

### 3 Molecular Detection of *SpnI/SpnR* and AHL-Mediated Quorum Sensing Signals Genes in *Serratia Marcescens*

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#### ABSTRACT

Quorum sensing process, bacteria connect with each other using secreted chemical signaling molecules called autoinducers. a quorum-sensing signaling molecule suggested to be involved in related species communication. Twelve isolates *Serratia marcescens* were collected from Baghdad hospitals. Of the 12 *S. marcescens* isolates examined, only 8 (66.66%) produced prodigiosin pigment. This work describes a high frequency of isolation of pigmented *S. marcescens* from clinical specimens, indicating that pigmented strains become clinically significant. The antibiotic sensitivity test showed multi drug resistant against (8- 18) antibiotics, all isolates were resistant (%100) against Beta lactam group, an indication of the comprehensive resistance to beta-lactam antibiotics, as a result of the irresponsible use of these antibiotics, which made them lose the effective therapeutic role that they previously required. In another hand *S. marcescens* 100% sensitive for to Meropenem and Imipenem and varied in their response to other antibiotics used in this study. The results showed a different distribution in *S. marcescens* (*AI-2 kinase*, *Tsq*, *rpoS* and *SpnI/SpnR*) genes. Eleven out of (92%) isolates namely were negative for *AI-2 kinase* gene, while (100%) 12/12 isolates observed positive for *Tsq* gene. 1\12 (8%) were positive for the presence of *rpoS* gene, whereas 12/12 isolates were positive, *spnI/spnR* gene was found with the highest percentage ratio (100%) when only one isolate were harboring all sets of genes. Our study suggested that expression of *spnI/spnR* by *S. marcescens* is independent of AHL signals synthesis.

**Key words:** *Serratia marcescens*, Quorum sensing, *AI-2 kinase*, *Tsq*, *rpoS* and *SpnI/SpnR*

#### INTRODUCTION

*Serratia marcescens* is a Gram-negative bacterium that causes infections in many organisms including humans [1]. There are two types of *Serratia marcescens*; pigmented (red) and non pigmented (white) strains, Pigmented *Serratia marcescens* strains have been shown to cause infections in much less frequency than non-pigmented strains, thus reducing the risk of infection during mass production of pigment [2].The ability of *S. marcescens* to adapt to and survive in both hostile and changing environments also relates to the bacterial capacity to express a wide range of secreted enzymes, including lipases, phospholipases, chitinases, proteases, and nucleases [3].*S. marcescens* is able to develop biofilm associated with either

biotic or abiotic surfaces [4]. This ability is associated with the capacity of *Serratia* to colonize and persist in medical devices, such as catheters or prostheses [5], and to enhance bacterial resistance to antibiotics [6]. The treatment of infections caused by some strains of *Serratia marcescens* infections is problematic due to its high resistance to many antibiotics including  $\beta$ -lactam, aminoglycosides in addition to fluoroquinolone antibiotics [7].

*S. marcescens* utilizes the quorum sensing (QS) system to regulate the production of prodigiosin pigment, virulence factors such as proteases, lipase, nuclease and hemolysin in addition to swimming and swarming motilities and biofilm formation [3]. In *Serratia marcescens*, Smal/SmaR is the main type of Q.S signals in [8]. *Serratia* strains utilize AHLs like C4-homoserine lactone (C4-HSL), and C6-HSL to manage the expression of genes encoding virulence and biofilm formation and play important role in the increasing of antibiotic resistance of the bacteria [9]. *Serratia marcescens* may also use spnI/spnR as alternative system for Q.S instead of smal/smaR system, The SpnI/R system regulates flagellum-independent population surface migration (sliding) and synthesis of biosurfactant, prodigiosin, and nuclease in *S. marcescens* [10]. Many genes also play vital role in the process of signal transduction in *S. marcescens* including Lsrk, TsqA and rpoS. Therefore, this study aims to investigation of Quorum sensing genes and AHL-mediated quorum sensing signals genes, in the other hand study their correlation with *S. marcescens* pathogenesis.

## Material and Methods

**Bacterial isolates.** The study was performed with *S. marcescens* isolates that had been recovered from the four hospitals in Baghdad. Of the 12 isolates of the organism identified over the whole period, from 1st October 2019 – 1 st March 2020 were maintained and included in the present analysis. Presumptive Identification was made by determination of DNase on DNase-test medium , Nutrient agar, and MacConkey agar (Himedia, India), microscopic examination after Gram staining, and biochemical tests according to the manufacturer's recommendations. Bacteria were stored at  $-4^{\circ}\text{C}$  in aliquots of 1.5 ml brain heart infusion broth (Biolife, Italy) containing 15% glycerol (as stock culture).

**Biofilms assay.** The test was done by using congo red agar test, it was prepared by Suspending 47 g of BHIA in 1000 ml of distilled water with 0.08% (w/v) Congo red supplemented with 5% (w/v) sucrose. It is Recommended for detection of biofilm formation [11]

**Antimicrobial agents.** Antibacterial susceptibility of *S. marcescens* was tested on Mueller-Hinton agar by the disk diffusion method according Patel *et al* (2017)[12]. The following antibiotic used are obtained from Mast disc Company, UK: Meropenem, Imipenem, Ceftazidime, Gentamicin, Amikacin, Netilmicin, Tetracycline, Doxycyclin, Ciprofloxacin, Levofloxacin, Ampicillin, Amoxicillin, Amoxicillin/clavulenic acid, Ampicillin/Salbutum, Cefixime,

Ceftriaxone, Cefotaxime, Cefepime, Sulfamethoxazol\Trimethoprim, Colistin and compared the result with standard according to CLSI (2020). Each isolate was tested on three separate occasions.

**DNA extraction of *S.marcescens* isolates.** The DNA *S. marcescens* was extracted by using boiling method, in this method two colonies of overnight growth bacteria were used. The colonies were put in a test tube containing one ml of distilled water and boiled for 10 minutes in a water bath, and then were centrifuged for five minutes at 1000 rpm. Five microliters of the supernatant were used for the PCR [13].

**Protocol of gene amplification.** Conventional PCR technique was carried out to amplify of *spnI/spnR*, *AI-2 kinase*, *TsqA* and *rpoS* genes ,(Table; 1) . Each PCR mixture consisted of 12.5 µl of master mix, 1µl of each forward and reverse primer, 5.5 µl of extracted DNA and 5 µl of deionized water to reach 25 µl as a total volume, and then the PCR mixture was transported to a thermal cycler. We used gradient PCR to all genes to reach the optimum temperature for annealing at temperature degree ranging from 51 C to 63 C.

**Table (1) primer sequences and the product size for each one.**

Gene ID	Reference	Product Size	Primers sequence (5'→3')	Primers	
NZ_HG3 262231	This study	472 bp	GATTTGCTGCCAGAAGGTGC GAAAGAGCTGCACAACCACG	<i>Primer-1 f</i> <i>Primer-1 r</i>	<i>AI-2 Kinase</i>
NZ_HG3 262231	This study	520 bp	TGGGGTGATCGTCTGGATCT CCGCCGCGATTATCCTTTG	<i>Primer-1 f</i> <i>Primer-1 r</i>	<i>TsqA</i>
[14]	This study	354 bp	AACGGTATTGGCCTTGCCTT TGCCCCTGATGGCGATAACTG	<i>Primer-1 f</i> <i>Primer-1 r</i>	<i>rpoS</i>
AB23486 91	This study	268 bp	CGTCCCATGCAAAGGGAGAT GACTGCAACGGAGCCTGTAT	<i>Primer-9 f</i> <i>Primer-9 r</i>	<i>spnI/spnR</i>

**Agarose Gel Electrophoresis.** Bacterial DNA electrophoresis was accomplished as it is described by Ream *et al.* (2013)[15]

## RESULTES:

### 1.Identification of *S. marcescens* isolates

A total of 12 different clinical sources isolates were collected from patients whom visited as “out-patients” at Baghdad city which were cultured on Nutrient agar,

MacConkey agar and DNase agar. Twelve isolates identified as *S.marcescens*, The identification and characterization of the isolates were carried out according to certain morphological, cultural and biochemical tests as described by Brooks *et al* )2001(.

## 2.Antimicrobial susceptibility testing.

The antibiotic sensitivity test was done by using (20) antibiotics, Bacterial isolates showed that *S.maacescens* 100% sensitive for to Meropenem and Imipenem, and showed high levels of resistance by percentage of 100% to ampicillin ,amoxicillin, amoxicillin\clavulenic acid, cefipim, ceftazidime, cefotaxime and doxycycline, it was also have resistance to ampcillin\sabactum, , cefixim, ceftriaxone, ciprofloxacin, levofloxacin ,amikacin, gentamicin netlmicin,tetracycline, and co-trimaxazol by percentage 33%, 66%, 58%, 8%, 8%, 8%, 33%, 25%, 41%, 41% respectively. Urin isolates showed highest antibiogram resistance than other isolating sources. results revealed that 33.3% and 66.6% were MDR and non-MDR of total isolates respectively. Figure 1.

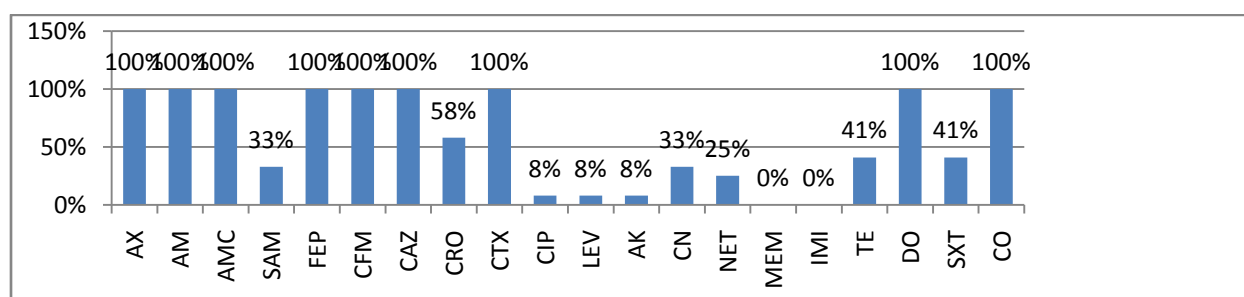
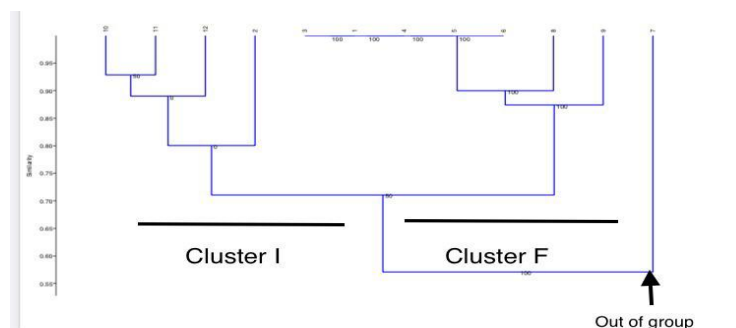


Figure (1) Antimicrobial resistance of *S. marcescens* isolates.

**3.Biofilm assay.** Results obtained by Congo red agar method in this study showed that 59% of *S.marcescens* isolates had the ability to produce biofilms.

**4.Antibiogram typing.** According to dendrogram in the figure (2), we classified 12 isolates of *S.marcescens* into two cluster I and F , only one isolate S7 was consider out of the group. The cluster I classified into three group A, B and cluster F contain only one group C according data of antimicrobial sensitivity test. The group A isolates were characterized by high resistance to Gentamicin, ,Tetracycline, Sulfamethoxazol\Trimethoprim and Colistin. group B isolates characterized by highly resistance to Ampicillin, Amoxicillin, Amoxicillin/clavulenic acid and Cefixime.. The group C were characterized by resistance to Ceftazidime, Cefotaxime, Cefepime and Amoxicillin. The out group isolate name S7 was extremely drug resistant (XDR) highly resistance to all types of antibiotics except meropeneme and imipeneme.

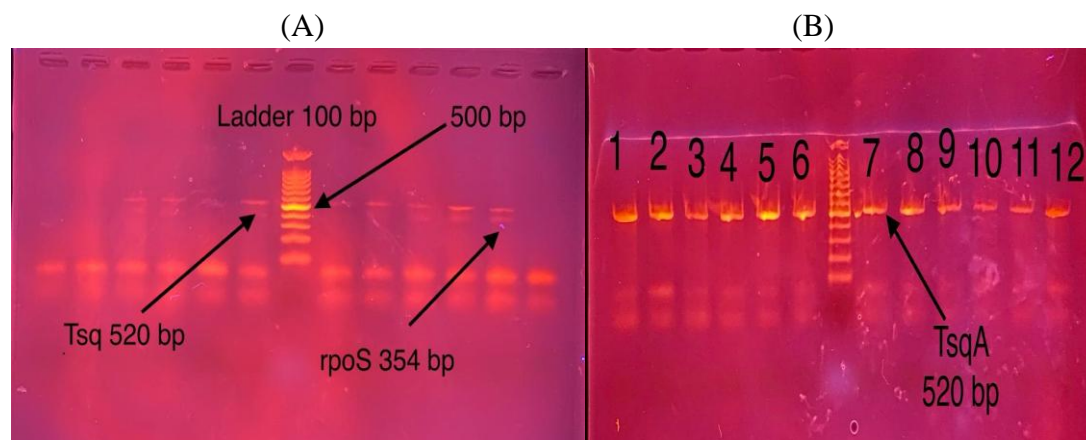


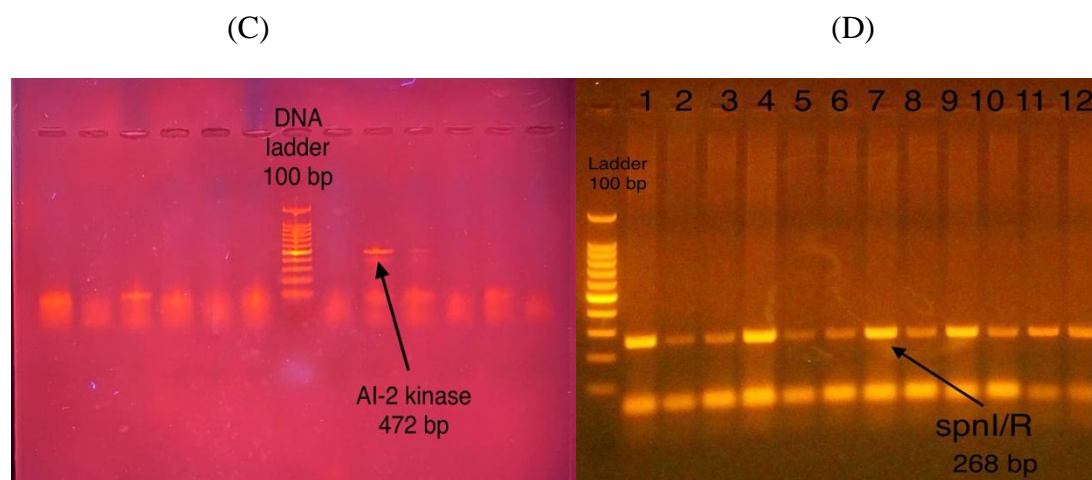
**Figure (2) Dendrogram analysis according to antibiogram data**

**5.Detection of some quorum sensing genes in *S.marcescens* by PCR.** The results showed a different distribution in *S. marcescens* (*AI-2 kinase*, *Tsq*, *rpoS* and *SpnI/SpnR* genes) (Table; 2). Eleven out of (92%) isolates namely were negative for *AI-2 kinase* gene, while (100%) 12/12 isolates observed positive for *Tsq* gene. 1\12 (8%) were positive for the presence of *rpoS* gene, whereas 12/12 isolates were positive, *spnI/spnR* gene was found with the highest percentage ratio (100%) when only one isolate were harboring all sets of genes.

**Table (2): The percentage and number of *S. marcescens* isolates positive for the presence of screened AHL- mediated quorum sensing and QS genes.**

QS genes	NO. of isolates	percentage
Autoinducer- kinase	1	(8%)
TsqA	12	(100%)
rpoS	1	(8%)
spnI/spnR	12	(100%)
spnI/spnR, AI-2 kinase , rpoS and TsqA	1	8(%)





**Figure (3)**Agaros gel electrophoresis 1% for for (A)Tsqa 520 bp and rpoS 354 bp, (B) Tsqa 520 bp (C), AI-2 kinase 472 bp, (D) spnI/spnR 268 bp of *Serratia marcescens* compared with (100 bp) DNA ladder lane.

## DISCUSSION :

*S. marcescens* isolates grown on MacConkey agar appeared pale color result from non-lactose fermentation in the medium [16]. *Serratia marcescens* have ability to produce red non-soluble pigment which is called Prodigiosin which differ from lactose fermentation colonies on MacConkey agar. , in the same manner Srimathi *et al* (2017) [17] mentioned that non- lactose fermenting is the reason where *S. marcescens* appeared in yellow color on the MacConkey agar. *S. marcescens* isolates differ in their ability to produce Prodigiosin pigment on nutrient agar medium at different temperatures, 6(50% ) of the isolates were pigment producers at both of 28 and 37 °C, while 6( 50% ) of *S. marcescens* isolates were non pigment producers at same temperatures. Similar results were obtained by other researchers, a study by Ali *et al* (2008) [18]noticed that their *S. marcescens* isolates had the ability to produce prodigiosin at 30°C and the rate was reduced as the temperature increases, Arivizhivendhan *et al* (2015) [19] Noticed most *S. marcescens* demonstrated the ability to prodigiosin production at 29 C. *S.marcescens* was positive for DNAase activity , and have been changed the colour from blue to pink purple around the growth , in the same line Ryan and Ray (2004) reported that DNase production is associated to *Serratia marcescens* identification further more considered major virulence factor of these bacteria.

From the study results, *S.marcescens* showed that 59% of isolates had the ability to produce biofilms, at the same line Bronowskil *et al*, (2014) [20] showed the common strategies for bacterial survival in hard environment conditions, is the biofilm production , Amorim *et al* (2018) [21] have been indicated that (85%) of *S. marcescens* isolates produced biofilm, appearing as black colonies, while non-producing isolates have become depigmented or red.

In our results noticed that *S. marcescens* isolates were isolated from patients were mixed between Prodigiosin and non Prodigiosin producer, these results came partially agree with Ali *et al* (2013) [22], which showed the *S. marcescens* frequently linked with hospitalized patients this reflects the ability as opportunistic pathogen. In this manner Alsakini *et al* (2020) [23] make out Non-pigmented *S. marcescens* is a main cause of infection in hospitals.

The antibiotics of the carbapenem group (Meropenem and imipenem) still maintain their therapeutic efficacy for *S. marcescens*, sensitivity of *S. marcescens* to Meropenem and Imipenem are 100% While the resistance to other antibiotics were high which make it useless for treating the infection figure (1). This finding is in agreement with the conclusion mentioned in studies in local, nearby and foreign countries. In study conducted in Saudi Arabia found out that all their (81) *S. marcescens* clinical isolates were susceptible to Meropenem and Imipenem (Faida *et al.*, 2015) [24] in another study by Moradigaravand *et al.*, (2016) [25] had found out that, their majority of multidrug resistant *S. marcescens* were susceptible to Imipenem.

characterized by high level of resistance to beta-lactam group of antibiotics penicillins and cephalosporins, in the same manner, many research found to confirm this finding about *S. marcescens* to penicillin, Amoxicillin, Amoxicillin plus clavulenic acid, , Ceftazidime, cefixime , Cefotaxime and ceftriaxone [25,26,27,28,29].

The resistance of *S. marcescens* isolates to fluoroquinolone (Ciprofloxacin and Levofloxacin) was only 8%, Our results close to the result obtained by Sethuraman *et al.*, (2011) [30] when their clinical *S. marcescens* isolates (100%) were all sensitive to ciprofloxacin and levofloxacin. The resistance to aminoglycoside antibiotics were variable. In the same context Şimşek (2019) [31] found the resistance of *S. marcescens* isolates to Amikacin was only 6.3% and this results are close to our result, he also reported that only 17 out of 185 isolates of *S. marcescens* from various clinical specimens were resistant to Netilmicin, while Ogba *et al.*, (2014) mentioned that only 32% of their *S. marcescens* isolates were resistant to Gentamicin.

In study by Fusté *et al.*, (2012) conducted in Spain indicated that all of their clinical and environmental *S. marcescens* isolates were resistant to Tetracycline, in another study by Alexandre *et al*, (2019) revealed that their isolates of *S. marcescens* had intermediate resistance to Doxycycline.

Bitew *et al.*, (2018) revealed that their *S. marcescens* isolates from wound infection were 50% sensitive to Trimethoprim/Sulfamethoxazole, their result agree with the result obtained in our study.

All isolates of *S. marcescens* were resistant to Colistin 100%. In study conducted by Abdellatif Daoudi *et al*, 2019 they mentioned that all of collected clinical isolates of *S. marcescens* were resistant to Colistin.

Our study suggested that AHL signals synthesis by *S. marcescens* is not dependent

on *spnR* expression, as we noticed only one isolate produce AHLs while all study isolates were positive for *SpnI/SpnR*. In the same line Horng and his colleague (2002) [32] find *spnI* transcripts level detected was not affected by the presence or absence of multicopy *spnR*, confirming that AHL synthesis independent of *spnR*. The information presented here suggest that *SpnR* is probably to form DNA-binding dimers in the lack of AHL, that suggest that *SpnR* can act as an stimulator of *spnR* gene expression. Same regard Horng and his colleague (2002) predict that *SpnR* stimulate its own expression by reacting with this lux box-like element. lux box-like sequence is not found in *spnI* promoter region, so it appears reasonable that, *spnI* expression not regulate by *SpnR*. A similar case is noticed in *P. stewartii* (von Bodman *et al.*, 1998) where the expression of both *esaR* and *cps* operons repressed by *EsaR*, in which the elements of lux box-like are all existing at the -10 region, suppressing access for transcription [33].

The exchange of extracellular signaling molecules must be mediated by specific transporters, some involved in molecular uptake, others catalyzing efflux, *TsqA* is a membrane-spanning protein that is conserved in many bacteria needed for transportation of AI-2 and have great effect on Q.S process [34]. Walters *et al* (2006) [35] reported the reason for presence of *TsqA* in all isolates is the vital role that it play in signal transduction in by mediating the exportation of AI-2 molecules.

In the same context Herzberg *et al* (2006) [36] revealed that *TsqA* was shown to control biofilm and It influences resistance to several antimicrobials, including crystal violet and streptomycin, Deletion of *TsqA* caused 31% of the bacterial chromosome to be differentially expressed in biofilms.

The other gene determined by this study and have a big influence on survival of the bacteria in harsh environment are *RpoS*, known to play an important role in the adaptation of the cell to general stresses such as carbon starvation, high temperature and oxidative stress [37]. The gene was detected in one isolate and the reason for this result are the absence of the plasmid containing the gene since it's portable on plasmid the differences in gene sequence from the registered sequences, as well as the or the mutations which can happened in the downstream region of the gene [38].

In compatibility with this results Naba'a *et al* 2018 [14] reviewed that in pathogenic bacteria, the gene *rpoS* involved in some virulence genes controlling to enable those bacteria to resist harsh environments given by the host which lead to many genes controlling that involved in maintenance of cellular viability in stationary phase like hyper-osmolality, oxidative stress, , reduced PH and starvation.

The information presented in this study clearly indicated that different isolates of the same organism may employ distinct negative or positive Q.S circuits to regulate the different or same traits. These results reflected that *Serratia* possess complicated quorum-sensing circuits.

The most frequent genes were *spnI/spnR* and *TsqA* appeared in 12 isolates, one of these



isolates have the full set of genes. According to phenotypic characters, we noticed that the isolate produced pigment prodigiosin in higher level than other isolates in the study, as well as, the isolate also expressed all of virulence factors were tested for e.g. DNase, and biofilm produced in much high manner when compared to other isolates. The resistance profile of the the same isolate was distinctive, it proved that most of the tested 20 antibiotics are ineffective for its eradication, only meropeneme and imipeneme were effective to get rid of it

## CONCLUSION:

The study pointed that AHL signals synthesis by *S. marcescens* is not dependent on *spnR* expression and the presence of the full set of genes is necessary for optimum operation of Q.S system in *S. marcescens*. These results reflected that *Serratia* possess complicated Q.S circuits, as well as, the production of prodigiosin and virulence factors are under control of more than one system of Q.S in *S. marcescens*

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