Modifications in Environmental Microbiome and the Evolution of Viruses Through Genetic Diversity

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Pola Sudhakar and Dhanalakshmi Padi

Abstract

The microbiome present in the environment is changing due to climate, chemical composition, biodiversity, and also even human activities. Biodiversity is vital for the maintenance of a healthy ecosystem and environment, and this includes genetic diversity which helps to maintain the gene variations among species and also aids in the evolution of better species that can withstand the changing environment. Therefore, genetically diverse species are more resistant to infectious pathogens, which cause dreadful diseases.

Keywords

Microbiome · Biodiversity · Genetic diversity · Major histocompatibility (MHC) · Evolution · Biogeography

7.1 Introduction

7.1.1 Modifications in Environmental Microbiome

Microbes are ubiquitous on the Earth; they can be found on the surface and in the deeper layers of the Earth. Microbes can also be found in the air and even in higher altitudes. The environmental microbes are continuously changing due to many factors such as climatic changes, chemical composition, and biodiversity. Also,

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P. Sudhakar (✉)
Department of Biotechnology, AUCST, Andhra University, Visakhapatnam, Andhra Pradesh, India
e-mail: sudhakar@andhrauniversity.edu.in

D. Padi
Düsseldorf, North Rhine-Westphalia, Germany

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human activities like plant and animal extinction may lead to the loss of useful microbial strains; therefore, this affects the microbes present in the environment. The richest amounts of microbes are found in the soil because it has all kinds of nutrients that are necessary for the growth of microbes (Bardgett and Van Der Putten 2014). Microbes help modulate the biogeochemistry; therefore, the chemical composition and properties in the Earth are due to the integrated microbial action. Microbes cause many diseases to humans and their secondary metabolites such as antibiotics have medicinal properties (Zhu and Penuelas 2020).

7.1.2 Microbiome Diversity

The changes that occurred due to biodiversity are necessary for evolutionary development; however, the Earth's microbiome is highly redundant and extremely diverse. Biodiversity is useful for a healthy ecosystem; it balances all the living organisms on the earth. Biodiversity is divided into three main categories; they are genetic diversity, species diversity, and ecosystem diversity.

- **Genetic diversity**: This focuses on the variations of genetic material (DNA) among individuals.
- **Species diversity**: In this category, different types of species in a particular area have been included.
- **Ecosystem diversity**: Differences in the ecosystem, which is within a geographical location, are focused on.

At these three levels of variations, the balances in nature are maintained and thus play an important role. The diversity in genes, species, and ecosystem among individuals, communities, and areas is helpful in evolutionary development. A wild variety of species is necessary for high biodiversity. However, the advent of molecular and genomic tools and techniques plays a crucial role in studying microbial diversity.

The depletion of biodiversity may affect the environment and the ecosystem. These effects on biodiversity impact the emergence and evolution of microbes (Rodríguez-Nevado et al. 2018). Biodiversity help in the development of human well-being, a better ecosystem, and sustainable development (Tydecks et al. 2018). European Environment Agency initiated the program to manage and protect biodiversity globally (Barbault 2011).

Low biodiversity affects the climate change and weather of the environment, which, in turn, affects the living organisms and ecosystem (Mawdsley et al. 2009). The journal, *Trends in Ecology & Evolution* mentioned that the species which are introduced show resistance to the parasite's prevalence. In contrast to that, global homogenization increases the susceptibility to diseases (Young et al. 2017). Review literature by the researcher Jessica says that the pathogens are increased due to the agricultural practices, and the domestic animals play a crucial role in spreading the diseases by pathogens to humans. Also, it is said that modification in the environment affected the ecology and thus laid a path to the development and emergence of pathogens, which causes infectious diseases (Pearce-Duvet 2006).

Human-made changes are also the reason for the evolution and emergence of pathogens; the two significant changes which were mentioned in the journal *Vector-Borne and Zoonotic Diseases*, by the researcher Loh et al., depicted the land-use changes and the agricultural industry changes. Also, climate changes and medical industry changes made humans susceptible to emerging infectious diseases (Loh et al. 2013).

7.2 Genetic Diversity Drifted Through Evolution

Genetic diversity covers the areas of genomics, ecology, and evolutionary biology, which are useful for a better understanding of biodiversity. The difference in the genes among species or organisms is known as genetic diversity; thus, these differences make two individuals look different from each other. Variations in a gene are caused when mutations occur; a mutation can show a positive or negative effect on a species. However, the selection of the mutated genes is dependent on the flow of those genes. The positive mutation or the addition of the valuable genes in the genome of the reproductive genes can be carried along with the generations (Wright 2005).

Microbial biogeography occurred when microorganisms developed an ability to acquire foreign DNA; therefore, the movement of genes occurred through the ecosystems. The microbes which can withstand the genetic changes can pass these genes to other organisms (Gillings 2017; Reed et al. 2014). Newly discovered viruses are developed and implemented with new standards and transformed for our understanding of microbial ecology, evolution, and biogeochemical cycles. These are also useful in leading innovative paths in many diverse fields such as environmental, agricultural, and biomedical sciences (Call et al. 2021).

Genetic polymorphism spreads among species; the two or different forms of traits in an entire genome are drifted through evolution (Ellegren and Galtier 2016). Genetic variations can be seen in the wild species, whereas the domesticated species have a low level of genetic diversity because mankind selects few traits. The organisms which are naturally selected are highly resistant to the artificially chosen organisms.

Genetic diversity is beneficial for the evolution of a better species which can adapt to the changing environment (Frankham 2005). The species with the potential to adapt to the environment can fight off bacteria and viruses. These can pass on the favorable characteristics to the generations, whereas the susceptible organisms cannot carry on their genes further (Doehring 2020).

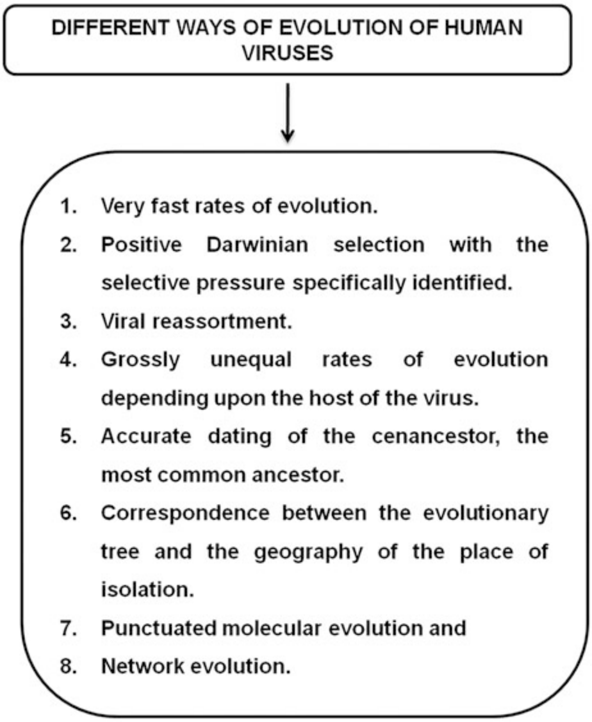
The viruses or bacteria can easily infect the species which are artificially selected as they have similar genes; therefore, the wild variety species possess genes that are diverse and can show resistance to pathogenic viruses and bacteria. Every organism has the blueprint of its genome, and thus, they vary from every individual. The genetically diverse species are more resistant to the changing environment and can quickly adapt to the changes. Therefore, these species can withstand adverse conditions.

7.3 Evolution of Viruses Through Genetic Diversity

Pathogens such as viruses, particularly RNA viruses, have the potential to reemerge and can infect multiple hosts. These pathogens cause infectious diseases, which can be a dangerous threat to human lives and economies (Cleaveland et al. 2001). There are mainly three different types of evolutionary paths for the RNA viruses (Reanney 1982); they are positive-sense single-stranded viruses, negative-sense single-stranded viruses, and double-stranded RNA viruses. Among these RNA viruses, single-stranded RNA viruses share the genes during their evolution, whereas double-stranded RNA viruses have a different evolutionary line (Baltimore 1980).

In the article, *Cellular and Molecular Life Sciences*, the mechanism of viral mutation are explained. It was mentioned that the RNA viruses (Lauring and Andino 2010) are more prone to mutations when compared to the DNA viruses, and single-stranded viruses undergo mutations faster than double-stranded viruses. Also, some viruses can adapt to the new environment and the host quickly, and therefore, their potentiality for quick adaptation is based on the generation of de novo diversity (Sanjuán and Domingo-Calap 2016) (Fig. 7.1).

In 1996, Walter M. Fitch in the article *Molecular Phylogenetics and Evolution* mentioned the different ways of the evolution of human viruses (Fitch 1996). They included:



1. Very fast rates of evolution.
2. Positive Darwinian selection with the selective pressure specifically identified.
3. Viral reassortment.
4. Grossly unequal rates of evolution depending upon the host of the virus.
5. Accurate dating of the cenancestor, the most common ancestor.
6. Correspondence between the evolutionary tree and the geography of the place of isolation.
7. Punctuated molecular evolution and
8. Network evolution.

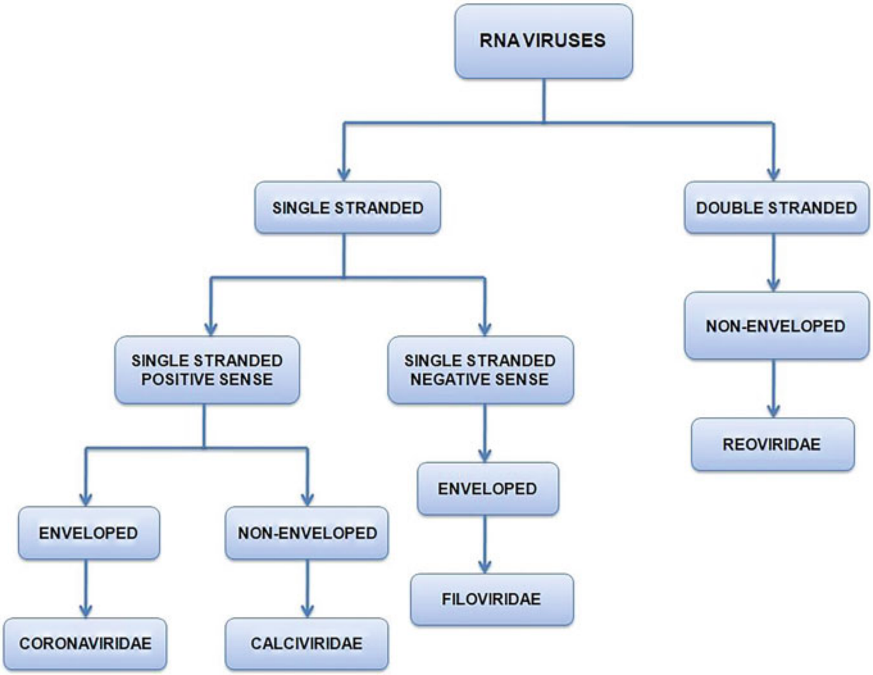


Fig. 7.1 Different types of evolutionary paths in the evolution of RNA viruses. The three major evolutionary lines are positive-sense single-stranded viruses, negative-sense single-stranded viruses, and double-stranded viruses

The rate of viral mutations and their genetic diversity depend on the multiple viruses and the host-dependent processes; also there are some selective processes involved in the development of mutations (Domingo and Holland 1997). The changes in the nucleotide bases caused the evolution and reemergence (Wang et al. 2020) of SARS-CoV-2, and many types of research are carried out to find out the mutations that occurred in the virus.

The researcher Phan. T of the University of Pittsburgh Medical Centre, USA, conducted genetic analyses on 86 genomes of SARS-CoV-2, which were collected from the source GISAID (Global Initiative on Sharing All Influenza Data) (https://www.gisaid.org/) and mentioned that they have revealed 93 mutations overall the entire genomes of SARS-CoV-2. Therefore, these analyses provided the data regarding the mutations and deletions in the coding and noncoding region of SARS-CoV-2 and also gave the evidence for the evolution of the novel coronavirus-2019 (nCoV-2019) (Phan 2020a, b).

The emergence and reemergence of infectious viruses need to understand better to overcome the global issues related to outbreaks and pandemics. The researches covering the areas such as evolutionary biology, epidemiology, and genomics need to be focused more. The advanced genome technologies and computational biology are useful to sort out the problems and, however, focus on the evolutionary emergence of viruses to be increased. Various methods and challenges need to be fulfilled in controlling the disease. Also, the further possible reemergence of infectious viruses to be studied thoroughly to avoid future outbreaks (Pybus et al. 2015).

7.4 The Role of MHC (Major Histocompatibility) in the Evolution

Jones and Partridge in 1983 in the *Nature* journal explained that the MHC system is used primarily for sexual selection, and thus to achieve gene recombination, the inbreeding of the species has been avoided. These selections of the MHC genes can be detectable when a series of selective pressure is applied for a short time (Garrigan and Hedrick 2003). MHC gene sequence's role in the reproduction, mate selection, and fitness to survive in the changing environment is also reviewed in many research papers (Zhu et al. 2019). The gene organization of MHC complexes is different among species in terms of size, complexity, and gene order (Flajnik and Kasahara 2001).

MHC diversity plays an essential role in the genetic drift of the traits and is thus involved in evolution (Kaufman 2018). The genetic drift is useful in shaping the genetic diversity and population, whereas the limited gene flow may cause massive differentiation in the genetic variations of the MHC complex (Lan et al. 2019). MHC variant molecules are useful in making the population resistant to pathogens. The pathogens are rapidly mutating and evolving; therefore, they can flow easily through the species with similar genes. Thus, the variants of MHC molecules are helpful for not passing the pathogens further.

7.5 MHC Diversity in Humans Makes Resistance Against Evolving Pathogens

In vertebrates, MHC genes, especially antigen-presenting cells, i.e., class-I and class-II MHC molecules, are highly variable. Pathogen-mediated selection has been focused more on because they play a crucial role in the selection of MHC genes (Hughes 2002). For instance, the two MHC types and the two MHC variants can produce ten different types of genotypes, which are resistant to the pathogens. The alleles of the different genotypes of MHC genes encode the different proteins; thus, the population with these genotypes shows resistance against the rapidly mutating pathogens (Fig. 7.2).

Also, during the inheritance of the haplotypes of MHC gene sequences to the offspring, the gene conversion and the gene recombination (Schaschl et al. 2006) make the MHC gene sequences polymorphic, and thus the new variants of MHC molecules are produced during the inheritance of haplotypes (Yamaguchi and Dijkstra 2019). The MHC genotypes, which are produced in response to the pathogens, are having the genes which show the phenotypic character fitness to the pathogens (Wegner et al. 2003).

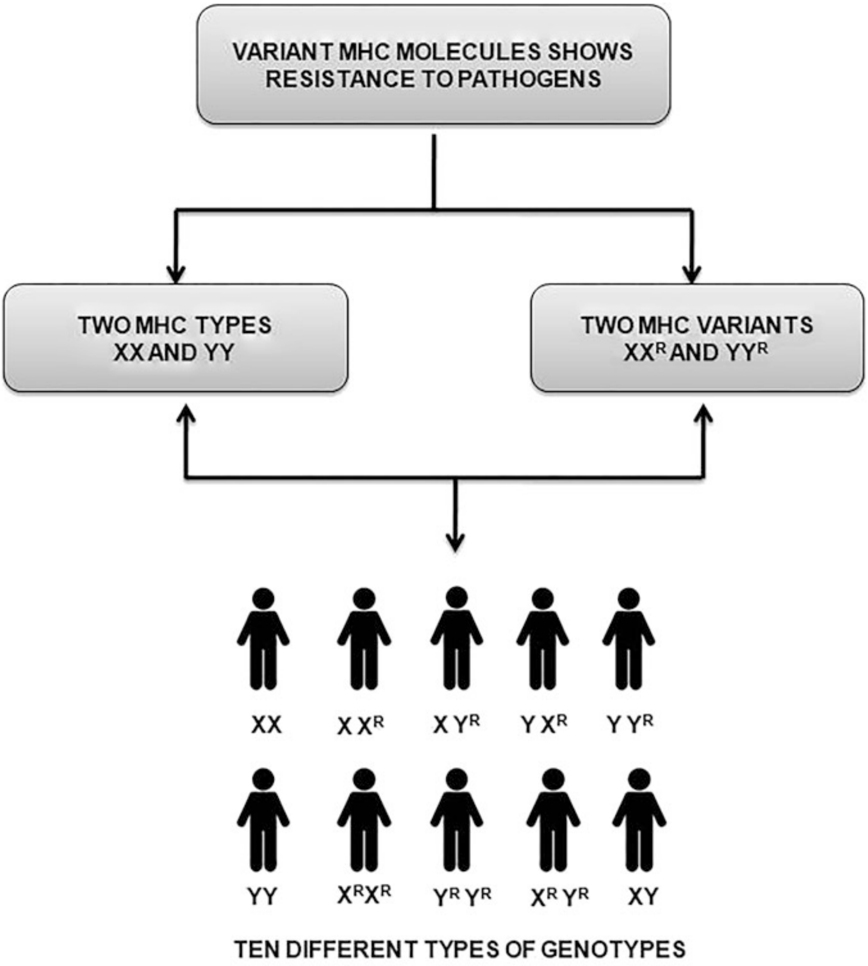


Fig. 7.2 Variant MHC molecules that are produced during the evolution show resistance to the pathogens. Ten different types of genotypes which are produced from two MHC types and two MHC variants help to avoid the infection caused by the viruses among species of similar genes

MHC complexes are mainly involved in the recognition of the foreign particles that invade our immune system; these genes at the MHC loci produce antibodies by activating the immune responses to fight against antigens (Dawkins and Lloyd 2019). MHC is represented by the immune cells and acts as a stalk that anchors the pathogens to the cells and, therefore, produces antibodies against them (Altuvia and Margalit 2004; Kelly and Trowsdale 2019).

7.6 Concluding Remarks

From this review, we conclude that the changes in the environmental microbiome need to be controlled as it affects the helpful bacteria in the environment. Also, maintenance of biodiversity is essential for sustainable development, and also genetic diversity is necessary among the species to stop the reemergence of infectious disease. Genetic diversity also makes the species to be fit and resistant to emerging pathogens. Thus, the research should be more focused on the areas of epidemiology, evolutionary biology, and genomics, which help us to be prepared for the subsequent outbreaks or pandemics.

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