

## MICROBIOLOGICAL ANALYSIS OF THE MAIN TYPES OF STAPHYLOCOCCI THAT ARE IMPORTANT FOR THEIR DISTRIBUTION AND MEDICAL PRACTICE

*Kuralay Kadirova Abdullaevna*

*Assistant of the Department of Microbiology, virology and immunology of Tashkent Medical Academy,  
Tashkent, Uzbekistan*

*Abdulaziz Nazirov Qakhramon ugli, Charoskhon Egamberganova Otabek qizi,  
Zebo Bokhodirova Zafarovna, Mokhinabonu Abdumalikova Alisher qizi.*

*Student of the 2nd Faculty of Medicine 2nd year of 225a group of the Tashkent Medical Academy*

**Abstract:** The microscopic organisms are a driving cause of nourishment harming, coming about from the utilization of nourishment sullied with enterotoxins. Staphylococcal nourishment inebriation includes fast onset of sickness, spewing, stomach torment, issues, and loose bowels. Side effects as a rule resolve after 24 hours. Creature chomps can result in nearby contaminations, cellulitis, erythema, delicacy, mellow fever, adenopathy, and lymphangitis (seldom). Burnt skin disorder is caused by exfoliative poisons emitted on the epidermis and for the most part influences neonates and youthful children. Other skin conditions caused by Staphylococcal exfoliative poisons incorporate rankles, skin misfortune, pimples, furuncles, impetigo, folliculitis, abscesses, destitute temperature control, liquid misfortune, and auxiliary disease. *S. aureus* can moreover cause necrotizing fasciitis in immunocompromised people, in spite of the fact that typically exceptionally uncommon. Necrotizing fasciitis is life-threatening and causes serious dreariness. *Staphylococcus aureus* is an astute pathogen that can cause a assortment of self-limiting to life-threatening illnesses in people. *Staphylococcus aureus* could be a common pathogen causing both healing center and community-acquired contaminations. Hemolysin is one of the critical harmfulness components for *S. aureus* and causes the normal  $\beta$ -hemolytic phenotype which is called total hemolytic phenotype as well. As of late, *S. aureus* with an fragmented hemolytic phenotype (SIHP) was disconnected from clinical tests. To ponder the microbiologic characteristics of SIHP, the extraordinary hemolytic phenotype of SIHP was confirmed on the sheep blood agar plates provided by distinctive producers. Species recognizable proof and demonstrative issues challenging for diagnosticians are displayed. Concluding comments with respect to the nearness of CoNS in people and their dissemination, especially beneath the impact of encouraging variables, are specified.

**Keyword:** Microscopic organisms, *Staphylococcus aureus*, coagulase-negative staphylococci, methicillin-sensitive *S. aureus*, life undermining contaminations, microbiological research.

**Introduction.** Microscopic organisms within the class *Staphylococcus* are pathogens of man and other warm blooded animals. Customarily they were separated into two bunches on the premise of their capacity to clot blood plasma (the coagulase response). The coagulase-positive staphylococci constitute the foremost pathogenic species *S. aureus*. The coagulase-negative staphylococci (CNS) are presently known to contain

over 30 other species. The CNS are common commensals of skin, in spite of the fact that a few species can cause contaminations. It is presently self-evident that the division of staphylococci into coagulase positive and negative is artificial and indeed, deceiving in a few cases. Coagulase may be a marker for *S. aureus* but there's no coordinate prove that it could be a harmfulness calculate. Too, a few characteristic segregates of *S. aureus* are imperfect in coagulase. In any case, the term is still in broad utilize among clinical microbiologists [1-5]. *S. aureus* communicates a assortment of extracellular proteins and polysaccharides, a few of which are related with harmfulness. Harmfulness comes about from the combined impact of numerous variables communicated amid contamination. Antibodies will neutralize staphylococcal poisons and proteins, but immunizations are not accessible. Both anti-microbial treatment and surgical seepage are frequently essential to remedy abscesses, expansive bubbles and wound contaminations. Staphylococci are common causes of contaminations related with indwelling restorative gadgets. These are troublesome to treat with anti-microbials alone and regularly require expulsion of the gadget. A few strains that contaminate hospitalized patients are safe to most of the anti-microbials utilized to treat contaminations, vancomycin being the as it were remaining medicate to which resistance has not created [5-11]. *Staphylococcus aureus* is an critical human pathogen disconnected from hospitalized patients around the world, which causes both healing center and community-acquired contaminations. This pathogen is the etiological operator of a few diverse systemic diseases, influencing skin and delicate tissue, as well as musculoskeletal and circulatory frameworks. It was detailed that *S. aureus* can survive in human monocyte-derived macrophages. The harmfulness of *S. aureus* is closely related with a assortment of emitted proteins and poisons delivered by the microbes. Hemolysin, leukocidin (PantonâValentine leukocidin, PVL), and harmful stun disorder toxin-1 (TSST-1), encouraging for harming the ruddy cell layer, harming phagocytic work of leukocytes, and actuating harmful stun disorder separately, are basic for the pathogenic forms of *S. aureus*. Later considers have illustrated that hemolysin too takes an interest within the arrangement of the *S. aureus* biofilm [12-16]. The expanding predominance of multidrug-resistant *S. aureus* strains inside healing center and community situations encourage increments the perils of *S. aureus* and postures a genuine challenge for clinical treatment. As of late, a number of strains having a place to a lesson of *S. aureus* with an fragmented hemolytic phenotype (SIHP) have been found in our healing center. Hemolysis caused by these SIHP strains is altogether diverse from the total hemolytic ring ( $\hat{I}^2$ -hemolytic phenotype) created in other *S. aureus* strains. Be that as it may, these SIHP strains have not however been distinguished and characterized comprehensively. To investigate the microbiological characteristics of these SIHP strains, we collected 60 SIHP strains and considered them utilizing numerous criteria counting hemolytic phenotype, expression of the hemolysin quality, drug-resistance highlights, and destructiveness. This think about illustrates that SIHPs are methicillin safe strains that profoundly express  $\hat{I}^2$ -hemolysin and have a tall harmfulness potential [17-21].

**The study of disease transmission of *Staphylococcus Aureus* diseases.** Since *S. aureus* may be a major cause of nosocomial and community-acquired contaminations, it is essential to decide the relatedness of separates collected amid the examination of an episode. Writing frameworks must be reproducible, oppressive, and simple to decipher and to utilize. The conventional strategy for writing *S. aureus* is phage-typing. This strategy is based on a phenotypic marker with destitute reproducibility. Too, it does not sort numerous separates (20% in a later overview at the Center for Illness Control and Anticipation), and it requires support of a huge number of phage stocks and proliferating strains and subsequently can be performed as it were by master reference research facilities [1,2,3,5-9]. Numerous atomic writing strategies have been connected to the epidemiological investigation of *S. aureus*, in specific, of methicillin-resistant strains (MRSA). Plasmid examination has been utilized broadly with victory, but endures the impediment that plasmids can effectively be misplaced and procured and are in this way inalienably questionable. Strategies outlined to recognize confinement part length polymorphisms (RFLP) employing a assortment of gene tests, counting rRNA qualities (ribotyping), have had constrained victory within the the study of disease

transmission of methicillin-resistant *S. aureus* (MRSA). In this strategy the choice of limitation chemical utilized to cleave the genomic DNA, as well as the tests, is significant. Irregular groundwork PCR offers potential for separating between strains but a suitable primer has however to be distinguished for *S. aureus*. The strategy as of now respected as the foremost solid is beat field gel electrophoresis, where genomic DNA is cut with a limitation chemical that produces huge parts of 50-700 kb [11-18].

**MRSA transmission between people and creatures.** Transmission of MRSA among diverse has is essentially known to happen by physical contact with source. The capability of exchange of MRSA among diverse have species counting people and creatures is the characteristic highlight of MRSA ancestries. HA-MRSA is basically procured from clinic settings such as sullied rebellious, bedding, entryways, and equipmentâs whereas CA-MRSA is basically procured by physical contact with tainted or solid individual as *S. aureus* could be a commensal bacterial within the nares of sound people. LA-MRSA transmission to people when the person has physical contact with creature and environment. Firstly, LA-MRSA was limited as it were to creatures until 1961 some time recently the Hungarian bovine was detailed to be the source of LA-MRSA transfer to its caretaker by testing throat swabs. This was the primary report of MRSA transmission from creature to human which demonstrated the capacity of MRSA flat transmission among creatures and people [39-45]. Afterward on a number of reports were distributed by different creators from diverse districts of world from distinctive animalâs species such as poultry, pigs, cattle, sheep and goat, equines, and companion creatures. These reports famous number of clonal complexes (CCs) such as CC5, CC8, CC9, CC59, CC1, CC30, CC45, CC22, CC130, CC97, and CC398 with multi-locus arrangement sorts (STs) were found comparable among human confined MRSA strains and creature separated MRSA strains. On the other hand, different HA-MRSA and CA-MRSA strains are moreover found comparative to other LA-MRSA strains [46]. Among those hazard variables, creature wellbeing status, contamination on body, long term anti-microbial treatment, veterinarians, pet get to to room were found critical chance variables in transmitting MRSA to people whereas the estimate of canine, ownerâs sex, and test location were found to be non-significant hazard variables related with MRSA transmission. Another ponder conducted highlighted the conceivable chance components of MRSA transmission from poultry to people are cultivate specialists, people having contact with live fowls at slaughterhouse, sort of butchering strategy, and butchering environment are altogether related with higher carriage of MRSA among people [24,25,28,33,39,41].

**Concepts in general and clinical manifestations.** Staphylococci are capable of causing a wide range of infections. (1) In addition to localized abscesses in other locations, *S. aureus* causes superficial skin lesions such as boils and styes. (2) In addition to more severe skin infections like furunculosis, *S. aureus* causes deep-seated infections like osteomyelitis and endocarditis. (3) *S. aureus* and *S. epidermidis* lead to infections linked to indwelling medical devices and are a major cause of hospital acquired (nosocomial) infections of surgical wounds. (4) *S. aureus* releases enterotoxins into food, which results in food poisoning. (5) By releasing superantigens into the bloodstream, *S. aureus* causes toxic shock syndrome. (6) UTIs, particularly in females, are caused by *S. saprophiticus*. (7) Other uncommon pathogens include *S. lugdunensis*, *S. haemolyticus*, *S. warneri*, *S. schleiferi* and *S. intermedius* [22-29].

**Species recognizable proof and diagnostics issues.** Challenging distinguishing proof forms may lead to a need of famous contaminations caused by staphylococci other than *S. aureus* and their spread within the environment. Commonly utilized schedule demonstrative strategies, such as culture-dependent phenotypic tests, counting robotized frameworks such as Vitek 2 (bioMÃ©rieux, La Balme Les Grottes, France), BD Phoenix (BD Demonstrative Frameworks, Flashes, MD, USA), and matrix-assisted laser desorption ionizationâ time of flight mass spectrometry (MALDI-TOF MS), both with 16S rRNA quality sequencing, are ordinarily not exact sufficient to carefully allot *Staphylococcus species*. Numerous individuals of the Staphylococcus sort are closely phylogenetically related, and the genuine affect of CoNS species as irresistible etiological components may stay underreported [31-37]. The execution of dependable hereditary

strategies in clinical hone will move forward the recognizable proof handle and result in speedier and more exact determination of staphylococcal contaminations. As appeared in our survey article, in laryngological contaminations, staphylococci regularly coexist with other astute and pathogenic microbes, complicating the distinguishing proof handle. The modern hereditary diagnostics approach, based on another era sequencing, may be utilized for the recognizable proof of entire species substance in polymicrobial clinical tests. The well-curated and freely accessible reference arrangement dataset for *Staphylococcus species* will permit the presentation of this approach in all microbiological research facilities with get to to NGS (next-generation sequencing) stages and may be utilized in diagnosing laryngological diseases [38-43].

**Discussion.** *Staphylococcus aureus* is recognized as commensal as well as deft pathogen of people and creatures. MRSA has developed as a major pathogen in healing centers, community and veterinary settings that compromises the open wellbeing and animals generation. MRSA fundamentally developed from MSSA after procuring SCCmec component through quality exchange containing mecA quality dependable for encoding PBP-2<sup>+</sup>. This protein renders the MRSA safe to most of the  $\beta$ -lactam anti-microbials. Due to the nonstop expanding predominance and transmission of MRSA in healing centers, community and veterinary settings posturing a major danger to open wellbeing. Moreover, tall pathogenicity of MRSA due to a number of harmfulness variables created by *S. aureus* together with anti-microbial resistance offer assistance to breach the insusceptibility of have and capable for causing extreme contaminations in people and creatures [1,2,3,5,11,17]. The pathogenic bacterium *Staphylococcus aureus* is the foremost common pathogen separated in skin-and-soft-tissue contaminations (SSTIs) within the Joined together States. Most *S. aureus* SSTIs are caused by the scourge clone USA300 within the USA. These contaminations can be genuine; in 2019, SSTIs with *S. aureus* were related with an all-cause, age-standardized mortality rate of 0.5 universally. Clinical introductions of *S. aureus* SSTIs shift from shallow contaminations with nearby side effects to monomicrobial necrotizing fasciitis, which can cause systemic signs and may lead to genuine complications or passing. In arrange to cause skin contaminations, *S. aureus* utilizes a have of harmfulness variables counting cytolytic proteins, superantigenic components, cell wall-anchored proteins, and atoms utilized for resistant avoidance [21,25,27,28,29,30]. The safe reaction to *S. aureus* SSTIs includes introductory responders such as keratinocytes and neutrophils, which are bolstered by dendritic cells and T-lymphocytes afterward amid contamination. Treatment for *S. aureus* SSTIs is ordinarily verbal treatment, with parenteral treatment saved for serious introductions; it ranges from cephalosporins and penicillin operators such as oxacillin, which is by and large utilized for methicillin-sensitive *S. aureus* (MSSA), to vancomycin for MRSA. Treatment challenges incorporate antagonistic impacts, chance for *Clostridioides difficile* contamination, and potential for anti-microbial resistance [33,34,35,36]. The clinical signs of MRSA comprise of skin and delicate tissues contamination to bacteremia, septicemia, harmful stun, and burnt skin disorder. Besides, due to the expanding resistance of MRSA to number of anti-microbials, there's have to be approach options ways to overcome financial as well as human misfortunes. This audit is progressing to examine different viewpoints of MRSA beginning from rise, transmission, the study of disease transmission, pathophysiology, malady designs in has, novel treatment, and control methodologies [21,22,23,31,32,33].

**Conclusion.** Methicillin safe strain of *S. aureus* is found to be flexible and eccentric pathogen with differences of ancestries common between people and creatures shown its transmission between human and creatures. The heredities found common between human and creature were CC398, CC9, CC130, CC97, CC398. But this, few HA-MRSA and CA-MRSA heredities were recognized in creatures and LA-MRSA ancestries were recognized comparative to HA-MRSA and CA-MRSA. Subsequently, expanding predominance and hereditary adjustment of this pathogen at creature and human cadre uncovering it a major danger for open wellbeing. Nowadays, based on later reports from progressed microbiological research facilities utilizing atomic demonstrative strategies, it is known that CoNS are extreme pathogens and require expanded disease anticipation programs with cleanliness teach in healing centers. Additionally, progressed



educational programs are required to way better get it the part of CoNS in laryngological maladies with the essential point of decreasing the number of staphylococcal diseases in patients.

This pathogen holds a differing qualities of have species extending from people to nourishment and companion creatures and numerous more. This pathogen has the capacity to stand up to numerous anti-microbials and to elude safe instruments through different destructiveness components that incapable this pathogen to cause mellow to life undermining contaminations. Due to the expanding anti-microbials resistance, this article highlighted the significance of elective ways such as phytochemicals, bacteriophages, nanoparticles, and probiotics alone and in combination to utilize them as substitution of anti-microbial. There's got to work more on these approaches to combat anti-microbial resistance and making them accessible at commercial scale for open. One more approach is to work on fruitful immunization generation and immunization against MRSA.

### References.

1. Zhang H, Zheng Y, Gao H, Xu P, Wang M, Li A, Miao M, Xie X, Deng Y, Zhou H, Du H. Identification and Characterization of *Staphylococcus aureus* Strains with an Incomplete Hemolytic Phenotype. *Front Cell Infect Microbiol.* 2016 Nov 18;6:146. doi: 10.3389/fcimb.2016.00146.
2. Changchien C. H., Chen S. W., Chen Y. Y., Chu C. (2016). Antibiotic susceptibility and genomic variations in *Staphylococcus aureus* associated with Skin and Soft Tissue Infection (SSTI) disease groups. *BMC Infect Dis.* 16:276. 10.1186/s12879-016-1630-z
3. Otto M. (2014). *Staphylococcus aureus* toxins. *Curr. Opin. Microbiol.* 17, 32–37. 10.1016/j.mib.2013.11.004
4. Abdullaevna, K. K., qizi, N. M. T., Farkhodovich, A. D., Furkatovich, R. S., & ugli, B. K. S. (2024). Analysis of the Importance of Microbiota in the Human Body in the Formation of Immunity or Immune Reactions. *American Journal of Bioscience and Clinical Integrity*, 1(11), 109–115. Retrieved from <https://biojournals.us/index.php/AJBCI/article/view/317>
5. Shoymardonovna, G. D., qizi, I. A. A., qizi, I. K. O., & qizi, Q. M. Z. (2024). Analysis of Methods for Detecting Bacteria and Fungi in Various Pathologies or Growing Environments and Their Differentiation by Main Functions. *American Journal of Bioscience and Clinical Integrity*, 1(11), 123–129. Retrieved from <https://biojournals.us/index.php/AJBCI/article/view/319>
6. Lowy F. D. (1998). *Staphylococcus aureus* infections. *N. Engl. J. Med.* 339, 520–532. 10.1056/NEJM199808203390806
7. Löffler B., Hussain M., Grundmeier M., Brück M., Holzinger D., Varga G., et al. (2010). *Staphylococcus aureus* panton-valentine leukocidin is a very potent cytotoxic factor for human neutrophils. *PLoS Pathog.* 6:e1000715. 10.1371/journal.ppat.1000715
8. Shaydullaevna, M. F., qizi, I. A. A., qizi, Q. M. Z., & qizi, S. S. E. (2024). The Serious Danger of Viral Infections to Health and the Health Care System and the Urgency of Combating Them. *American Journal of Bioscience and Clinical Integrity*, 1(11), 116–122. Retrieved from <https://biojournals.us/index.php/AJBCI/article/view/318>
9. Howden, B.P., Giulieri, S.G., Wong Fok Lung, T. et al. *Staphylococcus aureus* host interactions and adaptation. *Nat Rev Microbiol* 21, 380–395 (2023). <https://doi.org/10.1038/s41579-023-00852-y>
10. Course of Diseases. *American Journal of Bioscience and Clinical Integrity*, 1(10), 133–138. Retrieved from <https://biojournals.us/index.php/AJBCI/article/view/246>
11. Aliyev, S. R., & Abdullayev U. M. (2024). Expression of Circulating Microrna-199a and Microrna-155 in Chronic Viral Hepatitis B and Chronic Viral Hepatitis C. *International Journal of Integrative and*

- Modern Medicine, 2(10), 119–123. Retrieved from <https://medicaljournals.eu/index.php/IJIMM/article/view/1047>
12. Nuruzova, Z. A., O‘rinbaeva, Z. N., & Ergashev, O. I. (2024). Study the Effect of the Combination of Flavonoids of the Crocus Sativus Plant on Opportunistic Intestinal Microorganisms Against the Background of Acute Toxic Hepatitis Caused in Mice Under Study Conditions. *International Journal of Integrative and Modern Medicine*, 2(10), 113–118. Retrieved from <https://medicaljournals.eu/index.php/IJIMM/article/view/1046>
  13. Foster T. Staphylococcus. In: Baron S, editor. *Medical Microbiology*. 4th edition. Galveston (TX): University of Texas Medical Branch at Galveston; 1996. Chapter 12. Available from: <https://www.ncbi.nlm.nih.gov/books/NBK8448/>
  14. Mamatmusaeva, F. ., Raimkulova, D. ., Gulmurotova, D. ., & Ermatov, B. . (2024). Analysis of the prevalence and risk factors of infectious diseases in pediatric practice. *Евразийский журнал медицинских и естественных наук*, 4(6), 124–129. извлечено от <https://in-academy.uz/index.php/EJMNS/article/view/34058> DOI: <https://doi.org/10.5281/zenodo.12197569>
  15. Mo‘minova Madinakhon Abdulkhaq qizi. (2024). The Incidence of Nosocomial Infections and Their Role in the Course of Chronic Diseases. *American Journal of Pediatric Medicine and Health Sciences (2993-2149)*, 2(5), 49–52. Retrieved from <https://grnjournal.us/index.php/AJPMHS/article/view/4714>
  16. Rustamzhanovna, R. N., Shotursunovna, B. R., & Baratovna, Z. Z. (2024). Nosocomial Infections, Their Complications and the Relevance of Combating Them. *American Journal of Pediatric Medicine and Health Sciences (2993-2149)*, 2(3), 336–342. Retrieved from <https://grnjournal.us/index.php/AJPMHS/article/view/3952>
  17. Linz MS, Mattappallil A, Finkel D, Parker D. Clinical Impact of Staphylococcus aureus Skin and Soft Tissue Infections. *Antibiotics*. 2023; 12(3):557. <https://doi.org/10.3390/antibiotics12030557>
  18. Krismer, B., Weidenmaier, C., Zipperer, A. & Peschel, A. The commensal lifestyle of Staphylococcus aureus and its interactions with the nasal microbiota. *Nat. Rev. Microbiol.* 15, 675–687 (2017).
  19. Spaan, A. N., van Strijp, J. A. G. & Torres, V. J. Leukocidins: staphylococcal bi-component pore-forming toxins find their receptors. *Nat. Rev. Microbiol.* 15, 435–447 (2017).
  20. V. O. Masharipov, U.M. Abdullaev, F.R. Boltaev. Diseases caused by infections caused by various viruses and the importance of their risk factors in modern medicine. *Journal of Healthcare and Life-Science Research* Vol. 3, No. 03, 2024. 62-70. <https://jhlsr.innovascience.uz/index.php/jhlsr/article/view/462>
  21. Kushnazarova, N. ., Li, L. ., Ishmurodov, M. ., Mirzaeva, R. ., & Hakimova, M. . (2024). Uzoq muddatli antibiotikoterapiyaning ichak bakteriyalari guruhiga ta’sirini tahliliy baholash. *Евразийский журнал медицинских и естественных наук*, 4(3), 272–278. извлечено от <https://in-academy.uz/index.php/EJMNS/article/view/29377> DOI: <https://doi.org/10.5281/zenodo.10902890>
  22. V. O‘. Masharipov, U. M. Abdullaev, F. R. Boltaev. The role and risk factors of infection caused by various viruses in the practice of gynecology. *European journal of modern medicine and practice* Vol. 4 No. 3 (Mar - 2024). 42-49. <https://inovatus.es/index.php/ejmmp>
  23. N. G. Gulyamov, G. Kh. Razhabov, N. N. Bakhramova, R. A. Abidova, & O. I. Ergashov. (2023). Evolution of the Development of Typhoid Vaccines in Medical Practice. *Procedia on Economic Scientific Research*, 9, 35–42. Retrieved from <https://procedia.online/index.php/economic/article/view/1280>
  24. N.N. Bakhramova, R.A. Abidova, Kh.I. Ergasheva, & R.U. Mirzaeva. (2024). The importance of vaccination in achieving a positive trend in the prevention and treatment of paratyphs in the practice of

- infectious diseases. *Journal of universal science research*, 1(12), 819–827. <https://doi.org/10.5281/zenodo.10457639>
25. N. G. Gulyamov, G. Kh. Razhabov, N. N. Bakhranova, R. A. Abidova, O. I. Ergashov. Evolution of the Development of Typhoid Vaccines in Medical Practice. *Procedia on Economic Scientific Research. Procedia on Digital Economics and Financial Research*. Volume 15. 2024. 35-42. <https://procedia.online/index.php/economic>
  26. Chen Q., Hou T., Wu X., Luo F., Xie Z., Xu J. (2016). Knockdown of TNFR1 suppresses expression of TLR2 in the cellular response to *Staphylococcus aureus* infection. *Inflammation* 39, 798–806. [10.1007/s10753-016-0308-4](https://doi.org/10.1007/s10753-016-0308-4)
  27. Nargiza Rustamzhanovna Rakhimova, Valizhon O‘rinovich Masharipov, Ra‘no Shokhtursinovna Boltaeva. Conducting a literature analysis of antibacterial properties of oxadiazole derivatives. *Procedia of Theoretical and Applied Sciences*. Volume 15 | Jan 2024. 59-66. <http://procedia.online/index.php/applied/index>
  28. Kosecka-Strojek M, Sabat AJ, Akkerboom V, Becker K, van Zanten E, et al. Development and validation of a reference data set for assigning staphylococcus species based on next-generation sequencing of the 16S-23S rRNA region. *Front Cell Infect Microbiol*. 2019;9:278. <https://doi.org/10.3389/fcimb.2019.00278>.
  29. Ayeni FA, Andersen C, Nørskov-Lauritsen N. Comparison of growth on mannitol salt agar, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, VITEK 2 with partial sequencing of 16S rRNA gene for identification of coagulase-negative staphylococci. *Microb Pathog*. 2017;105:255–9. <https://doi.org/10.1016/j.micpath.2017.02.034>.
  30. Masharipov Valizhon O‘rinovich, Boltaeva Ra‘no Shokhtursinovna, & Rakhimova Nargiza Rustamzhanovna. (2023). The importance of improving the disturbed intestinal microflora in the prognosis of nonsteroidal ulcerative colitis. *European journal of modern medicine and practice*, 3(11), 81–86. Retrieved from <https://inovatus.es/index.php/ejmmp/article/view/2077>
  31. V. U. Masharipov, N. A. Srimbetova, & F. R. Boltaev. (2023). The role of intestinal microflora in the occurrence and treatment of irritable bowel syndrome. *European journal of modern medicine and practice*, 3(11), 72–80. Retrieved from <https://inovatus.es/index.php/ejmmp/article/view/2076>
  32. Kosecka-Strojek M, Ilcyszyn WM, Buda A, Polakowska K, Murzyn K, et al. Multiple-locus variable-number tandem repeat fingerprinting as a method for rapid and cost-effective typing of animal-associated *Staphylococcus aureus* strains from lineages other than sequence type 398. *J Med Microbiol*. 2016;65(12):1494–504. <https://doi.org/10.1099/jmm.0.000378>.
  33. Fayzullaeva Zamira Raxmatovna. Homiladorlik davrida mikrofloraning o‘zgarishi va uni yaxshilashning ahamiyati. *Central asian journal of academic research*. Volume 1, Issue 2, November 2023. 5-10. <https://doi.org/10.5281/zenodo.10208505>
  34. Becker K, Harmsen D, Mellmann A, Meier C, Schumann P, Peters G, et al. Development and evaluation of a qualitycontrolled ribosomal sequence database for 16S ribosomal DNA-based identification of *Staphylococcus* species. *J Clin Microbiol*. 2004;42:4988–95. <https://doi.org/10.1128/JCM.42.11.4988-4995.2004>.
  35. Bakhranova, N. N. (2023). Determination of the Immunostimulating Activity of a Biologically Active Compound under Experimental Conditions. *Journal of Nursing Research, Patient Safety and Practise*, 3(04), 17–22. <https://doi.org/10.55529/jnrpsp.34.17.22>

36. Эргашева Х.И., Юнусходжаев П.Ю., Максудова Г.А. Қандли диабет билан оғриган беморларда оғиз бўшлиғи микрофлораси ўзгаришининг аҳамияти ва уни яхшилашнинг долзарблиғи. *Journal of universal science research*. 2023. 90-101.
37. LisowskaŁysiak K, Kosecka-Strojek M, Białocka J, Kasproicz A, Garbacz K, et al. New insight into genotypic and phenotypic relatedness of *Staphylococcus aureus* strains from human infections or animal reservoirs. *Pol J Microbiol*. 2019;68(1):93–104. <https://doi.org/10.21307/pjm-2019-011>.
38. Бахрамова Н.Н., Абидова Р.М., Эргашов О.И., Боймуродов Б.Т. и Каландарова Ф.С. (2023). Оценка антибактериальной и противогрибковой активности биологически активного вещества, приготовленного из местных растительных экстрактов. *Американский журнал инноваций в сельском хозяйстве и садоводстве*, 3(04), 29-36. <https://doi.org/10.37547/ajahi/Volume03Issue04-06>
39. Ithomovich, E. O. . ., Sobirjonovich, A. S. ., & Raxatovna, A. G. (2022). Talabalar og'iz boshlig'i gigienasida tish pastasi va cho'tkasining patogen bakteriyalarga ta'siri. *Innovative Society: Problems, Analysis and Development Prospects (Spain)*, 79–81. Retrieved from <https://www.openconference.us/index.php/ISPADP/article/view/160>
40. Catherine Liu, Arnold Bayer, Sara E. Cosgrove, Robert S. Daum, Scott K. Fridkin, Rachel J. Gorwitz, Sheldon L. Kaplan, Adolf W. Karchmer, Donald P. Levine, Barbara E. Murray, Michael J. Rybak, David A. Talan, Henry F. Chambers, *Clinical Practice Guidelines by the Infectious Diseases Society of America for the Treatment of Methicillin-Resistant Staphylococcus aureus Infections in Adults and Children*, *Clinical Infectious Diseases*, Volume 52, Issue 3, 1 February 2011, Pages e18–e55, <https://doi.org/10.1093/cid/ciq146>
41. Ozodjon Ilkhomovich Ergashov. (2023). The Importance of Plant Extract in Improving the Microflora of the Gastrointestinal Tract in the Treatment of Diseases of the Stomach and Duodenum. *Journal Healthcare Treatment Development(JHTD) ISSN : 2799-1148*, 3(05), 12–18. <https://doi.org/10.55529/jhtd.35.12.18>
42. Aqib, A. I., Ijaz, M., Farooqi, S. H., Ahmed, R., Shoaib, M., Ali, M. M., et al. (2018b). Emerging discrepancies in conventional and molecular epidemiology of methicillin resistant *Staphylococcus aureus* isolated from bovine milk. *Microb. Pathog.* 116, 38–43. doi: 10.1016/j.micpath.2018.01.005
43. Awad, M., Yosri, M., Abdel-Aziz, M. M., Younis, A. M., and Sidkey, N. M. (2021). Assessment of the antibacterial potential of biosynthesized silver nanoparticles combined with vancomycin against methicillin-resistant *Staphylococcus aureus*–induced infection in rats. *Biol. Trace Elem. Res.* 199, 4225–4236. doi: 10.1007/s12011-020-02561-6
44. Aliev Shavkat Rozimatovich. (2023). Prospects for Improving the Microflora in Diseases of the Urinary Tract Encountered in Gynecological Practice. *Journal Healthcare Treatment Development(JHTD) ISSN : 2799-1148*, 3(05), 7–11. <https://doi.org/10.55529/jhtd.35.7.11>
45. qizi, M. M. A., qizi, K. M. K., & ugli, N. U. U. (2024). Epidemiology, Risk Factors and Measures to Combat Diseases Caused by *Klebsiella* Bacteria. *American Journal of Bioscience and Clinical Integrity*, 1(11), 102–108. Retrieved from <https://biojournals.us/index.php/AJBCI/article/view/316>
46. Gudiol, F., Aguado, J. M., Almirante, B., Bouza, E., Cercenado, E., and Domínguez, M. Á, et al. (2015). Executive summary of the diagnosis and treatment of bacteremia and endocarditis due to *Staphylococcus aureus*. A clinical guideline from the Spanish society of clinical microbiology and infectious diseases (SEIMC). *Enferm. Infecc. Microbiol. Clin.* 33, 626–632.