OZIQLANISH TURIGA QARAB CHAQALOQLARDA ICHAK MIKROFLORASINING OʻZGARISHI.

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Annotatsiya: Chaqaloqlik davri inson ichak mikroflorasining shakllanishi uchun eng muhim bosqichlardan biri hisoblanadi.Bu davrda inson mikroflosasining tarkibi va funksional imkoniyatlari organizmning immun tizimini rivojlanishi, metabolizm va keyingi hayotdagi turli kasalliklarga moyillikni belgilab beradi.Asosan chaqaloqlar ichak mikroflorasining shakllanishida oziqlanish turning (ona suti va suniy ovqatlanish) bu oziqlar ta'sirida mikroflorada yuzaga keladigan chuqur oʻzgarishlar, ularning biologik mexanizmlari va uzoq muddatli klinik ahamiyati tahlil qilingan.Bifidobacterium va bacteroides kabi dominant bakteria turlari, sut oligoxaridlaring (HMOlar)mikroflora shakllanishidagi ahamiyati yoritilgan. Molekulyar-genetik usullardan foylalangan holda ichak disbiyozining patogenetik mexanizmlari, immun disfunksiyalar va metabolitik buzilishlar oʻrtasidagi bogʻliqlik muhokama qilingan. Erta yoshdagi bolalarda sogʻlom mikroflorani shakllantirishning fundamental ahamiyatini takidlaydi va davolash strategiyalarini optimallashtirishda oziqlanish omilini hisobga olish zarurligiga asoslanadi.

Kalit soʻzlar: Chaqaloqlik davri, ichak mikroflorasi,ona suti, suniy ovqatlanish, dizbioz, sut oligoxaridlari (HMOLAR), Bifidobacterium,bacteroides, 16SrRNK sekvensiyalash, immune tizimi,metobolizm.

ИЗМЕНЕНИЯ КИШЕЧНОЙ МИКРОФЛОРЫ МЛАДЕНЦЕВ В ЗАВИСИМОСТИ ОТ ТИПА ВСКАРМЛИВАНИЯ.

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Аннотация: Младенческий период является одним из наиболее важных этапов формирования кишечной микрофлоры человека.В этот период состав и фунционалные возможности микрофлоры опредеяют развитие иммуной ситемы организма, метаболизм и предрасположенность к различным заболеваниям в дальнейшей жизни.В данной статье подробно проанализированы ключевая роль типа вскармливания (грудное молоко и искусственное питание) в формиравании кишкечной микрофлоры младенцев,

глубокие изменения микрофлоры под влиянием этого питания, их биологические механизмы и дологосрочное клиническое значение. Освещена роль доминирующих видов бактерий, таких как Bifidobacterium и Bacteroides а также олигосахаридов грудного молока ОГМ/НМО в формировании микрофлоры. С исползованием молекулярно- генетических метод обсуждена взаимосвязь между патогенетическими механизмами дизбиоза кишечника, иммунными дисфункциями и метаболическими нарушениями. Статья подчеркивает фундаментальное

значение формирования здоровой миркофлоры у детей микрофлоры у детей раннего возраста и обосновывает необходимость учета фактора птиания при оптимизации статегиий лечения.

Ключевые слова: Младенческий возраст, кишечная микрофлора, грудное вскармливание, искусственное вскармливание, дисбиоз, олигосахариды грудного молока (ОГМ/HMOs), Bifidobacterium, Bacteroides, секвенирование 16S рРНК, иммунная система, метаболизм.

INFANT GUT MICROBIOTA: PROFOUND CHANGES DRIVEN BY FEEDING TYPE.

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Anntasion: Infancy represents one of the most crucial stages for the development of the human gut microbiota. During this period, the composition and functional capabilities of the microbiota determine the development of the organism's immune system, metabolism, and predisposition to various diseases later in life. This article comprehensively analyzes the pivotal role of feeding type (breastfeeding vs. formula feeding) in shaping the infant gut microbiota, the profound changes in the microbiota induced by these nutritional factors, their underlying biological mechanisms, and their long-term clinical significance. The importance of dominant bacterial species suchas *Bifidobacterium* and *Bacteroides*, as well as human milk oligosaccharides (HMOs), in microbiota development is highlighted. The interrelationship between the pathogenetic mechanisms of gut dysbiosis, immune dysfunctions, and metabolic disturbances is discussed using molecular-genetic methods. The article emphasizes the fundamental importance of establishing a healthy microbiota in early childhood and substantiates the necessity of considering the nutritional factor in optimizing treatment strategies.

Keywords: Infancy, gut microbiota, breast milk, formula feeding, dysbiosis, human milk oligosaccharides (HMOs), Bifidobacterium, Bacteroides, 16S rRNA sequencing, immune system, metabolism.

Introduction: a person is a set of billions of microorganisms that exist in the body - microbiota, which plays an important role in maintaining health and pathogenesis of diseases. The infancy period, especially the first 1,000 days of life, is a period in which the formation, maturation and stabilization of intestinal microfolation are of particular importance [1]. During this time, the specificity and diversity of the composition of microbial communities in the intestine directly affects the development of the body's immune system, digestive processes, metabolictic functions, and even the shallowing of the central nervous system [2]. The formation of intestinal microflora in infancy is influenced by a number of factors, including the method of birth (natural or caesarean section), gestational age, genetic predisposition, antibiotic therapy of the mother and baby, the environment and, most importantly, the type of nutrition [3, 4]. In particular, the unique role of breast milk in the optimal formation of infant intestinal microflora is one of the main objects of modern medical and microbiological research [5]. The composition of breast milk is not just a nutrient value, but a rich source of immunoglobulins, protective factors such as lactoferrin, lycosim, as well as human milk oligocharids (HMOs) [6]. HMOs perform a specific prebiotic function, selectively stimulating intestinal growth of certain beneficial bacterial species, notably Bifidobacterium [7]. Artificial nutrition, an alternative to breast milk nutrition, is widely used for a number of reasons. However, artificial milk formulas, although their composition is maximally approximated to breast milk, lack important biologically active components such as HMOs and living bacteria in breast milk [8]. As a result, infants who have switched to artificial feeding experience

profound and drastic changes in the intestinal microflora compared to infants who have been fed breast milk. These changes are evident in microbial diversity, the proportion of dominant species, and the metabolite activity of microbial communities [9]. Our goal is to analyze the deep changes of the intestinal microflora of the intestines in relation to the type of nutrition on the basis of scientific literature, to highlight the molecular and biological mechanisms of these changes, and to discuss their long-term clinical significance for infant health. The role of modern molecular-genetic methods in determining these differences was considered Ham.

Purpose of the work: study of the condition of intestinal microbiocenosis of babies with natural and artificial nutrition

Materials and methods: infants have intestinal mkiroflora according to changes related to the type of nutrition .From the 7th family polyclinic of Samarkand, 20 natural and artificially fed babies were selected, and their feces were examined in the bacteriological laboratories of the Department of Microbiology, Virology and immunology of the Samarkand medical multidisciplinary clinic.

Literature review:

The reviewed scientific sources were carefully studied in order to assess the structural and functional changes of the intestinal microflora of infants depending on the type of feeding, the biological mechanisms causing these changes, and the long-term effects of these changes on children's health. The importance of *Bifidobacterium* and *Bacteroides* species, the selective effect of HMOs, and the consequences of intestinal dysbiosis are taken into account. In microbiological analysis, modern molecular-genetic methods are widely used in the analysis of infant intestinal microflora. 1. 16S ribosomal RNA gene sequencing: This method allows determining the taxonomic composition of microorganisms through amplification and sequencing of specific regions of the bacterial 16S ribosomal RNA gene. Using this method, even non-cultivable bacteria can be identified. [10] 2. Shotgun metagenomics: This includes sequencing the complete DNA of all microorganisms in the microflora. This method allows analyzing not only microbial species but also their genetic potential and metabolic functions. [11] 3. Metabolomics: By measuring metabolites in infant stool samples, it serves to directly assess the functional activity of the microflora. [12]

Results. In March 2025, bacteriological examination of stool samples from 20 infants under 1 year of age, both breastfed and artificially fed, from Samarkand city Family Polyclinic No. 7 was conducted, and the following results were obtained. Of the infants, 12 (60%) were girls and 8 (40%) were boys. Among them, 85% of infants were breastfed, and 15% were artificially fed (Nestogen, NAN, Nuppi Gold). In bacteriological examination, 15 indicators were identified. In 8 infants, grade I dysbiosis was detected, that is, a relative decrease in normal microorganisms; among conditionally pathogenic microorganisms *Klebsiella spp.* was identified in 2 infants; among pathogenic microorganisms *S. aureus* was detected in 8 infants; and among strict anaerobic microorganisms *Clostridium spp.* was identified in 2 infants.

Discussion: Breast milk (in a healthy mother) is considered the most optimal biological nutrition. Breast milk consists of various components and is adapted to the immature gastrointestinal tract mucosa and plays an important role in the formation of the nervous system, immune system, endocrine system, and other organ systems. Breast milk contains vitamins, minerals, and important components, namely nucleotides and DNA. This is not present in any artificial formula. During artificial feeding, within a certain time period, an atypical "bifidoflora" is formed with anaerobes other than bifidobacteria and facultative anaerobic bacteria. In other scientific studies, the amount of bifidobacteria in infants born in large urban maternity hospitals was consistently detected, which was not related to whether they were breastfed or artificially fed. It has been suggested that to improve the condition of the gastrointestinal tract and to form intestinal colonization, at least 1×10° colony-forming units (live microorganisms—probiotics) should be present. These bacteria have several functions, improving intestinal immunological protection and preventing penetration through the intestinal wall by pathogens. The intestinal microbiota of infants is a complex ecosystem consisting of many bacterial strains, species, and genera. This large cell mass performs many unique functions. This affects the physiology of the large intestine and systemic physiology. Its main functions include nutritional, metabolic, immunological, and protective functions.

Conclusion. Deep changes in the intestinal microflora of infants depending on the type of feeding are of fundamental importance for human health. Breastfeeding forms a healthy microbiota characterized by *Bifidobacterium* dominance, strengthens the immune system, and reduces the risk of various diseases later. Artificial feeding often leads to intestinal dysbiosis, and understanding changes in the intestinal microflora and managing them effectively, in particular through breastfeeding and, when necessary, through HMO-enriched formulas, is important in improving infant health. Grade I dysbiosis was detected in 40% of infants, and Grade II dysbiosis in 60% of infants.

In breastfed infants, the state of intestinal microflora was contaminated with the pathogenic microorganism *S. aureus* (40%), which indicates that breast milk is not sterile.

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