Hypothesis

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Why Does Immortality Not Exist, and Can It Be Achieved?

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Abstract

In this work, we analyze the reasons for the absence of immortality from the perspective of "genetic information metabolism." All living organisms synthesize and release genes, including novel and previously unknown genes, into the external environment through the process of genetic information metabolism. As a result, new genes become available for inclusion in the unified complex of genetic information represented by all living and non-living carriers, which has been termed the "Pangenome," ensuring the maintenance of life on Earth under changing biotic and abiotic conditions. Part of the newly created genetic information remains inaccessible to spreading to other members of the Pangenome during the lifetime of an organism and can only be released after its death. We hypothesize, to our knowledge for the first time, that the absence of immortality is associated with the necessity of releasing novel genes for spread within the Pangenome, which can happen efficiently only after an organism's death. We define the spread of genes and their integration into the genomes of other organisms as "gene reincarnation." Within the Pangenome, genes are redistributed, ensuring the further evolution of life. We formulate a new definition of death as "a stage in the metabolism of genetic information during which all genes of an organism become available for reincarnation." This understanding for the first time views death as a crucial part of the genetic cycle of life. Based on above novel concepts, we propose certain properties that immortal organisms should possess.

Keywords: immortality; Pangenome; metabolism of genetic information; reincarnation of genes; longevity; ageing; extracellular nucleic acids; universal receptive system; lifespan

Introduction

All living organisms are mortal. Malignant cells in multicellular organisms are the only example of relative immortality, achievable only under laboratory conditions; in the natural environment, their immortality is limited by the lifespan of the host organism, and the death of the host ultimately leads to their demise. Although death is perceived as an objective and inevitable phenomenon, its universal cause remains understudied. According to modern concepts, most diseases resulting in death, including cancers, neurodegenerative disorders, and cardiovascular and endocrine diseases, are related to microorganisms (Balloux and van Dorp 2017; DiMaio et al. 2022; Doocey et al. 2022; Blackhurst and Funk 2023; Zhang et al. 2022; Walker and Czyz 2023; Sipilä et al. 2023; Tetz and Tetz 2019; Tetz et al. 2020; Tetz et al. 2019). Based on this concept, it can be assumed that Adam did not wash the apple before eating the forbidden fruit in the Garden of Eden—where all creatures were immortal—which marked the beginning of infections and, consequently, the emergence of death.

Today, it is assumed that the emergence of diseases and the absence of immortality on Earth have another reason. In this work, we consider death and its causes to be necessary for the existence of life. We analyze potential reasons for the absence of immortality on the basis of the concept of "genetic information metabolism" as a fundamental characteristic of life.

The term “genetic information metabolism” was coined in 2020 to describe the functioning, reproduction, and creation of genes and their distribution among living and non-living carriers of genetic information. Based on this concept, a new biological definition of life was redefined as: ““Life is an organized matter that provides genetic information metabolism” (Tetz and Tetz 2020). Genetic information metabolism is the foundation of the existence of the functionally active complex “Pangenome,” which represents the totality of genes in all living and non-living carriers of genetic information (Tetz 2005). Data on non-living genetic elements (NLGEs) in the Pangenome have been significantly expanded in recent years, and NLGEs are represented by large numbers of DNA and RNA molecules that can exist both inside cells and in a free, extracellular state, or be encapsulated in protein coats, as seen in viruses. NLGEs include viruses, virusoids, viroids, plasmids, transposons, insertion sequences, and extracellular DNA and RNA in multicellular microbial biofilms (Liang and Bushman 2021; Tetz and Tetz 2023; Siguer et al. 2015). The genetic information of the Pangenome includes DNA and RNA molecules that form the basis for protein synthesis as described in classical biology but also encode previously unknown functions not associated with protein synthesis, as recently described under the New Biology concept. For example, polymeric DNA and RNA molecules can function as pliers, altering the properties of other molecules (primarily proteins) (Tetz and Tetz 2019). This was the first example of environmental change caused by the direct action of DNA and RNA molecules on existing proteins. Another previously unknown function of nucleic acid molecules besides protein-coding is related to the recently discovered “Universal Receptor System,” in which DNA and RNA molecules act as receptors capable of recognizing and responding to different environmental factors. This receptor system has been found throughout the tree of life, from prokaryotes to eukaryotes, including animals, plants, and fungi (Tetz and Tetz 2022a; Tetz and Tetz, 2022b; Tetz et al., 2024; Tetz et al. 2025a; Tetz et al. 2025b).

The Pangenome ensures the maintenance of life on Earth under changing biotic and abiotic conditions through constant improvement of the information it receives. Genetic information metabolism is the primary tool for maintaining and developing this unified functionally active complex and involves three major processes: 1) increasing the amount of genetic information through the reproduction of living organisms, increasing the number of NLGEs, and gene amplification, 2) alteration of the genes in an organism, ensuring adaptation and the occupation of new ecological niches, and 3) the spread of genes within the Pangenome. In multicellular organisms, all these processes occur within the organism. Importantly, all multicellular organisms have an individual microbiota, which largely controls their life cycle (Stencel and Proszewska 2017; Huitzil et al. 2018; Sonnert et al. 2024; Siguer et al. 2015; Hutzil et al. 2023). Microbiota cells outnumber host cells by 10 times, and NLGEs, by hundreds of times (Liang and Bushman 2021). In the symbiosis of multicellular and unicellular organisms and NLGEs, genetic changes are largely interconnected (Maritan et al. 2024; Henry et al. 2021). Any change in the genetic information of multicellular organisms will alter the genetic information of their predominantly unicellular microbiota, and vice versa.

Microbiota genomes and host genes closely interact, with host genes being transferred to the microbiota and NLGEs, and vice versa, microbiota genes spreading to cells of the multicellular host (Li et al. 2020; Haimlich et al. 2024; Keeling and Palmer 2008; Wells et al. 2022). The possibility of lateral gene transfer between eukaryotes and bacterial viruses (bacteriophages) has recently been discussed (Bordenstein 2016). Thus, multicellular organisms serve as a source of diverse new genes that are distributed over eukaryotic and prokaryotic cells, as well as NLGEs.

An important process in genetic information metabolism is the spread of genes within the Pangenome. Various pathways are involved in gene spread in nature, the most important being gene transfer between related and non-related eukaryotic and prokaryotic organisms (Gregorius 2009; Vogt 2022; Erven et al. 2022; Boll et al. 2023). Gene redistribution among unrelated organisms allows organisms to acquire fundamentally new properties, ultimately ensuring the existence of the Pangenome. The Earth’s microbiota, which represents the largest part of living nature, comprises more than 10^{30} bacteria spread across all ecological niches (Rappuoli et al. 2023; Locey and Lennon 2016). The microbiota of multicellular organisms, including humans, is closely interconnected with that of the environment. The continuous exchange of microorganisms and genes between the microbiota of multicellular organisms and the soil microbiota is essential for maintaining their life processes (Blum et al. 2019). Genes are continuously released into the environment and absorbed through food chains or various other pathways (Week et al. 2024; Van Wert et al. 2023; Arim et al. 2006)

The most significant function of the Pangenome is the spread of previously non-existent gene variants. Throughout an organism's life, the gene composition in its cells changes significantly, including the emergence of unique genes. Aging and lifespan have been associated with the accumulation of changes in the genes of the macroorganism, microbiota, and associated NLGEs (Tetz and Tetz 2018)

From the perspective of genetic information metabolism, not only the formation and preservation but also the release of genes upon death is important, particularly for multicellular organisms. For example, patients with progressed cancer or certain other diseases feature increased levels of extracellular DNA and RNA with altered properties (Gotoh et al. 2005; Widschwendter and Jones 2002; Gould et al. 2015; Hawes et al. 2015; Hajizadeh et al. 2003). This extracellular DNA consists of unique fragments of the human genome. It contains genes associated with cancer progression, including microsatellites, which have a higher mutation frequency than other regions of the genome, leading to greater genetic diversity (Genkin et al. 2005; Schwarzenbach et al. 2007; Hao et al. 2014; Iqbal et al. 2015; Zhu et al. 2013). Accordingly, the significance of an organism as a source of new and variant genes for the genetic information metabolism of the Pangenome increases with age and the development of various diseases.

A Reason for the Lack of Immortality

Available data suggest that the routes through which genes and associated NLGEs can be released during the lifetime of a macroorganism are limited. Despite the flow of genes released by organisms during their life, only a small fraction of these genes enter the environment and therefore are not included in the metabolism of genetic information.

Genes of unicellular and multicellular organisms, as well as some NLGEs, including extracellular DNA and RNA associated with cell surfaces, present in the matrix of microbial biofilms, or circulating in blood and tissue fluids, are either released into the environment in very limited amounts or are not released at all during an organism's lifetime. Further, it has been established that only a portion of the bacteria that make up the microbiota of multicellular organisms is released with feces (Eckburg et al. 2005; Can et al. 2014).

Thus, the inclusion of variant genes that arise in an organism into the collective metabolism of genetic information within the Pangenome becomes possible only after the organism's death. After the death of unicellular and multicellular organisms, large numbers of genes are released and spread in the external environment, most of which did not enter the environment during the organisms' lifetime.

In our view, the fact that these novel genes cannot be distributed fully within the Pangenome during the lifetime of organisms, corresponding to the third process of genetic information metabolism (i.e., gene distribution within the Pangenome), is the reason for the absence of immortality. Genes of unicellular and multicellular organisms, in the form of DNA fragments suitable for spreading to other cells, are released during programmed cell death, as observed in both prokaryotes and eukaryotes (Elmore 2007; Holmgren et al. 1999; Bayles 2013; Bergsmedh 2001; Iranzo et al. 2014). As a result of the death of multicellular organisms, in addition to the genes of the macroorganism, large amounts of cellular and extracellular DNA and RNA from microbiota are released into the external environment.

The fate of genes of multicellular organisms after death has been the subject of various studies, which have shown that genes do not readily degrade after the death of a multicellular organism and even remain active for some time (Ferreira et al. 2018; Pozhitkov et al. 2017; Javan et al. 2024; Dachet et al. 2021). For example, specific synthetic activity in cells is preserved for more than 48 h after death.

During this period, various genes, including the gene encoding histone acetyltransferase, which is necessary for the activation of proviruses, are actively transcribed (Benkirane 1998). These data suggest that after death, certain genes are activated, which may contribute to the preservation and spread of NLGEs.

The fate of the majority of genes in deceased organisms is determined by their distribution between unicellular and multicellular participants in the destruction of the macroorganism. The microbiota of multicellular organisms participates in the destruction of the host and captures some of the released genes but loses its uniqueness as a stable complex that is preserved in each organism and passed down from generation to generation.

The fate of the numerous intra- and extracellular NLGEs that are released upon cell death is an important part of genetic information metabolism and deserves special attention. NLGEs are widespread in bacteria more than for 10% of the bacterial genome (Canchaya et al. 2003). Most eukaryotic cells and nearly half of all sequenced bacterial genomes contain NLGEs in the form of prophages (Touchon et al. 2016; Barth and Aylward 2024). Bacteria can contain more than four full-size prophages, most of which are capable of lytic cycling (Figueroa-Bossi et al. 2001). The induction of the bacterial SOS response to DNA damage can trigger the lytic cycle in many prophages, leading to bacterial death (Nanda et al. 2013). Simultaneously, bacterial death can be accompanied by the release of a significant number of plasmids into the environment. Plasmids can increase in number through amplification, which occurs under protein synthesis suppression, for example, due to antibiotics produced by other microbes (Kohanski et al. 2010). Proviruses and other NLGEs from eukaryotic cells are released in a similar manner.

Thus, a significant portion of variant genes and NLGEs are not released and do not spread within the Pangenome during life; however, mechanisms and pathways exist for their preservation and spread after death. Based on this data, we hypothesize that death exists by the necessity of the release of variant genes and their redistribution within the Pangenome, which is critically important for maintaining its potential under constantly changing environmental conditions. This is indirectly supported by the comparatively short lifespan of most organisms, which is expected to maintain a high intensity of genetic information metabolism.

Notably, there is an obvious contradiction between lifespan and the necessity for releasing and redistributing new genes within the Pangenome; an increase in lifespan promotes the formation and accumulation of novel gene variants, but hinders their spread within the Pangenome. This contradiction is resolved differently in different species and may depend on their living conditions. The dominance of annual plants in unfavorable conditions, which is believed to contribute to variability and adaptation to environmental conditions (Poppenwimer et al. 2023; Charnov and Schaffer 1973), supports this notion.

Life and death are inseparably intertwined. The performance of biological life functions aimed at accumulating and improving genetic information predetermines the existence of death for all organisms as a means to release and spread this information. Therefore, it is evident that death is a crucial element in genetic information metabolism, creating conditions that allow genes to be fully released for spread within the Pangenome.

Accordingly, the absence of immortal organisms in nature is a result of the necessity of death to ensure the diversity of the Pangenome, which supports the existence of life. This conclusion is closely related to the first Tetz biological law: “The general biological function of life is to provide genetic information metabolism” and may be formulated as Tetz’s second law: “Death is required to sustain life,” and Tetz’s paradox: “The Pangenome is necessary for the existence of life, and death is necessary for the existence of the Pangenome” (Tetz and Tetz 2020).

The fate of the released genes when acquired by other organisms can be considered “gene reincarnation.” In this respect, the death of an organism can be viewed as the release of all of its genes and their redistribution within the Pangenome. The definition of death from a biological perspective has various interpretations (Murphy et al. 2023; Sarbey 2016; DeGrazia 2021; Howard 2021). We propose a new definition: "Death is a stage in genetic information metabolism during which all genes of an organism become available for reincarnation."

Thus, the life and death of individual organisms in nature do not play the roles that human consciousness assigns to them. Individual life and death are necessary components of the genetic information metabolism within the Pangenome, which requires a constant increase in the quantity and diversity of the genetic information contained within it, for the continuation of life in general.

The Pangenome comprises the genes of organisms of all levels of complexity, from unicellular to the most complex and "young" in evolutionary terms, and represents the history of the development of life on Earth under various conditions. The information contained in it represents an independent and hitherto underestimated value. It can be assumed that the value of the information stored in the Pangenome is substantially greater than currently known.

The astonishing possibilities of DNA and RNA beyond genetic coding are related to the fact that information in these molecules can be recorded in various ways simultaneously. On the most basic level is the genetic code, which consists of three-nucleotide codons that correspond to specific amino acids, which make up proteins (Nirenberg and Matthaei 1961). Other methods of encoding are the subject of recent research, mainly in the emerging field of "natural computing," in which DNA and RNA are used to store information using the binary information currently employed in computers (Koch et al. 2020). Great success has been achieved in this field, with DNA data encoding not only in vitro but also in vivo (Lim et al. 2023). Another possible application of DNA encoding in the future of computer technology are DNA quantum computers (Riera et al. 2024).

These scientific achievements in solving the challenges of developing new information technologies suggest that in nature, the Pangenome may contain other information encoded by yet-unknown mechanisms. This supports the idea of the potential spread of Pangenome information and its establishment on other planets. From a biological perspective, the most promising Pangenome representatives for space dissemination are sporobiota. Bacterial spores can remain viable for millions of years and can survive in space (Cano and Borucki 1995; Kminek et al. 2003; Vreeland et al. 2000; Zhou et al. 2023; Horneck et al. 2012). It should be noted that the genomes of spore-forming bacteria are generally substantially larger than those of non-spore-forming bacteria and thus carry a larger volume of information (Tetz and Tetz 2017).

An important aspect of the information carried in the Pangenome is memory, which both unicellular and multicellular organisms possess. We encountered previously unknown features of cellular memory while studying the Universal Receptor System of prokaryotes and eukaryotes, formed by DNA and RNA molecules which is capable of recognizing various biological, chemical, and physical factors in the environment (Tetz and Tetz 2022a; Tetz and Tetz 2022b). This discovery allowed us to find new tools that enabled us to manage cellular memory for the first time. We were able to erase the memory of any type of cells, resulting in the emergence of previously non-existing traits in these cells (Tetz and Tetz 2022b). The results were reproducible, indicating that the process of memory changes in cells, leading to the emergence of novel traits, is encoded in their genomes.

The extraordinary possibilities for storing and spreading vast amounts of information encoded in various ways on a single DNA or RNA molecule suggest that these molecules in cells carry not only the information for reproduction and survival but also the individual memory of any multicellular, memory-capable organism, including humans. In other words, our individual memory, which stores past events and experiences, knowledge, and skills, may be encoded in our DNA and RNA molecules. Research findings on the roles of DNA and RNA in the onset and preservation of memory support this possibility (Li et al. 2019; Day and Sweatt 2010; Jovasevic et al. 2024; Carney 2018).

It can be assumed that cells store individual memory and spread it to the Pangenome. Moreover, the rationality of genetic information metabolism, perfected over billions of years, has culminated in a means to record individual memory, marking its connection to a specific host through the use of unique genetic markers, which we are only beginning to understand through genome sequencing. In future, we expect that it will be possible to identify individual memory genes reincarnated in different organisms by certain markers and to reconstruct the memory of organisms that lived in the past (once we learn how to read such information). It may even be possible to reproduce an individual, including their memory, up until their death. This type of memory uploading would open up a fundamentally new direction in biology: Artificial Immortality.

Considering all of the above regarding the Pangenome and the information it presumably carries, a paradox arises—the "Tetz Paradox:" "Life and death exist to create and spread new genetic information. "In other words, the Pangenome is the key to life and death.

How to Achieve Immortality

Is immortality achievable? We have come closer to understanding the characteristics that an immortal organism should possess. Such an organism would require a different immune system and an entirely different, open genetic system.

It is commonly believed that microbes, which cause the vast majority of diseases, and diseased or dysfunctional host cells must face the protective action of the immune system. However, this is only partially true, as the immune system, when overactivated in response to microbes or altered host cells, often becomes the cause of the host's death. In particular, immune cells tend to support malignant tumor cells by providing nourishment and protecting them from other immune defense mechanisms, aiding in the spread of metastases (Anderson and Simon 2020; Gay and Felding-Habermann 2011; de Visser and Joyce, 2023). Excessive production of cytokines and chemokines by immune cells triggers a "cytokine storm," which exacerbates the severity of various diseases and often is the primary cause of the host's death (Hsu et al. 2022; Fajgenbaum and June 2020; Lin et al. 2022). Such behavior of the immune system can be viewed as a programmed action aimed at "growing" new genes in pathogenic microbes and diseased host cells, followed by their release to actively participate in genetic information metabolism. For immortal organisms, the immune system should follow a different algorithm: on the one hand, it should not interfere with the organism's ability to spread new genetic information created in the host's diseased cells, pathogenic microbes, and NLGEs to the Pangenome; on the other hand, it should prevent this to cause the death of the organism.

Second, immortal organisms should have open genetic systems in which genes change and are continuously released into the environment throughout life for inclusion in genetic information metabolism and for maintaining gene diversity in the Pangenome.

However, in a world populated by immortal organisms, new dangers would arise for them. Immortal organisms would be less able to adapt to changes in abiotic environmental factors. Moreover, overpopulation would lead to a decrease in the emergence rate of new organisms, thus reducing Pangenome diversity. This could lead to inefficiency of the Pangenome in maintaining life under changing environmental conditions. This danger can be described as a new Tetz paradox: "In a world of immortals, the threat of death for all living organisms increases."

Key concepts of the theory:

1. The total genetic information of all living and non-living carriers forms a single, functionally active complex, i.e., the Pangenome, which supports life on Earth under changing biotic and abiotic conditions.
2. Genetic information metabolism, encompassing the reproduction, alteration, and distribution of genetic material among Pangenome participants, ensures the existence of the Pangenome.
3. Genetic information metabolic processes in all living organisms generate unique genes and make them available for distribution and incorporation in the Pangenome.
4. During an organism's lifetime, a significant portion of new genetic information remains inaccessible to spreading to other elements in the Pangenome.
5. Immortality is absent because of the necessity of the release of new genes, which cannot spread to other organisms or be integrated into genetic information metabolism during the lifetime of an organism.

6. An immortal organism should possess an open genetic system in which genes change and are continuously released into the environment for the maintenance of Pangenome diversity, as well as an immune system that does not cause the death of the host in response to pathogens or diseased/dysfunctional host cells.

Here, wee examined the features of genetic information metabolism related to pre- and post-mortem gene release from unicellular and multicellular organisms and NLGEs into the environment within the frameworks of classical biology and new biology.

Key Concepts of the Theory

During an organism's lifetime, various DNA and RNA molecules are retained within cells or cell communities or in the extracellular spaces of multicellular organisms and their microbiota and are not released into the environment. The release of a significant portion of altered genetic information for distribution in the Pangenome is possible only after the death of an organism, which clarifies the absence of immortality. Therefore, the absence of immortal organisms in nature is a result of the necessity of death for spreading new genes within the Pangenome for the maintenance of life. The fate of the released genes when acquired by other uni- or multicellular organisms can be considered "gene reincarnation." In this respect, the death of an organism can be viewed as the release of all of its genes for capture by and continuation in other living organisms. This allows us to formulate a new definition of death as "Death is a stage in genetic information metabolism in which all genes of an organism become available for reincarnation."

As the Pangenome includes genes from organisms ranging from the most primitive unicellular forms to the most advanced and "young" in evolutionary terms, it represents the history of life on Earth under various conditions of existence. Viewing the Pangenome from this perspective allows us to hypothesize that it is the main reason for the existence of both life and death. We termed this the "Tetz Paradox:" "Life and death exist to create and spread new genetic information."

Based on the analysis conducted, we formulated some properties that immortal organisms should possess. First and foremost, they should be able to continuously generate new gene variants for distribution in the Pangenome and participation in genetic information metabolism. Second, they should have an immune system that provides complete protection against any external pathogenic factors, while not interfering with the spread of new genetic information originating from host cells, microbes, and NLGEs and preventing it from turning against the host.

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