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Virus taxonomy and megataxonomy (Vira domain) – current status

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Abstract

For nearly 80 years since the discovery of the first virus by the Russian scientist D.I. Ivanovsky, it has been recognized that all organisms of Earth's biosphere serve as natural hosts for viruses. Viruses, grouped within the informal domain *Vira*, infect all three domains of cellular life: archaea – *Archaea*, bacteria – *Bacteria*, and eukaryotes – *Eucarya* (algae, fungi, protozoa, plants, invertebrates, and vertebrates). The formation of viral population gene pools through interactions with the gene pools of their hosts has taken place under changing environmental conditions over 3.5 billion years, giving rise to the vast diversity of the virosphere. The accumulation of data on the Earth's virosphere, facilitated by the advent of high-throughput sequencing technologies (NGS), has necessitated a reassessment of approaches to virus classification and, since 2018, has led to a reform of viral taxonomy through the introduction of higher taxonomic ranks (megataxonomy). As of September 2025, the International Committee on Taxonomy of Viruses (ICTV) recognizes 15 taxonomic ranks for viruses, the most significant being: realm – 7, kingdom – 11, phylum – 23, class – 49, order – 93, family – 368, genus – 3769, and species – 16,215. Ongoing advances in metagenomics, metatranscriptomics, and the global ecology of the virosphere will inevitably drive further changes in viral taxonomy and megataxonomy. These developments are of fundamental importance for understanding the evolution of the biosphere and of practical relevance for developing new strategies to strengthen biological security and to mitigate the consequences of epidemic emergencies associated with emerging and reemerging infections.

Keywords: *virus taxonomy; ICTV (International Committee on Taxonomy of Viruses); global virosphere ecology; domain Vira; virosphere; megataxonomy*

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РЕДАКЦИОННАЯ КОНЦЕПЦИЯ

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Таксономия и мегатаксономия вирусов (домен Vira) – текущий статус

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Резюме

Спустя 80 лет с момента открытия первого вируса нашим соотечественником Д.И. Ивановским установлено, что все организмы биосферы Земли являются природными хозяевами вирусов. Вирусы, объединенные в неформальный домен Vira, инфицируют все три домена биосферы: археи – *Archaea*, бактерии – *Bacteria*, эукариот – *Eucarya* (водоросли – *Algae*, грибы – *Fungi*, простейшие – *Protozoa*, растения – *Plantae*, беспозвоночные – *Invertebrata*, позвоночные – *Vertebrata*). Процесс формирования популяционных генофондов вирусов в результате взаимодействия с популяционными генофондами их хозяев происходил в условиях меняющейся среды обитания на протяжении 3,5 млрд лет и обеспечил огромное многообразие виросферы. Накопление данных о виросфере Земли, связанное с внедрением технологий массового параллельного секвенирования (NGS), привело к необходимости реконструкции подходов к классификации вирусов и реформированию, начиная с 2018 г., таксономии вирусов с введением новых высших рангов (мегатаксономия). На сентябрь 2025 г. для представителей виросферы Международным комитетом по таксономии вирусов (ICTV) приняты 15 таксономических рангов, основные из которых: надцарство (Realm) – 7, царство (Kingdom) – 11, тип (Phylum) – 22, класс (Class) – 49, отряд (Order) – 93, семейство (Family) – 368, род (Genus) – 3768, вид (Species) – 16 213. Дальнейший прогресс использования метагеномики, метатранскриптомики и глобальной экологии виросферы неминуемо приведет к дальнейшим изменениям в таксономии и мегатаксономии вирусов. Это будет иметь фундаментальное значение в понимании эволюции биосферы и прикладную значимость для разработки новых подходов обеспечения биологической безопасности и минимизации последствий чрезвычайных эпидемических событий, связанных с проблемой новых и возвращающихся (emerging and reemerging) инфекций.

Ключевые слова: таксономия вирусов; ICTV; глобальная экология вирусов; домен Vira; виросфера; мегатаксономия

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Финансирование. Авторы заявляют об отсутствии внешнего финансирования при проведении исследования.

Конфликт интересов. Авторы декларируют отсутствие явных и потенциальных конфликтов интересов, связанных с публикацией настоящей статьи.

Introduction

Viruses are a form of extracellular life and are subject to all the laws of population genetics, evolution, and ecology. Viruses are defined as mobile genetic elements that encode at least one structural protein of the virion (capsid), into which the viral genomic RNA or DNA is packaged at a certain stage of the virus's life cycle. In this regard, viruses can be characterized as capsid-encoding organisms, in contrast to cellular organisms. All viruses are grouped into a separate informal domain,

Vira, alongside the three other (cellular) domains of the biosphere: *Archaea*, *Bacteria* (prokaryotes) and *Eukarya*.

The unified system for virus classification and nomenclature is developed and maintained by the International Committee on Taxonomy of Viruses (ICTV), an international scientific body operating under the auspices of the Virology Division of the International Union of Microbiological Societies (IUMS). The Committee defines taxonomic ranks (from realm to species), establishes naming rules, reviews proposed

changes, and publishes official reports and databases on virus taxonomy on its official website: <https://ictv.global>.

A *virus species* is defined as a monophyletic group of viruses with a shared gene pool, that can be distinguished from other groups (species) based on accepted parameters such as shared evolutionary history (genetic and phenotypic similarity), replicative properties, and shared ecological niche (host range and vectors). The species share a single population gene pool, the formation and evolution of which occur as a result of interaction with the host and vector population gene pools in a constantly changing habitat [1]. Genetic changes in the population gene pool determine the evolution of viruses, and in some cases, also that of their hosts: both prokaryotes (bacteria, archaea) and eukaryotes (algae, plants, fungi, protists, invertebrates and vertebrates, including humans).

In recent years, as a result of the development of high-throughput sequencing technologies (next-generation sequencing, NGS), there has been a huge qualitative and quantitative leap in the field of genetic data accumulation and the description of new species, genera, and families of viruses. As a result, the classification of viruses within known families was significantly altered, and many new families were added. New taxonomic ranks have been introduced to group families into orders (Order), classes (Class), phyla (Phylum), kingdoms (Kingdom), and realms (Realm) (Table 1).

Fundamentals of Viral Antigenic Classification

The discovery of viruses in eukaryotes (plants) – 1892 [2, 3], animals – 1897 [4], human – 1901 [5], and prokaryotes (bacteria – 1917 [6, 7], archaea – 1974 [8, 9]) (Figure) took approximately 80 years. Then, as the number of isolated viruses accumulated, the question of standardizing methods for their identification and classification became urgent. The methods and approaches available at that time were based on the use of serological reactions. Based on the adopted criteria (a 4-fold difference in the titer of the homologous immune serum at which a positive result is observed), the first system for determining the relationship between viruses and grouping them into antigenic groups was developed. The first antigenic groups were described for arboviruses transmitted by mosquitoes and ticks: groups *A*, *B*, *C* and *D*, which formed the basis for the genera and families of viruses: *Alphavirus*, *Flavivirus* and *Bunyavirus*, respectively [10, 11]. Later, the antigenic groups either became part of the established genera and families or formed their own. Nevertheless, the antigenic group (or serocomplex) remained the basic taxonomic unit in the intrageneric classification of viruses for a long time. Antigenic classification has not lost its significance today and practically completely coincides with the classification of viruses within the genus based on phylogenetic analysis.

Table 1. The number of species, genera, families, and orders accepted by ICTV by 2005

Таблица 1. Число видов, родов, семейств, отрядов, принятых ICTV к 2005 г.

Report Отчет	Reference Ссылка	Reporting ICTV Proceedings at the International Congress of Virology held in: Отчет ICTV о работе Международного конгресса по вирусологии, состоявшегося в:	Content Содержание
First Первый	Wildy (1971)	Helsinki, 1968 Хельсинки, 1968	43 families and groups 43 семейства и группы
Second Второй	Fenner (1976)	Budapest, 1971, and Madrid, 1975 Будапешт, 1971, и Мадрид, 1975	47 families and groups 47 семейств и групп
Third Третий	Matthews (1979)	The Hague, 1978 Гаага, 1978	50 families and groups 50 семейств и групп
Fourth Четвертый	Matthews (1982)	Strasbourg, 1981 Страсбург, 1981	54 families and groups 54 семейства и группы
Fifth Пятый	Francki et al. (1991)	Sendai, 1984, Edmonton, 1987, and Berlin, 1990 Сендай, 1984, Эдмонтон, 1987, и Берлин, 1990	2420 viruses belonging to 73 families or groups 2420 вирусов, принадлежащих к 73 семействам и группам
Sixth Шестой	Murphy et al. (1995)	Glasgow, 1993 Глазго, 1993	1 order, 50 families, 9 subfamilies, 164 genera and more than 3600 virus species 1 отряд, 50 семейств, 9 подсемейств, 164 рода и более 3600 видов вирусов
Seventh Седьмой	van Regenmortel et al. (2000)	Jerusalem, 1996 Иерусалим, 1996	3 orders, 63 families, 9 subfamilies, 240 genera, 1550 species 3 отряда, 63 семейства, 9 подсемейств, 240 родов, 1550 видов
Eighth Восьмой	Fauquet et al. (2005)	Sydney, 1999, and Paris, 2002 Сидней, 1999, и Париж, 2002	3 orders, 73 families, 11 subfamilies, 289 genera and 1898 species 3 отряда, 73 семейства, 11 подсемейств, 289 родов и 1898 видов

					
Dmitriy Iosifovich Ivanovsky (Дмитрий Иосифович Ивановский) 1864–1920 1892 – plant-based viruses (вирусы растений) (<i>Tobacco mosaic virus</i> , табачной мозаики)	F. Loeffler (Фридрих Леффлер) 1852–1915 1897 – animal viruses (вирусы животных) (Foot-and-mouth disease, ящур)	Walter Reed (Вальтер Рид) 1851–1902 1901 – human viruses (вирусы человека) (<i>Yellow fever virus</i> , желтой лихорадки)	Frederik Twort (Фредерик Туорт) 1877–1950 1915 – bacterial viruses (вирусы бактерий) (bacteriophage, бактериофаг)	Felix d'Herelles (Феликс д'Эрель) 1893–1949 1917 – bacterial viruses (вирусы бактерий) (bacteriophage of dysentery bacillus, бактериофаг дизентерийной бациллы)	Carl Woese (Карл Везе) 1928–2012 1977 – description of archaea as a separate domain of the biosphere (описание архей как отдельного домена биосферы) Terje Torsvik: (Терье Торсвик) 1974 г. – archaea virus вирусы архей (Bacteriophage of <i>Halobacterium salinarium</i> , бактериофаг <i>Halobacterium salinarium</i>)
<i>Eucarya</i> (Эукариоты)			<i>Procarya</i> (Прокариоты)		
<i>Algae</i> (Водоросли) <i>Fungi</i> (Грибы) <i>Protozoa</i> (Простейшие) <i>Plantae</i> (Растения) <i>Invertebrates</i> (Беспозвоночные) <i>Vertebrates</i> (Позвоночные)			<i>Bacteria</i> (Бактерии)		<i>Archaea</i> (Археи)

Fig. Virus discoverers (informally the Vira domain), infecting representatives of all domains of Earth's biosphere.

Рис. Первооткрыватели вирусов (неформальный домен Vira), инфицирующих представителей всех доменов биосферы Земли.

Fundamentals of Virus Taxonomy and the Work of the International Committee on Taxonomy of Viruses (ICTV)

With the development of molecular and genetic methods as well as electron microscopy, virus taxonomy has been able to rely not only on antigenic relationships but also on physicochemical characteristics such as virion morphology, type of nucleic acid, presence or absence of a lipid envelope, and so on. This led to the formation of a large number of classic viral genera and families, which united most of the most relevant pathogens of human and animal infections. During this period, the need arose to develop official standardized criteria for virus nomenclature and classification, which ultimately led to the creation of the International Committee on Nomenclature of Viruses (ICNV).

The ICNV, which was later renamed the International Committee on Taxonomy of Viruses (ICTV), was founded on July 22, 1966, in Moscow during the 9th Congress of the International Union of Microbiological Societies (IUMS) at the initiative of Viktor Mikhailovich Zhdanov. The temporary steering

committee, established three years earlier, invited a virologist representative from each member country of the National Microbiological Society. The appointed representatives became founding members of ICTV. The Executive Committee (EC) they elected to oversee the activities of the ICTV developed a set of rules that were approved by the national members at a subsequent meeting during the same congress. The important decisions of these inaugural meetings were that ICTV would create a universal system of virus classification and nomenclature (i.e., one for all viruses regardless of host), that the bacterial nomenclature code would not apply to viruses, and that the rule of publication priority would not be followed. These principles established a system where ICTV decisions would determine both the creation and naming of taxa, thus separating viral taxonomy from most biological taxonomy (botanical, zoological, etc.), as international codes only regulate the names used in biology. At the founding meeting of ICTV, the task of moving toward the implementation of a Latinized binomial nomenclature for viruses was also set.

The EC established four subcommittees based on the classification of the host type infected by the viruses. Subcommittee members proposed genera and families for known viruses of insects, vertebrates, plants, and bacteria. Each subcommittee, chaired by a member of the EC, consisted of experts representing the main group of viruses within its competence. These specialists, in turn, headed study groups that proposed classifications and nomenclature within the families under consideration. The taxonomy proposed by the working groups was discussed by the relevant subcommittee and the EC, and after agreement was reached, it was to be given final approval by the entire ICTV membership. The same basic scheme is still in place today – most taxa and taxon names originate from proposals made by specialized working groups, whose work is coordinated and overseen by the EC. The main work on developing taxonomic criteria, forming new species and genera, proposing species names (binomial, non-Latinized), etc., is carried out in the relevant working groups. Moreover, these criteria are developed independently for each individual family. Working groups make decisions by voting, and not only members of the working group but also any virologist specialist (or a team of specialists) can propose changes or additions to the current status.

Since the first ICTV report, the main taxonomic ranks that the working groups have been working with have been genus and family. The first report on the work of the ICTV was published in 1971 and included descriptions of only 290 viruses, grouped into 19 genera, two families (*Papovaviridae* and *Picornaviridae*), and 24 groups that had not yet been taxonomically formalized (Table 1). For each group, a “typical representative” was chosen – often a human pathogen, after whose name the group, genus, or family was named accordingly. A list of viruses belonging to the group was also provided, using the established virus names. It should be noted that we are specifically talking about viruses and their original or historical names, as the concept of a viral *species* was gradually introduced later. For each group, a list of viruses that are also possibly members of that group and will be included in it in the future was also provided.

The concept of a viral species. The concept of a viral species was introduced gradually and was formally adopted by the ICTV in 1991 [12, 13]. In subsequent reports, study groups began classifying different viruses by species, but the very concept of a viral species was undergoing changes. In the 1991 report, the virus species was defined as “a polythetic group of viruses that constitute a replicating line and occupy a specific ecological niche” [12]. By 2013, this concept had been changed to the following definition: “A species is the lowest level of the taxonomic hierarchy approved by the ICTV. A species is a monophyletic group of viruses whose properties can be differentiated from those of other species using multiple criteria.” Or, in a more modern version, a species is “a monophyletic group of viruses that can be separated from other groups (*species*) based on accepted criteria.” For naming species, non-Latinized binomial names have been introduced, where the first word corresponds to the genus

name, and the second is specialized, often formed based on the Latinized transliteration of the historical name of the type virus or the resulting nosology.

Currently, the main criterion for determining *species*, *genera* and *families* is the genetic distance between viruses or groups of viruses, determined by pairwise comparison of genomic sequences. Genetic distance values that allow for the differentiation of viruses within families at a hierarchical level are determined by the relevant working groups, typically using specialized bioinformatic approaches (e.g., DEmARC [14, 15]). Nucleotide and amino acid sequences of conserved viral proteins (e.g., the RdRp polymerase protein or the nucleocapsid) are used, where the established threshold of 90–93% amino acid sequence identity can be the criterion for differentiation. The officially accepted ICTV characteristics of genera, families, orders, and higher taxonomic ranks are periodically published in the “ICTV Taxonomy Profiles” section of the Journal of General Virology (<https://www.microbiologyresearch.org/content/ictv-virus-taxonomy-profiles>)

Taxonomic ranks above family. As mentioned above, the main taxonomic units initially used by the ICTV were genera and families, with the lowest rank – species – being gradually introduced. But there were also attempts to combine families into higher taxonomic ranks – orders – based on shared characteristics in genome strategy, virion morphology, and the presence of phylogenetic relationships according to the most conserved proteins and motifs. By the 8th ICTV Report (2005), three orders were established, uniting tailed phages (*Caudovirales*), viruses with a single-stranded large (+)RNA genome (*Nidovirales*), and viruses with a single-stranded large (–)RNA genome (*Mononegavirales*). Due to their polyphyletic origin and high degree of genetic divergence, establishing evolutionary relationships at a higher level was considered impossible. In this regard, the Baltimore classification, proposed in 1971 as an attempt to group viruses into larger categories based on their genome type and replication strategy, was particularly significant. In the Baltimore classification, viruses were divided into 7 groups (I–VII) based on their genome type (DNA or RNA, single-stranded or double-stranded, positive or negative polarity, presence of reverse transcriptase, etc.). However, it is important to emphasize that this system does not reflect evolutionary relationships within or between groups of viruses. Viruses belonging to the same group can be evolutionarily unrelated but use similar replication mechanisms. Thus, this classification is fundamentally different from the taxonomy developed by the ICTV, which aims to map the evolutionary lineages of different virus groups [16].

Features of modern virus taxonomy and megataxonomy

At the beginning of the second decade of the 21st century, with the development of NGS technology, a large amount of genetic data began to accumulate, demonstrating the enormous diversity and ubiquitous distribution of viruses in the biosphere. In-depth analysis of the evolutionary relationships between different

groups of viruses and their coevolution with cellular life has changed assessments of the importance of the viral world in the origin and evolution of life on Earth [17, 18]. These data necessitated a review of previously adopted virus taxonomy criteria, which are based, among other things, on virus phenotype and ecology. In this regard, in 2016, ICTV approved the possibility of including in the official taxonomy viruses known solely from their genomic sequences. According to this provision, the formation of new species and other taxonomic units can occur without prior determination of the virus phenotypic characteristics (host range, pathogenicity), without its isolation in cell culture or model animals, and without morphological visualization of virions [19, 20]. Subsequently, principles were developed and published that define minimum standards for viral genome data. These standards stipulate that viruses included in the ICTV taxonomy must be represented by complete or coding-complete genomic sequences that are accurately assembled and free of sequencing artifacts (errors) [21–23]. Adopting this approach has significantly expanded the official taxonomy by including a large number of new taxa, primarily based on data obtained from large-scale metagenomic studies [24]. At the same time, the discussion about the appropriateness of using different criteria for the taxonomic classification of individual virus groups continues. Specifically, for viruses that infect animals and plants, the focus has traditionally been on biological properties, whereas for prokaryotic viruses, genetic characteristics are used in most cases, ranging from the species to the order level.

On the other hand, the possibilities of structural analysis of viral proteins – signatures (Hallmark genes), such as the type of RNA/DNA polymerase, or the type of nucleocapsid protein folding within the virion, and even the identification of certain patterns in their composition, have allowed viruses to be grouped into super-groups whose evolutionary relationship cannot be traced through gene and genome comparison analysis [25–27].

One of the structural motifs characteristic of viruses is a specific fold found in capsid proteins, comprising eight antiparallel β -strands arranged into two β -sheets that are tightly packed against each other. When observed from a certain perspective, this fold resembles a jelly roll, which has led to its widely accepted designation as the **single jelly-roll (SJR)** fold [28]. This architectural motif confers structural stability to the capsid and is observed in many DNA viruses. In many viral capsids, two sequentially linked SJR domains form a composite structure known as the **double jelly-roll (DJR)** fold. This configuration also represents an important taxonomic marker in viral classification.

By 2017, based on a large body of such work, higher taxonomic ranks (megataxonomy) were formed: Class, Phylum, Kingdom, Realm (with intermediate ranks). In 2018 and 2019, these changes were adopted by the ICTV [29]. Thus, the current classification of viruses within the informal Vira domain includes 15 officially recognized ICTV taxonomic ranks from species to realm (**Tables 2 and 3**).

The realm *Riboviria* encompasses almost all known RNA viruses, whose genomes can be represented by different forms of RNA: segmented or non-segmented single-stranded RNA of positive (ss(+)RNA) or negative (ss(-)RNA) polarity, or double-stranded RNA. This realm also includes viruses with a reverse transcription stage in their replication cycle, with either an RNA or DNA genome. All viruses in this group encode an RNA-dependent RNA polymerase (RdRp) or reverse transcriptase [30].

The realm *Monodnaviria* includes single-stranded DNA viruses (ssDNA) as well as small double-stranded DNA viruses (dsDNA) with a circular genome, typically 2–10 thousand nucleotide pairs long. A characteristic feature of the representatives of the realm is the presence of a viral signature gene encoding an endonuclease (HUH) that initiates genome replication via the rolling circle mechanism. Depending on the virion type (icosahedral, filamentous, or pleomorphic form) and host range (archaea, bacteria, eukaryotes), monodnaviruses are divided into 4 kingdoms.

The realm *Varidnaviria* is represented by a diverse group of dsDNA viruses characterized by icosahedral capsid morphology and a double jelly-roll (DJR) fold in the major capsid protein (MCP). Viruses in this realm infect representatives of all domains of life [31].

The realm *Duplodnaviria* unites dsDNA viruses that encode 4 signature viral genes: the major capsid protein with a HK97-like fold, the portal protein, a protease required for capsid maturation, and an ATPase-nuclease required for DNA packaging into the capsid. This realm includes tailed double-stranded DNA viruses of bacteria and archaea (Caudoviricetes), which are considered among the most numerous viruses on Earth, as well as viruses of various single-celled eukaryotes and animal herpesviruses [32].

The realm *Adnaviria* unites viruses with dsDNA that is packaged in a capsid in the A-form DNA (right-handed). Adnaviruses have only been found in thermophilic archaea. Another unique feature of the realm is the unique α -helical structure (folding) of the main capsid protein [33].

The realm *Ribozyviria* includes a single family – *Kolmioviridae*. This family includes human hepatitis D virus (genotypes 1–8, *Deltavirus* genus) and related viruses that infect vertebrate and invertebrate animals. These viruses are viroid-like circular RNA replicons that encode the nucleocapsid protein (δ -antigen). Similar to viroids, riboviruses utilize cellular transcriptional mechanisms for genome replication and are dependent on other viruses for the formation of infectious enveloped particles (e.g., hepatitis B virus) [34, 35].

The realm *Singelaviria* unites viruses of archaea and bacteria with a DNA genome (dsDNA) in linear or circular form. Viruses belonging to the realm encode two main capsid proteins (MCP and mCP), both of which are characterized by a single jelly-roll fold (SJR), as well as an ATPase necessary for packaging DNA into the nucleocapsid.

Table 2. Vira Domain Hierarchy (taxonomic ranks accepted by the ICTV¹ for virus classification)**Таблица 2.** Иерархия домена Vira (таксономические ранги, принятые ICTV¹ для классификации вирусов)

Taxonomy ranks Таксономический ранг	Suffix Суффикс	Main criteria and characteristics Основные критерии и характеристики	Number (July 2025) Количество (на июль 2025 г.)
Realm (Надцарство)	-viria	The highest taxonomic rank that unites viruses based on fundamental biological characteristics such as nucleic acid type, genome replication type, and the presence of certain signature viral genes Высший таксономический ранг, объединяющий вирусы на основе фундаментальных биологических характеристик, таких как тип нуклеиновой кислоты, тип репликации генома, наличие определенных вирусных генов-сигнатур	7
Kingdom (Царство)	-virae	A megataxon that unites <i>Phyla</i> based on shared viral signature genes or their individual motifs at the structural level Мегатаксон, объединяющий <i>Типы</i> на основе общих вирусных генов-сигнатур или их отдельных мотивов на структурном уровне	11
Phylum (<i>Tun</i>)	-viricota	A megataxon, uniting <i>Classes</i> based on a shared evolutionary history manifested thru genome type and the presence/similarity of viral hallmark genes (VHG), often at a structural level, such as RNA and DNA polymerases, capsid proteins, and their assembly method Мегатаксон, объединяющий <i>Классы</i> на основе общей эволюционной истории, проявляющейся через тип генома и наличие/схожести вирусных генов-сигнатур (viral hallmark genes, VHG), часто на структурном уровне, таких как РНК-, ДНК-полимеразы, белки капсида и способ их сборки	22
Class (<i>Класс</i>)	-viricetes	Unites <i>Orders</i> into major evolutionary branches based on shared highly conserved characteristics (replicative module, genome strategy, characteristic capsid structures). It is an intermediate rank between classical virus taxonomy and megataxonomy Объединяет отряды в крупные эволюционные ветви на основе общих высококонсервативных характеристик (репликативный модуль, стратегия генома, характерные структуры капсида). Является промежуточным рангом между «классической» таксономией вирусов и «мегатаксономией»	49
Order (<i>Отряд</i>)	-virales	Groups <i>Families</i> based on common structural features: similar virion shape, comparable size and genome organization, and similarities in replication and genome expression strategy (subgenomic RNAs, polyprotein maturation method, etc.). Phylogenetic similarity in the conserved domains of key proteins of the replication complex (RNA and DNA polymerases, replication factors) Объединяет <i>Семейства</i> на основе общих структурных признаков: схожая форма вириона, сопоставимые размеры и организация генома, схожесть стратегии репликации и экспрессии генома (субгеномные РНК, способ созревания полипротеина, и т.д.). Филогенетическая схожесть по консервативным доменам ключевых белков репликативного комплекса (РНК-, ДНК-полимеразы, репликативные факторы)	93
Family (Семейство)	-viridae	It unites viral <i>Genera</i> with similar genome organization (type, size, structure) and virion morphology. Within the family, genera exhibit phylogenetic proximity when comparing the amino acid sequences of conserved viral proteins Объединяет <i>Роды</i> вирусов со схожей организацией генома (тип, размер, структура) и морфологией вириона. Внутри семейства роды обладают филогенетической близостью при сравнении аминокислотных последовательностей консервативных вирусных белков	368
Genus (<i>Род</i>)	-virus	A monophyletic group of species united based on a shared evolutionary history and expressed by genetic and phylogenetic proximity Монофилетическая группа видов, объединенных на основе общей эволюционной истории и выраженной генетической и филогенетической близости	3769
Species (<i>Вид</i>)	—	A monophyletic group of viruses, separated from other groups of viruses within the genus based on genetic, biological, and ecological criteria Монофилетическая группа вирусов, отделенная от других групп вирусов внутри рода на основе генетических, биологических, экологических критериев	16215

¹International Committee on Taxonomy of Viruses

Taxonomy of viruses infecting humans and vertebrate animals

Viruses that infect humans and vertebrates belong to at least 45 families and 25 orders and are represented by all types of RNA and DNA genomes (Table 4). Most human and vertebrate viruses are RNA viruses (*Riboviria*) (31 families, 15 orders). Changes in the taxonomy of human and vertebrate viruses in recent years have

been mainly related to the reorganization of “classic” families by raising their rank to orders and classes, with a corresponding revision of the status and expansion of the number of genera and species included in them.

Viruses with a single-stranded negative-sense RNA genome are classified under the phylum *Negarnaviricota* (*Riboviria*: *Orthornavirae*). Within the *Negarnaviricota*, 4 classes are formed based on the type of genomic

Table 3. Realms of domain Vira**Таблица 3.** Надцарства домена Vira

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Realm Надцарство	Genome type, Replication strategies Тип генома, стратегии репликации	Number of members Число членов					Areal in Biosphere Ареал в Биосфере								
		Kingdom Царство	Phylum Тип	Class Класс	Order Отряд	Family Семейство	Archaea Археи	Bacteria Бактерии	Algae Водоросли	Fungi Грибы	Plantae Растения	Protozoa Простейшие	Invertebrate Беспозвоночные	Vertebrate Позвоночные	Human Человек
							Procarya Прокариоты	Eucarya Эукариоты							
Adnaviria	dsDNA, linear A-form DNA, the main capsid protein (MCP) has a SIRV2-type structure (fold) dsDNA, линейная ДНК в виде А-формы, главный белок капсида (MCP) имеет структуру (укладку) типа SIRV2	1	1	1	3	6	+	–	–	–	–	–	–	–	–
Singelaviria	dsDNA, the major (MCP) and minor (mCP) capsid proteins have a single jelly-roll (SJR) fold dsDNA, главный (MCP) и минорный (mCP) капсидные протеины имеют укладку по типу single jelly-roll (SJR)	1	1	1	1	3	+	–	–	–	–	–	–	–	–
Duplodnaviria	dsDNA, linear DNA, the main capsid protein (MCP) has an HK97-like structure (fold) dsDNA, линейная ДНК, главный белок капсида (MCP) имеет структуру (укладку) HK97-подобного типа	1	2	2	12	108	+	+	–	+	–	–	+	+	+
Monodnaviria	ssDNA and dsDNA, circular form; replication occurs via a rolling circle mechanism ssDNA и dsDNA, кольцевая форма; репликация проходит по типу катящегося кольца (rolling-circle).	4	7	10	22	35	+	+	+	+	+	–	+	+	+
Varidnaviria	dsDNA, linear form, capsid proteins have a vertical double jelly-roll (DJR) structure (fold) dsDNA, линейная форма, белки капсида имеют структуру (укладку) по типу вертикального double jelly-roll (DJR)	2	3	10	18	35	+	+	+	–	+	+	–	+	+
Riboviria	RNA genome, including ss(+)RNA, ss(–)RNA, dsRNA, segmented and non-segmented forms; also includes retroviruses and mobile genomic retro-elements РНК-геном, включая ss(+)RNA, ss(–)RNA, dsRNA, сегментированные и несегментированные формы; также включает ретровирусы и мобильные геномные ретроэлементы	2	8	24	36	150	–	+	+	+	+	+	+	+	+
Ribozyviria	ssRNA in a circular form, self-splicing using a ribozyme is used during replication ssRNA в циркулярной форме, при репликации используется самосплайсинг с использованием рибозима	–	–	–	–	1	–	–	–	–	–	–	–	+	+
	Unclassified classes and familie Неклассифицированные классы и семейства				1	1	30								

RNA. Viruses with a single-stranded, non-segmented RNA genome are classified under the class *Monjiviricetes*, which includes the order *Mononegavirales*, encompassing important families of pathogenic viruses (*Paramyxoviridae*, *Pneumoviridae*, *Filoviridae*, *Rhabdoviridae*, etc.). Viruses with a segmented ss(–)RNA genome (2–3 segments) are classified under the class *Bunyaviricetes*, which includes orders *Elliovirales* and *Hareavirales*. The order *Elliovirales* includes hantaviruses (*Hantaviridae*) and orthobunyaviruses (*Peribunyaviridae*) as independent families. The order *Hareavirales* includes arenaviruses (*Arenaviridae*), phleboviruses (*Phenuiviridae*), and nairoviruses (*Nairoviridae*). Thus, the current taxonomic position of important pathogens such as the pathogens of hemorrhagic fever with renal syndrome (Hantaan virus) and Crimean-Congo hemorrhagic fever is as follows: *Bunyaviricetes*: *Elliovirales*: *Hantaviridae*: *Mammatavirinae*: *Orthohantavirus*: *Orthohantavirus hantaanense* and *Bunyaviricetes*: *Hareavirales*: *Nairoviridae*: *Orthonairovirus haemorrhagiae*, respectively. Viruses with a segmented ss(–)RNA genome (6–10 segments) are classified in the class *Insthoviricetes*, including the family *Orthomyxoviridae* (order *Articulavirales*), to which influenza A (*Alphainfluenzavirus influenzae*) and B viruses belong [36–38].

Viruses with an ss(+)RNA genome are classified into two phyla – *Kirtinovicota* and *Pisuviricota*. *Kirtinovicota* includes important families of pathogenic viruses: *Flaviviridae* (class *Flasuviricetes*, order *Amarillovirales*) and *Togaviridae* (class *Alsuviricetes*, order *Martellivirales*). Thus, the taxonomic position of an important pathogen – the hepatitis C virus – is as follows: *Flasuviricetes*: *Amarillovirales*: *Flaviviridae*: *Hepacivirus*: *Hepacivirus hominis*. Based on the family *Hepeviridae*, the order *Hepelivirales* (*Kirtinovicota*: *Alsuviricetes*) was established, which also includes the family *Matonaviridae*, to which the rubella virus belongs (*Alsuviricetes*: *Hepelivirales*: *Matonaviridae*: *Rubivirus*: *Rubivirus rubellae*).

Viruses with segmented dsRNA genomes are classified under the phylum *Duplornaviricota*, class *Resentoviricetes*, order *Reovirales*, which was formed based on the family *Reoviridae* by elevating the rank of its constituent subfamilies to families *Sedoreoviridae* and *Spinareoviridae* and reorganizing the number and structure of the genera and species within them. The family *Sedoreoviri-*

dae includes the pathogens of intestinal infections – rotaviruses (*Reovirales*: *Sedoreoviridae*: *Rotavirus*) and the genus *Orbivirus* (*Reovirales*: *Sedoreoviridae*: *Orbivirus*) – arboviruses, which includes the pathogens of animal diseases (bluetongue virus (*Orbivirus caerulinguae*) and epizootic hemorrhagic disease (*Orbivirus ruminantium*)) and human diseases (Kemerovo fever group viruses *Orbivirus magninsulae*).

Several examples above demonstrate the principles by which, starting in 2018, virus taxonomy has been expanded and supplemented both by the introduction of binomial species names and the formation of higher taxonomic ranks. Information on accepted and ratified ICTV taxonomy changes for various groups is periodically published in the “ICTV Virus Taxonomy Summaries” section of the Journal of General Virology (<https://www.microbiologyresearch.org/content/ictv-virus-taxonomy-summaries>).

Conclusion

Recent advancements in metagenomics and metatranscriptomics have significantly expanded our knowledge of viral diversity and their role in the evolution of life. It can be confidently stated that viruses are the most numerous and diverse representatives of life on Earth. The total number of viral particles existing on Earth at any given time is estimated to be $\sim 10^{30}$ – 10^{31} [39, 40]. Virus taxonomy has been dynamically developing for over 50 years and today represents a reconstruction of the evolution of major virus groups, from species and genera to evolutionary groups of the highest ranks. The fundamental importance of virus taxonomy is evident in both its theoretical and applied aspects, given the ubiquitous distribution of viruses on Earth among all representatives of the three domains (*Archaea*, *Bacteria*, *Eucarya*) of the biosphere. All organisms on Earth are hosts to a variety of viruses. Further progress in studying the virosphere will be achieved using megataxonomic and global viral ecology approaches. Currently, the Vira domain includes 7 realms of viruses, which are formed based on fundamental biological properties of viruses, such as genome replication type and the type of proteins that make up the viral capsid. And while the main criteria for forming species, genera, families, and orders can be considered definitively established, ongoing research suggests that the structure of megataxonomic ranks may need to be revised [41].

Table 4. Megataxonomy of pathogenic for vertebrates viruses and their areal among domen Eucarya
Таблица 4. Мегатаксономия патогенных для позвоночных вирусов и их ареал среди домена Эукариотов

Viruses Вирусы						Areal in Biosphere (Eucarya) Ареал в биосфере (Эукариоты)																	
Realm Надцарство	Kingdom Царство	Phylum Тип	Class Класс	Order Отряд	Family Семейство	Type of genome Тип генома	Fungi Грибы	Protozoa Простейшие	Algae Водоросли	Plant Растения	Arthropoda Членистоногие	Molluscs Моллюски	Reptilia Пресмыкающиеся	Amphibia Земноводные	Ichtha (Рыбы)	Aves (Птицы)	Mammalia Млекопитающие	Human (Человек)					
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19					
Adnaviria	Zilligvirae	Taleaviricota	Tobkiviricetes	Ligamenvirales	6 families of archaeal viruses 6 семейств вирусов архей																		
				Maximovirales																			
				Primavirales																			
Singelaviria	Helvetiavirae	Dividoviricota	Laserviricetes	Halopanivirales	3 families of archaeal viruses 3 семейства вирусов архей																		
Duplodnaviria	Heunggongvirae	Peploviricota	Herviviricetes	Herpesvirales	Alloherpesviridae	dsDNA								x									
					Malacoherpesviridae																		
					Orthoherpesviridae																		
Monodnaviria	Shotokuvirae	Commensaviricota	Cardeaviricetes	Sanitavirales	Anelloviridae	ssDNA											x	x					
				Sepolyvirales	Polyomaviridae																		
		Cossaviricota	Papovaviricetes	Zurhausenvirales	Papillomaviridae																		
				Piccovirales	Parvoviridae																		
		Cressdnaviricota	Arfviricetes	Cirlivirales	Circoviridae																		
					Cycloviridae																		
Varidnaviria	Bamfordvirae	Nucleocyotoviricota	Arfviricetes	Recrevirales	Endolinaviridae	dsDNA																	
					Vilyaviridae																		
					Redondoviridae																		
					Asfarvirales		Asfarviridae																
					Chitovirales		Poxviridae																
Riboviria	Orthornavirae	Preplasmiviricota	Megaviricetes	Pimascovirales	Iridoviridae	dsDNA																	
				Rowavirales	Adenoviridae																		
				Reovirales	Sedoreoviridae																		
		Duplornaviricota	Resentoviricetes	Spinareoviridae	Cystoviridae (bacteriophages)	dsRNA сезм. (segmented)																	

For continuation of the table, see page 411.

For continuation of the table, see page 412.

Viruses Вирусы							Areal in Biosphere (Eucarya) Ареал в биосфере (Эукариоты)																						
Realm Надцарство	Kingdom Царство	Phylum Тип	Class Класс	Order Отряд	Family Семейство	Type of genome Тип генома	8	9	10	11	12	13	14	15	16	17	18	19											
			Bunyaviricetes	Elliovirales	Crulviridae	ss(-)RNA сезм. (segmented)					x																		
					Fimoviridae																								
					Hantaviridae																								
					Peribunyaviridae																								
					Phasmaviridae																								
					Tospoviridae																								
					Tulasviridae																								
					Arenaviridae																								
					Discoviridae																								
					Konkoviridae																								
					Leishbuviridae																								
					Mypoviridae																								
					Nairoviridae																								
					Phenuiviridae																								
					Tosoviridae																								
					Wupedeviridae																								
				Annooviridae																									
				Orthomyxoviridae																									
				Pisuviricota	Duploviricetes			Durnavirales	Amalgaviridae	dsRNA сезм. (segmented)				x															
									Curvulaviridae																				
									Fusariviridae																				
									Hypoviridae																				
									Partitiviridae																				
									Picobirnaviridae																				
									Soropartitiviridae																				
									Nidovirales		Abyssoviridae (плоские черви, планарии) (flatworms, planarians)																		
												Arteriviridae																	
												Cremegaviridae																	
				Gresnaviridae																									
								Olifoviridae																					

For continuation of the table, see page 413.

Viruses Вирусы						Areal in Biosphere (Eucarya) Ареал в биосфере (Эукариоты)										Human (Человек)			
Realm Надцарство	Kingdom Царство	Phylum Тип	Class Класс	Order Отряд	Family Семейство	Type of genome Тип генома	Fungi Грибы	Protozoa Простейшие	Algae Водоросли	Plant Растения	Artropoda Членистоногие	Illuices Мякотелые	Reptilia Пресмыкающиеся	Amphibia Земноводные	Ichtha (Рыбы)	Aves (Птицы)	Mammalia Млекопитающие	Human (Человек)	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	
				Picornavirales	<i>Medioniviridae</i> (морские хордовые – туникиаты) (marine chordates – tunicates)														
					<i>Mesoniviridae</i>						x								
					<i>Mononiviridae</i> (планарии)														
					<i>Nanghoshaviridae</i>										x				
					<i>Nanhypoviridae</i>										x				
					<i>Euroniviridae</i>						x								
					<i>Roniviridae</i>						x								
					<i>Tobaniviridae</i>								x		x		x	x	
					<i>Caliciviridae</i>										x		x	x	
					<i>Dicistoviridae</i>						x								
					<i>Iflaviridae</i>						x								
					<i>Marnaviridae</i>			x											
					<i>Noraviridae</i>						x								
					<i>Picornaviridae</i>									x	x	x	x	x	
					<i>Polycipiviridae</i>						x								
					<i>Secoviridae</i>					x	x								
					<i>Soliniviridae</i>						x								
					<i>Astroviridae</i>								x	x	x	x	x	x	
				<i>Stellavirales</i>	<i>Hepadnaviridae</i>	<i>dsDNA-RT</i>							x	x					
	<i>Paramavirae</i>	<i>Arteriviricota</i>	<i>Reptraviricetes</i>	Blubervirales Orterivirales	<i>Belpaoviridae</i> (ретроэлементы) (retroelements)	<i>ssRNA-RT</i>													
					<i>Caulimoviridae</i>						x				x				
					<i>Metaviridae</i> (LTR- ретроэлементы эукариот) LTR-retroelements of eucaryotes)														
					<i>Pseudoviridae</i>		x			x			x		x		x	x	
					<i>Retroviridae</i>		x												
<i>Ribozyviria</i>					<i>Kolmioviridae</i>	<i>циркулярная ss(-)RNA (circular)</i>													

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