SCIREA Journal of Agriculture
ISSN: 2995-6935
http://www.scirea.org/journal/Agriculture
December 26, 2023
Volume 8, Issue 3, June 2023
https://doi.org/10.54647/agriculture210392

The law of biological variation:

offspring like parents, offspring are not parents

Linyun Wang[1]

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

Email: 1055905815@qq.com

Abstract

At present, there are 5 million to 30 million species of organisms on the Earth, how did so many kinds of organisms come into being? What is the pattern of their variation? So far, there is no satisfactory theory to explain it. Since Watson and Crick proposed the double helix structure model of genetic material DNA in 1953, human understanding of the causes of biological evolution has entered the era of molecular genetics. Over the past 70 years, human understanding of genetic phenomena has increased a lot, among which two points are very noteworthy. (1)The genome of organisms will undergo mutations and recombination in the course of generations. Mutation and recombination are the key processes that cause genome changes. (2) In the continuation of generations, regardless of sexual reproduction or asexual reproduction, heterozygous effects will occur. Heterozygous effects include: variation of DNA nucleotide sequence; Differences in mRNA expression (differences in gene expression rate and gene expression amount); Differences in protein structure; DNA methylation in certain regions; Multiplication of nucleotide sequences, entire genomes, or chromosomes; Heritable

gene expression changes that are not caused by changes in DNA sequence, etc.The variation characteristics of organisms in the succession of generations show microdegree, gradualism, pluralism and randomness. Micro and progressive means that the variation of each genome is micro and progressive, the so-called "offspring like parents, offspring are not parents"; The diversity of variation refers to the variation of the nucleotide sequence in the offspring, which does not occur in one place, but in multiple places compared with the parent, which includes both nucleotide sequence variation and epigenetic phenomenon of non-nucleotide sequence change. The randomness of biological variation means that mutation and recombination are random, non-directional, and not affected by the environment. Beneficial mutations get positive selection and harmful mutations get negative selection. This is the main genetic cause of biodiversity on Earth. Due to the different length of time between generations of various organisms, some change faster, the reproductive cycle is only a few hours, a few days (such as some viruses, bacteria), and some change slower, to several years, even hundreds of years, thousands of years. The result of evolution is that some prosper, some become blind, some become new species, and some become dead.

Keywords: biodiversity, gene recombination and mutation, heterozygous effect

Grandfather, father, son, son gave birth to grandchildren, grandchildren, generation after generation, the life of the earth, children and grandchildren are endless. Where did we come from? Where are you going again?

So far, scientists have discovered and named about 2 million species of living things on Earth, of which 260,000 plants, 750,000 insects, 500,000 vertebrates, and the rest are a large number of microorganisms. Scientists estimate that there are between 5 and 30 million species of living things on Earth, most of which have yet to be named （Qingyu Wu ,2002）.These organisms are all different from each other, even between different individuals within the same species, and that's biodiversity.

What causes biodiversity on Earth? How do species evolve? So far, there is no satisfactory theory to solve.

1.Where did life on Earth come from?

The Earth is one of the eight planets in the solar system, the third in order of distance from the Sun.

Life on earth did not fall from the sky, nor did it come out of the ground. It was formed gradually after a long period of evolution after the earth had water. Chemical evolution of preorganisms - biological evolution - Prokaryotes - Eukaryotes - single-celled eukaryotes - multicellular metaphyta and Metazoa - Cambrian Marine animal explosion - early terrestrial life (land plants, moss plants - vascular plants; Arthropods) - vertebrates (fish) - reptiles - birds (angiosperms) - mammals, and so on. (Shougang Hao et al., 2000a) formed the present biodiversity.

The origin of life on Earth can be traced back to the origin of life-related elements and chemical molecules, the evolution of pre-organisms before the emergence of primitive life with cellular structure, and the transition from chemical evolution to biological evolution. 3.8 billion years ago, hot, even boiling water on Earth gave rise to primitive life, and today's extremely thermophilic archaea and methanobacteria may be the most ancient forms of life on Earth. [3] （Shougang Hao et al., 2000b）

The "black chimneys" found today in the deep ocean are a surviving example. On December 11, 2012, China's "Dayang No. 1" research ship "completed the 22nd voyage of ocean scientific research after 369 days and 64,162 nautical miles, and returned to Qingdao, China. A total of 16 hydrothermal areas were discovered during the voyage. Seawater seeps into the ground from cracks in the earth's crust and is heated when it encounters molten rock, dissolving gold, silver, copper, zinc, lead and other metals in the surrounding rocks, and then sprays out of the ground. These metals are deposited into the sea floor by chemical reactions to form sulfides, which are piled up like chimneys, so it is called "black chimneys." Temperatures near the "Black chimney" range from 100°C to 300°C, but there are still plenty of organisms around it, starting with microbes, which can use hydrogen and alkane produced when water and submarine lava react chemically. Microbial organics are used by large organisms, such as blind shrimp and hydrothermal fish. (Xinhua News Agency of China，2011)

After the emergence of a large number of microorganisms, plants and animals, various organisms depend on each other and use each other to form a food chain.From the microorganisms in the "black chimney" gradually evolved to the modern variety of animals and plants.

At present, the earliest organisms found on the Earth are 3.5 billion years ago, some filamentous bacteria and cyanobacteria fossils of only a few microns to ten microns in size were found in the Pilbara region of northern Australia, (they are the simplest and most primitive prokaryotic cell organisms on the Earth). (Jiayu Rong et al., 2014a)

In the early Paleozoic Cambrian period, 542 million to 520 million years ago, the Earth ushered in an explosion of life. It includes at least nine animal phyla, and by the second act of the Cambrian explosion 520 million years ago, the number of animal groups had increased, making the Cambrian explosion even more prominent. This fauna includes more than 20 phyla, including Brachiopods, Molluscs, ungulates (including phyllophyla), Cypris, Echinoderma, Ctenophores, Endoprocta, Starworm, Phoronida, Hemicordate, Chordate, Archaea, annelida, and many other taxonomic types. That is to say, almost all the animal groups in the world today were already present at that time. In addition, strange shrimp up to 2 meters long with a pair of large predators were also found in the fauna, fully indicating that the food chain had existed at that time, with both predators and prey, and the complex ecosystem of life had entered a new period of development from then on.

Through the exploration of ancient life, scientists have found that since more than 500 million years ago, there have been at least five large-scale cluster extinctions (referred to as mass extinctions) of organisms on the Earth, including three times in the Paleozoic era (late Ordovician, late Devonian and late Permian), and two times in the Mesozoic era (late Triassic and late Cretaceous). The dinosaurs that many people are familiar with died out in the Great extinction at the end of the Cretaceous period. But the most tragic prehistoric event occurred at the end of the Permian Period 252 million years ago, when about 95 percent of the world's oceans and 75 percent of all life on land died out forever.

Each mass extinction did not kill all life on Earth, and there were always different numbers and types of organisms that survived the mass extinction and then began to reproduce and enter a new stage of evolution when conditions improved. There is a "coping" effect (resilience adaptation) in all kinds of organisms that experience catastrophic environments. Organisms with good adaptability and strong vitality can survive; Otherwise, they are eliminated. So, survival is the end of the mass extinction and the prelude to the Great Radiation. During the evolution of life, the mass extinction played an accelerated and catalytic role, especially in the substitution of dominant taxa. Life on Earth is like this, after many large and small extinction events and recovery radiation, it has evolved to such a magnificent scene today. （Jiayu Rong et al., 2014b）

2. To explore the main reasons for the evolution of organisms in the continuation of generations from the perspective of molecular biology

Human beings gradually understand the living things on earth and the reasons for the evolution of living things.

For a long time in history, certain religions have preached that the various species of life on Earth were created by God. It was not until 1859 (more than 160 years ago) that Charles Darwin (1809-1888) published On the Origin of Species, in which he proposed for the first time that "species are not independently created, but, like varieties, descended from other species." "Natural selection is the most important, though not the only, route of variation." In 1871, in another great work, The Descent of Man and Sexual Selection, Darwin used a large number of facts to prove that human beings were evolved from apes. In this way, human beings have a basic understanding of the evolution of species and varieties.

In 1928, Morgan published the famous "Gene Theory", which believed that there were pairs of genetic elements (genes) in the reproductive matter of organisms, and combined with the results of Mendel's pea hybridization experiment in 1865, proposed the three laws of heredity, and he regarded genes as each grain on the chromosome. Therefore, it can be called "particle genetics", and it is believed that genes are dominant and recessive.

In 1953, Watson and Crick proposed the double helix structure model of genetic material DNA based on three concepts obtained from a large number of experiments by scientists at that time, indicating that genes are actually nucleotide sequences. He also proposed the "central law" that the genetic information contained in DNA and RNA flows only one way to proteins. The human understanding of biological variation has entered the age of molecular biology from the age of particle genetics.

Molecular genetics holds that the genetic material of living things is the DNA in the chromosomes of sex cells. The genetic information in DNA determines the primary structure of protein through the mediation of mRNA (messenger ribonucleic acid), that is, the nucleotide sequence of DNA determines the nucleotide sequence of mRNA, and the nucleotide sequence of mRNA determines the amino acid sequence of protein. Thus appeared "genetic code", "central law", "cistron", "operon", "exon and intron", "overlapping gene", "transposon" and so on a series of phenomena and terms.

From 1953 to 2023, 70 years have passed, and human understanding of biological heredity

and variation is still increasing. The following points are worth noting：

1. Various types of organisms contain a large number of genomes (nucleotide sequences). Analysis of the genome sizes of large taxa shows that the genome minimum increases with species. The genomes of mycoplasma (Mycoplasma pneumoniae) are only 1.0×106 bp, bacteria (E. coli) 4.2×106 bp, yeast (Saccharomyces cerevisiae) 1.3×107 bp, nematode (Caenorhabditis elegans) 8.0×107 bp, and insects (Drosophila melanogaster) 1.4×108 bp. It was 1.2×109 bp for birds, 3.1×109 bp for amphibians (Xenopus) and 3.3×109 bp for mammals (humans) (Lewin B., 2005a)

2. Not all nucleotide sequences in the DNA double helix are genes. Genes are not beads on a spiral string of DNA on a chromosome. Instead, a nucleotide "region" corresponds to a genetic unit. (Jie Tang,2006)

3. Analysis of the genetic composition of nucleotide sequence in a 50kb region of human chromosome 7 shows that (this region forms a part of the human ßT cell receptor locus). There is one gene (TRY4), two gene fragments (V28 and Y29-1, which are not complete genes and must be linked to other gene fragments in this segment), one pseudogene (which is a non-functional copy of the gene because it has been mutated), 52 repeats, two microsatellites, and, in addition, two microsatellites. 50% of nucleotide sequences are single copy DNA sequences whose function and significance are unknown. (Brown T.A.,2002f) In the human genome, the coding sequence capable of making proteins accounts for only about 1.5% of the total length. According to January 2013 statistics from the Ensembl database, there are 13,430 pseudogenes in the human genome, almost two-thirds of the "real" genes. (hao Jia, 2019)

4. Duplicate sequences can induce replication slippage to produce new variants of different lengths.

5. The nucleotides of the genome are divided into coding and non-coding regions, and mutations in the coding region of the gene have a greater impact on the progeny.

6. DNA methylation plays an important role in the formation and stabilization of biological species. In eukaryotes, cytosine in chromosomal DNA can sometimes be converted to 5-methylcytosine by the addition of a methyl group by DNA transferase, a phenomenon called DNA methylation. In vertebrate genomes, up to 10% of cytosine is methylated. Methylation is related to the inhibition of gene activity, and the inactive genes are located in the methylated region. (Brown T.A.,2002g) There is no dominant or recessive gene.

7. In 1987, British molecular biologist Holiday reformulated the systematic expression of "epigenetics" according to the consensus that DNA methylation can change gene activity. The now widely accepted concept of epigenetics is the study of heritable changes in gene expression that are not caused by changes in DNA sequence. In 2013, the National Institutes of Health, based on the extension of epigenetics research, considered epigenetics to include both genetic changes in the activity and expression of cells or individual genes, as well as stable, long-term, and no genetic changes at the level of cellular transcriptional bands. Currently identified epigenetic processes include methylation, acetylation, phosphorylation, ubiquitination, and protein modification. With further research, other epigenetic mechanisms will be identified.(Life Science Association of China Association for Science and Technology, 2018)

8. In the structure of DNA, the insertion/deletion of a nucleotide (In/del) causes a series of mutations around it. A comparative analysis of the gene sequences of human, chimpanzee, rhesus monkey, mouse, fruit fly, rice and saccharomyces cerevisiae by bioinformation technology shows that the insertion/deletion (In/del) of a nucleotide in DNA can cause a series of mutations around it. Tian Dacheng et al. (2008) proposed the hypothesis of the mechanism of spontaneous mutation induced by In/del. (Dacheng Tian, et al.,2008)

Studies of COVID-19 viruses that have emerged in recent years have shown that in RNA organisms, the codon (codon) of each nucleotide triad can change its properties as long as (at important sites) one of the nucleotides is replaced by another nucleotide in replication. For example, on June 18, 2020, China's National Center for Disease Control and Prevention announced that the D614G mutation of COVID-19 virus in Beijing in June is the s-protein (spike glycoprotein) of the virus with a conversion from arginine to tyrosine at the 614 position. This mutation causes the spike glycoprotein to form a trimer on the surface of the virus, and the three spike heads form a three-dimensional structure, which makes it more stable, and the spike glycoprotein is not easy to fall off the surface of the virus, which increases the infectiosity of the virus. [14] The same is true of many new variants (such as Delta, Omicron, etc.) that have emerged since the COVID-19 virus (Yi Mo, 2020).

Changes in biological traits caused by the replacement of a single nucleotide do not only occur in RNA organisms, but also in DNA organisms. A case in point is the malignant hyperthermia syndrome of pigs (mammals, DNA creatures).

Malignant hyperthermia syndrome (MHS) refers to the non-specific stress response caused by

the stimulation of a variety of adverse factors, such as the pig may die under transportation, high heat, herd shifting, fighting, and hunger conditions, or the pork is pale and soft after slaughter. Water seepage and so on, thus affecting the quality of pork, to the pig industry has brought huge economic losses. FUJII J, OTSU K, ZORZATO F, et al.1991; VOGELI P, BOLT R, FRIES R, et al.1994) found that Ryanodine receptor 1 on pig chromosome 6 (Ryanodine receptor 1, Nucleotide No. 1 843 of the c DNA of RYR1 is mutated from cytosine (C) to thymine (T), resulting in the transformation of arginine to cystine at 615, which leads to structural and functional changes, resulting in Malignant hyperthermia syndrom in pigs. MHS). (Ming Yang et al., 2018)

9. Biological genomes are mutated and recombined in the process of generation continuation (i.e. "heterozygote hybridization"). Mutation is a change that leads to a smaller sequence, and recombination is the cumulative result of a larger sequence rearrangement. Mutation and recombination are the key processes that lead to genome evolution.

There are a large number of microsatellite repeats in the non-coding sequences of biological genomes. In the continuation of generations, the sequence of two nucleotides repeating in tandem is easy to occur through random point mutations, and the number of duplicate copies increases from 2 to 3, 4, and even more copies through replication slip.(Shouyuan Zhao et al., 2001a) This variation first occurs in non-coding sequences, and for most genes, the alteration of nucleotide sequence will become a non-functional pseudogene.

Replication "errors" are one of the sources of point mutations. E. coli can synthesize DNA with an error rate of 1/107. These errors are not evenly distributed between the two progeny DNA molecules, and the error rate of the trailing strand is often 20 times that of the leading strand. This asymmetry may indicate that the base selection and correction activity of DNA polymerase I, which only plays a role in the trailing strand replication, is less efficient than that of the main replicase, DNA polymerase III. (Brown, T.A. 2002a) "errors" also occur in the imbalance between the two tautomers. The organism itself has a "mismatch repair system" that can reduce the replication error rate, and because of its effect, the overall error rate of DNA synthesis in E. coli is only 1/1010 to 1/1011, that is, there is only one uncorrected "replication error" per 1,000 copies of the E. coli genome. (Brown, T.A.2002b)

Not all replication errors cause point mutations. Abnormal replication may also result in the insertion of a small number of excess nucleotides in the synthesized polynucleotides or the uncopied partial nucleotides in the template. Insertion or deletion in the coding area can cause

the reading frame of the gene encoding a specific protein to shift, so it is often called a frameshift mutation. (Brown, T.A. 2002c)

Frameshift mutations can occur at any location, not only in genes, and not all insertions and deletions of coding regions result in frameshift; insertions or deletions of three or three integer multiple nucleotides merely add or remove some codons or separate adjacent codons without affecting the reading cabinet (ORF) (Brown,T.A. 2002d)

Most changes in protein sequences are the result of many small mutations that accumulate slowly over time. Point mutations, small insertions and deletions occur randomly and may occur with similar probabilities throughout the gene, except for a few point mutation hotspots, many mutations causing amino acid sequences are harmful and thus removed by natural selection. A very small number of mutations are beneficial, and it spreads to the entire population, eventually replacing the previous sequence. (Lewin, B.2005b)

10. In the continuation of generations, regardless of sexual reproduction or asexual reproduction, heterozygous effects will occur. The heterozygous effect is not a simple cross between two varieties. Nor is one gene particle replacing another. Offspring traits cannot be measured by removing 2 from the sum of two parental traits. The heterozygous effects after hybridization include: ① variation of DNA nucleotide sequence; ② mRNA expression difference (gene expression rate and gene expression quantity difference); ③ Differences in protein structure; ④ DNA methylation or epigenetic phenomena in certain regions; ⑤Nucleotide sequences, entire genomes or chromosomes, and so on. The offspring will separate and develop new traits.

There are two ways in which the genome can acquire new genes, one by doubling all or part of what is already in the genome and the other by acquiring them from other species. Shouyuan Zhao et al., 2001b)

This law of biological variation in generations, I call: children like parents, children are not parents. In other words, the nucleotide sequence of the offspring is mostly the same as that of the parent, and only differs from the parent in some (especially the key part) loci (haplotype or nucleotide). When this difference accumulates to a certain extent, the two produce reproductive isolation and form a new species.

The evolution and emergence of man on Earth is a case in point. Humans evolved from apes, and, from the perspective of molecular biology, this is a long process of "offspring like

parents, children are not parents". In 2006, scientists at the Broad Institute of Massachusetts Institute of Technology and Harvard University, after comparing human and chimpanzee DNA, concluded that chimps and humans last split no earlier than 6.3 million years ago, and most likely around 5.4 million years ago. The researchers concluded that ancient humans and chimpanzees first split 10 million years ago, and each evolved in a different direction over the next four million years. Later, chimps and humans experienced a brief reunion. During this time, two populations with slightly different genes interbred, creating a third type of hybrid population with characteristics of both. It was this third group of hybrids that eventually gave rise to the two branches of humans and chimpanzees. (China Daily, 2006-05-19),

The project to study the chimpanzee genome was completed in December 2003. By comparing the genetic structure of humans and chimpanzees, we found that the main genetic difference between humans and chimpanzees is that chimpanzees have 24 pairs of chromosomes in their genome, while humans have only 23 pairs of chromosomes. During evolution, two ancestral chromosome pairs fused at their telomeres to form human chromosome 2. There are also some other variants, such as different inversions of chromosome segments on chromosomes 1, 4, 5, 9, 12, 15, 16, 17 and 18, and the FOXP2 transcription factor and chimpanzee hearing gene are different from human ones. [24] (genetic differences between humans and chimpanzees, [EB/OL] https://cn.weblogographic. com/based - the difference between...

In the process of evolution from primitive human to modern human, there have been many mutant subgroups. For example, predecessors (can walk upright, but can not make tools), real people (can walk upright, can make tools), Homo habis, Homo erectus (Peking man), Homo sapiens, elder Homo sapiens, early Homo sapiens (Neanderthals), etc. (Hujun Li , 2003), due to various reasons, some mutated branch groups died out. For example, prehistoric Homo Floresiensis (" dwarf "), found on the Indonesian island of Flores in October 2004, which lived 18,000 years ago, and Neanderthals, which became extinct 35,000 years ago, were both blind. (Ji Qiu, 2005) Some mutant subgroups flourished and eventually developed into modern humans.

A team of scientists in the United States has compared the DNA sequences of human and chimpanzee genomes and found that the two are about 98.5% similar, and the nucleotide difference between humans and chimpanzees is only 1.5-3%. The difference between the two was found in about 3 percent of genomes where a "species genome" was inserted into a section of DNA, or where a section of DNA was removed from the genome altogether. In

other words, there is a "species genome" within the same species. (Tarjei S. Mikkelsen, et al.,2005)

There are fewer differences in nucleotide sequences between races. According to a report in the journal Science (2005.2.18), scientists from the US company Perlegen analyzed the genomic data of 71 people of European, African and Chinese descent in the United States, and identified 1.58 million single nucleotide DNA sites. A single nucleotide site in the white, black and yellow human genome was labeled, and the difference map of different human genome was preliminatively drawn. It turns out that the world's different human genomes (3.01 billion pairs) share at least 99.99 percent of the same base pairs. But the remaining difference of less than 0.01% (300,000 pairs) determines not only our susceptibility to certain diseases, but also our differences in height, skin color and body type. (Science, 2005.2.18)

From the above situation, the process of chimpanzee evolution into human is a long gradual process. The same is true of variation in other organisms. The main reason for this is errors in DNA replication and the "heterozygous effect" caused by parental mating. In a 2014 article, I proposed that there are at least three rules in the evolution of living things: (1) The influence of parental traits on offspring traits is not equal, some traits of offspring are biased towards the father, and some are biased towards the mother, which does not follow the Hardy-Weinberg law of genetic balance (1908), and the existing formula for calculating inbreeding coefficient is also wrong; This is proved by the different traits of the offspring of cross-breeding between different breeds of livestock.(2) Progeny variation shows familial phenomenon, but there are some differences among individuals in the same family. Within the same family, certain genomes (nucleotide sequences or fragments) are conserved in the continuation of generations. I call it mutated familial phenomena. This is the conservative side of biological evolution. However, within the same family, there were some nucleotide sequence differences between individuals. The degree of difference of these nucleotide sequences varies according to the difference of family, group, strain, variety, genus, family, order, class, phylum, etc. Biological variation is absolute, random, no direction, this variation is difficult to clear those are "favorable" or those are "unfavorable", under the joint action of the environment, some variations will be fixed to form a new species, and some variations will make the species gradually into the blind branch. (Linyun Wang, 2014) I expressed this idea again in an article in 2015 (Linyun Wang, 2015) and again in another article in 2018. (Mei Li,and Linyun Wang,*, 2018)

The variation characteristics of organisms in the succession of generations show microdegree, gradualism, pluralism and randomness. As described above, the diversity of variation refers to that compared with the parents, the variation in the nucleotide sequence of the offspring does not occur in one place, but in multiple places, with both nucleotide sequence variation and epigenetic phenomenon of non-nucleotide sequence change. Randomness of biological mutation is an important concept in biological variation. The Darwinian view of evolution holds that changes in biological characteristics occur randomly and are not dictated by their environment. Beneficial mutations get positive selection and harmful mutations get negative selection.(Brown T.A.,2002g) Biological variation does not present the elements of human feelings such as "evil", "cunning", or "good".

Due to the different length of time between generations of various organisms, some change faster, their generation cycle is only a few hours, a few days (such as some viruses, bacteria), and some change slower, to several years, even hundreds of years, thousands of years. The result of evolution is that some prosper, some become blind, some become new species, and some become dead.

For example, mutations in the COVID-19 virus occur frequently. However, not all mutated COVID-19 viruses survive. In fact, most mutations often have adverse effects on the survival of the virus, and the virus strain carrying the adverse mutation can not adapt to the environment, and gradually disappear. But a few mutations increase the infectivity or transmissibility of the virus, slowly evolving into a dominant mutant strain.

In February 2021, a paper was published in the authoritative journal Cell Host & Microbe, taking 355,067 COVID-19 virus genome sequences from the GISAID database as of January 11, 2021 as research objects. The researchers found nearly 30,000 mutations (8.57%) in more than 350,000 genome sequences. Among them, 3823 (12.74%) COVID-19 virus mutants were representative, that is, genetic mutations affected the characteristics of the virus; 130 (3.4%) of these nucleic acid mutation sites are persistent (these mutations can spread and spread in the population); 75 mutations (1.96%) were non-synonymous mutations (causing changes in viral proteins, affecting transmissibility or disease-causing ability); 24 (0.628%) were parallel mutation sites (the same mutation site was produced by the novel coronavirus in different regions at the same time). Such mutations have the potential to improve the adaptability and survival of the virus. It can be seen that the virus mutated in these more than 350,000 genome sequences can spread and spread in the population and affect the transmission ability (0.037%) or the disease ability (0.021%) is very small. But as long as it exists, it's always evolving.

The COVID-19 virus mutant that caused the repeated upward movement of the global epidemic is the mutated virus that stands out from so many COVID-19 virus mutants. From the mutant strain Alpha (Alpha B.1.1.7) to Beta B.1.351, to Gamma P.1 and Delta B.1.617.2, COVID-19 virus has shown greater transmistibility with each mutation (Gen Chen, 2021). But at the same time, its pathogenicity is sometimes diminished, and its mutation is random. This is caused by human ignorance about the COVID-19 virus allowing it to spread freely.

This is the main genetic cause of biodiversity on Earth. From RNA organisms to DNA organisms, from plants to animals to microbes, there are many examples.

In the past 70 years, although molecular genetics has made a lot of achievements, most of our current research still adopts horizontal research, that is, only studying the relationship between certain nucleotide sequences or epigenetic phenomena and certain traits or certain diseases, and rarely adopts longitudinal research, that is, rarely studying the changes of certain nucleotide sequences or epigenetic phenomena between parents and offspring.Few studies have been conducted on the differences and changes in nucleotide sequence or epigenetic phenomena of progeny caused by different consanguineous matching between parents (inbreeding, hybridization and outbreeding). There is still a long way to go to correctly understand the law of biological variation from the perspective of molecular genetics.

REFERENCES

[1] Brown T.A., 2002a, Genomes, Jiangang Yuan et al. Trans. , [M] Beijing: Science Press, August 2002 : 10

[2] Brown T.A., 2002b, Genomes, Jiangang Yuan et al. Trans., [M] Beijing: Science Press, August 2002:199

[3] Brown, T.A., 2002c, Genomes, Jiangang Yuan et al. Trans. , [M] Science Press, August 2002, Edition: 375

[4] Brown, T.A., 2002d, Genomes, Jiangang Yuan et al. Trans. , [M] Science Press, August 2002, Edition: 376

[5] Brown, T.A., 2002e, Genomes, Jiangang Yuan et al. Trans. , [M] Science Press, August 2002, Edition: 376-379

[6] Brown, T.A., 2002f, Genomes, Jiangang Yuan et al. Trans. , [M] Science Press, August

2002, Edition: 379

[7] Brown T.A., 2002g, Genomes, Jiangang Yuan et al. Trans. , [M] Science Press, August 2002, Edition: 392

[8] China Daily [N](2006-05-19), Online edition of Nature 2006-05-17 [EB/OL], http://www.sina.com.cn 18:02 May 19, 2006 [N] Information Times

[9] Dacheng Tian , et al.,2008, Single-nucleotide mutation rate increases close to insertions/deletions in eukaryotes . [J] Nature 07175 . 2008. Vol. 455(4): 105-108

[10] Gen Chen, 2021, Delta Variant strains are prevalent in the world, Why does the novel coronavirus mutate? [EB/OL] Phoenix News 2021-06-21 09:07

[11] Genetic differences between humans and chimpanzees, [EB/OL] https://cn.weblogographic.com/genetic - difference between....

[12] Hao Jia, 2019, Genome Biology, the Third National College Genomics Teaching Seminar (2019, Chongqing)[EB/OL], July 22, 2019

[13] Hujun Li, 2003, we are from Ethiopia? [N] Southern Weekend,2003-6-26,

[14] Ji Qiu, 2005, The Life of human Beings. [J] Life World, 2005, 3: 37-38

[15] Jiayu Rong, et al., 2014a, Ancient Disaster, [M] Nanjing: Jiangsu Fenghuang Science and Technology Publishing House, December 1, 2014:14

[16] Jiayu Rong, et al., 2014b, Ancient Disaster, [M] Nanjing: Jiangsu Fenghuang Science and Technology Publishing House, December 1, 2014: Preface

[17] Jie Tang, 2006, What are genes? [J] Advances in Biochemistry and Biophysics, 2006, 33 (7) : 607-608, compiled from Helen Pearson, "What Is a Gene?" [J] Nature, 2006,441:399-401

[18] Lewin B., 2005a, Genes VIII, Long Yu et al., Trans. [M] Beijing: Science Press, February 2005 (1) : 62

[19] Lewin, B. 2005b, Genes VIII, Long Yu et al. Trans. , [M] Science Press, February 2005 :100

[20] Life Science Association of China Association for Science and Technology, 2018 , Research history and global status of epigenetics [DB/OL] Sohu: 2018-02-23 12:00

[21] Linyun Wang, 2014, Gene exchange is an important driving force for changing pig Traits

and on Gene exchange between Chinese local pig breeds and foreign pigs [J], Journal of Swine Science, 7 (2014)：38-42

[22] Linyun Wang, 2015, On the top-level design of pig small group preservation, [J] Animal Husbandry and Veterinary Medicine, 2015 (47), No. 4：1-4

[23] Mei Li and Linyun Wang*, 2018，Some novel rules of the biological heterozygous effects [J] Indian Joural of Animal Research , 52(6):811-815

[24] Ming Yang et al., 2018, Molecular marker-assisted selection of fluoroalkyl in Pitland pigs, Journal of South China Agricultural University, 2018, 39(6): 1-4

[25] Qingyu Wu ,2002, Basic Life Sciences, [M] Higher Education Press, May 2002, Edition ：14

[26] Science [J]2005.2.18, Genome Difference Map of different ethnic groups, [J] Life World 2005, 3:9

[27] Shougang Hao et al., 2000a, Origin and Evolution of Life, [M] Beijing: Higher Education Press, Springer, May 2000 ： 37-47

[28] Shougang Hao et al., 2000b, Origin and Evolution of Life, [M] Beijing: Higher Education Press, Springer, May 2000 ： 37

[29] Shouyuan Zhao et al., 2001a, Modern Genetics [M], Higher Education Press, August 2001:305

[30] Shouyuan Zhao et al., 2001b, Modern Genetics, [M], Higher Education Press, August 2001:298-305

[31] 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,dol:10.1038:69-87

[32] Xinhua News Agency, Discovery of "black chimneys", capture of new species, [N] Jinling Evening News, 2011-12-12, B06

[33] Yi Mo 2020, the virus strain in Beijing has mutated, with a nine-fold increase in infectivity! [EB/OL] wechat 2020-06-25