Scientific Research Publishing

Journal of Quantum Information Science, 2026, 16(3), 387-397
https://www.scirp.org/journal/jqis
ISSN Online: 2162-576X
ISSN Print: 2162-5751

Bio-Quantum Evolution of the Human Brain

Jianzhong Zhao

Department of Geophysics, Yunnan University, Kunming, China
Email: jzhzhao@ynu.edu.cn

How to cite this paper: Zhao, J.Z. (2026) Bio-Quantum Evolution of the Human Brain. *Journal of Quantum Information Science*, **16**, 387-397.
https://doi.org/10.4236/jqis.2026.163013

Received: June 11, 2026
Accepted: August 21, 2026
Published: August 24, 2026

Abstract

The human brain evolves generation by generation. In the present paper I discover, by means of theoretical research into the process of gene transmitting and inheriting of a typical family (a family without loss of its any genes), that the bio-quantum computational speed (the Grover Iterations per second) of mankind increases in the human hereditary process. That means that the ability of the human brain (the central processing unit of biological information and controller of biological process of humans) to control bio-quantum computation strengthens or develops in the human hereditary process. This is the bio-quantum evolution of the human brain. Thus, this work explores the bio-quantum mechanical nature of human brain evolution.

Keywords

Modern Theory of Genetics, Modern Theory of Evolution of the Human Brain, Quantum Biology, Bio-Quantum Computation, Bio-Quantum Evolution of the Human Brain, Law of Evolution of Human Bio-Quantum Intelligence, Bio-Quantum Selection

1. Introduction

Exploration of biological evolution is an important and significant subject of biology, genetics and anthropology. Modern theories of human brain evolution, based on modern genetic theories, have been developed. Volume of researches on human brain evolution, in terms of development of human genes, DNA and genome, has been published.

Enard, W. *et al.* study molecular evolution of a gene related to development of human speech and language [1]. Dorus, S. *et al.* examined the evolution of genes involved in human nervous system development [2]. Evans, P. D. *et al.* find that an important brain gene, Microcephalin (MCPH1) regulating brain size, has continued to evolve adaptively in modern humans [3]. Mekel-Bobrov, N. *et al.* find

that one genetic variant of ASPM, a specific regulator of brain size in humans, arose merely about 5800 years ago and has since swept to high frequency under strong positive selection, suggesting that the human brain is still undergoing rapid adaptive evolution [4]. Results of Prabhakar, S. *et al.* suggest that widespread cis-regulatory changes in human evolution may have contributed to unique features of development and function of the human brain [5]. Pollard, K.S. *et al.* show that the ability to compare our genome to that of our closest relative, the chimpanzee, presents new approaches to link genetic and phenotypic changes in the evolution of the human brain [6]. McLean, C.Y. *et al.* search for putative regulatory mutations specific to the human lineage by looking for sequences deleted in the human genome, illustrated by means of two examples, one of which affects brain size [7]. Paar, V. *et al.* identify two particular intragene repeat structures of noncoding human DNA, genomic patterns underlying the evolution of the human brain and its emergent advanced cognitive capabilities [8]. The results of Charrier, C. *et al.* show that inhibition of SRGAP2 function by its human-specific paralogs has contributed to the evolution of the human neocortex and plays an important role during human brain development [9]. Somel, M. *et al.* review a strategy to yield some of the first hints about the mechanisms of human cognition [10]. Geschwind, DH and Rakic, P. describe how advances in neurobiology, associated with those in genetics, provide insights into the evolutionary mechanisms in the human cerebrum to understand the emergence of human higher cognition [11]. Boyd, J. L. *et al.* conclude that changes in HARE5 function unique to humans alter the cell-cycle dynamics of a critical population of stem cells during corticogenesis and may underlie some distinctive anatomical features of the human brain [12]. Florio, M. *et al.* find that human-specific gene ARHGAP11B may have contributed to evolutionary expansion of human neocortex [13]. Fiddes, I.T. *et al.* Discover that the emergence of human-specific NOTCH2NL genes may have contributed to the rapid evolution of the larger human neocortex [14]. Heide, M. *et al.* show that the human-specific gene ARHGAP11B drives changes in development in the nonhuman primate marmoset that reflect the changes in evolution that characterize human neocortical development [15]. Trujillo *et al.* conclude, in their article, that the reintroduction of an ancestral amino acid substitution in the protein NOVA1 drastically alters the development of brain organoids. The comment of Maricic, T. *et al.* shows that cell lines used by the authors carry heterozygous deletions of the target DNA sequence, providing another plausible explanation for the effects observed [16]. The comment of Herai, R. H. *et al.* shows that the "putative Neanderthal variant" of TKTL1 is present in modern human backgrounds, disputing the argument that this genetic variant is responsible for brain differences in modern humans as opposed to Neanderthals [17]. Joshy, D, Santpere, G and Soojin, V.Y. support the acceleration of cell-type-specific functional programs as an important feature of human brain evolution [18]. Rickelton, K. *et al.* identified genes with variation in expression most correlated with brain siz [19]. Cui, X. *et al.* find the endogenous gene regulatory functions of HARs, potentially contributing to

human brain evolution [20]. Pal, A. *et al.* support that HARs alter the expression of ancestral gene targets shared between human and chimpanzee, influencing brain evolution [21]. Soto, D.C. *et al.* discover two genes, GPR89B and FRMPD2B, possibly contributing to hallmark features of the human brain [22]. The study of Kaur, N. *et al.* advances the knowledge of the development and evolution of the ventrolateral pallial (VLp) [23]. Zhang, D. *et al.* discuss human brain development, exploring its spatial dynamics [24]. Rickelton, K. and Babbitt, C. C. understand the evolution of astrocytes across primates, focusing on gene expression evolution and gene regulation in astrocytes [25]. Raza, R. Z., Nazir, F. and Abbasi, A.A. build a perspective on an already determined set of human accelerated brain enhancers (HABEs) with 34 putative target brain genes for their role in human cognitive enhancements. They conclude that HABE, associated with IRX3, and the Homo sapiens-specific substitution P422L in the IRX3 protein serve as examples of the accelerated evolution of human brain regulatory circuits [26]. Liu, Y., Li, J. and Liu, Q. find that the inactivation of CMAH (CMP-N-acetylneuraminic acid hydroxylase), resulting from natural selection, reduced the level of N-glycolylneuraminic acid (Neu5Gc) in brain tissue. And the low level of Neu5Gc promoted the development of human brain tissue [27]. Soorajkumar, A. *et al.* synthesize current knowledge of brain cell diversity and highlight key gene markers that define cellular identity and function, exploring how cellular diversity shapes brain function and contributes to disease mechanisms [28]. Chen, Y.-C., Maupas, A. and Nowick, K. developed a software TEKRABber to reconstruct regulatory networks of TEs (transposable elements) and KRAB-ZNFs (TE silencing factors KRAB zinc finger genes) during human brain evolution. They discovered that the human brain displays a notably denser TE:KRAB-ZNF network compared to NHPs, particularly for more recently evolved TEs and KRAB-ZNFs [29]. Liu, J. *et al.* find that small changes in regulatory DNA can directly affect critical signalling pathways to modulate human brain development, uncovering new functions of HARs (Human accelerated regions) as key regulatory elements crucial for the expansion and complexity of the human cerebral cortex [30]. Caglayan, E. and Konopka, G. use DNA sequence substitutions within cellularly resolved GREs (gene regulatory elements) to gain insight into human brain evolution, and identify ancestral evolutionary patterns of the human brain epigenome at cellular resolution [31]. Yoo, D.A. *et al.* present complete sequencing of ape genomes for their study of evolution of humans and our closest living ape relatives [32]. In their discussion, the expansion, contraction and restructuring of SDs lead to concurrent gene innovation and chromosomal structural changes [32]. In the case of humans, three gene family expansions, namely NOTCH2NL, SRGAP2C and TBC1D3, have been functionally implicated over the past decade in the expansion of the frontal cortex of the human brain [32].

All researches and results above are based on biological chemistry.

Quantum biology's origins are often traced back to 1944 and the publication of Erwin Schrödinger's famous book, What is Life? [33] [34]. In the book, the author

declares three results. Firstly, the durability or permanence of genes is unexplainable by classical physics, but is explicable by quantum theory. The mechanism of heredity is closely related to, or founded on, the very basis of quantum theory. Secondly, it seems possible to point out in a more direct manner the connection between "quantum jumps" and mutations of genes. Thirdly, new physical laws are expected in the organism, and the new physical principle is nothing else than the principle of quantum theory over again [33]. Quantum biology is a field of research that applies quantum theory to understand biology, and has unique contributions to life science. Researchers made contributions to quantum biology [33]-[47]. Davies, P. reviewed researches suggesting that living systems process information quantum mechanically, and life will eventually be created as a by-product of quantum information processing and nanotechnology [34]. McFadden, J. developed an evolution theory resorting to quantum tunnelling in base pair formation [35]. McFadden, J. and Al-Khalili, J. reviewed the origin and development of quantum biology, arguing that some of the insights of those quantum pioneers of the early twentieth century, including Erwin Schrödinger, remain relevant to our understanding of quantum biology today [36]. The result of Dikshit, B. shows that life originates out of establishment of quantum coherence in a group of inanimate particles [37]. Tuszynski, J. A. discussed quantum consciousness, commented, based on quantum theory, on the merits, challenging issues and possible developments of the hypotheses suggested to introduce a scientific basis to consciousness theory [38]. Kim, Y. *et al.* reviewed the progress in quantum biology, concerning the areas of enzyme-catalysed reactions, photosynthesis, spin-dependent reactions, DNA, fluorescent proteins and ion channels, and discussed questions, challenges, expecting further development of quantum biology [39]. Ogryzko, V. V. and McFadden, J. & Al-Khalili, J. study directed or adaptive mutations, based on the principles of quantum theory [40] [41]. Pullman, B. reviewed developments in the quantum mechanical researches on the electrical structure of the nucleic acids [42]. Steele, R. H. discussed the quantization of simple systems in quantum theory, introducing quantum physics into biology in an intuitive way [43]. Wu, L.-A., Wu, S.S. and Segal, D. demonstrated a universal DNA breathing dynamics by means of an approximate method in quantum mechanics [44]. Ruggiero, M. and Pacini, S. discuss quantum processes of DNA that have played a role in the evolution of the human brain and consciousness [45]. Zhao, J. established the System of Bio-Quantum Genetics; proposed the Bio-Quantum Genetic Model of Plant Heredity, theoretically proving Mendel's results of experiments on plant hybrids; suggested the Bio-Quantum Genetic Model of Human Genetics, explaining human normal inheriting, reversion and atavism [46]. Zhao, J. discussed DNA forming and replicating process within the theoretical framework of the System of Bio-Quantum Genetics established in [46] and reached the conclusion that DNA forming and replicating is a process of bio-quantum entangling, de-entangling and re-entangling [47].

In the present paper, I apply quantum mechanics to understand evolution of

the human brain. A typical human family provides the baby with the genes of his/her seniors, and the baby searches the genes of the seniors for his/her parents' ones and inherits them. In terms of quantum mechanics, an initial bio-quantum state of the seniors' genes of the human family is established, and the baby searches the initial bio-quantum state of the seniors' genes for the bio-quantum state of his/her parents' genes. The search succeeds by using Grover's fast quantum mechanical algorithm for database search [48]-[51], operating $O\left(\sqrt{N}\right)$ Grover Iterations. Thus, it is found that the ability of the human brain to process bio-quantum information, or, to control bio-quantum computation, strengthens or develops in the human hereditary process. This is bio-quantum evolution of the human brain, or development of human bio-quantum intelligence (human intelligence defined and explored by means of quantum mechanics and quantum computation). Then a law of human bio-quantum intelligence is suggested, consistent with Schrödinger's expectation [33]. Then bio-quantum selection (selection defined and explored by means of quantum mechanics and quantum computation) is suggested.

2. Modeling Human Family in Terms of Quantum Mechanics

A typical human family consists of n generations of seniors and an offspring baby ($n \gg 1$). Every senior is probable to transmit his/her genes to the baby. Because of this, it is possible for the parents of the baby to transmit their genes to the baby (normal heredity), and, it is possible for the grandparents of the baby to transmit their genes to the baby (reversion), and, it is possible for the remote ancestors of the baby to transmit their genes to the baby (atavism). In fact, normal heredity, reversion and atavism are three phenomena of human genetics.

Genes are micro-entities, ruled by laws of quantum mechanics, the physical science of the micro-world. Also, genes are bio-quantum bits, controlled and transformed by quantum computation. Therefore, the underlying physical mechanism of family heredity is quantum mechanical and quantum computational processes. Logically, establishing a bio-quantum theory of family heredity is reasonable.

Using Dirac Notation [52] [53], $\left|F_{-1,1}\right\rangle = \left|00\cdots001\right\rangle$ is the bio-quantum state of the genes of the baby's parents (the father and the mother); $\left|F_{-2,1}\right\rangle = \left|00\cdots010\right\rangle$ and $\left|F_{-2,2}\right\rangle = \left|00\cdots011\right\rangle$ are the bio-quantum sub-states of the genes of the baby's grandparents (the two couples of grandfather and grandmother); $\left|F_{-3,1}\right\rangle = \left|00\cdots100\right\rangle$, $\left|F_{-3,2}\right\rangle = \left|00\cdots101\right\rangle$, $\left|F_{-3,3}\right\rangle = \left|00\cdots110\right\rangle$ and $\left|F_{-3,4}\right\rangle = \left|00\cdots111\right\rangle$ are the bio-quantum sub-states of the genes of the baby's grand-grand-parents (the four couples of grand-grand-father and grand-grand-mother);……; $\left|F_{-n,1}\right\rangle = \left|10\cdots000\right\rangle$,……, $\left|F_{-n,2^{n-1}}\right\rangle = \left|11\cdots111\right\rangle$ are the bio-quantum sub-states of the genes of the baby's ancestors of *nth* senior generation.

In terms of quantum mechanics, the spectrum of genes of a typical family is a bio-quantum superposition state. The initial probabilities of the sub-states are

evenly distributed, because no couple of seniors is, logically and genetically, initially superior to any couple else in the family. Then the initial bio-quantum state of the genes transmitted to the baby by his/her seniors is

$$\begin{aligned}\left|F\right\rangle &= \frac{1}{\sqrt{N}}\sum_{i=1}^{n}\sum_{j=1}^{2^{i-1}}\left|F_{-i,j}\right\rangle \\ &= \frac{1}{\sqrt{N}}\left(\left|00\cdots001\right\rangle\right. \\ &+\left|00\cdots010\right\rangle+\left|00\cdots011\right\rangle \\ &+\left|00\cdots100\right\rangle+\left|00\cdots101\right\rangle+\left|00\cdots110\right\rangle+\left|00\cdots111\right\rangle \\ &+\cdots \\ &\left.+\left|10\cdots000\right\rangle+\cdots+\left|11\cdots111\right\rangle\right)\end{aligned} \tag{1}$$

where

$$N = 2^n - 1, \left\langle F_{-k,m}\middle|F_{-i,j}\right\rangle = \delta_{ki}\delta_{mj}. \tag{2}$$

3. Normal Inheriting by Quantum Computing

The parents are the generation closest to the baby. The baby is borne by his/her parents. Therefore, normal inheriting should be defined as inheriting the parents' genes rather than genes of the generations far from the baby. To inherit his/her parents' genes normally, the baby has to search the spectrum of the family genes for his/her parents' genes and inherits them. Therefore, in terms of quantum mechanics, the parents' gene state is the unique target. The baby searches $\left|F\right\rangle$ for $\left|F_{-1,1}\right\rangle$ by means of bio-quantum computation. The baby prefers to use a quantum algorithm following Grover's fast quantum mechanical algorithm for database search , because Grover's fast quantum mechanical algorithm for database search is the optimal and efficient database search algorithm [48]-[51], the baby finds his parents' genes, $\left|F_{-1,1}\right\rangle$,with a probability of $O(1)$, by searching $\left|F\right\rangle$ in $O\left(\sqrt{N}\right)$ steps ($N = 2^n - 1$). The details of the algorithm are following.

1) Defining a function $f\left(F_{-i,j}\right)$:

$$f\left(F_{-i,j}\right) = \begin{cases} 1, & \left|F_{-i,j}\right\rangle = \left|00\cdots001\right\rangle \\ 0, & \left|F_{-i,j}\right\rangle \neq \left|00\cdots001\right\rangle \end{cases} \tag{3}$$

2) Repeating the following operations (a) and (b) for $O\left(\sqrt{N}\right)$ times (Grover Iterations):

a) Applying the oracle operation:

$$\left|F_{-i,j}\right\rangle \xrightarrow{O} (-1)^{f\left(F_{-i,j}\right)}\left|F_{-i,j}\right\rangle \tag{4}$$

where $f\left(F_{-i,j}\right)$ is the function defined by Equation (3).

b) Performing Grover operation (in terms of *inversion about average operation*) [48] [49]

$$D|F\rangle \tag{5}$$

where the diffusion transform D can be implemented as

$$D = WRW \tag{6}$$

where W is the Walsh-Hadamard Transform Matrix and R is the phase rotation matrix [48] [49].

3) Measuring the resulting state of $|F\rangle$.

4. Bio-Quantum Computational Speed in Hereditary Process

The $(n+1)th$ generation of the family inherits his/her parents' genes by $O\left(\sqrt{2^n-1}\right)$ Grover Iterations according to Section 3. This fact means that the family increases its bio-quantum computational speed in its hereditary process.

For example, for $n = 100$, the bio-quantum computing speed of the baby of $101th$ generation is $O\left(4\times10^7\right)$ Grover Iterations per second during pregnancy of 280 days, but for $n = 200$, the bio-quantum computing speed of the baby of $201th$ generation is $O\left(4\times10^{22}\right)$ Grover Iterations per second, much bigger than that of the baby of $101th$ generation, also during pregnancy of 280 days. One Grover Iteration should correspond to one physical operation of the brain.

5. Bio-Quantum Evolution of the Human Brain

A brain is a CPU (central processing unit) of biological information of a person. The human brain controls the bio-quantum computational process and bio-quantum computational speed. The increase, generation by generation, of the bio-quantum computational speed of the family in Section 4 means that the ability of the human brain to control the bio-quantum computation strengthens or develops in the human hereditary process. This is defined as bio-quantum evolution of the human brain.

6. A Law of Evolution of Human Bio-Quantum Intelligence

Human bio-quantum intelligence is developing with the order $O\left(\sqrt{2^n-1}\right)$, where $\sqrt{2^n-1}$ is defined as Human Bio-quantum Intelligence Root, n is the number of the generations of the seniors of the human family.

7. Bio-Quantum Selection

A human family of $(n+1)$ generations, whose baby of the last generation is successful to perform $O\left(\sqrt{2^n-1}\right)$ Grover Iterations for quantum computation during pregnancy of 280 days, is chosen as a normal family with normal heredity, or, a normal family of normal evolution. This is defined as bio-quantum selection.

8. Discussion

1) Evolution described by Darwin is a process of natural selection.

Human brain evolution is a bio-chemical process in modern evolutionary theories, based on molecular genetics.

Human brain evolution is a bio-quantum computational process in the bio-quantum evolutionary theory suggested in this research, based on quantum mechanics.

2) The bio-quantum evolutionary theory suggested in this research is validated as long as quantum mechanics and quantum computation are valid.

Conflicts of Interest

The author declares no conflicts of interest.

References

[1] Enard, W., Przeworski, M., Fisher, S.E., Lai, C.S.L., Wiebe, V., Kitano, T., *et al.* (2002) Molecular Evolution of FOXP2, a Gene Involved in Speech and Language. *Nature*, **418**, 869-872. https://doi.org/10.1038/nature01025

[2] Dorus, S., Vallender, E.J., Evans, P.D., Anderson, J.R., Gilbert, S.L., Mahowald, M., *et al.* (2004) Accelerated Evolution of Nervous System Genes in the Origin of Homo Sapiens. *Cell*, **119**, 1027-1040. https://doi.org/10.1016/j.cell.2004.11.040

[3] Evans, P.D., Gilbert, S.L., Mekel-Bobrov, N., Vallender, E.J., Anderson, J.R., Vaez-Azizi, L.M., *et al.* (2005) Microcephalin, a Gene Regulating Brain Size, Continues to Evolve Adaptively in Humans. *Science*, **309**, 1717-1720. https://doi.org/10.1126/science.1113722

[4] Mekel-Bobrov, N., Gilbert, S.L., Evans, P.D., Vallender, E.J., Anderson, J.R., Hudson, R.R., *et al.* (2005) Ongoing Adaptive Evolution of ASPM, a Brain Size Determinant in Homo Sapiens. *Science*, **309**, 1720-1722. https://doi.org/10.1126/science.1116815

[5] Prabhakar, S., Noonan, J.P., Pääbo, S. and Rubin, E.M. (2006) Accelerated Evolution of Conserved Noncoding Sequences in Humans. *Science*, **314**, 786. https://doi.org/10.1126/science.1130738

[6] Pollard, K.S., Salama, S.R., Lambert, N., Lambot, M., Coppens, S., Pedersen, J.S., *et al.* (2006) An RNA Gene Expressed during Cortical Development Evolved Rapidly in Humans. *Nature*, **443**, 167-172. https://doi.org/10.1038/nature05113

[7] McLean, C.Y., Reno, P.L., Pollen, A.A., Bassan, A.I., Capellini, T.D., Guenther, C., *et al.* (2011) Human-Specific Loss of Regulatory DNA and the Evolution of Human-Specific Traits. *Nature*, **471**, 216-219. https://doi.org/10.1038/nature09774

[8] Paar, V., Gluncic, M., Rosandic, M., Basar, I. and Vlahovic, I. (2011) Intragene Higher Order Repeats in Neuroblastoma Breakpoint Family Genes Distinguish Humans from Chimpanzees. *Molecular Biology and Evolution*, **28**, 1877-1892. https://doi.org/10.1093/molbev/msr009

[9] Charrier, C., Joshi, K., Coutinho-Budd, J., Kim, J., Lambert, N., de Marchena, J., *et al.* (2012) Inhibition of SRGAP2 Function by Its Human-Specific Paralogs Induces Neoteny during Spine Maturation. *Cell*, **149**, 923-935. https://doi.org/10.1016/j.cell.2012.03.034

[10] Somel, M., Liu, X.L. and Khaitovich, P. (2013) Human Brain Evolution: Transcripts, Metabolites and Their Regulators. *Nature Reviews Neuroscience*, **14**, 112-127. https://doi.org/10.1038/nrn3372

[11] Geschwind, D.H. and Rakic, P. (2013) Cortical Evolution: Judge the Brain by Its

Cover. *Neuron*, **80**, 633-647. https://doi.org/10.1016/j.neuron.2013.10.045

[12] Boyd, J.L., Skove, S.L., Rouanet, J.P., Pilaz, L., Bepler, T., Gordân, R., *et al.* (2015) Human-Chimpanzee Differences in a FZD8 Enhancer Alter Cell-Cycle Dynamics in the Developing Neocortex. *Current Biology*, **25**, 772-779. https://doi.org/10.1016/j.cub.2015.01.041

[13] Florio, M., Albert, M., Taverna, E., Namba, T., Brandl, H., Lewitus, E., *et al.* (2015) Human-Specific Gene ARHGAP11B Promotes Basal Progenitor Amplification and Neocortex Expansion. *Science*, **347**, 1465-1470. https://doi.org/10.1126/science.aaa1975

[14] Fiddes, I.T., Lodewijk, G.A., Mooring, M., Bosworth, C.M., Ewing, A.D., Mantalas, G.L., *et al.* (2018) Human-Specific NOTCH2NL Genes Affect Notch Signaling and Cortical Neurogenesis. *Cell*, **173**, 1356-1369.e22. https://doi.org/10.1016/j.cell.2018.03.051

[15] Heide, M., Haffner, C., Murayama, A., Kurotaki, Y., Shinohara, H., Okano, H., *et al.* (2020) Human-Specific ARHGAP11B Increases Size and Folding of Primate Neocortex in the Fetal Marmoset. *Science*, **369**, 546-550. https://doi.org/10.1126/science.abb2401

[16] Maricic, T., Helmbrecht, N., Riesenberg, S., Macak, D., Kanis, P., Lackner, M., *et al.* (2021) Comment on "Reintroduction of the Archaic Variant of nova1 in Cortical Organoids Alters Neurodevelopment". *Science*, **374**, eabi6060. https://doi.org/10.1126/science.abi6060

[17] Herai, R.H., Semendeferi, K. and Muotri, A.R. (2023) Comment on "Human TKTL1 Implies Greater Neurogenesis in Frontal Neocortex of Modern Humans than Neanderthals". *Science*, **379**, eadf0602. https://doi.org/10.1126/science.adf0602

[18] Joshy, D., Santpere, G. and Yi, S.V. (2024) Accelerated Cell-Type-Specific Regulatory Evolution of the Human Brain. *Proceedings of the National Academy of Sciences*, **121**, e2411918121. https://doi.org/10.1073/pnas.2411918121

[19] Rickelton, K., Zintel, T.M., Pizzollo, J., Miller, E., Ely, J.J., Raghanti, M.A., *et al.* (2024) Tempo and Mode of Gene Expression Evolution in the Brain across Primates. *eLife*, **13**, e70276. https://doi.org/10.7554/elife.70276

[20] Cui, X., Yang, H., Cai, C., Beaman, C., Yang, X., Liu, H., *et al.* (2025) Comparative Characterization of Human Accelerated Regions in Neurons. *Nature*, **640**, 991-999. https://doi.org/10.1038/s41586-025-08622-x

[21] Pal, A., Noble, M.A., Morales, M., Pal, R., Baumgartner, M., Yang, J.W., *et al.* (2025) Resolving the Three-Dimensional Interactome of Human Accelerated Regions during Human and Chimpanzee Neurodevelopment. *Cell*, **188**, 1504-1523. https://doi.org/10.1016/j.cell.2025.01.007

[22] Soto, D.C., Uribe-Salazar, J.M., Kaya, G., Valdarrago, R., Sekar, A., Haghani, N.K., *et* al. (2025) Human-Specific Gene Expansions Contribute to Brain Evolution. *Cell*, **188**, 5363-5383. https://doi.org/10.1016/j.cell.2025.06.037

[23] Kaur, N., Kovner, R., Gulden, F.O., Pletikos, M., Andrijevic, D., Zhu, T., *et al.* (2025) Specification of Claustro-Amygdalar and Palaeocortical Neurons and Circuits. *Nature*, **638**, 469-478. https://doi.org/10.1038/s41586-024-08361-5

[24] Zhang, D., Rubio Rodríguez-Kirby, L.A., Lin, Y., Wang, W., Song, M., Wang, L., *et al.* (2025) Spatial Dynamics of Brain Development and Neuroinflammation. *Nature*, **647**, 213-227. https://doi.org/10.1038/s41586-025-09663-y

[25] Rickelton, K. and Babbitt, C.C. (2025) Exploring the Expanded Role of Astrocytes in Primate Brain Evolution via Changes in Gene Expression. *Brain, Behavior and Evo-*

lution, **100**, 200-208. https://doi.org/10.1159/000544004

[26] Raza, R.Z., Nazir, F. and Abbasi, A.A. (2025) Genetic Foundations of Human Brain Evolution: A Study of IRX3-Associated Human Accelerated Enhancer and the P422L Mutation. *Evolutionary Biology*, **52**, 182-196. https://doi.org/10.1007/s11692-025-09654-x

[27] Liu, Y., Li, J. and Liu, Q. (2025) Inactivation of the *CMAH* Gene and Deficiency of Neu5Gc Play a Role in Human Brain Evolution. *Inflammation and Regeneration*, **45**, Article No. 5. https://doi.org/10.1186/s41232-025-00368-3

[28] Soorajkumar, A., Balan, B., Nassir, N., Akter, H., Shahin, Z., Berdiev, B.K., *et al.* (2025) Mapping Human Brain Cell Type Origin and Diseases through Single-Cell Transcriptomics. *Translational Psychiatry*, **15**, Article No. 349. https://doi.org/10.1038/s41398-025-03562-6

[29] Chen, Y.C., Maupas, A. and Nowick, K. (2025) Regulatory Networks of KRAB Zinc Finger Genes and Transposable Elements Changed during Human Brain Evolution and Disease. *eLife*, **14**, RP103608. https://doi.org/10.7554/elife.103608

[30] Liu, J., Mosti, F., Zhao, H.T., Lollis, D., Sotelo-Fonseca, J.E., Escobar-Tomlienovich, C.F., *et al.* (2025) A Human-Specific Enhancer Fine-Tunes Radial Glia Potency and Corticogenesis. *Nature*, **643**, 1321-1332. https://doi.org/10.1038/s41586-025-09002-1

[31] Caglayan, E. and Konopka, G. (2025) Decoding DNA Sequence-Driven Evolution of the Human Brain Epigenome at Cellular Resolution. *Nature Communications*, **16**, Article No. 5625. https://doi.org/10.1038/s41467-025-60665-w

[32] Yoo, D., Rhie, A., Hebbar, P., Antonacci, F., Logsdon, G.A., Solar, S.J., *et al.* (2025) Complete Sequencing of Ape Genomes. *Nature*, **641**, 401-418. https://doi.org/10.1038/s41586-025-08816-3

[33] Schrödinger, E. (1944) What Is Life? Cambridge University Press.

[34] Davies, P. (2004) Quantum Mechanics and the Origin of Life. *IAU Symposium*, **213**, 237-243. https://doi.org/10.1017/s0074180900193349

[35] McFadden, J. (2000) Quantum Evolution. Harper Collins.

[36] McFadden, J. and Al-Khalili, J. (2018) The Origins of Quantum Biology. *Proceedings of the Royal Society A*: *Mathematical*, *Physical and Engineering Sciences*, **474**, Article 20180674. https://doi.org/10.1098/rspa.2018.0674

[37] Dikshit, B. (2018) Origin of Quantum Mechanical Results and Life: A Clue from Quantum Biology. *NeuroQuantology*, **16**, 26-33.

[38] Tuszynski, J.A. (2020) From Quantum Chemistry to Quantum Biology: A Path toward Consciousness. *Journal of Integrative Neuroscience*, **19**, 687-700. https://doi.org/10.31083/j.jin.2020.04.393

[39] Kim, Y., Bertagna, F., D'Souza, E.M., Heyes, D.J., Johannissen, L.O., Nery, E.T., *et al.* (2021) Quantum Biology: An Update and Perspective. *Quantum Reports*, **3**, 80-126. https://doi.org/10.3390/quantum3010006

[40] Ogryzko, V.V. (1997) A Quantum-Theoretical Approach to the Phenomenon of Directed Mutations in Bacteria (Hypothesis). *Biosystems*, **43**, 83-95. https://doi.org/10.1016/s0303-2647(97)00030-0

[41] McFadden, J. and Al-Khalili, J. (1999) A Quantum Mechanical Model of Adaptive Mutation. *Biosystems*, **50**, 203-211. https://doi.org/10.1016/s0303-2647(99)00004-0

[42] Pullman, B. (1965) Some Recent Developments in the Quantum-Mechanical Studies on the Electronic Structure of the Nucleic Acids. *The Journal of Chemical Physics*, **43**, S233-S243. https://doi.org/10.1063/1.1701497

[43] Steele, R.H. (2008) Harmonic Oscillators: The Quantization of Simple Systems in the Old Quantum Theory and Their Functional Roles in Biology. *Molecular and Cellular Biochemistry*, **310**, 19-42. https://doi.org/10.1007/s11010-007-9662-8

[44] Wu, L.A., Wu, S.S. and Segal, D. (2009) Looking into DNA Breathing Dynamics via Quantum Physics. *Physical Review E*, **79**, Article 061901. https://doi.org/10.1103/physreve.79.061901

[45] Ruggiero, M. and Pacini, S. (2018) On the Impact of Quantum Biology and Relativistic Time Dilation in Autism. *AIMS Molecular Science*, **5**, 90-95. https://doi.org/10.3934/molsci.2018.1.90

[46] Zhao, J. (2024) A Theory of Bio-Quantum Genetics. *Journal of Quantum Information Science*, **14**, 15-27. https://doi.org/10.4236/jqis.2024.141002

[47] Zhao, J. (2025) Quantum Mechanical Mechanism of DNA Forming and Replicating. *Journal of Quantum Information Science*, **15**, 101-112. https://doi.org/10.4236/jqis.2025.153006

[48] Grover, L.K. (1996) A Fast Quantum Mechanical Algorithm for Database Search. *Proceedings of the* 28*th Annual ACM Symposium on Theory of Computing*, Philadelphia, 22-24 May 1996, 212-219. https://doi.org/10.1145/237814.237866

[49] Grover, L.K. (1997) Quantum Mechanics Helps in Searching for a Needle in a Haystack. *Physical Review Letters*, **79**, 325-328. https://doi.org/10.1103/physrevlett.79.325

[50] Nielsen, M.A. and Chuang, I.L. (2000) Quantum Computation and Quantum Information. Cambridge University Press.

[51] Zalka, C. (1999) Grover's Quantum Searching Algorithm Is Optimal. *Physical Review A*, **60**, 2746-2751. https://doi.org/10.1103/physreva.60.2746

[52] Dirac, P.A.M. (1958) The Principles of Quantum Mechanics. 4th Edition, Oxford University Press.

[53] Shankar, R. (1994) Principles of Quantum Mechanics. 2nd Edition, Plenum Press.