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| Book Name: | [**Microbiology and Biotechnology Research: An Overview**](https://www.bookpi.org/bookstore/product/microbiology-and-biotechnology-research-an-overview-vol-1/) |
| Manuscript Number: | **Ms\_BPR\_4727** |
| Title of the Manuscript: | **Centrosomes and Not-Coding DNA during the Emergence and Evolution of Bilaterally Symmetric Complex Organs: Computational Models** |
| Type of the Article | **Book Chapter** |

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**Source Article:**

**This chapter is an extended version of the article published by the same author(s) in the following journal.**

**Advances in Bioscience and Biotechnology, 16(2): 30-64, 2025.**

[**https://doi.org/10.4236/abb.2025.162003**](https://doi.org/10.4236/abb.2025.162003)

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| PART 1: Comments | | |
|  | Reviewer’s comment | Author’s Feedback *(Please correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)* |
| **Please write a few sentences regarding the importance of this manuscript for the scientific community. A minimum of 3-4 sentences may be required for this part.** | Scientists have long been intrigued by the emergence and evolution of bilaterally symmetric complex organs in metazoans. Central to this discussion are the roles of centrosomes and non-coding DNA, mainly DNA tandem repeats, in morphogenesis and evolutionary processes. The article tackles the intricate problem of how complex, bilaterally symmetric organs evolve and integrate seamlessly into existing anatomical frameworks without disrupting function. This is a central question in evolutionary biology, and the authors' focus on this issue is both relevant and timely, underlining the urgency and importance of the topic. The study adopts an interdisciplinary methodology by combining computational modeling with biological insights. This approach allows for the simulation of complex evolutionary processes that are challenging to observe directly, providing a platform to test hypotheses about the roles of DNA tandem repeats and centrosomes in morphogenesis. |  |
| **Is the title of the article suitable?**  **(If not please suggest an alternative title)** | Yes |  |
| Is the abstract of the article comprehensive? Do you suggest the addition (or deletion) of some points in this section? Please write your suggestions here. | The abstract argues that DNA tandem repeats and centrosomes are crucial in the genesis of bilaterally symmetric complex organs. Its merits reside in tackling a substantial evolutionary inquiry through an interdisciplinary perspective and contesting established paradigms. The abstract would greatly benefit from a more detailed description of the computational methods employed, as this would enhance the credibility and reproducibility of the study. Meticulous adherence to language and a more nuanced depiction of the biological processes involved are also recommended. These modifications offer a more lucid and persuasive summary of the study's contributions to the discipline. |  |
| **Is the manuscript scientifically, correct? Please write here.** | **2.1. Centrosome Theoretical Models: Intracellular Trafficking.**  The section states, *“Euclidean geometry precludes the construction of a mirror-symmetric structure out of chiral components without the simultaneous use of their mirrored partners.”* While this is true in a strict mathematical sense, it does not necessarily apply to biological systems. In living organisms, molecular interactions, biochemical gradients, and developmental constraints often override geometric considerations. For instance, the formation of a spiral shell in mollusks is not dictated by strict geometric rules but by the interaction of the developing organism with its environment. Centrosomes, operate within a highly dynamic and non-Euclidean cellular environment.  The claim that *“cells are externally identical but intrinsically chiral”* is somewhat oversimplified. While cellular components (such as actin filaments and microtubules) exhibit chirality, cells' external symmetry varies depending on tissue context, cell type, and developmental stage. For example, in a developing embryo, cells may initially appear symmetrical but as they differentiate into various cell types, their external symmetry changes. The phrase *“deterministic cleavage patterns with stereotyped division geometries, coded in DNA, are peculiar to each species”* is a key aspect of our understanding of biology. While genetic information plays a significant role in influencing cleavage patterns, it's important to remember that they are also modulated by cytoplasmic factors, maternal determinants, and environmental cues. The term “coded in DNA” oversimplifies this multifactorial process, but it's a crucial starting point in our exploration of cleavage patterns.  **Section 2.2: About in Silico**  This section presents an interesting perspective on in silico modeling of biological processes but **overgeneralizes certain claims about recursion and memory in biology**. The claim that recursive functions are not biologically compatible oversimplifies the nature of biological processes. While cellular systems do not recall function calls in the way that computer stacks do, recursive-like processes do occur in biology—such as gene regulatory networks, fractal branching in vascular and neural structures, and developmental morphogenesis. Thus, recursion may not be directly analogous to biological execution but is still invaluable for modeling and understanding these complex processes. A more precise, structured, and balanced discussion would strengthen its arguments.  **Section 4.1. Bilateral Symmetry**  Provide a more nuanced view of bilateral symmetry's evolution, acknowledging that it was likely refined over multiple evolutionary steps rather than arising instantaneously. Expand on the molecular basis of symmetry formation, integrating developmental genetics and known signaling pathways. Clarify how the computational model aligns with real biological processes, specifying its assumptions and limitations. Discuss alternative theories of symmetry emergence and compare them to the proposed computational framework.  **Section 4.2 Bilateral Symmetry and Zygote Centrioles**  While the hypothesis that centrioles are chiral tools influencing bilateral symmetry is plausible, it requires more empirical validation. The inheritance of a single sperm centriole and its subsequent duplication raises important questions about symmetry establishment, but other developmental cues likely contribute. Bilateral symmetry is a complex trait shaped by molecular, cellular, and evolutionary processes, and centriole chirality may be one of several contributing factors rather than the sole determinant. It is crucial to conduct further research integrating molecular genetics, developmental biology, and evolutionary theory to fully understand this relationship.  **4.3. Bilateral Symmetry and Centrosomes**  This section introduces a thought-provoking hypothesis on the role of centrosomes in bilateral symmetry. However, it's crucial to underline that this hypothesis, while intriguing, is heavily reliant on theoretical models and analogies. The absence of sufficient empirical support is a significant gap that needs to be addressed to enhance the credibility of the hypothesis.Cite experimental studies that examine the molecular mechanisms of centrosome-mediated symmetry. It's crucial to maintain precision in scientific language and avoid overgeneralizations across species. This will ensure that the hypothesis is accurately applied and understood within the context of developmental biology.It's essential to delve into alternative explanations for left-right asymmetry, particularly the role of cilia and nodal signalling in vertebrates. This comprehensive approach will enrich the discussion and provide a more holistic view of the topic.Provide evidence or references to studies supporting the claim that a simple genetic mutation could result in rotationally symmetric centrosomes.  **4.4. Bilateral Symmetry and TRs**  Emphasize the importance of providing empirical data or references to experimental studies supporting the proposed function of TRs in spindle orientation. This will ensure that our audience feels well-informed and confident in the research proposal.  Emphasize the need to clarify terminology and avoid excessive reliance on computational analogies that may not translate directly to biological reality. This will reassure our audience and ensure they have a clear understanding of the concepts.  Stress the importance of discussing alternative mechanisms for spindle orientation to give a more balanced perspective. This will make our audience feel open-minded and considerate of different perspectives. Address potential limitations of the model, including the impact of cellular microenvironments on morphogenesis.  **4.5. A Second Evolutionary Lever to Accelerate the Genomic Capacity of Creating Novelties**  The section presents an intriguing but largely speculative hypothesis. While TRs are highly dynamic and can contribute to genetic novelty, their direct role in shaping morphology through cell division control remains unsupported by empirical data. A more cautious and evidence-based discussion is necessary.  **5. Discussion**  Provide more direct experimental evidence linking TRs and centrosomes to morphogenesis.  Clarify whether correlations imply causation and acknowledge alternative factors influencing symmetry.  Balance computational models with empirical validation, discussing their limitations.  Address counterarguments, such as morphogen-based models of symmetry formation.  **6. Conclusion**  Overall, while the hypothesis is thought-provoking, the conclusion requires refinement in clarity, evidential support, and mechanistic explanations to strengthen its scientific credibility. |  |
| **Are the references sufficient and recent? If you have suggestions of additional references, please mention them in the review form.**  **-** | The reference list contains a mix of older and more recent publications, Authors should onsider to replace older studies with recent reviews/meta-analyses (2018–2024) on tandem repeats, genome instability, and forensic genetics.. Also, the authors should consider incorporating forensic-specific references if your work is related to forensic science, particularly forensic DNA markers. Additionally, check for missing landmark papers from 2022–2024 in fields such as repetitive DNA evolution, genome stability, and forensic genetics. |  |
| Is the language/English quality of the article suitable for scholarly communications? | Yes |  |
| Optional/General comments | While the article presents an interesting computational hypothesis, it requires stronger empirical support and a more nuanced discussion of biological complexity. |  |

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| **PART 2:** | | |
|  | Reviewer’s comment | Author’s comment *(if agreed with the reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)* |
| **Are there ethical issues in this manuscript?** | *(If yes, Kindly please write down the ethical issues here in detail)* |  |