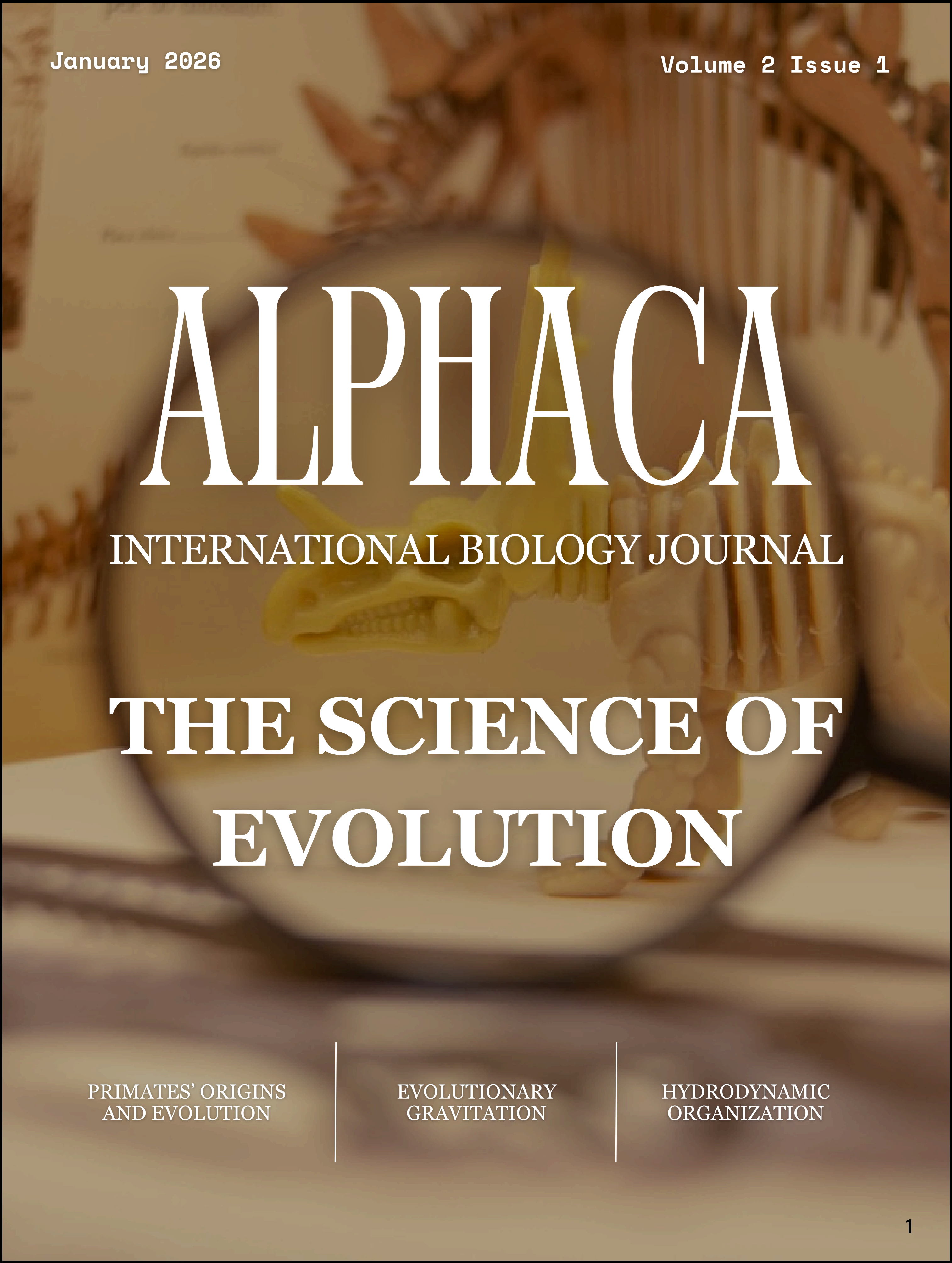

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INTERNATIONAL BIOLOGY JOURNAL

THE SCIENCE OF EVOLUTION

PRIMATES' ORIGINS AND EVOLUTION

EVOLUTIONARY GRAVITATION

HYDRODYNAMIC ORGANIZATION

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Citations for the articles referenced, listed in the order by which they appear in the journal publication.

Wang, Zirui. "View of the Origin and Evolution of Primates." Drpress.org, Darcy & Roy Press, 2024, drpress.org/ojs/index.php/HSET/article/view/21957/21495. Accessed 28 Jan. 2026.

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THE ORIGIN AND EVOLUTION OF PRIMATES

An overview of primate evolutionary history and the genetic mechanisms shaping modern lineages.

Original Article by: Zirui Wang
Digest by: Nicole Ekanem

Lots of progress regarding the study of human evolution (paleoanthropology), genetics and comparative behavior of primates, but multiple issues about human evolution still exist (i.e. environmental factors, behavior/social structure of early primates, etc). Studying the origin and separation process of different primate species, like humans, evolution of them, both genetically, socially and physiologically will aid us in understanding the nature of human beings themselves, our connections with other organisms, as well as human culture. This study, through exploring fossil records, genetic data, and primate behaviour studies, will provide a thorough explanation of human evolution.

A study done by researchers on guenons, a group of African primates, was done, and it showed that gene flow and ancient hybridization occurred often between lineages, even though they had ecological and physical differences. Hybridization seems to have played an important role in adaptation and the diversification of species, especially through immune-related genes, unlike traits like pigmentation and morphology that seem to have contributed to reproductive isolation. These results show that reproductive barriers are not definite, that genes can be exchanged across distinct species, challenging the traditional views of species evolution.

Figure 1: Guenon Primate

Existing research shows that primate sex chromosomes, particularly the Y chromosome, which is used to help understand male-specific traits and disorders, shows conclusive evidence of the quick evolution and diversification of the Y chromosome in primates, as shown in Figure 2. This reflects a complicated history of structural changes and gene modifications, which have contributed to different phenotypes, which are "observable characteristics or traits in an individual based on the expression of their genes. The phenotype is determined by the individual's genotype and possibly influenced by other factors, such as environmental factors," according to the National Cancer Institute. But these findings have limitations due to incomplete genetic sequences and potential gaps in the data, which could possibly affect the generalizability of the findings.

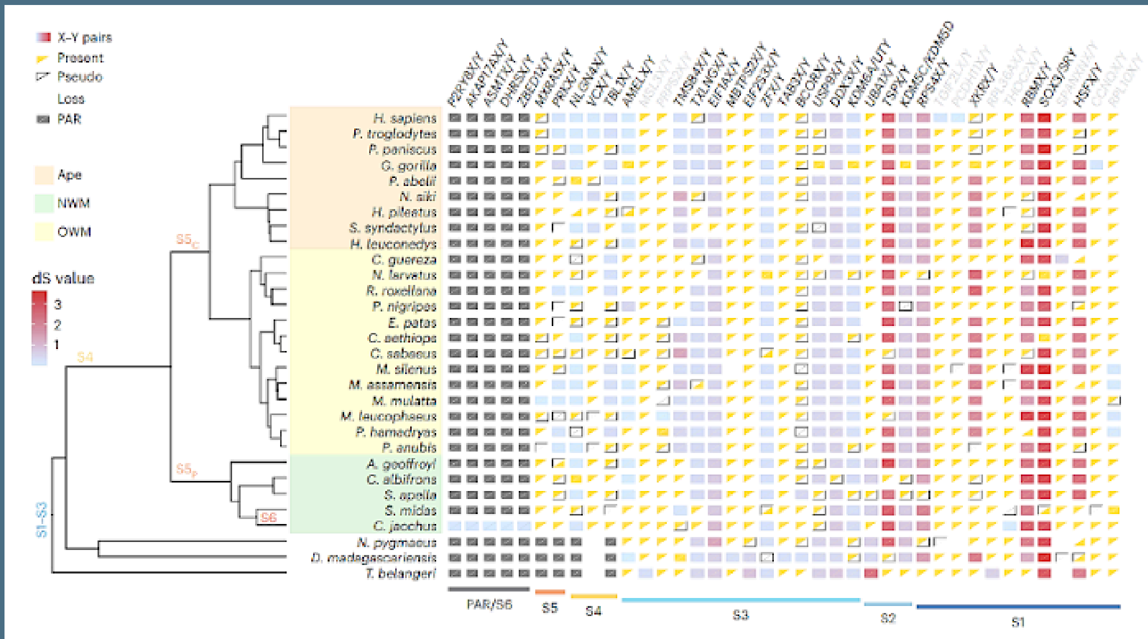

Figure 2: X/Y Gametologues and the Evolutionary Strata

Regulatory sequences have evolved rapidly in the primate lineage, and by using comparative genomic, transcriptomic, and epigenomic analyses, the brain genes' evolution and regulatory sequences from ancestral primates to humans have been highlighted. The rapid evolution of regulatory sequences are seen to drive high cognitive functions and increased brain complexity, possibly influencing key developmental processes and the cognitive and neural complexity characteristics in primates, including humans. Unfortunately, applying this to every primate lineage and species is difficult because of various evolutionary histories.

APOL1 is a gene that has been studied, and has evolved uniquely in primates and has been connected to kidney disease and potentially harmful effects when misoriented in the endoplasmic reticulum. APO2, unlike APO1, is not considered to be toxic. These genes were found across different species, indicating ancient origins, and the cellular localization of APO1 variants were studied, showing that it can insert into the endoplasmic reticulum membrane in different shapes and orientations.

The findings also contribute to the understanding its role in human disease, especially in kidney function and pathology. The practical uses in a clinical setting may need further translational research to be completely understood and applied.

The genetic mechanisms driving the brain evolution of primates, with a focus on humans, were analyzed regulatory elements that evolved rapidly in the ancestors of Simiiformes, which is a suborder that includes humans. These rapidly evolving conserved elements (RECEs) were investigated using comparative genomics and various bioinformatics, and they may play an important role in human brain development, advanced cognitive development, and neurodegenerative diseases, like Alzheimer's. The findings support the idea that changes in gene regulation, rather than just protein-coding genes, were crucial in shaping the complex primate brain. Some limitations include difficulty in establishing direct causal roles of RECEs because of lack of direct experimentation, as well as the biases and some novel elements not yet characterized being overlooked due to the reliance on available databases and bioinformatic predictions.

A reverse chemical ecology approach was used to investigate the evolution of pheromone detection in primates, from lemurs to humans, by analyzing soluble carrier protein (SAL) orthologs from different species. The results show that SAL proteins have conserved ligand-binding properties across primate evolution, with large macrocyclic ketones and lactones identified as the most likely pheromone candidates. These compounds may have been used for chemical communication in early human ancestors before the SAL gene became nonfunctional in humans. Some strengths of this study are its innovative approach and comparative analysis across primate species, which gives insight into the evolution of pheromone communication. But, the study has some flaws, such as assumptions being made based on ligand-binding properties without direct behavioral or ecological evidence, as well as the challenge of generalizing findings from a few species to the complexity of pheromone communication in primates.

Previous research has shown that rapidly evolving regulatory sequences have played a major role in primate brain evolution. Using comparative genomic, transcriptomic, and epigenomic analyses across primate species, these studies identify regulatory elements, like promoters, silencers, insulators, and enhancers that influence gene expression location and timing. These elements are essential for brain developmental processes like neurogenesis, synaptic plasticity, and neuronal differentiation, and may explain the advanced cognitive ability seen in humans. Strengths of this work are the use of comprehensive omics technologies and the cross-species analysis of regulatory sequences. Weaknesses include the challenges of interpreting complex genomic data and the applicability of the findings across all primate species.

Another study focuses on DNA methylation to reconstruct primate phylogenetic trees.

It shows that CpG methylation levels, except for enhancers, have enough evolutionary information to produce phylogenies that could be compared to those based on nucleotide sequences. The research finds that methylation at individual CpG sites is highly conserved and predicts methylation rates in one species better than the closest neighboring CpGs within the same species. It also highlights the role of epigenetic conservation in controlling transcription factor binding density and accelerated CpG methylation evolution in humans within key pathways like the Polycomb Repressive Complex 2 and telomerase. Even though this approach represents the potential of integrating genomic and epigenomic data in understanding the evolution of gene regulatory mechanisms, the methodology’s success heavily depends on the quality and quantity of the data, and its focus on primates limits how broadly it can be applied

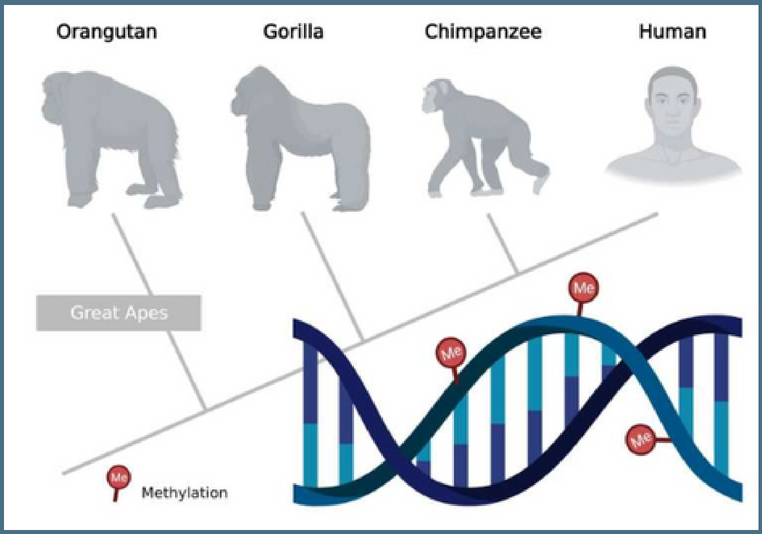

Figure 3: Epigentic changes in DNA, e.g. through methylation, can be used to reconstruct phylogentic trees

This entire article provides a comprehensive overview of primate brain evolution, especially in humans, showing that complex brain structures and cognitive functions are shaped by rapidly evolving regulatory sequences that influence gene expression. It highlights the value of DNA methylation data in revealing evolutionary relationships, species diversity, and brain development in humans. The role of gene flow and interspecies hybridization in primate evolution is also emphasized in the research. Combined, these findings deepen researchers' understanding of human origins and brain evolution while providing crucial implications for biodiversity conservation, disease prevention, and treatment, while improving human self-awareness of origins and health.

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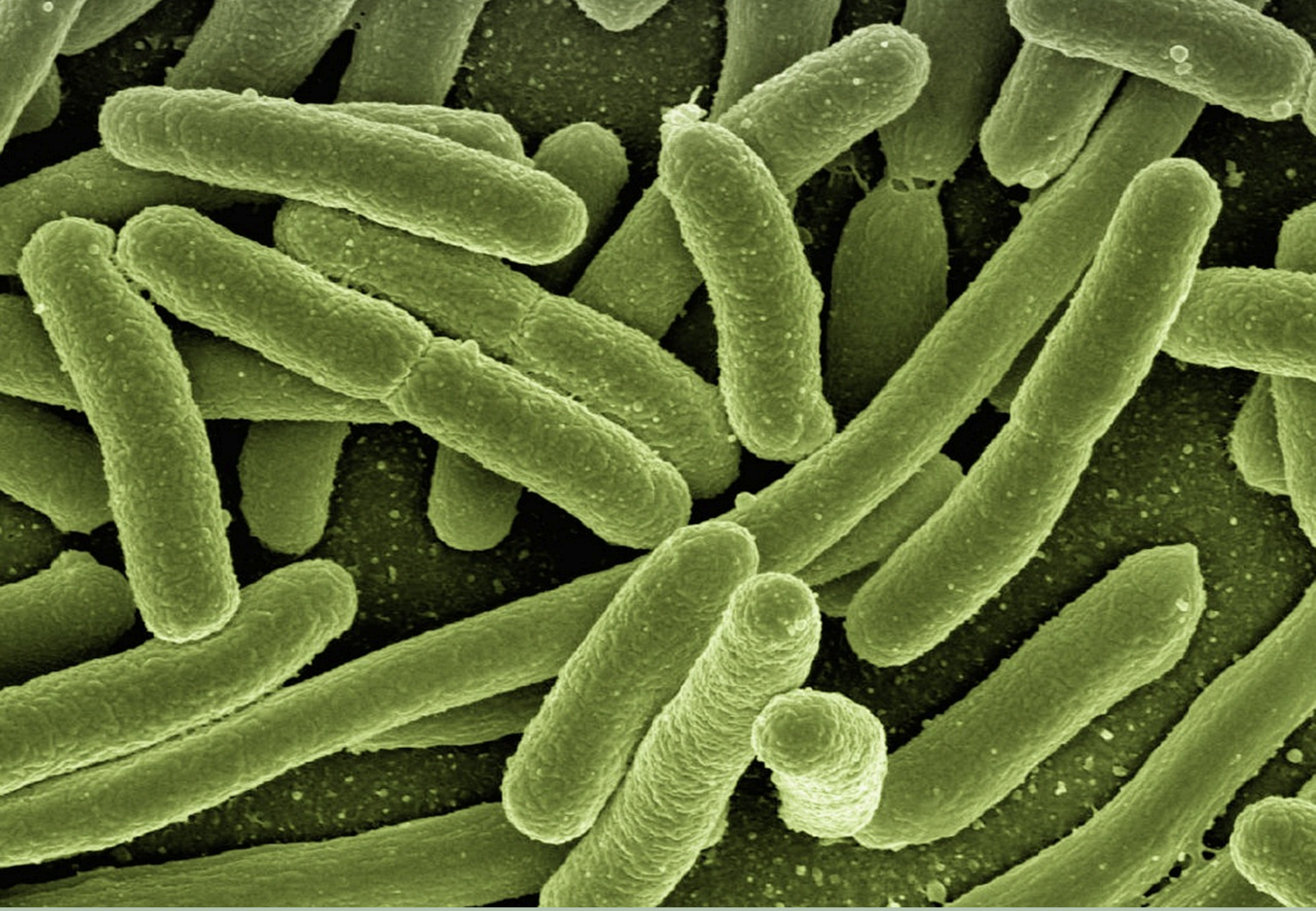


EVOLUTIONARY GRAVITATION: HOW BACTERIA 'CHOOSE' THE FITTEST PATH

Original Article by:
Haoyuan Wu & Yonghua Wu

Digest by: Daniella Ling

Most people know Darwinian evolution as the idea that the “fittest” traits survive. Traditionally, this means that small variations in a trait—for example, running speed in wolves or nectar production in flowers—can make a difference in survival and reproduction. Over time, these beneficial traits become more common in a population. However, this traditional view mainly describes evolution within a single adaptive path—it explains how a trait can improve but does not explain why species often evolve in one direction and not others, even when multiple options could work.

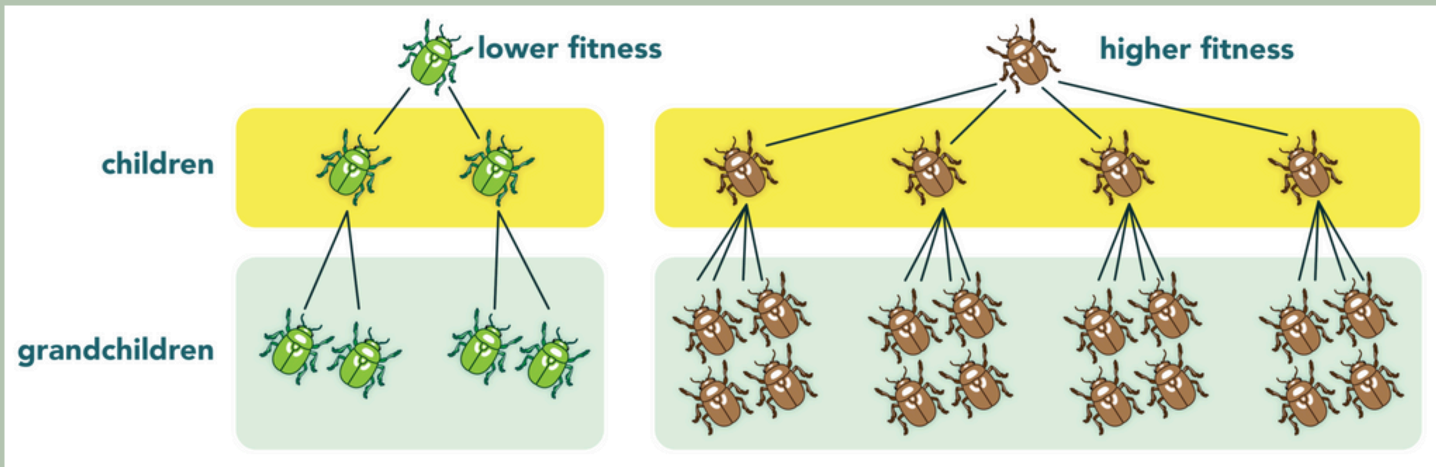


Figure 1: Population gravitating towards the higher-fitness path

This study looks at this question using Escherichia coli (E. coli), a common bacterium. The strain we used, called K-12 GM4792, normally cannot digest lactose because it has a deletion in the genes responsible for lactose metabolism. Sometimes, random mutations can restore this ability, producing lactose-utilizing mutants called lac+. By observing how these mutants compete with the original lactose-negative (lac-) bacteria, we investigated a broader form of natural selection, which we call inter-directional selection. In this process, different "adaptive directions" (strategies for survival and growth) compete with each other, and the most successful one dominates. Understanding this helps explain why evolution seems biased toward certain paths rather than exploring all possibilities equally.

Tracking Competition and Fitness

To study how bacteria decide—or are "pushed"—toward the fittest path, E. coli grew in two types of nutrient solutions. One, called L medium, contained lactose and acetate. The other, G medium, contained lactose and glucose. In L medium, only lac+ bacteria can digest lactose, giving them a potential advantage. In G medium, lac- bacteria can survive on glucose, giving them an advantage there.

They tracked which bacteria were lac+ or lac- using blue-white screening, a simple method where lactose-digesting colonies turn blue and non-digesting colonies stay white. This allowed us to see how the populations changed over time.

Growth curves, tracking how fast bacteria grow over time, were also measured alongside carbon consumption analysis, which shows how efficiently bacteria use the available food. By comparing growth rates and nutrient use, metabolic ability could be linked to competitive success.

Finally, DNA of the bacteria was sequences to see what mutations occurred. This step revealed exactly which genes changed to restore lactose metabolism and showed whether different populations evolved similar or different mutations. By combining genetics, metabolism, and competition, we could observe how evolution works on both the genetic and population level.

Inter-Dimensional Selection: Choosing the Fittest Path

The experiments showed a clear pattern: in L medium, lac+ mutants grew faster and outcompeted lac- bacteria. This is inter-directional selection in action. Unlike traditional Darwinian selection, inter-directional selection compares entire adaptive strategies. The "direction" that produces higher growth and survival dominates, while the weaker strategy is gradually eliminated.

It was also seen that this selection creates evolutionary bias. Bacteria don't randomly explore all possible paths—they are "pulled" toward the one with the highest fitness. We call this phenomenon evolutionary gravitation. It works much like gravity: populations are attracted to the most productive path and kept from exploring less profitable ones.

For example, aphids tend to eat young leaves because they provide better nutrition. Similarly, lac+ bacteria dominate in lactose-rich environments because lactose metabolism provides higher growth gains. In both cases, the environment shapes which adaptive direction is favored, creating a predictable evolutionary path.

Linking Genetics, Growth, and Competition

The DNA sequencing results helped explain why lac+ bacteria were so successful. Different lac+ strains had slightly different mutations in the lactose operon, but all restored the ability to digest lactose. This shows genetic convergence: different mutations can lead to the same adaptive result if it improves survival.

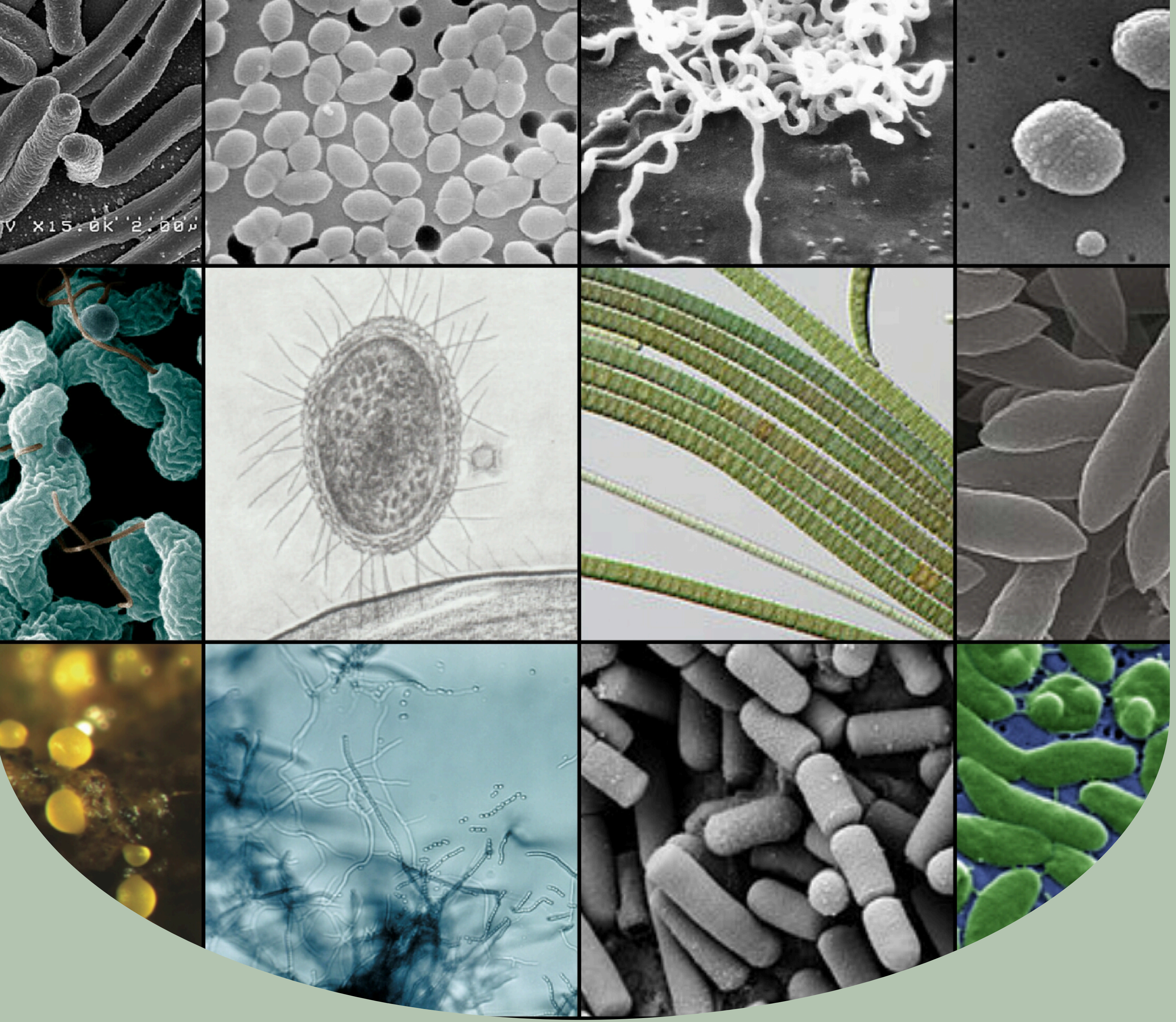
Growth curves and nutrient measurements confirmed the competitive advantage. Lac+ populations grew faster and used lactose efficiently, while lac- populations struggled to survive on acetate alone. When paired in competition experiments, lac+ bacteria consistently increased in number while lac- declined.

Together, these results show that evolution is shaped by both the genetic changes that occur and the competitive environment. Traditional selection explains how traits improve along one path, but inter-directional selection explains why certain paths are chosen over others. High-fitness strategies dominate not only by growing faster but also by limiting opportunities for less-fit alternatives.

Conclusion: The Direction of Evolution

This study demonstrates that evolution is not simply a collection of random improvements. It is guided by competition between different adaptive strategies, producing what is known as evolutionary gravitation. High-fitness strategies dominate and suppress weaker strategies, causing populations to consistently evolve along particular paths.

In the case of E. coli, lac+ mutants thrived in lactose-rich conditions while lac- bacteria declined, showing how inter-directional selection shapes population outcomes. This principle likely applies to many organisms and environments: evolution is biased toward the most rewarding strategies, not random exploration. By combining genetic, metabolic, and ecological data, we can see how natural selection operates on multiple levels, guiding species along specific evolutionary paths. This concept helps explain why some adaptations repeatedly appear in nature, why certain ecological niches are filled predictably, and how evolutionary "choices" are made in response to environmental opportunities.



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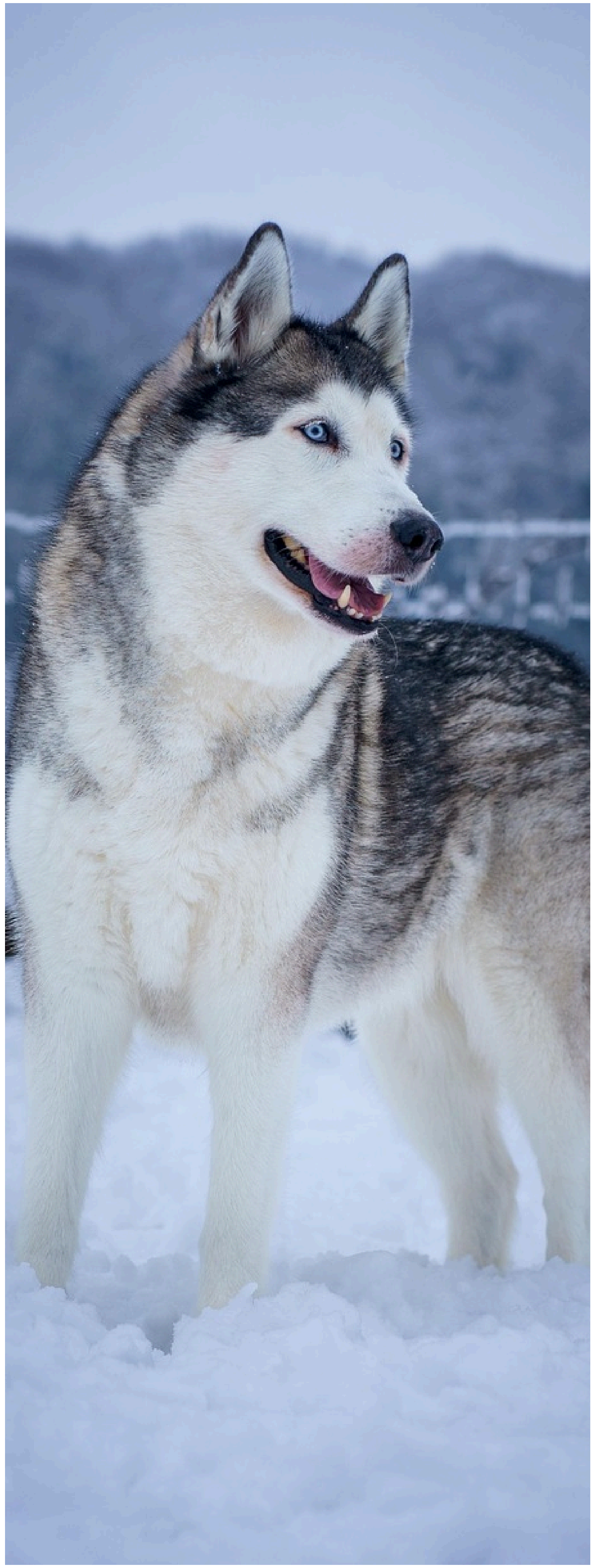

THE ROLE OF LEARNING AND SAMPLING STRATEGIES IN HYDRODYNAMIC ORGANIZATION

Original Article by: Long Zheng & Shunhuai Chen
Digest by: Nathan Zhuang

In recent years, the field of Differential Evolution (DE), the act of iteratively optimizing complex mathematical or engineering problems, has advanced at an alarming rate. The goal of DE is to improve design efficiency and performance based on specific environmental requirements, thus minimizing both energy loss and operational cost. Traditional DE algorithms have been extensively employed in a wide range of optimization tasks; however, their practical performance is often hindered by issues such as premature convergence and limited search efficiency.

This has allowed the rise of a novel variant termed Learning and Sampling strategies collaborative Aided Differential Evolution (LADE). The reason that this is significant is due to the help it gives in navigating high-dimensional search spaces and finding effective global solutions based on data-driven variations. This shift mirrors the transition in medicine from broad-spectrum treatments to personalized care, where the algorithm no longer guesses the best path but learns the "genetic" blueprint of the problem at hand to make informed decisions.

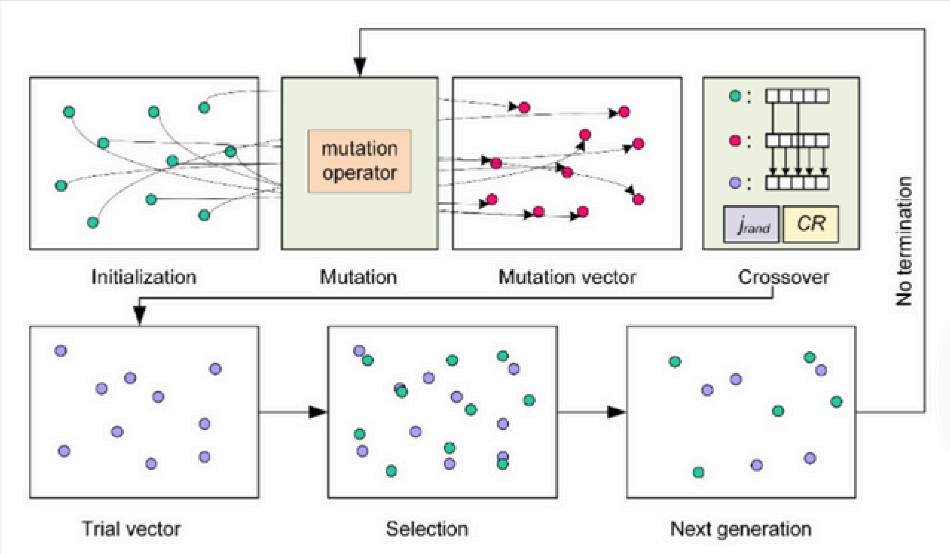

Figure 1: Graphical Abstract of the LADE Model

The Foundation of LADE

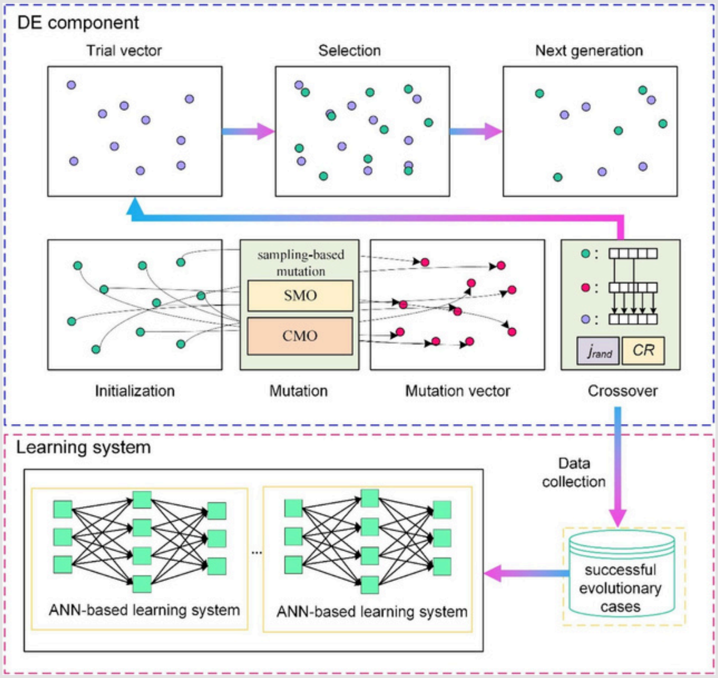

Figure 2: ANN-based learning system incorporated into the pipeline

The foundation of LADE was laid through decades of research into metaheuristic algorithms and modern machine learning frameworks, evolving from simple trial-and-error methods into highly sophisticated, self-correcting systems. Just as early genomic projects mapped the human genetic structure to understand disease, researchers in the maritime engineering field have mapped the complex "fitness landscapes" of fluid dynamics to understand how water interacts with metal.

This international initiative to enhance DE successfully integrated an artificial neural network (ANN) into the evolutionary loop, creating a synergy between raw computational power and intelligent prediction. This collaborative approach is driven by an ANN-based Learning System that acts much like a physician analyzing a patient's historical genomic data to predict future health outcomes. It specifically extracts knowledge from successful evolutionary cases, instances where offspring surpassed their parents in performance, to dynamically predict and control key parameters like the scaling factor (F) and crossover rate (Cr). By learning from the successes of the past, the algorithm avoids the "side effects" of poor parameter choices that lead to stagnation. Alongside this, a Sampling-aided Mutation Operator (SMO) works by identifying potential "genetic" variations in the population to construct localized search subspaces. This process identifies promising directions for improvement, contributing to the diversity of the candidate solutions and preventing the algorithm from getting stuck in a local optimum, which is the mathematical equivalent of a biological dead end.

Significant Results in Engineering

Just as genetic profiling identifies risks for diseases before they manifest, LADE identifies the most effective paths to an optimal engineering solution with unprecedented foresight. The effectiveness of this method was validated through rigorous and extensive testing on international benchmark problems, including the highly challenging CEC2017 and CEC2022 sets. In these tests, LADE demonstrated a better ability to find global minima in complex, non-convex functions that typical algorithms failed to resolve. In a practical application involving a full CFD-based (Computational Fluid Dynamics) hydrodynamic propeller optimization, the algorithm demonstrated its real-world utility by successfully improving the propeller's efficiency by approximately 5.1% compared to the original design.

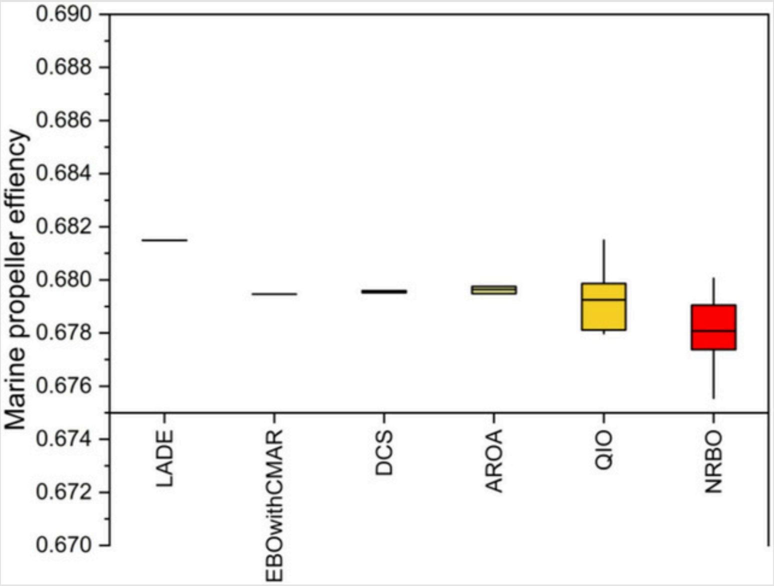

Figure 3: Results for varying pipeline efficiencies

This is not merely a theoretical gain; it represents a massive reduction in fuel consumption and carbon emissions for large-scale vessels. Furthermore, it managed the complex trade-offs of constraint management by maintaining all necessary thrust requirements while simultaneously reducing torque. This delicate balance is comparable to the precision required in balancing medication dosage to maximize therapeutic effect while strictly avoiding toxicity. Finally, experimental results indicate that LADE achieves significantly higher precision and stronger robustness than state-of-the-art algorithms, much like how modern high-throughput sequencing provides more accurate diagnoses than traditional, manual imaging techniques.

Hurdles & the Future

Despite its transformative potential, LADE faces certain hurdles that reflect the early days of any technological revolution. Currently, the implementation is computationally expensive for widespread commercial use, as it requires massive high-performance computing resources to run the CFD simulations that verify each iteration. Another major issue is the complexity of the data archive itself; while a larger archive of evolutionary data undoubtedly improves the ANN's accuracy, it also creates a data management burden. Much more research is needed to allow these systems to be implemented into everyday industrial design processes without the overhead costs that currently restrict them to high-end research facilities.

The future of LADE lies in the deeper integration of evolutionary data with other engineering disciplines. Just as the Updated Genomic Model (GIFT) shows a multidisciplinary approach to medicine, the integration of surrogate models, which act as digital twins of the physical propeller, with LADE could further reduce the cost of extensive testing. This would allow engineers to simulate thousands of variations in a fraction of the time and at a fraction of the cost. Personalized engineering through LADE represents a huge shift in the field, moving away from "one-size-fits-all" propeller designs toward components tailored for specific ship types and environmental conditions. By using data-driven information, it not only enhances our ability to optimize ship hulls and propellers but also paves the way for greener maritime strategies that improve overall energy outcomes across the globe. As research progresses and computing power continues to follow its own version of Moore's Law, the computational cost for LADE should become more accessible to all small and medium-sized shipyards. Integration of LADE into mainstream industrial design holds the promise of a more efficient, sustainable, and more precise future for all.

References & Comparisons

Standard Differential Evolution remains a broad and reliable tool in the engineer's toolkit, yet it is often slow to find the perfect solution in complex landscapes because it lacks the ability to learn from its own history, essentially treating every new generation as if it were starting from scratch. In contrast, the LADE algorithm utilizes an Actionable Knowledge Threshold through its integrated Artificial Neural Network to significantly speed up results by identifying which parameter adjustments are most likely to yield success based on previous generations.

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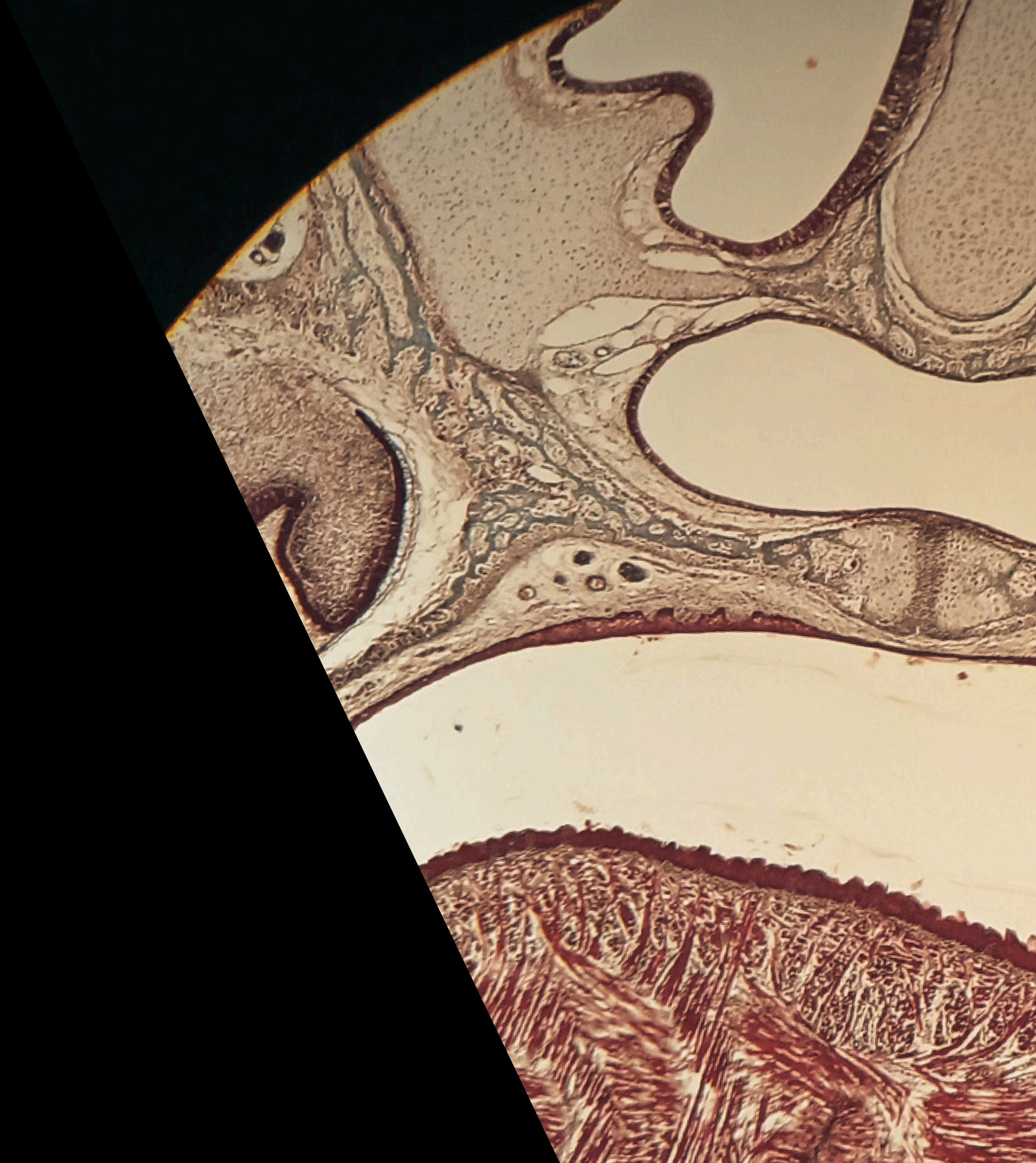
Zheng, L., & Chen, S. (2026). A learning and sampling strategies collaborative aided differential evolution algorithm and application in hydrodynamic optimization. Results in Engineering, 29, 109261. https://doi.org/10.1016/j.rineng.2026.109261


“Nothing in biology makes sense
except in the light of evolution.”
- Theodosius Dobzhansky



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