Review Article ISSN 2766-2624

Advances in Earth and Environmental Science

Species Variation is Irresistible

Linyun Wang[1*] **and Taoran Du, Ph.D**[2]

[1]College of Animal Science and Technology, Nanjing Agricultural University, Nanjing-210095 China.

[2]Institute of Swine Science, College of Animal Science & Technology, Nanjing Agricultural University, Nanjing 210095, China.

***Corresponding author**

Linyun Wang,
College of Animal Science and Technology,
Nanjing Agricultural University, Nanjing- 210095 China.

Submitted : 18 Sept 2025 ; Published : 7 Oct 2025

Citation: Wang, L. & Du, T. (2025). Species Variation is Irresistible. *Adv Earth & Env Sci; 6*(4):1-13.
DOI : https://doi.org/10.47485/2766-2624.1073

Abstract

Species variation is a biological phenomenon. When organisms reproduce, they produce offspring, and during the reproduction process of successive generations, variations occur. However, many people are unaware of or have disputes about this, believing that biological species do not vary during their generations. Scientists believe that life already existed on Earth 3.8 billion years ago. Over the past 500 million years, due to various reasons, at least five major mass extinctions (referred to as major extinctions) have occurred on Earth. After each major extinction, the remaining organisms would recover and thrive. Up to now, there are 500,000 to 300 million species of various organisms on Earth. Where did the original species come from? How did the species inherit and continue from generation to generation? What are the causes of biological variation? After the mass extinction, how did living beings reproduce and recover, and why did the number of species become increasingly larger and more complex, forming the biodiversity of the Earth? Up to now, there is still no satisfactory theory to explain it. Human beings have gradually come to understand the causes of biological variation. From the superstition of "God created all things" to Darwin's first proposal in 1859 that a species could evolve from other species. From Morgan's speculation in 1928 that there are paired genetic elements (genes) within the reproductive material of organisms to the confirmation of biological genetic material DNA in 1953. Human understanding of biological variation has entered the era of molecular biology. Over the past 70 years, human understanding of biological variation has continued to increase. Among them, the most important is: it is believed that the genetic material genome of organisms undergoes mutations and recombination during the continuation of generations. Mutations and recombination are the key processes causing changes in the genome. The heterozygous effect produced within a species during its continuation is the main driving force for species variation and evolution. This can be found in the history of variation and evolution of humans, animals, plants, and microorganisms. Some of the main rules of genetic heterogeneity effects are as follows: 4.1 Heterogeneity effect is not the replacement of one gene particle by another. The influence of parental traits on offspring traits is not symmetrical. The offspring traits are not the sum of the related traits of the two parents minus 2. It cannot be expressed as 50% of the father: 50% of the mother; it should be expressed as 50 ±% of the father: 50 ±% of the mother. The heterogeneity effect also varies depending on the degree of heterogeneity of the parents themselves. The F1 generation self-crossing results in the F2 generation, which will separate. The situation is even more complex. 4.2 The variation between the offspring and the parents shows microscopicality, gradualness, and multiplicity. 4.3 The variation between the offspring and the parents is random, without directionality. Without human intervention, it is not subject to the will of the organism itself. 4.4 The nucleotide sequences of the offspring after biological mutations can be inherited or separated again. The newly generated nucleotide sequences in the offspring can be fixed and passed on through appropriate inbreeding. Both good and bad traits can accumulate and be passed down from generation to generation. However, some nucleotide sequences are very conservative and do not change, while others may undergo re-separation or mutation, and the traits will also change accordingly. 4.5 The speed of various biological mutations varies. 4.6 Molecular genetics holds that genes do not have dominant and recessive traits, but there are DNA methylation and demethylation, as well as epigenetic phenomena. 4.7 Biological genomic variations are generally irreversible. 4.8 The same biological species will undergo nucleotide sequence variations in different living environments. The same species will have nucleotide sequence variations during their generations when they are in different altitudes and under different environmental conditions on Earth. The theory of species variation has extensive applications in the evolution of living beings. 5.1 It can provide a reasonable explanation for the causes of biodiversity on Earth. 5.2 During the 4.5 million-year evolution of humans, through hybridization, they have continuously changed their genetic structure to adapt to survival on Earth and to better adapt to the environment on Earth, resulting in longer life spans. 5.3 Humans have applied the theory of species variation not only to domesticate wild plants and animals into crops and livestock, changing their genetic structure, but also to continuously improve their yield and quality. 5.4 Microorganisms on Earth are also constantly undergoing variations. Studying the variations of harmful microorganisms to humans can enable humans to take preventive measures against them in advance, while studying the variations of beneficial microorganisms to humans can make them better serve humanity. 5.5 Applying the theory of biological hybridization to the variations of other lower species under lunar conditions is also very promising. It can accumulate data for humans to live on the moon. The issue of species variation and whether there will be a biological extinction on the Earth are two distinct matters.

Keywords: Species variation Genetics Gene Nucleotide Biodiversity.

1. Species Variation is a Biological Phenomenon That is Irresistible

There are many natural phenomena on the earth. Light, microwaves, gravity etc. are called physical phenomena. The neutralization of acidic and alkaline substances is called a chemical phenomenon. The growth, development, reproduction and variation of living things are called biological phenomena. The biological phenomena of organisms have two basic manifestations. First, growth and development, the material exchange between organisms and their surrounding environment, and the growth and development of the organisms themselves. Second, reproduction produces offspring, and mutations occur during generations of reproduction. That is: "The offspring are like parents, offspring are not parents." The first manifestation of biological phenomena has been recognized by many people, but regarding the species variation in the second manifestation, there are still many people who do not understand or are not very clear about it, believing that biological species do not change during the continuation of generations.

Scientists believe that living things on Earth emerged 3.8 billion years ago. Over the course of more than 3.8 billion years, organisms have undergone the chemical evolution of pre-organisms - biological evolution - prokaryotes - eukaryotes - single-celled eukaryotes - multicellular metaphyta and metazoa - the Cambrian explosion of Marine animals - early terrestrial life (terrestrial plants, moss plants - vascular plants;) Arthropods - vertebrates (fish) - reptiles - birds (angiosperms) - mammals, and many other stages. (Shougang Hao et al. 2000a)

Over the past 500 million years, at least five large-scale mass extinctions (referred to as mass extinctions) have occurred on Earth, including three in the Paleozoic Era (the end of the Ordovician, the end of the Devonian, and the end of the Permian), and two in the Mesozoic Era (the end of the Triassic and the end of the Cretaceous). Most of the dinosaurs familiar to many people died out in the mass extinction at the end of the Cretaceous Period (a small number evolved into birds) (William Wahl et al., 2005). But the most tragic event in prehistoric times occurred at the end of the Permian period 252 million years ago, when about 95% of the creatures in the world's oceans and about 75% on land died out forever.

Each mass extinction does not wipe out all life on Earth. There are always different numbers and types of organisms that survive after the mass extinction. When the environment improves, they start to reproduce again and enter a new stage of evolution. All kinds of organisms will produce a kind of "coping" effect (struggle to adapt) when experiencing a catastrophic environment. All creatures with good adaptability and strong vitality can survive. On the contrary, they will be eliminated. So, survival is the outcome of the mass extinction and also the prelude to the Great Radiation. During the evolution of life, mass extinctions have played an accelerating and catalytic role, especially in the substitution of dominant groups. Life on Earth is like this: after going through numerous major and minor extinction events and then recovering from radiation, it has evolved into the magnificent scene it presents today (Jiayu Rong et al., 2014).

Up to now, there are 5 to 30 million species of various creatures on the Earth, most of which have not yet been named. Approximately 2 million species of organisms have been discovered and named, including 260,000 species of plants, 750,000 species of insects, 500,000 species of vertebrates, and the rest are a large number of microorganisms (Qingyu Wu, 2002a).

What are the causes of biological variation? Why do organisms multiply and recover after the mass extinction, and the number of species becomes increasingly large and complex? What are the causes of the biodiversity that forms the Earth? So far, there is still no satisfactory theory to analyze it.

2. Human Understanding of the Numerous Organisms on Earth and the Causes of Their Variations

How to get to know so many creatures on the earth?. In 1753 (271 years ago), Linnaeus, a Swedish plant taxonomist, published "Species Plantarum" and first proposed the "binomial nomenclature", giving each species a taxonomic name and biological location. In this way, people can have a basic understanding of biodiversity. Organisms are classified into seven major categories: kingdom, phylum, class, order, family, genus and species, and species is regarded as the basic unit within these seven major categories.

A "species" refers to a group of organisms that are basically the same in morphology, structure, function, developmental characteristics and ecological distribution. The distinction between species is based on the principle of "reproductive isolation". That is, species A and species B cannot naturally mate and reproduce offspring, or even if they can produce offspring, they cannot reproduce (for example, when a horse and a donkey cross to produce a mule, the mule cannot reproduce offspring.) . For hundreds of years, the "reproductive isolation" in this "biological species concept" has often been interpreted as "complete reproductive isolation". However, in nature, "complete reproductive isolation" has not been formed between most closely related species (even many closely related genera) (Jianquan Liu, 2016). The process of speciation is a dynamic process; The existing "species" are all at a certain moment or stage in the process of speciation. All species in nature are on the "path of species differentiation", in the middle or late stage of species formation. Or it is beginning a new round of species differentiation and is in the early stage of speciation. To deal with the complex challenges in the actual application process, The "integrative species concept", which emphasizes the integration of multiple criteria such as morphological differences, population genetic differentiation, reproductive isolation, niche differentiation, and phylogenetic relationships (monophyletic principle) for species definition, might be a more reasonable interpretation. (Zefu Wang, Jianquan Liu, 2025).

But where did the original species come from? How do species pass on from generation to generation? How do species mutate dynamically? Are species becoming more and more or fewer and fewer? People are still unclear or controversial.

Faced with all kinds of incomprehensible worlds of heaven and earth, early humans could only rely on immortals, religions and God. The first book of the Old Testament, Genesis, says, “God created heaven and earth and all things.”

It was not until 1859 (165 years ago) that Charles Darwin (1809-1888) published the book “On the Origin of Species”, proposing for the first time that “species were not independently created by (God), but, like varieties, were passed down from other species.” Natural selection is the most important way of variation, although not the only one. In 1871, Darwin, in another magnum opus, “The Origin and Sexual Selection of Man”, used a large number of facts to prove that humans evolved from ancient apes. In this way, human beings can have a basic understanding of the evolution of species. He also proposed for the first time that there are “variants” in species.

Sixty-nine years later, in 1928, Morgan published his famous “Theory of Genes”, arguing that there exist pairs of genetic elements (genes) in the reproductive plasm of living organisms. Combining the results of Mendel’s pea hybridization experiments in 1865, he proposed the three laws of inheritance, regarding genes as individual grains on chromosomes. And it is believed that genes can be divided into dominant and recessive ones.

Another 25 years passed. In 1953, two American scientists, Watson and Crick, based on three concepts obtained from a large number of experiments by other scientists at that time, proposed the double helix structure model of genetic material DNA, indicating that genes are actually nucleotide sequences. And it proposed the “central dogma” that the genetic information contained in DNA and RNA flows only unidirectionally to proteins. Human understanding of biological variation has entered the era of molecular biology from the Mendel-Morgan genetics era.

Molecular genetics holds that the genetic material of organisms is the DNA in the chromosomes of sex cells. The genetic information in DNA, mediated by mRNA (messenger ribonucleic acid), determines the primary structure of proteins. That is to say, the nucleotide sequence of DNA determines the nucleotide sequence of mRNA, and the nucleotide sequence of mRNA determines the amino acid sequence in proteins. Then it shows various traits.

From 1953 to 2024, more than 70 years have passed. Human understanding of biological genetics and variation has gone beyond the above-mentioned scope and is constantly increasing. In my article “The Law of Biological Variation: Offspring Are Like Parents, Offspring Are Not Parents” (Linyun Wang, 2023) published in 2023, I proposed 10 progress points. Among them,2 points require special attention:

1. Mutations and recombination occur in the biological genome during the course of generations. Mutation and recombination are the key processes that cause genomic changes.
2. In the course of generations of living organisms, whether they reproduce sexually or asexually, heterozygous effects occur. “Heterozygous effects” include: variations in DNA nucleotide sequences; The expression differences of mRNA (the differences in gene expression speed and gene expression level); Differences in protein structure DNA methylation in certain regions Doubling of nucleotide sequences, entire genomes or chromosomes; Heritable gene expression changes caused by non-DNA sequence variations, etc., are the main driving forces for genomic mutations and recombinations.

Before the emergence of human beings on Earth, species groups in different regions moved and interbred with each other. Under the influence of heterozygous effects, species kept mutating. Some died out while others developed into new species. Species utilize, restrict and depend on each other, giving rise to multiple biological food chains and forming an Earth life community composed of plants, animals and microorganisms.

3. Genetic Recombination Caused by Heterozygous Effects is The Main Driving Force for Species Variation and Evolution

The genetic recombination caused by heterosis within a species during its generational continuation is the main driving force for species variation and evolution. Many examples can be found in the history of variation and evolution of humans, animals, plants and microorganisms.

The continuous interbreeding and evolution of different groups after humans separated from apes is a good example. Between about 10 million and 4.5 million years ago, different groups of apes in various regions interbred, gradually separating from the ape population to become human. Under the influence of various factors such as trade, war, and disease, human groups in different regions moved outward and interbred. Under the effect of hybrid vigor, humans consciously or unconsciously changed their genetic combinations. Some branches were eliminated due to unsuitability to the environment, while others enhanced their survival ability on Earth. After several million years of development, modern humans gradually formed, becoming increasingly adapted to survival in the Earth’s environment.

Regarding the origin and evolution of human beings, there are various theories and hypotheses in the scientific community. Many scholars believe that although there were three migrations of Africans out of Africa, the African race did not “replace” the races in other regions but rather “hybridized and integrated” with them. As one of the representatives of the “multiregional evolution theory”, Academician Xinzhai Wu of the Chinese Academy of Sciences, together with Milford Wolpoff of the University of Michigan and Alan Thorne of the

Australian National University, co-authored an article in 1984, proposing the “multiregional evolution theory”, which holds that modern humans emerged and continuously evolved in four regions, and there was gene exchange among these regions.

In 1885, Professor Alan Templeton from Washington University in St. Louis, USA, designed a computer program called GEODIS. Using this program, he analyzed the DNA sequences of populations around the world and attempted to identify the genetic relationships among different groups. Templeton and other researchers focused on comparing the common chromosomes, sex chromosomes, and mitochondrial DNA of people in 10 regions based on genetic characteristics. The analysis results showed that humans left Africa 420,000 to 840,000 years ago and then underwent another large-scale migration outwards 80,000 to 150,000 years ago.

In 2005, Templeton expanded the 10 regions to 25 regions. As a result, it was discovered that in addition to the two migrations mentioned above, humans had already experienced “leaving Africa” 1.9 million years ago, which can be regarded as the earliest such occurrence.

In this study, Templeton used genetic analysis to find that the Homo erectus who left Africa had extensive genetic exchanges with the local population. It can be said that the time of their integration was earlier than what is currently recognized by the scientific community (Jianya Li, 2006).

The development of the Chinese nation is also the result of continuous gene exchanges among different groups.

In China, the unearthed artifacts from the existing Sanxingdui Ruins (discovered by a local farmer in 1929 and subsequently extensively excavated from the 1980s to the 1990s) and the related archaeological research have proved that as early as the late Neolithic period (approximately 4500 - 3600 BC) to the end of the Shang Dynasty and the early Western Zhou Dynasty (approximately 3100 - 2900 BC), multiple ethnic groups emerged in that region. The Sanxingdui Kingdom was an ancient state centered around the Sanxingdui Ruins in Guanghan during the Shang Dynasty and its predecessor, with its territory covering the entire Sichuan Basin and its surrounding areas. The central power structure of this state was jointly governed by the noble groups with “hairpinned” and “braided” hairstyles, who respectively held religious and secular powers. The bronze human statues buried in the Sanxingdui pits are evidence of this political structure. During the formation and development of the Sanxingdui culture, in addition to the factors of resources, technology, and art that moved along with exchanges and the movement of specific populations, multiple opposing city-states within the local Baodun Village culture in Chengdu gradually merged into two or three, and finally concentrated into the Sanxingdui City. This process indicates that the population composition of this ancient kingdom represented by the Sanxingdui culture was definitely not monolithic. Among them, there were both ancient tribes from the distribution area of the Erlitou Culture in the Yellow River Middle Basin and ancient tribes from the local Baodun Village and Yufan Village cultures in the Sichuan Basin (and perhaps also the ancient tribes from the Ling Valley in eastern Chongqing and the hills of central Sichuan). (Hua Sun, 2023)

The study of the nearly 2,000-year history of the Chinese nation also indicates that Dynasty ascended the throne in Xingyang, Henan Province (the Western Han Dynasty), to the end of the Qing Dynasty, over 2,000 years, there were five major population migrations, leading to nationwide population movement and ethnic integration. Marriages among various ethnic groups occurred, causing the Han ethnicity to incorporate many non-Han ethnic bloodlines (Yida Yuan and Cheng Zhang, 2002).

Apart from the Chinese nation, many other ethnic groups on Earth also have a history of genetic exchanges. After the discovery of the New World in the Americas, there was a second major population migration in the world. This population migration began in the late 15th century and ended in the early 19th century, lasting for more than 800 years. The main migration directions were: one was from Europe to the Americas, and the other was from Africa to the Americas. The initial migration was to search for gold and open up new living spaces in the new continents such as North and South America. The migrants were mostly bankrupt artisans, farmers, and merchants from Western Europe, as well as those who fled feudal oppression and religious persecution, and also adventurers seeking wealth. (Zhongguan Wu, 1997) Different populations merged in North America. After several hundred years of development, the hybrid effect was fully manifested. Today’s United States has achieved multiple firsts in terms of national economic production volume, military strength, and science and technology.

From an individual perspective, in modern humanity, there have emerged many individuals who are both long-lived and wise, such as Emperor Qianlong of the Qing Dynasty (Aisin-Gioro Hongli, 1711-1799, aged 89, a mixed-blood of Manchu, Han, Mongolian and other ethnic groups, with 1/16 ± 1% Han Chinese bloodline), modern Macau gambling tycoon Ho Hing Shan (aged 98, with multiple ethnic (clan) genetic exchanges, the heterozygous effect is manifested in individuals).

On the contrary, if a group does not exchange genes with the outside world and remains isolated, the consequence will be extinction due to inbreeding, or death from inability to resist foreign diseases.

In the history of European social development, there is a typical example. A dynasty was destroyed because of the long-term practice of consanguineous marriage within a closed small family group, which led to the emergence of genetic diseases in their offspring. This is the famous Habsburg Dynasty.

The House of Habsburg (6th century - 1918) was the most powerful and expansive royal family in European history, having ruled over the Holy Roman Empire, the Spanish Empire, the Austrian Duchy, the Austrian Empire, the Austro-

Hungarian Empire, and the Second Mexican Empire, among others. The Habsburg family is also known as the Austrian family. The Habsburg dynasty began its 640-year rule in Austria in 1278. In the early 18th century, the territory of the Habsburg dynasty expanded unprecedentedly. After the Congress of Vienna in 1815, a German Confederation led by Austria was established. In 1866, Austria was defeated in the Prusso-Austrian War, and the Confederation was dissolved. In 1867, an agreement was signed with Hungary, and the Austro-Hungarian Empire was formed. After the end of World War I in 1918, the empire disintegrated. This family, which ruled Europe for 1,300 years, suddenly declined in the 18th century, and the reasons for this are puzzling. According to research, incest and close marriage may have been the main causes.

One of the fatal disadvantages of consanguineous marriage is that the children born, whether male or female, are prone to premature death. The Habsburg dynasty in the early days indeed had a large number of royal members and numerous offspring. However, as generations of consanguineous marriage continued, the number of offspring gradually decreased. This was a factor contributing to the decline of the Habsburg dynasty. Historical records also show that out of the 11 significant marriages within the Habsburg family, 9 were consanguineous marriages. (Phoenix News, 2009).

In 1665, King Philip IV passed away. At the age of only 4, King Charles II succeeded to his father's throne. As he grew older, the bitter consequences of marrying a close relative were fully manifested in him: low intelligence, epilepsy, heart disease, deafness, impotence, infertility, and so on. He lived to be 39 years old, but unfortunately, he had no descendants because he simply had no reproductive ability. In 1918, the empire disintegrated and the emperor abdicated. The Habsburg family was no longer the ruler of Central Europe. The former territory was divided among 7 countries: three new countries - Czechoslovakia, Poland, and Yugoslavia, and four existing countries - Austria, Hungary, Italy, and Romania.

There is also an example in South America where a community faced extinction due to long-term isolation. According to the July 2003 issue of National Geographic of the United States, in the Amazon rainforest area of Brazil, there is a group of "archer tribe". The "archer tribe" is one of the 17 isolated tribes living deep in the Brazilian Amazonian forest. The indigenous area of the Javari River Valley is likely the largest closed indigenous living area in the world, with approximately 1,350 people. Most of them are descendants of those who survived the massacres carried out by white people over the past several centuries. They are descendants of the Indians. They have lived in the deep forest for a long time, isolated from the outside world. Most of them are unable to resist foreign infectious diseases, including common colds. Twenty-five years ago, after Brazilian officials came to this tribe, a large-scale epidemic death occurred in the tribe (mainly coughing). After several months of contact with the outside world, 350 people died in another tribe living in the Ituri River (the Matsi people). (Xiao Xiang Morning Post, 2003).

The role of genetic recombination and heterozygous effects in other biological variations is also very obvious. After the emergence of humans on Earth, humans have continuously utilized the heterozygous effect of organisms to change the genetic combinations of animals and plants, generating new traits, domesticating wild plants into crops, domesticating wild animals into livestock, and domesticating wild rice into cultivated rice (Yuehui Wu, 2024). Initially, wild wheat that appeared in the Mediterranean and the Middle East was domesticated into cultivated wheat all over the world. Two-grain wheat and rough goat grass (barley grass) hybridized approximately 8,000 years ago, eventually forming today's common wheat (Tong Xu, 2021). Wild teosinte underwent secondary domestication and transformed into corn (Jianbing Yan, 2023). About 10,000 years ago, humans domesticated wild pigs into domestic pigs and wild chickens into domestic chickens. These domesticated animals and plants followed the movement of humans and continued to flow, with crops, livestock, poultry, and microorganisms from different sources, different regions, and with different properties undergoing continuous hybridization, separation, re-hybridization, and re-separation within the same species. Through human and natural selection, various varieties and groups emerged to meet the growing demands of humans on the material for their lives on Earth.

Among the species with the largest number on Earth, the microorganisms have small genomes and simple structures, which make them prone to genetic heterogeneity and mutations. They have played a significant role in biological evolution and coexist in the bodies of many animals and plants. After the emergence of humans, humans have utilized many beneficial microorganisms and their variants, and widely applied them in industries such as brewing, fermentation, leather production, and medicine. For many harmful microorganisms and their variants, humans have also constantly fought against them, changing certain genetic structures of humans or generating corresponding immunity within the body to protect their own survival.

4. Some of the Main Laws of Biological Heterosis Effects

In the process of biological reproduction, whether sexual or asexual, hybridization effects occur. In my article "The Laws of Biological Variation: Offspring Resemble Parents, Yet Are Not Parents" (Linyun Wang, 2023), I have already presented some of the main laws of biological hybridization effects. Here, I will further supplement them as follows.

4.1 Hybridization effect is not a simple cross between two varieties. Nor is it one gene particle replacing another. The influence of parental traits on offspring traits is not equal. Some traits of the offspring tend to be like the father, while others tend to be like the mother. It does not follow the Hardy-Weinberg law of genetic equilibrium (1908), and the existing formula for calculating inbreeding coefficient is also incorrect. The fact that the offspring of reciprocal crosses between different varieties of livestock, crops, and microorganisms exhibit different traits proves this point.

The traits of the offspring are not the sum of the related traits of the two parents minus 2. It cannot be expressed as 50% from the father and 50% from the mother. Instead, it should be stated as 50±% from the father and 50±% from the mother.

The hybrid effect also varies depending on the degree of heterozygosity of the parents themselves. Here, let's use the example of "cooking vegetables" in daily life to illustrate. We take "50g of cucumber" as one parent (father) and "50g of shredded meat" as the other parent (mother). The offspring resulting from the cross between these two parents is "50g of cucumber + 50g of shredded meat" (100g). Suppose 50g of cucumber and 50g of cucumber are cooked together or 50g of shredded meat and 50g of shredded meat are mixed together, then the 100g of the dish is called "pure breeding". When 50g of cucumber and 50g of shredded meat are cooked together, the offspring is "50g of each type mixed with 50g of 100g cucumber and shredded meat" and is called "hybrid breeding". However, when "25g of cucumber + 25g of shredded meat" and "25g of cucumber + 25g of shredded meat" are mixed together, the offspring is also "50g of each type mixed with 50g of 100g cucumber and shredded meat". When "10g of cucumber + 40g of shredded meat" and "40g of cucumber and 10g of shredded meat" are cooked together, the offspring is also "50g of each type mixed with 50g of 100g cucumber and shredded meat". In fact, the ratio of cucumber to shredded meat can be in various different proportions, and the offspring can also exhibit various different proportions of "100g cucumber and shredded meat". The genetic material of living organisms (DNA) undergoes changes in the offspring produced after the mating of the two parents, which is much more complex than this "cooking vegetables" example.

After self-fertilization of the F1 generation, the F2 generation will undergo segregation, making the situation even more complex. The offspring produced by backcrossing the F1 generation with a certain parent can be represented as 75±%:25±%. More materials are needed for further research and analysis on this. The segregating offspring have both good and bad traits. There is a possibility of producing excellent individuals, or inferior varieties. Especially in "inbreeding", the offspring will have various genetic defects, deformities, and reduced vitality.

4.2 The Variations Between the Offspring and the Parents Are Characterized by Their Small Scale, Gradual Nature, and Diversity

Since life emerged on Earth 3.8 billion years ago, it has been constantly mutating and evolving, resulting in increasingly larger genomes. Scientists' analysis of the genome sizes of large biological groups has proved that the minimum genome size varies with different species. The genome of mycoplasma (pneumonia mycoplasma) is only 1.0×10^6 bp, that of bacteria (Escherichia coli) is 4.2×10^6 bp, that of yeast (Saccharomyces cerevisiae) is 1.3×10^7 bp, that of nematode (Caenorhabditis elegans) is 8.0×10^7 bp, that of insect (Drosophila melanogaster) is 1.4×10^8 bp, that of bird is 1.2×10^9 bp, that of amphibian (Xenopus laevis) is 3.1×10^9 bp, and that of mammal (human) is 3.3×10^9 bp (Lewin B., 2005). However, further analysis shows that after hybridization within the same species or between closely related species, the vast majority of the nucleotide sequences of their offspring remain unchanged, with only a few alterations. The nucleotide difference between humans and chimpanzees is only 1.5% - 3% (Tarjei S. et al., 2005). The genomes of different human races in the world (3.01 billion pairs) have at least 99.99% of base pairs that are the same. Only the remaining less than 0.01% (300,000 pairs) of differences determine whether we are prone to certain diseases and also determine our differences in height, skin color and body type, etc. (Science [J] 2005.2.18).

This is the aspect of the minuteness and gradualness of variation. The diversity of variation refers to the fact that compared with the parents, the variations in the nucleotide sequences of the offspring do not occur at one point, but at multiple points. There are both nucleotide sequence variations and epigenetic phenomena of changes in non-nucleotide sequences. The process of species continuation is a dynamic process. All species in nature are at the middle or late stage of speciation; or they are beginning a new round of species differentiation, or they are in the early stage of speciation. (Zefu Wang et al., 2025).

4.3 The variations between offspring and parents are random and directionless. Without human intervention, they are not subject to the will of the organisms themselves. Randomness is an important concept in biological variation. According to Darwin's evolutionary perspective, changes in biological traits occur randomly and are not influenced by the environment. Beneficial mutations are positively selected, while harmful mutations are negatively selected. (Brown T.A., 2002g) Biological variation does not contain human emotions such as "fierce", "cunning", or "kind".

It should be pointed out that biological evolution has no directionality and is unpredictable. Evolution does not equal progress; it is not about "survival of the fittest" or "the law of the jungle". In the process of life adapting to the environment, there is not only competition but also collaboration, coexistence, and even "altruism". Many weaker species can also find their ecological niches. (Edited by Jiayu Rong, 2024) Among living organisms, multiple food chains have formed, interdependent on each other. A multitude of species have formed a community of life on Earth. For instance, various plankton, crustaceans, small fish and shrimp in the ocean are the main food sources for squids, while squids are the primary food for whales and other large fish, and are also one of the important marine foods for humans.

4.4 The Nucleotide Sequences of the Offspring After Biological Variation Can Be Inherited or Separated Again

The newly generated nucleotide sequences in the offspring can be fixed and passed on through appropriate inbreeding. Both desirable traits and undesirable traits can accumulate and be passed down from generation to generation. However, during the continuation of generations, some of these nucleotide sequences remain very stable and do not change, while others may undergo re-segregation or variation, resulting in corresponding changes in the traits. The segregation of hybrid offspring does not follow the binomial expansion $(a + b)^2$, and the situation is even more complex. More research is needed in this area.

During the evolution process of organisms, certain genomic regions (or nucleotide sequences) are highly conserved. The offspring families produced by the same parent have similar genomic variations. That is to say, within the same family, certain genomic regions (nucleotide sequences or segments) remain relatively stable over generations. This is one aspect of the conservation in biological evolution.

Scientists have discovered that among the cytochrome C involved in electron transfer, there are 27 amino acids that are extremely conserved. These 27 amino acids are exactly the same in all organisms, including the more primitive yeast and the highly evolved humans. However, the amino acid variability in other parts of cytochrome C varies in degree (Qingyu Wu, 2002).

During the process of genetic inheritance, in addition to "point mutations" occurring in the nucleotide sequence, genes can also undergo duplication and divergence, which is the most important way to generate new genes. During the process of biological inheritance, the following several duplication situations can occur:

1. A single gene (a segment of the nucleotide sequence) or a group of genes (a longer segment of the nucleotide sequence) duplication;
2. The entire genome duplication;
3. The duplication of a chromosome or a part of a chromosome. For most genomes, when the nucleotide sequence changes, it will lose its function and become a pseudogene. Only occasionally, some additional gene copies will acquire new functions due to mutations, thereby generating new genes.

The Saccharomyces cerevisiae underwent cell division approximately 100 million years ago. A homology analysis of the genes of the Saccharomyces cerevisiae revealed that at least one "genomic segment consisting of 376 genes" had the same genes at three locations. These genes were located on different chromosomes, but their arrangement order was the same. (Shouyuan Zhao, 2001).

There are many examples in the genetic improvement of animals and plants where the nuclear acid sequences of the offspring of crossbreeding between parents result in trait variations. Taking the number of piglets born per litter as an example, someone began in 1955 to crossbreed pigs from the Huizhou breed (with an average of 12.46 ± 0.48 piglets per sow litter in 41 sow pens) as the maternal parent and Yorkshire pigs (with an average of 10.13 ± 0.30 piglets per sow litter in 46 sow pens) as the paternal parent. The resulting F1 generation (new Huizhou pigs, containing 50 ±% Yorkshire pig bloodline: 50 ±% Huizhou pig bloodline) had an average of 13.63 ± 0.57 piglets per sow litter. The F1 generation self-crossed to produce the F2 generation (still containing 50 ±% Yorkshire pig bloodline: 50 ±% Huizhou pig bloodline) and showed segregation, with an average of 12.10 ± 0.70 piglets per sow in 10 sows. (Weixin Chen et al., 1963). After 14 years of selection, when the new Huizhou pig population was evaluated and accepted in 1977, the average number of live piglets born per adult sow was 12.23. This example shows that the littering performance of the F1 generation is not the sum of the parental performances divided by 2, but leans towards the maternal parent. The traits of the F2 generation (still containing 50 ±% Yorkshire pig bloodline: 50 ±% Huizhou pig bloodline) after self-crossing show segregation, with an average of 12.10 ± 0.70 piglets per sow in 10 sows. (This indicates that multiple variations in the nucleic acid sequences occur, and there are differences between individuals.) Although at that time (1963) and the current research level did not have evidence using nucleic acid sequence variations to prove this point, because there are multiple factors affecting the reproductive capacity of pigs, involving the number of corpora lutea (ovulation rate), litter size, number of nipples, and the age of reaching puberty, and there are multiple related genes, not just one. (Feng'e Li et al., 2003) However, the changes in the phenotypic values of the littering performance have already proved that multiple variations in the nucleic acid sequences do exist, and there are individual differences.

An example of a hereditary bad gene can be illustrated by the "Habsburg big chin" that emerged in Europe from the 6th century to 1918. The most powerful and widely ruling royal family in European history, the Habsburg royal family, had a distinctive facial feature: a protruding chin and a large jaw, also known as the "Habsburg big chin". This feature persisted for several generations until the end of the dynasty (Phoenix Information, 2009).

4.5 The rates of various biological mutations vary. Due to the different generation intervals and genome sizes among various organisms, some undergo changes more rapidly, with their reproductive cycles lasting only a few hours or days (such as certain viruses and bacteria with smaller genomes). Others undergo slower changes, and those with larger genomes and longer reproductive cycles take several years, even several hundred or several thousand years. The result of evolution is that some thrive, some become extinct branches, some evolve into new species, and some die out. Not all individuals that undergo mutations can survive; some die halfway through.

For instance, the mutations of the COVID-19 virus occur frequently. However, not all the mutated COVID-19 viruses can survive. In fact, most mutations usually have adverse effects on the survival of the virus. Viruses carrying unfavorable mutations cannot adapt to the environment and gradually disappear; but a few mutations will enhance the infectivity or transmission ability of the virus, and gradually evolve into dominant variant strains.

In February 2021, an article was published in the authoritative journal "Cell Host & Microbe", using the 355,067 COVID-19 virus genome sequences from the GISAID database as the research object. The researchers found that there were approximately 30,000 mutations (accounting for 8.57%) in these over 350,000 genome sequences; among them, 3,823 (accounting for 12.74%) were representative COVID-19 virus mutant strains, meaning that the genetic mutations affected the characteristics of the virus; 130 (accounting for 3.4%) were nucleic acid mutation sites that could be continuously inherited (these mutations could spread and diffuse among the population); 75 (accounting for 1.96%) were non-synonymous mutations (which would cause changes in the virus proteins, affecting the transmission ability or pathogenicity); and 24 (accounting for 0.628%) were parallel mutation sites (the same mutations occurred simultaneously in the COVID-19 viruses from different regions). Such mutations may enhance the adaptability and survival ability of the virus. It can be seen that the viruses that mutated in these over 350,000 genome sequences were able to spread and diffuse among the population and affected the transmission ability (0.037%) or pathogenicity (0.021%) of the virus. However, as long as they exist, they are constantly evolving.

The mutated strain of the COVID-19 virus that has caused the resurgence of the pandemic on a global scale is precisely the variant virus that emerged from among so many COVID-19 virus mutations. From the variant Alpha (B.1.1.7), to Beta (B.1.351), to Gamma (P.1) and Delta (B.1.617.2), with each mutation, the COVID-19 virus has demonstrated greater transmissibility (Chen Gen, 2021). However, at the same time, its pathogenicity sometimes weakens. Its mutations are random.

The mutations of other microorganisms, animals and plants are similar.

4.6 *Unlike the assumptions of classical genetics, molecular genetics holds that genes do not have dominant and recessive traits, nor do they have supergenes or subgenes***.** However, there are DNA methylation and demethylation processes, as well as epigenetic phenomena.

4.7 *Genetic variations in biological genomes are generally irreversible.* Although biological variations are random and without directionality, the variations in the nucleotide sequences of the offspring produced by parental hybridization are generally irreversible. Small genome organisms can evolve into large genome organisms, but large genome organisms cannot evolve into small genome organisms.

After humans separated from the anthropoid apes, it is impossible for them to evolve back to the anthropoid apes (sometimes partial traits may return to their ancestral forms, but it is impossible for all traits to return.). After birds evolved from some dinosaurs, they could no longer evolve back into dinosaurs. The mutant strain of the COVID-19 virus, Alpha (Alpha B.1.1.7), evolved into Beta (Beta B.1.351), and the Beta virus strain (Beta B.1.351) could not evolve back into the Alpha virus strain (Alpha B.1.1.7).

However, in certain special circumstances (such as long-term inbreeding, etc.), some DNA may be methylated, preventing certain traits from being expressed. More experiments are needed to confirm this.

4.8 *The same biological species may undergo nucleotide sequence variations in different living environments.* Within the same species, when they persist across generations in different altitudes and under various environmental conditions on Earth, their nucleotide sequences will also change, although these variations are minor and gradual. Whales gradually evolved from terrestrial animals to aquatic animals in this way. For instance, if lower-level biological species on Earth (such as moss plants and the fungi that live symbiotically with them, ferns (such as the cycad), etc.) are first exposed to simulated lunar environment conditions on Earth for a certain period of time, their nucleotide sequences will also change. Then, when they are moved to areas with water on the moon, after an appropriate amount of time, their nucleotide sequences will gradually change as well. Some may die, while others can adapt to the lunar environment (such as microgravity, large day-night temperature differences, low oxygen levels, etc.) and survive.

5. Application of the Theory of Species Variation in the Evolution of Earth's Organisms

5.1 *The theory of species variation can provide a reasonable explanation for the causes of biodiversity on Earth.*

During the continuation of a biological species' generations, due to errors in DNA replication and the heterozygous effects resulting from interbreeding between parents, various variations occur. Under the influence of the environment or due to the reasons of these variations themselves, some species may become extinct or die out, while others can transform from the original species into another species.

Scientists have discovered that the earliest life on Earth originated from the microorganisms around the "black chimneys" in the deep ocean. These microorganisms continuously "mated" and mutated, with moderate inbreeding and relative stability, evolving into various aquatic proto-organisms, plants and animals. Then they "mated", mutated, and had moderate inbreeding and relative stability again. Aquatic organisms emerged on land, evolving into terrestrial organisms and animals, and some terrestrial animals returned to the ocean (such as whales). Life constantly "mated", mutated, had moderate inbreeding and relative stability; then "mated" again, mutated again, had moderate inbreeding again, and remained relatively stable again. This cycle repeats over and over, moving forward in a continuous loop. Through natural selection, some survived while others were eliminated. The variety of life species increased. This is the evolutionary process of biodiversity on Earth.

Animals evolved from aquatic to amphibian forms and then from amphibians to terrestrial reptiles (Shougang Hao et al., 2000b).

Cetaceans are mammals that evolved very early. The modern whales in the ocean were once four-legged land animals. Their ancestors, the ancient whales, shared a common ancestor with hippos, camels, and deer. Like other land mammals, they all had four legs and were even-toed ungulates. About 50 million years ago, because the ratio of food to predators in the water was more favorable for the survival of ancient whales than on land, they began to enter the water. Around 10 million years ago, the descendants of ancient whales evolved to be very similar to modern whales, and their hind legs also degenerated into fin-like appendages. From then on, they no longer came ashore, but they still retained the balance organ "inner ear" that land animals have. During the evolution of ancient whales, there were Pakicetus, Rodhocetus, and Basilosaurus, etc., and finally they became modern whales (Shougang Hao et al., 2000c). This variation was completed over a period of 40 million years (Jun Liu et al., 2012).

Dinosaurs once existed on Earth. They lived for approximately 140 million years. They disappeared from the Earth about 60 million years ago. Some scholars believe that not all dinosaurs died out; some of them evolved into birds. (Shougang Hao et al., 2000d)

The theory that birds originated from dinosaurs was first proposed by Huxley in the mid-19th century. It was popular for a long time but disappeared in 1927, being replaced by the toothed-origin theory. It was not until the 1970s in the 20th century that renowned dinosaur expert John Ostrom from Yale University in the United States re-proposed it. Since the 1980s, its influence has been expanding and it has gradually become the mainstream school of thought. Currently, most scholars have accepted the view that birds originated from dinosaurs and believe that birds evolved from a small-sized individual of a theropod dinosaur. At the annual meeting of the Society of Vertebrate Paleontology held in Arizona, USA on October 20, 2005, paleontologists announced a new species of dinosaur that lived at the same time as Archaeopteryx and was closely related to it. This dinosaur lived during the Late Jurassic period and has a history of 150 million years. It belongs to the genus Sinosauropteryx, a type of ornithomimid dinosaur. According to the discoverers, this is the most ancient fossil found that is closely related to birds. What is more important is that it lived at the same time as Archaeopteryx, which fills the "time gap" in the theory that birds originated from dinosaurs. (William Wahl et al., 2005)

Humans evolved from chimpanzees; whales evolved from elephants. A history of biological evolution is a history of the exchange of biological genes.

In the process of reproduction of any living species, it is always undergoing continuous variations. Variations are absolute, while the absence of variation is relative. The organisms on Earth have evolved from single-celled to multi-celled, from asexual reproduction to sexual reproduction, and from hermaphroditism to dioecy. From a general perspective, the biodiversity on Earth is not decreasing but increasing. In essence, the number of organisms on Earth is increasing and they are becoming more complex. If this were not the case, then the organisms on Earth would still be in the "black chimney" generation or the era of biological explosion to this day.

5.2 After humans separated from the apes, over the course of 4.5 million years of evolution, they continuously modified their genetic structure to adapt to life on Earth. Modern humans are better adapted to the environment on Earth and have a longer lifespan compared to ancient humans.

Throughout the history of human development, there have been countless disasters of various magnitudes. Among them, the ones that are particularly unforgettable are the Black Death from 1347 to 1353 and the influenza in 1918. Within just six years from 1347 to 1353, the Black Death (later proved to be the plague) claimed the lives of approximately 25 million Europeans, accounting for one-third of the total population at that time. (Daily Knowledge, 2020) However, when the vicious Black Death resurfaced in the 17th century, there was an exception. In September 1665, the plague once again invaded London with great ferocity. But in a small village outside London - the village of Eynsham, there were 433 survivors. After being studied by a scientist, Stephen O'Brien, it was believed that these survivors had a genetic mutation, which was called the "Delta32 mutation" (referring to "a deletion mutation in the receptor gene, losing 32 base pairs"). This mutated gene has an extremely high occurrence rate in Europe, indicating that its advantages are very prominent. This mutated gene was approximately present in large numbers in the European population about 700 years ago. (National Geographic Channel, USA, 2006)

Other examples of human modification of genetic structure can also be listed. For instance, the malaria parasite has been present since at least 30 million years ago. Humans have been attacked by the malaria parasite since their inception. To reduce mortality, during the process of evolution, humans have undergone genetic variations. Some people have a deficiency in a protein antigen on the surface of human red blood cells, known as Duffy antigen deficiency. People in the regions of West and Central Africa have a large proportion lacking the Duffy antigen, effectively eliminating the threat of intermittent and tertian malaria in these areas. Some people have a single-base mutation in the beta chain of the globin gene causing sickle cell anemia. Up to 40% of people in Africa, South Asia, and the Middle East have this genetic mutation, which can reduce the mortality rate of malignant malaria by 90%. However, this is a desperate measure because those who inherit sickle cell anemia have a 25% infant mortality rate. (Jing Huizi, 2015)

5.3 Humans, consciously or unconsciously, have applied the theory of species variation, not only domesticating crops and livestock and altering their genetic structure, but also continuously improving their yields and qualities.

Corn, as one of the most widely cultivated crops in the world, has always been subject to continuous controversy regarding its origin. By integrating various research methods such as archaeology, molecular biology, and population genetics, Chinese and American scholars jointly proposed a new model for the origin of corn, namely the "secondary origin hypothesis". Approximately 9,000 years ago, corn originated from the sub-species of small-grain tall grass; around 6,000 years ago, corn underwent a second hybridization with the Mexican plateau sub-species, resulting in a second domestication process. Modern corn is derived from the offspring of two different tall grasses. The secondary origin has significantly enhanced the adaptability of modern corn, and the Mexican plateau sub-species provided high-altitude adaptability and extensive resistance genes to modern corn. (Jianbing Yan, 2023)

In the process of domesticating and improving animals, the British crossed the local Yorkshire pigs with Chinese pig breeds and domesticated them into the modern Large White pigs that are distributed all over the world, which is a representative example.

As early as 1818, local breeds of pigs appeared in the area near Yorkshire in southern England. They are descendants of European wild boars. The early Yorkshire pigs were large, with thick bones and long legs, white in color, and had a large body size. Adult pigs could weigh over 1000 pounds. Their backs were rounded, their spines like those of a carp, their hind legs were underdeveloped, their heads were narrow and straight, their ears were large and drooping, they had very developed snouts and four sharp teeth. Their skin was thick and their bodies were covered with dense and coarse bristles. Some had a light yellow or brownish red color. They matured slowly, had rough meat, were very wild in temperament, had fierce eyes, and each litter could produce 5 to 8 piglets.

According to Plumb (1920), at that time, the British introduced the small-eared pig from Guangdong in China and crossed it with other breeds, resulting in multiple different hybrid groups. Some were called small Yorkshire pigs, some were called Leicesters, and some were called Yorkshire pigs. These different groups then interbred with each other, gradually forming the improved Yorkshire pigs of the 18th century. (C.S. Plumb, 1920) This was the first hybridization between Chinese pig breeds and British native pig breeds.

The second improvement of Chinese pig breeds over European pig breeds occurred in modern times. In October 1979 and December 1981, France imported Mei Shan pigs from China and crossed them with French Large White pigs. After about 20 years, a "French Large White pig breed" was selected and bred, with a significant increase in the number of piglets born. In 1999, among the "French Large White pigs" imported from France, it was found that while maintaining a high lean meat rate of the carcass, the number of piglets born increased significantly (according to a report in 2000, the average number of piglets born in 29 litters with 3 births per litter was 13.97). However, the abdomen became larger, and a few of the offspring piglets showed a small amount of black hair or black spots, which is strong evidence that it contains a small amount of the Chinese Mei Shan pig bloodline. (Linyun Wang, 2014)

Modern molecular genetics analysis also provides further evidence for this. Fang et al. (2006) used pyrosequencing technology to sequence the mitochondrial CytB gene and D-loop region of 45 pig populations worldwide, including 934 European pig individuals and 21 Chinese local pig breeds, and conducted genetic polymorphism analysis. In the selected Longbei and Dabai pig populations, the proportions of mtDNA haplotypes (haplotype refers to the combination of alleles at multiple loci on the same chromosome that are subject to common genetic inheritance) of different strains varied, with an average of 12.8% and 73.2% of haplotypes respectively; statistically, the average proportion of Chinese pig breeds' haplotypes in the entire population of commonly used commercial pigs in Europe was 29%. (FANG M Y, et al., 2006) Now in both the northern and southern regions of China, there are many large white pig or Yorkshire pig populations from different countries. Depending on their origin from different countries, they are called varieties such as the German line, the Japanese line, the Danish line, etc. Whether it is the earliest 18th-century original Yorkshire pigs from Britain and the Yorkshire pigs introduced from the United States and other places to China before the 1950s, or the Yorkshire pigs imported from the UK to China in the 21st century. Although they are all called "Yorkshire pigs", "Large Yorkshire pigs", or "Large White pigs", due to the continuous genetic exchange between the local pig populations and the same-named groups outside the region, from the perspective of genetic structure (nucleotides, haplotypes, etc.), there have been certain differences among them. As a result, there are also certain differences in performance and appearance.

According to the theory of species variation, the existing breeding theories for living organisms (domestic animals, domestic birds and crops) also need to be innovated and changed. From the perspective of nucleotides, no two organisms on Earth have exactly the same nucleotide sequence. The "pure" and "mixed" of species are relative, and the "pure" and "mixed" of varieties (subspecies, subtypes) within the same species are also relative. There is no absolute pure breed; all biological varieties are hybrids. There are certain differences in appearance and performance between different groups within the same species (such as groups, varieties, etc.), which enriches the genetic structure of the species and is not a bad thing but a good thing. Within the same variety, certain differences in appearance and performance between different groups (subspecies, subtypes, etc.) are not bad but good, as it can prevent inbreeding and incompatibility.

"Purebred breeding" (between different strains, breeds, or bloodlines) refers to the breeding where the nucleotide sequences of the parents differ minimally. "Hybrid breeding" (between different breeds) refers to the breeding where the nucleotide sequences of the parents differ significantly. Simply relying on "purebred selection" - "purebred selection" of a single variety to improve yield and quality is not comprehensive enough. Instead, a cycle of "pure breeding" - "hybrid breeding" - "re-pure breeding" - "re-hybrid breeding" should be adopted to rapidly enhance yield and quality.

5.4 Microorganisms on Earth are also constantly undergoing mutations. Studying the mutations of microorganisms that are harmful to humans can enable us to take preventive measures against them in advance, while researching the mutations of beneficial microorganisms can help them serve humanity better.

Over the past 30 years, China's pig farming industry has been hit by several major and severe infectious diseases. In 1996 and 2006, it was invaded by swine fever twice, resulting in the death of millions of breeding pigs and piglets. In 2006, 40% of pregnant sows were infected. On August 3, 2018, African swine fever invaded China. A large number of sows died across the country, and the total number of sows in the country decreased from 31.3 million in August 2018 to 19.04 million in September 2019. The main reasons for the occurrence of these three major infectious disease epidemics were that a small number of pathogen pigs (African swine fever first occurred in Shenyang, Shenyi New District, Liaoning Province) entered the country first, and then spread rapidly throughout the country through the large circulation of live pigs (pork pigs). During the spread process, the virus hybridized, mutated, then hybridized again, and mutated again. The original vaccines were unable to control it. Therefore, to control the hybridization and mutation of the virus, the best solution is to change "live pig circulation" to "pork circulation". Because the virus only attaches to live pigs, while on the pork after slaughter, the virus cannot survive for a long time.

The evolution history of influenza virus strains is another example of harmful microbial mutation. The influenza virus is one of the earliest viruses to appear on Earth, being the main culprit causing influenza in humans and animals. It belongs to the Orthomyxoviridae family and causes acute respiratory infections, spreading rapidly through the air.

The Spanish flu that broke out in 1918 claimed the lives of 20 to 40 million people. It was caused by the H1N1 influenza virus, which is closely related to swine flu. It was not until the 20th century that humans first isolated the influenza virus. However, the understanding of influenza symptoms began long before the Common Era. In 412 BC, the renowned Greek physician Hippocrates began to describe the prevalence of influenza, which is recognized as the earliest description of the epidemiological symptoms of influenza.

Based on the different characteristics of the influenza virus genome, it can be classified into human influenza virus, swine influenza virus and avian influenza virus, etc. According to the antigenicity of the viral nucleoprotein and matrix protein, it can be further divided into three types: type A, type B and type C.

The large-scale outbreak and prevalence of influenza should have occurred after the Industrial Revolution. "Influenza can be cured and patients can recover within 5-7 days. The influenza virus cannot remain dormant in humans for a long time. The Industrial Revolution led to a rapid increase in urban population, establishing a human-to-human biological transmission chain." After the Industrial Revolution, the outbreaks of influenza became more frequent and on a much larger scale than before.

Among the three types of influenza viruses - type A, type B, and type C - the type A influenza virus has the greatest variability. The three major influenza pandemics that occurred in the last century were all caused by type A influenza viruses. This shows the path of the variation of type A influenza viruses.

The influenza virus undergoes mutations during its transmission among humans. 70% of those infected with the flu develop antibodies, which also cause the virus to mutate. After the first wave of the 1918 influenza pandemic, the virus spread from humans to pigs, resulting in the emergence of influenza in pig populations. For nearly 40 years after that, the descendants of the A(H1N1) virus were the main influenza virus strains. Until 1957, the human H1N1 virus recombined with the Eurasian avian-origin H2N2 influenza virus to produce the A(H2N2) influenza virus, causing the outbreak of the Asian flu. Approximately 11 years after the epidemic, the H2N2 virus recombined with the avian-origin H3 virus to form the A(H3N2) virus, which was the virus strain that caused the 1968 Hong Kong flu. (Ying Zhang, 2009).

It is necessary to closely monitor the mutations of viruses such as avian influenza virus and swine vesicular disease virus, which have close relationships with humans. Their further mutations may pose greater risks to humans. It is not recommended to conduct high-density breeding of livestock and poultry and to prevent people (especially those infected with infectious diseases) from being concentrated in high-density groups, as these are effective methods to prevent further mutations of the viruses.

5.5 Applying the theory of biological hybridization to the study of variations in other lower species is also very promising. For instance, if humans want to live on the moon, they can first study how lower organisms (such as moss plants and the fungi and ferns that live symbiotically with them, as well as the cycads) survive in simulated lunar environments on Earth (with microgravity, large temperature differences, and low oxygen content), and then transport them to the moon. Other animals and plants can also be tested in the same way. This will help accumulate data for humans to live on the moon.

6. Species Variation and Whether There Will Be a Mass Extinction on Earth Are Two Different Issues

For nearly 300 years, human society has entered the industrial civilization era after experiencing tens of thousands of years of agricultural civilization (most people believe that it started from the appearance of the first steam engine in 1698, which is now 320 years). Human beings have achieved unprecedented results in controlling and transforming nature with the weapons of science and technology. Steam engines, electric motors, computers and nuclear reactors, each technological revolution has established a new monument of "humanized nature", and armed agriculture with industry, while also discharging a large amount of carbon dioxide, waste plastics, sewage, etc. Ecological, resource and population problems have also faced unprecedented crises, causing great damage to the environment. The earth's temperature has risen, the probability of extreme weather has increased, thus affecting the survival of some species. Some species on the earth are on the verge of extinction, and many species die out and become extinct every year. According to incomplete statistics, starting from the dodo that became extinct in 1681, to the death of the Galapagos tortoise George in June 2012, at least 44 species of animals have become extinct in 331 years (1681-2012). Currently, many animals and plants such as giant pandas and finless porpoises are in a state of endangered numbers.

Over the past 3.8 billion years, there have been five major mass extinctions on Earth. Will there be a sixth large-scale mass extinction? This is a question that many scientists are concerned about. I believe that whether there will be a mass extinction is a different issue from biological variation and the increase in biodiversity. As long as there are living things on Earth, biological variation will always exist and biodiversity will increase. However, whether there will be an extinction is determined by the relationship between living things and the Earth's environment.

Will the Earth experience the 6th major mass extinction? I believe it is related to two factors. The first is that the number of living organisms on Earth is constantly increasing, especially the human population, which is growing too rapidly in terms of quantity, leading to environmental deterioration and making it impossible for organisms to survive. According to research, the global population has grown astonishingly in the past 2,000 years. In the year 1 AD, there were only 188 million people, and by 1900 AD, it had increased to 1.65 billion (Yuan Liu, 2022). By mid-November 2022, this figure had reached 8 billion. Therefore, the American environmental organization "Global Ecological Footprint Network" (GFN) and the British think tank "New Economic Foundation" proposed the theory of "Earth Ecological Overshoot Day" in 2012. According to GFN's calculation, in 1961 (when the world population was 307.3 million), humans consumed only about two-thirds of the Earth's annual renewable resources, and most countries still had an ecological surplus. However, both global consumption and the population are increasing. Since the early 1970s, human demand for Earth resources has exceeded the Earth's ability to regenerate resources, and this situation is called ecological overload (Chuo Feng Dang, 2016).

Starting around 1970 (with a global population of 376.8 million in 1971), human beings began to demand more from nature, exceeding the ecological threshold of the Earth. The trend over the past few decades shows that this day approaches one month earlier every 10 years. The Earth's overloading day in 1994 (with a global population of 564.2 million) was October 22nd. The Earth's ecological overloading day in 2022 (with a global population of 8 billion) was July 28th. If humans continue to increase their population in an uncontrolled manner, the Earth will be overwhelmed. Therefore, whether humans can consciously control population growth is the key to whether life will become extinct.

The second reason for the sixth major mass extinction of species is the changes in the Earth's external environment, such as asteroid impacts on the Earth, climate change, etc. The conditions on Earth no longer suit the survival of species, and species will again become extinct.

Reference

1. Baidu Knows (2020), How did the Black Death sweep across medieval Europe? And how did it eventually come to an end? Daily Knowledge, July 24, 2020
2. Brown, T. A. (2002), Genomes, [M] (Translater: Jiangang Yuan et al.Chinese verssion) Beijing Press, : 392
3. C. S. Plump, (1920) Type and Breeds of Farm Animal, 1920, New York
4. Dang Chaofeng (2016), "The Earth has entered an 'ecological overdraft' state today. The rate of consumption of renewable natural resources is the fastest in history. China Daily, August 8, 2016.
5. FANG M Y, et al. (2006), Mitochondrial diversity in European and Chinese pigs is consistent with population expansions that occurred prior domestication. Proc Biol Sci ,2006, 273(1595):1803-1810e
6. Feng'e Li, et al. (2003), Research Progress on Major Genes and QTLs Affecting Pig Reproduction Capacity, Foreign Animal Husbandry - Pigs and Poultry, Volume 23, Issue 4, July 2003, pp. 31-35
7. Gen Chen (2021), The Delta variant is prevalent worldwide. Why has the novel coronavirus mutated? [EB/OL] Phoenix News 2021-06-21 09:07
8. Hua Sun (2023), The Structure and Characteristics of the Sanxingdui National System, "Chinese Social Sciences", Issue 1, 2023, February 27, 2023
9. JianbingYan (2023), "The Century Debate on the Origin and Evolution of Corn", Journal of Maize Science 2023, 31(6): 1-6
10. Jianquan Liu, (2016), "The Concept of Integrated Species" and "Species on the Road of Diversification". Biodiversity, 2016, 24(9): 1004 - 1008.
11. Jianya Li, (2006) Humans Have "Left Africa" Three Times (Group Photos), The Beijing News, Sohu, February 16, 2006, 09:29
12. Jiaru Rong et al., (2014), "Ancient Catastrophes" [M], Nanjing: Jiangsu Fenghuang Science and Technology Press, December 2014, 1st edition: Preface
13. Jia-yu Rong, et al., (2024), Fossil Secrets, reported by "Chinese Academy of Sciences" on July 18, 2024.
14. Jing Huizi, (2015), From Quinine to Artemisinin: The History of the War Against Malaria, Sina Weibo, Real Estate Gossip Lady, 2015-10-07 23:4

15. Jun Liu et al. (2012), “Whales Entering the Ocean”, [J] Life World, October 2012, Vol. 276 No. 10: pp.32-35
16. Lewin B. (2005), Genes Volume VIII, Yu Long et al. (main translators), [M] Beijing: Science Press, 2005, First Edition: pp. 62
17. Linyun Wang, (2014), Gene exchange is an important driving force for altering pig traits, “Pig Science” 2014, Issue 7: pp.38-42
18. Linyun Wang, (2023), The law of biological variation: offspring like parents, offspring are not parents, SCIREA Journal of Agriculture, Volume 8, Issue 3, June 2023, pp. 137-151
19. National Geographic Channel, USA, (2006) [Science People] website of Beijing Science and Technology Daily 2006-02-27
20. Phoenix News, (2009) Close relatives’ marriage led to the extinction of the Spanish Habsburg family. Guangming Daily, 2009-4-7
21. Qingyu Wu (editor), (2002a), Basic Life Sciences, [M], Higher Education Press, May 2002 First Edition: 14
22. Qingyu Wu, (2002b) Basic Life Sciences, Higher Education Press, May 2002, First Edition, pp. 21.
23. Science [J] 2005.2.18, “Genome Differences among Different Races”, Life World [J] 2005, No. 3: pp.9
24. Shougang Hao et al. (2000a), The Origin and Evolution of Life - Life in Earth’s History. [M]. Beijing: Higher Education Press, Springer Verlag, May 2000, 1st Edition: 37-47.
25. Shougang Hao et al. (2000b), The Origin and Evolution of Life - Life in Earth’s History, [M] Beijing: Higher Education Press, Springer-Verlag, May 2000 Edition: pp. 128-136
26. Shougang Hao et al. (2000c), The Origin and Evolution of Life - Life in Earth’s History, [M] Beijing: Higher Education Press, Springer-Verlag, May 2000 Edition: pp. 221
27. Shougang Hao et al. (2000d), The Origin and Evolution of Life - Life in Earth’s History, [M] Beijing: Higher Education Press, Springer-Verlag, May 2000 edition: pp184-186
28. Shouyuan Zhao et al., (2001), “Modern Genetics”, Higher Education Press, 2001 August Edition, pp.229
29. Tarjei S. Mikkelsen, et al. (2005), The Chimpanzee Sequencing and Analysis Consortium, Initial sequence of the chimpanzee genome and comparson with the humam genome, [J] Nature04072, 2005,DOI:10.1038,69-87
30. Tong Xu, (2021) “Bring me the grain of Li Mu” - The imperial decree ordered Yu Er to cultivate it - A brief discussion on the origin of wheat in China, “Rural · Agriculture · Farmers”, Culture, 2021.6A, pp: 59-60
31. Weixin Chen, et al. (1963), Selection and Breeding of New Huai Pig (Second Report), Journal of Animal Husbandry and Veterinary Science, March 1963, Volume 6, Issue 1, pp. 4-5
32. William Wahl et al, (2005), Hypotheses on the Origin of Several Bird Species. Science, October 21, 2005. [EB/OL] http://www.baidu. Baidu Knows
33. Xiao Xiang Morning Post,(2003, Getting Close to the “Arrow People Tribe” of the Amazon. Xiao Xiang Morning Post, July 31, 2003, 08:27
34. Yida Yuan, Cheng Zhang. (2002), Chinese Surname Population Genetics and Population Distribution [M]. Shanghai: East China Normal University Press. 2002, 2nd edition. pp. 5-8.
35. Ying Zhang, (2009) The Past and Present of Influenza Viruses, Guangming Daily, June 15, 2009
36. Yuan Liu, (2022), Global Population Shifts, Their Impact and China’s Response, China Political Economy Think Tank, 24 March 2022, 17:37
37. Yuehui Wu, (2024) From wild to domesticated, this research uncovers the 100,000-year evolution history of rice. People’s Daily, May 24, 2024
38. Zefu Wang, Jianquan Liu (2025), Studies on speciation in the genomic era: Genetics. Hereditas (Beijing) 2025, January, 47(1): 71-100.
39. Zhongguan Wu (1997). Dictionary of Population Science. Southwest University of Finance and Economics Press. 1997. The Second Great Population Migration.