



Biofilm Formation by Uropathogenic *Serratiamarcescens*

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Received: July 9, 2024 / Accepted: July 31, 2024 / Published: November 3, 2025

Abstract: Gram-negative nosocomial *Serratiamarcescens* is responsible for severe urinary tract infections (UTIs) in hospitalized individuals. *S. marcescens*'s quorum sensing (QS) system regulates biofilm formation. This study aimed to test *S. marcescens*'s capacity to establish biofilms. Out of 150 clinical specimens were collected from patients admitted to Baghdad Medical City, only 23 were positive growth of *S. marcescens*. The *S. marcescens* isolates were identified by CHROMagar *Serratia* and the VITEK-2 system compact. Microplate technique was employed to investigate biofilm formation. DNA extractions were conducted on all positive isolates to confirm their identity through PCR amplification of a fragment of *rplU* gene. *S. marcescens* was identified in all 23 isolates. 11 (47.8%) and 12 (52.2%) isolates were capable of establishing moderate and weak biofilms, respectively. However, none of the isolates was a robust biofilm-former. *Serratiamarcescens* isolates from catheter-associated and UTIs have shown a significant capacity for biofilm formation, indicating potential for UTIs.

Keywords: Biofilm, *rplU*, *Serratiamarcescens*, Uropathogenic.

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Introduction

Serratiamarcescens is human pathogen from the *Enterobacteriaceae* family that is gram-negative and opportunistic, *Serratiamarcescens* is responsible for hospital-acquired infections and outbreaks in critically ill or severely immunocompromised patients (1). *S. marcescens* is a pathogen that has the potential to induce a variety of illnesses, such as urinary tract infections (UTI), meningitis, pneumonia, wound infections, septicemia, keratitis, and lung infections (2). It is believed that the bloodstream is the most common location for the transmission of infections when the respiratory and digestive systems are compromised. *S. marcescens* is capable of producing

virulence factors, such as the capacity to establish biofilms on abiotic or biotic surfaces (3). Furthermore, *S. marcescens* can be isolated from soil samples as well (4). Through a sequence of predetermined stages, *S. marcescens* generate biofilms that essentially consist of cell chains, cell clusters, and filaments, resulting in a highly porous, filamentous biofilm. This biofilm is contingent upon the quorum sensing (QS) system (5).

Labbate *et al.* (6) reported that the process of biofilms developing in *S. marcescens* is genetically regulated. As the biofilm matures, the development of interconnected cell aggregates, bacterial cell assemblages alongside the threadlike cells, and extended threadlike

cells is indicative of the resulting cell and structure differentiation.

A bacterial community can benefit from the formation of biofilms in a variety of ways. Biofilms offer protection against protozoan graze, resistance to a variety of antimicrobials, and defence against host immunity(7).The bacteria's formation of a highly filamentous and porous biofilm, which is composed of filaments and cell chains, is the result of a sequence of distinct stages(8).Protruding organelles, known as fimbriae or pili, are primarily responsible for inert surfaces or living tissue adhesion, entry into host cells, and interactions of bacterium-to-bacterium that result in bacterial aggregation and biofilm formation(9).The pathogenesis of *S. marcescens* is likely influenced by biofilm formation, which is the adhesion of microbes to surfaces such as contact lenses(10).The biofilms growth enables populations of bacteria to survive more effectively in inhospitable conditions when a hostile immune system or antibiotics are present (11).

The objective of this study was to examine *S. marcescens*'s capacity to establish the biofilms.

Materials and Methods

Bacterial Isolates

The bacterial isolation was carried out during the period from September to December 2023, a total of 150 different specimens, including mid-stream urine and indwelling urinary catheter, were collected from patients referring to Baghdad Medical City. All the specimens were cultured on the blood agar and MacConkey agar at 37°C for 24 hrs.Colourless colonies (lactose non-fermenters) were chosen for identification of *S. marcescens* as they were cultured on

CHROMagar*Serratia*(CHROMagar, France) and incubated at 37°C for 24 hours. The resulting isolates were then subjected for identification by VITEK 2 compact system (BioMérieux, France), which utilizes a sophisticated colourimetric approach. *S. marcescens* was identified with a probability of 99% using a Gram-negative (GN) card (12, 13).

Biofilm assay

Biofilm formation was quantified using microplate technique(14). All 23 isolates were cultured in brain heart infusion broth at 37°C for 18 hours. Next, each isolate was diluted in tryptic soy broth (TSB) containing 1% glucose. The 0.5 McFarland standard was used to adjust the cell suspension. Subsequently, addition of 200 µl of the isolated culture to 3 wells of 96-well U-shaped bottom polystyrene microplates. At 37°C, the microplates were incubated for 24 hours and kept covered. The microplates were rinsed twice with distilled water to eliminate loose bacteria, tapped on paper towels to remove any remaining water, and then air-dried. 200 µl of absolute methanol was used to fix each well at room temperature for 20 minutes. Subsequently, application of a volume of 200 µl of 0.1% crystal violet for 15 minutes. The excess dye was eliminated through repeated washing with distilled water. The plates were subsequently air-dried for approximately 30 minutes. 200 µl of 95% ethanol was added to each well after drying, and the crystal violet dye attached to the adherent cells was allowed to dissolve for 10 minutes. This experiment was conducted in triplicate, with the absorbance of bacteria-free wells that contain TSB serving as the negative control. A microplate reader was employed to quantify the samples at an optical density of 600. The classification of bacterial adherence as

shown in (Table 1) was employed to conduct the data simplification and computation, which was derived from the OD₆₀₀ values of individual *S.*

marcescens isolates. The cut-off value (OD_c) was established as follows (15):
OD_c = OD₆₀₀ of the negative control + 3 standard deviation.

Table (1): Biofilm intensity calculation.

Mean OD ₆₀₀	Biofilm intensity
OD ≤ OD _c *	Non-biofilm producer
OD _c < OD ≤ 2OD _c	Weak
2OD _c < OD ≤ 4OD _c	Moderate
OD > 4OD _c	Strong

Molecular Detection of

Serratiamarcescens

Extraction of DNA

Presto Mini gDNA bacteria kit (Geneaid, Taiwan) was used for genomic DNA extraction from the bacterial isolates. The amplification of a fragment of *rpIU* gene was performed using conventional PCR by which the extracted DNA, forward primer (5'-GCTTGGAAAAGCTGGACATC-3') and reverse primer (5'-

TACGGTGGTGTTCACGACGA-3'), were used in the PCR master mix with 20 µl as total volume (Table 2). The DNA amplification was carried out in accordance with the conditions outlined in (Table 3). Subsequently, the amplicons were resolved in a 1.5% agarose gel (16).

Table (2): Components of master mix of conventional PCR.

No.	Component	Concentration	Volume (µl)
1	GoTaq Green Master Mix	2X	10
2	Forward primer (10 µM)	10 µM	1
3	Reverse primer (10 µM)	10 µM	1
4	Nuclease free water	-	6
5	Template DNA	25 ng	2
6	Final volume	-	20

Table (3): PCR amplification program (16).

No.	Step	Temperature (°C)	Time	Cycles
1	Initial denaturation	95	5 min.	1
2	Denaturation	95	45 sec.	40
3	Annealing	57	45 sec.	
4	Extension	72	50 sec.	
5	Final extension	72	5 min.	1
6	Hold temperature	4	∞	1

Statistical analysis

Shapiro-Wilk test was adopted to test the normality. Biofilm data were expressed as mean ± standard deviation, whereas the ANOVA test followed by

the least significant difference were adopted for comparing these data. P value ≤ 0.05 was considered significant (17).

Results

Isolation and identification of *Serratiamarcescens*

Out of 150 specimens, 23 (34.5 %) developed positive bacterial growth when cultured on CHROMagarSerratia. Plates incubated for 24 hours at 37°C (Figure 1). The inhibition of the majority of the microorganisms implies

a relevant characteristic of CHROMagarSerratia(18). The VITEK-2 compact system verified this identification, as all of the isolates were identified as *S. marcescens*. The highest isolation rate was 19 (19%) isolates from 100 mid-stream urine specimens and 4 (8%) isolates from 50 indwelling urinary catheters.

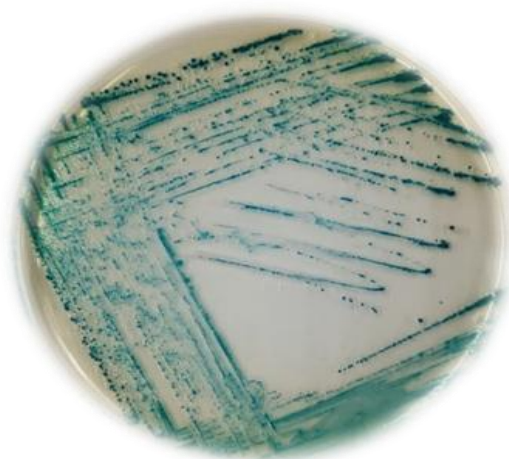


Figure (1): Growth of *Serratiamarcescens* on CHROMagarSerratia after incubation at 37°C for 24 hrs.

Biofilm formation by *Serratiamarcescens*

Biofilm was produced by all twenty-three *S. marcescens* isolates. Nevertheless, a one-way ANOVA revealed substantial differences ($P < 0.05$) among the biofilms that were

generated. Furthermore, weak and moderate biofilms were produced by 11 and 12 isolates, respectively. None of the isolates was capable of establishing strong biofilm (Figure 2).

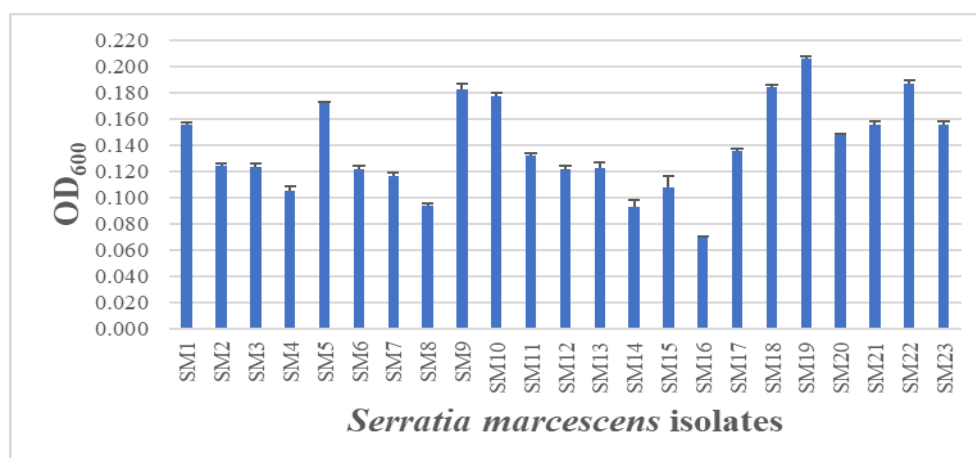


Figure (2): Biofilm formation capacity expressed as OD₆₀₀ of *Serratiamarcescens* isolates. Error bars represent standard deviation. P value = 2.827×10^{-22} , $LSD_{0.05} = 0.016$.

Detection of *rplU* gene

The PCR results (Figure 3) showed that *rplU* gene existed in all 23 *S. marcescens* isolates. Markedly, this

result may reflect more accurate detection of molecular diagnosis in comparison with CHROMagar *Serratia*, and VITEK 2 compact system methods.

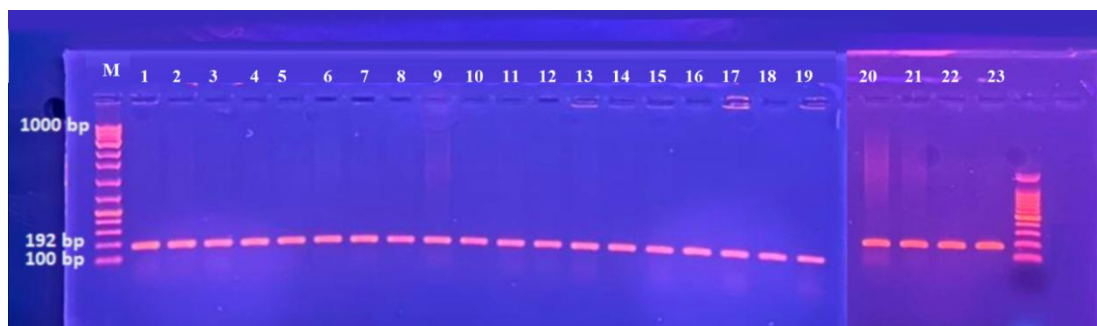


Figure (3): Agarose gel electrophoresis of PCR products using 1.5% at 10 V/cm for 1hr. M:100 bp DNA ladder. Lanes: 1-23 PCR product of *rplU* gene (192bp).

Discussion

A previous recent study has established the pathogenic nature of uropathogenic *Serratia marcescens* in causing urinary tract infections (UTIs) (19). *S. marcescens*, has now been acknowledged as a frequent cause of nosocomial extra-intestinal infection (20). *S. marcescens*'s infectious dose can fluctuate based on the individual's susceptibility who is infected. Nevertheless, it's generally believed that a relatively low number of *S. marcescens* can be sufficient to cause an infection in a healthy individual (21). Fever, diarrhea, chills, and abdominal cramps are potential symptoms of *S. marcescens* infection (22). Regardless of the reservoir, the primary method of *S. marcescens* infection transmission is believed to be direct contact between hospital personnel, as evidenced by the relatively widespread distribution of the bacterium among patients with a variety of clinical presentations (23).

Twenty-three isolates of *S. marcescens* (out of 150 clinical specimens) were detected and confirmed using CHROMagar *Serratia* (Figure 1), which agreed with a previous study by Hatem (12, 13); which identified 27 out of 101

isolates as *S. marcescens* through CHROMagar culturing. The highest percentage of isolation rate was 16 (59.26%) from urine, 8 (29.63%) from blood, 2 (7.41%) from the burn, and one isolate (3.70%) from the wound. The identification of *S. marcescens* in this study was confirmed using the VITEK-2 compact system. In which the identification is in agreement with research carried out by Dhaife and Al-Attar (24) documented that from the 120 obtained specimens, four isolates were identified as *S. marcescens* using the VITEK-2 compact system.

Moreover, the present study isolated *S. marcescens* from UTI patients and hospitalized patients with indwelling urinary catheters. Based on the current results, *S. marcescens* isolation from mid-stream urine specimens was higher than those from indwelling catheter-patients. This is in accordance with Potrus (25), Sabaa *et al.* (26), and Al-azzawiet *et al.* (27), who all isolated *S. marcescens* from clinical samples in Baghdad, Iraq. Recently, Salim *et al.* (28) documented that 16, 2, and 1 isolates of *S. marcescens* were isolated from UTI, wound infections, and respiratory tract infections, respectively.

The present study confirms the importance of biofilm as an important virulence factor that characterizes *S. marcescens* clinical isolates causing UTI. Through a signal-mediated QS mechanism, *S. marcescens* produces biofilm and releases a variety of virulence factors (29). This research assessed biofilm formation and it shows *S. marcescens*'s ability to detect biofilm formation using a microtiter plate. The precise mechanism by which *S. marcescens* attaches to both (biotic and abiotic surfaces) remains unknown, despite the extensive understanding of its ability to adhere to various substrates (30).

The current results found that 11 and 12 isolates produced weak and moderate biofilms, respectively. While none was biofilm non-producer. These data are similar to a recent study conducted by Al-Fayyadh *et al.* (15), as they indicated that fifteen and thirty-five isolates, respectively were weak and moderate biofilm-former. None of which were strong biofilm-forming. Recently, Salim (28) demonstrated that 18 *S. marcescens* isolates had 100% biofilm production, with 16 (88.88%) isolates producing weak biofilm and 2 (11.11%) isolates forming moderate biofilms.

All the twenty-three *S. marcescens* isolated in this research detect the presence of the housekeeping gene (*rplU*). Similarly, Al-Fayyadh (15) conducted research that utilized the *rplU* gene as a housekeeping gene. A fragment of *rplU* gene was detected in all 50 (16.3%) *S. marcescens* isolates from 350 specimens. Commonly, housekeeping genes (HKG) are characterized as "essential for cellular existence regardless of their specific function in the tissue or organism" and "stably expressed irrespective of tissue type,

developmental stage, cell cycle state, or external signal." (31). HKG are genes that are ubiquitously expressed in all tissue compartments and cell types, irrespective of their developmental stage, physiological condition, and exposure to external stimuli (32). HKG genes are frequently employed as reference genes in gene expression studies to normalize the expression levels of target genes, as they are essential for the maintenance of basic cellular functions. The internal control was established as the *rplU* gene of *S. marcescens* (33, 34). The internal reference gene was *rplU*, and the calibrator was wild-type cells (35).

Exposure to medical interventions, protracted hospitalization, compromised clinical conditions of patients, and increased frequency and intensity of direct contact with healthcare personnel are all factors that influence the opportunistic nature of this bacterium. The importance of meticulous surveillance and preventative measures to mitigate the transmission of this pathogen is underscored by the heightened vulnerability of patients to *S. marcescens* infections in healthcare environments (36). *S. marcescens* produces biofilms that are distinct from those generated by other conventional bacteria that form biofilm, including *E. coli* and *P. aeruginosa*, in which undifferentiated cells are arranged in microcolonies (37). This pathogen is implicated in (2.5–7.7) % of catheter-associated infections, including central line-associated bloodstream infections and catheter-associated UTI. The formation of biofilms is facilitated by the survival advantage that bacterial colonization of catheters provides (38).

Ultimately, it can be stated that QS is an established mechanism in pathogenic and opportunistic bacteria that modulates biofilm, motility, secreted

toxins, enzymes, and different virulence determinants. Because there is little constraint on bacterial growth, targeting bacterial pathogenicity was much less likely to produce resistance. Alternatively, virulence suppression weakens pathogens and improves the immune system's capacity to destroy them (2).

Conclusion

The results indicated that *S. marcescens* isolates collected from patients with catheter-associated infections and urinary tract infections demonstrate a substantial capacity for biofilm formation. The extensive dissemination of a highly genotoxic strain in urinary tract infections in Iraq is a significant indication of the occurrence of biofilm from isolates. This specific strain has the potential to lead to the development of urinary tract infections. Nevertheless, additional research is necessary to restrict the capacity of *S. marcescens* to form biofilms.

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