



Morphological analysis of English-language biotechnology terms of the genomic era

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Abstract. The relevance of this study is determined by the growing importance of English-language biotechnology terminology in the context of the rapid development of genomic technologies, which necessitates a systematic analysis of its morphological structure to enhance scientific communication and deepen the understanding of cognitive processes in term formation. The aim of the study was to analyse the morphological structure of English-language biotechnology terms of the genomic era through the lens of the cognitive approach. To achieve this goal, the following methods were used: lexicographic, morphological, and statistical analysis, elements of the cognitive approach to terminology research, as well as methods of systematisation and generalisation. It was found that English-language biotechnology terminology actively employs term formation models involving nouns, adjectives, and participles. The vast majority of terms are represented by nouns (N), with the most common being suffixal and prefix-suffixal formations, which together account for approximately 46% of the entire term base. The distribution of terms by conceptual categories within the N morphological model shows that the largest portion is made up of objects (54%)-key elements of biotechnology research such as genomes, proteins, and cells-followed by tools (19%)-modern methods, devices, and technologies-processes (17.2%)-dynamic actions such as sequencing or editing-and goals/results (9.8%)-final products or intended outcomes. Each of the analysed structures (N, N + N, A + N, A + A + N, A + A + A + N, V-ed + N, V-ing + N) was found to be associated with specific aspects of the conceptual domain: noun-based models predominantly represent the object of study (e.g., gene expression, protein synthesis), adjective-noun constructions typically refer to tools and characteristics of processes (e.g., synthetic genomic technologies), while participial forms

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verbalise the results of actions, altered states, or acquired properties resulting from biotechnological interventions (e.g., engineered organism, modified gene), as well as functional features of objects (e.g., binding protein, binding site, coding sequence). Morphological analysis revealed not only the structural features of terms, but also the underlying conceptual models that reflect the patterns of scientific thinking in biotechnology and the cognitive-linguistic specificity of this dynamic field. The practical significance of the study lies in the possibility of applying the obtained results in teaching English for specific purposes to students majoring in “Biotechnology and Bioengineering”

Keywords: biotechnology terminology system; derivational structure; morphemic organisation; concept; cognitive approach

Introduction

Biotechnology is one of the most dynamic and interdisciplinary fields of knowledge, integrating advances in biology, chemistry, medicine, computer science, and engineering. This nature determines the constant updating of the terminological base, the emergence of new concepts, and the active development of the termino-system. Despite the active development of biotechnological terminology, in particular English-language terminology, its morphological structure remains insufficiently investigated from the standpoint of a cognitive approach. Awareness of the lack of research on this issue justifies the relevance of analysing biotechnological terminology within the cognitive paradigm. Focusing on the morphological analysis of biotechnological terms of the genomic era is quite reasonable, given a number of key factors. During this period, there was a rapid increase in the number of terms in biotechnological discourse, due to revolutionary discoveries in the fields of genomics, genetic engineering, synthetic biology, and bioinformatics.

During 2000-2020, English-language biotechnological terminology became the object of increased interest from linguists. Ye. Striuk (2020) reviewed the cognitive model of the concept of biotechnology in contemporary English, analysing in detail its structural components and ways of representation in scientific discourse. The researcher stressed the importance of combining conventional terminology

with cognitive interpretations, which contributed to a deeper understanding of the role of terms in the conceptual system of science. It was concluded that biotechnology is a flexible, prototype concept that does not lend itself to an adequate description due to classical definitions with fixed features. Therefore, an effective description of such concepts, according to the researcher's observations, requires alternative cognitive approaches that consider contextuality, interdisciplinarity, and variability of meaning. Consequently, cognitive terminography opens up new possibilities for describing complex scientific concepts, which allows considering both formal and content-cultural features of categorisation in scientific discourse.

O. Syrotina (2020) focused on the linguistic and cognitive aspects of metaphorisation in the English-language terminology of biotechnology, emphasising its role as a cognitive mechanism for creating new terms. The researcher came to the conclusion that one of the most productive types of metaphors is the anthropomorphic metaphor, when biotechnological terms are formed by analogy with a person or human activity, reflecting an active rethinking of scientific concepts through the prism of metaphorical images. The researcher also stressed that metaphorisation performs not only an explanatory, but also an innovative function, providing flexibility and adaptability of terminology to the rapid development of scientific

knowledge, technologies and interdisciplinary communication. Notably, the cognitive-discursive approach to the analysis of the biotechnological term system was deepened in the study by S. Molina-Plaza & A. Martínez-Sáez (2024), who investigated the functioning of metaphors in scientific texts on biotechnology. The researchers showed that metaphors not only perform a stylistic or heuristic function, but also actively participate in the conceptualisation of knowledge, contributing to the understanding of complex biotechnological processes through more understandable images. Metaphorical structures act as a tool of cognition, are fixed in scientific discourse and eventually become components of the term system, which confirms the expediency of a cognitive approach to analysing the morphological organisation of terms.

T. Almashadni & A. Jawad (2025) investigated the semantic content of the latest terms in biotechnology using methods of collocation analysis, discursive analysis, and semantic field theory. Discursive analysis has shown that these terms function in a variety of discourses – scientific, public, ethical, and political – often accompanied by conflicting interpretations. Through the application of semantic field theory, it was possible to group the latest terms into broader thematic domains, such as genetics, bioengineering, and medical biotechnology, reflecting the interdisciplinary nature and multifactorial nature of contemporary biotechnological terminology. The study confirmed and expanded on previous scientific developments in this area, while offering a new approach to the analysis of terms in both scientific and public speech. However, the study had certain limitations: the volume of the case was relatively small, and the selection of terms partly depended on the availability of sources. F.R. Adambaeva & N.A. Sadullayeva (2023) analysed eponym terms as part of biotechnological terminology, highlighting the historical and functional aspects of such terms and showing how personal names and discoveries become lexicalised

in scientific discourse. In a follow-up study, F.R. Adambaeva (2025) investigated semantic hierarchies in biotechnology terminology in English and Uzbek, in particular, the process-object and property-object relationships. Both papers emphasised the importance of systematising terms for the accuracy of scientific communication, facilitating translation, and developing bilingual dictionaries, which contributes to a better understanding of specialised concepts in biotechnology.

All these studies show that terms in biotechnology are not only tools of nomination, but also means of conceptualisation, social impact, and interdisciplinary communication. In the context of the active development of scientific communication and the expansion of international terminological interaction, there is an increasing need to analyse terms not only from the standpoint of their formal organisation, but also considering cognitive function. Morphological analysis, which covers part-language affiliation, word-forming mechanisms, types of morphemes and models of creation, allows identifying how language represents scientific knowledge, how the structure of the term correlates with mental processes and categorical schemes of scientific thinking. It is in this context that morphological analysis of the terms of the genomic era, which was a turning point in the development of the biotechnological industry, becomes particularly important.

The purpose of the study was to identify morphological features of English-language biotechnological terms of the genomic era, considering their cognitive representation, and to analyse the part-language structure of terms and conceptualisation mechanisms that reflect the specifics of contemporary scientific thinking in the field of biotechnology. Achieving this goal involved solving the following tasks: perform morphological analysis of English-language biotechnological terms of the genomic era with the definition of their part-language affiliation; identify productive morphological models and

describe the typical structural organisation of terms; interpret established morphological models through the prism of a cognitive approach to identify the concepts that they represent.

Materials and Methods

In this study, the terms that characterise genomic era were selected according to a number of well-defined criteria. This category includes terms that directly relate to technologies and approaches that have emerged or are widely used, in particular CRISPR-Cas technologies, new generation sequencing, synthetic biology, etc. The sample also included tokens related to post-genomic areas of modern science – genomics, transcriptomics, proteomics, metabolomics – and advanced practices in genetic engineering, genetic diagnostics, and gene therapy. Considerable attention was paid to the availability of terms in leading sources on biotechnology – dictionaries and glossaries. In particular, the Glossary of Biotechnology and Genetic Engineering (Zaid *et al.*, 2001) and Glossary of Biotechnology Terms (Kimball, 2002). The paper also considered the materials of the Encyclopaedia of Biotechnology (n.d.), Merriam-Webster (n.d.), and the American Heritage Dictionary of the English Language (2022). In addition, the Glossary of Genomics Terms (n.d.), National Human Genome Research Institute (n.d.a; n.d.b), and Genomics Glossary (n.d.) were analysed. Modern online resources dedicated to the creation of genetically modified organisms and biotechnological products were also considered. By drawing on a wide range of sources, from classic reference works to up-to-date glossaries of the genomic era, the authors compiled a representative sample of over 400 English-language terminology units. Thus, the terminology included in the analysis reflected the current state and dynamics of the development of biotechnological language in the context of genomic and post-genomic research.

In the process of studying the morphological features of English-language biotechnological

terms of the genomic era, considering their cognitive representation, lexicographic, morphological and statistical analysis, elements of a cognitive approach to the study of terms and methods of systematisation and generalisation were used. At the first stage of the study, a corpus of English-language biotechnological terms representing key concepts and processes of the genomic era (in particular, CRISPR technologies, new generation sequencing, gene therapy, proteomics, genome editing, etc.) was formed. For the selection of lexical units, the lexicographic method was used, which performed a double function: it served as a tool for the initial selection of terms from authoritative industry dictionaries and glossaries and ensured the recording of definitions and verification of the terminological status of units. The latter involved checking whether the token is an established term in the biotechnological term system, or whether it functions only in certain contexts of specialised scientific use. The final sample included only those terms that were certified in at least two independent professional sources with a clear interpretation and stable subject reference. At the second stage, morphological encoding of terms was performed. The use of the morphological method at this stage involved determining the part-language affiliation of each component of the term, establishing the morphological structure, and distributing terms according to standard models that reflect their internal grammatical and semantic organisation. Based on the data obtained, terms were classified according to morphological models such as N + N (for example, gene therapy), A + N (genetic material), V-ed + N (modified organism) and V-ing + N (binding site), and which grammatical categories are most productive in the process of term formation in the English-language biotechnological term system of the genomic era. At the third stage of the study, a cognitive approach was applied, which allowed interpreting the results of morphological analysis from the standpoint

of cognitive linguistics. This approach considered language as a tool for representing, conceptualising and categorising knowledge about the world, and allowing the study to identify how term elements and their morphological structures relate to conceptual categories relevant to a particular scientific field. Within the framework of cognitive interpretation, each of the identified morphological models was compared with the conceptual categories that form the structure of the concept of “genomic era biotechnology”. Methods of systematisation and generalisation at the final stage provided systematisation of the obtained data, identification of repeated structural models, and formulation of typical patterns of term formation in the English-language biotechnological term system. This synthesis of morphological, generalising and cognitive analysis helped to identify deep connections between the formal organisation of terms and the conceptual structure of knowledge that they represent.

Results and Discussion

Although biotechnology as a science was formed at the end of the 20th century, its terminological and practical foundations have a deep historical background, originating from the research of the heredity of Gregor Mendel in the 19th century and the use of microorganisms in fermentation processes, known since the 4th millennium BCE. This was highlighted in the paper by S. Rajak (2018), who noted that there are three main stages in the development of biotechnology: ancient, classical, and modern. It was modern biotechnology that became the basis for the development of the genomic era, which began in the second half of the 20th century and gained rapid development at the beginning of the 21st century. The genomic era became a defining stage in the development of scientific terminology, since its term system was not only replenished with new words, but also underwent a significant internal

transformation: the principles of word formation changed, elements from different disciplines were combined, and the set of word-forming models was expanded.

To identify the conceptual features of the concept of “biotechnology of the genomic era”, it is advisable to refer to the concept of concept. The term “concept”, which has many scientific definitions, is widely used in the social sciences and humanities – such as literary studies, philosophy, linguistics, psychology, and cultural studies – and is also the basic unit of linguoconceptology (Yuldashev & Haydarov, 2022). O. Selivanova (2006) considered the concept as “an information structure of consciousness, an organised unit of memory that contains a set of knowledge about the object of cognition, verbal and nonverbal, acquired through the interaction of the functions of consciousness and the extra-conscious”. This definition focuses on the cognitive nature of the concept, its connection with the conscious and subconscious experience of a person, and the multi-layered semantic content.

Since the concept of “biotechnology” functions mainly in the field of scientific discourse, it was appropriate to turn to the category of scientific (professional) concept, which helps to more deeply reveal the features of the term system and the knowledge content behind the corresponding term. The development of a scientific concept is carried out in the process of accumulation and development of special knowledge in a particular field, and the linguistic representation of concepts is terms. According to this opinion, terms are the result of cognitive activity, a reflection of professional concepts, and simultaneously – a link in communication between experts in a particular field. Thus, the term acts as a linguistic form of the concept, its sign expression, which ensures accurate and effective transfer of knowledge within the framework of scientific discourse. In this approach, the scientific concept is

considered not only as a set of knowledge, but as a metasense-value – that is, an important, meaningful term concept that is relevant for the subject of knowledge in specific circumstances. The scientific concept is the most important means of forming and developing a particular scientific field. Accordingly, the main function of a scientific concept is to represent knowledge, experience, meanings, associations, and scientific concepts that are most relevant to science or the scientific paradigm.

To determine the conceptual features of the concept of “biotechnology of the genomic era”, the definitions of the term genomics in leading sources were analysed, which helped to outline the boundaries and content of this concept. According to the Merriam-Webster (n.d.), genomics is a branch of biotechnology concerned with applying the techniques of genetics and molecular biology to the genetic mapping and DNA sequencing of sets of genes or the complete genomes of selected organisms, with organising the results in databases, and with applications of the data (as in medicine or biology). In the Genomics Glossary (n.d.) emphasises that genomics covers the identification and characterisation of all genes and functional elements of the genome, and the analysis of their interaction. In the glossary of the National Human Genome Research Institute (n.d.a), genomics is defined as the branch of biology that studies the entire DNA set of an organism – its genome. Key aspects include the identification and characterisation of all genes and functional elements of the genome, and the study of their interaction.

Based on a definitive analysis of the term “genomics” in leading sources, genomic era biotechnology is defined as an interdisciplinary field of biotechnology that emerged at the intersection of molecular biology, genetics, genomics, and bioinformatics. Within this field, genomic information is considered as a key object of research and practical application. It is based on technologies of high-performance

sequencing, genome editing (in particular CRISPR/Cas), synthetic biology and digital modelling and is aimed at developing innovative solutions in the field of medicine, agriculture, industry, and ecology. As a result of the definitive analysis of the concept “biotechnology of the genomic era”, it became possible to determine its cognitive features: the use of genomic information as an object of research and practical application; the use of innovative technologies for sequencing, editing, and synthetic biology; integration of biological and digital approaches; orientation to the creation of new products and solutions in applied areas. The identified cognitive features allow structuring the concept of “biotechnology of the genomic era” by identifying relevant concepts in its concept sphere: the object is the genome and related information; the process is research, sequencing, editing and use of genomes; the goal/result is the creation of new biotechnological products and solutions; the tool is modern methods of genomics, bioinformatics, and synthetic biology.

Analysis of the research material proved that certain concepts are verbalised by most of the identified term-forming models, which include in their morphological composition the same parts of speech – noun, adjective, and verb (in participial form). Based on the results of morphological analysis, it was found that the structure of the English-language biotechnological terminological system is represented by the following models: N, N, N + N, A + N, A + A + N, A + N + N, A + A + A + N, and P + N, where N – noun, A – adjective, P – participle (verb in the form of a participle). Nouns play a key role in building the term system of the English biotechnological language, since they verbalise most industry concepts and are part of the structure of almost all terminological models. K. Deroey (2007) showed that noun compounds in scientific and technical texts in English occur significantly more often than in texts of a general thematic nature, which determines their

special functional load. This phenomenon has attracted the attention of researchers who have studied noun compounds from various scientific approaches, in particular: semantics (Bogachyk & Bihunov, 2020) and cognitive studies (Matvieieva & Torgovets, 2022), corpus linguistics (Bauer & Renouf, 2001), morphology and syntax (Junya, 2017).

Nouns fall into various lexical and grammatical categories: concrete, abstract, and proper nouns. In linguistic research, specific nouns are considered as nouns denoting physical objects or creatures that can be directly perceived through the senses. According to R. Matthews (2014), a specific noun is “a noun denoting a physical entity, an object that can be perceived by the senses”. Specific nouns refer to various objects or beings that are key to human understanding. They contain in their semantics information about the properties, appearance, functions, and relationships of these objects with others, which is important for the categorisation process. In the biotechnological terminology of the genomic era, terms expressed by specific nouns verbalise the concept of “object”. Examples of such terms: allele, codon, exon, gene, genome, histone, homolog, kinase, intron, neuron, vector, pathway, plasmid, promoter, transposon (Kimball, 2002). Specific nouns allow scientists to uniquely identify objects and results in biotechnological activities, ensuring accuracy and logical consistency in the development of a terminological system. To verbalise the concept of “goal/result” in biotechnology, terms expressed by specific nouns are also actively used. They usually denote the final effect, achieved goal or product of a biotechnological process, giving the terms clarity, concreteness and completeness, which is extremely important for the accuracy of the scientific term system. Examples of such nouns are the following terms: construct, mutant, strain, clone, biomarker, isolate, metabolite, knockout.

Specific nouns in the N + N model are widely used to verbalise the concepts of “object”

and “process” in genomic era biotechnology. This model ensures accuracy and unambiguity of terminology, allowing scientists to clearly identify objects, phenomena, and processes. Examples of terms for objects: protein complex, plasmid vector, antibody molecule, lipid vesicle (Kimball, 2002), cell line, DNA sequence, membrane protein, virus particle (Zaid *et al.*, 2001). The concept of “process” is verbalised in biotechnological terminology through terms such as gene expression, protein synthesis, virus replication, cell division. A special role in this is played by the gerund, which, acting as a noun, is one of the most common morphological means of expressing processuality. It provides: nominativity – naming processes as independent objects (cloning, sequencing, culturing) and consistency – including complex terms in the structure, for example: genome editing, genetic engineering, gene cloning, molecular cloning, protein cloning, cell culture, tissue culture (Zaid *et al.*, 2001). Thus, the use of specific nouns in the N + N model is an effective morphological means of nominating key concepts of biotechnological terminology, which allows clearly reflecting both static objects and dynamic processes, and accurately reflecting the relationships between objects and their characteristics or processes in the scientific discourse of biotechnology.

Abstract nouns are names of immaterial entities that denote an abstract feature, action, or general concept. Most often, these are nouns that refer to phenomena or processes that do not have a real physical embodiment and are perceived by the imagination. In the English terminology of biotechnology, abstract nouns are used to verbalise the concept of “process”. Abstract nouns are used to represent concepts related to processes, functions, properties, or states of biological systems, such as replication, transcription, expression, regulation, interaction, transformation, differentiation, and mutation. The vast majority of nouns with abstract meaning are words with derived bases

of adjective (active → activation) or verb origin (replicate → replication). These examples indicate the abstract nature of the phenomenon reflected in the term. These phenomena cannot be counted, they cannot be measured or their limits determined, etc., but the characteristic features of these phenomena can be distinguished. Abstract nouns are symbiotic formations that combine in their categorical semantics the meaning of a phenomenon as a process and its qualities and form a special zone in the class of nouns. They allow describing dynamic and functional aspects of objects that cannot be directly observed, and thus play a key role in scientific discourse and categorisation of knowledge in the field of biotechnology.

Proper nouns that denote the individual name of a particular object and distinguish it from a number of objects of the same type are widely used in the verbalisation of the concept of “object”. They allow describing concepts related to specific biological or technological objects. The use of proper nouns helps to accurately identify specific objects and their unique properties, which is important for scientific description and communication in the field of biotechnology. Proper names serve as a constant source for the formation of eponyms. In terminology, eponyms are terminological units used to name concepts that reflect unique objects, discoveries, processes, or technologies associated with specific individuals, organisations, or projects. Proper nouns are part of models of multicomponent eponymic terms and can be classified into several groups. These include the names of specific organisms or strains that uniquely identify biological objects, such as *Escherichia coli*, *Saccharomyces cerevisiae*, Watson-Crick; the names of cell lines, molecular tools, or enzymes that denote laboratory materials or technologies, such as HeLa cells, CRISPR-Cas9, Taq polymerase, Sanger sequencing method; and the names of large scientific projects, databases, or organisations that have become eponyms for large-scale research and initiatives,

for example: Human Genome Project, ENCODE project, BioBricks Foundation (Kimball, 2002). The use of proper names in terminology allows accurately identifying objects and emphasising their unique properties, which is important for scientific description, communication, and standardisation of knowledge in biotechnology.

Thus, words denoting objects of reality, play an active role in the nomination process in the biotechnological sphere, since they provide accuracy and clarity in defining concepts, serve as the basis for the formation of terminological units and reflect key objects, phenomena, and processes around which scientific knowledge is built. By performing a quantitative analysis of the terms of the selected term system, it was revealed that the absolute majority are terms represented by a noun, which is quite natural for the scientific and technical industry. The total number of such terms was 206 units out of a total sample of 400 terms, which corresponded to 51.5% and indicated their dominant presence in the material under study. Similar dynamics were recorded by A.A. Tyutyunyk (2021), who noted that although the leading position is still occupied by simple terms (45.5%), phrase terms (41.34%) also make up a significant share, which indicates the relevance of multi-component structures in modern term-making. This trend was also observed by G. Bondarenko (2020), who in the study of terminological vocabulary noted the dominance of nouns.

The morphological method of term formation is the basis for the development of English-language terms – nouns in biotechnology of the genomic era, since it is the foundations and affixes that carry the main word-forming load, since the morphological structure of the term formed by affixation organically lays the foundations of structural systematisation, which are of primary importance for terminology, because they allow tracing changes in the semantics of the word associated with the addition of so-called formal indicators – suffixes and affixes (Bondarenko, 2020). Using word-forming

analysis to distinguish between productive and unproductive ways of forming English-language terms represented by nouns in the field of biotechnology of the genomic era, several main groups were identified depending on the nature of their word-forming structure. This classification includes suffix formations – terms created by adding suffixes to bases that denote processes, phenomena, properties, or carriers of action. Such units as docking, transcription, replication, modification, stability, sequencer, activator (47 units – 22.8%) demonstrate high performance in expressing dynamic and static characteristics.

Prefix formations are formed by adding a prefix to the generating base without involving suffixes; the prefix changes or clarifies the meaning of the base word. In biotechnological terminology, such structures are less common, but they perform an important function of semantic modification, as illustrated by the examples of anticodon, antigen, remark, pretest, and postgenome (29 units, 14.1%). A separate group consists of prefix-suffix formations, in which prefixes and suffixes simultaneously modify the meaning of the base, indicating the processality, state or action characteristic of scientific terminology. These include reprogramming, demethylation, misfolding, deactivation, reexpression, uncoating, rereplication, and misregulation (47 units – 22.8%). An important place among word-forming structures is also occupied by composite (root-forming) formations created by combining two or more bases, which can be either independent words or root morphemes. This type of creation is productive in biotechnological terminology, as it allows forming capacious, accurate, and semantically rich names of complex objects, processes and phenomena, for example: mutagen, bacteriophage, bacteriostat, immunosensor, ribosome, carcinogen, biotechnology, pharmacogenomics (41 units – 19.9%). A separate group consists of terms with Latin and Greek roots, which are formed on the basis of classical languages, which ensures their international clarity

and stability in scientific use. These include epigenome, transcriptome, cytokine, mutagen, proteome, and metagenomics (41 units, 19.9%).

Terms represented by nouns in the English-language biotechnology terminology of the genomic era are often formed using neoclassical components such as bio-, geno-, -omics. Some researchers consider them the same status as ordinary words, while others give them a special status and consider them as a separate category. According to the rethinking of the status of these morphemes in the English derivation system, neoclassical components should be considered as a separate class of combining forms. They occupy an intermediate position between roots and affixes, since they have their own lexical meaning, but do not function as independent words. These forms are productive elements of the word-forming system, which allows creating new terms using regular morphological rules. This approach allows more accurately describing the structure and mechanisms of creating modern biotechnological terminology, which is especially relevant for the analysis of language units of the genomic era. This was also confirmed by a number of researchers. I. Plag (2018) emphasised the semi-autonomous nature of such forms, emphasising their ability to function as independent elements in word formation. A similar opinion was expressed by G. Booij (2005), who drew attention to their ability to form new words in regular, though somewhat limited, patterns. Similar observations were expressed by O. Garmash (2014; 2016), who analysed the verbalisation of English-language biocentric and technocentric concepts of affixal type and emphasised the active use of neoclassical morphemes as productive word-forming components in the development of complex scientific terms that reflect the latest concepts of genomics, bioinformatics, proteomics, etc. The results of quantitative analysis of the formulation of biotechnological nouns in the genomic era are presented in Table 1.

Table 1. Distribution of nouns by word-forming structure

No.	Type of word-forming structure	Number of terms	Share
1	Suffix formations	47	22.8%
2	Prefix formations	29	14.1%
3	Prefix-suffix formations	47	22.8%
4	Composite (basic) formations	41	19.9%
5	Terms with Latin and Greek roots	41	19.9%
	Total	206	100%

Source: compiled by the author

The word-forming analysis of English-language noun terms in the field of biotechnology of the genomic era showed different degrees of productivity of word-forming models. Suffix and prefix-suffix formations were the most commonly used, which together cover almost half of the entire term base (about 46%). This indicates the high productivity of suffixing as the main method of creating scientific terminology, which allows denoting processes, phenomena, and actions characteristic of the biotechnological sphere. Composite formations and terms with Latin and Greek roots also occupy a significant share – 19.9% each. This is conditioned by the need to create succinct and precise terms that ensure interethnic clarity and consistency in scientific discourse. The relative low productivity of prefix nouns in term systems, which is 14.1%, is confirmed by studies of other researchers. In this context, Yu. Togano (2024) also noted that the prefix in English basically does not change the grammatical category of a word, but only expands its lexical and semantic meaning. Prefixes, according to the researcher, function more as lexemes or full-meaning units than as classical morphemes, which also limits their role in the creation of nouns in scientific terminology.

However, it should be noted that the study by M. Bogachyk & D. Bihunov (2020), devoted to the structural and semantic features of computer terminology in English, prefix formations account for 14.3% of the total number of analysed units, while prefix-suffix formations account for only 1.8%. This distribution

demonstrates that the performance of word-forming models largely depends on the industry specifics of the term system. In the terminology of biotechnology, models related to the description of biological processes and structures predominate, where suffixation and basic assembly play a more important role, while in the computer sphere, the active use of prefixes is more often recorded due to the need to quickly create new functional names based on existing terms. Prefixes mostly only change the meaning of a word without changing its grammatical category, which narrows their word-forming use. Thus, the results of the analysis confirm the dominance of suffix and combined (prefix-suffix) models in the structure of English-language biotechnological terms, and the importance of composite formations and classical language elements in ensuring the scientific accuracy and universality of biotechnological terms – nouns of the genomic era.

Categorisation of the world at the level of features involves structuring knowledge about various characteristics of the surrounding reality, primarily qualities and properties, and finds its linguistic reflection at the level of the adjective category, which is an integral part of the terms that implement this concept. The adjective is an important part of speech, often found in syllabic models of English terms that verbalise concepts of genomic era biotechnology. In terminological phrases of attribute models, the noun fixes an object or object, and the adjective specifies its properties, origin, or functional specifics, for example: genomic sequence,

cellular pathway, recombinant protein, molecular marker, transgenic mouse, regulatory element, viral vector, bacterial strain, synthetic pathway, specific promoter (Zaid *et al.*, 2001). The presence of adjectives in models of English-language biotechnological terms indicates that during the nomination process, experts emphasise the essential features of objects necessary for their accurate scientific description and categorisation. Adjectives in terms of the genomic era mostly reflect properties that can be perceived or conceptualised through parameters of size (long-read sequencing), structure (structural genomics), shape (circular DNA), colour (green fluorescent protein), functional characteristics (functional genomics), spatial orientation (spatial transcriptomics), and temporal dynamics (real-time PCR, time-dependent expression) (Genomics Glossary, n.d.). Based on these features, adjectives play a key cognitive role: they highlight the most important characteristics of objects and processes, systematise knowledge, and clarify the meaning of terms. Thus, adjectives become not only a grammatical, but also a conceptual tool for term formation.

In genomic era biotechnology terminology, the A + N model is used to verbalise various concepts. The concept of “object” is represented by an adjective that specifies the type, kind, or characteristic of an object (for example: human genome, viral vector, or bacterial strain). The concept of “goal/result” is implemented through an adjective that emphasises the properties or functions of the final product (for example: recombinant protein, therapeutic molecule, therapeutic protein, transgenic organism). The A + N model provides high consistency and logic of terms, since it allows combining the basic concept (noun) with its refinement (adjective), which is especially important in genomic and molecular biotechnology. It allows accurately identifying both the objects of research and the final results of experimental activities, emphasising their properties, origin, and functions. This makes terms more specific,

analytical, and unambiguously understandable in a scientific context.

In the analysed terminological system, two main types of adjectives can be distinguished: qualitative and relative. In the field of biotechnology, where accuracy, quality and efficiency play an important role, the language of science should be not only informative, but also as clear as possible. That is why qualitative adjectives and phrases constructed with them are an important tool for scientific description. They help to convey specific properties of biological processes, materials, and technologies. As part of multicomponent models such as A + A + N, A + N + N, or A + A + A + N, qualitative adjectives detail the properties of an object, for example: comprehensive functional genomic study, sensitive diagnostic test, stable gene expression, stable protein structure, strong promoter activity, pure DNA sample, robust experimental design, efficient delivery system, or advanced genomics methods: accurate measurement technique, efficient fermentation process. Phrases with high-quality adjectives are not only a way to decorate the language, but also a tool for scientific accuracy, which allows communicating effectively in an area where every characteristic matters. Knowledge and active use of such constructions increases the level of scientific literacy and professionalism of the specialist. Qualitative adjectives reflect the qualitative characteristics of an object or process.

Relative adjectives are adjectives that indicate a feature of an object because of its relation to another object or phenomenon. In a biotechnological context, such adjectives are widely used to accurately describe processes, materials, technologies, and equipment. In the field of biotechnology, relative adjectives in the A + N model indicate the relationship of an object to a particular industry, process, environment, or property. In biotechnology, this model is widely used for scientific accuracy, time creation, and classification of phenomena. Relative

adjectives in the A + N model allow verbalising concepts formally and clearly: specify a method, material, property, or industry, for example: genetic engineering, genetic variation, genetic material, recombinant DNA, recombinant protein, microbiological analysis, microbiological safety, immunological response, immunological assay, viral vector, viral infection, chromosomal abnormality, chromosomal mapping, biotechnological innovation, biotechnological production, antigenic determinant, metabolic pathway, enzymatic reaction, enzymatic degradation (Zaid *et al.*, 2001).

In the biotechnological term system of the genomic era, the adjective+noun (A + N) model is one of the most common key concepts for verbalisation: 89 (45.9%) term units out of 194 were formed using this structural model, which allows simultaneously reflecting the main object of research and its characteristic, property or function, which significantly improves the accuracy of terminology. The noun + noun (N + N) model also plays an important role and makes up 57 phrases, which is 29.4% of the total number of terminological phrases. Model A + N is used with greater frequency because adjective-noun constructions provide a higher level of terminological accuracy, structural flexibility, and semantic transparency, which is critical for scientific discourse in biotechnology. It is these characteristics that allow the A + N model to act as a basic tool for nominating new concepts in the industry.

This conclusion was also reached by H. Syrotina (2022), who, as part of its research on the categories of concepts expressed in English-language terms of the biotechnological sphere, analysed grammatical models of term combinations and found that, despite the lower performance compared to the A + N model, the N + N structure remains relevant for denoting substantive terms with an attributive meaning, where the main component is located at the end of the phrase. O.A. Brana (2023) found that in English-language scientific texts, the

frequency of using attributes-nouns exceeds the frequency of attributes-adjectives, although in the linguistic tradition it is common to use relative adjectives as terminological attributes that form complex terminological phrases, carrying a feature meaning and providing the synthetics of knowledge necessary to reveal the semantic potential of terms. The composition of terminology depends on the field of sciences – humanities, social sciences, natural sciences, or technical sciences. Common to them is the naming of beings, things, and phenomena, but in the terminology of the sciences of the humanities and the social cycle, there is an attraction to more nouns. But in the natural and technical sciences, the quantitative meaning of nouns.

The study by K. Pitkänen-Heikkilä (2015), dedicated to the analysis of adjectives as terms in the field of plant morphology, made similar observations, but with a focus on a specific subject area. The researcher noted that almost half of the terms in plant morphology are adjectives that function not only as modifiers, but also as full-fledged terminological units with a stable meaning. The researcher stressed that the traditional practice of terminography, which included the nominalisation of adjectives, was unsuitable for the field of plant morphology. This is conditioned by the fact that such nouns are not used in authentic scientific texts, and the transformation itself can lead to semantic distortions. Both researchers emphasised the conceptual significance of attributive adjectives, which do not act as secondary grammatical elements, but, on the contrary, play a key role in the formation of terminological meaning. If O.A. Brana (2023) considered this issue in a broader interdisciplinary context, K. Pitkänen-Heikkilä (2015) argued for the expediency of preserving adjectives as independent terms in specialised dictionaries.

Multicomponent adjective models, in particular A + A + N and A + A + A + N, play an important role in the classification of objects, since they allow reflecting in detail several features

of the concept under study simultaneously, for example: recombinant viral vector, robust experimental design, functional genomic analysis, experimental genetic manipulation, comprehensive functional genomic study. Despite the relatively low frequency, they remain significant in the structure of the terminological system: the model A + A + N is 11 units (5.7%), and A + A + A + N – 7 units (3.6%) of the total number of analysed term combinations. Their use indicates the need for a more accurate, multi-level characterisation of concepts in scientific discourse. They allow simultaneously conveying qualitative traits, attitudes, and affiliation, making the term more informative and accurate. This approach contributes to the effective systematisation of terms and facilitates communication between specialists in the field of biotechnology of the genomic era. The tendency to increase multicomponent terms in biotechnological terminology was noted by E. Myshak (2017) and A. Syrotin (2017), who emphasised their importance for accurately conveying complex concepts that have emerged in the development of scientific knowledge. E. Myshak (2017) noted that multicomponent terms often occur in biotech discourse, and their number increases with the complexity of the subject area. The researcher noted that “the more components in a term, the lower its polysemy”, that is, the highest degree of accuracy and unambiguity, which is especially important for professional scientific communication. Similar observations were made by researchers in related fields. Arguments in favour of multicomponentence were also supported by F. Remy *et al.* (2023), who, when analysing clinical terminology, emphasised the importance of accurate recognition of verbose (idiomatic) terms, since they provided adequate encoding of complex concepts in specialised subsections. Thus, in the context of the rapid development of scientific disciplines, multicomponent terms are not only a natural consequence of the complexity of knowledge, but also an effective tool for

avoiding ambiguity, improving accuracy, and forming new nominations.

As a result of morphological analysis of terms of the English terminological system, a term formation model was identified that includes such a language unit as the participle. By its origin, the participle has a noun basis, but in the process of language evolution, it has acquired verbal characteristics, in particular, signs of state and time. From the standpoint of cognitive linguistics, a participle is considered as an intermediate language category that differs from both a verb and an adjective, but reflects the cognitive processes of adjectivation of an action based on verbal semantics. The participle retains procedural features in its meaning, that is, it reflects a new way of perceiving an object in human consciousness. Its formation is based on the heterogeneity of cognitive processes, which is manifested in varying degrees of expression of verbal and adjective properties. A participle is a verb form in which an action, process, or state, while remaining procedural in nature, acquires the meaning of a feature or property.

In the structure of English terms built on the model (participle + noun), verbalising the concepts of biotechnology, the participle is presented in two main forms – present (present participle, -ing) and past (past participle, -ed). Both forms perform an important cognitive and term-forming function, but differ in semantics and pragmatics of use. The past participle in the V-ed + N model performs the function of indicating the properties of objects or materials obtained as a result of biotechnological processes, for example: engineered organisation, cultured cells, isolated DNA, modified vector; denatured enzyme, activated pathway, inhibited expression, targeted delivery; integrated system, controlled release, immobilised biocatalyst, encapsulated microorganism (Zaid *et al.*, 2001). The V-ed + N model is represented by 16 units, which is 8.2% of the total number of analysed term combinations. The past participle in terms of the biotechnological field

not only performs a nominative function, but also serves as a cognitive marker that reflects the result, method or nature of an action, fixing important aspects of complex biotechnological processes in a linguistic form.

Present participles in the V-ing + N model structure serve as markers of the active action, process, or functional ability of an object. Such participles, unlike forms with the suffix -ed, do not focus on the result of the action, but reflect the processality, dynamics, incompleteness or continuing nature of the event, for example: binding protein, coding region, splicing site, signalling molecule, targeting system, processing enzyme, emerging pathogen (Genomics Glossary, n.d.). This is especially true in the genomic era biotechnology concept sphere,

where constantly updated knowledge about the functioning of living systems, genomic processes, and molecular interactions is key. The V-ing + N model was recorded in 14 term combinations (7.2% of the total). Although the proportion of conjugations with participial forms – models V-ed + N and V-ing + N – is relatively small (8.2% and 7.2%, respectively), their use in biotechnological terminology is significant. Such constructions allow nominating complex scientific concepts compactly, accurately and cognitively motivated, which, in turn, contributes to effective communication within the framework of research, applied and educational activities. The results of quantitative analysis of morphological models of biotechnological terms of the genomic era are presented in Table 2.

Table 2. Frequency of morphological models of biotechnological terms of the genomic era

No.	Morphological model	Number of cases	Percentage of total (%)
1	N + N	57	29.4
2	A + N	89	45.9
3	A + A + N	11	5.7
4	A + A + A + N	7	3.6
5	V-ed + N and V-ing + N	30	15.5
Total		194	100

Source: compiled by the author

The analysis of the data presented in Table 2 allowed identifying the most productive morphological models of terms, identifying the relationship between noun and adjective structures, and trace trends in the dominance of individual types in the formation of terms of the genomic era. The most productive model is A + N (45.9%), which is actively used to indicate tools, methods and characteristics of processes in the field of genomic research. Noun structures N + N (29.4%) reflect objects of research and phenomena, while participial forms (V-ed + N, V-ing + N, 15.5%) verbalise the dynamic aspect – the process or result of an action. Models with two and three adjective components (A + A + N, A + A + A + N) are

less common (9.3% together) and perform the function of detailing complex concepts. Thus, the predominance of adjective-noun constructions indicates the trend of biotechnological terminology of the genomic era towards analyticity, compactness, and accuracy of scientific nomination. To clarify the relationship between the morphological model N and the conceptual categories “object”, “process”, “goal/result” and “tool”, an integrative analysis was carried out, which helped to identify which aspects of scientific knowledge are most often represented through a certain morphological structure. Table 3 shows the results of the distribution of model N terms by main conceptual categories.

Table 3. *Distribution of conceptual categories by model N*

Conceptual category	Number of terms	Percentage of total (%)
OBJECT	110	54.0
PROCESS	35	17.2
GOAL/RESULT	20	9.8
TOOL	39	19.0
Total	204	100

Source: *compiled by the author*

The distribution of terms by conceptual categories within morphological model N shows that the largest share is occupied by objects – 54%, which indicates that in the terminology of the genomic era, considerable attention is paid to the name of key objects of research, such as genomes, proteins, cells, and other biological structures. This is logical, because objects are the basis for further analysis, experiments, and development. The second most frequent category is “instrument” (19%). They include terms that refer to advanced methods, devices, and technologies that are actively used to study genomes and modify them. The high proportion of this category highlights the role of technological progress in biotechnology and genomics. The category “process” is 17.2%, which indicates the active use of terms that describe various dynamic phenomena – research, sequencing, editing, etc. This reflects the importance of the procedural component in scientific

research and practical applications. A smaller share falls on the “goal/result” category (9.8%), which includes terms that denote the final products or goals of biotechnological activities. This may indicate that compared to objects, tools, and processes, the concepts of results or goals are still less formalised in terminology.

Thus, the analysis demonstrates that model N mainly verbalises static, object concepts, which is the basis for building further descriptions of processes, tools, and results in the field of genomic biotechnology. This division reflects the nature of the development of scientific knowledge in this dynamic field. In order to summarise the results of the study and identify the relationship between morphological models and conceptual categories, an integrative analysis of the terms of the genomic era was carried out. Table 4 shows a comparison of the main conceptual categories with typical models of their morphological implementation and frequency indicators.

Table 4. *Correlation of morphological models and conceptual categories in genomic era terminology*

Conceptual category	Morphological models	Number of terms	Share of the total number
OBJECT	N, N + N, A + N	108	55.7%
PROCESS	V-ing + N, V-ed + N, A + N	33	17.0%
GOAL/RESULT	A + A + N, A + A + A + N	20	10.3%
TOOL	N + N, A + N	33	17.0%
Total	-	194	100%

Source: *compiled by the author*

The above table shows the distribution of terms by main conceptual categories and their morphological models, which helps to better

understand the structure and functionality of terminology in the field of genomic biotechnology. The largest share is made up of terms in the

“object” category (55.7%). This dominance reflects a focus on naming specific research objects – genomes, genetic structures, molecules, and other elements that form the basis for further scientific action and technological applications. The most common morphological models in this category are simple noun constructions (N) and phrases like N + N and A + N, which ensures compactness and accuracy in names. The second largest category is “process” (17.0%), which includes participle models (V-ing + N, V-ed + N) and adjective-noun constructions (A + N). This indicates the active use of terms that describe actions, operations, methods, and technological processes within genomic era biotechnology. This morphology contributes to a concise and understandable reflection of the dynamic aspects of scientific activity.

The tool category (17.0%) covers terms that refer to tools, methods, and technologies used in genomics and related disciplines. Here, too, noun models predominate, which emphasises the importance of clear identifiers for naming technical means and techniques. The smallest category – “goal/result” (10.3%) – reflects terms related to the final products of research and their meaning. They are represented by more complex adjective models (A + A + N, A + A + A + N), which is explained by the need for a detailed description and classification of new scientific concepts and products. Thus, the analysis confirmed that genomic era terminology is dominated by simple noun constructs for designating objects, and more complex models predominate in categories that require more accurate characterisation and description of processes and results. This division reflects the general tendency to conciseness in the names of objects and to expand in the designation of dynamic and functional aspects of scientific knowledge.

Conclusions

Morphological analysis of the terms of the English-language biotechnological terminology of the genomic era showed that its

structure is represented by a number of productive models: N, N + N, A + A + N, A + N + N, A + A + A + N, and V-ing + N, V-ed + N, which include nouns, adjectives, and participles. The noun conceptualises phenomena of objective reality, such as processes, materials, structures, and technologies, while the adjective and participle refine the characteristics of an object by adding information about qualitative, quantitative, functional, spatial, or temporal parameters. Among the terms, the noun model N dominates (206 out of 400 terms, 51.5%), which indicates its leading role in the term system. The most productive model is A+N (45.9%), which denotes objects, tools, methods, and process characteristics. A smaller share is occupied by N + N structures (29.4%), which reflect the objects of research, and participial forms (15.5%), which verbalise the dynamics of processes or the results of actions. Models with multiple adjectives (9.3%) perform the function of detailing complex concepts, while simultaneously conveying qualitative features, attitudes, and belonging to the object. Comparing linguistic models with conceptual categories – “object”, “process”, “goal/result”, “tool” – allows tracing how language structures scientific knowledge. Noun models mostly represent the object of research, adjective-noun constructions represent tools and characteristics of processes, and participial forms verbalise actions or target processes. The term system of the genomic era is dominated by the concept of “object” (55.7%), which reflects the priority of accurate naming of fundamental elements of research – genomes, molecules, structures. The “process” category (17%) includes participle and adjective-noun constructions, while the “tool” category (17%) covers tools and methods, mostly noun constructions. The smallest category – “goal/result” (10.3%) – is represented by more complex adjective models, which reflects the need for a detailed description of the final products of research. Thus, morphological

and cognitive analysis of terminological models demonstrated the relationship of formal language organisation with the conceptual content of the biotechnological terminosphere. Multicomponent models provide the accuracy, compactness, and detail of terms needed to describe complex biological processes and structures. A promising area of further research is the investigation of the dynamics of term formation in the context of the rapid development of the latest technologies, in

particular, CRISPR, artificial intelligence in bioinformatics, and synthetic biology.

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Морфологічний аналіз англomовних біотехнологічних термінів геномної ери

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Анотація. Актуальність дослідження зумовлена зростанням значення англomовної біотехнологічної термінології в контексті інтенсивного розвитку геномних технологій, що потребує системного аналізу її морфологічної структури для покращення наукової комунікації та глибшого розуміння когнітивних процесів термінотворення. Мета роботи полягала в аналізі морфологічної структури англomовних біотехнологічних термінів геномної ери крізь призму когнітивного підходу. Для досягнення поставленої мети використано такі методи: лексикографічний, морфологічний та статистичний аналіз, елементи когнітивного підходу до вивчення термінів, а також методи систематизації та узагальнення. Встановлено, що в англomовній біотехнологічній терміносистемі активно використовуються термінологічні моделі, до структури яких входять іменники, прикметники та дієприкметники. Абсолютну більшість становлять терміни, представлені іменниками (N), причому найбільш уживаними виявилися суфіксальні та префіксально-суфіксальні утворення, які разом охоплюють близько 46 % усієї термінної бази. Розподіл термінів за концептуальними категоріями у межах морфологічної моделі N показав, що найбільшу частку займають об'єкти (54 %) – ключові елементи біотехнологічного дослідження, такі як геноми, білки, клітини, за якими слідує інструменти (19 %) – сучасні методи, прилади й технології, процеси (17,2 %) – динамічні дії на кшталт секвенування чи редагування, та мета/результат (9,8 %) – кінцеві продукти або цілі. Кожна із проаналізованих структур (N, N + N, A + N, A + A + N, A + A + A + N, V-ed + N, V-ing + N) виявилась пов'язаною з окремими аспектами концептуальної сфери: іменникові моделі здебільшого репрезентують об'єкт дослідження (наприклад, gene expression, protein synthesis), прикметниково-іменникові конструкції – інструменти та характеристики процесів (наприклад, synthetic genomic technologies), тоді як дієприкметникові форми вербалізують результати дії, змінні стани або властивості, набуті внаслідок біотехнологічного втручання (наприклад, engineered organism, modified gene) або функціональні властивості об'єктів (наприклад, binding protein, binding site, coding sequence). Морфологічний аналіз дозволив виявити не лише структурні особливості термінів, а й ті концептуальні моделі, що лежать в основі наукового мислення у сфері біотехнологій, відображаючи динаміку розвитку галузі та її лінгвокогнітивну специфіку. Практичне значення дослідження зумовлене можливістю використання отриманих результатів у процесі викладання іноземної мови за професійним спрямуванням для студентів спеціальності «Біотехнології та біоінженерія»

Ключові слова: терміносистема біотехнології; словотвірна структура; морфемна організація; концепт; когнітивний підхід