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REVIEW ARTICLE

Quenching the quorum sensing system: potential antibacterial drug targets

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Abstract

Emergence of antibiotic and multi-drug resistant pathogenic bacteria has created the need for new drugs and drug targets. During pathogenesis bacteria release signals which regulate virulence and pathogenicity related genes. Such bacteria co-ordinate their virulent behaviour in a cell density dependent phenomenon termed as quorum sensing (QS). In contrast, microbes interfere with QS system by quenching the signals, termed quorum quenching (QQ). As a consequence of disrupted QS, pathogens become susceptible to antibiotics and drugs. In this article, the biodiversity of organisms with potential to quench QS signals and the use of QQ molecules as antibacterial drugs have been reviewed.

Keywords: Antibiotics, Bacillus, enzymes, pathogens, signal, virulence

Introduction

In the present era, one of the primary concerns in public health is the emergence and proliferation of multidrug resistant microbial strains (Cars et al. 2008). The magnitude of the problem is enhanced by the rapid genetic changes in microbes which confer resistance even to the most recently developed drugs (Wright 2005; Marris 2006; Sundaramurthy & Pieters 2007; Courvalin 2008). This scenario has forced researchers to look for novel microbes for producing antibiotics (Kalia et al. 2007) or alternatives to manipulate the virulence genes in pathogens, which get expressed through bacterial co-ordination (Rasmussen & Givskov 2006a). Bacteria ensure appropriate and robust coordination by communicating through signal molecules (Chen et al. 2005; Dunny et al. 2008; von Bodman et al. 2008), which are released in a cell-density dependent manner, termed as quorum sensing (QS) (Winzer et al. 2002) (Figure 1). QS is a true cell-to-cell communication behaviour widely observed among prokaryotes (Zhu et al. 2002) not only for interacting among those living in their close proximity (Flannery 2006) but also for making collective decisions (von Bodman et al. 2008). It leads to the expression and regulation of processes which extend beyond the normal cellular responses such as i) bioluminescence, ii) biofilm formation, iii) regulation of virulence genes, iv) antibiotic production, v) nitrogen fixation, vi) conjugal transfer of plasmid DNA, vii) swarming, viii) biocorrosion, ix) spore formation, x) competence, x) fruiting body formation, and so on (Baca-DeLancey et al. 1999; Winans & Bassler 2002; Wisniewski-Dyé & Downie 2002; Zhu et al. 2002; Wright et al. 2004; Waters & Bassler 2005; Chevrot et al. 2006; Dunny et al. 2008; Defoirdt et al. 2010). These biological activities ensure better survival in natural environments, where microbes within a community compete for scarce resources (Chen et al. 2005; Hibbing et al. 2009). In response to these specific survival mechanisms, quite a few bacteria produce bioactive molecules to disturb the QS system by a process termed as quorum quenching (QQ). It primarily attenuates the expression of virulent behaviour in pathogenic bacteria (Chen et al. 2009) without restricting their growth (Manefield et al. 2000; Defoirdt et al. 2006). In the absence of any harsh selective

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Abbreviations

AHL, Acylhomoserine lactone

HSL, Homoserine lactone

C4HSL, N-butanoyl-L-HSL

C6HSL, N-hexanoyl HSL

C7HSL, N-heptanoyl-HL

C8HSL, N-octanoyl HSL

C10HSL, N-decanoyl HSL

C12HSL, N-dodecanoyl HSL

C14HSL, N-tetradecanovl-HSL

C16HSL, N-hexadecanoyl-HSL

30C6HSL, 3-oxo-N-hexanoyl-HSL

30C8HSL, 3-oxo-N-octanoyl-HSL

30C10HSL, 3-oxo-N-decanoyl-HSL

30C12HSL, 3-oxo-N-dodecanoyl-HSL

30C14HSL, 3-oxo-N-tetradecanoyl-HSL

OHC4HSL, 3-hydroxy-N-butanoyl-HSL

OHC10HSL, 3-hydroxy-N-decanoyl-HSL

OHC14HSL, 3-hydroxy-N-tetradecanoyl-HSL

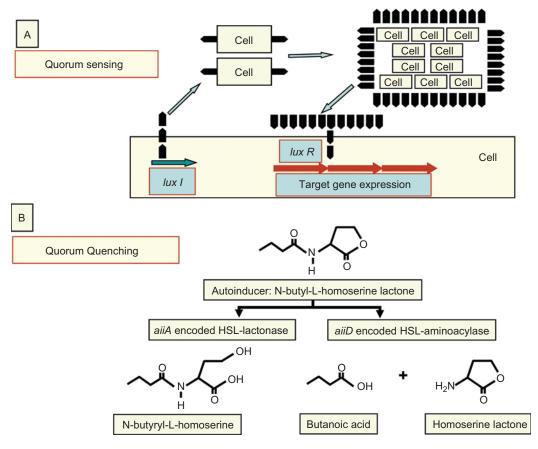


Figure 1. A: Quorum sensing. QS initiates with the activation of *lux*I leading to the production of signal molecules (, filled arrow) (acylhomoserine lactones, acyl-HSL), which are released into the environment. At high cell densities, these signal molecules are retrieved into the cell resulting in the expression of target genes (virulence, etc.) through *luxR*. B: Quorum quenching. QQ is initiated by the inactivation of quorum sensing signal (acyl-HSL) by enzymes—lactonase (Hydrolysis of lactone ring) and acylase (Cleavage of the acyl side chain) generally produced by gram-positive (*Bacillus* sp.) and gram-negative bacteria (*Ralstonia* sp.) respectively.

pressure being imposed on bacteria, the pressure to develop resistance to antibiotics is negligible (Rasmussen & Givskov 2006b; Defoirdt et al. 2008). The excitement on the possibilities of interference with microbial communication to prevent expression and dissemination of virulence factors among pathogens has lead to the emergence of an interesting and innovative system for searching novel drug targets and drug designing (Chowdhary et al. 2007; Dobretsov et al. 2007; Opal 2007; Purohit et al. 2007; Turovskiy et al. 2007; Uroz et al. 2007, 2008; Uroz & Heinon 2008; Adonizio et al. 2008; Romero et al. 2008; Schaefer et al. 2008; von Bodman et al. 2008). In this article, we are attempting to present the diversity of the potential organisms and the mechanisms, which can be

exploited for developing antibacterial drugs through QQ (Czajkowski & Jafra 2009).

Quorum sensing systems

Pathogenic microbes have been bestowed with a unique ability to grow and multiply without displaying their virulent behaviour until they have reached a certain threshold of cell population density (Figure 1). At this stage, they release signals which activate their arsenal of virulence genes and a cascade of activities follows there after (Wagner et al. 2006; Bjarnsholt & Givskov 2008). QS allows bacteria to change their behavior from individual activity to a collective coordinated expression and act like

a "multicellular" organism (Schauder & Bassler 2001). Multiplicity of QS systems, signals, and the differences in their operational level and activities provide bacteria with a resilient and adaptable signaling network (Decho et al. 2010). It may enable bacteria to do a quick survey of their surrounding and develop a strategy to counter the threats (Yang et al. 2006). The following few examples provide a glimpse of the diversity of bacterial behaviours manifested through QS.

Bioluminescence

The emission of light observed in a symbiotic association between marine bacterium—*Photobacterium fischeri* (Formerly known as *Vibrio fischeri*) and its host, the squid—*Euprymna scolopes* is among the first few examples found to be regulated by QS. Here *P. fischeri* obtains its nutrients from the host, which in exchange uses the light produced by *P. fischeri* at high cell density for attracting prey, avoiding predators or finding its mating partner (Nealson et al. 1970; Schauder & Bassler 2001).

Biofilms and infections

QS systems, which are very important from medical application point of view include biofilm development and expression of virulence factors (Schertzer et al. 2009). *Pseudomonas aeruginosa*, a human opportunistic pathogen forms QS regulated biofilms in the lungs of cystic fibrosis patients. These biofilms are secondarily colonized by *Burkholderia cepacia* strains (Schauder & Bassler 2001), the only pathogen more dreadful than *P. aeruginosa*, and virtually spells "death sentence" for CF patients (Hassett et al. 2009). These matrix-enclosed structures are responsible for persistence and severity of *P. aeruginosa* (Rahme et al. 2000; Ueda & Wood 2009).

Among the Gram-positive bacteria are members of Streptococci which colonize epithelial, mucosal, and tooth surfaces (Suntharalingam & Cvitkovitch 2005). In dental plaques colonized by *Streptococcus intermedius, S. mutans, S. pneumoniae, S. gordonii,* and so on competence-stimulating peptide mediated QS is closely linked with biofilm formation (Petersen et al. 2004; Antunes et al. 2009). Another pathogen of concern is *Staphylococcus aureus,* which manifests skin and lung infections through QS dependent biofilms (Schauder & Bassler 2001; Yarwood & Schlievert 2003).

Antibiotic production

QS mechanism is often used by a wide range of microbes for producing antibiotics. QS signals (peptides) are used by Gram-positive microbes belonging to Firmicutes—*Streptococcus*, *Lactococcus*, and *Bacillus* to produce antibacterial peptides, Nisin and Subtilin, respectively (Kuipers et al. 1995; Stein et al. 2002; Hazan & Engelberg-Kulka 2004). Production of antibiotics violacein by *Chromobacterium violaceum* and phenazine by

Pseudomonas chlororaphis PCL1391 are regulated by AHL mediated QS ((McClean et al. 1997; Molina et al. 2003). AHLs act as signaling molecules among proteobacteria such as *Pseudomonas* spp., *Erwinia, Burkholderia, Serratia,* and so on for regulating antibiotic production (Hibbing et al. 2009; Raina et al. 2009).

Rhizospheric activities

In plant associated bacteria such as *Rhizobium* and *Agrobacterium*, QS participates in rhizospheric specific genes, conjugal DNA transfer, symbiotic nitrogen fixation, growth, production of secondary metabolites, antifungal compounds, antibiotics, and a large number of extracellular enzymes (Somers et al. 2004). Conjugal transfer of DNA in *Agrobacterium tumefaciens*, a soil phytopathogenic bacterium to the plant host is mediated by Ti plasmid encoded *vir* (virulence) genes in response to certain phenolic compounds, which are released from the plant wounds (Luo & Farrand 1999; Zhu & Winans 1999).

Quorum sensing signals

Bacteria have evolved a number of diffusible chemical signals to control various biological activities (Newton & Fray 2004). The QS signals vary from organism to organism: i) AHLs in *Vibrio* (Fuqua et al. 1994; Fuqua & Greenberg 1998), ii) The Lux-S-derived family of furanone signals (AI-2) in *Vibrio harveyi* (Schauder & Bassler 2001; Xavier & Bassler 2003), iii) Volatile fatty acid and methyl ester signal in *Ralstonia solanacearum* (Flavier et al. 1997), iv) PQS: 2-heptyl-3-hydroxy-4-quinolone and diketopiperazines in *P. aeruginosa* (Pesci et al. 1999), v) Peptidoglycan in *Myxococcus* (Kaplan & Plamam 1996), and vii) diketo piperazines (Holden et al. 1999).

In Gram-negative bacteria, the most widely studied QS signaling system is based on AHLs (Koutsoudis et al. 2006). The specificity of the AHL signals depends up on the length (typically 4-12 carbons) of the fatty acyl group, degree of saturation and substitution at carbon number 3 (carboxyl, hydroxyl, or fully reduced) of the acyl chain (Fuqua et al. 2001; Hoang et al. 2002; Watson et al. 2002; González & Marketon 2003; Wang et al. 2004). However, the variety of signals is limited (Ryan & Dow 2008; Schaefer et al. 2008; Decho et al. 2010). In contrast to the fatty AHL QS signals used by most Proteobacteria (Waters & Bassler 2005), Rhodopseudomonas palustris CGA009, Bradyrhizobium sp. BTAi1 and Silicibacter pomeroyi DSS-3 produce p-coumaroyl-HSL (aryl-HSL) QS signals (Larimer et al. 2004; Schaefer et al. 2008). The diversity QS systems are well illustrated by a single LuxI/R pair in P. fischeri (Schaefer et al. 1996), two AHL signal-receptor pairs in P. aeruginosa (Balaban et al. 2008), and three systems in V. harveyi (Henke & Bassler 2004). On the whole this system regulates more than 300 genes, primarily implicated in virulence and biofilm formation (Soberón-Chávez et al. 2005; Schuster & Greenberg 2007).

Quorum-sensing system in Gram-positive bacteria—-Bacillus subtilis, Enterococcus, S. aureus, and S. pneumoniae (Firmicutes), and Streptomyces sp. (Actinobacillus) (Solomon et al. 1995; Park et al. 2005; Dunny 2007) operates through processed linear or cyclic oligopeptide signals (Solomon et al. 1995) and a two component regulatory system consisting of a membrane associated sensor histidine kinase and an intracellular response regulator (Hakenbeck & Stock 1996). In these bacteria, oligopeptides act as AIs, which contain side chain modifications such as isoprenyl groups in B. subtilis or thiolactone rings in Staphylococcus spp. (Otto et al. 1998; Ansaldi et al. 2002). QS in Streptomyces sp. is regulated by AIs such as γ -butyrolactones, which are structurally similar to AHLs of Gram-negative bacteria (Khmel & Metlitskaya 2006).

Another class of QS signaling system is a hybrid between the Gram-positive and Gram-negative systems. It was identified in the marine bacterium *V. harveyi* which has the ability to produce and detect two distinct AIs: AI-1 and AI-2 (Bassler et al. 1994) and a CAI-1 (Henke & Bassler 2004). Here, AI-1 is similar to AHL of Gram-negative QS (Cao & Meighen 1989), whereas AI-2 is a furanosyl borate diester, which does not show any resemblance to other AIs (Chen et al. 2002). In contrast to overlapping QS systems in *P. aeruginosa*, (Yarwood et al. 2005), QS signal mechanisms operate in parallel in *V. harveyi* and *B. subtilis* and act together to regulate target genes in a concerted manner (Miller et al. 2002; Mok et al. 2003).

Quorum Quenching: Mechanisms

A brief description of the QS process will enable us to appreciate the potential targets, which have been identified for inhibiting it. The most widely studied QS signaling system is based on AHLs (Figure 1) (Koutsoudis et al. 2006). The biosynthesis of AHL involves intermediates from fatty acid biosynthetic pathway: S-adenosyl methionine and an acylated acyl carrier protein (Schaefer et al. 1996). Gram-negative bacteria in general, employ two proteins, LuxI and LuxR during QS process. In the beginning of cell growth at low cell population densities, AHL synthase LuxI produces AHLs at low concentrations. These are diffused out of the cell. With increase in cell densities, AHLs above a threshold concentration in the environment are diffused back into the cell (Flagan et al. 2003). Here the QS signals bind to transcription regulator (LuxR) and activate the operon such as those responsible for virulence, and so on (Decho et al. 2010).

Several QQ strategies have recently been discovered in a few organisms primarily as a defense mechanism against competitors. The different QQ mechanisms operate by blocking different steps involved in QS. At low population densities, inhibition of signal generation and accumulation occurs by blocking fatty acid pathway. QQ mechanisms operating at high cell-population densities involve (i) R protein (Lux R type) inhibitor to prevent signal reception, (ii) AHL signal degradation enzymes, inhibitors for I and R proteins—autoinduction and activation and (iii) decay of the signal molecule (Dong et al. 2007).

Blocking signal generation and accumulation:

Two major potential targets identified in the synthesis of AHL-type signals are (i) enoyl-ACP reductase (ENR) and (ii) S-adenoysl methionine (SAM), substrate for the ENR enzyme (Zhang 2003; Dong et al. 2007). Triclosan, a widely used biocide, acts as an inhibitor of the enoyl-ACP reductase (Hoang and Schweizer, 1999), and Closantel inhibits histidine kinase sensor of 2 component system (Stephenson et al. 2000) to suppress AHL gene in vitro (Zhang 2003).

Preventing signal reception:

Inhibition of reception of signal molecule by antagonist molecule is another mechanism for controlling QS mediated infections (Antunes et al. 2009). These antagonist molecules compete or interfere with the binding of the signal molecule to the receptor. Inactivation of the receptor results in failure to express virulence factors. Diketopiperazines (DKP) are cyclic dipeptides which share structural similarity to signaling peptides in mammalian tissues (Draganov et al. 2005). They are produced by a range of bacteria (*P. aeruginosa, P. mirabilis, Citrobacter freundii* and *Enterobacter agglomerans*) (Holden et al. 1999) and yeast, fungi, and lichens (Draganov et al. 2000). DKP act as AHL antagonists in LuxR based QS and as agonists in others (Holden et al. 1999).

Inhibiting autoinduction and activation:

(i) Signal degradation

Three different mechanisms have been reported for degradation of QS signals: i) chemical, ii) metabolic, and iii) enzymatic. The chemical degradation has been reported primarily at alkaline pH, which leads to opening of the lactone ring (Yates et al. 2002) and results in loss of activity of the AHL signal in Erwinia (Byers et al. 2002). However, at acidic pH, the ring re-cyclizes and the activity gets restored. A few organisms such as Variovorax paradoxus and P. aeruginosa PAI-A have the ability to metabolize AHL to suppress QS bacteria and in the process they gain a competitive edge (Leadbetter & Greenberg 2000; Huang et al. 2003). Enzymatic degradation of QS signal molecules has been observed in a wide range of prokaryotes and a few eukaryotes (Figure 1, Table 1). Broadly, the QQ enzymes hydrolyze either the amide bond (Lin et al. 2003) or the lactone ring (Dong et al. 2000; Lee et al.

Organism	Enzyme and gene	Target ^a	Reference(s)
Bacillus sp.	AHL lactonase, <i>aiiA</i>	Short chain and long chain AHLs: C4HSL, C6HSL, C8HSL, C10HSL, 3OC4HSL, 3OC6HSL, 3OC8HSL, 3OC10HSL, 3OC12HSL, 3OHC4HSL	Dong et al. 2000; Dong et al. 2001; Fuqua et al. 2001
Bacillus thuringiensis	AHL lactonase, aiiA	AHL	Lee et al. 2002; Dong et al. 2004; Liu et al. 2005
Bacillus anthracis (expressed in Burkholderia thailandensis)	AHL lactonase, aiiA	C6HSL, C8HSL, C10HSL	Ulrich 2004
Bacillus cereus A24 (exprssed in Pseudomonas aeruginosa PAO1)	AHL lactonase, aiiA	AHL	Reimmann et al. 2002
Bacillus sp. (expression in plant pathogen Erwinia carotovora)	AHL lactonase, aiiA	AHL	Dong et al. 2000
Bacillus megaterium	Cytochrome P450 oxidation at ω -1, ω -2, and ω -3 of the acyl chain Lactonolysis, P450BM-3	AHLs and acyl homoserine	Chowdhary et al. 2007
Acidobacteria	AHL lactonase, qlcA	C6HSL, C7HSL, C8HSL	Riaz et al. 2008
Agrobacterium tumefaciens	AHL lactonase, attM	AHL	Zhang et al. 2002; 2004
Agrobacterium tumefaciens C58	AHL lactonase, aiiB	AHL	Zhang et al. 2002; Carlier et al. 2003; Zhang et al. 2004
Agrobacterium radiobacter K84	AHL lactonase, aiiS	AHL	Uroz et al. 2009
Arthrobacter sp. IBN110	AHL lactonase, ahlD	AHL	Reimmann et al. 2002; Park et al. 2003
Klebsiella pneumoniae KCTC2241	AHL lactonases, ahlK	AHLs: C6HSL, C7HSL, C8HSL	Park et al. 2003
Rhodococcus erythropolis W2	Lactonases (PTE family: Phosphotriesterase) ^b , <i>qsdA</i>	AHLs: C6 to C14, with or without substitution at carbon 3	Uroz et al. 2008
	Oxidoreductase (converts to corresponding 3-hydroxy derivatives), <i>qsdA</i> (alleles)	C6HSL, 3OC6HSL, 3OC8HSL, C10HSL, 3OC10HSL, C12HSL, 3OC12HSL, 3OHC12HSL, 3OC14HSL AHL analogues: i) N-(3-oxo-6-phenylhexanoyl)HSL (aromatic acyl-chain substituent); ii) 3-oxo- dodecanomide (lacks HSL ring) [3OC12-NH ₂]	Uroz et al. 2003; Uroz et al. 2005
	Amidolytic (cleaves the acyl chain) hydrolase	3OC10HSL	Uroz et al. 2005
Streptomyces sp. strain M664	AHL-acylase, ahlM	Effectively degrades AHLs (with chain length more than 8 carbon): C8HSL, C10HSL and 3OC12HSL Low activity on short-acyl-chain AHLs: C6HSL and 3OC6HSL	Park et al. 2005
Comomonas strain D1	AHL-acylase, Not known	N-AHSL with acyl-side chains C4 to C16 with or without 3-oxo- or 3-hydroxy substitutions. C12HSL, 3OC12HSL, 3OHC12HSL, 3OC14HSL, 3OHC14:1-HSL, C16HSL	Uroz et al. 2007
Ralstonia eutropha XJ12A, XJ12B	AHL-acylase, <i>aiiD</i>	Long chain AHLs: 3OC8HSL, 3OC10HSL, 3OC12HSL Short chain AHLs with less efficiency	Lin et al. 2003
Ralstonia solanacearum GMI 1000	AHL-acylase, aac	Long chain AHL with acyl side chains >6C: C7HSL, C8HSL, 3OC8HSL, C10HSL	Chen et al. 2009
Shewanella sp. strain MIB015	AHL-acylase, aac	Long chain-AHLs:	Morohoshi et al. 2005

Table 1. Continued

Organism	Enzyme and gene	Target ^a	Reference(s)
Pseudomonas aeruginosa PAO1	AHL-acylase, PA2385 (qcs112/pvdQ), PA1032	Long chain-AHLs: C7HSL, C8HSL, C10HSL, C12HSL	McClean et al. 1997; Huang et al. 2003; Uroz et al. 2003; Lamont & Martin 2003; Huang et al. 2006
Anabaena (Nostoc) sp. PCC 7120	AHL-acylase, <i>aii</i> C	Long chain AHLs: OC12HSL,OC12HSL, OHC12- HSL, C14 HSL, OC14 HSL, OHC14HSLMedium chain AHLs: C10 HSL, OC10HSL, OHC10HSL	Romero et al. 2008
Laminaria digitata (Marine algae)	Haloperoxidases	3-oxo-AHLs	Borchardt et al. 2001
Delisea pulchra (Red algae)	Halogenated furanones	C6HSL and autoinducer (AI-2) [Furanosyl borate diester]	Givskov et al. 1996; 1997; Manefield et al. 1999; 2001; Ren et al. 2001; Hentzer & Givskov 2003; Delalande et al. 2005
Fungi: Phialocephala fortinii, Ascomycetes, Meliniomyces variabilis	Lactonase	C6HSL, 3OC6HSL	Uroz & Heinon 2008
Porcine kidney Acylase I.	AHL-acylase, ACY1	C4HSL, C8HSL	Xu et al. 2003
Eukaryotes: Human airway epithelial cells	Lactonase-like enzymes: Paraoxonases, PON1, PON2, PON3: <i>PON1, PON2, PON3</i>	Long chain AHLs: 3OC12-HSL of <i>P. aeruginosa</i> Less efficient with short chain AHLs: C6-HSL	Draganov et al. 2000; Chun et al. 2004; Hastings 2004
Recombinant PONs from human airway epithelial cells	Lactonase-like enzyme:PON2 Paraoxonases, <i>PON2: PON2</i>	DL-3OC6HSL, DL-C7HSL, DL-C12HSL, DL-C14HSL	Yang et al. 2005
Rabbit AiiA sp. antiserum	AHL lactonase, aiiA	3OC12HSL	Chun et al. 2004
Lotus corniculatus seedlings	Unknown	C6HSL, 3OC6HSL, 3OC8HSL, 3OC10HSL	Delalande et al. 2005

a: AHL: Acylhomoserine lactone, HSL: Homoserine lactone, C4HSL: N-butanoyl-L-HSL, C6HSL: N-hexanoyl HSL, C7HSL: N-heptanoyl-HL, C8HSL: N-octanoyl HSL, C10HSL: N-decanoyl HSL, C12HSL: N-dodecanoyl HSL, C14HSL: N-tetradecanoyl-HSL, C16HSL: N-hexadecanoyl-HSL, 3OC6HSL: 3-oxo-N-hexanoyl-HSL, 3OC8HSL: 3-oxo-N-octanoyl-HSL, 3OC10HSL: 3-oxo-N-decanoyl-HSL, 3OC12HSL: 3-oxo-N-dodecanoyl-HSL, 3OC14 HSL: 3-oxo-N-tetradecanoyl-HSL, OHC4HSL: 3-hydroxy-N-butanoyl-HSL, OHC10HSL: 3-hydroxy-N-decanoyl-HSL, OHC14HSL: 3-hydroxy-N-tetradecanoyl-HSL

b: QsdA belong to PTE of zinc dependent metallic proteins. It is unrelated either i) N-AHL lactones which belong to the Zinc-dependent glyoxylase family or N-AHSL amidohydrolases which belong to β -lactam acylases (Uroz et al. 2008).

2002) of AHL. The two reactions are largely mediated by the enzymes AHL-acylase, AHL-lactonase, lactonase like enzymes (paraoxonases), and oxidoreductases. A few cases of organisms possessing the enzymes acting as quenchers of QS signals have been presented below.

a) In prokaryotes

Bacteria belonging to the genus *Bacillus-B. anthracis, B. cereus, B. mycoides, B. subtilis, B. thuringiensis, Arthrobacter* spp., *Acidobacteria, Agrobacterium* spp., and *Klebsiella* spp. produce an enzyme—AHL-lactonase (AiiA) belonging to the superfamily—metallohydrolase. It hydrolyzes the lactone ring to form acyl-homoserine, which ceases to function as a QS signal (Dong et al. 2000, 2002, 2004; Lee et al. 2002; Park et al. 2003; Ulrich 2004; Liu et al. 2005; Thomas et al. 2005; Dong & Zhang 2005; Bai et al. 2008; Riaz et al. 2008; Uroz et al. 2009). In *Bacillus* AHL lactonases have a broad substrate specificity (Fuqua et al. 2001) but are quite selective for (s)-configuration (Thomas et al. 2005). *Bacillus* spp. could degrade

V. harveyi AHL signal HAI-1 (Dong et al. 2002; Bai et al. 2008). Many homologues of this AHL-lactonase have been identified (Ulrich 2004) (Table 1) and expressed in different closely related species (Reimmann et al. 2002). Heterologous expression of the B. cereus strain A24 AiiA lactonase in P. aeruginosa PAO1 negatively affected quite a few QS controlled functions such as AHL accumulation, swarming motility and expression and secretion of virulence factors (Reimmann et al. 2002). The plant-colonizing bacterium Pseudomonas fluorescens carrying aiiA borne plasmid prevented soft rot disease in potatoes and egg plants (Dong et al. 2000) caused by Pectobacterium carotovorum (previously Erwinia carotovora) and crown gall disease caused by A. tumefaciens in tomatoes (Molina et al. 2003). Co-culturing P. chlororaphis with Fusarium oxysporum controls tomato vascular wilt caused by the latter. However, its co-culturing with AiiA-producing bacterium, Bacillus sp. A24 resulted in loss of its biocontrol activity (Molina et al. 2003). Similarly aiiA expression in transgenic tobacco plants made them less susceptible

to *P. carotovorum* (Dong et al. 2001). Phylogenetic studies have revealed that lactonase genes of *Bacillus* (aiiA) cluster together with attM (pAt plasmid borne) and aiiB (pTi plasmid borne) of *A. tumefaciens*, (Zhang et al. 2004) along with aiiA homologues from other α - and γ -Proteobacteria and an ORF from *Deinococcus radiodurans* (Carlier et al. 2003).

The enzyme AHL-acylase has also been reported from a wide range of prokaryotes belonging to Gram-positive and Gram-negative bacteria. The range of activities is relatively large in this case compared to that of AHLlactonase, since AHLs have varying acyl-chain lengths, they provide variability of substrates to AHL-acylases (Table 1). AHL-acylase AiiD from Ralstonia eutropha strains are quite specific in their activity as they are more effective on long chain AHLs with chain length more than 8 carbons (Lin et al. 2003). In contrast, AHL-acylase of Streptomyces sp. strain M664 shows high efficiency with AHLs having chain length less than 8 carbons. The most interesting feature of this organism is the secretion of AHL-degrading enzyme into the culture medium, increasing the range of its action (Park et al. 2005). The diversity of organisms showing AHL-acylase has been widened by the work of Chen et al (Chen et al. 2009), who have recently shown that a putative aculeacin A acylase from R. solnacearum GMI1000 is an acylase with distinct QQ activity. Comamonas is yet another Gram-negative microbe which exhibited a wide range of AHL degradative patterns (Uroz et al. 2003), varying with acyl chain lengths between 4 and 16 carbon, with or without 3-oxoor 3-hydroxy substitutions (Uroz et al. 2007). Quite a few alleles of AHL-acylase of P. aeruginosa PAO1 have preference for degrading long chain AHLs (Lamont & Martin 2003; Zhang & Dong 2004; Huang et al. 2006; Sio et al. 2006). The AHL-acylase type enzyme from filamentous nitrogen-fixing cyanobacterium Anabaena (Nostoc) sp. PCC7120 exhibits homology to the acylase QuiP of P. aeruginosa PAO1 (Romero et al. 2008). Shewanella sp. are known to possess acylase activities for AHL degradation (Morohoshi et al. 2005). Phylogentically, AHL-acylases share well conserved amino acid residues, which are important for autoproteolytic activities (Lin et al. 2003). The two residues important for their substrate specificity are Ile50 and Ser57 in Ralstonia sp. XJ12B (Lin et al. 2003), Leu⁵⁰- and Glu⁵⁷ in Actinoplanes utahensis (Dong et al. 2007), Leu⁵⁰ and Asp⁵⁷ in P. aeruginosa PAO1 (Huang et al. 2003) and Leu⁵⁰ and Ser ⁵⁷ in Streptomyces sp. (Park et al. 2005).

A series of studies have revealed that *Rhodococcus erythropolis* strains have a wide spectrum of QQ abilities (Table 1). *R. erythropolis* W2 has been reported to possess AHL-lactonase, oxidoreductase as well as AHL-acylase activities (Uroz et al. 2005, 2008; Park et al. 2006). *In vitro*, *R. erythropolis* W2 strongly interfered with AHL dependent violacein production by *C. violaceum* and transfer of pathogenicity in *A. tumefaciens*. In planta, *R. erythropolis* W2 markedly reduced pathogenicity of *P. carotovorum* sub sp. *carotovorum* in potato tubers (Uroz et al. 2003).

AHLs were shown to be modified and degraded by amidolytic and novel oxidoreductase of *R. erythropolis* W2 (Uroz et al. 2005). *Acinetobacter* sp. has been shown to degrade C6HSL and C8 HSL, however much characterization is to be done (Kang et al. 2004).

Salmonella typhimurium, Escherichia coli, and V. harveyi produce AI-2 signals, which activate other genes leading to its metabolism and consequently inhibition of QSS (Taga & Bassler 2003; Xavier & Bassler 2005, Roy et al. 2009). LsrK (AI-2 kinase) phosphorylates AI-2 to phospho-AI-2, which confers a negative charge on AI-2. It restricts its reentry into the cell through Lsr transporter. Here quenching of the signal happens ex vivo and is advantageous since it is not limited by the need to overcome the barrier (the cellular membrane) (Roy et al. 2009).

b) In Eukaryotes

Human epithelial cells have enzymes paraoxonases PON1, PON2, and PON3 which exhibit important hydrolytic activity related to drug metabolism and detoxification of organophosphate (Ng et al. 2005; Dong et al. 2007). The capacity of human respiratory epithelia to inactivate P. aeruginosa QS signals was reported by Chun et al. (Chun et al. 2004). It was speculated that host defense mechanism targets 3OC12-HSL which is necessary for activation of *P. aeruginosa* QS C4-HSL system (Hastings 2004). Mammalian cells expressing three mouse paraoxonases (PONs) genes showed AHL degradation activities quite similar to that of lactonase enzymes (Yang et al. 2005). Human paraoxonases (PON1, PON2, and PON3) have lactonase activities with overlapping substrates but are quite specific as well. PON2 hydrolyzes and inactivates AHL, QS signals of pathogenic bacteria, whereas PON1 catalyzes the hydrolysis of aromatic and aliphatic lactones and lactonization of γ - and δ -hydroxy carboxylic acids. PON2 completely hydrolyzes 3OC6HSL (Draganov et al. 2005). Another interesting feature of the PON lactonases is their specificity to hydrolyze six-member ring lactones more efficiently than their 5-member ring analogs (Draganov et al. 2005). Expression of human paraoxonase showing lactonase activity in Drosophila melanogaster protected it from the lethality of P. aeruginosa (Stoltz et al. 2008). AHL inactivating activity was observed in the sera of mammalian animals including human and rabbit but not in chicken and fish (Draganov et al. 2000; Yang et al. 2005). These enzymes were less efficient on AHLs of short acyl chain lengths of 6 carbons (Chun et al. 2004; Yang et al. 2005).

Fungi such as *Phialocephala, Ascomycetes*, and *Melinimyces* have been shown to possess lactonase activity with ability to act upon the lactone ring of C6HSL and 3OC6HSL (Uroz & Heinon 2008). In addition to paraoxonases reported from animals, certain acylases from porcine kidney have also been recognized with ability to degrade AHLs (Reimmann et al. 2002; Xu et al. 2003). These findings although limited at present but are consistent with the idea that cells derived from human epithelia

tissue exposed to pathogens can inactivate the QS signal (Liu et al. 2005).

(ii) Antagonists

Antagonists molecules can compete or interfere with native AHL signal molecule for binding to Lux R-type receptor. This complex fails to activate QS signal transduction. Blocking the transduction through inhibitors of I and R proteins also helps in manipulating QSS (Antunes et al. 2009). AHLs with C10 and C12 acyl side chains can inhibit the C4HSL dependent expression of exproteases in Aeromonas hydrophila (Swift et al. 1999), violacein production in C. violaceum (McClean et al. 1997) and suppression of filament in pathogenic yeast Candida albicans (Hogan et al. 2004). 3OC12-HSL - AI produced by P. aeruginosa plays dual roles as QS signal and also as an effective bactericidal agent against Gram-positive bacteria (EC50 in the range of 22.1 to more than 100 μM) and not against Gram-negative (Kaufmann et al. 2005). 3OC12HSL from P. aeruginosa showed inhibitory effect on the production of exotoxins and cell wall fibronectin proteins and could also inhibit agr expression of S. aureus. 10 µM of 3OC12HSL completely inhibited growth dependent bioluminescence of S. aureus RN6390 (pSB2030) (Qazi et al. 2006). Human pathogen S. aureus is responsible for causing skin and lung infections. S. aureus group employ thiolactone-based auto-inducing peptide based QS to regulate agr virulence (Ji et al. 1997) and also to inhibit virulence in other S. aureus groups (categorized on the basis of their peptide sequences) (Ji et al. 1997; Schauder & Bassler 2001; Khmel & Metlitskaya 2006; Geisinger et al. 2008). In the human oral cavity, interaction between S. gordonii and S. mutans results in disruption of QS regulated bacteriocin production by the later, the organism causing dental caries (Fuqua et al. 2001). Fungi - Penicillium radicicola produce panicillic acid and Penicillium coprobium produce patulin to target LasR and RhlR QS regulators in *P. aeruginosa* (Koch et al. 2005; Rasmussen et al. 2005b). Plants such as tomato, pea, garlic are effective antagonists on LuxR based QS but not effective against P. aeruginosa (Teplitski et al. 2000; Rasmussen et al. 2005a). Bryozoan Flustra foliacea AHL act as antagonist to combat potential pathogenic bacteria (Peters et al. 2003).

Status of Quorum Sensing Inhibitors

(i) Natural

Natural compounds such as furanones and enones from the marine macro alga *Delisea pulchra* (Manefield et al. 2001; Ren et al. 2004) act by accelerating turnover of the LuxR protein there by lowering its availability to AHL. Furanones are structurally similar to HSLs and bind to LuxR-like proteins and thereby affecting the binding of the AI. This mechanism consequently results in reduced transcription (Manefield et al. 2002; Zhang 2003; Clatworthy et al. 2007). Furanone produced by marine alga *D. pulchra* consists of a fural ring structure with a

substituted acyl chain at C-3 position and a bromine substitution at C-4 position. D. pulchra produces more than 30 different species of halogenated furanone compounds (de Nys et al. 1993), which quench the AHL molecules used by the pathogenic bacterium Serratia liquefaciens and P. fischeri (Givskov et al. 1996). The inactivation of AHL-mediated motility of S. liquefaciens MG1, results in preventing bacteria from colonizing within the algal cells (Eberl et al. 1996; Givskov et al. 1997; Manefield et al. 1999; Rasmussen et al. 2000). Oxidized halogens produced as a result of haloperoxidase activity in alga, Laminaria digitata react specifically with C3-oxo-AHLs and destroy their signaling ability by penetrating the biofilm (Borchardt et al. 2001). Similarly chloroperoxidases produced by marine algae also specifically inactivates C3-oxoAHLs. These enzymes thus prove microbicidal in nature (Taga & Bassler 2003). Natural furanones could enhance the survival rate of brine shrimps challenged with pathogenic Vibrio spp. at a concentration of 20 mg/l of cultured water (Defoirdt et al. 2006). It is however highly toxic to larvae at 50 mg/l and is too reactive to be used for treating bacterial infections (Hentzer & Givskov 2003; Defoirdt et al. 2006). Chlamydomonas reinhardtii can also interfere with QS by producing molecules which mimic bacterial QS signaling molecules (Teplitski et al. 2004).

Plants and animals which associate with microbes need to detect for their presence in a rapid and reliable manner (Mathesius et al. 2003). Among plant-microbial associations, Medicago truncatula, Pisum sativum, etc. develop a symbiotic relationship with AHL producing, nitrogen fixing bacterial symbiont—Sinorhizobium meliloti and Rhizobium sp. P. sativum and M. truncatula secrete substances, which mimic AHL signals to stimulate or inhibit AHL-regulated responses in bacteria (Cook 1999; Teplitski et al. 2000; Bauer & Robinson 2002; Gao et al. 2003; Mathesius et al. 2003) including Pseudomonas spp. (Marketon et al. 2002). Recombinant plants of potato and tobacco expressing lactonase (AiiA) could degrade AHLs and showed resistance to QS-dependent bacterial infection (Dong et al. 2000, 2001; Leadbetter & Greenberg 2000; Zhang et al. 2002; Lin et al. 2003). Recent studies have revealed the diversity of these systems and have shown that Lotus corniculatus seedlings exhibit some unique properties of stabilizing the AHL signal and may even inactivate them (Delalande et al. 2005).

Plants such as crown vetch, carrot, soybean, water lily, tomato, pea seedlings, habanero, and garlic produce compounds which can act as QSIs (Teplitski et al. 2000; Rasmussen et al. 2005a). Garlic extracts contain different QSIs (Rasmussen et al. 2005a), which show improved clearing and remarkable reduction in mortality of mouse lungsinfected with *P. aeruginosa* (von Bodman et al. 2008). QSI compounds extracted from food sources especially garlic has been found to quite effective in inhibiting *in vitro* QS regulated biofilm during *P. aeruginosa* infections (Bjarnsholt et al. 2005). Bark of *Combretum albiflorum* contains flavan-3-ol catechin (a flavonoid) with abilities

to quench the production of QS-dependent factors such as pyocyanin and elastase and biofilm formation in *P. aeruginosa* (Vandeputte et al. 2010). Hamamelitannin, (2′,5-di-O-galloyl-D-hamamelose) a natural product present in the bark of *Hamamelis virginiana* was found to prevent device-associated Staphylococcal infections by acting as a QSI. It inhibits RNA III production, a component of agr QSS. The range of inhibition extended to infections caused by methicillin-resistant *Staphylococcus epidermidis* and *S. aureus* strains (Kiran et al. 2008).

Other natural QS inhibitors are fatty acids derived from ground beef and poultry meat (Roy et al. 2009), metabolites from plant extracts (Adonizio et al. 2008), and secondary fungal metabolite, Ambuic acid, which inhibits the biosynthesis of a cyclic peptide quormone in *S. aureus, Listeria innocua*, and *Enterococcus faecalis* (Nakayama et al. 2009).

(ii) Synthetic

The possible ways which can be envisaged for developing the chemical analogues of the AHL molecule to act as QS inhibitors (QSIs) are: a) substitution(s) in the acyl side chain; b) alteration(s) in the lactone ring; or c) changes in both the components. Acyclic or cyclic alkyl substituent especially those developed by replacing C3 with S in the acyl side chain resulted in analogues with ability to block the expression of LuxR- and LasR- controlled QS receptors (Olsen et al. 2002; Persson et al. 2005). Replacement of C-1 carbonyl group of the side chain with a sulphonyl group- Aryl substituent further enhanced the QSI activity (Castang et al. 2004). AHLs with C10 to C14 long acyl chains when substituted at C3, inhibited light output and growth in S. aureus. Incidentally, short chain AHLs did show any effect (Qazi et al. 2006). A significant reduction (from 50 to 90%) in the activity in P. carotovorum was recorded with AHL-analogs with extended acyl chain length (Chhabra et al. 1993). It was suggested that AHL analogs should be longer than the native AHL to act as efficient inhibitors (Hentzer & Givskov 2003). Specific N-acyl-cyclopentylamine (C_n-CPA) with an acyl chain length in the range of C₅-C₁₀ showed strong inhibitory effects on Lux QSS. Its efficacy was higher than those recorded with halogenated furanones (Wang et al. 2008). C₁₀-CPA was most effective inhibitor on Las and Rhl based QS in *P. aeruginosa* (Ishida et al. 2007). C₀-CPA has been shown to be inhibitory to Spn QS of Serratia marcescens (Morohoshi et al. 2005) and Aeromonas hydrophila (Swift et al. 1999). Synthetic HSL derived sulfonyl ureas and N-phenylacytanoyl-L-HSL have been supported to inhibit Lux-QSS (Geske et al. 2007; Frezza et al. 2008). Another possibility is the introduction of unsaturated bond near the amide bond, which was shown to completely abolish bonding of the QS signals to the receptor (Chhabra et al. 1993). Analogues with variation in the length of acyl side chain of 3OC12HSL as in the 3OC12-(aminocyclohexanone) could strongly influence the two QS systems of P. aeruginosa (Smith et al. 2003a; Rasmussen & Givskov 2006b) by inhibiting the QS regulated expression of *plasI-gfp* fusion and virulence factors (Smith et al. 2003a). Replacing phenol ring with a hexanone ring 3OC12-(2-aminophenol) led to a further improvement in the efficacy of this compound, which act as a potent inhibitor of QS controlled LasR in *P. aeruginosa* (Smith et al. 2003b). Synthetic signal analogues containing lactones or lactam rings alone were found to be effective as inhibitors of Staphylococcal infections (Winans & Bassler 2002; Lyon & Novick 2004). Softening of bacterial biofilms by the action of these compounds made them more susceptible to conventional antibiotics and the action of host immune system (Rasmussen & Givskov 2006b).

Screening of a library of compounds such as 4-nitropyridine-N-oxide (4-NPO), indole, p-benzoquinone, 2,4,5-tribromoimidazole, indole and 3-nitrobenzene sulphone amide proved quite effective in reducing the expression of the QS regulated genes in P. aeruginosa (Rasmussen et al. 2005a). Prof. Greenberg's group identified small molecules inhibitors of LasR (Mattmann et al. 2008), which function as agonists for QscR, which is critical for pathogenic abilities of *P. aeruginosa* (Fuqua 2006) and can be exploited to reduce the virulence caused due to the expression of LasR and QscR (von Bodman et al. 2008). Synthetic analog, N-phenyl-4-{[(phenylamino) thioxomethyl]amino}-benzenesulfonamide was identified from a library of small organic molecules for its ability to inhibit the binding of the QS signal (norepinephrine) to its adrenergic receptor QseC. This resulted in inhibition of the expression of virulence genes and reduced morbidity and mortality in a wide range infection models (Rasko et al. 2008). Similarly, antibody RS2-1G9 protects macrophages from cytotoxic effects of the P. aeruginosa QS signal (3OC12HSL) (Kaufmann et al. 2008). Efforts to inhibit the synthesis of QS signal molecule (AI-2) by employing synthetic analogues at submicromolar range have helped to increase the chances of successful application of this strategy (Alfaro et al. 2004; Shen et al. 2006). Anthranilate analog represses PQS production but does not affect bacterial growth. Methyl-anthranilate caused dose dependant reduction in elastase activity of P. aeruginosa PAO1 (Calfee et al. 2001). It has raised the possibilities for novel anti-infective therapies (Williams 2002; Sio et al. 2006).

Quite a few efforts have gone in to modulate QS to reduce the production of toxins or to activate the QS at low cell density. It will provide an opportunity to the immune system to attract them (Martin et al. 2008). These have resulted in potential QS-modulating therapies such as macrolide antibiotics, QS vaccines and competitive QS inhibitors (Martin et al. 2008).

Microlides such as azithromyzin inhibit QS (Tateda et al. 2001) by reducing the production of several virulence factors of *P. aeruginosa*, such as elastase, rhampolipids and alginate synthesis (Ichimiya et al. 1996; Imamura et al. 2004; Nalca et al. 2006). Azithromycin acts by reducing LasI and RhII, leading to reduction in HSL by 94% and 72%, respectively and consequently virulence in

P. aeruginosa (Imamura et al. 2004; (Tateda et al. 2001) especially in cystic fibrosis cases (Saiman et al. 2003). It inhibits QS at sub-inhibitory concentrations (Nalca et al. 2006). Its chemically related antibiotics, erythromycin and Clariothromycin affect HSL production and reduce production of virulence factors such as protease and elastase (Molinari et al. 1993; Mizukane et al. 1994; Sofer et al. 1999). Virstatin inhibits the V. cholerae Tox T, transcriptional regulator involved in the expression of virulence factors (i) the toxin—coregulated pilus and (ii) cholera toxin. Administration of virstatin during in vivo experiments on infant mice, protected its intestine from Vibrio cholerae (Hung et al. 2005).

Furanones with varied side chain lengths and substitution in the ring structure particularly those compounds which lacked a side chain but had a electronegative substituent on the furanone ring effectively inhibited the QSS of P. aeruginosa (Hentzer et al. 2002; Manefield et al. 2002). Halogenated furanones were found to inhibit the production of carbapenem (in E. carotovora) by regulating Lux R homolog CarR (Manefield et al. 2001). A halogenated furanone derivative, (5Z)-4-bromo-5-(bromomethylene)-3-butyl-2(5H-furanone) was found to inhibit biofilm formation and swarming motility in E. coli and B. subtilis (Ren et al. 2001; 2002). Four synthetic furanones were found to significantly affect biofilm formation by S. epidermidis (Lonn-Stenrud et al. 2009). Since two of the furanones: (Z)-5-(bromomethylene) furan-2(5H)-one and (Z)-3-bromo-5-(bromomethylene) furan-2(5H)-one were found to be non-irritative and non-genotoxic, they represented promising therapeutic agents for protecting surface colonization by S. epidermidis (Lonn-Stensrud et al. 2009). Of the two synthetic furanones, the former appeared to inhibit AI-mediated QS and decrease the severity of mice lung infections caused by P. aeruginosa (Wu et al. 2004). Compared to natural furanones, the efficiency of synthetic analogues such as C30 and C56 with varying side chain length and substitutions were found to be effective in inhibiting QSS of P. aeruginosa (Hentzer et al. 2002; 2003). The effectiveness of furanone (compound C-30) treated biofilms of P. aeruginosa was evident by higher susceptibility of biofilms to tobramycin in comparison to untreated ones (Hentzer et al. 2002; 2003). Vibrio anguillarum treatment with furanone C-30 significantly reduced the mortality of rainbow trout (Rasch et al. 2004). Halogenated furanones specifically inhibits bacterial QS, such as surface colonization by Serratia liquefaciens (Givskov et al. 1996).

Analog of SAM such as S-adenosylhomocysteine, 8-adenosyl cysteine and sinefungin act as inhibitors of AHL synthesis (catalyzed by *P. aeruginosa* RhII protein) (Parsek et al. 1999). Imine adduct resulting from the condensation of a halogenated salicylaldehyde and 3-aminoacetophenone affected the transcription of T3SS without affecting other important properties like growth or motility in *E. coli* EPEC (Gauthier et al. 2005). QSI, RNAIII-inhibiting peptide has been found to effectively inhibit phosphorylation of TRAP (Target of RAP),

in animal model infected with *S. aureus* (Gov et al. 2001; Balaban et al. 2007). This antagonism of RAP has the potential to act as therapeutic is exciting but its future is still unclear (Martin et al. 2008). Its potential appears to lie in preventing biofilms formed by *S. epidermidis* (Joelsson et al. 2006). The promise of RIP was evident from the augmentation in the antibacterial action of ciprofloxin, imipenem, and vancomycin (Cirioni et al. 2006).

Structural mimics of signal molecules such as synthetic AI peptides interfere with signal binding to the receptor (Lyon et al. 2000]. Analog of QS signal—HSL, [N-(2-oxocyclohexyl)-3-oxododecanamide)] were found to antagonize HSL activity which consequently lead to reduction in *P. aeruginosa* induced pyocyanin, elastase and biofilm formation (Smith et al. 2003a). A high throughput screening of 150,000 small organic compounds lead to the identification of LED 209 (N-phenyl-4-[(phenylamino)thioxomethyl]amino]-benzene sulfonamide) (Rasko et al. 2008). It blocks the binding of signals - (i) AI-3 (a bacterial autoinducer produced by normal gut intestinal flora) and (ii) epinephrine/norepinephrine (hormones produced by the host) (Sperandio et al. 2003)—to QseC (membrane bound sensor kinase) mediated activation of virulence gene expression in entero hemorrhagic E. coli (EHEC) (Walters & Sperandio 2006). The scope of such small molecules could be highly valuable as pathogenic blockers (Njoroge & Sperandio 2009) in the treatment of EHEC infections since QseC homologues have been found to be present in more than 25 microbial pathogens of significance to humans and plants (Rasko et al. 2008).

More recent approach to target oral microbial pathogens such as *Streptococcus mutans* and related species has been through a novel class of antimicrobials, called specifically-targeted antimicrobials peptides (STAMPS) (Eckert et al. 2006). STAMPSs are made up of two functionally independent linearly arranged peptide moities. These have a very strong potential to develop into novel therapeutics (Li et al. 2010).

AHL sequestration by antibodies

Biochemical studies have revealed the effect of AHL such as 3-oxo-C12-HSL on mammalian cells. It promotes induction of apoptosis in macrophages and neutrophils (Tateda et al. 2003). Kaufmann et al. pioneered an immuno-pharmacotherapeutic approach to QS mediated microbial infections by developing anti-AHL monoclonal antibodies (mAbs). They demonstrated the inhibitory effect of mAb RS2-1G9 on AHL based QS in P. aeruginosa (Kaufmann et al. 2006). Further efforts have been made on the synthesis of QQ catalytic antibodies (sulfones) which resemble the transition-state structure of AHL-ring hydrolysis leading to attenuation of bacterial virulence (Kapadnis et al. 2009). 3-oxo-C₁₂-HSL-protein conjugate based immunization in mice proved effective in preventing motility caused by P. aeruginosa infections (Miyairi et al. 2006).

Metals targeting QS

Metals have been found to affect biofilm related activities. Ionic silver has antibacterial properties which affect P. aeruginosa caused infections (Melaive et al. 2005), where as Gallium acts by interfering with iron metabolism (Banin et al. 2008; Patriquin et al. 2008) to prevent biofilm formation (Yamamoto et al. 1994; Banin et al. 2005, 2006). Nitric oxide is a reactive free radical which kills cells within established biofilms (Barraud et al. 2006; Ghaffari et al. 2006; Hetrick et al. 2008; Hetrick et al.

Potential anti-bacterial opportunities

Bacteria are highly adaptive to fluctuations in environmental conditions (Zhang & Dong 2004), which enable them to coexist and co-evolve in natural environments, symbiotically or even as pathogen with their host. The worry which looms large on our minds is the ever increasing resistance of pathogens to antibiotics (Marris 2006; Cars et al. 2008; Courvalin 2008; Defoirdt et al. 2008). The focus is largely on P. aeruginosa, which causes life-threatening infections such as cystic fibrosis, leading to high rates of morbidity and mortality among human beings (Lyczak et al. 2002). The solution to this problem can be found out by understanding bacterial behaviour particularly in the case of chronic infection diseases. Here, bacteria prefer to remain silent and evade human immune responses (Otto 2004) until they have reached a cell density sufficient enough to produce enzymes which can destroy the host cell (Schauder & Bassler 2001; Winans & Bassler 2002; Waters & Bassler 2005). Quite a few examples of organisms with an ability to counter this phenomenon and retarding the expression of virulent behaviour of these pathogens have given some hope of finding a solution to this problem. The possibilities of succeeding lies either with a microbe (natural isolates or genetically engineered) or genetically engineer plants (Ferrer-Miralles et al. 2009), for producing QQ molecules. These molecules should be highly specific to QS regulator, stable, resistant to degradation by the host (Rasmussen & Givskov 2006b), versatile in production and non-toxic (Rasmussen & Givskov 2006a). Alternatively, a combination of QS signal degrading molecules may be exploited (Dong et al. 2000; 2001; Reimmann et al. 2002; Uroz et al. 2003). This method can be complemented by saturating a given environment with AHL molecules (Fray et al. 1999; Mae et al. 2001; Fray 2002) to initiate QS at a suboptimal cell density, which will be detrimental for the survival of pathogenic bacteria. Engineering plants with ability to induce QS at sub-optimal bacterial population has shown mixed behaviour among the non-target microbial community in the rhizosphere: i) yenI (from Yersinia enterocolitica) encoding for AHL synthase in the chloroplast of transgenic plants resulted activation

of QS of Erwinia and Pseudomonas with the release of QS signaling molecules (Fray et al. 1999; Dong et al. 2001; Mae et al. 2001; Fray 2002), ii) a negative impact of AHL produced by plants and bacteria was the reduction in biocontrol ability of Pseuodmonas aureofaciens (Fray et al. 1999), and iii) a no evident impact of rhizospheric microbial populations was recorded by C6HSL and 3OC6HSL signals produced by transgenic tobacco plants (D'Angelo-Picard et al. 2004).

C. albicans, a fungal pathogen is normally a component of human microflora. However, in immunocompromised individuals, they can cause systemic candidiasis. In mixed infections, it is often associated with P. aeruginosa. Within the conducive host physiological conditions, C. albicans turns virulent and invasive upon transformation from a budding to a hyphal morphology (Dhillon et al. 2003). At this stage, the farnesol produced by C. albicans interferes with the quinolone signal specific QS system in P. aeruginosa. In the presence of farnesol, the Pseudomonas quinolone signal binding with pqsA promoter (which regulates expression of virulence factors) (Déziel et al. 2005) is non-productive (Calfee et al. 2001). Farnesol at a concentration level of 25 µM lead to 39% reduction in PQS and at a concentration of 250 µM resulted in 85% decrease in extracellular PQS levels. Consequently, 250 µM farnesol to the medium of P. aeruginosa strain PA14 cultures resulted in 72% reduction in pyocyanin (a redox-active phenazine) production and 95% in the case of P. aeruginosa PAO1 in comparison to the control cultures. It thus has the potential to control Pseudomonas infection by blocking the production of virulence factor without inhibiting its growth. This places farnesol in the class of QS inhibitory molecules (Cugini et al. 2007). These studies demonstrate that strategies which affect the virulence process or the ability of bacteria to modulate the host immune system (Dunn et al. 2009) hold promise for effective management of chronic bacterial infections.

Limitations of QSI

Most of the QQ effects have been recorded on nonmucoid P. aeruginosa, which is observed in early stages of pulmonary infection in CF patients. Chronic patients have mucoid P. aeruginosa, which may not be cured through QSI treatments (Bjarnsholt & Givskov 2007). Halogenated furanones exhibit toxic side effects with potential to cause cancer and is likely to be unsuitable for human beings (Bjarnsholt & Givskov 2007), due to their base labile nature and are substrates for mammalian paraoxonases (Yates et al. 2002; Dragnov et al. 2005; Yang et al. 2005). In certain situations such as blocking the agr system leads to increased biofilm formation along with enhanced antibiotic resistance (Vuong et al. 2000, 2004). Thus targeting agr system to control staphylococcal infections may be counterproductive (Harraghy et al. 2007).

Selective pressure and QSI resistance

The basic science is being revealed for most QSIs and incidentally the efforts during the past two decades have not led them to be in the clinical stage. Since G+ve and G-ve bacteria do not show similarity in their QSS and does not communicate at high frequency, the chances of a broad spectrum QSI are bleak Bjarnsholt & Givskov 2008). The basic assumption and emphasis has been that disruption of QS is unlikely to put harsh selective pressures on pathogenic microbes, which are thus "unlikely" to develop resistance to QSIs (Hentzer & Givskov 2003; Defoirdt et al. 2010). However, it will be premature to assume that bacteria will not develop resistance against QSIs, such that we may not see an end to this battle against infections (Bjarnsholt & Givskov 2008). Quite a few cases provide evidences to support the likelihood of development of QSI resistance among pathogenic microbes: (i) variation in the specificity of AHL synthases in E. carotovora strains SCC3193 and SSC1 (Brader et al. 2005), (ii) variability in the presence of signal receptors in Burkholderia mallei—2-5 LuxR homologs (Case et al. 2008). Point mutations in the receptor of LuxR signal make them insensitive to N-(propylsulfanylacetyl)-L-HSL. This synthetic antagonist acts as an agonist for the mutant form (Koch et al. 2005). Further support follows from high mutation rate in the QS of different V. cholerae strains, which lead to constitutive or even non-functional QS regulation (Joelsson et al. 2006). The occurrence of QSS on a transposon in S. marcescens provide it with an opportunity to overcome any disruption in their QSS (Wei et al. 2006). Finally, Diggle et al. have shown the influence of nutrient medium on the growth of wild type and lasI and lasR mutants of P. aeruginosa (Diggle et al. 2007). These evidences have led to the apprehension that pathogenic microbes may exploit their genetic reservoir to develop resistance to QSI treatment. In view of the limited discoveries leading to novel modes of action against hospital pathogens, it has been estimated that it may take 10-15 years before novel antimicrobials are made available (Clatworthy et al. 2007; Payne et al. 2007). Prof. Givskov feels that it will take 5-10 years before QSI drugs can be seen in the market (Bjarnsholt & Givskov 2008). Although many of these compounds are quite promising, their clinical utility is yet to be proven. They however, expand the range of well and urgently needed armamentarium against highly resistant microbes (Martin et al. 2008). The need is to expand our strategies to find novel anti-microbials and anti-virulence targets (Njoroge & Sperandio 2009).

Opinion

QQ may be effective in disturbing the biofilm structure and increasing its susceptibility to the action of antibiotics (de Kievit & Iglewski 2000; Dong et al. 2000; Parsek & Greenberg 2000; Ren et al. 2001; Lin et al. 2003; Ueda & Wood 2009). However, caution need to be exercised on

the practical application of this strategy (Hibbing et al. 2009) as non-biofilm cells (of P. aeruginosa) are much more likely to express their virulence factors, toxins and proteases than non-planktonic cells in the biofilm (Resch et al. 2005). It may also be realized that a conclusive relation between QQ and its exploitation for gaining competitive advantage has not been established (Hibbing et al. 2009). So far, the approach of QS inhibition has met with limited success (Otto 2004; Wu et al. 2004; Persson et al. 2005; Rasmussen et al. 2005a), however, it has the potential to allow us to overcome the problem of rapidly evolving multi-drug resistant bacteria (Alksne & Projan 2000). It has been proposed that in natural environments, such altered signal molecules may provide cells with important sensory information about their physiochemical conditions (Decho et al. 2010). Such studies suggest that the most effective treatment regimen may be a combination of antibiotics and QSIs (Rasmussen et al. 2005a). The long-term goal of such studies is to develop novel biocontrol agents (Fray 2002; Hentzer et al. 2003; Bjarnsholt & Givskov 2008; Uroz et al. 2009), therapeutic strategies (Cámara et al. 2002), directed at infection control in both plants and animals (Uroz et al. 2005), and to effectively prevent widespread epidemic outbreaks.

Rhodococcus, Comomononas, Pseudomonas, and Ralstonia spp. are among the top contenders as organisms which may be exploited in the future as a source of QQ enzymes. It is primarily because of their abilities to quench a wide range of QS signals with varying acyl side chain lengths. However, the dependence of their QQ activity upon the chain length of the AHL molecules can be regarded as a major limiting factor in using them as "universal" antipathogenic drug producers. The best target may be to disrupt the QS signals outside the cell and here AHL lactonase may be the best approach since it is active against a wide range of AHLs with little influence of the length of the acyl chain on its efficiency (Dong et al. 2008). Here, Bacillus is more likely to succeed as an organism of choice because they produce AHL-lactonases, whose QQ activity is not limited by acyl chain length or substitutions at C3 position (Uroz et al. 2009). Another very interesting feature reported recently has been the high frequency of AHL based QS systems among Proteobacteria (Case et al. 2008). It has also revealed that quite a few organisms have the potential to detect and respond to exogenous signals, though they themselves are not able to produce QS signals as they lack genes for AHL synthase (Case et al. 2008). Bacillus being independent of AHL type QS (the only reported exception is that of Ren et al. 2002), AHL-lactonase will not prove inhibitory to itself. On the other hand, it can affect not only the QS of the AHL producers but also those which are non-AHL producers including the orphan QS systems (Fugua 2006; Case et al. 2008; Decho et al. 2010). In addition, Bacillus can be used in a wide range of environments including treatment of human beings, as it is a known probiotic organism, which has been accorded the status of GRAS: generally regarded as safe by FDA (Porwal et al. 2009). Furthermore, because of its ability to sporulate and a capacity to produce a range of antibiotics, it is less susceptible to attack by antibacterial agents and other antibiotic producing organisms (Arguelles-Arias et al. 2009). It is further recommended that plant or algal extracts might pose relatively less risk of QSI resistance development (Defoirdt et al. 2010) and it may be better to target major virulence factors instead of blocking their expression (Clatworthy et al. 2007; Charkowski 2009). Quorumex's first product (Topic-Qx), from plant materials claims to have anti-QS properties. Incidentally, it has met with a very aggressive response from public, who have shown apprehensions about its utility and authenticity (http://www.boingboing.net/2010/06/22/ do-quorum-sensing-me.html).

Declaration of interests

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