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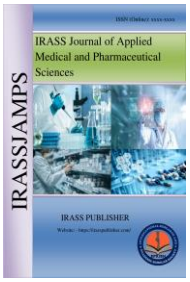

Bacteriology Identification of Quorum Sensing Genes in Serratia SSP

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Abstract: Cell-to-cell communication is exploited by a wide range of bacteria in order to monitor the density of their population, synchronize their behavior, and participate in social contact with one another. In the end, coordinated gene regulation will develop as a consequence of this mode of communication, which is more popularly known as quorum sensing. Acylated homoserine lactones, also known as AHLs, are the quorum signal molecules that are found in gram-negative bacteria the majority of the time. Alternative low-molecular-mass signaling molecules, such as Autoinducer-2 (AI-2), have also been reported. Nevertheless, these molecules have been reported. AHL-regulated Serratia phenotypes are diverse, biologically and ecologically important, and often braided with other global regulators. This is because AHLs are responsible for interacting with other global regulators. The reason for this is because AHLs are the ones that are in charge of controlling these actions. Additionally, AHL- and AI-2-mediated mechanisms, which have been explored to a lesser extent, are continuously being identified and researched when it comes to Serratia species. There are a lot of these systems that offer fascinating variations on the primary content. The goal of this review is to concentrate on the quorum sensing systems that are now known to exist in Serratia species, including the major nosocomial pathogen Serratia marcescens. This review will be conducted in order to achieve this conclusion.

Keywords: Quorum Sensing Genes in Serratia SSP.

1. Introduction

Bacteria are not solitary, as scientists from all over the globe have learned in the last several decades, and cell-cell communication influences the behaviour of individuals, populations, and communities. "Words" those bacteria create and release are little molecules that can communicate with other cells and get responses. Bacteria employ a chemical language called quorum sensing to communicate with one another (Mukherjee and Bassler, 2019).

When a single bacterium releases a low-molecular-mass signaling molecule, the extracellular concentration drops below a particular threshold. This is the fundamental notion that underpins the communication that occurs between cells. When, on the other hand, the cell density reaches a certain concentration, the signaling molecule may be detected, and the bacteria are able to react to (Pena et al., 2019b). Numerous chemical categories have been assigned to the chemicals that are responsible for bacterial signaling. N-acyl-homoserine lactones, also known as AHLs, are utilized by the vast majority of gram-negative quorum sensors as

signaling molecules(Abisado et al., 2018). Furthermore, other signalling molecules are produced by certain gram-negative bacteria. For example, Pseudomonas aeruginosa produces diketopiperazines and 2-heptyl-3-hydroxy-4-quinolone (PQS) (Azimi et al., 2020), while the plant pathogen Ralstonia solanacearum produces 3OH palmitic acid methyl ester (3OH PAME). According to Defoirdt (2018) gram-positive bacteria frequently use amino acids and brief peptides that have been post-translated to regulate genes depending on the density of their cells. The g-butyrolactones used by actinomycetes are also structurally comparable to AHLs. A new form of communication utilised by both gram-negative and gram-positive bacteria has been proposed as autoinducer-2 (AI-2), which was initially found in Vibrio harveyi (Abisado et al., 2018).

Gram-positive and gram-negative bacteria' quorum sensing mechanisms regulate biofilm formation, Ti plasmid conjugation, and antibiotic synthesis (Mukherjee and Bassler, 2019) additionally noted Streptococcus pneumoniae expertise. Quorum sensing in Serratia marcescens, a nosocomial pathogen, has been extensively studied. This review shows the complexity of quorum sensing and the variety of signalling molecules and target genes in Serratia strains (Abisado et al., 2018).

2. The Serratia Genus

Italian chemist Bartolomeo Bizio was motivated to investigate a phenomenon in 1819 after it caused widespread consternation and mystery due to an extraordinary reddish-brown stain in polenta (corn mush). In a letter he sent to the renowned priest Angelo Bellani in 1823, he detailed the occurrence and the linked organism's unique traits. The culprit was a microbe that Bizio dubbed *Serratia marcescens*. The name was chosen to honour *Serafino Serrati*, an Italian physicist whom Bizio thought had a claim on the steamboat invention ahead of time. Marcescens comes from the Latin word for decay, which Bizio thought was appropriate given how rapidly the blood pigment deteriorated (Mukherjee and Bassler, 2019).

This rod-shaped bacterium belongs to the gram-negative Serratia genus. As of this writing, the following species are known to belong to this family: Serratia entomophila, S., which measures 0.9-2 mm in length and 0.5-0.8 mm in diameter. fungal, S. Santos, Fonticola. grimesii, S.I. slippery feet, *S. scutellaria, O. aromatica, sp. plantae, S. salamanders, S. scavengers*, S. as well as (Pena et al., 2019a) found ureilytica. Even if Serratia spp. are able to move around with the use of peritrichous flagella, and they are chemoorganotrophic bacteria that can use both aerobic and anaerobic metabolism. Serratia spp. are found all over the place, whether it's in the dirt, water, or on the surfaces of plants. are often found in raw food ingredients and can lead to food deterioration. As opportunistic pathogens, they can cause food poisoning and can colonise many different surfaces in the digestive systems of animals and humans.

3. The N -acyl-L-homoserine lactones

According to Asfour (2018a), the marine symbiotic bacterium Vibrio fischeri was one of the earliest known bacterial communication systems. This particular bacterium can either live independently in the water at low densities or form symbiotic relationships with fish and squid. The presence of a quorum sensing system dependent on AHL is associated with the bacterial luminescence, which occurs only under the later conditions. This system, which has become a model for quorum sensing in gram-negative bacteria, comprises two key proteins: the I protein, which is similar to LuxI of Vibrio fischeri, and the R protein, which is similar to LuxR. The R protein activates transcription and processes, while the I protein synthesizes N-acyl-L-homoserine lactone (AHL) signaling molecules (Defoirdt, 2018). The basal level of AHL synthesis occurs at low cell densities, and newly synthesized AHLs exit the cell through active transport by antibiotic export pumps or diffusion across the cell membrane. A higher concentration of intracellular AHL results from a higher influx of AHL, which in turn is caused by an increase in the population and the concentration of AHL outside of cells. When AHL attaches to the transcriptional regulatory R protein, it activates the protein. Then, the complex binds to certain sequences in DNA promoter regions, which cause downstream target genes to be expressed. Autoinduction of AHL synthesis occurs in many systems when the quantity of AHL reaches a particular threshold, leading to an upregulation of transcription of the I gene, which is a target gene for the R protein (Azimi et al., 2020).

4. Synthases of LuxI-type AHLs and concurrent AHLs

The literature says AHLs are SAM and acyl-ACP. A two-substratum, three-product reaction is suggested. AHL synthase releases ACP from SAM and acyl-ACP. The acyl group from acyl-ACP is then transferred to the amine of SAM. After then, methylthioadenosine (MTA) and the AHL molecule are released (Zhao et al., 2020). These processes make unique use of acyl-ACP and SAM, which are typically utilized in lipid biosynthesis and SAM as a methyl donor, respectively. A wide range of acyl chain lengths (from 4 to 18 carbons), oxidation states at the C3 position, and saturation levels are produced by AHLs produced by various bacterial species' I protein. AHLs and production patterns vary among Serratia species, showing the diversity and specificity of quorum sensing signal molecules and regulation in this genus (Asfour, 2018b). AHLs from various Serratia species are included in Table 1. either by mass spectrometry (MS) or targeted bioassays using thin-layer chromatography (TLC) analysis and an agar overlay containing a reporter bacterium with a mutation that prevents it from producing AHL molecules but which contains an AHL-responsive reporter gene. The chemical most frequently found in Serratia sp. is nhexanoyl-L-homoserine lactone (C6-HSL). M. ATCC 39006, L. types marcescens MG1, 12, and SS-1, S. strains of plymuthica and S. class B proteobacteria. Aside from

C4-HSL, another common lactone generated by Serratia sp. is 3-oxo-C6-HSL, although N-3-oxo-hexanoyl- L-homoserine lactone is also present. M. ATCC 39006, L. Markerfish strains MG1 and 12, as well as S. by S. plymuthica RVH1. species marcescens SS-1, S. strains of plymuthica and S. class B proteobacteria (Krzyżek, 2019).

AHL production depends on the cellular acyl-ACP pool and AHL synthase (I protein) substrate selectivity. Structural studies of Pantoea stewartii's EsaI and Pseudomonas aeruginosa's LasI show that they both bind the acyl-ACP phosphopantetheine prosthetic group. The AHL synthase EsaI has a hydrophobic pocket that can accommodate an acyl-ACP, but it can't accommodate a longer AHL. In contrast, the tunnel structure of LasI does not seem to limit the length of the acyl chain. (Azimi et al., 2020)found that hydrogen bonding to the 3-oxo position of acyl-ACP is dependent on a specific threonine in the acyl-chain binding site. Also, according to Zhao et al. (2020), when looking at AHL synthase sequences and their AHL production profiles, it was found that threonine at that position (which is the same as threonine-140 in EsaI) is associated with 3-oxo-substituted AHLs, unsubstituted AHLs are associated with alanine and glycine, and 3-hydroxy-substituted AHLs are associated with serine. According to (Padder et al., 2018), the AHL-synthases SplI from S. cerevisiae were found to induce the synthesis of the unsubstituted C6-HSL when the threonine-140 residue in EsaI was replaced with alanine. RVH1, S. plymuthica SprI, and IC1270. Bacteria B5a and SpnI from *S. marcescens* encode mostly 3-oxo-substituted AHLs and have a threonine residue at position 140, similar to Pantoea stewartii's EsaI. SmaI and SwrI create AHLs without a 3-oxo substituent and have an alanine residue at position 140, unlike EsaI (Yu et al., 2019). See Table 1 for details.

Table 1. AHL-dependent quorum sensing systems identified in *Serratia* spp

Species	Strain	AHLs	LuxI/LuxR	Regulated phenotypes	Reference
Serratia sp.	ATCC 39006	C4-HSL*, C6-HSL*	SmaI/SmaR	Production of carbapenem, prodigiosin, pectate lyase and cellulase	Thomson *et al.* (2000)
Serratia marcescens	MG1‡	C4-HSL†, C6-HSL†	SwrI/SwrR	Swarming motility; production of serrawattin, protease and S-layer protein; biofilm formation; butanediol fermentation	Eberl *et al.* (1996a, b)
	SS-1	C6-HSL†, 3-oxo-C6-HSL†, C7-HSL†, C8-HSL†	SpnI/SpnR	Sliding motility; production of biosurfactant, prodigiosin and nuclease	Horng *et al.* (2002)
	Strain 12	C4-HSL†, C6-HSL†	SmaI/SmaR	Swarming motility; haemolytic activity; production of caseinase and chitinase; biofilm formation	Coulthurst *et al.* (2006)
Serratia plymuthica	IC1270	3-hydroxy-C6-HSL*, 3-hydroxy-C8-HSL*	SplI/SplR		Ovadis *et al.* (2004)
	RVH1	C4-HSL†, C6-HSL†, 3-oxo-C6-HSL†	SplI/SplR	Production of nuclease, chitinase, protease and antibacterial compound; butanediol fermentation	Van Houdt *et al.* (2007)
Serratia proteamaculans B5a		C6-HSL*, 3-oxo-C6-HSL*	SprI/SprR	Production of lipase, protease and chitinase	Christensen *et al.* (2003)

*,†AHLs were identified by specific bio-assays (*) or by MS (†).
‡*Serratia liquefaciens* MG1 was recently identified as *Serratia marcesens* MG1 (Rice *et al.*, 2005).

5. Serratia phenotypes controlled by AHL

Isolated from liquefied plant tissue, Serratia marcescens MG1 (formerly *S. liquefaciens*) may alternate between swimming and swarming, two types of flagellum-driven motility that are dependent on the viscosity of the growing media. Long, multinucleated, aseptate, hyperflagellated cells with the remarkable ability to float on top of the agar surface are produced during swarming by differentiation. Two important regulators, as shown in Fig1., govern this swarming motion. These genes regulate two distinct pathways, one involved in biosynthesis and the other in development. The complete flagellar hierarchy for enteric bacteria is regulated by the transcriptional regulators FlhD and FlhC. *S. aureus* shows a high degree of homology with the flagellar hierarchy of Escherichia coli. marcescens MG1 (based on data not released by Christensen and Visick (2020).The flhDC mutant strain of S. Because it lacks the ability to synthesise flagella, marcescens MG1 is totally immobile and unable to swim or swarm. However, when the flhDC operon is controlledly expressed, swimming and swarming are both restored. Additionally, it has been shown that swarm cell differentiation in liquid medium can be induced by overexpressing flhDC(Prazdnova et al., 2022). Thus, surface sensing is a key trigger for swarm cell differentiation, and artificially stimulating flhDC expression can circumvent the ordinarily necessary surface contact. *S. cerevisiae* regulates the metabolic route.

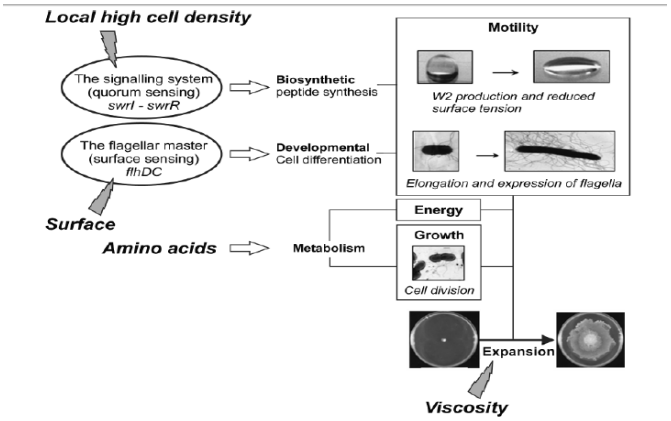

Fig. 1. Swarming motility in *Serratia marcescens* MG1 is controlled by two key regulatory systems (ovals). Inducing stimuli (lightning) point to their respective system. The wide horizontal arrows indicate the pathways targeted by the regulatory systems. The rectangles summarize the biological processes the combined action of which leads to expansion of the colony (adapted with permission from Eberl *et al.*, 1999).

The gene product may produce serrawettin W2, a cyclical lipodepsipentapeptide with a 3-hydroxy-C10 fatty acid side chain. (Fig. 2a). This gene product has been found to have similarities to a large family of complex enzyme complexes responsible for the synthesis of no ribosomal peptides. Figures 2b and c show that water droplets collapse due to the surface tension-reducing effects of this released extracellular lipopeptide. Exogenous addition of C4-HSL to the medium restores surface conditioning and

serrawettin W2 synthesis in a swrI mutant. Furthermore, the swarming phenotype of S bacteria deficient in surfactant can be restored by supplementing the media with pure serrawettin W2. marescens MG1 (swrI mutant and the swrI swrA double mutant) (Fig. 2c), showing that S swarming movement relies on the generation of molecules that reduce the medium's surface tension. MG1 marcescens(Antonioli et al., 2019). The swarming motility of marcescens strain 12 was shown to be reliant on smaI; further research could shed light on whether or not this strain employs the same or different regulators. The capriciousness of S. Even when the ability of the marcescens SS-1 flagellum to swim or swarm is impaired, the bacterium may yet spread quickly on a 0.35% agar Luria-Bertani plate. This movement that does not rely on flagellar movement is called "sliding motility" and is different from swarming movement (Preda and Săndulescu, 2019)

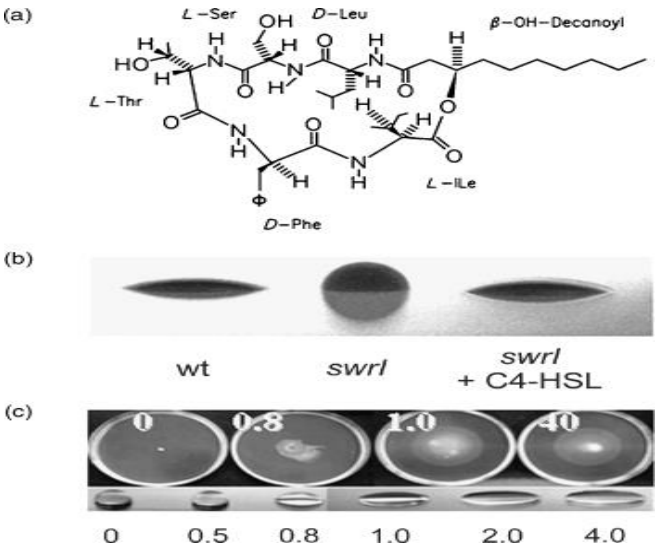

Fig. 2. (a) Symmetry of serrawettin W2 molecules. (b) The impact on water surface tension as shown by side views of cultures using the drop-collapsing test

6. The exo-enzymes and LipB translocation framework

Unrelated proteins like LipA, PrtA, and SlaA must be secreted by marcescens' lipBCD operon. ATP-binding cassette (ABC) protein superfamily transporters with type I secretion include the LipB protein translocation system. These transporters participate in the transportation of a wide range of substances, both into and out of cells. The system consists of three proteins: LipC, an MFP, and lipD, an outer-membrane polypeptide. With S. Markescens MG1 and S. proteamaculans B5a, the quorum sensing system SwrI/SwrR and its associated AHL, C4-HSL, and 3-oxo-C6-HSL, are shown to regulate the lipB gene transcription (Mitra and Das, 2022). S. aureus extracellular PrtA metalloprotease activity is regulated in this way. S. marcescens MG1 and of lipase and protease activities outside of cells. Tripathi et al. (2023) also showed that for S. Fig. 3 shows that the degradation of milk is aided by these quorum sensing-controlled exo-enzymes secreted by the LipB apparatus, which are proteamaculans B5a. Quorum sensing also regulates the generation of chitinase activity. Additional reports have shown that certain serratia strains, such as S. aureus, can produce extracellular enzymes such as protease, chitinase, and hemolytic activity in response to quorum sensing. S. marcescens strain 12 nuclease productions (Kostylev et al., 2019). The synthesis of nuclease, chitinase, and protease in S. marcescens SS-1 was studied by (Prazdnova et al., 2022). Serratia sp. pectate lyase and cellulase synthesis, and Rhizobium plymuthica RVH (Yi et al., 2021). The ATC code is 39006, as reported by (Tian et al., 2021).

7. production of Prodigiosin

Three Serratia species are S. scutellaria, O. Rhododendron, and S. Occasionally, the fungus plymuthica generates prodigiosin, a dark red to light pink colour. Prodigiosin (2-methyl-3-pentyl-6-methoxyprodiginine) has an unusual structure with three pyrrole rings, two of which are directly linked and a third attached by an amethene bridge to produce a pyrryldipyrrylmethene. Prodigiosin, a common secondary metabolite, may contribute to metabolic "overflow" for primary metabolism products, but its physiological relevance in the animals that make it is unclear. However, prior research suggests it may affect dispersion and competitive survival. Ramanathan et al. (2018) found that prodigiosin and its relatives had extraordinarily broad antibacterial, antimalarial, antifungal, and antiprotozoal activity. The immunosuppressive, proapoptotic, and anticancer effects of prodigiosins have been well-documented. There is great hope for the pharmaceutical business in the present result status, which implies that prodigiosin or prodigiosin analogues may be a new class of anticancer medications (Kalia et al., 2019).

8. Production of Antibiotic

The primary focus of this section is 1-carbapen-2-em-3-carboxylic acid, but the antibacterial activity of the secondary metabolite prodigiosin is also discussed earlier. Car, similar to other carbapenem antibiotics, is a potent b-lactam antibiotic that hinders the production of peptidoglycan in the cell walls of bacteria, hence exhibiting a broad range of effectiveness. Carbapenems are characterized by the presence of an unsaturated carbon ring with five members that is connected to the nitrogen and one carbon atom on the b-lactam ring. For more information, refer to the

review of (Antonioli et al., 2019). Streptomyces cattleya and a few gram-negative species, including Erwinia carotovora ssp., have the ability to produce carbapenems. Specifically, this capability is seen in the carotovora group, the photoluminescent TT01 group, and Serratia species. Different from the biosynthesis of penicillin and cephalosporins, the carA-E genes encode biosynthetic enzymes in the second organism that produce car from precursors derived from acetate and glutamate (Tsunetsugu-Yokota et al., 2016). The innate resistance to Car requires CarF and CarG through an as-yet-unknown mechanism, although CarH's role is unclear. Separate from the carA-H operon, the carR gene produces a transcriptional activator that is similar to LuxR (Chung et al., 2016). With E. carbotovora ssp. In carotovora, the LuxI homologue CarI synthesises 3-oxo-C6-HSL, and CarR triggers carA-H expression in response to that concentration of cells. The CarR gene in Serratia sp.

9. Formation of biofilms

Prodigiosin synthesis and quorum sensing, which is released by LipB and is an extracellular enzyme, are essential for normal biofilm growth and complex differentiation in S. Labbate et al. (2004) described marcescens MG1. According to Davenport et al. (2015), biofilms consist of a community of surface-adherent bacterial microcolonies that are encased in exopolymeric substances that the bacteria themselves produce. Corrosion, decreased mass and heat transmission, and other issues can arise when bacterial biofilms in industrial settings transform into biofouling. The development of biofilms on foodstuffs, surfaces that come into touch with them, and water distribution systems poses a threat to the food industry's products by increasing the likelihood of spoiling and the presence of harmful microbial communities. Because they can induce long-lasting infections, the bacteria that form biofilms on medical devices like implants or catheters are a major cause for medical concern (Davenport et al., 2015). In addition, as discussed in (Gohil et al., 2018), a phenotypic shift occurs when planktonic cells differentiate into a complex mature biofilm. This transition has significant ramifications, such as an increase in resistance to antimicrobial drugs and removal by host defences. (Eickhoff and Bassler, 2018)shown the other day that in S. An attachment test to a plastic microtiter plate was used to examine the biofilm formation of marcescens strain 12, and it was found that smaI was the key factor. Investigating the steps involved in biofilm formation and the function of quorum sensing in this context for S. aureus would be an intriguing endeavour. marcescens strain 12, which is almost identical to S. Swarming motility in the marcescens strain MG1 is regulated by quorum sensing in a manner that is dependent on AHL.

10. Butanediol fermentation

It was recently discovered that at least two Serratia species are quorum sensing regulators of 2,3-butanediol fermentation (Jo et al., 2020). The majority of glucose fermentation in the family Enterobacteriaceae occurs in Klebsiella, Serratia, Enterobacter, and several other genera. The mixed acid route is utilised by members of the Escherichia, Salmonella, and Shigella genera, which result in the production of acetate, lactate, succinate, and formate, among other acidic end products, in enormous quantities. The environment becomes highly acidic during mixed acid fermentation, although the butanediol route limits the formation of acidic end-products when a large amount of pyruvate from glycolysis is directed there. Butanediol fermenters are able to avoid fatal acidification as cells approach stationary phase by producing neutral chemicals, which is ecologically relevant (Jung et al., 2017). For both S. strains of plymuthica and S. In the presence of fermentable sugars, early growth arrest occurs when the AHL synthase encoding gene in marcescens MG1 is inactivated. This is because the production of 2,3-butanediol is reduced and acidic end-products are continued to be produced both at the end of the exponential and throughout the stationary growth phase. These results could potentially help with metabolic engineering efforts to increase 2,3-butanediol fermentation yields. Worldwide, the demand for 2,3-butanediol is on the rise (by 4-7% every year) for a number of reasons, including its use as a liquid fuel additive and the rising demand for polybutylene terephthalate resin, g-butyrolactone, spandex, and related products (Kim et al., 2019)

11. Quorum sensing integration in intricate networks

Certain phenotypes are not always absolutely regulated by quorum sensing; in fact, phenotypes are frequently subject to multifactor control that integrates information from several physiological signals. See Figure for details. Two important regulators, the flhDC operon and the swr quorum sensing system, govern marcescens MG1. On top of that, the quorum sensing reliant S. When it comes to marcescens MG1, nutritional cues can actually prevent biofilm formation. Kaur et al. (2018) found that MG1 could not swarm in minimum medium supplemented with glucose, regardless of the presence of exogenously supplied AHL signals. In minimal medium that contained 0.05% glucose and 0.05% casamino acids, the swrI mutant produced biofilms that were thin and undifferentiated, in contrast to the parent strain's filamentous biofilm that was made up of cell chains and clusters. However, in 0.1 LB medium, both strains produced biofilms that resembled the architecture of the wild type. In addition, changes in biofilm morphology were shown to be influenced by changes in medium composition. Under nutrient-limiting conditions, a filamentous biofilm type can reversibly transition to a microcolony biofilm,

showcasing how biofilm structures respond to their environment (Jiang et al., 2019). Furthermore, the esterase EstA, which is part of the class II of lipolytic enzymes and is supplied by S, is encoded by the constitutively expressed estA gene, which is situated upstream of swrR. This class is defined by the active-site consensus pattern G-D-S-L, as described by A Zhou et al. (2019). When cells are cultured on specific lipidic substrates, like Tween, marcescens MG1 with the precursors needed for AHL production.

In Serratia sp. In ATCC 39006, a number of environmental factors regulate the production of the secondary metabolites carbapenem and prodigiosin. Using what is likely the same derepressive mechanism, the SmaIR quorum sensing system controls the transcription of pigR, rap, and pigQ, three regulators involved in prodigiosin production. (Ramanathan et al., 2018)found that the transcriptional activators Rap (SlyA/MarR family) and PigQ (a potential response regulator of a GacAS family two-component system PigQW) influence prodigiosin production. A two-component signal transduction system similar to the GacA/GacS cascade controls the production of AHLs in numerous bacteria, including S. aureus and Pseudomonas species. This cascade is a worldwide regulator of gene expression in gram-negative bacteria. IC1270 belonging to the plymuthica plant. However, quorum sensing controls the PigQW system, which in turn does not regulate AHL synthesis (Prescott and Decho, 2020). An emerging family of new regulatory proteins in bacteria, the SlyA/MarR transcriptional regulators are essential controllers of many facets of bacterial physiology on a global scale (Luo et al., 2021).

12. Horizontal gene transfer and threshold sensing

It has been previously established that the capacity and pattern of AHL generation by Serratia strains vary across species and strains (Rémy et al., 2018). In addition, strains of Serratia that do not manufacture AHLs nonetheless exhibit quorum-sensing-regulated phenotypes (Saxena et al., 2019). Interestingly, it was found by Ravindran et al. (2018)that in S. TnTIR is a new transposon in the Tn3 family that contains the spnIR quorum sensing genes from marcescens SS-1. According to Wang et al. (2020), the quorum sensing genes are currently distributed across different bacterial species in large part because of horizontal gene transfer, which is facilitated by placing spnIR on a mobile genetic element. Wu et al. (2020)proved that a full cluster of genes responsible for prodigiosin synthesis could be transferred to the S. cerevisiae strain using phage-mediated horizontal gene transfer. The natural quorum sensing system was able to control prodigiosin synthesis in marcescens strain 12. Further, the smaIR locus of S. can be transferred using phage. strain 12 of marcescens to S. The synthesis of prodigiosin was regulated by the foreign quorum sensing locus in marcescens strain 274, which does not have SmaIR homologues.

13. Amino acid AI-2

In the quorum sensing circuit of the marine bacterium Vibrio harveyi, the AI-2 molecule was initially described as being one of at least three parallel systems that synthesise, detect, and respond to different signalling molecules. Each system controls bioluminescence in its own unique way. The gene products of luxL and luxM do not resemble the LuxI family of AHL synthases mentioned earlier; rather, they are responsible for synthesising HAI-1, an AHL, N-3-hydroxybutanoyl-Lhomoserine lactone. System 3 is similar to Vibrio cholerae system 1 and uses the CAI-1 autoinducer of unknown structure, while AI-2 is a furanosyl borate diester and its synthesis is dependent on luxS. Patel et al. (2023)found that at a specific cell density, cognate sensor histidine kinases begin to convert from kinase mode to phosphatase mode, relaying phosphate to the common response regulator LuxO. According to (Bettenworth et al., 2019), the phosphorylated LuxO and s54 are involved in the activation of sRNA-encoding genes. These sRNAs, along with the RNA chaperone Hfq, destabilise the LuxR mRNA. Despite not being a homologue of V. fischeri's LuxR, this LuxR is the supreme quorum sensing regulator. According to Zhang et al. (2019), V. harveryi is able to assimilate various AI signals because to this communication architecture.

14. Tasks Performed by AI-2 in Serratia

According to reports from thurst (Zhang et al., 2019), luxS is present in Serratia sp. and influences several phenotypes. yeast strain ATCC 39006, S. bacteria S. marcescens ATCC 274 and T. The previous evidence of extracellular AI-2 activity in Serratia strains was confirmed and expanded upon by marcescens strain 12, as previously shown (Van Houdt et al., 2004). As a result, Serratia sp. Samples of ATCC 39006 and S. marcescens ATCC 274 was found to produce carbapenem, prodigiosin, and haemolysin, in that order (Luo et al., 2021). The luxS mutant strain of S. marcescens ATCC 274 showed slightly less pathogenicity in a Caenorhabditis elegans model as well. With S. The absence of AI-2 synthesis in marcescens strain 12 led to a marginal increase in biofilm formation when contrasted with the parent strain. In the case of S. There was no discernible impact on biofilm formation or AHL-regulated phenotypes in plymuthica RVH1 deletion of luxS. Ravindran et al. (2018) found that RVH1 strains with luxS on a multicopy plasmid exhibited reduced growth due to overproduction

of AI-2. These results do not suggest a role for LuxS and AI-2 in cell-cell communication in S, since the signal transduction pathway has not been discovered. rather than implying that the luxS knockout phenotypes seen in other Serratia species are due to plymuthica RVH1. can be a variety of side effects caused by an imbalance in metabolic processes (Zuniga et al., 2017).

15. Discussion

Quorum sensing (QS) mechanisms in bacteria, particularly within the Serratia genus, are complex and multifaceted. This study sheds light on the intricate regulatory networks mediated by QS, primarily through small signaling molecules such as N-acyl-L-homoserine lactones (AHLs) and autoinducer-2 (AI-2). These molecules enable bacteria to coordinate gene expression in response to changes in population density, thereby influencing various phenotypes crucial for bacterial survival and adaptation (Mukherjee and Bassler, 2019).

One notable finding is the diversity of AHLs produced by different Serratia species, indicating a species-specific regulation of QS. For instance, Serratia marcescens MG1 demonstrates swarming and sliding motility, both of which are regulated by AHLs, showcasing the diverse roles of QS in bacterial motility dynamics. Furthermore, AHLs play a significant role in regulating the synthesis of extracellular enzymes such as lipase and protease, which are essential for nutrient acquisition and environmental adaptation. The study also highlights the role of QS in the production of secondary metabolites, including prodigiosin and antibiotics such as 1-carbapen-2-em-3-carboxylic acid. These metabolites exhibit diverse biological activities, including antimicrobial and anticancer properties, indicating the potential of QS-regulated metabolites for biomedical applications (Pena et al., 2019a).

Moreover, QS plays a crucial role in biofilm formation, a key survival strategy for bacteria. By modulating biofilm architecture and resistance to environmental stressors, QS influences the adaptability and persistence of bacterial communities. Understanding the molecular mechanisms underlying biofilm formation could provide insights into strategies for combating biofilm-associated infections (Azimi et al., 2020).

Furthermore, QS interacts with other regulatory pathways, such as nutrient sensing, to modulate bacterial behavior in response to environmental cues. This crosstalk between QS and other signaling pathways underscores the complexity of bacterial regulatory networks and their adaptive significance in diverse ecological niches. Horizontal gene transfer (HGT) emerges as a pivotal mechanism for disseminating QS genes across bacterial species, facilitating the evolution of QS-mediated behaviors. The identification of transposons carrying QS genes highlights the genetic plasticity of bacterial QS systems and their potential for rapid adaptation to changing environments (Zhao et al., 2020).

In conclusion, this study significantly advances our understanding of the multifaceted roles of QS in bacterial physiology and ecology. By elucidating the molecular mechanisms underlying QS-mediated phenotypes, future research can explore the potential applications of QS in biotechnology and medicine (Preda and Săndulescu, 2019).

16. Conclusions

Understanding the physiology of (mixed) bacterial populations is crucial for medical and commercial purposes, and cell-cell communication is now well understood. Thus, understanding communication routes and their formation is crucial. AHL-dependent quorum sensing and AI-2-mediated communication are crucial to biology and ecology. Because Serratia species use both communication systems in intricate neural networks that channel exoenzymes, antibiotic chemicals, and other virulence features. Additionally, additional instances of Serratia spp. cell-cell communication systems, such as AI-2 and AHL-mediated systems, are continually being discovered and researched. These systems are examples. along with many additional species, many of which offer interesting twists on the main idea. Increasing instances of infections caused by Serratia species other than S. The genus Marcescens, which has communication systems, needs more investigation into its physiology, pathogenicity, and classification. This research should also investigate enhanced cell-cell communication disruption methods to prevent or cure illnesses.

References

1. Abisado, R. G., Benomar, S., Klaus, J. R., Dandekar, A. A., & Chandler, J. R. (2018). Bacterial quorum sensing and microbial community interactions. *MBio*, *9*(3), 10-1128.
2. Antonioli, L., Blandizzi, C., Pacher, P., Guilliams, M., & Haskó, G. (2019). Rethinking communication in the immune system: the quorum sensing concept. Trends in immunology, 40(2), 88-97.
3. Asfour, H. Z. (2018). Anti-quorum sensing natural compounds. Journal of microscopy and ultrastructure, 6(1), 1-10.
4. Azimi, S., Klementiev, A. D., Whiteley, M., & Diggle, S. P. (2020). Bacterial quorum sensing during infection. Annual review of Microbiology, 74(1), 201-219.

5. Bettenworth, V., Steinfeld, B., Duin, H., Petersen, K., Streit, W. R., Bischofs, I., & Becker, A. (2019). Phenotypic heterogeneity in bacterial quorum sensing systems. Journal of molecular biology, 431(23), 4530-4546.
6. Christensen, D. G., & Visick, K. L. (2020). Vibrio fischeri: laboratory cultivation, storage, and common phenotypic assays. Current protocols in microbiology, 57(1), e103.
7. Chung, J. H., Song, G. C., & Ryu, C. M. (2016). Sweet scents from good bacteria: case studies on bacterial volatile compounds for plant growth and immunity. Plant Molecular Biology, 90, 677-687.
8. Davenport, P. W., Griffin, J. L., & Welch, M. (2015). Quorum sensing is accompanied by global metabolic changes in the opportunistic human pathogen Pseudomonas aeruginosa. Journal of bacteriology, 197(12), 2072-2082.
9. Defoirdt, T. (2018). Quorum-sensing systems as targets for antivirulence therapy. Trends in microbiology, 26(4), 313-328.
10. Eickhoff, M. J., & Bassler, B. L. (2018). SnapShot: bacterial quorum sensing. Cell, 174(5), 1328-1328.
11. Jiang, Q., Chen, J., Yang, C., Yin, Y., & Yao, K. (2019). Quorum sensing: a prospective therapeutic target for bacterial diseases. BioMed Research International, 2019(1), 2015978.
12. Jo, H., Tagele, S. B., Pham, H. Q., Kim, M. C., Choi, S. D., Kim, M. J., ... & Shin, J. H. (2020). Response of soil bacterial community and pepper plant growth to application of Bacillus thuringiensis KNU-07. Agronomy, 10(4), 551.
13. Jung, B. K., Khan, A. R., Hong, S. J., Park, G. S., Park, Y. J., Park, C. E., ... & Shin, J. H. (2017). Genomic and phenotypic analyses of Serratia fonticola strain GS2: a rhizobacterium isolated from sesame rhizosphere that promotes plant growth and produces N-acyl homoserine lactone. Journal of biotechnology, 241, 158-162.
14. Kalia, V. C., Patel, S. K., Kang, Y. C., & Lee, J. K. (2019). Quorum sensing inhibitors as antipathogens: biotechnological applications. Biotechnology advances, 37(1), 68-90.
15. Kaur, A., Capalash, N., & Sharma, P. (2018). Quorum sensing in thermophiles: prevalence of autoinducer-2 system. BMC microbiology, 18, 1-16.
16. Kim, D., Paggi, J. M., Park, C., Bennett, C., & Salzberg, S. L. (2019). Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. Nature biotechnology, 37(8), 907-915.
17. Kostylev, M., Kim, D. Y., Smalley, N. E., Salukhe, I., Greenberg, E. P., & Dandekar, A. A. (2019). Evolution of the Pseudomonas aeruginosa quorum-sensing hierarchy. Proceedings of the National Academy of Sciences, 116(14), 7027-7032.
18. Krzyżek, P. (2019). Challenges and limitations of anti-quorum sensing therapies. Frontiers in microbiology, 10, 2473.
19. Luo, H. Z., Zhou, J. W., Sun, B., Jiang, H., Tang, S., & Jia, A. Q. (2021). Inhibitory effect of norharmane on Serratia marcescens NJ01 quorum sensing-mediated virulence factors and biofilm formation. Biofouling, 37(2), 145-160.
20. Mitra, B., & Das, A. (2022). Microbes and environment sustainability: An in-depth review on the role of insect gut microbiota in plastic biodegradation. Synergistic Approaches for Bioremediation of Environmental Pollutants: Recent Advances and Challenges, 1-25.
21. Mukherjee, S., & Bassler, B. L. (2019). Bacterial quorum sensing in complex and dynamically changing environments. Nature Reviews Microbiology, 17(6), 371-382.
22. Padder, S. A., Prasad, R., & Shah, A. H. (2018). Quorum sensing: A less known mode of communication among fungi. Microbiological research, 210, 51-58.
23. Patel, R., Soni, M., Soyantar, B., Shivangi, S., Sutariya, S., Saraf, M., & Goswami, D. (2023). A clash of quorum sensing vs quorum sensing inhibitors: an overview and risk of resistance. Archives of Microbiology, 205(4), 107.
24. Pena, R. T., Blasco, L., Ambroa, A., González-Pedrajo, B., Fernández-García, L., López, M., ... & Tomás, M. (2019). Relationship between quorum sensing and secretion systems. Frontiers in microbiology, 10, 1100.
25. Pena, R. T., Blasco, L., Ambroa, A., González-Pedrajo, B., Fernández-García, L., López, M., ... & Tomás, M. (2019). Relationship between quorum sensing and secretion systems. Frontiers in microbiology, 10, 1100.
26. Prazdnova, E. V., Gorovtsov, A. V., Vasilchenko, N. G., Kulikov, M. P., Statsenko, V. N., Bogdanova, A. A., ... & Chikindas, M. L. (2022). Quorum-sensing inhibition by Gram-positive bacteria. Microorganisms, 10(2), 350.
27. Preda, V. G., & Săndulescu, O. (2019). Communication is the key: biofilms, quorum sensing, formation and prevention. Discoveries, 7(3).
28. Prescott, R. D., & Decho, A. W. (2020). Flexibility and adaptability of quorum sensing in nature. Trends in microbiology, 28(6), 436-444.
29. Ramanathan, S., Ravindran, D., Arunachalam, K., & Arumugam, V. R. (2018). Inhibition of quorum sensing-dependent biofilm and virulence genes expression in environmental pathogen Serratia marcescens by petroselinic acid. Antonie Van Leeuwenhoek, 111, 501-515.
30. Ravindran, D., Ramanathan, S., Arunachalam, K., Jeyaraj, G. P., Shunmugiah, K. P., & Arumugam, V. R. (2018). Phytosynthesized silver nanoparticles as antiquorum sensing and antibiofilm agent against the nosocomial pathogen Serratia marcescens: an in vitro study. Journal of applied microbiology, 124(6), 1425-1440.
31. Rémy, B., Mion, S., Plener, L., Elias, M., Chabrière, E., & Daudé, D. (2018). Interference in bacterial quorum sensing: a biopharmaceutical perspective. Frontiers in pharmacology, 9, 203.
32. Tian, X., Ding, H., Ke, W., & Wang, L. (2021). Quorum sensing in fungal species. Annual Review of Microbiology, 75(1), 449-469.

33. Tripathi, S., Purchase, D., Govarthanan, M., Chandra, R., & Yadav, S. (2023). Regulatory and innovative mechanisms of bacterial quorum sensing–mediated pathogenicity: a review. Environmental Monitoring and Assessment, 195(1), 75.
34. Tsunetsugu-Yokota, Y., Kobayahi-Ishihara, M., Wada, Y., Terahara, K., Takeyama, H., Kawana-Tachikawa, A., ... & Meyerhans, A. (2016). Homeostatically maintained resting naive CD4+ T cells resist latent HIV reactivation. Frontiers in Microbiology, 7, 1944.
35. Wang, S., Payne, G. F., & Bentley, W. E. (2020). Quorum sensing communication: molecularly connecting cells, their neighbors, and even devices. Annual review of chemical and biomolecular engineering, 11(1), 447-468.
36. Wu, S., Liu, J., Liu, C., Yang, A., & Qiao, J. (2020). Quorum sensing for population-level control of bacteria and potential therapeutic applications. Cellular and Molecular Life Sciences, 77, 1319-1343.
37. Yi, L., Dong, X., Grenier, D., Wang, K., & Wang, Y. (2021). Research progress of bacterial quorum sensing receptors: Classification, structure, function and characteristics. Science of the Total Environment, 763, 143031.
38. Yu, Z., Yu, D., Mao, Y., Zhang, M., Ding, M., Zhang, J., ... & Yin, J. (2019). Identification and characterization of a LuxI/R-type quorum sensing system in Pseudoalteromonas. Research in microbiology, 170(6-7), 243-255.
39. Zhang, J., Feng, T., Wang, J., Wang, Y., & Zhang, X. H. (2019). The mechanisms and applications of quorum sensing (QS) and quorum quenching (QQ). Journal of Ocean University of China, 18, 1427-1442.
40. Zhao, X., Yu, Z., & Ding, T. (2020). Quorum-sensing regulation of antimicrobial resistance in bacteria. Microorganisms, 8(3), 425.
41. Zhou, J. W., Ruan, L. Y., Chen, H. J., Luo, H. Z., Jiang, H., Wang, J. S., & Jia, A. Q. (2019). Inhibition of quorum sensing and virulence in Serratia marcescens by hordenine. Journal of agricultural and food chemistry, 67(3), 784-795.
42. Zuniga, A., Donoso, R. A., Ruiz, D., Ruz, G. A., & González, B. (2017). Quorum-sensing systems in the plant growth-promoting bacterium Paraburkholderia phytofirmans PsJN exhibit cross-regulation and are involved in biofilm formation. Molecular Plant-Microbe Interactions, 30(7), 557-565.