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THE MAIN TAXONOMIC FEATURES OF THE CAUSATIVE AGENTS OF URINARY TRACT INFECTIONS AND A DESCRIPTION OF THEIR VARIABILITY

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ABSTRACT

After evaluating the microbial landscape of the cultured microorganisms, they analyzed and evaluated the results of Scientific work on taxonomic traits and their changes, ie the manifestation of atypical traits that are not specific to the species. We found it necessary to differentiate each generation and species separately in order to facilitate the evaluation of the results obtained, to characterize the taxonomic characteristics of the grown pathogens, and to strengthen the identification results.

KEYWORDS: *Escherichia coli. microorganisms.,pathogen strains*

INTRODUCTION

The description of the microorganisms was given in sequence according to their growth rate.

Escherichia coli. Escherichia coli has been identified as a genus of Escherichia coli. They grew in their own universal (meat-peptone agar) and differential-diagnostic nutrient media. All studied strains of this gram-negative bacterium did not differ from each other in morphological and tinctorial properties. When observed under a microscope (7x90 = 630), the field of view

appeared to be medium-sized, short, rod-shaped (100%), irregularly spaced (100%), and stained red (100%) with control dye (aqueous fuchsin) when stained on Gram[1,4,6,8,9].

As for the cultural feature, the colonies grown in the Endo environment were bulging, the edges smooth, the surface smooth, C-shaped, mostly fuzzy (100%), metallic radiant, reddish, and sometimes dark pink. All strain colonies were of solid consistency (100%).

Result and methods

Study of the biochemical properties of E.coli strains isolated from the urine sample of women of childbearing age showed that it utilizes glucose, lactose, maltose, arabinose, mannitol, sodium citrate, does not break down sorbitol, inositol, sodium Malone, does not produce hydrogen sulfide, urease, arginine dehydrola (Table 1).

According to the results of the analysis, practically half of the pathogen strains isolated from women diagnosed with UTI did not break down the enzyme sucrose. All studied strains (except 19 strains of E.coli) did not have hemolytic activity.

Strains that did not fully represent all taxonomic traits were assessed as atypical strains, however, their scarcity and the fact that there was only a change in 1-2 taxonomic traits allowed us to describe this pathogen as Escherichia coli[5,9].

Proteus srr. We did not find it necessary to identify the species because they are not pathogenetically different from each other. All strains of this microorganism were similar to other enterobacteria in morphological (100%), tinctorial (100%), and cultural (100%) properties. In this respect, similar characteristics were observed in other members of the family he represented.

TABLE 1 INDICATORS OF BIOCHEMICAL PROPERTIES OF E.COLI STRAIN ISOLATED FROM URINE SAMPLE (FROM N = 12)

Characteristics of strains	Acute UTI	Chronic UTI
Fermentation of carbohydrates		
Glucose utilization	+	+
Lactose fermentation	+	+
Mannitol fermentation	+	+
Sucrose fermentation	+	+ (58,3%)
Inositol fermentation	–	–
Sorbitol fermentation	–	–
Arabinose fermentation	+	+
Maltose fermentation	+	+
Citrate Na Fermentation	–	–
Malonate Na	–	–
Fermentation		
Lysindecarboxylase	+	+
Ornimindecarboxylase	+(50,0%)	+ **(**75,0%)
Arginine dehydrolase	–	–
Phenylalanine deaminase	–	–
Urease	–	–

B-galactosidase	–	–
Hydrogen formation	–	–
Hemolytic activity	+ (66,7%)	+ (41,7%)

Note: the percentage is given the number of strains with these characteristics; in the percentage not specified (+) the result was 100.0%.

According to Shukevich, the main differentiating features are "creeping growth" (100%), lactose fermentation (100%), sorbitol degradation (83.3 ± 15.2%), lysine decarboxylase activity (83.3 ± 15.2%), indole we can cite positive results of additional bacteriological tests such as formation (100%), malonate activity (83.3 ± 15.2%). Bacteriological studies did not reveal pathogenic factors (0%). Apparently, the percentage of atypical strains is low, so there was no doubt that they belonged to the Proteus family.

Klebsiella SRP. In terms of morphological, tinctorial, cultural, and enzymatic properties (100%) showed taxonomic traits specific to this generation, as with other gram-negative bacteria analyzed, no atypical strains, i.e. no generational taxonomic traits were observed, no pathogenic factors were identified (0%).

Thus, strains of uropathogenic enterobacteria (Escherichia coli, Proteus SRP, Klebsiella SRP) collected from the urine of sick women were typical strains of all genera and species-specific to all studied taxonomic traits. detected.

Pseudomonas aeruginosa. This microorganism, which belongs to the genus Pseudomonas, along with other non-fermentable gram-negative bacteria (NFGNBs) has good growth properties in all nutrient media, so we did not choose a separate nutrient medium and grew it in Endo medium. we have described.

Colonies suspected of being the causative agent were replanted on 2% glycerin-containing oblique frozen agar. On its surface, Pseudomonas aeruginosa grew abundantly and densely, forming oily green pigmented (pyocyanin) colonies and distinguished by its distinctive ‘blooming purple’ odor.

For differentiation from other gram-negative microorganisms, especially enterobacteria, Pseudomonas aeruginosa was evaluated for the following characteristics:

- good growth (100%) in normal nutrient media (meat-peptone agar);
- mobility (100%);
- formation of green pigment (piocyanin) (100%);
- solubility of gelatin at 22ºC (100%);
- Positive result of the Hugh Leifson test (90.9 ± 8.7%);
- Occurrence of the phenomenon of "rainbow lysis" (90.9 ± 8.7%).

The phenomenon of “rainbow lysis” (formation of a mucous membrane of different colors on the surface of a colony of microorganisms) was recommended as an additional test in the identification of Pseudomonas aeruginosa in the bacteriological diagnosis of UTI. Since the atypicality of the strains was associated only with additional tests - the Hugh-Leifson positive

test and the “rainbow lysis” phenomenon, we relied on key taxonomic features in identification[].

Staphylococcus aureus. When the described stimulus was stained on Gram, it was observed in the field of view that it was stained with the primary dye in 100% of cases. Under a microscope (7x90 = 630) it was observed that they were ball-shaped and arranged in a “grape bunch” shape (100%).

The following taxonomic characteristics of cultured strains were identified: bulging, dull, larger than 5 mm in diameter, large, C-shaped colonies (100%) grew on the surface of the nutrient medium; the presence of the causative colony in the golden pigment (100%); Growth in a nutrient medium containing 10% NaCl (83.3 ± 15.2%); the colonies were found to be of solid consistency (100%).

Based on the above morphological, tinctorial, and cultural characteristics, the strains described were identified as belonging to the Staphylococcus genus.

The results of the identification of strains of the genus Staphylococcus by type are given below:

- coagulase activity of strains (coagulase-positive strains) was detected (83.3 ± 15.2%);

- Growing in nutritious juice (83.3 ± 15.2%);

- fermented mannitol in the Giss series under anaerobic conditions (100%);

- showed sensitivity to novobiocin (83.3 ± 15.2%);

- One of the signs of pathogenicity of the strain is the activity of lecithovetilase or the breakdown of lecithin, which forms the appearance of a "rainbow circle" around the colony (83.3 ± 15.2%);

- breaks down glucose (100%), lactose (100%), mannose (100%), sucrose (83.3 ± 15.2%) (enzymatic activity).

The results show that basically all strains exhibited taxonomic traits specific to the genus Staphylococcus aureus. In some cases, i.e., in reactions, less than 100%, strains that showed atypical reactions that differed from typical strains specific to the Staphylococcus aureus species were also identified. However, the percentage of these cultures was low, and these strains differed from typical strains by only 1–2 characters. With this in mind, strains with an atypical reaction were also recognized as belonging to the genus Staphylococcus aureus[2,3,9].

Staphylococcus epidermidis. Morphologically, it is difficult to distinguish this microorganism from Staphylococcus aureus in terms of tinctorial properties, so it was not difficult to identify the generation by these taxonomic traits, in all strains (100%) these features were fully manifested.

The percentage of typical and atypical strains relative to Staphylococcus acc did not differ significantly.

The Main differential taxonomic features that distinguish Staphylococcus epidermidis from Staphylococcus aureus are the absence of golden pigment formation, the absence of coagulase activity (coagulase-negative), and the absence of hemolytic activity of pathogenicity.

Thus, Staphylococcus epidermidis was close to Staphylococcus aureus in morphological, tinctorial, cultural, enzymatic properties, differentiated by some cultural properties (absence of golden pigment), lack of coagulase activity and a low percentage of pathogenic factors and closeness to healthy women.

Staphylococcus saprophyticus. In the identification of these strains, differences in their typical properties were not observed in practice. While it was acknowledged that staphylococcal traits were observed during microbiological identification, there was no difficulty in bacteriological identification.

Enterococcus faecalis. These identified enterococci were differentiated using tests used in the following microbiological diagnosis: gram-positive, chain-like in the visual field; grass-esculin agar formed C-shaped, dark-colored colonies, grown in a nutrient medium with 6.5% NaCl, on obliquely hardened meat-peptone agar (this test was used to differentiate from streptococci); fermented lactose, glucose, and mannitol to acid but without gas[1,9].

Candida spr. The overgrown strains were spherical and oval in shape, they did not break down lactose, they broke down sucrose to acid. The main differential signs - no ascospores, formed pseudomycelium, verticillas, chlamydospores, without breaking down lactose, breaking down glucose, maltose, and sucrose, sprouting from the tip.

Bacteroides spp. Identification of this anaerobic microorganism was based on gram-negative, rod-like, inactive, sequential location in the visual field, growth under strict anaerobic conditions, C-shaped, pale, small colonies on blood agar, no hemolysis, hydrogen sulfide, glucose, lactose, sucrose breakdown.

The pathogenic properties of strains grown as large uropathogenic pathogens were characterized by the percentage of detection of pathogenic factors.

A total of 35 strains of acute UTI pathogens and 25 strains of chronic UTI pathogens were studied as pathogenic factors.

Strains with plasma coagulase, lecithinase, hyaluronidase activity accounted for a large percentage.

It is noteworthy that the hemolytic property was detected in low percentages only in E.coli (n = 19).

No significant differences were found between gram-negative bacteria and gram-positive cocci in the detection of pathogenic factors, and no similar convincing differences in this parameter were observed between acute and chronic UTI.

Thus, there were no significant differences in the identification of the main taxonomic features between strains that are considered uropathogenic pathogens and strains of microorganisms belonging to the same species derived from other biotopes. The variability of biological properties was also low, which did not prevent the identification of pathogens by generation and type.

CONCLUSION

No practically convincing differences were found in the biochemical and pathogenic properties of the strains in the acute and chronic forms of UTI. This suggests that the main taxonomic features of uropathogenic strains that cause UTI in women of childbearing age are that there are no changes to the extent that can be included in the diagnostic algorithm of microbiological studies on the characteristics of their variability.

This situation showed that the results obtained differed significantly from the results of Scientific studies published by the other researchers mentioned above.

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