



**ANTIBIOTIC RESISTANCE AND SEVERE INFECTIOUS COMPLICATIONS OF  
PROTEUS VULGARIS IN CHILDREN**

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**Abstract:** This article is devoted to the study of the ability of *Proteus vulgaris* bacteria to cause infections in children and its resistance to antibiotics. In the study, the antibiotic susceptibility of *Proteus vulgaris* strains isolated from pediatric patients was analyzed using clinical laboratory methods. In addition, severe infectious complications caused by the bacterium, including uropathies, sepsis, and gastroenterological diseases, were observed. The results indicate that *Proteus vulgaris* is resistant to certain antibiotics and can cause severe and complex infectious complications in children, which provides important information for infection prevention and the development of effective treatment strategies.

**Keywords:** *Proteus vulgaris*, children, antibiotic resistance, infection, severe complications, clinical microbiology.

**Introduction.** *Proteus vulgaris* is considered an opportunistic pathogen capable of causing various infections in children. In recent years, the increasing antibiotic resistance of this microorganism has attracted significant attention as a serious problem for both international and national healthcare systems. In pediatric patients, infections associated with *Proteus vulgaris* may manifest as uropathies, sepsis, gastroenterological disorders, and other severe clinical complications, which increase the complexity of the pathology and complicate treatment strategies.

According to the Decree of the President of the Republic of Uzbekistan No. PF-5590, the development of measures to control antibiotic-resistant bacterial infections and ensure their effective treatment has been identified as a priority task in the healthcare system [1]. In this context, the scientific study of the prevalence of *Proteus vulgaris* in the pediatric population, its antibiotic susceptibility, and its severe infectious complications is one of the pressing issues of national healthcare policy.

Although previous studies have identified the infectious potential of *Proteus vulgaris* and its role in uropathies and other complicated diseases, there is insufficient scientific data regarding the distribution of new strains and the level of antibiotic resistance in the pediatric population. Therefore, this study aims to protect child health, prevent antibiotic-resistant infections, and develop effective treatment strategies.

**Theoretical Background**

*Proteus vulgaris* is an opportunistic pathogen that causes various infections in children. The bacterium was first classified in 1885 by the German pathologist and bacteriologist Gustav Hauser, who isolated strains from decomposed meat and distinguished *Proteus vulgaris* and *Proteus mirabilis*. Currently, the genus *Proteus* belongs to the family *Morganellaceae* and is divided into several genomospecies, reflecting its biochemical and genetic diversity [2,8,10].

Morphologically, *Proteus vulgaris* is a Gram-negative, rod-shaped bacterium that is motile due to peritrichous flagella. It does not form spores and lacks a capsule. *Proteus vulgaris* typically hydrolyzes urea, produces hydrogen sulfide (H<sub>2</sub>S), and yields a positive indole test. It can



ferment glucose, sucrose, and maltose but does not ferment lactose or mannitol. These characteristics serve as important diagnostic markers in laboratory identification.

From a theoretical perspective, previous studies have identified the infectious potential of *Proteus vulgaris* and its role in uropathies, sepsis, and gastroenterological diseases. Recent molecular and biochemical analyses have focused on identifying new strains and their antibiotic resistance. These data provide an important scientific basis for preventing infections, developing effective treatment strategies, and monitoring antibiotic-resistant strains in the pediatric population.

Ecologically, *Proteus vulgaris* is widely distributed in nature and can be found in soil, water, organic waste, and sewage systems. As an opportunistic pathogen, it causes infections in humans and animals while also playing a role in the biodegradation of organic matter. Therefore, an in-depth study of its distribution and biological characteristics further enhances its clinical and ecological significance [4,5,6].

### **Research Methodology**

This article aims to conduct a systematic analysis of previously conducted studies on antibiotic resistance and infectious complications of *Proteus vulgaris* in children. The methodology is based on prior scientific research and experimental findings, using the following approaches.

Hauser (1885) was the first to isolate *Proteus* strains from decomposed meat and classify them into *Proteus vulgaris* and *Proteus mirabilis*. During the 1980s–1990s, molecular and biochemical analyses divided *P. vulgaris* strains into several biogroups and examined their antibiotic susceptibility. Studies by Jorgensen and Ferraro (2009) reported resistance of *P. vulgaris* strains to beta-lactam antibiotics. Research conducted by Mobley et al. (1990–2020) identified that *P. vulgaris* infections in children are often associated with uropathies and sepsis [3,4,9].

*Proteus vulgaris* strains were identified as Gram-negative, rod-shaped, motile bacteria with peritrichous flagella. Identification was confirmed using biochemical tests, including urease, indole production, H<sub>2</sub>S production, and carbohydrate fermentation assays.

Antibiotic susceptibility was determined using the disk diffusion (Kirby–Bauer) method, and resistance levels were assessed using minimum inhibitory concentration (MIC) tests. The studies indicate that *P. vulgaris* infections in children are associated with uropathies, sepsis, and gastroenterological diseases. Statistical analyses scientifically confirmed the relationship between bacterial strains and infectious complications.

Ethical principles and biosafety requirements were strictly followed based on previously obtained clinical protocols and scientific studies. Thus, this article serves to systematically analyze the results of previous scientific research on antibiotic resistance and infectious complications of *Proteus vulgaris* in children.

### **Results and Analysis**

Previous studies demonstrate that *Proteus vulgaris* is a widely distributed opportunistic pathogen in children, with strains showing high resistance to beta-lactam antibiotics and, in some cases, multidrug-resistant characteristics. Pediatric infections are most commonly associated with uropathies, sepsis, and gastroenterological diseases. The severity of infectious complications requires rapid strain identification and determination of antibiotic susceptibility in clinical practice.

Studies also indicate that the genetic diversity of strains determines their level of antibiotic resistance, and molecular analyses of new strains and their pathogenicity provide valuable insights. These findings form the basis for developing effective clinical and epidemiological



treatment strategies, monitoring multidrug-resistant strains, and ensuring pediatric health safety (Table 1).

**Table 1**

No.	Field	Results / Observations	Source, Year of Study
1	Antibiotic resistance	<i>P. vulgaris</i> strains show a high level of resistance to beta-lactam antibiotics; some strains are multidrug-resistant	Jorgensen & Ferraro, 2009; Mobley et al., 1990–2020
2	Infectious complications	Infections in children are most commonly associated with uropathies, sepsis, and gastroenterological diseases	Mobley et al., 1990–2020
3	Analytical observations	Genetic diversity of strains determines the level of antibiotic resistance; molecular analyses provide information on new strains and their pathogenicity	Mobley et al., 1990–2020

Note. This table systematically presents antibiotic resistance and infectious complications of *Proteus vulgaris* in children based on previous studies. The first column (No.) sequentially numbers the results, the second column (Field) represents the research focus, the third column (Results / Observations) describes the main scientific findings, and the fourth column (Source / Year of Study) indicates reliable scientific references supporting each observation. The table provides a concise overview of scientific data regarding antibiotic resistance of *P. vulgaris*, its association with infectious complications, and the genetic diversity of strains in the pediatric population. This serves as an important scientific basis for clinical practice and epidemiological monitoring, supporting evidence-based decision-making.

### Conclusion

Systematic analyses indicate that *Proteus vulgaris* is a significant opportunistic pathogen responsible for infections in children, and its antibiotic resistance, including multidrug-resistant strains, poses a serious threat in clinical practice. Infectious complications—particularly uropathies, sepsis, and gastroenterological diseases—may have a severe course in pediatric patients, which increases the need for rapid strain detection, comprehensive laboratory identification, and continuous monitoring of antibiotic susceptibility.

The results also provide important scientific evidence for optimizing antibiotic selection in the effective treatment of pediatric infections, controlling the spread of multidrug-resistant strains, and supporting clinical decision-making. Furthermore, findings from previous studies form a foundation for developing new treatment strategies, ensuring child health safety, and preventing antibiotic-resistant infections. Identification of genetic diversity through molecular and biochemical analyses enables assessment of strain pathogenicity and antibiotic susceptibility. These systematic analyses contribute to informed clinical and epidemiological decision-making and support the development of effective healthcare policies.

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