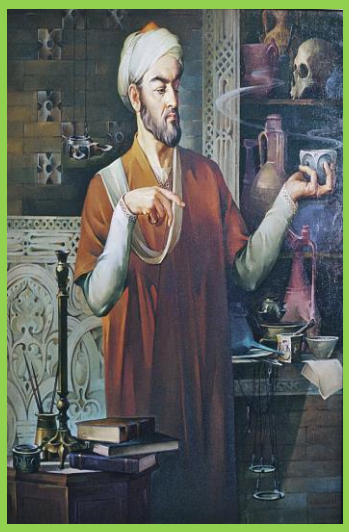
MEDICAL-SOCIAL INSTITUTE OF TAJIKISTAN

CENTER FOR BOTANICALS AND CHRONIC DISEASES

INTERNATIONAL SYMPOSIUM METABOLOMICS OF PLANTS, HUMANS, AND MICROORGANISMS



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METABOLOMIC PROFILING AND BIOACTIVITY OF APHID-INDUCED GALLS IN TAJIKISTANI PISTACIA VERA L. (PISTACHIO)

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Purposeofthestudy. Study of phytochemical properties of two species of *Pistaciavera* L. (pistachio) galls in Tajikistan caused by aphids.

Materials and methods. In 2024, two expeditions, one each in the spring and the summer months, were undertaken within the Danghara District, Tajikistan to collect *Pistaciavera* leaf, gall, resin, and fruit samples from wild populations of trees, especially to focus on comparing immature and mature gall stages of one type of abaxialmidvein gall (*Geoicautricularia)*, one type of leaf margin gall (*Forda formicaria*), and the unaltered leaf tissues themselves. Galls are induced by woolly aphids in the tribe Fordini that alternate between*Pistacia spp.* and the roots of grasses. A sample of a commercially available woolly aphid gall, a horn gall harvested from *Pistaciaintegerrima* (*Baizongiapistaciae*, India's Creation brand), was included for comparison in some analyses. Fresh plant materials from Tajikistan were dried in a forced air oven and placed in long-term storage in a freezer (-20 °C) before further preparation. Extracts for materials analyzed were from 7:3 ethanol/water macerations (200 mg in 5 mL).

Results and discussion. *Pistaciavera* gall materials and other comparative tissues from Tajikistan, as well as a commercially available *Pistaciaintegerrima* gall, are differentiated from each other particularly based ontheir polyphenol and terpenoid contents. Gallotannin, flavonoid, and other polyphenolic components of *Pistacia spp*. extracts (except for resins, which comparatively lack polyphenols) are shown to bear significant antioxidant activity in HPTLC profiles. Volatile terpenoids and polyphenols are also demonstrated to have differing profiles in leaf and gall materials. Analyses of LC-MS-MS, GC-MS, and HPTLC data show that triterpenoids are enriched in the galls, particularly in *Geoica utricularia* galls and in *Baizongiapistaciae* galls, with triterpenoids predominating especially in gall-derived resinsamples (from *Geoica utricularia*), and the data is also suggestive of potential differences between spring and summer collections. Further interrogation of the data is required to fully

show the extent of these patterns, but LC-MS-MS data and global analyses of annotated metabolites with principal component analysis (PCA)show that the parent leaf tissue, leaf margin gall, and fruit tissues are more similar to each other than to the abaxial midvein gall and the commercially available horn gall, which are all in turn all distinct from the resin samples. Preliminary MALDI imaging studies of immature *Geoicautricularia* gall tissues are showing gallic acid and gallo tannins being ionized and may suggest greater abundance of these compounds closer to the gall lumen as well as noticeable differences even between two sides of a 30 μm slice. More method development is required for dried tissue sections, however. Lastly, one resin extract (sample code 23) exhibited anti-lipolytic activity in 3T3-L1 cells at a nontoxic dose. Follow-up research would be required to better characterize this effect and demonstrate any anti-inflammatory activity *Pistacia vera* resins may bear.

Conclusions. A study of the phytochemical and biological activity of two species of *Pistaciavera* L. (pistachio) galls in Tajikistan caused by aphids showed differences in abundance of polyphenols, including hydrolysable tannins and flavonoids, as well as terpenoids between gall tissue types and the parent leaf tissue as well as the gall-derived resinsample. Preliminary MALDI imaging studies of immature *Geoicau tricularia* gall tissues confirm the presence of gallic acid and gallotannins, especially concentrated closer to the lumen side. Resins exhibited anti-lipolytic activity in 3T3-L1 mouse adipocytes, with research in additional cell types like macrophages needed to more fully demonstrate anti-inflammatory activity for *Pistacia vera* resins.

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MICROSCOPIC STUDY OF ENDEMIC FERULA SPECIES

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Purposeofthestudy. To study the root structure of three endemic *Ferula* species: *F. violacea, F. kuhistanica,* and *F. gigantea.*

Materials and methods. Microscopic examination of the roots of the *Ferula* species included in the study was conducted using generally accepted microstructural analysis techniques.

Results and discussion. In the first stage of the study, a microscopic examination of the roots of the *Ferula* species included in the study was conducted. Cross-sectional analysis revealed that the cork extends around the entire circumference of the root and consists of 9-16 rows of thick-walled cells. The cork is dark brown. Microscopic examination of the surface reveals that the root cork cells are tightly packed and have a polygonal (4-5 angles) and slightly smoothed shape. Phloem, xylem vessels, and parenchyma cells are clearly visible in the cross-section. The cavities of the parenchyma cells are filled with starch. The main part of the cortical parenchyma consists of loosely arranged cells and consists of numerous cavities and ruptures. The pericyclic zone of the central cylinder is represented by ground tissue filled with numerous plasma crystals.

In the second stage of the study, a microscopic examination of the roots of a regional endemic species of *Ferula, F. kuhistanica*, was conducted. It was found that, like the roots of *Ferula violacea,* it has a rounded shape. Microscopic examination of a cross-section of the root of this species reveals three zones: the cork, the primary cortex, and the central cylinder. The cork is brownish in color and covers the root externally. It consists of 7-8 layers of equal size that are tightly adhered to each other. The cells of the primary parenchyma are large, with slightly thickened sheaths and a round or oval shape. Most of the cells are partially or completely filled with starch grains. In cross-section, small starch grains are visible, with a simple structure and round or oval shape. The cells of the medullary rays are characterized by the presence of large amounts of starch. In the parenchyma, cells containing yellow pigments are noticeable. As might be expected, xylem vessels, phloem, and parenchyma cells are visible in the section, all of which are round and elongated. The third stage of the anatomical and morphological study of the roots of the *Ferula s*pecies included in the study was a microscopic examination of the F. gigantea root. The rhizome has a rounded structure. The cortex occupies the majority of the root. Microscopic analysis of a root section of this *Ferula* species reveals two types of vessels: densely spiral and scalloped. The phloem portion is narrower, and the phloem rays extend to the cortex parenchyma. The xylem is well developed. Numerous xylem vessels extend to the center of the root. Vessels located closer to the center are larger than those located at the periphery. The xylem consists of single and clustered vessels. Cortex parenchyma cells, like other cells, contain reserve nutrients (starch), a schizogenous receptacle, parenchymatous cells, and xylem vessels.

Conclusions. In *F. violacea,* prismatic crystals are found in the cells of the main root parenchyma, which are not observed during anatomical examination of the roots of *F. kuchistanica*and *F. gigantea.* The parenchyma cells of the root of *F. violacea,* unlike F. *kuchistanica*and *F. gigantea,* are filled with starch grains and have more developed vessels.

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ANTIBACTERIAL PROPERTIES OF ALCOHOL EXTRACTS OF PLANTS OF THE GENUS SWIDADARVASICA (POJARK.) SOJAK.

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Purposeofthestudy. To study the antibacterial properties of various organs of the endemic plant of the genus *Swida darvasica* (Pojark.) Sojak.

Materials and methods. The antibacterial activity of the obtained extracts was studied against four standard museum strains of microorganisms: *S. aureus, E. coli, Ps. aeruginosa, and Kl. pneumoniae.* The plant's antimicrobial properties were assessed using the solid agar disc diffusion method, according to standard EUCAST-2024 protocols. Alcohol extracts were obtained using the GIBEX method at Rutgers University. Statistical analysis of the results was performed using the Statistica 10.0 software package (Statsoft, USA).

Results and discussion. Various organs (parts) of the endemic plant *Swida darvasica* (Pojark.) Sojak., growing at altitudes over 3000 m above sea level, were studied. It was found that the branches and leaves of the studied plant exhibited varying degrees of antibacterial activity against the standard museum strain of *Staphylococcus aureus,* while the berries themselves did not. It is worth noting that all other strains used in the study demonstrated bacterial resistance to extracts of this plant. Thus, an ethanol extract from the leaves inhibited pathogen growth by 18 mm, while the bark of the plant exhibited a weaker inhibitory effect, delaying pathogen growth by only 12 mm.

Conclusions. Various organs of the *Swida darvasica* (Pojark.) Sojak. plant exhibited varying degrees of antistaphylococcal activity, demonstrating no antimicrobial effect against the other bacterial strains used in the study.

S.Kh. Nazarmamadova

PHENOLOGICAL CHARACTERISTICS OF *ROSA DAMASCENA* MILL. IN THE CONDITIONS OF THE GISSAR VALLEY AND THEIR IMPORTANCE FOR ADAPTATION AND COMMERCIAL CULTIVATION

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Purpose of the study. To evaluate the phenological rhythms of *Rosadamascena* Mill. in the Gissar Valley, identify the features of their morphogenesis, and determine the potential for using the variety in industrial cultivation and landscape design.

Materials and Methods:

• Study Object: *Rosadamascena* Mill., cultivated in the Shakhrinav District.

• Observation Period: 2020–2025.

• **Methods:** Phenological observations according to I.N. Beideman (1979) and the methodological guidelines for botanical gardens (1975).

• Observation Frequency: Every 2–3 days, daily during the active growth period.

• Statistical Analysis: According to Zaitsev (1973, 1991), Borovikov (2001).

Research and discussion.

1. Key Phenorrhythmic Phases

- Bud swelling begins when the temperature steadily rises above +5°C.
- Bud break occurs within 10–15 days, with foliage appearing in early April.
- Flowering occurs in late April and lasts 25–45 days.
- If not picked, fruits form in 70–85 days.

2. Seasonal Rhythmic Patterns

- Rosadamascena Mill. lacks a pronounced natural winter dormancy period: buds enter winter at stages I–II of organogenesis.
- Winter damage to the aboveground parts is compensated for by the activation of dormant buds in the underground renewal zone.

3. Growth Processes

- Maximum shoot growth is recorded in the first year (106 cm), then declines: 30 cm in the second year, 11 cm in the third, 6 cm in the fourth.
- The main growth is provided by lateral shoots. Activated after weakening apical dominance.

- With age, an increase in branching order and the formation of a dense crown are observed.
- 4. Organogenesis and generative development
- Formation of floral organs begins in February–March (stage III), with active growth and budding occurring in March–April.
- The duration of stage VIII (budding) varies from 6 to 28 days, depending on temperature.
- The synchronicity of the development of phenological phases confirms the key role of temperature.

Conclusions.

• *Rosa damascene*Mill. demonstrates a high degree of adaptation to the conditions of the Hissar Valley.

• Temperature is a determining factor in growth and flowering rhythms.

• The specific phenological rhythms allow for the optimization of agronomic measures: pruning timing, watering regimens, and fertilization.

• The obtained data confirm the potential of the variety for industrial cultivation and use in ornamental horticulture.

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EFFECT OF ORGANS AND SAMPLE PROCESSING METHODS ON *F. VIOLACEA* METABOLITE COMPOSITION

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Purpose of the study. To evaluate the impact of plant organ type and sample processing method on the metabolite composition of *Ferula violacea* Korovin.

Materials and methods. Roots and seeds were collected in Maykhura, Tajikistan, and subjected to hydroethanolic extraction or juicing. Metabolite profiling was conducted using UHPLC–QTOF mass spectrometry, followed by untargeted data analysis in Bruker MetaboScape with in silico fragmentation (SIRIUS) and spectral matching against MoNA,

BrukerMetaboBASE, COCONUT, and HMDB libraries. Metabolites were structurally annotated using NPClassifier and ClassyFire. Principal component analysis (PCA) and PERMANOVA were employed to assess chemical profile differences between organs and processing methods, and to identify organ-specific and differentially enriched metabolites.

Results and discussion. A total of 532 metabolites were identified in root samples, with 21 being exclusive to roots, while 519 were detected in seed samples, of which only 8 were unique to seeds (Figure 4B). Sample processing method also significantly influenced metabolite composition (PERMANOVA, variable: processing method, R2: 35 %, p-value: 0.009).In addition, metabolite differences between organs were dependent on the sample processing method as shown by PCA and confirmed by PERMANOVA (variable: organ+processing method, R2: 30 %, p-value: 0.013). Metabolite comparison between sample processing methods revealed 512 total metabolites in ethanol extracts, with 2 metabolites exclusively found in extracts. In juice samples, 538 total metabolites were identified, with 28 unique to juices, demonstrating juice samples were able to capture nearly all the metabolite diversity in F. violacea. These metabolic distinctions underscore the impact of sample processing methods on metabolite composition and the specialized biosynthetic capacities of each organ, likely reflecting their distinct physiological and ecological functions.

Conclusions. Sample processing methods markedly influenced the metabolite profiles of *F. violacea*, resulting in method-specific compound enrichment, particularly within the shikimate and terpenoid pathways. The traditional hydroethanolic extraction yielded a higher number of metabolites related to shikimates, phenylpropanoids, and terpenoids, whereas the juicing method revealed distinct compounds within these pathways.

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METABOLIC DIFFERENCES BETWEEN *F. VIOLACEA* ROOTS AND SEEDS

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Purpose of the study. Study of the metabolic characteristics between the roots and seeds of *F. violacea.*

Materials and methods. Roots and seeds were collected in Maykhura, Tajikistan, and subjected to hydroethanolic extraction or juicing. Metabolite profiling was performed using UHPLC-QTOF mass spectrometry, followed by untargeted data analysis with BrukerMetaboScape with *in-silico* fragmentation (SIRIUS), and spectral matching against MoNA, BrukerMetaboBASE, COCONUT, and HMDB spectral libraries. Metabolites were structurally annotated using NPClassifier and ClassyFire. Principal component analysis (PCA) and PERMANOVA were used to assess chemical profile differences between organs and processing methods. Metabolites specific to and differentially enriched between organs and processing methods were identified.

Results and discussion. The classification of organ-specific metabolites indicates that metabolites unique to roots and seeds are primarily associated with the shikimate and phenylpropanoid, terpenoid, and alkaloid biosynthetic pathways. The majority of these compounds were detected at relatively low abundance, with intensities below 1 million. Notably, root-specific metabolites included a distinct group of flavonoids and phenolic acids from the shikimate and phenylpropanoid pathway, which were exclusively detected in root juice samples. This finding suggests organ-specific metabolic adaptation, potentially associated with root defense mechanisms or specialized biosynthetic functions.

Differential abundance analysis identified a total of 60 root-enriched and 83 seed-enriched metabolites (log2-fold change > 1, FDR < 0.05). Most metabolites with significant differences in abundance between organs (FDR < 0.05) exhibited log2-fold changes below 5, though a few metabolites displayed log2-fold changes above 8 (Figure 6), which included the seed-enriched terpenoid farnesyl-4-hydroxybenzoesaure (CID: 54248366). Other seed-enriched metabolites with intensities exceeding 1 million were predominantly alkaloids and amino acids. This suggests that seeds prioritize alkaloid biosynthesis, likely for chemical defense or germination-associated metabolic functions. In contrast, root-enriched metabolites with intensities exceeding 1 million were primarily terpenoids.

Conclusions. Differential analyses of roots and seeds revealed organ-specific metabolite enrichment, showcasing distinct biosynthetic specializations. Seeds were enriched in amino acids and alkaloids, while roots displayed a higher abundance of terpenoids, suggesting tissue-specific metabolic pathways.

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FERULA VIOLACEA METABOLOMICS: ORGAN-AND EXTRACTION-DEPENDENT PHYTOCHEMICAL PROFILES REVEALED BY UNTARGETED UHPLC-QTOF ANALYSIS

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Purpose of the study.*Ferula violacea*Korovin, an endemic Tajik species with longstanding medicinal use, remains chemically underexplored. This study aimed to apply a rigorous untargeted metabolomics framework to delineate how plant organ (roots versus seeds) and processing method (hydroethanolic extraction versus juicing) shape phytochemical composition.

Materials and methods. Roots and seeds were collected in Maykhura, Tajikistan, and subjected to hydroethanolic extraction or juicing. Metabolite profiling was performed using UHPLC-QTOF mass spectrometry, followed by untargeted data analysis with BrukerMetaboScape with *in-silico* fragmentation (SIRIUS), and spectral matching against MoNA, BrukerMetaboBASE, COCONUT, and HMDB spectral libraries. Metabolites were structurally annotated using NPClassifier and ClassyFire. Principal component analysis (PCA) and PERMANOVA were used to assess chemical profile differences between organs and processing methods. Metabolites specific to and differentially enriched between organs and processing methods were identified.

Results and discussion. The analysis revealed 540 metabolites, of which 419 were newly reported for the genus *Ferula*. Terpenoids represented the dominant pathway, followed by phenylpropanoids and amino acid derivatives. Roots were enriched in terpenoids and unique phenylpropanoids, whereas seeds exhibited higher levels of alkaloids and amino acids. Processing strongly influenced chemical recovery: juices captured nearly the complete metabolome, including unique phenylpropanoids and terpenoids, while hydroethanolic extracts yielded greater enrichment in terpenoids. PCA and PERMANOVA confirmed significant clustering by organ and processing method, underscoring the analytical resolution of this approach.

Conclusions. This study delivers the first systematic metabolomic survey of *F. violacea*, expanding the known *Ferula* chemical space by 419 metabolites. It demonstrates that both organ identity and extraction method critically modulate phytochemical profiles. These results highlight the importance of analytical strategy in natural products research and suggest that optimized sampling and processing protocols are essential for accurate bioactive discovery.

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HERBAL PRODUCTS USED IN PURULENT-INFLAMMATORY DISEASES

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Purpose of the study. To evaluate the antimicrobial activity of herbal remedies in purulent-inflammatory diseases.

Materials and methods. To evaluate the antimicrobial activity of herbal remedies, the following were used:

- Determination of microbial counts and sanitary indicator microorganisms: inoculation of aqueous extracts on nutrient media (MPA, Sabouraud agar, MacConkey agar), counting total bacterial counts, yeasts, and molds, identification of *E. coli, S. aureus, P. aeruginosa* and *Salmonella spp.* - Evaluation of antibacterial activity: Kirby-Bauer disk diffusion method, determination of MIC and MBC by serial dilution.

- Study of the effect on biofilm: modeling of pathogen biofilms (*S. aureus, P. aeruginosa*) in 96-well plates followed by treatment with plant extracts. Antifungal activity: determination of MIC against *Candida albicans* and mold fungi by microdilution.

Results and discussion. In the raw material samples studied, the total microbial count did not exceed pharmacopoeial standards, and pathogenic microorganisms (*E. coli, Salmonella spp.*) were not detected.

Extracts of wormwood, calendula, sage, and thyme demonstrated pronounced antibacterial activity against *S. aureus* and *E. coli* (inhibition zones of 12–18 mm). The MIC of aqueous extracts was 0.5–2.0 mg/ml; ethanol extracts were more effective (0.25–1.0 mg/ml).

Efficacy against *P. aeruginosa* was lower due to the pathogen's inherent resistance.

Essential oils of thyme and sage demonstrated high activity against *Candida albicans* (MIC = 0.125–0.5 mg/ml).

Alcohol extracts of calendula and sage caused partial destruction of bacterial biofilms.

Conclusions. Microbiological studies confirm the potential of medicinal plants for the treatment of purulent-inflammatory diseases. Extracts of wormwood, calendula, sage, and thyme demonstrated the greatest activity, effective against gram-positive bacteria and yeasts.

Herbal remedies have potential as an alternative to synthetic antibiotics due to their low toxicity and lack of resistance. Further research should be aimed at isolating active components, studying their mechanisms of action and creating effective herbal preparations**.**

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EXPRESSION OF CIRCULATING MICRORNA-199A AND MICRORNA-155 IN CHRONIC VIRAL HEPATITIS B AND CHRONIC VIRAL HEPATITIS C

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Purpose of the study. To study the expression level of microRNA-199a and microRNA-155 in CHB and CHCV.

Materials and methods. The material for the study was blood plasma samples from 76 patients with chronic viral hepatitis: chronic viral hepatitis B (CVHB) - 36, chronic viral hepatitis C (CVHC) - 40, the control group consisted of 30 healthy individuals who had no markers of infection HBV and HCV infections.

Research methods. Total RNA was isolated from blood plasma using the MiRNeasy Serum/Plasma Kit according to the manufacturer's instructions. To normalize the reaction and as an internal control, the “MiRNeasy Serum/Plasma Spike-In Control” kit containing C.elegans miR-39 miRNA mimic was used. Reverse transcription PCR (RT-PCR) was carried out using the MiScript II RT Kit. RT-PCR reaction conditions: 37°C-60 min; 95°C-5 min. Real-time PCR was carried out using the MiScript SYBR® Green PCR Kit. To detect internal control, a universal reverse primer, forward primer Ce_miR-39_1 miScript® Primer Assay and specific reverse primers (microRNA-199a and microRNA-155) were used. PCR conditions: 95°C - 15 min; 94°C-15 sec; 55°C-30 sec; 70°C-30 sec – 40 cycles. Interpretation of the results of quantitative assessment of microRNA expression was carried out using the following indicators: ΔCt indicator - the difference between the Ct values of the microRNA under study and the internal control; ΔΔCt indicator is the difference between the ΔCt values of the test sample and the control sample. The 2^-ΔΔCt method proposed by K.J.Livak was used to analyze relative

expression. Statistical processing of the obtained results was carried out using the Mann-Whitney U test.

Results and discussion. As a rule, during pathology, the level of a particular microRNA changes depending on its function in regulating the pathological processes of the affected organ. Many authors point out the non-random nature of the identified associations of various microRNAs with the development of pathological processes. The function of microRNA-199-a suggests, according to the literature, a protective function in the process of cell proliferation and the life of hepatocytes. According to some studies, liver damage by the hepatitis B virus is accompanied by an increase in the level of microRNA-199-a, which may not only reflect pronounced disturbances in immune regulation in the liver tissue during viral damage, but also indicates the decisive role of 199-a as a regulator of viral replication.

Similar studies were carried out by Chang C.C. et al. for HCV. In patients with HCV, the expression levels of miR-199a, miR-16, miR-193b, miR-222 and miR-324 were significantly higher compared to the healthy group. According to the authors, the expression levels of the above microRNAs may play a role as significant biomarkers of the risk of developing HCV infection. Based on the results of the studies, the authors came to the conclusion that miR-122 can be used in laboratory monitoring of the management of patients with hepatitis C as an indicator of the severity of liver damage in acute hepatitis C and the rate of formation of liver fibrosis in chronic hepatitis C. Other authors have shown that microRNA-199a is a potential biomarker that reflects the therapeutic effectiveness of treatment.

Conclusions:

1. Expression of microRNA-199a content is significantly higher in CHBV compared to CHCV.
2. The quantitative change in miR-155 in CHCV was significantly higher compared to CHB.
3. Further study of the expression of miR-199a and miR-155 as promising non-invasive markers will determine the potential of these miRNAs as early predictors of the development of liver fibrosis, liver cirrhosis and HCC.

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LOCAL IMMUNITY AND SPECIFIC SENSITIZATION TO BACTERIAL ANTIGENS IN CHILDREN WITH TONSILLITIS

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Purpose of the study. To study local immunity and specific sensitization to bacterial antigens in children with tonsillitis.

Materials and Methods. The study was conducted in 2024 at the ENT Clinic of the Tashkent State Medical University. The study included 178 patients aged 3 to 12 years (mean age 3.1 ± 0.5 years) diagnosed with moderate chronic tonsillitis. The gender distribution of the patients was 48.9% male and 51.1% female. The biological material for analysis consisted of tonsil swabs collected in sterile containers within the first 24 hours of hospitalization and stored at 37°C. Bacteriological testing and ELISA were used for diagnosis.

Results and discussion. In our studies, lysozyme and secretory immunoglobulin A levels in saliva in children of various ages with community-acquired pneumonia were almost three times lower than those in healthy peers. Thus, lysozyme, by actively participating in the formation of the microbiocenosis of various biotopes in the host body, is one of the most important factors in local protection of the mucous membranes. The effect of exogenous lysozyme depends not only on its dose but also on the functional state of the body, its cellular and humoral systems, and the maintenance of homeostasis. Lysozyme helps reduce the antigen load on the body of frequently ill children, as it... Prevents the penetration of foreign agents into the body's internal environment by stimulating phagocytosis and enhancing the cooperative functions of T-lymphocyte populations, as well as the bacteriological and anti-adhesive properties of immunoglobulins. Lysozyme accelerates reparative processes and increases the susceptibility of microbes to antibiotics.

Conclusions. When assessing the state of local humoral immunity in the oral cavity in patients with chronic tonsillitis (CT) and apparently healthy individuals (PHI), differences were identified. Patients with CT have a local immunoglobulin imbalance due to reduced levels of complement-activating antibodies (IgM and IgG), which play a key protective role against bacterial infections. It is known that in patients with CT and bacterial sensitization, the phagocytic response is suppressed and incomplete compared to patients without bacterial or fungal sensitization. Lysozyme's stimulation of nonspecific resistance and immunity in children is most pronounced when they are suppressed: in frequently and long-term ill children, in

weakened individuals, and in children at risk. Therefore, the use of Lysobact® is advisable in this category. We studied bacterial and fungal sensitization as an indicator of impaired anti-infective defense, when evolutionarily ingrained mechanisms for antigen (infective) elimination fail and the body limits inflammation through DTH. During an exacerbation of chemotherapy, sensitization to the Staphylococcus aureus antigen was detected in one-third of those examined, and to Streptococcus sp. and Candida sp. in one-twentieth of those examined. During remission, sensitization was detected in 1/6, 1/6, 1/15, and 1/6 of those examined, respectively.

V.U. Masharipov

NEW APPROACHES TO ASSESSING IMMUNE STATUS IN CHRONIC INFECTIOUS AND INFLAMMATORY PROCESSES OF THE RESPIRATORY TRACT

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Purpose of the study. To identify new approaches to assessing immune status in chronic infectious and inflammatory processes of the respiratory tract**.**

Materials and Methods. We examined 38 patients with upper respiratory tract diseases using the Ritchii concentration method. IL-4 and IFN-gamma levels using a sandwich enzyme-linked immunosorbent assay we also determined. The control group (healthy individuals) consisted of 25 individuals. The use of immunotherapy leads to a temporary restoration of reduced parameters and a slight prolongation of remission. All this necessitates the search for new approaches to assessing immune status that could help physicians improve the quality of treatment for patients with immune disorders.

Results and discussion. We found that during exacerbations of chronic bacterial infections (bronchitis), more than half of the examined individuals lack a specific cellular response to the antigens of the etiotropic agent. Approximately two-thirds of patients lack a general specific humoral and cellular response to opportunistic pathogens of the normal microflora of the body, and the neutrophil response in the opsonophagocytic reaction with the sera of the examined individuals is reduced. Similar changes were also detected during exacerbations of chronic, long-term infections.

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METHODS FOR DETECTING PSEUDOMONAS AERUGINOSA IN BURN PATIENTS

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Purpose of the study. To study the properties and antibiotic susceptibility of *Pseudomonas aeruginosa* in secondary purulent infections.

Study Materials and Methods: We examined 120 patients diagnosed with secondary purulent infection in the burn unit between 2023 and 2024. Clinical signs during examination included the appearance of bluish-green purulent discharge with a characteristic odor. In some cases, fever and the risk of sepsis were observed.Smears from the burn surface, exudate, and blood samples were collected in cases of suspected sepsis, with strict adherence to aseptic technique.

Bacteriological diagnosis was performed using selective media (Cetrimideagar, MacConkeyagar). Colonies growing on the nutrient medium were blue-green in color and had a characteristic "grape" odor.

Microscopy revealed gram-negative rods, singly or in pairs, and motile.

Biochemical tests revealed positive oxidase and catalase reactions, growth at 42°C, and oxidative metabolism.

Modern methods include MALDI-TOF MS for rapid identification, PCR (oprL, exoA), 16S rRNA sequencing, and qPCR for assessing microbial load.

Antibiotic susceptibility testing was performed using the Kirby-Bauer disk diffusion method, with mandatory detection of multidrug-resistant strains.

Monitoring included repeat wound cultures, monitoring for nosocomial infections, and molecular typing (PFGE, WGS) for epidemiological surveillance. Results and discussion. Timely detection and identification of *P. aeruginosa* in burn patients is critical for selecting appropriate antibacterial therapy and reducing mortality. The level of virulent *P. aeruginosa* in the current study is alarming, particularly among burn patients, as they lack protective measures to resist this pathogen. Furthermore, older age groups were more susceptible, increasing the risk, as older patients have weak immune systems, and most of them have other medical conditions, such as diabetes, which increase the complications associated with burn infections.

Conclusions. According to numerous studies, detection of this pathogen in burn patients delays or prevents recovery and increases the likelihood of death in those infected. Furthermore,

virulent bacterial strains are exceptionally adaptive and resilient to adverse environmental factors.

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THE ROLE OF REGULAR GREEN TEA CONSUMPTION IN THE PREVENTION OF METABOLIC SYNDROME COMPONENTS IN STUDENTS

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Purpose of the study. To study the impact of regular green tea consumption on key metabolic syndrome-related indicators—body weight, body mass index, waist circumference, blood pressure, and lipid metabolism—in medical students of Uzbekistan, in order to determine its potential role in the prevention of early metabolic disorders.

Materials and Methods: Forty-five students (mean age ≈21 years; men n=26, women n=19) participated in our study. Participants were randomized into three groups:

- Control Group - 500 ml of water/day, 0 mg of catechins
- Study Group 1 - 500 ml of green tea/day, ≈200 mg of catechins
- Study Group 2 - 500 ml of green tea/day, ≈400 mg of catechins

The intervention lasted 4 weeks. Participants underwent comprehensive measurements at the beginning and end of the study. We recorded the following parameters:

- Anthropometry
- Percentage of body fat
- Exhaled CO2 and respiratory exchange ratio
- Pulse wave velocity (PWV)

Results and discussion. No statistically significant changes in body weight or body mass index (BMI) were observed in either group, indicating that short-term green tea consumption does not significantly affect anthropometric parameters. However, body composition analysis revealed a significant reduction in relative body fat percentage exclusively in the group receiving 400 mg of catechins per day (Intervention II). Furthermore, as the catechin dose increased, there was a significant trend toward a decrease in body fat percentage, suggesting a dose-dependent effect.

Changes in respiratory and metabolic parameters were also characteristic of the group receiving the higher catechin dose: a significant decrease in carbon dioxide production and a change in the respiratory exchange ratio (RER) were observed. These data indicate a shift in energy metabolism toward lipid oxidation over carbohydrate oxidation. Regarding pulse wave

velocity (PWV), no statistically significant changes were observed during the 4-week intervention period. This suggests that such short-term regular green tea consumption does not significantly affect arterial stiffness parameters in young, healthy individuals.

Conclusions. Thus, green tea, especially when consumed in higher doses of catechins,may be considered a potential preventative factor against early metabolic disorders. Given the increasing incidence of obesity and metabolic syndrome in young adults, further larger, longer-term studies in student populations are highly relevant.

S.T. Jumamurodov, Z.A.Nuruzova

GENOTYPE OF BACTERIAL MICROFLORA IN NASOPHARYNGEAL SWABS OF COVID-19 PATIENTS

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Purpose of the study. To identify the genotype of bacterial microflora associated with COVID-19 and investigate their pathogenic impact to understand their role in the infectious process.

Materials and methods. The study analyzed nasopharyngeal swabs collected in 2021 from COVID-19-positive patients admitted to the Specialized Republican Zangiota Infectious Diseases Hospital № 2. Modern molecular-genetic and laboratory methods were employed for the analysis of the nasopharyngeal swabs.

Results and discussion. This study was conducted at the Virology Laboratory of the Tashkent City Center for Sanitary-Epidemiological Welfare (SEW) and the Biotechnological Research Center at the Tashkent Medical Academy (TMA). For identifying the bacterial microflora genotype in SARS-CoV-2 positive samples, 16S rRNA genes were utilized.16S rRNA is a ribosomal RNA molecule essential for bacterial genetic identification and phylogenetic studies. It plays a pivotal role in determining bacterial types and classification, as its sequence varies significantly across different bacterial species. Electrophoresis was conducted on samples from 36 COVID-19-positive patients, and bacterial fragments were detected in 75% (n=27) of the cases. These fragments indicate the presence of bacterial infections among the patients, which may co-occur with viral infections like COVID-19. The findings emphasize the need for further analyses and investigations.

Conclusion.These indicators are of great importance for determining treatment strategies and identifying potential bacterial infections. The results must be carefully analyzed to monitor infections and take timely action.

Z.N. Orynbaeva, Z.A. Nuruzova

NASALSPECIFIC MICROBIOTA IN ALLERGIC RHINITIS IN THE POPULATION OF THE ARAL SEA REGION

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Purpose of the study.To study the composition of the nasal mucosa microbiota in children with allergic rhinitis (AR) living in the ecologically disadvantaged Aral Sea region.

Materials and methods. The study included 82 patients aged 7–17 years (mean age 12.7 ± 3.65 years) who visited the Republican Multidisciplinary Medical Center of Karakalpakstan named after U. Khalmuratov and Muynak District Medical Institution. Samples for bacteriological examination were collected using sterile swabs; cultures were performed on standard nutrient media (mannitol-saline, Endo, Sabouraud, blood, and neutral agar).

Results and discussion. In year-round AR (allergic rhinitis), the leading microorganism was *Staphylococcus aureus* (65.0%), followed by *S. epidermidis, S. haemolyticus, Corynebacterium spp., Streptococcus viridans,* and *Enterococcus spp.*

In seasonal AR, coagulase-negative staphylococci were detected more frequently *(S. haemolyticus* - 41.2%, *S. epidermidis* - 29.4%), while *S. aureus* was recorded less frequently (17.6%). In patients with allergic rhinitis combined with atopic bronchial asthma, *S. aureus* was detected in 39.4% of cases; in the seasonal AR + BA subgroup, *S. haemolyticus* was predominant (62.5%).

In patients with allergic rhinitis combined with atopic dermatitis, the carriage rate of S. aureus was highest (66.7%).

Conclusions. Children with allergic rhinitis living in the Aral Sea region exhibit significant changes in the nasal mucosal microbiome, with a predominance of opportunistic microorganisms, particularly *Staphylococcus aureus.* Its carriage is associated with a more severe course of rhinitis, a risk of chronicity, and the development of sinusitis. These data highlight the importance of considering the microbiota in the diagnosis and treatment of allergic respiratory diseases in ecologically disadvantaged regions.

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PROBLEMS IN DIAGNOSIS OF PATHOGENIC INTESTINAL BACTERIA

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Purpose of the study. Determination of etiological agents in patients admitted to the infectious diseases hospital with a diagnosis of acute intestinal infection using the polymerase chain reaction (PCR) method.

Materials and methods. At the Center for Biomedical Technologies of the Tashkent Medical Academy, 96 patients' feces were examined using RT-PCR in 2024.

Results and discussion. The RT-PCR method is based on molecular diagnostics and allows for the identification of the genetic material of microorganisms or pathogens. To isolate NK from the collected biomaterial, the "SilicSorbNA" set, produced by the domestic company ROSSA, which holds international certification, was used. According to the obtained results, positive results were found in 94.79% of the total number of examined individuals (n=96). As a result of molecular genetic research, bacterial and viral pathogens were identified. Among the bacteria, nail infections predominated, accounting for 95.3%. The number of monoinfections was significantly lower - 5.4%. Claw and monoinfections with viral content were relatively close to each other. That is, monoinfections accounted for 46.2%, and mixed infections - 54.1%.

Conclusions. As a result of the high accuracy and sensitivity of the RT-PCR method, the probability of false results (false positive or false negative) is reduced. This allows for making the diagnosis reliable and proven, thereby ensuring the proper treatment of patients. The use of the RT-PCR method allows for quick and efficient obtaining of test results, which saves time for monitoring the patient's condition and initiating the necessary treatment. The high percentage of positive results identified during the study indicates the need for wider implementation of molecular genetic methods in practice.

S.B. Ashurova

SECONDARY RESPIRATORY DISEASES IN HIV-INFECTED PATIENTS: CLINICAL AND LABORATORY FEATURES AND PROGNOSTIC FACTORS

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Purpose of the study. To study the structure of secondary respiratory diseases in HIV-infected patients, their clinical and laboratory characteristics, and to identify factors influencing their severity.

Materials and Methods.A retrospective analysis of the medical records of 440 patients with HIV infection hospitalized at the Republican AIDS Center in 2024–2025 was conducted. Inclusion criteria were: confirmed HIV diagnosis and the presence of a respiratory disease, ages 20–70 years. Clinical data, laboratory parameters (complete blood count and biochemistry), immunological parameters (CD4+), virological and molecular genetic tests (PCR) were analyzed. Descriptive statistics, χ^2, and multivariate logistic regression were used for statistical analysis.

Results and discussion. The average age of the subjects was approximately 42 years, with a predominance of men. Approximately 75% of patients were in stage 4 HIV infection, while ART coverage remained low. At the first stage, the etiologic structure of respiratory infections was determined: bacterial pneumonias (approximately three-quarters of cases) and encephalitis of unspecified etiology were prevalent. Among opportunistic infections, CMV infection, Pneumocystis pneumonia, candidiasis, cerebral toxoplasmosis, and their combinations were frequently identified. A significant proportion of patients had two or more secondary diseases simultaneously (115 different combinations). Severity of the disease and high risk of death were associated with low CD4+ lymphocyte counts, high viral load, and lack of antiretroviral therapy.

Conclusions. Bacterial pneumonia and encephalitis are the most common and prognostically unfavorable secondary infections in HIV-infected patients. Their timely diagnosis requires mandatory PCR, extensive microbiological testing, and neuroimaging methods. CD4+ and viral load indicators are key prognostic factors for outcome and justify their regular monitoring and early initiation of ART. In clinical practice, it is advisable to use screening indicators (CD4 <100, high viral load, multiple secondary infections) to promptly refer patients to specialized hospitals and optimize treatment strategies.

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HEPATITIS A INCIDENCE AND ITS CONSTITUENT FACTORS (CASE STUDY IN NUKUS DISTRICT)

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Purpose of the study. To study the spread of hepatitis A infection and its relationship with environmental factors using Nukus District as an example.

Materials and Methods. Annual survey data from the Department of Sanitary and Epidemiological Welfare and Public Health of the Nukus District of the Republic of Karakalpakstan were used. Bacteriological, statistical, and epidemiological methods were used in the study.

Results and discussion: Between 2019 and 2024, hepatitis A incidence rates in Nukus District varied. Specifically, in 2019, this indicator was 47.3%, in 2020 – 26.2%, in 2021 – 9.9%, in 2022 – 13.7%, and in 2023, it was recorded at 96.4%. Over the past year (2024), the analysis was intensified, and cases were examined across 13 mahallas in the district. This approach allowed us to assess the sources of the disease and its spread. By the end of 2024, only 68 cases of hepatitis A were identified in the district. The distribution by mahalla was as follows: Akmangyt – 14.7%, Tok-Tau – 5.8%, Bakanshakly – 1.4%, Arbashi – 10.3%, Samanbay – 20.5%, Krantau – 16.7%, Kerder – 1.4%, Takhyrkul – 14.7%, Kutankul – 1.4%, and Diykhan-Arna – 13.2%. However, no cases of hepatitis A were recorded in the Akterek, Darsan, and Ulgili-Makan mahallas.

The analysis revealed that the main factor causing hepatitis A is exposure to the virus through contaminated water and food. We compared the incidence data with the results of water samples from open water bodies for the corresponding years. Samples that did not meet the requirements of the State Standard of the Republic of Uzbekistan (UzGOST) were distributed as follows: 2019 – 35.1, 2020 – 0, 2021 – 0, 2022 – 40, 2023 – 25, 2024 – 49. The correlation coefficient between these indicators was $r = 0.41$, with $p = –0.415$.

Conclusion. Based on the results obtained, the following can be concluded: by the end of 2024, the incidence of hepatitis A was higher in the Akmangyt, Samanbay, and Krantau street block of the Nukus district compared to anotherstreet block. A moderate positive correlation was found between the two sets of indicators for the years studied; however, due to a p value of > 0.05, this relationship is not statistically significant.