Research Article

Isolation and Molecular Identification and Antimicrobial Susceptibility of Providencia spp. from Raw Cow’s Milk in Baghdad, Iraq

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A total of sixty raw milk samples were collected from (street vendors and shops) from Baghdad city, Iraq. The samples were inoculated into peptone water and, then, subcultured onto MacConkey agar and Blood agar. Identification of isolates was confirmed by microscopic examination, cultural characteristic, biochemical tests, Vitek (VITEK®2 system), and Biolog GN substrate reactions followed by 16S rRNA and specific genes sequencing. Of 60 raw cow’s milk samples, Providencia spp. were identified only in 4 samples (6.67%) and P. rettgeri was the most common, 2/4 (50%), followed by P. stuartii and P. vermicola, 1/4 (25%). Antimicrobial susceptibility tests were conducted against ten antibiotics by the disc diffusion method. All Providencia isolates showed multidrug resistance (MDR), and the absolute resistant was 100% to tetracycline, erythromycin, and doxycycline and 50% against ampicillin/sulbactam and amoxicillin/clavulanic acid. They were highly susceptible (100%) to trimethoprim, imipenem, and chloramphenicol. These findings indicate that milk might be contaminated with Providencia spp. leading to transmission to humans causing poisoning, diarrhea, and other infections. This is the first study of isolated Providencia spp. from raw cow’s milk.

1. Introduction

Before 2005, the genus Providencia was including six species; after that, a new species was identified to become nine species which are P. alcalifaciens, P. rustigianii, P. stuartii, P. rettgeri, P. friedericiana, P. heimbachae, P. vermicola, P. sneebia, and P. thailandensis [1–3]. The Providencia spp. are urease-producing Gram-negative, belonging to the family Enterobacteriaceae. Although these species are present as normal flora in the human intestinal tract, they are opportunistic pathogens, especially in immunocompromised people causing traveler’s diarrhea, gastroenteritis and infection of the urinary tract and endocardium, sepsis in neonatal, and ocular inflammations [4–9]. Animals such as cattle, sheep, insects, worms, cats, birds, dogs, guinea pigs, and reptiles are reservoirs to Providencia spp., as well as this bacterium present in environment such as water (river, cows, and waste) [10–14]. These may explain the isolation of them from different food and food products [9, 15–17].

The laboratory identification of Providencia spp. is depending on culturing and biochemical characteristics. Providencia spp. grow in enteric agars such as MacConkey, Salmonella-Shigella (SS), Eosin Methylene Blue (EMB), and Hektoon Enteric (HE), and selective agars are Simmons Citrate, Tergitol, and HardyCHROM™ UTI [18, 19]. The commercial identification kits currently available include the Analytical Profile Index (API20) Esystem, Vitek GNI and GNI1 cards, and Microscan Rapid Neg ID3panel [20–23] in addition to the molecular identification using 16S rRNA and specific species genes [10, 24, 25].

Providencia spp. reported resistant to antimicrobials and multidrug resistance (MDR), and both P. stuartii and P. rettgeri reported resistant against many antimicrobial drugs. Providencia isolates were investigated to be MDR.
2. Materials and Methods

2.1. Isolation and Morphological Identification. Sixty raw milk samples were collected from vendors and shops in Baghdad city from March to June 2019. Ten ml of milk samples was taken and inoculated into peptone water, incubated at 37°C for 24 hrs, then subcultured on MacConkey agar and Blood agar (HiMedia, India), and incubated at 37°C for 24 hrs. The suspected Providencia spp. colonies which appear as pale colonies, lactose nonfermenter on MacConkey agar were picked, and conventional biochemical tests were applied including urease, phenylalanine, and triple sugar iron (TSI). They were further identified using the VITEK®2 system and Biolog GN substrate (Biomerieux, France) reactions for more differentiation according to [1, 41].

2.2. Molecular Identification. Molecular identification was applied on three isolates to confirm and differentiate between them. DNA was extracted from isolates growth using the Wizard Genomic DNA Purification Kit protocol (Promega, USA). PCR amplification of bacterial 16S rRNA was applied with 27 forward primer AGAGTTT-GATCCTGCGTCA and 1492 reverse primer TACGGTTACCTTGTTACGACTT 1, 300bp. The PCR reaction mixture final volume of 25 μl contains PCR premix 12.5 μl, forward primer 1 μl, reverse primer 1 μl, nuclease free water 8.5 μl, and DNA 2 μl. The PCR scheme performed was as follows: initial denaturation at 95°C for 30sec, annealing at 62°C for 30sec and extension at 72°C for 1 min, and final extension 72°C for 7 min [25].

After amplification, 1% agarose gel electrophoresis was applied to confirm the presence of amplification, then PCR products were purified and sent to sequenced, and the results were analyzed using genius software and compared to known sequences in the GenBank and Sepsitest BLAST databases.

2.3. Detected Antimicrobial Susceptibility. Susceptibility against antimicrobial drugs was determined by disk diffusion protocol using Mueller-Hinton (MH) agar (Oxoid, UK). The inhibitory zones around these antimicrobial discs were measured using a millimeter (mm) unit utilizing a metric ruler, and the results were read [43, 44]. Ten antibiotic disks (Merseyside, U.K.) used included amoxicillin 20 μg, clavulanic acid 10 μg (AUG 30C), trimethoprim (TM, 15 μg), ampicillin10 μg, sulbactam 10 μg (SAM, 20 C), tetracycline (T, 30 μg), erythromycin (E, 10 μg), cefixime (CFM 5 μg), doxycycline (DXT, 30 μg), imipenem (IPM, 10 μg), chloramphenicol (C 30 μg), and streptomycin ($ 25 μg). Multi-drug resistance (MDR) was detected according to the work of Magiorakos et al. [45]. The isolates resistant against three or more separate antimicrobial classes are considered as MDR. The multiple antibiotics resistance (MAR) index was calculated by dividing (a): the number of antimicrobial drugs resistant of isolate by (b): the total number of antimicrobial drugs, where the same isolate which exposed the results more than 0.2 was considered high risk [46].

3. Results

3.1. Characterization and Molecular Identification of Providencia Species. Providencia species were identified in 4 (6.67%), P. rettgeri were the most dominant species, 2/4 (50%), and P. stuartii and P. vermicola were 1/4 (25%). The isolates were Gram-negative coccobacilli. On MacConkey agar, lactose nonferment colonies are circular with entire edges, shining, smooth, slim, and convex, P. vermicola showed a dense brownish center and hyaline periphery colonies, and the isolate on blood agar are nonhemolysis. Biochemically, it is motile, negative reactions for oxidase, positive for catalase and tryptophan deaminase, on TSI, gives alkaline/acid (pink/yellow) reaction without H₂S and gases production, the isolates were suspected of Providencia spp.,
and by using the VITEK®2 system, reactions give the positive for three isolates of P. rettgeri and one isolate was P. stuartii.

P. rettgeri isolates (unfortunately, P. stuartii isolate died before completing molecular identification) were sent to be sequenced and analyzed for similarity using a database at the NCBI. The partial gene sequence of 16S RNA established that these isolates had high similarity between P. rettgeri/P. vermicola in both databases, when using Provi_foward and Provi_reverse (detected both P. rettgeri and P. vermicola), and a band of approximately 1306 bp was observed on the agarose gel (Figure 1). The results of the sequence were as follows: 1st isolate was 99.91% similar with P. rettgeri, the 2nd gave 100% similarity to P. rettgeri/P. vermicola, while the 3rd isolate was 99.81% similar to P. vermicola/P. rettgeri in the Gen bank database and in the Sepsi test BLAST database; similarity were as follows: the 1st was P. vermicola/P. rettgeri, 99.5%; the 2nd was P. vermicola/P. rettgeri, 99.9%, while the 3rd was P. vermicola, 99.8%, and when using Provi_forward and P_Verni_reverse primer (detected only P. vermicola), the 1st and 2nd isolates give no bands, that is, these two isolates were P. rettgeri, while the 3rd one gives two bands, which were not of the same expected size of 1366 bp; therefore, this isolate was more differentiated from P. rettgeri based on Biolog GN substrate reactions for more biochemical tests and the sequencing result gives that the 3rd isolate was P. vermicola, 99.8%; thus, the three isolates were deposited in GenBank with accession nos: MT032351.1, MT032352.1, and MT032359.

3.2. Antimicrobial Susceptibility. As total, all Providencia isolates showed absolute resistance (100%) against tetracycline, erythromycin, and doxycycline, 50% to Amoxicillin/clavulanic acid and ampicillin/sublactam, and 25% to cefixime. P. vermicola was resistant 100% to amoxicillin 20 μg/clarulanic acid and ampicillin/sublactam compared with P. rettgeri which was 50% and P. stuartii was 0%. The resistance against streptomycin reported 50% in P. rettgeri. Also, resistance to cefixime was 100% against P. vermicola, while 0% (sensitive) in both P. rettgeri and P. stuartii. All isolates were 0% resistant (100% sensitivity) to trimethoprim, imipenem, and chloramphenicol. The results also revealed that these isolates were MDR. MAR index values were 0.6 in P. rettgeri and P. vermicola and 0.3 in P. stuartii that reveals all isolates were high risk (Table 1).

4. Discussion

Infections with Providencia spp. including P. rettgeri and P. stuartii which cause food poisoning, diarrhea, and UTI have been increased in the world, especially in developed and developing countries [9, 32, 47–51]. P. vermicola was investigated for the first time in infective nematodes, later from a diseased fresh water fish and from an acute watery diarrhea patient [1, 25, 52]. Therefore, in the present study, we investigate for Providencia spp. in raw milk collected from shops and vendors in Baghdad city. Our results indicate that raw milk is contaminated with P. rettgeri, P. stuartii, and P. vermicola. Providencia spp. including P. rettgeri and P. stuartii were isolated from food [9, 15–17, 53, 54]. In Iraq, out of bacterial content of fish gut, P. rettgeri reported 1/50 [55]. This is the first report of isolated Providencia from raw milk in Iraq; there is a study in Kenya, where 0.6% Providencia spp. was isolated from the milk of goats with subclinical mastitis, and 2% P. stuartii and P. alcalifaciens were isolated from clinical healthy cows (subclinical mastitis) in Algeria [39, 40]. This study is also the first isolating P. vermicola from a food source such as milk. Milk may be contaminated by the environment such as soil, water, feces of the carrier or infected cattle, unhygienic conditions during milking, or used contaminated containers.

Phylogenetically, the family of Enterobacteriaceae has a highest similarity (16S rRNA gene sequence similarity), particularly with the members of genus Providencia (>98.1%), and a higher similarity 99.5% was found between P. rettgeri and P. vermicola [1]. In agreement with that found in the present study, the similarity was ranging from 99.81 to 99.9% even in used species-specific gene. In contrast, the primer Provi_foward and P_Vermi_revers primers confirmed that the two isolates were P. rettgeri (no bands), but the 3rd one gives more one band in suspected P. vermicola. For this reason and because of the fact that the VITEK®2 system does not contain automated identification of P. vermicola in the list of card Gram negative, we used Biolog GN substrate reactions for more biochemical tests to differentiate P. vermicola from P. rettgeri such as urease,
erythritol and 2-ketogluconate, L-arabinose, D-glucosaminic acid, and D-glucuronic acid reactions and depending on the cultural characterization according to [1, 41]. In addition to the sequence, results confirmed that this isolate was *P. vermicola*.

In the current study, the results showed multiple resistance to antibiotics with high risk, these results were similar to other research studies, and resistance against multiple antimicrobials including tetracycline, ampicillin, and streptomycin were recorded in *Providencia* isolates in farm animals [56]. On the other hand, MDR *P. rettgeri* from UTI patients recorded high resistance to amikacin, aztreonam, cephalosporins, ciprofloxacin, ertapenem, and meropenem [41]. MDR (43%) showed in *Providencia* spp. including *P. stuartii* and *P. rettgeri* isolated from retail meats, and most of the isolates were resistant (91%) against tetracycline, ampicillin (69%), and streptomycin (49%) [54].

In addition, the results are similar with some differences in percentage of resistance to the study in Iraq; *P. alcalifaciens* and *P. rettgeri* isolated from clinical sputum and wastewater showed a high resistance against nitrofurantoin (100%), ampicillin (94.4%), amoxicillin/clavulanic acid (72.2%), and ampicillin/sulbactam and tetracycline (38.8% and 33.3%), respectively, while resistance to imipenem and cefotaxime were 5.6% each, and the most effective antibiotics were 100% resistant to norfloxacin, chloramphenicol, and cefixime and 88.9% resistant to trimethoprim recorded by the authors in [14] which are accordance with our results. High drug resistance against chloramphenicol, trimethoprim, and tetracycline and susceptibility to streptomycin of *P. vermicola* were recorded in diarrheal patients [25]. Despite MDR and the risk of the *Providencia* spp. isolates, all the isolates were susceptible to important antimicrobials which are used clinically such as imipenem, trimethoprim, and chloramphenicol in the present study.

### 5. Conclusions

Our results showed that raw milk is a potential source of *Providencia* spp. that may lead to infection in humans and risk to public health, especially the bacteria found as MDR. The present *Providencia* spp. in milk may be attributed to contamination after milking from the environment such as animal feces, or it is source from subclinical mastitis cow.

### 6. Recommendations

More studies should be conducted for more identification of this microorganism in food and its products in Iraq. Conventional methods and commercial kits beside molecular techniques should be used to identify *Providencia* spp. in level species.

### Data Availability

Data used to support the findings of this study can be obtained from the corresponding author on request.

### Conflicts of Interest

The author declares no conflicts of interest.

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### References


