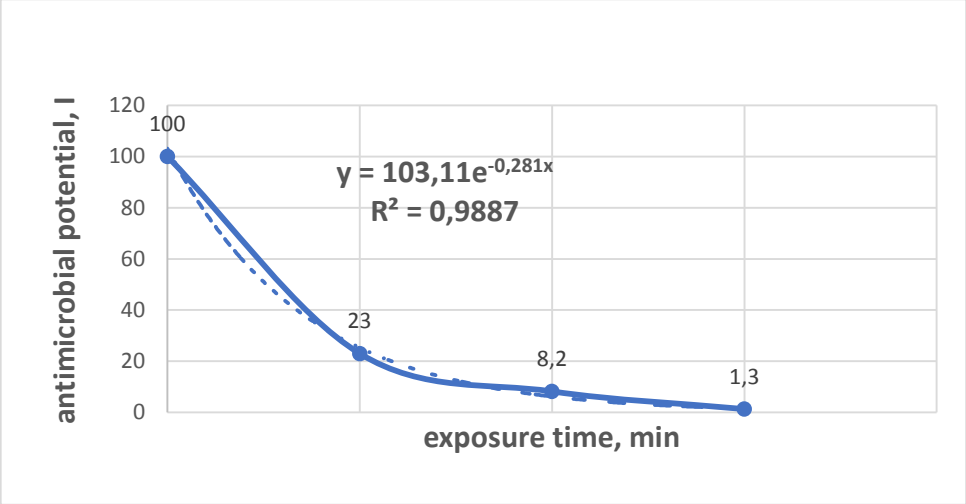

Figure 1 – Dependence of antimicrobial potential of plasma on time of exposure to *Staphylococcus aureus* population

A regular dependence of the efficiency of plasma exposure on the time of exposure to the population of test microorganisms *Staphylococcus aureus* was obtained, which was described by an exponential function. The approximation coefficient of 0.9887 allows one to conclude that the chosen mathematical model describes the obtained dependence with a high degree of reliability.

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THE ROLE OF SINGLE NUCLEOTIDE VARIANTS (SNVS) IN GENOMIC INNOVATION

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Summary. *Single nucleotide variants (SNVs) represent the most common type of genetic variation, with significant applications in genomic research, disease understanding, and personalized medicine. This paper discusses the role of SNVs in modern research and technological advances, particularly in the development of diagnostic and therapeutic innovations.*

Single nucleotide variants (SNVs) refer to variations in a single nucleotide that occur at a specific position in the genome. SNVs are pivotal in understanding genetic diversity and are linked to numerous inherited traits and diseases.

Their study is instrumental in advancing personalized medicine, where patient-specific genetic information guides individualized healthcare [1]. This paper explores the role of SNVs as the key genetic variation, and innovative usage of the knowledge about them in personalized medicine, while also addressing the challenges and future directions in SNV research.

SNVs are distinguished from other genetic variations by their simplicity and prevalence, accounting for the major part of known genetic variations in the human genome [2]. Of all clinically classified SNVs, approximately 16.8 % are pathogenic or likely pathogenic, 40.2 % show positive or likely positive effects, and the majority (40.5 %) are still unclear [3]. They can potentially influence susceptibility to diseases, response to medications, and other health-related traits. Due to their simplicity, SNVs are easier to analyze than more complex genetic variants, making them a key area of interest in genetic research [4].

There is a wide range of SNVs application in medicine and research. One of the most significant areas is personalized medicine. SNVs are instrumental in the field of pharmacogenomics, where they help predict drug response based on genetic makeup [5]. Identifying SNVs associated with adverse drug reactions enables clinicians to tailor treatments, thereby increasing drug efficacy and reducing side effects.

SNVs also can be used for disease diagnosis and prognosis. Certain SNVs are the markers for genetic diseases, including cystic fibrosis, sickle cell anemia, and various cancers [6]. Research on SNVs linked to cancer, for instance, has contributed to the development of targeted therapies that specifically address the molecular changes associated with a patient's tumor [7].

Despite significant advancements, several challenges remain in fully utilizing SNVs. One major obstacle is the difficulty in interpreting their functional impact, as many SNVs have unknown effects on gene function or phenotype. This complexity arises from the intricate interaction between genetic and environmental factors, as well as variability in how different populations are affected. Furthermore, while technologies for detecting SNVs are improving, the large volume of data generated requires sophisticated bioinformatics tools to accurately assess their biological consequences. These challenges hinder the integration of SNVs into clinical practice, particularly for personalized medicine, where precise knowledge of their effects is essential for predicting the risk of disease appearence and tailoring treatments [8].

In conclusion, SNVs are crucial to the continued progress in genomics, holding transformative potential across various fields, particularly in medicine. Their continued exploration, coupled with innovations in sequencing technology and bioinformatics, will undoubtedly lead to new breakthroughs in personalized healthcare, marking a significant step forward in the application of genomic knowledge for societal benefit.

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