highly specialized organs as follows:

Sharks possess a network of jelly-filled pores on their snouts called the Ampullae of Lorenzini. These are extremely-sensitive voltmeters capable of detecting fields as weak as 5 nanovolts per centimeter and help in locating their prey even if they are buried completely under the ocean sand.

While sharks passively listen to prey currents, animals like the electric eel use active electro-location by emitting low-voltage pulses.

3. Aerial Predators:

Spiders are master predators that utilize the atmospheric potential of the bioelectric landscape through a process called ballooning. Spiders use their specialized sensory hairs (trichobothria) to sense the electrical currents in the air.

A predatory spider can travel hundreds of miles through the sky purely on static electricity by releasing silk threads from a high point.

A unique phenomenon observed in certain species of cuttlefish:

Freezing behaviour facilitates bioelectric crypsis in cuttlefish faced with predation risk.

Over the years prey species have evolved ways to actively camouflage their electricity, via a process known as electro-crypsis.

A novel cryptic mechanism in *S. officinalis* species of cuttlefish has been studied in which bioelectric cues are reduced via a behavioral freeze response to a predator stimulus. This resulted in a possible decrease in shark predation risk by reducing detectability. The cuttlefish presses its body flat against the seabed and physically constricts its breathing gills and body cavities which reduce the cuttlefish’s bioelectric voltage output by up to 80%. It effectively becomes an electrical ghost, blending perfectly into the background voltage of the ocean floor.

Conclusion

It could thus be understood that the language in millivolts is the loudest. From the ion-swept membranes of single cells to the entire electrically interconnected meshworks of the forests, bioelectric landscapes showcase an ancient and continuous conversation where plants sense, signal and coordinate one another using living voltmeters and are more effective than artificial electronic sensors. Conversely, crop management and breeding programs can select for more robust electrical signalling processes, while urban green infrastructure can be designed to minimize electromagnetic interference while preserving beneficial bioelectric feedback and early-warning systems may one day detect ecosystem stress through voltage anomalies rather than waiting for irreversible morphological decline. Hence, it can be confirmed that life has always spoken in a silent language where it intricates all its components into an electrical web.

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Bio-Inspired Engineering and Biomimicry for Aquatic Environmental Solutions

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Semester 3

Postgraduate & Research Department of Biotechnology

Keywords: Biomimicry, Environmental Innovation, Aquatic Conservation

Introduction

The process of translating biological traits into physical prototypes to see how organisms function into environmental technology rather than simply copying their appearance is known as biomimicry or bio-inspired design. The shift is from passively observing nature toward building systems that can sense, predict and intervene. This structured engineering pipeline moves from discovering a biological mechanism to manufacturing a functional, real-world prototype like soft robotics, non-toxic coatings or bio-materials. Aquatic environments create a major engineering challenge because underwater surfaces are continuously exposed to microorganisms, algae and other organisms that can accumulate and interfere with equipment. Biomimicry offers a way to address this problem by studying how marine organisms naturally resist such environmental pressures and translating their functional adaptations into engineered solutions. Soft robotics help in expanding the scope of research studies in robotics to serve new needs that are linked to adaptation and safety. Living organisms depend on real-time and stored information for their response, whereas soft robotics often suffer from nontrivial integration with aids like actuators, sensors and controllers. This shows that effective underwater interaction arises from the synergy of materials, morphology, and environment.

Sharkskin-Inspired Anti-fouling and AI Vision

Sharkskin denticles alter boundary-layer flow and discourage biological attachment which has made them a model for micro-patterned surfaces used in aquatic equipment. Such sur-

faces could protect desalination membranes and underwater sensors from fouling. Bio-inspired textured surfaces physically stop algae and bacteria from adhering to surfaces without using any dangerous chemicals or toxic heavy metals. Micro-structures that cover sea vehicles and marine equipment keep optical sensors clean. AI vision technology collects reef health status and determines the presence of hazardous species without impact from the bio-fouling layer.

Manta Ray Gill Rakers for Bio-Inspired Smart Filtration

Manta rays have a unique “ricochet separation” mechanism in their gill rakers in which particles collide with wing-like filter lobes and are redirected allowing high-flow filtration with larger pores and less clogging. CFD, particle tracking and 3D-printed models set the fluid-mechanical basis of this system. This architecture has inspired self-cleaning microfluidic chips and nanofibrous membranes for efficient particle and oil-water separation illustrating how marine biomimicry can be translated into sophisticated environmental filtration technology

Fish-Inspired Robots for Aquatic Monitoring

Fish achieve great agility via body and fin movements having inspired the design of robotic fish which use flexible bodies, smart material actuators and hydrodynamic control. A fish inspired robot is able to look at hard to access environments, map out pollution and study bio growth. Bio-mimetic fish-shaped Autonomous Underwater Vehicles (AUVs) are able to propel due to their tails made of soft robotics. Integration of cameras, sonar, water quality probes and machine learning into the device brings the

tech alive. Silent underwater robots can swim next to marine species that are threatened by over-exploitation and gather necessary information without posing any danger.

Mussel-Inspired Water Remediation

Mussels attach firmly to wet surfaces which has inspired the development of poly-dopamine based coatings which create a very flexible interface for water treatment. The coating improves membrane hydrophilicity, reduces foul-ant adhesion putting down functional layers which capture pollutants. Innovative sticky materials like bio-resins and aerogels with mussel-like active groups are released into water bodies which connect to heavy metals and micro-plastics, effectively drawing pollutants out from wastewater. This engineering has been put to use in filtration, contaminant adsorption, catalysis and photo-thermal evaporation. Thus, mussel chemistry becomes an underwater “glue”.

Automated eDNA Biodiversity Monitoring

Aquatic organisms release DNA through normal bodily functions into their environment which is now collected by machines as a replacement for almost total manual sampling. Usage of automated filters and sequencing along with machine learning as a way to turn water bodies into molecular laboratories will collect biodiversity data without researchers having to go into the field. Underwater robotic platforms constantly collect shed genetic material from surrounding waters with the help of in-water sampling and automated sequencing techniques making the destructive use of fishing equipment unnecessary. The system enables generation of detailed biological maps that can help identify endangered species, identify the loss of biodiversity and prevent the initial introduction of invasive species.

Multi-Robot Marine Cleanup

Collective behaviour among fish schools influences distributed robotic coordination with multiple machines to do the work rather than divide and conquer with one vehicle. The SeaClear system combines surface vehicles, aeri-

al drones, an observation underwater robot and an underwater collection robot having a bio-mimetic gripper. The drone and the observation underwater vehicle create bottom maps based on AI analysis where AI detects the litter, autonomous navigation estimates its location and robotic hardware retrieves it allowing separation of round litter on the bottom from living sea creatures. Then, the collecting robot picks up bottom plastics and industrial waste, thus allowing deeper water remediation which cannot be performed by divers as it is unsafe. SeaClear shows how bio-mimetic coordination can transform environmental intervention transitioning from pollution awareness to autonomous detection and collection.

Coral-Inspired 3D Environmental Infrastructure

Coral skeletons form complex surfaces and flow pathways hosting diverse communities in the cavities. Using Computational Fluid Dynamics, topology optimization and additive manufacturing, engineers recreate this functional architecture. Instead of printing voids, utilization of a specific mixture of geopolymers similar to natural coral reefs pertaining to their complexity and porous geometry use 3D printing for building structures. These structures serve for dispersing wave energy to tackle coastal erosion processes and provide natural habitat niches for marine life. Sensors enable the measurement of several parameters like temperature, oxygen, pH and ecological performance. Thus, what results is a reef that is not simply an artificial structure but one capable of being programmed to create habitat.

From Laboratory to Ecosystem

Scaling up these lab-scale models to global, field-deployed environmental technologies is an effort of addressing critical engineering constraints:

1. **Manufacturing and Scaling Up Costs:** Micro-textured surfaces like sharkskin and bio-resins are expensive to manufacture on a large scale and so, engineers are scaling up to roll-to-roll nanoimprinting and bio-

based 3D printing feedstock vessels.

2. Circular Life Cycle Design: Integrating technology into natural ecosystems introduces the danger of producing additional waste through this process. To enforce circularity, bio-inspired sensors and soft robotics technologies are increasingly manufactured from biodegradable polymers which are harmless if accidentally lost in the ocean. 3D artificial corals are constructed from recycled waste or CO₂ capturing cement making sure the technology is sequestering CO₂ during its entire life cycle.

Conclusion

Biomimicry perfectly bridges the gap between evolutionary sciences and engineering providing a revolutionary model for marine conservation and ecosystem restoration. It transforms biological principles into scalable engineering solutions that preserve and restore our planet's ecosystems. Concurrently, integrating the concepts of the circular economy plays a big role in the technology introduction. For example biodegradable materials are used in soft robotics, CO₂-absorbing compounds are uti-

lized in coral reefs recovery and recycled feedstock is used for 3D-printing. Lastly, employing digital technologies like digital twin technology and drone technology for continuous tracking of environmental changes allow scientists to monitor pollution trends and anticipate the water cleaning processes before their commencement.

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Coral Bleaching and the Collapse of a Marine Symbiosis: Impacts on the Web of Life

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Keywords: Coral bleaching, coral-algal symbiosis ocean warning, marine biodiversity, ecosystem resilience

Introduction

Coral reefs have some of the highest levels of biological diversity of any ecosystem found on Earth and support nearly 25% of all marine species that exist, despite covering less than 1% of the ocean floor. These ecosystems sustain high

levels of biological diversity partly because of the symbiotic association between corals and microscopic algae known as zooxanthellae. Zooxanthellae reside inside coral tissue and utilize photosynthesis to produce energy for both themselves and the coral. The association between corals and zooxanthellae is what pro-

vides the basis for coral symbiosis. Symbiotic associations are required for the long-term survival of corals because they can provide up to 90% of a coral's nutritional requirements and allow them to exhibit bright colours. As a result of rising sea surface temperature related to climate change, there has been an increase in the pressure being placed upon this symbiotic association, resulting in many corals expelling their algae and turning white in a condition called coral bleaching. This article will investigate the biological mechanisms involved in coral bleaching and the subsequent cascading effects on the biodiversity of coral reefs and the broader food chain.

The Symbiotic Partnership

Zooxanthellae exist inside the gastrodermal layer of cells of their coral polyp host within a membrane known as the symbiosome. Here, the coral provides algae with a sheltered place in the sun where it can access supplies of carbon dioxide and nitrogen-rich waste material generated by the coral's metabolism. Zooxanthellae provide their host with sugars and other organic material generated from photosynthesis directly to the coral host, satisfying up to 90% of its energy needs. This exchange of nutrients takes place at various scales, ranging from individual polyp cellular level transfer of carbon, to whole reef productivity. Corals and their symbiotic algae are very sensitive to changes in their environment. Rising sea temperatures can have devastating effects on this relationship. This close metabolic dependence also creates a vulnerability: when environmental conditions disrupt algal photosynthesis, the same partnership that supports coral productivity can become a source of cellular stress.

The Bleaching Mechanism

If the temperature of seawater goes above the range that corals can normally tolerate, heat stress has an adverse effect on the photosynthetic apparatus of their algal symbionts. Because of the high temperature, photosystem II may suffer damage to its structure and its repair mechanisms, which in turn lowers the efficien-

cy by which light energy is turned into chemical energy. The damage can be made worse by intense sunlight especially in case of shallow reefs. When photosynthesis is impaired, the excess electrons react with oxygen to form reactive oxygen species. When produced in small quantities, these molecules are handled by the antioxidant defenses. However, when exposed to prolonged heat and light stress, the amount produced can go beyond the protective ability of both the algae and coral host. This leads to oxidative stress which damages the cell membranes, the proteins, the DNA and the photosynthetic structures.

This damage interferes with usual exchange of carbon and nutrient between the two partners. The coral gets less photosynthetic energy at the same time as its own level of physiological stress rises. In response, the host can expel the algae, digest them by means of cellular processes or lose the host cells which contain them. The algae may also lose their photosynthetic pigments. As both the algal cells and the pigments decrease, the transparent tissue of the coral exposes the white calcium carbonate skeleton underneath. Bleaching is not an immediate death sentence; a coral can recover if the stress is of short duration, the living tissue is still there and the colony is able to regain its symbionts or get further food.

However, if the high temperatures continue, the loss of photosynthetic energy results in an energy deficit. Alongside, growth, calcification, reproduction and immune functions all decline, thus raising the risk of disease, tissue loss and mortality.

Ecosystem-Wide Consequences

The impact of coral bleaching goes beyond that which is seen in individual colonies since living corals form the physical framework of reef ecosystems. When bleaching leads to a large number of deaths in corals, the dead skeletons are gradually broken down by waves, storms and organisms that bio-erode the coral. As a result, the reef's structural complexity decreases and the crevices and shelter that many fish and

invertebrates use for protection, feeding and breeding are lost. It therefore follows that a severe loss of coral can lead to a reduction in the number of fish species and have an effect on the abundance of various feeding groups.

Bleaching also changes the composition of reef communities. When their food source is lost, fish and invertebrates that feed on coral may decrease while herbivores may increase temporarily as algae take over the dead coral surfaces. However, this change is not always advantageous. Dense growth of algae can compete with the remaining corals and inhibit new coral larvae from settling and growing. If herbivorous fish and sea urchins are not able to keep the algae in check, the reef can change from a system dominated by corals to a system dominated by algae. These changes reorganize the way energy flows through the food web since the death of the coral decreases the habitat available to small reef fish, which in turn can have an effect on larger predators that feed them. The changing grazing pressure may affect the balance between algae and coral recruits, and the loss of complex habitat can lead to a reduction in nursery areas for juvenile fish. After the 2016 bleaching event, researchers recorded a decline in fish that feed on coral and more widespread changes in the various trophic groups on the Great Barrier Reef. The consequences of bleaching can still be observed even when the temperature has gone back to normal. If this kind of event occurs repeatedly, it may stop corals from being able to reproduce and recover before the next disturbance arrives. As the dead carbonate structures wear away, the reefs lose their complexity, support fewer species and offer less protective coastal protection. Lower habitat levels can also result in reduced fish recruitment and lower fisheries productivity. Coral bleaching is therefore, not just a simple physiological reaction; it can develop into a disturbance that affects the whole ecosystem.

Conclusion

Coral bleaching shows that the failure of a microscopic partnership can destabilize an en-

tire ecosystem. When heat stress disrupts the coral-algal symbiosis, corals lose an important source of energy. As a result, their growth, reproduction and resistance to disease decline. If bleaching becomes too severe or occurs repeatedly, coral mortality destroys reef structure and alters food webs. This affects the species and communities that depend on these habitats including humans. Although some corals can recover or become more heat tolerant, increasingly frequent marine heatwaves may leave too little time for recovery and gradually weaken reef resilience. Protecting coral reefs requires local action, such as improving water quality and protecting herbivores as well as rapid reductions in greenhouse gas emissions. The future of reefs depends on preserving the symbiosis that sustains them.

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Developmental Bias and the Evolutionary Accessibility Of Strategies

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Keywords: Developmental bias, evolutionary game theory, natural selection, phenotypic variation, evolutionary dynamics

Introduction

Evolution is a process where natural selection acts upon heritable variation, allowing phenotypes with greater reproductive success to become more common over generations. Now the question is, where do the phenotypes available for natural selection arise from, and are all phenotypes equally likely to arise? Developmental biology suggests that they are not. Developmental systems are organized in such a way that some phenotypic variants are more readily generated than others, a phenomenon called developmental bias.

This means that natural selection acts upon the phenotypic variation made available through developmental processes, rather than on all theoretically possible phenotypes. However, the presence of a phenotype does not necessarily mean that it will become more common. Its frequency also depends on its fitness and on how it performs in interactions with other organisms.

In this article, we explore how evolutionary game theory can be used to quantify changes in the frequencies of such phenotypes under natural selection. Evolutionary game theory provides a framework for understanding how the frequencies of phenotypes, when considered as evolutionary strategies, change according to their reproductive fitness when organisms interact with one another.

Developmental Bias and Phenotypic Variation

An organism does not develop from its genet-

ic material in an unrestricted manner. Genes interact with regulatory networks, cells, and tissues through a structured developmental process. Therefore, genetic or environmental changes may not produce corresponding phenotypic changes with equal probability. Some changes may readily produce viable phenotypes, while others may be difficult to generate because they may require multiple coordinated changes during development.

For example, vertebrate limbs are produced through highly coordinated developmental processes. Changes in these processes can alter the size, shape, and proportions of an existing limb, allowing variations to arise. However, producing a completely different and novel structure may require changes across several interacting developmental pathways. Thus, developmental systems do not make every possible phenotype equally accessible.

Therefore, some phenotypes are more readily generated than others, creating a bias in the variation available to natural selection. Developmental bias does not determine which phenotype will be favoured; instead, it influences which phenotypes are more likely to become available for natural selection.

Evolutionary Game Theory and Natural Selection

Natural selection becomes more complex when the fitness of a phenotype depends on its interactions with other organisms. Evolutionary game theory provides a framework to understand such situations.

For example, an organism may display aggressive or non-aggressive behaviours, and the outcome of its behaviour depends on the behaviour of the organism it is interacting with. In evolutionary game theory, these behaviours or phenotypic types are termed strategies. A strategy refers to a heritable type that influences how an organism behaves during an interaction. The outcome of an interaction is represented as a payoff, which describes its fitness consequence.

Therefore, the success of a strategy (phenotype) depends on both its own characteristics and the other strategies present in the population. The replicator equation quantifies how strategy frequencies change according to their relative fitness:

$$dx_i/dt = x_i(f_i - \bar{f})$$

Here, x_i is the frequency of strategy i , f_i is its fitness, and $\bar{f}$ is the average population fitness.

Strategies with above-average fitness increase in frequency, while those with below-average fitness decrease.

Developmental Bias in Evolutionary Strategy Spaces

Evolutionary game theory begins with a defined set of strategies (phenotypes or behaviours) and examines how their frequencies change according to their relative fitness. Developmental bias suggests that these strategies may not be equally accessible. As mentioned earlier, developmental systems influence how readily different phenotypes arise in a population; therefore, some phenotypes may enter a population more frequently than others.

Thus, two factors can influence evolutionary change: reproductive fitness and developmental accessibility. Developmental accessibility determines how readily a particular phenotype can arise, while reproductive fitness determines how successfully that phenotype persists and increases in frequency once it is present. These factors act at different stages but can jointly influence evolutionary trajectories.

For example, consider three possible pheno-

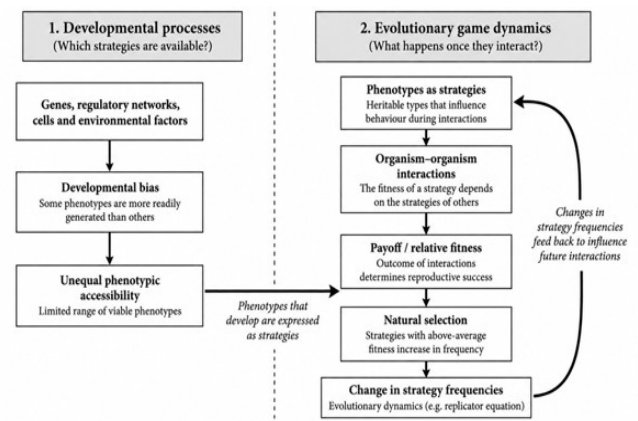


Figure 1: Conceptual relationship between developmental bias and evolutionary game dynamics. Developmental processes influence the accessibility of phenotypic variants, which may function as evolutionary strategies. Interactions between strategies generate fitness consequences that influence their frequencies through natural selection. (Source: Author's own illustration.)

types- A, B and C. Suppose A is more readily generated by the developmental system, while C is much more difficult to produce but has a higher payoff during interactions. Evolutionary game theory predicts that, once C is present, its higher fitness can allow its frequency to increase under appropriate conditions. However, developmental bias may make C less likely to arise in the first place. Thus, a strategy with a high fitness payoff may not be equally likely to appear as one that is developmentally more accessible.

This suggests that developmental bias and evolutionary game theory describe complementary aspects of natural selection. Developmental bias influences which phenotypic variants are more readily available for selection, while evolutionary game theory describes how natural selection changes the frequencies of these phenotypes according to their fitness during interactions. Thus, developmental accessibility may influence the variation on which natural selection can act, while fitness determines which of the available variants are favoured.

Evolutionary Implications

Considering developmental accessibility alongside fitness may provide a different per-

spective on evolutionary predictability. If certain phenotypes are more accessible through development, they may be more likely to enter evolutionary trajectories, even when other theoretically possible phenotypes could provide greater fitness. This could help explain the repeated evolution of similar phenotypic variations in different populations or species.

This perspective may also help to explain why evolution does not always reach the theoretically optimal outcome predicted from fitness alone. A highly advantageous strategy may have little evolutionary impact if the developmental system rarely produces the corresponding phenotype. However, a moderately advantageous phenotype that can be readily generated may have a greater opportunity to be acted upon by natural selection.

Therefore, incorporating developmental accessibility into evolutionary game theory could potentially improve our understanding of which evolutionary outcomes are not only favourable, but also accessible.

Conclusion

An example of this can be seen in the domestication syndrome observed across several domesticated mammals. Despite domestication occurring independently in different species, similar traits such as reduced aggression, al-

tered pigmentation and changes in craniofacial morphology have repeatedly appeared. These similarities have been proposed to arise partly from shared developmental pathways, suggesting that certain phenotypic changes may be more developmentally accessible than others. This illustrates why evolutionary outcomes may depend not only on traits are favoured by natural selection, but also on traits development makes more readily accessible. Evolution may therefore be influenced not only by which strategies are favourable, but by which strategies are developmentally reachable.

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The Purple Earth: the Archaea World

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Keywords: Archaea, Retinal, Chlorophyll, Halophile

Introduction

The Earth appears a beautiful bluish green planet from outer space. The photos taken from the satellites and spaceships might have looked different when our earth was young

many years ago. There was a time when the Earth was less green and blue, and more purple. The Purple Earth hypothesis, proposed by two Professors of Molecular biology and Astrobiology in 2007, Shiladitya Das Sarma and Ed-

ward W Schwieterman tells the story of a purple earth of the Haloarchaeons. Haloarchaeons are considered as the main organisms who imparted this violet color to our earth.

Position in Biological Classification

Haloarchaeons or halophiles are positioned in the archaea or archaeobacteria domain of the three-domain system classification by Carl Woese. These are not purple sulfur bacteria which are in Eubacteria (true bacteria domain).

First Appearance of Life on Earth

One of the earliest life forms that came into existence in the Early Archean or possibly in late Hadean Eons which could date back to 4 Ga (molecular clock) about 4000 million years ago. It is reasonable to believe that evolution of the retinal pigment (the main purple pigment of archaea) is a metabolic invention that closely coincided with the development of cellular life. Polypeptide attached to a retinal chromophore formed a chromoprotein like bacteriorhodopsin. This results in direct photoautotrophy rather than photosynthesis. When sunlight hits the archaea cell, the cell changes shape physically and the pigments use this solar energy to exude H^+ ions from the cell. When they return to the cell they can only do so by ATP turbine gated channels forcing ATP generation. This does not produce any complex carbon backed carbohydrates which also explains why it cannot be called photosynthesis which produces glucose (note: it also helps to differentiate purple sulfur bacteria which produce glucose and not just ATP) and also does not produce oxygen.

The retinal theory is considered plausible because retinal has a rather simple structure compared to other complex pigments like chlorophylls which have porphyrin rings. Also, retinal compounds are found rather abundantly in nature marked by their characteristic absorption of green yellow paths of the light spectrum. They are found at the intersection of lipid metabolism and bioenergetics studies, so all these factors support the evolutionary theory of retinal being the first pigment of photoautotrophs rather than chlorophyll.

Prevalent Environment and Ultimate Transition

The purple world hypothesis has another interesting dimension as the primitive earth had a different environment. It is essential to note that this purple earth existed before the oxygen revolution (or Great Oxygenation Event, simply GOE). In fact, the advent of cyanobacteria and modern algae which released the oxygen killed this huge Archaeon population. It was not an instant event and was delayed due to mechanisms like geological absorption, however, the change when it came was permanent.

The environment was strictly anoxic, filled with CO_2 and CH_4 was reducing in nature. These archaea which had purple pigment were halophiles which means they lived in a highly salty environment. In such huge numbers in oceans that Earth was hypothesized to give off a purplish hue. The oceans at that time had more mineral and salts to support this halophilic population.

Another major point of difference between modern pigments like chlorophyll and bacteriorhodopsin versus retinal based bacteriorhodopsin pigments was the absorption range. The most intense solar absorptions are at the range of 500 to 600 nm. Retinal absorption peaks at 568 nm (green to yellow range) reflecting off red and blue (combining to give purple hue) but chlorophyll and modern pigments absorb more at red and blue wavelengths reflecting off green and yellow. These suggests the evolutionary relevance of the development of retinal pigment was primarily to absorb sunlight while chlorophyll and other similar pigments that developed later are some sort of 'compromise'.

What sort of compromise? Evolutionarily speaking the cyanobacteria and green algae appeared (both oxygenic and anoxygenic photosynthesizers) later, but coexisted and even coevolved with their Archaea counterparts. However, as mentioned before, GOE got delayed. During this period, cyanobacteria and green algae evolved to use the otherwise non useful red and blue wavelengths to promote

coexistence by resource partitioning and niche specialization (to avoid Gauche's exclusion) as a 'compromise'. Later during the inevitable GOE, these green autotrophs were naturally selected over the purple ancestors as they had mechanisms to use or at least dispose off toxic peroxide radicals. These archaea were killed in mass due to poisoning and lagging in competition and survivors were either forced into high salt anoxic environments in deep seas (main cause of disappearing of purple hue) or rarely into symbiotic mutualism with these green autotrophs who guarded them from oxygenic environments.

Modern Existence of Haloarchaeon

Professor Das Sarma put forward the argument that the abundance of retinal pigments, and the existence of the Archaeon cells in nature even today proves the existence of a purple world in the past. Indeed, in some salt rich lakes blooming in Australia, the water appears purple. These even can be isolated and cultured (though special conditions required) in vitro to get purple cultures. Though modern halophiles are facultative aerobes, they are close phylogenetic relatives of the original anoxic halophiles.

Future Astro-biological use and Conclusion

The most significant astro-biological use of this hypothesis is the change in approach to how we try to discover extraterrestrial life. Formerly scientists tried to hunt for only red edge, which is a dramatic dip in reflected red

light since it will be absorbed by photosynthetic green vegetation. However, this hypothesis implies even a green edge is a possible positive response to the question of existence of life on the planet under consideration because primitive vegetation by this hypothesis could be purple too. This can be detected by employing remote sensing UV and Visible spectroscopy. Extremophile biology has seen recent progress and can almost translate directly to astrobiology progress, since space often has the conditions extremophiles tide over. Halophilic archaeon even survives launches into Earth's stratosphere, which mimics the condition of the surface of Mars. This validates the assertion above.

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Smaller and Smarter : The AI Revolution in Nanomedicine

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Keywords: Artificial Intelligence(AI), Machine Learning(ML), Nanoparticles(NP), Molecular Docking

Development of this field called Nanomedicine has garnered a lot of attention from the pharmaceutical industry. However, not every nanoparticle has been able to perform optimally in targeted drug delivery but they certainly performed better than the traditional non-compartmental pharmacokinetic approach of treating diseases like cancer. To synthesize better therapeutic drugs, a lot of structural and physicochemical data of the nanoparticles as well as structural, physiological data of the targeted type of tissue or cell along with the knowledge on their signaling systems is required. Assessing such a large quantity of datasets manually only to produce drugs that have subpar performance which sometimes does not even pass the AD-MET(Absorption, Distribution, Metabolism, Excretion, Toxicity) profiling is wasteful and time-consuming. To reduce the cost of drug development as well synthesize better performing therapeutics, researchers have stepped up to using artificial intelligence and machine learning to try and simulate all different conformations of molecules, ligands with the help of digital models and database information including multi-omics data (genomics, transcriptomics, proteomics, metabolomics, electronic health record (EHR) data; imaging data; and high-throughput experiments of nanoparticle libraries). This article is a brief dive into the world of drug discovery using AI and nanotechnology and its workflow.

Why do we need Targeted Therapeutics and better Nanoparticles?

Multiple datasets from different studies per-

formed from 2005 to 2018 have revealed that targeted drug therapy has a better performance than non-compartmentalized one-size-fits-all approach that causes damage to non-target cells as well. A meta-analysis paper by Cheng. Et al analyzed 376 datasets using Physiologically Based Pharmacokinetics (PBPK) method of delivering the medicines to solid tumor sites using varieties of different nanoparticles and found that mean delivering efficiency was 2.24% ID (Injected Dose) and median delivering efficiency was 0.76 %ID at the last sampling point time after 24hrs of injecting and it dropped to 1.23% and 0.35 %ID after 168 hours. Comparing the previous results to the studies that used non-physiologically based models which had the mean delivery efficiency of only 1.48 %ID and the median delivering efficiency of 0.70 %ID, we observe improvement. However, despite this slight increase, the overall delivery efficiency remains quite low and presents a major hurdle for clinical translation. This is where deep analysis of previously collected practical and experimental data comes, in the form of bioinformatics and computational biology both of which as of current require the use of AI to a significant extent. The type of nanoparticles (liposomes, dendrimers, carbon nanotubes, etc) used to treat a particular disease also differs and directly affects their ability to deliver therapeutics. The size and shape, the material type, the cellular/tissue microenvironment (tumor microenvironment as considered in the aforementioned meta-analysis) and whether the nanocarrier is targeted or passive

plays an important role in determining the efficacy of the nanomedicines.

Why use AI in drug development?

The advent of nanomedicine as we speak is now heavily intertwined with techniques that include machine learning and deep learning used widely for predictive sampling and simulation in the process of drug development. Deep learning and machine learning form the two core principles of training and development of AI in any field. The reason on the surface level might seem to be reducing production cost and enhancing efficiency of the entire process but recent research in the field of targeted therapy using nanotechnology reveals the more scientific reason behind the integration of machine learning along with nanotech. Lower bioavailability, complex physicochemical nature of the nanocarriers, multidrug resistance inside a patient or the superbug in them and toxicity prediction are some of the challenges currently faced by the industry today.

Using AI would essentially help us predicting better models of drug with better bioavailability and cytotoxicity, synthesize better APIs (Active Pharmaceutical Ingredient), quicker and earlier screening of complex diseases such as cancer or neurological diseases like Alzheimer's and Parkinson's using nanocarriers in medical imaging (MRI, PET), etc. Molecular docking and QSAR (Quantitative Structure-Activity Relationship) modeling are some of the most important tools we use today to predict binding of a ligand with a target molecule and predict its toxicity, biological activity by mathematically mapping to its chemical structure respectively. DiffDock, AlphaFold-3, Boltz-2 are a few examples of software widely used in molecular docking applications such as production of diffuse models to predict the binding and interactions between ligands and poses or score the poses based on deep learning techniques of convoluted neural networks (CNN), etc with prediction accuracies upto approximately 86% (in case of AlphaFold-3). OECD QSAR Toolbox, KNIME Analytics Platform are two popular no code workflow tools used in QSAR

modeling by researchers.

Methodology and Application

The type of disease that is being dealt with is taken as the model whose cell receptor and signaling pathway data is collected from databases which have both in-silico as well as in-vivo experimental results, a suitable API is formulated using QSAR modelling and molecular docking algorithms and the best scored ligand-pose interaction is further analyzed to choose an optimal nanocarrier that is compatible with the therapeutic and has minimum possible toxicity inside tissue systems. For example Doxorubicin (DOX), a member of the anthracycline class, is a chemotherapeutic agent that is used to treat different sorts of blood cancers, solid tumors and sarcomas, is cardiotoxic and causes severe suppression of hematopoiesis. Hence, targeting of DOX by means of SWCNTs (Single Walled Carbon Nanotubes) may help reduce the toxicity and improve the clinical utility of this highly active therapeutic agent and to reduce the damage on the non-target cells, use of magnetic SWCNT in which nanotubes are tagged with iron oxide particles is preferred as seen in a study conducted by Faraj. Et al. After the in-silico analyses, in-vitro study and/or animal studies are given a shot. If it performs well enough, it's ultimately approved for clinical trials on selected few candidates before getting approval for commercial availability by medical boards across the world such as FDA. Another example to illustrate this workflow would be the synthesis of mRNA Vaccine Lipid Nanoparticles. Beginning with antigen identification and target selection by using tools like AlphaFold and BLAST for multi-sequence alignment and analysis of the viral or bacterial genomic sequences, we move on to the in-silico design process where mRNA sequence optimization is done to rewrite the mRNA script inside the human body safely without eliciting a severe toxic immune reaction by codon optimization, nucleoside modification, etc. Free energy minimization and ribosome bottleneck screening is done computationally before the manufacturing process so that hairpin loops created do not

stall translation inside the patient body. Finally MD (Molecular Dynamic) simulation and QSAR modeling is done to design effective delivery of the vaccine into the human target cells.

Conclusion

The synergy between all three distinctive fields marks a paradigm shift in achieving true personalized medicine enabling the engineering of smart nanotherapeutics which are tailored to patient-specific molecular profiles. Although there are still many challenges remaining for achieving clinical translation of AI-based nanomedicines including data heterogeneity, regulatory gaps, batch-to-batch variability, scalability, and ethical issues that need to be resolved the collaboration of medical investigators, computational biologists, clinical practitioners and various other experts can help in solving these issues much faster. In summary, the application of AI to nanomedicines could revolutionise precision medicine through improved efficacy, safety, and flexibility of treatments for cancer and neurological diseases. Despite the challenges, there has been an obvious enhancement in drug development with the use of AI and ML that has bypassed the empirical, slow moving trial-and-error methodology of

drug discovery and thus this line of biomedical engineering needs to be explored further.

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Beyond The Veil, To The Abyss

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The harmony, in which all resides,
The symphony created by raging tides,
But beneath this vast world lies what,
If not, an abyss full of stars and lies?

"This blank canvas, covered with a thousand strokes,"
"I speak of the heart where your silence awoke,"
With clarity and hint of a tormenting smile,
She spoke the words my mind denied.

"There's naught a heart which hasn't undergone"
"Under trials and tribulations, foregone."
"How innocent, 'twas, that heart of yours,"
"Just like clay, soft and pure."
"Just like a canvas, blank and white,"
"With pictures drawn, but none seemed right."
"You used to fill the pages bright,"
"With colours and the hope of light,"
"But now all that's left for you,"
"Is an unfinished drawing,"
"An unfinished song,"
"An unfinished script for LIFE ANEW"
"Fear not" she implored,
"And strike the harp once again,"
"And with this newfound melody,"
"Sing songs galore of life and pain"
"Cause, once you sing this song you seek,
"Life will seem a little less bleak,"
"For, beneath this vast world lies
What? If not, an abyss full of stars and lies?"

Leaves Of A Tree

Sarvarish Sarkar

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My life like leaves of a tree--- waits for Your breeze to
blow
and from this tiny instrument of my being, make the
music flow.

I stare still at the valley far away, roses blooming and
blossoms in sway.

A passion rises within, like melody stuck midway.
My body aches, and this idle gaze, I can no longer bear.
Sitting still as the poised leaves of a tree, I wait---
for Your breeze to blow and set my song free.
I see people come and go and life racing past, not
leaving a trace.

Unfazed by sorrow, unmoved by pain, untouched by all
joy and triumph---
they move on in tireless motion, completing the same
chores of the day.

There is no time to stay and as if in a sprint, moments
pass by---
restless and quick, in the blink of an eye!
And when all the work is done, the gathering disperses
away.

Time slows down as dusk sets in on empty roads.
The leaves crumble with weight and bend low. I with
sighing hope, stare still---
the pain of songs unsung, deepening within.

In all this humid void, I can hear faintly the sound of
rustling leaves,
and feel the blowing of Your breeze!
Out flows my music with the rustling of the leaves and
into the ocean of Your rhythm,
like a small stream it merges, the song of my heart in
waves of glee.

And when the breeze has blown and the song is sung,
light falls as it recedes---
upon the pale, brown leaves.

The wait of a lifetime concludes at Your feet for when
the last verse is sung
and I have no more to offer, I lie at peace--- like leaves
in an autumn fall.

Hestia's Hearth

Pramita Dan

Semester 9

Postgraduate & Research Department of
Biotechnology

To care and to love so greatly
That hell fire seems warm like
The sun rays on a winter morning
Cries of a newborn and the giggles
Like symphony so great that the Gods' sway
Small felines tip tapping over the huge hands
Unaware and innocent from all things wrong
To hold a bundle of precious life, Midas cries
As he holds his living daughter again
The drums of life beat so rhythmic
Tuning out the bombs and cries of the dead
To live is to move, to hold, to kiss so tender
Hades returns the pomegranates, and
Demeter smiles and sways her branch of
Peonies and the daisies bloom with carnations.

Communion Without Tongue

Aryan Ahmed

Semester 3

Postgraduate & Research Department of
Biotechnology

Where does the cedar leave off and the loam begin?
A ghost-thread slips beneath the basalt floor,
neither quite self nor stranger, taking in
what loneliness could never fathom for.
Beneath the heels, an unsaid covenant breathes—
pale hyphae knotting sugars into bone,
the dark traffic of moss and lichen-sheaths
that proves no living thing survives alone.
We carve our names in bark to mark the skin,
absurdly solitary in our pride,
while subterranean conspirators draw in
the quiet water from the other side.
The boundary is an altar, not a fence:
We are the crossing and the consequence.

The Tax of Becoming

Tahira Afroza

Semester 3

Postgraduate & Research Department of
Biotechnology

They borrow stature from an older cold,
a currency of salt and borrowed sun
that uncoils quietly inside the fold
of muscle, till the brief arithmetic is done.
No tendon snaps without a debt repaid;
the leaf surrenders what the root desires,
an ache of ash through which the world is made,
fed by the embers of discarded fires.
It is not ruin, this deliberate slow yield—
the beetle's mandibles, the softening rind,
the marrow leaching into fallow field,
leaving no scaffold or remorse behind.
To enter life is to accept the tear:
a stitch of light unraveling into air.

Trip To The Hills

Swastik Khan

Semester 9

Postgraduate & Research Department of Biotechnology

"Let's take a trip to the hills, it's been a while since I've felt the cool breeze."

Araj recalled saying these words to his mother a week ago. The cold wind stung his face. He could no longer see the hills in the distance, as the sun hid behind them, and the pink and orange hues of dusk dissolved into darkness. He rubbed his palms together, and turned to face the fire.

The pyre burned a fierce orange. The crackling sounds overpowered the babbling and gurgling of Teesta flowing nearby. Apparently one's not supposed to leave till the fire burns out. Araj didn't mind the warmth for a bit. His clothes were soaked with the rain. He hadn't had a change of clothes in almost thirty hours.

(felt like sixty to him.)

Eventually, he decided to take a walk. He took his phone out of his pocket. He searched for a name in his contacts.

no contact found.

Oh right, he changed it to a nickname only he used. Didn't make a lot of sense, that.

"Are you going to the movies tomorrow?" Araj had to start somewhere.

"Yes. You're coming too, right?"

"No."

ask me why.

"Oh too bad. Guess I'll see you in college on Monday then," came the reply, in an undecipherable tone.

"Hm." Araj hung up. He felt cold. The pyre has burned out, he thought. He turned to see it still ablaze. He felt cold, nonetheless. The sky had cleared, the stars kept him company. He shrugged and put his hands in his pockets, gripping his mobile in his right. His father's

phone lay unattended on a bench nearby. A curious mountain dog had its eyes on it from a distance.

Araj's phone rang.

He took it out and his eyes widened. He swiftly turned his head. His father's phone was still on the bench. He peered at his mobile screen again. He must've been mistaken.

He wasn't.

Sweat trickled down his forehead. His hands trembled.

"Hello?" Araj managed to say.

"You must go back if you don't feel like staying here."

"You never called me. It was always me calling you."

"Better late than never?" Araj didn't know what to say to that. He looked at the bench again, the pyre, then the name of the caller. He surely wasn't mistaken. The wind had died down.

"Mom okay?"

"Don't."

"Alright."

There was silence. "I wish things did not have to be this way," Araj said.

"Don't we all?" the voice let out a sigh, "Things barely go the way we want them to. We can just hope it's for the better."

Silence again.

"I'm sorr-"

The line dropped. Araj saw the fire had gone out, leaving behind a pile of ash. The river could be heard again, splashing against the rocks. The mountain dog sat quietly next to the phone on the bench, its white coat glistening in the moonlight.

শহরের প্রথম পাঠ

সুমন পাল

Semester 3

Postgraduate & Research Department of Biotechnology

হাওড়া স্টেশনে ট্রেনটা থামতেই অর্ণবের বকের ভেতর এক অচেনা কাঁপুনি। বাবার হাতটা শক্ত করে ধরে ছিল সে, যেমন ছোটবেলায় মেলায় হারিয়ে যাওয়ার ভয়ে ধরত। বাবাও তো গ্রামের মানুষ, সারাজীবন ধানখেতের সবুজ দেখে বড় হয়েছেন। আজ এই লোহার শহরে, মানুষের চেউয়ের মধ্যে দাঁড়িয়ে, তাঁর চোখেও সেই একই বিস্ময়, একই অস্থিরতা। হোস্টেলের শেষ তারিখ কখন ফুরিয়ে গেল বোঝাই গেল না, দাদুর কাছে সাফাই গাইতেও হল, তারপর সারাদিন হেঁটে অবশেষে একটা পিজি জুটল, ভাড়া শুনে বুক ধক করে উঠলেও আর উপায় ছিল না।

দ্বিতীয় দিনই এক সিনিয়র নিয়ে গেল এলাকা চেনাতে। হিন্দিতে জিভ জড়িয়ে যাচ্ছিল বারবার, তোতলাচ্ছিল প্রতিটা বাক্য। “একটু স্মার্ট হ,” সিনিয়র হেসে বলল, কথাটা শেষ হতে না হতেই একটা বেপরোয়া গাড়ি প্রায় ছুঁয়ে চলে গেল দুজনকে – বুক কাঁপিয়ে দেওয়া এক মুহূর্ত। সেই ধাক্কা কাটতে না কাটতেই দুজনে ঢুকল একটা ছোট্ট দোকানে। “এক প্লেট ম্যাগি হবে?” জিজ্ঞেস করতেই দোকানদার দাম বলল, আর সেই শুনে অর্ণবের মাথায় যেন বাজ পড়ল – গ্রামে যা দামে সে সবসময় খেত, এ যে তার প্রায় আট গুণ! মনে মনে হিসেব কষছিল, এই টাকায় গ্রামে কতগুলো প্লেট হয়ে যেত। আর আপেক্ষা? সে যেন আরেক পরীক্ষা – মিনিটের পর মিনিট গড়িয়ে যাচ্ছিল, অথচ প্লেট আসার নামগন্ধ নেই। শহরটা যেন প্রথম দিনেই শিথিয়ে দিল, এখানে সময় আর টাকা, দুটোরই হিসেব আলাদা।

বন্ধু খাঁজার সাহস তখনও জোগাড় করে উঠতে পারেনি অর্ণব। এক সন্ধ্যায় ডর্মের বাইরে অন্ধকারে বসে সে একা একা খাচ্ছিল – পিজির মালিক আমিষ খাওয়া নিষেধ করে রেখেছিলেন, যদিও তা নিছকই ভয় দেখানোর কৌশল ছিল, তখন সেটা জানা ছিল না। ঠিক তখনই তার বয়সী একটা ছেলে এসে দাঁড়াল, জিজ্ঞেস করল, “তুই এখানে অন্ধকারে বসে খাচ্ছিস কেন?” মুহূর্তের মধ্যে, বিদ্যুৎগতিতে হাত চালিয়ে মুরগির প্যাকেটটা সে লুকিয়ে ফেলল আলুর তরকারির আড়ালে, ছেলেটির চোখ এড়িয়ে। তারপর শুরু হল পরিচয়পর্ব – কোথা থেকে এসেছে, আগে কী করত, ইত্যাদি। এটাই ছিল তার প্রথম কথোপকথন সমবয়সী

কারো সাথে, অথচ কী বিদ্যুটে রকমের অস্বস্তিকর! মনে মনে শুধু প্রার্থনা করছিল, ছেলেটা কখন যাবে। হিন্দিতে কথা এগোচ্ছিল থেমে থেমে, কিন্তু ছেলেটা কিছুতেই উঠতে চাইছিল না। শেষমেশ হয়তো বুঝল, অর্ণবের মন এই আড্ডায় নেই, তাই “গুড নাইট” বলে চলে গেল। লম্বা এক নিঃশ্বাস ফেলে বাকি খাবারটুকু শেষ করল অর্ণব – অথচ এই অস্বস্তিকর সন্ধ্যাটাই একদিন পাকা বন্ধুত্বে বদলে যাবে, তা তখন কে জানত।

সময় গড়াল। সেই ছেলে, আরেকজন নিজে থেকে আলাপ করা বন্ধু, আর বয়সে বড় এক কর্মরত দাদা – সবাই মিলে একটা দল হয়ে উঠল। তারপর এল সেই দিন, যেদিন পরীক্ষা চলাকালীন খবর এল, দাদু আর নেই। এক মুহূর্তে পাথর হয়ে গেল অর্ণব, নড়তেও পারছিল না। বন্ধুরা নিজেদের মতো করে, হাসি-ঠাট্টার মধ্যে দিয়ে সান্ত্বনা দেওয়ার চেষ্টা করল, তারপর জোর করে টেনে নিয়ে গেল একটা মলে, মনটা একটু হালকা করার জন্য। মনের কষ্ট তখনও পুরোপুরি যায়নি, কিন্তু তাদের সেই জোরা জুরিতে মনটা কিছুটা হলেও হালকা হয়েছিল।

ফেরার পথে বাসে উঠে যোগাযোগ-দক্ষতা বাড়ানোর অজুহাতে বড়দা জোর করলেন কন্ডাক্টরের সাথে কথা বলতে। বেশ ভালোভাবেই এগোচ্ছিল কথা, কিন্তু হঠাৎ জিভ কেটে অর্ণব বলে ফেলল, “কন্ডাক্টর স্যার...” – গোটা বাসভর্তি যাত্রী সেই মুহূর্তে তার দিকে তাকিয়ে, কন্ডাক্টর নিজেও অবাক আর করুণ দৃষ্টিতে চেয়ে আছেন, আর বন্ধুরা হাসতে হাসতে প্রায় লুটিয়ে পড়ছে। রাঙা হয়ে যাওয়া গাল নিয়ে চারদিকে পালানোর পথ খুঁজছিল অর্ণব, কিন্তু কোথাও লুকোনোর জায়গা না পেয়ে নিজেও হেসে ফেলল শেষমেশ। পুরো বাসযাত্রা জুড়ে চলল সেই হাসি-ঠাট্টা।

পিজিতে ফিরে সে চুপচাপ বসে গেল পরদিনের পরীক্ষার পড়ায়। বন্ধুরা কিছুক্ষণ পর ফিরে ক্ষমা চাইল, হাসি মিশিয়েই। রাগ কমেনি ঠিক তখনই, কিন্তু এইটুকু বোঝা গেল – শহর একা একা শেখায় না, শিথিয়ে দেয় হাত ধরে থাকা মানুষগুলোও, তাদের হাসি, তাদের বিরক্তিকর ভালোবাসা দিয়ে।

Anti-Parallel

Anindya Sundar Ghosh

Semester 1

Postgraduate & Research Department of Biotechnology

Every morning, two boys entered the same school through the same gate. Yet they belonged to two completely different worlds. Aryan arrived in a shining car. His uniform was always perfectly pressed, his shoes reflected the sunlight, and his lunchbox carried more food than he could ever finish. A few minutes later came Rafiq. He walked. His shoes were old, with a small tear near the side. His uniform had been washed so many times that its colour had begun to fade. Sometimes, when the morning assembly lasted too long, his stomach growled—not because he disliked breakfast, but because there had been none.

They sat in the same classroom. They studied the same chapters. They dreamed under the same sky. But their lives moved in opposite directions—anti-parallel.

One afternoon, during lunch break, Aryan opened his lunchbox. Sandwiches, fruit, chocolate and juice covered his desk. Rafiq sat quietly beside him. Aryan noticed that Rafiq had nothing. “Didn’t your mother give you food today?” Aryan asked. Rafiq looked down. Before he could answer, Aryan laughed and said loudly, “Oh, I forgot. Maybe your family cannot afford lunch every day.” The classroom erupted in laughter. Rafiq did not say a word. He simply held his empty bag closer to his chest. Aryan did not know that morning Rafiq’s mother had divided one piece of bread into two halves—one for herself and one for Rafiq’s younger sister. Rafiq had lied and said he was not hungry.

That evening, rain fell heavily over the city. Aryan’s car stopped near a flooded road. He stepped out, irritated, trying to protect his expensive shoes from the muddy water. Then

he saw someone—Rafiq, standing beneath the rain with a small umbrella, completely drenched. Aryan looked surprised. “Why are you still here?” Rafiq pointed towards the road. “Your driver said the car cannot go further. I know another way home.”

They began walking. The rain grew heavier. At one point, Aryan slipped into the muddy water. Before anyone else could help him, Rafiq stretched out his hand. Aryan looked at it. Those hands were rough—hands that carried groceries and helped his mother wash clothes. Hands Aryan had once considered inferior. For a moment, Aryan could not move. Then he took Rafiq’s hand. Rafiq pulled him up. Neither of them spoke.

That night, Aryan remembered the empty lunchbox. For the first time, he wondered how hunger felt. The next morning, Aryan entered the classroom carrying two lunchboxes. He placed one silently on Rafiq’s desk. Rafiq looked at him. “I don’t need your pity,” he whispered. Aryan lowered his eyes. “It isn’t pity,” he said softly. “Yesterday, you helped me when I didn’t deserve it. I’m sorry for making you feel small.”

Outside the classroom window, a spider was weaving its web between two branches. Aryan watched it carefully. Two separate branches, growing in different directions, yet connected by delicate threads. Perhaps life was like that. Two boys could be born into different worlds—one surrounded by abundance, the other by absence. Their lives could move anti-parallel, never truly equal. But compassion could still create a connection. And sometimes, one small thread was enough to hold two worlds together.



PHOTOGRAPHY & ARTWORKS



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Semester 9



Aishani Bhattacharya
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Shehala Dhar
Semester 9



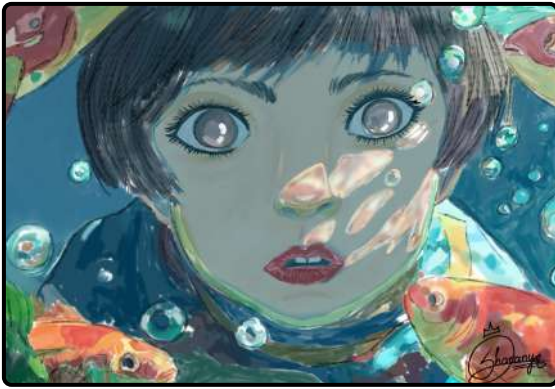
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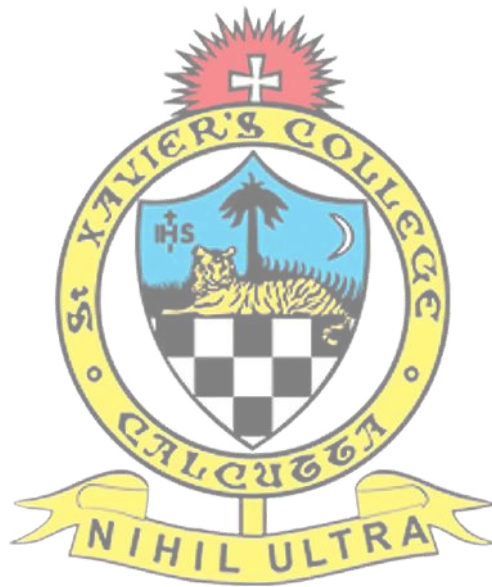
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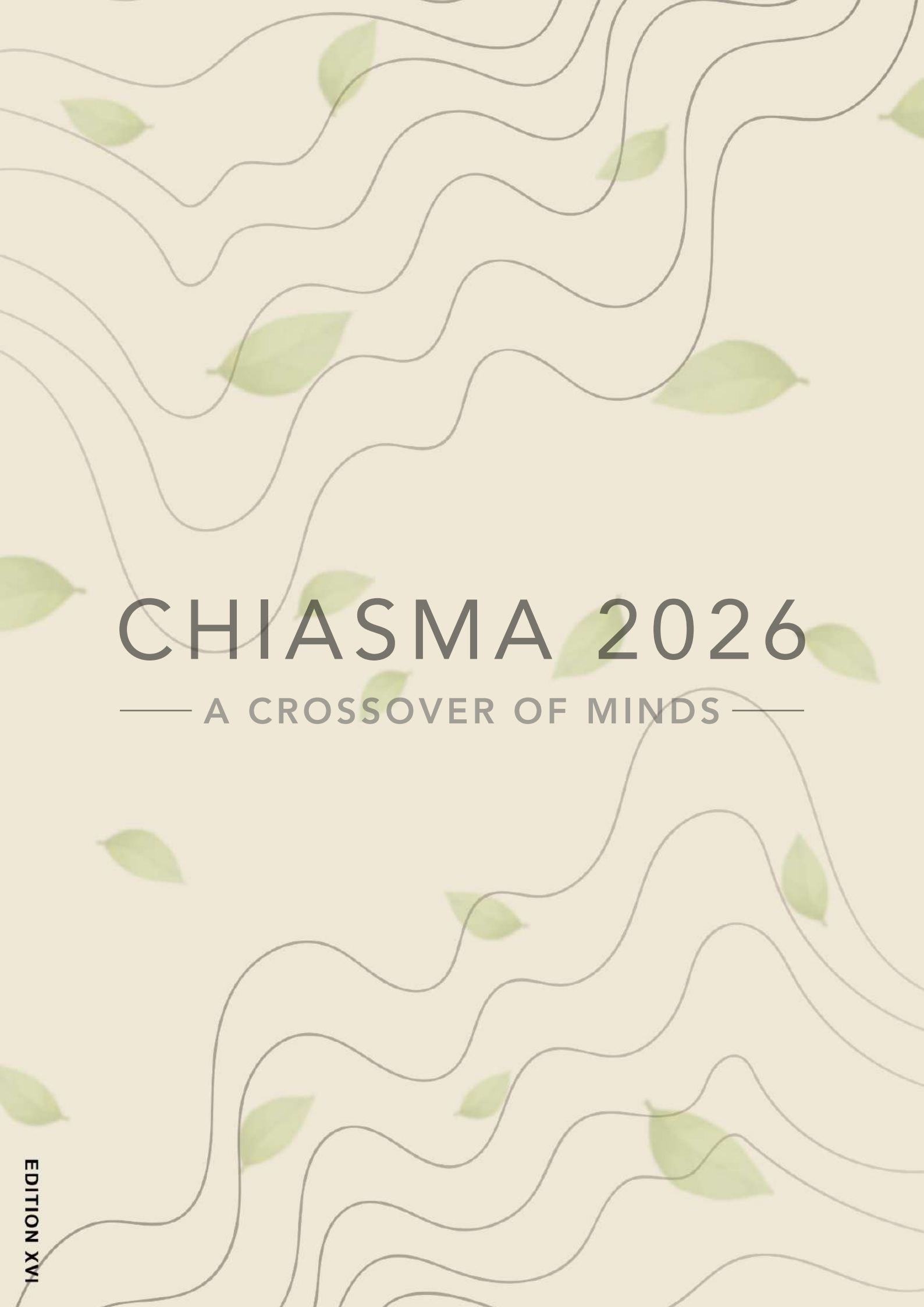
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CHIASMA 2026

A CROSSOVER OF MINDS

The background of the entire page is a light beige color. It features a pattern of thin, dark grey wavy lines that flow across the page. Scattered throughout this pattern are several green leaves of varying sizes and orientations, some appearing as simple outlines and others with a slight gradient.

CHIASMA 2026

— A CROSSOVER OF MINDS —