

Mutational Analysis of *Burkholderia thailandensis* Quorum Sensing and Self-Aggregation^{∇†}

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Received 6 May 2009/Accepted 20 July 2009

Acyl-homoserine lactone (acyl-HSL) quorum-sensing signaling is common to many *Proteobacteria*. Acyl-HSLs are synthesized by the LuxI family of synthases, and the signal response is mediated by members of the LuxR family of transcriptional regulators. *Burkholderia thailandensis* is a member of a closely related cluster of three species, including the animal pathogens *Burkholderia mallei* and *Burkholderia pseudomallei*. Members of this group have similar *luxI* and *luxR* homologs, and these genes contribute to *B. pseudomallei* and *B. mallei* virulence. *B. thailandensis* possesses three pairs of *luxI-luxR* homologs. One of these pairs, BtaI2-BtaR2, has been shown to produce and respond to 3OHC₁₀-HSL and to control the synthesis of an antibiotic. By using a markerless-exchange method, we constructed an assortment of *B. thailandensis* quorum-sensing mutants, and we used these mutants to show that BtaI1 is responsible for C₈-HSL production and BtaI3 is responsible for 3OHC₈-HSL production. We also show that a strain incapable of acyl-HSL production is capable of growth on the same assortment of carbon and nitrogen sources as the wild type. Furthermore, this mutant shows no loss of virulence compared to the wild type in mice. However, the wild type self-aggregates in minimal medium, whereas the quorum-sensing mutant does not. The wild-type aggregation phenotype is recovered by addition of the BtaI1-R1 HSL signal C₈-HSL. We propose that the key function of the BtaR1-BtaI1 quorum-sensing system is to cause cells to gather into aggregates once a sufficient population has been established.

Members of the genus *Burkholderia* constitute a large group of metabolically diverse species. We are interested in a subgroup that is closely related at the genomic level and is comprised of the three species *Burkholderia thailandensis*, *Burkholderia pseudomallei*, and *Burkholderia mallei* (63). Of these species, *B. mallei* is the only obligate animal pathogen. *B. mallei* causes glanders in horses, donkeys, and mules and less frequently in humans (61). *B. pseudomallei*, the causative agent of the human disease melioidosis, can be isolated from soil and water in Southeast Asia and northern Australia (7, 34, 43). Both *B. pseudomallei* and *B. mallei* are highly infectious to humans, and both are considered bioterrorism threats (45). Melioidosis is an emerging disease (43, 61). *B. thailandensis* has a limited potential to cause disease (15, 21, 33). Evidence suggests that *B. mallei*, *B. pseudomallei*, and *B. thailandensis* evolved from a common *B. pseudomallei*-like ancestor (37).

We are interested in *N*-acyl-homoserine lactone (acyl-HSL) quorum sensing in *B. mallei*, *B. pseudomallei*, and *B. thailan-*

densis primarily because quorum sensing has been reported to influence the virulence of *B. mallei* and *B. pseudomallei* and because there are multiple quorum-sensing circuits in each species (53–55). Quorum sensing allows bacteria to sense and respond to their population density (4, 19, 58). In *Proteobacteria*, quorum sensing is often mediated by diffusible acyl-HSL signals. At a critical concentration, acyl-HSLs bind LuxR family transcriptional regulators and affect changes in gene expression (20). Acyl-HSLs are produced by members of the LuxI family of synthases. Different synthases catalyze the production of acyl-HSLs that vary in the nature of the acyl side chain (20, 47). LuxI and LuxR homologs that are adjacently encoded in the genome form cognate pairs. Many bacterial genomes contain multiple cognate pairs and can also contain unpaired orphan LuxR signal receptors that do not have a cognate *luxI* gene nearby in the genome. Relatively little is known about the functions of the orphans (12, 31, 32, 38, 41). Quorum-sensing systems are found in dozens of different *Proteobacteria* species and can affect the transcription of tens or hundreds of different genes in a given species (1, 50, 57, 60). Genes coding for extracellular enzymes and factors are commonly activated by acyl-HSL quorum sensing, and members of the quorum can share these public goods (60).

B. pseudomallei and *B. thailandensis* possess three cognate receptor-synthase pairs (systems 1, 2, and 3) and at least two orphan receptors (53, 55). *B. mallei* possesses the same complement of quorum-sensing genes, except it is missing the system 2 cognate pair (54). It was first reported that the *B. thail-*

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† Supplemental material for this article may be found at <http://jb.asm.org/>.

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[∇] Published ahead of print on 31 July 2009.

TABLE 1. Bacterial strains and plasmids used

Bacterial strain or plasmid	Genotype or phenotype ^a	Reference or source
Bacterial strain		
<i>E. coli</i>		
DH5 α		Invitrogen
DH5 α (pECP61.5)	Acyl-HSL bioreporter	40
<i>A. tumefaciens</i> KYC55	Acyl-HSL bioreporter; R10 (pJZ384, pJZ410, pJZ372)	65
<i>P. fluorescens</i> 1855	Acyl-HSL bioreporter; WT (pSF105, pSF107)	30
<i>R. capsulatus</i> ALS1	Acyl-HSL bioreporter; WT (pYP)	49
<i>B. thailandensis</i>		
E264	Soil isolate from central Thailand	6
JBT101	E264 $\Delta btaI1$	This study
JBT102	E264 $\Delta btaI2$	This study
JBT103	E264 $\Delta btaI3$	This study
JBT107	E264 $\Delta btaR1$	This study
JBT108	E264 $\Delta btaR2$	This study
JBT109	E264 $\Delta btaR3$	This study
JBT110	E264 $\Delta btaR4$	This study
JBT111	E264 $\Delta btaR5$	This study
JBT104	E264 $\Delta btaI2 \Delta btaI3$	This study
JBT112	E264 $\Delta btaI1 \Delta btaI2 \Delta btaI3$	This study
Plasmids		
pBAD24	Arabinose-inducible expression vector; Amp ^r	23
pBTI1	pBAD24 with arabinose-inducible <i>btaI1</i> ; Amp ^r	This study
pBTI3	pBAD24 with arabinose-inducible <i>btaI3</i> ; Amp ^r	This study
pBBR1Tp	Broad-host-range vector; Tp ^r	14
pJRC112	pBBR1Tp with <i>B. thailandensis</i> mutant <i>pheS</i> (304AG); Tp ^r	This study
pEX18Tc	<i>P. aeruginosa</i> suicide plasmid; Tet ^r	25
p34S-Tp	Antibiotic resistance cassette vector; Tp ^r	13
pEX18Tp	pEX18Tc with <i>dhfrIII</i> from p34S-Tp; Tet ^r and Tp ^r	This study
pJRC115	Mobilizable suicide vector with the <i>B. thailandensis pheS</i> counterselectable marker (304AG); Tp ^r	This study
pJRC115 <i>btaI1</i>	pJRC115 with $\Delta btaI1$ extending from +13 to +597 with respect to the translational start site; Tp ^r	This study
pJRC115 <i>btaI2</i>	pJRC115 with $\Delta btaI2$ extending from +13 to +606 with respect to the translational start site; Tp ^r	This study
pJRC115 <i>btaI3</i>	pJRC115 with $\Delta btaI3$ extending from +19 to +594 with respect to the translational start site; Tp ^r	This study
pJRC115 <i>btaR1</i>	pJRC115 with $\Delta btaR1$ extending from +13 to +699 with respect to the translational start site; Tp ^r	This study
pJRC115 <i>btaR2</i>	pJRC115 with $\Delta btaR2$ extending from +22 to +686 with respect to the translational start site; Tp ^r	This study
pJRC115 <i>btaR3</i>	pJRC115 with $\Delta btaR3$ extending from +19 to +675 with respect to the translational start site; Tp ^r	This study
pJRC115 <i>btaR4</i>	pJRC115 with $\Delta btaR4$ extending from +16 to +690 with respect to the translational start site; Tp ^r	This study
pJRC115 <i>btaR5</i>	pJRC115 with $\Delta btaR5$ extending from +13 to +708 with respect to the translational start site; Tp ^r	This study

^a Tp^r, trimethoprim resistant; Amp^r, ampicillin resistant; Tet^r, tetracycline resistant; WT, wild type.

landensis quorum-sensing signals were hexanoyl-HSL (C₆-HSL), octanoyl-HSL (C₈-HSL), and decanoyl-HSL (C₁₀-HSL) (55); however, a careful analysis of *B. thailandensis* system 2 (encoded by *btaR2* and *btaI2*) revealed that the primary signal was *N*-3-hydroxy-decanoyl-HSL (3OHC₁₀-HSL), and the system also produced significant amounts of, and responded to, *N*-3-hydroxy-octanoyl-HSL (3OHC₈-HSL) (18). The studies of the BtaR2-BtaI2 quorum-sensing system raise questions about the signals that are specific to the other two *B. thailandensis* systems. We can speculate about the signals based on findings with the conserved systems 1 and 3 in *B. mallei* (16, 17) and system 1 in *B. pseudomallei* (51). The *B. mallei* and *B. pseudomallei* systems 1 both involve C₈-HSL (17, 51), and system 3 in *B. mallei* involves 3OHC₈-HSL (16).

In addition to the signals produced by quorum-sensing system 2, our group has also shown that system 2 controls a number of genes required for synthesis of an antibiotic (18). However, it is unclear what the signals are for systems 1 and 3 and what behaviors other than antibiotic synthesis are con-

trolled by quorum sensing in *B. thailandensis*. Here, we describe a method for the construction of *B. thailandensis* quorum-sensing mutants. We describe studies with various mutants that establish the principal acyl-HSLs for systems 1 and 3, and we show that a primary function of system 1 in *B. thailandensis* is to induce self-aggregation. Quorum sensing did not appear to contribute to the virulence of *B. thailandensis* in our mouse infection model.

MATERIALS AND METHODS

Bacterial strains, growth conditions, and chemicals. The bacterial strains used are described in Table 1. *Escherichia coli* and *B. thailandensis* were grown in Luria-Bertani (LB) broth, 20% LB broth, M9 minimal medium (35) with either 0.4% glucose or 20 mM succinate as a carbon and energy source and additional supplements as indicated, or Biolog IF-0 inoculation medium. Agar plates contained 1.5% Bacto agar (BD). Antibiotics were at the following concentrations (per ml): 30 μ g trimethoprim (Tp), 30 μ g kanamycin, 100 μ g ampicillin, and 30 μ g gentamicin for *E. coli*, and 100 μ g Tp for *B. thailandensis*. For counterselection during mutant construction, we used M9 minimal agar plates with glucose and 10 mM *para*-chloro-phenylalanine (*p*-Cl-Phe). For arabinose

promoter activation in *E. coli*, we used 0.2% (wt/vol) L-arabinose. To assess the aggregation of *B. thailandensis*, we used M9 minimal medium with glucose and MOPS (morpholinepropanesulfonic acid) buffer (50 mM; pH 7.0). The starting optical density at 600 nm (OD₆₀₀) for aggregation experiments was 0.01, and the inocula were from LB broth cultures grown with shaking for 24 h at 37°C. Acyl-HSLs were added to media where indicated at the following concentrations: 2 μM of D,L-C₈-HSL and 1 μM L-3OHC₈-HSL.

DNA manipulations and transformation procedures. Routine procedures were used for DNA manipulations (46). Plasmid DNA was isolated using Qia-prep mini-spin kits (Qiagen). PCR and plasmid fragments were isolated by using Qiaquick PCR purification or gel extraction kits (Qiagen). Chromosomal DNA was prepared by using Genra Puregene Cell kits (Qiagen). PCR products were generated using an Epicentre Failsafe PCR System or a Roche ExpandLong Template PCR system.

Transformation of *B. thailandensis* was by electroporation in a 0.2-cm electroporation cuvette with 100 μl of competent cells at a voltage of 2.5 kV and a time constant of approximately 5 ms. This was followed by a 2-h recovery in 500 μl LB broth with shaking at 37°C before the cells were plated on LB agar plates containing appropriate antibiotics. We used at least 2 μg nonreplicative plasmid DNA for allelic recombination. Preparation of competent *B. thailandensis* cells was as follows. Overnight cultures were diluted 1:500 in 100 ml of LB broth. When the OD₆₀₀ reached 0.5, the cells were pelleted by centrifugation, washed twice with equal volumes of cold water, and then washed once and suspended in 0.2 ml of cold 10% glycerol. These cell suspensions constituted our competent cell preparations.

Plasmid and strain construction. The plasmids we used are described in Table 1. The sequences of oligonucleotide primers are available upon request. To construct the BtaI1 and BtaI3 expression vectors pBTI1 and pBTI3, the open reading frames of *btaI1* (BTH_II1512) and *btaI3* (BTH_II0804) were PCR amplified from *B. thailandensis* genomic DNA. The primers were designed to incorporate EcoRI and XbaI restriction sites at the ends of the PCR products. The PCR products were digested with EcoRI and XbaI and ligated to EcoRI-XbaI-digested pBAD24 (23) to generate pBTI1 and pBTI3, which contained *btaI1* and *btaI3*, respectively. The plasmids were constructed so that *btaI1* and *btaI3* expression was driven by the L-arabinose-inducible promoter (P_{BAD}) present in the parent plasmid pBAD24.

We developed a method for making *B. thailandensis* quorum-sensing mutants that is similar to a recently developed method for making unmarked chromosomal mutations in a variety of *Burkholderia* species (3). Mutations were introduced by markerless allelic exchange. Unmarked mutations were made during two homologous recombination steps. In the first recombination step, a nonreplicative plasmid with a modified gene was introduced into the recipient strain, where it could integrate into the chromosome at the target gene. For this step, we selected for Tp resistance encoded by the plasmid-borne dihydrofolate reductase gene, *dhfrIIIa*. In the second recombination step, the integrated plasmid was excised from the chromosome, leaving behind either the original wild-type allele or the desired modified allele. The plasmid contained a counterselectable *pheS* allele with an A304G mutation, which conferred sensitivity to *p*-Cl-Phe (3, 27, 29).

The suicide plasmid pJRC115 was used to deliver quorum-sensing-gene deletions to the *B. thailandensis* chromosome. This plasmid has *dhfrIIIa* and the *B. thailandensis* mutant *pheS* allele. To construct pJRC115, we excised the *dhfrIII* cassette from p34S-Tp (13) by KpnI digestion, treated the cassette with Klenow fragment (New England Biolabs) to create blunt ends, and ligated this DNA to EcoRV-BstZ171-digested pEX18Tc (25), thereby creating pEX18Tp. The mutant *pheS* allele was introduced into pEX18Tp to make pJRC115. To construct the mutant *pheS* allele, the *B. thailandensis pheS* (BTH_I2591) open reading frame and upstream promoter were PCR amplified to make two products from bp -406 to +906 and from bp +885 to +1081 relative to the predicted translational start site. During amplification, a primer-incorporated missense mutation in codon 304 (A304G) was created. We used a second PCR to anneal and amplify the two products. Primer-incorporated XbaI and BamHI sites were created at the ends of this product during amplification. The product was digested with XbaI and BamHI and ligated to XbaI-BamHI-digested pBBRTp (14) to make pJRC112, a replicative vector with the mutant *pheS* allele. pJRC112 was digested with XbaI and SmaI to release the mutant *pheS* allele, and this was ligated to NheI-NruI-digested pEX18Tp to make pJRC115 (Table 1).

To construct gene deletion vectors, we used overlap extension PCR to generate PCR products with about 1 kb of DNA homologous to DNA flanking the intended sites of deletion. We annealed and amplified the products by PCR. Primer-encoded restriction enzyme sites were introduced into the ends of the PCR products during amplification. The *btaR4* deletion allele was digested with NheI and HindIII. The other alleles were digested with XbaI and HindIII. The

digested PCR products were ligated to XbaI-HindIII-digested pJRC115. To construct the single-mutant strains JBT101-103 and 107-111, the relevant pJRC115-derived suicide vector was used to transform *B. thailandensis* by electroporation, and Tp-resistant transconjugants were identified on selective LB agar plates. The transformants were grown in LB broth for 10 h in the absence of selection to allow excision of the plasmid from the chromosome and then counterselected on minimal medium-plus-glucose agar plates supplemented with *p*-Cl-Phe. Mutations were confirmed by sequencing PCR products generated with primers targeting chromosomal DNA flanking the recombination sites. To make strains with multiple gene deletions, alleles were sequentially introduced by the method described above. The double mutant JBT104 ($\Delta btaI2 \Delta btaI3$) was constructed from JBT103 ($\Delta btaI3$) as an intermediate step to make JBT112 ($\Delta btaI1 \Delta btaI2 \Delta btaI3$).

Acyl-HSL identification. We used three different approaches to analyze acyl-HSL production; liquid chromatography/mass spectrometry/mass spectrometry (LC/MS/MS), radioisotope analysis, and measurements of biological activity as described below.

For LC/MS/MS, acyl-HSLs were extracted from 5-ml cultures grown with shaking in LB broth to stationary phase (OD₆₀₀ = 4.0). The cells were removed from the culture fluid by centrifugation, and the culture fluid was extracted with two equal volumes of acidified ethyl acetate (0.1 ml/liter glacial acetic acid). The extracts were dried under a stream of nitrogen gas, suspended in 100 μl of 100% methanol, and subjected to LC/MS/MS analysis as described previously (22). We used deuterated C₆-HSL and deuterated C₁₂-HSL as internal standards.

We used a radiotracer assay similar to that described previously by Schaefer et al. (48) to monitor acyl-HSLs produced by recombinant *E. coli*. Briefly, 5-ml cultures of *E. coli* DH5α containing pBTI1 or pBTI3 were grown in LB broth plus 0.2% L-arabinose (starting OD₆₀₀ 0.025). When the OD₆₀₀ reached 0.5, we pelleted the cells by centrifugation at 2,750 × *g* for 10 min and suspended the cells in the pellet in 5 ml of M9 minimal medium containing L-arabinose and succinate. After 10 min at 37°C with shaking, 5 μCi of L-[1-¹⁴C]methionine (American Radiolabeled Chemicals) was added to the cell suspension. After a further 3 h of incubation at 37°C, the cell suspension was extracted with two equal volumes of acidified ethyl acetate (glacial acetic acid; 0.1 ml/liter). The ethyl acetate fraction was evaporated to dryness under a stream of nitrogen gas, and the residue was dissolved in 50% methanol. The dissolved acyl-HSLs were separated by C₁₈ reverse-phase high-performance liquid chromatography (HPLC) in a 10 to 100% methanol gradient with a flow rate of 1 ml/min over 70 fractions.

We used four different bioassays to monitor acyl-HSLs produced by *B. thailandensis* and *B. thailandensis* quorum-sensing mutants. To prepare samples for analysis, 5-ml cultures were grown to an OD₆₀₀ of 4.0 in LB broth with MOPS (50 mM; pH 7.0), the cells were removed from the culture fluid by centrifugation, the culture fluid was extracted twice with acidified ethyl acetate, and the ethyl acetate fraction was evaporated to dryness under a stream of nitrogen gas. The residue was dissolved in 1 ml acidified ethyl acetate, and the ethyl acetate solutions were used in bioassays. For the bioassays, we used *Agrobacterium tumefaciens* KYC55(pJZ372)(pJZ384)(pJZ410) with *traI::lacZ* and *traR* on separate plasmids (65), *Pseudomonas fluorescens* 1855(pSF105)(pSF107) with *phzA::lacZ* and *phzR* on separate plasmids (30), *E. coli* DH5α(pECP61.5) with *rhlA::lacZ* and *ptac-rhlR* on the same plasmid (39, 40), and *Rhodobacter capsulatus* ALS1(pYP) with *orf2::lacZ* on the plasmid and *gtaR* on the chromosome (49). Details of the bioassay procedures have been described elsewhere (17, 30, 40, 49).

PM analysis. We used a Phenotype MicroArray (PM) system (Biolog, Hayward, CA) according to the manufacturer's instructions. We screened carbon, nitrogen, and phosphorus sources by using PM-1, PM-2, and PM-3 microtiter plates. Inocula were prepared by scraping colonies from 20% LB agar plates, suspending the cells in Biolog IF-0 inoculating fluid, and adjusting the transmittance to 85%. The cell suspensions were then diluted 1:200 in IF-0 containing Biolog Redox Dye Mix A, which contains a redox dye used to measure cell respiration. These cell suspensions were used as inocula for PM plates, which were incubated without shaking at 37°C in an OmniLog instrument. The respiration-dependent color changes in each well were measured at 15-min intervals for 3 days.

Mouse infection experiments. Specific-pathogen-free BALB/c mice were obtained from Jackson Laboratories (Bar Harbor, ME). All animals were housed in laminar flow cages and were permitted ad lib access to sterile food and water. Euthanasia was accomplished with intraperitoneal pentobarbital, followed by exsanguination by cardiac puncture. The Institutional Animal Care and Use Committee of the University of Washington approved all experimental procedures. For infection, 20 ml LB broth was inoculated with a single colony of *B. thailandensis* E264, JBT101 ($\Delta btaI1$), or JBT112 ($\Delta btaI1 \Delta btaI2 \Delta btaI3$). After 18 h with shaking at 37°C, the bacteria were washed twice and suspended in

TABLE 2. Relative amounts of acyl-HSLs produced by *B. thailandensis* wild type and quorum-sensing mutants

Acyl-HSL	Relative acyl-HSL abundance in culture extracts ^a			
	E264 (wild type)	JBT101 (<i>ΔbtaI1</i>)	JBT103 (<i>ΔbtaI3</i>)	JBT112 (<i>ΔbtaI1</i> <i>ΔbtaI2</i> <i>ΔbtaI3</i>)
3OHC ₄ -HSL	4 (1)	ND ^b	ND	ND
C ₈ -HSL	30 (2)	ND	39 (1)	ND
3OHC ₈ -HSL	21 (0.5)	22 (1)	7 (1)	ND
3OHC ₉ -HSL	1	ND	ND	ND
3OHC ₁₀ -HSL	43 (0.3)	78 (1)	55 (2)	ND

^a The values are the average relative abundances (percent) of acyl-HSLs from two independent cultures, and the range is indicated in parentheses.

^b ND, none detected.

phosphate-buffered saline to the desired density. The mice were exposed to aerosolized bacteria by using a snout-only inhalation system (In-Tox Products) (59). Aerosols were generated from a MiniHeart hi-flo nebulizer (Westmed) driven at 40 lb/in². Airflow through the system was maintained for 10 min at 24 liters per min, followed by a 5-min air purge. Bacterial deposition in each experiment was determined from quantitative culture of the left lungs from four sentinel mice sacrificed immediately after infection with each strain. Lung tissue was homogenized in 1 ml phosphate-buffered saline, and serial dilutions were plated on LB agar. Colonies were counted after 2 to 4 days at 37°C under 5% CO₂. For the number of recovered CFU per lung from sentinel mice sacrificed immediately after infection, see the legend to Fig. 5. Infected mice (four female and four male for each strain) were monitored for 14 days postexposure. The animals were examined daily for illness or death, and abdominal surface temperatures were measured using a Ranger MX4P digital infrared thermometer (Raytek). Ill animals with temperatures of <23°C, ruffled fur, eye crusting, hunched posture, and lack of resistance to handling were deemed terminal and were euthanized.

RESULTS

***btaI1*- and *btaI3*-dependent production of acyl-HSLs.** We used LC/MS/MS (22) and a [¹⁴C]methionine incorporation assay (48) to determine what acyl-HSLs are produced by *B. thailandensis*. Both of these methods detect acyl-HSLs in a complex mixture without bias toward acyl side chain length or substitution and provide information on the relative abundances of the acyl-HSLs in the sample (22, 48). LC/MS/MS was used to analyze acyl-HSLs in ethyl acetate extracts of stationary-phase culture fluid from wild-type *B. thailandensis*. We found that extracts had C₈-HSL, 3OHC₈-HSL, 3OHC₁₀-HSL, and a relatively small amount of *N*-3-(hydroxybutanoyl)-HSL (3OHC₄-HSL) and *N*-3-(hydroxynononyl)-HSL (3OHC₉-HSL) (Table 2). The levels of 3OHC₄-HSL and 3OHC₉-HSL were about 4% and 1% of the total fatty acyl-HSL content, respectively (Table 2).

The *B. thailandensis* signal synthase BtaI2 was characterized in a separate study and shown to catalyze 3OHC₈-HSL and 3OHC₁₀-HSL synthesis (18). To determine which acyl-HSLs were produced by each of the other two *B. thailandensis* acyl-HSL synthases, we constructed strains with individual in-frame deletions of the signal synthase genes (*btaI1* and *btaI3*) and analyzed the acyl-HSL production of these strains by LC/MS/MS. The *btaI1* mutant (JBT101) produced 3OHC₈-HSL and 3OHC₁₀-HSL but did not produce detectable levels of C₈-HSL (Table 2), supporting the conclusion that BtaI1 is a C₈-HSL synthase. The *btaI3* mutant (JBT103) produced detectable levels of C₈-HSL, 3OHC₈-HSL, and 3OHC₁₀-HSL; however, the

relative abundance of 3OHC₈-HSL was threefold less than that of the wild type. It is important to note that Table 2 shows relative abundances of acyl-HSLs and not absolute values. Based on these results, we hypothesized that BtaI3 is a 3OHC₈-HSL synthase and that the 3OHC₈-HSL detected in the *btaI3* mutant strain is produced by BtaI2.

To verify that BtaI1 is a C₈-HSL synthase and that BtaI3 is a 3OHC₈-HSL synthase, the proteins were each expressed in *E. coli*, and acyl-HSL production was monitored by using a radiotracer assay, which incorporates one ¹⁴C atom into each acyl-HSL molecule regardless of side chain length or substitution (48). Recombinant *E. coli* expressing BtaI1 incorporated ¹⁴C into one major product that coeluted with C₈-HSL by C₁₈ reverse-phase HPLC (Fig. 1). Recombinant *E. coli* expressing BtaI3 had one major product that coeluted with 3OHC₈-HSL (Fig. 1). These results are consistent with the conclusion that BtaI1 is a C₈-HSL synthase and BtaI3 is a 3OHC₈-HSL synthase.

Quorum sensing and metabolic capabilities. In other bacteria, such as *Pseudomonas aeruginosa* and *Vibrio fischeri*, quorum sensing affects the range of utilizable carbon and energy sources. In particular, proteases are often under quorum control (1, 40, 50, 52). To test whether quorum sensing controls metabolism in *B. thailandensis*, we used Biolog phenotype microarrays to compare the abilities of the wild type and a quorum-sensing mutant to utilize 344 different compounds (5). We constructed a quorum-sensing mutant with unmarked, in-frame deletions of all three of the acyl-HSL synthase genes (*btaI1*, *btaI2*, and *btaI3*) by using a *pheS* counterselection method (see Materials and Methods). This strain did not produce any acyl-HSLs that were detectable by LC/MS/MS (Table 2) or by any of four bioassays that in combination should detect the majority of described fatty acyl-HSLs (Table 3). The wild-type strain produced acyl-HSLs that were detectable by LC/MS/MS and by three of the four bioassays (Tables 2 and 3). The Biolog phenotypic-array method measures the respiration rate as an indication of growth. Both the wild type and the mutant metabolized a wide range of nutrients (detailed in Table S1 in the supplemental material). Interestingly, the mutant showed greater respiration rates on most substrates tested. This is

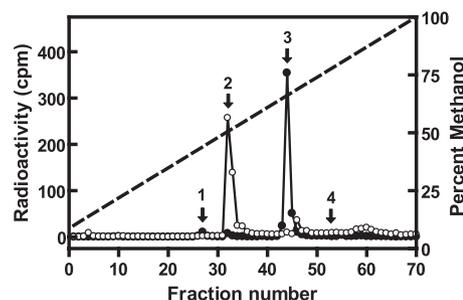


FIG. 1. Methanol gradient HPLC separation of radioactive acyl-HSLs produced by recombinant *E. coli* expressing *B. thailandensis* signal synthases. Shown is *E. coli* containing the *btaI1* vector pBTI1 (●) or the *btaI3* vector pBTI3 (○). The y-axis values are radioactive counts per minute (cpm) divided by 10³ for pBTI1 or 10² for pBTI3. The radiotracer assay provides a measure of the relative abundances of all acyl-HSLs produced, regardless of side chain length or substitution. The arrows indicate the fractions in which synthetic C₆-HSL (1), 3OHC₈-HSL (2), C₈-HSL (3), or C₁₀-HSL (4) was eluted.

TABLE 3. Activation of acyl-HSL reporters by culture extracts of *B. thailandensis* wild type and an acyl-HSL synthesis mutant

Bioassay strain ^a	Range of acyl-HSLs detected	β -Galactosidase activity (fold induction) of:	
		E264 (wild type)	JBT112 ($\Delta btaI1$ $\Delta btaI2$ $\Delta btaI3$)
<i>A. tumefaciens</i> KYC55(pJZ372)(pJZ384)(pJZ410)	Broad range	2×10^5 ($\pm 9\%$)	1 ($\pm 11\%$)
<i>P. fluorescens</i> 1855(pSF105)(pSF107)	3OHC ₆ -HSL, 3OHC ₈ -HSL	4×10^2 ($\pm 7\%$)	1 ($\pm 5\%$)
<i>E. coli</i> DH5 α (pECP61.5)	C ₄ -HSL, C ₆ -HSL	13 ($\pm 12\%$)	1 ($\pm 11\%$)
<i>R. capsulatus</i> ALS1(pYP)	C ₁₄ -HSL, C ₁₆ -HSL	1 ($\pm 8\%$)	1 ($\pm 9\%$)

^a Bioassays are described in Materials and Methods. The induction was in comparison to controls with no culture extracts added. The values are the averages from at least two independent cultures, and the range is indicated in parentheses.

exemplified by the examples shown in Fig. 2. We tested the abilities of the parent and the quorum-sensing mutant to degrade proteins. Both strains were capable of degrading gelatin and casein (data not shown). Our results led us to suggest that *B. thailandensis* quorum sensing does not affect the metabolic diversity of *B. thailandensis* as it does in *P. aeruginosa* (40, 50), for example. However, quorum sensing does have a negative influence on the rate of respiration on most carbon, nitrogen, or phosphorus substrates under the conditions of our experiments.

***B. thailandensis* quorum sensing and intercellular aggregation.** Our phenotype microarray results suggested that quorum sensing has a global affect on the rate of cellular growth and metabolism. We propose that this could result from control of processes that affect cellular respiration or by the imposition of a metabolic burden on dividing cells. A possible explanation

arose from our observation that wild-type *B. thailandensis* aggregated and formed macroscopic clumps when grown in a minimal medium similar to that used for phenotype microarray experiments, whereas the acyl-HSL synthase-deficient mutant JBT112 did not form clumps (Fig. 3A). Aggregation of the mutant strain was restored when we added C₈-HSL and 3OHC₈-HSL to the minimal medium (Fig. 3A). Although there was no obvious aggregation of the wild type or mutant in LB broth, wild-type cultures spotted on LB agar plates and grown for 4 days exhibited a wrinkly appearance associated with the production of an exopolysaccharide (EPS), whereas the mutant colonies were not wrinkly (Fig. 3B). We suspect that in our phenotype microarray experiments aggre-

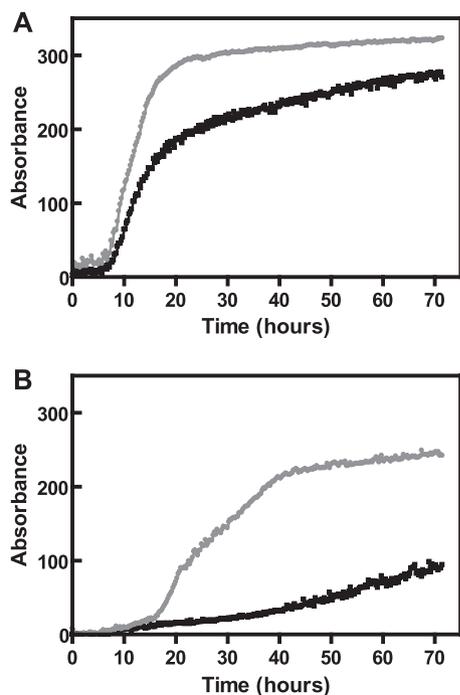


FIG. 2. Metabolism of α -D-glucose (A) and L-isoleucine (B) by *B. thailandensis* wild-type and JBT112 ($\Delta btaI1$ $\Delta btaI2$ $\Delta btaI3$) strains. Metabolism was monitored as respiration with glucose or L-isoleucine as the sole source of carbon in Biolog phenotype microarray experiments. Respiration was measured at 15-min intervals for 72 h. Shown are the *B. thailandensis* wild type E264 (black) and the quorum-sensing signal synthase-deficient mutant JBT112 (gray).

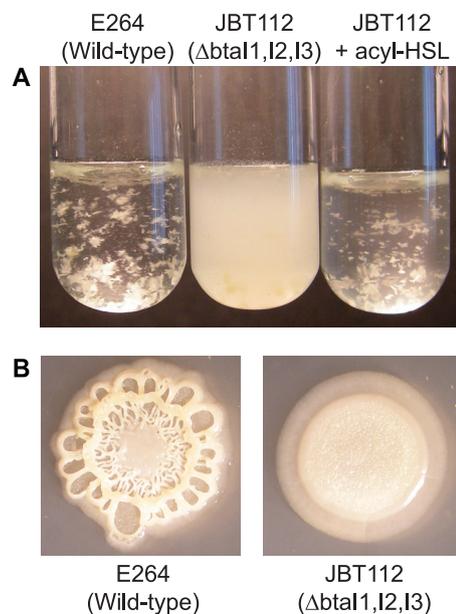


FIG. 3. Phenotype of a quorum-sensing signal synthase-deficient mutant. (A) Aggregation in shaken liquid cultures. When grown in minimal medium, the wild-type E264 cells aggregate and form clumps. The quorum-sensing mutant JBT112 ($\Delta btaI1$ $\Delta btaI2$ $\Delta btaI3$) does not show visible aggregation. The cultures were agitated just prior to image acquisition. Ethyl acetate solutions of C₈-HSL and 3OHC₈-HSL were added to a sterile glass culture tube and dried to completion just prior to addition of the culture medium and inoculum. (B) Growth of wild-type E264 and the mutant JBT112 on solid medium. The inoculum was 5 μ l from stationary-phase cultures grown for 24 h in LB broth. The photographs were taken with a digital camera mounted on an Olympus SZX12 dissecting microscope after incubation for 24 h at 37°C and an additional 72 h at room temperature. The colonies measured approximately 1 cm in diameter.

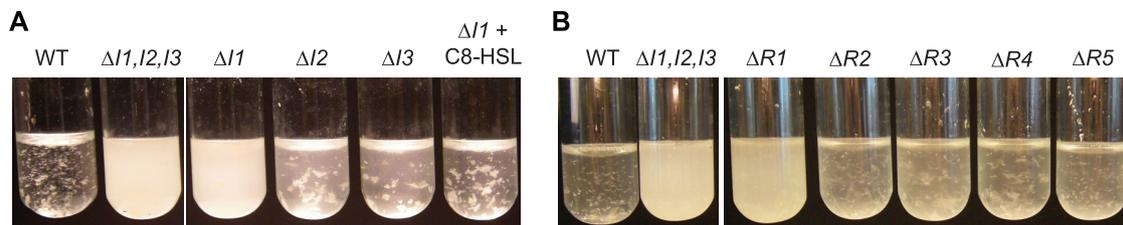


FIG. 4. *B. thailandensis* BtaR1 and BtaI1 are required for cell aggregation. *B. thailandensis* wild-type (WT) and quorum-sensing mutant strains were grown in minimal medium to assess aggregation, as for Fig. 3. (A) The following strains were studied: JBT101 ($\Delta btaI1$), JBT102 ($\Delta btaI2$), JBT103 ($\Delta btaI3$), and JBT101 with C₈-HSL (added as described for acyl-HSL additions in the legend to Fig. 3). (B) Aggregation of *B. thailandensis* signal receptor mutant strains JBT107 ($\Delta btaR1$), JBT108 ($\Delta btaR2$), JBT109 ($\Delta btaR3$), JBT110 ($\Delta btaR4$), and JBT111 ($\Delta btaR5$). Strain JBT112 ($\Delta btaI1 \Delta btaI2 \Delta btaI3$) is also shown.

gation has a negative influence on respiration, because cells deep within aggregates have limited access to oxygen. The conclusion that aggregation affects cellular respiration is supported by the following result. We monitored the growth of both the wild type and the quorum-sensing mutant in LB broth, a medium in which neither strain forms aggregates, and we found that the growth rates were identical (both strains had a doubling time of 36 min at 37°C with shaking) (data not shown).

The *btaI1-btaR1* quorum-sensing system is required for cell aggregation. Next, we sought to determine which of the multiple *B. thailandensis* quorum-sensing systems is required for cell aggregation. To address this issue, we constructed strains with mutations in individual signal synthase genes or signal receptor genes. Our *btaI1* mutant did not aggregate, whereas the *btaI2* and *btaI3* mutants formed aggregates indistinguishable from wild-type aggregates (Fig. 4A). Aggregation was restored in the *btaI1* mutant strain by the addition of C₈-HSL (the acyl-HSL product of BtaI1 activity) to the growth medium (Fig. 4A). This leads to the conclusion that clumping is dependent on the BtaI1-BtaR1 system. In support of this conclusion, we found that a *btaR1* mutant lost the clumping phenotype but *btaR2*, *-R3*, *-R4*, and *-R5* mutants all formed aggregates (Fig. 4B).

Quorum sensing and virulence of *B. thailandensis*. The published literature shows that the virulence of a variety of *B. pseudomallei* and *B. mallei* quorum-sensing mutants is attenuated in animal models, including airborne mouse infection models (53, 54, 56). Like *B. pseudomallei*, *B. thailandensis* infects, causes a melioidosis-like disease, and can kill mice when administered by aerosol, as described elsewhere (28, 59). Thus, we compared the virulence of *B. thailandensis* quorum-sensing mutants to that of the wild-type strain by administering about 5×10^4 bacteria per lung (a dose sufficient for the wild type to kill about 75% of infected mice) by aerosol (28). As expected, seven out of eight wild-type-infected mice died within a week (Fig. 5). The triple acyl-HSL synthase mutant JBT112 and the *btaI1* mutant JBT101 were also tested and were as virulent as the wild type. At least in our model, quorum sensing does not appear to be a *B. thailandensis* virulence determinant.

DISCUSSION

We have been interested in the conserved quorum-sensing circuits of *B. thailandensis*, *B. pseudomallei*, and *B. mallei* because these bacteria are closely related at the genomic level but

have divergent lifestyles. Here, we report a characterization of quorum-sensing signals, and we report that quorum sensing activates a self-aggregation system in *B. thailandensis*. To perform our analysis, we developed an allelic replacement strategy that allowed the construction of strains with multiple unmarked, in-frame deletions in an otherwise genetically unmodified strain of *B. thailandensis*. During the course of our studies, a somewhat similar technique was developed by Barrett et al. (3). Because *B. thailandensis* is naturally resistant to many antibiotics as a result of antibiotic efflux, genetic manipulations prior to this study were commonly done in a strain with an efflux pump mutation that confers sensitivity to a wider range of antibiotics (8, 36). However, efflux pumps have been reported to influence quorum-sensing signaling in *B. pseudomallei* (9, 10).

An earlier publication on quorum-sensing signal production by *B. thailandensis* indicated that *btaI1* directed synthesis of C₈-HSL, *btaI2* directed synthesis of C₁₀-HSL, and *btaI3* encoded a C₆-HSL synthase (55). We recently found that *B. thailandensis* produces primarily C₈-HSL, 3OHC₈-HSL, and 3OHC₁₀-HSL and only very small amounts of other acyl-HSLs (18). Furthermore, we found that BtaI2 is not a C₁₀-HSL synthase but is a 3OHC₁₀-HSL synthase that also produces some 3OHC₈-HSL (18). Thus, a first step in the study de-

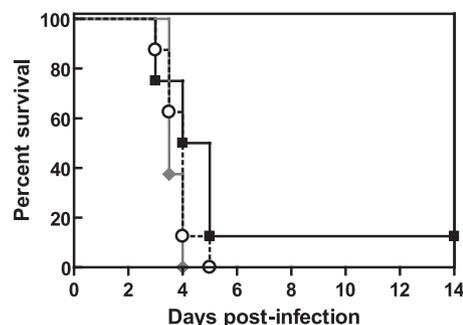


FIG. 5. Virulence of *B. thailandensis* quorum-sensing mutants in a BALB/c mouse respiratory-infection model. Shown is survival following infection with aerosolized suspensions of wild-type *B. thailandensis* strain E264 (■), strain JBT112 (◆), or strain JBT101 (○). The target dose was 5×10^4 CFU/lung, and the actual number of CFU per lung recovered from sentinel mice sacrificed immediately after infection was $3.7 (\pm \text{SEM of } 0.3) \times 10^4$ for E264, $3.8 (\pm \text{SEM of } 0.4) \times 10^4$ for JBT112, and $5.0 (\pm \text{SEM of } 0.4) \times 10^4$ for JBT101. Twelve mice were infected with each strain, and four sentinel mice were harvested immediately after infection.

scribed here was to determine the relevant signals produced by the other two *B. thailandensis* acyl-HSL synthases, BtaI1 and BtaI3. Our evidence with unmarked synthase deletion mutants and with recombinant *E. coli* indicates that, in agreement with the initial report, BtaI1 is a C₈-HSL synthase but BtaI3 is a 3OHC₈-HSL synthase. It is not clear why the initial report presented a different picture for BtaI2 and BtaI3, but we believe there were two potential explanations. First, an efflux pump mutant was used in the study, and efflux pumps have since been shown to affect acyl-HSL production by members of the *B. thailandensis*-*B. pseudomallei*-*B. mallei* group (9, 10). Second, the acyl-HSLs were detected by a single bioassay, the *A. tumefaciens* assay. Because this assay is particularly sensitive to aliphatic acyl-HSLs in the C₆-C₁₀ chain length range, the investigation could have easily missed the most abundant hydroxy-acyl-HSLs and focused on minor acyl-HSL species. It now seems clear from the results reported here and elsewhere (16, 17, 51) that in *B. thailandensis*, as well as *B. mallei* and *B. pseudomallei*, quorum-sensing system 1 involves a C₈-HSL signal and system 3 a 3OHC₈-HSL signal.

Previously, we reported that the *B. thailandensis* BtaI2-BtaR2 quorum-sensing circuit induces the production of an antibiotic predicted to be a nonribosomal peptide-polyketide hybrid molecule (18); but what else might be regulated by quorum sensing in *B. thailandensis*? The initial report on *B. thailandensis* quorum sensing showed that signal synthase and receptor mutants generated from the efflux pump-defective strain showed motility defects and minor differences in hemolysin production and utilization of some carbon sources compared to the parent, but these phenotypes were not complemented with plasmid-borne copies of the relevant genes or by addition of the appropriate signals in the case of the signal synthase mutants (55). We used our quorum-sensing signal-deficient strain JBT112 to reexamine these phenotypes and found a motility phenotype similar to that reported but no discernible quorum-sensing-dependent differences in hemolysin production (data not shown). In addition, our extensive screen of carbon, nitrogen, and phosphorus sources did not reveal any substrates for which *B. thailandensis* quorum sensing was required. Our results suggest that the hemolysin and carbon utilization defects previously reported (55) might have been strain specific and perhaps unrelated to quorum sensing.

We also found that the virulence of *B. thailandensis* in a mouse infection model was unaffected by quorum-sensing mutations. Our model and our dosing were similar to those used in *B. pseudomallei* experiments that suggested a role for quorum sensing in virulence (53). Perhaps there is a fundamental difference in the roles of the highly conserved *B. thailandensis*, *B. pseudomallei*, and *B. mallei* quorum-sensing systems that is related to the divergent niches these species are thought to occupy. However, it will be important to revisit the issue of quorum-sensing control of virulence in *B. pseudomallei* and *B. mallei* now that it is possible to generate unmarked deletions in wild-type strains. Due to past difficulties in working with *B. mallei* and *B. pseudomallei*, the virulence phenotypes of quorum-sensing mutants were not complemented.

Although virulence and metabolic diversity were not affected in our quorum-sensing mutant, we did find that the strain lost a characteristic clumping phenotype exhibited by the wild-type strain when grown in minimal medium and exhibited a smooth

colony morphology on LB agar compared to the rough or wrinkly colony morphology of the parent (Fig. 3). We were able to demonstrate that the clumping or self-aggregation phenotype was dependent on BtaR1 and BtaI1 and could be restored in a *btaI1* mutant by addition of the BtaI1-generated signal C₈-HSL (Fig. 4). The molecular basis for self-aggregation in *B. thailandensis* remains unknown; however, two lines of evidence support the view that it is at least in part mediated by EPS production: (i) the rough or wrinkly colony morphology reported in this study (Fig. 3) has been associated with EPS production in other bacteria, such as *Vibrio cholerae* (62) and *P. aeruginosa* (24), and (ii) we used microarrays to identify quorum-sensing-controlled genes, and a number of these are predicted to be involved in EPS production. Mutations in two of these quorum-sensing-controlled putative EPS synthesis genes, BTH_II0551 and BTH_II0695, caused aggregation defects (J. R. Chandler and E. P. Greenberg, unpublished data). Quorum-sensing control of cell aggregation is a common theme that has been observed in other organisms, including *Yersinia pseudotuberculosis* (2), *Pseudomonas aerofaciens* (64), *Erwinia chrysanthemi* (26) *Rhodobacter sphaeroides* (42), and many clinical isolates of *P. aeruginosa* (L. Hoffman and S. I. Miller, personal communication). In some cases, quorum sensing induces aggregation (26) and, in other cases, dispersion (2, 42, 64). One controversy that has arisen in the quorum-sensing field is whether acyl-HSL signaling is in fact a system that enables cooperativity among members of a group or whether it might serve a different purpose. Others have proposed that such systems are not quorum-sensing systems but systems for diffusion sensing (44) that benefit individual cells by enabling them to monitor the diffusion of small molecules (acyl-HSLs) before inducing expression of more metabolically expensive secreted protein products. The recurring theme of acyl-HSL induction of cell-cell aggregation is another argument that signaling is involved in cooperative behavior. The aggregation response requires multiple cells, and it is not likely to benefit a solitary individual.

It is not yet clear what the survival advantage is for a cell density-dependent switch from dispersed cells to aggregation in *B. thailandensis*. Among the possibilities, aggregation may enable the establishment of microcolonies in the natural habitat of *B. thailandensis*, such as in mixed microbial communities in Southeast Asian rice paddies or soils. Aggregates consist of *B. thailandensis* cells at very high density, and because the BtaR2-BtaI2 system activates antibiotic synthesis, one might expect the local antibiotic concentration to be high and to serve to protect the aggregate from competing bacteria. As we learn more about quorum sensing in *B. thailandensis*, we hope to gain an understanding of why clumping and antibiotic synthesis are controlled by two separate quorum-sensing systems. Finally, it is interesting that rough colony morphology has been described for the great majority of *B. pseudomallei* clinical isolates, with about 10% of isolates showing a smooth colony morphology (11). It will be interesting to determine whether at least some *B. pseudomallei* smooth-colony isolates have defects in quorum-sensing system 1.

ACKNOWLEDGMENTS

This work was funded by a National Institute of Allergy and Infectious Disease (NIAID) award from the Northwest Regional Center

of Excellence for Biodefense and Emerging Infectious Diseases (U54AI057141) to E.P.G., S.J.S., and T.E.W.; a National Science Foundation Grant (MCB-0821220) to M.E.A.C.; and the Lipid Maps Large Scale Collaborative Grant (NIH GM069338). J.R.C. was funded by the NIAID (NRSA 1 F32 AI073027-01A2), and B.A.D. was funded in part by the National Institute of General Medical Sciences (NRSA T32 GM07270).

We thank Bradley Borlee, Kelly Colvin, Dao Nguyen, Snow Brook Peterson, and Amy Schaefer for helpful discussions regarding the manuscript.

REFERENCES

- Antunes, L. C., A. L. Schaefer, R. B. Ferreira, N. Qin, A. M. Stevens, E. G. Ruby, and E. P. Greenberg. 2007. Transcriptome analysis of the *Vibrio fischeri* LuxR-LuxI regulon. *J. Bacteriol.* **189**:8387–8391.
- Atkinson, S., J. P. Throup, G. S. Stewart, and P. Williams. 1999. A hierarchical quorum-sensing system in *Yersinia pseudotuberculosis* is involved in the regulation of motility and clumping. *Mol. Microbiol.* **33**:1267–1277.
- Barrett, A. R., Y. Kang, K. S. Inamasu, M. S. Son, J. M. Vukovich, and T. T. Hoang. 2008. Genetic tools for allelic replacement in *Burkholderia* species. *Appl. Environ. Microbiol.* **74**:4498–4508.
- Bassler, B. L. 2002. Small talk. Cell-to-cell communication in bacteria. *Cell* **109**:421–424.
- Bochner, B. R., P. Gadzinski, and E. Panomitros. 2001. Phenotype microarrays for high-throughput phenotypic testing and assay of gene function. *Genome Res.* **11**:1246–1255.
- Brett, P. J., D. DeShazer, and D. E. Woods. 1998. *Burkholderia thailandensis* sp. nov., a *Burkholderia pseudomallei*-like species. *Int. J. Syst. Bacteriol.* **48**:317–320.
- Brett, P. J., D. Deshazer, and D. E. Woods. 1997. Characterization of *Burkholderia pseudomallei* and *Burkholderia pseudomallei*-like strains. *Epidemiol. Infect.* **118**:137–148.
- Burtnick, M., A. Bolton, P. Brett, D. Watanabe, and D. Woods. 2001. Identification of the acid phosphatase (*acpA*) gene homologues in pathogenic and non-pathogenic *Burkholderia* spp. facilitates TnphoA mutagenesis. *Microbiology* **147**:111–120.
- Chan, Y. Y., H. S. Bian, T. M. Tan, M. E. Mattmann, G. D. Geske, J. Igarashi, T. Hatano, H. Suga, H. E. Blackwell, and K. L. Chua. 2007. Control of quorum sensing by a *Burkholderia pseudomallei* multidrug efflux pump. *J. Bacteriol.* **189**:4320–4324.
- Chan, Y. Y., and K. L. Chua. 2005. The *Burkholderia pseudomallei* BpeAB-OprB efflux pump: expression and impact on quorum sensing and virulence. *J. Bacteriol.* **187**:4707–4719.
- Chantratita, N., V. Wuthiekanun, K. Boonbumrung, R. Tiyawitsuri, M. Vesaratchavest, D. Lumthirotsakul, W. Chierakul, S. Wongratanaheewin, S. Pukritiyakamee, N. J. White, N. P. Day, and S. J. Peacock. 2007. Biological relevance of colony morphology and phenotypic switching by *Burkholderia pseudomallei*. *J. Bacteriol.* **189**:807–817.
- Chugani, S. A., M. Whiteley, K. M. Lee, D. D'Argenio, C. Manoel, and E. P. Greenberg. 2001. QscR, a modulator of quorum-sensing signal synthesis and virulence in *Pseudomonas aeruginosa*. *Proc. Natl. Acad. Sci. USA* **98**:2752–2757.
- Dennis, J. J., and G. J. Zylstra. 1998. Plasmids: modular self-cloning minitransposon derivatives for rapid genetic analysis of gram-negative bacterial genomes. *Appl. Environ. Microbiol.* **64**:2710–2715.
- DeShazer, D., and D. E. Woods. 1996. Broad-host-range cloning and cassette vectors based on the R388 trimethoprim resistance gene. *BioTechniques* **20**:762–764.
- Dharakul, T., B. Tassaneetrithep, S. Trakulsomboon, and S. Songsivilai. 1999. Phylogenetic analysis of Ara⁺ and Ara⁻ *Burkholderia pseudomallei* isolates and development of a multiplex PCR procedure for rapid discrimination between the two biotypes. *J. Clin. Microbiol.* **37**:1906–1912.
- Duerkop, B. A., J. P. Herman, R. L. Ulrich, M. E. Churchill, and E. P. Greenberg. 2008. The *Burkholderia mallei* BmaR3-BmaI3 quorum-sensing system produces and responds to N-3-hydroxy-octanoyl homoserine lactone. *J. Bacteriol.* **190**:5137–5141.
- Duerkop, B. A., R. L. Ulrich, and E. P. Greenberg. 2007. Octanoyl-homoserine lactone is the cognate signal for *Burkholderia mallei* BmaR1-BmaI1 quorum sensing. *J. Bacteriol.* **189**:5034–5040.
- Duerkop, B. A., J. Varga, J. R. Chandler, S. B. Peterson, J. P. Herman, M. E. A. Churchill, M. Parsek, W. C. Nierman, and E. P. Greenberg. 2009. Quorum-sensing control of antibiotic synthesis in *Burkholderia thailandensis*. *J. Bacteriol.* **191**:3909–3918.
- Fuqua, C., M. R. Parsek, and E. P. Greenberg. 2001. Regulation of gene expression by cell-to-cell communication: acyl-homoserine lactone quorum sensing. *Annu. Rev. Genet.* **35**:439–468.
- Fuqua, C., S. C. Winans, and E. P. Greenberg. 1996. Census and consensus in bacterial ecosystems: the LuxR-LuxI family of quorum-sensing transcriptional regulators. *Annu. Rev. Microbiol.* **50**:727–751.
- Glass, M. B., J. E. Gee, A. G. Steigerwalt, D. Cavuoti, T. Barton, R. D. Hardy, D. Godoy, B. G. Spratt, T. A. Clark, and P. P. Wilkins. 2006. Pneumonia and septicemia caused by *Burkholderia thailandensis* in the United States. *J. Clin. Microbiol.* **44**:4601–4604.
- Gould, T. A., J. Herman, J. Krank, R. C. Murphy, and M. E. Churchill. 2006. Specificity of acyl-homoserine lactone synthases examined by mass spectrometry. *J. Bacteriol.* **188**:773–783.
- Guzman, L. M., D. Belin, M. J. Carson, and J. Beckwith. 1995. Tight regulation, modulation, and high-level expression by vectors containing the arabinose P_{BAD} promoter. *J. Bacteriol.* **177**:4121–4130.
- Hickman, J. W., and C. S. Harwood. 2008. Identification of FleQ from *Pseudomonas aeruginosa* as a c-di-GMP-responsive transcription factor. *Mol. Microbiol.* **69**:376–389.
- Hoang, T. T., R. R. Karkhoff-Schweizer, A. J. Kutchma, and H. P. Schweizer. 1998. A broad-host-range Flp-FRT recombination system for site-specific excision of chromosomally-located DNA sequences: application for isolation of unmarked *Pseudomonas aeruginosa* mutants. *Gene* **212**:77–86.
- Hussain, M. B., H. B. Zhang, J. L. Xu, Q. Liu, Z. Jiang, and L. H. Zhang. 2008. The acyl-homoserine lactone-type quorum-sensing system modulates cell motility and virulence of *Erwinia chrysanthemi* pv. zea. *J. Bacteriol.* **190**:1045–1053.
- Ibba, M., P. Kast, and H. Hennecke. 1994. Substrate specificity is determined by amino acid binding pocket size in *Escherichia coli* phenylalanyl-tRNA synthetase. *Biochemistry* **33**:7107–7112.
- Jeddeloh, J. A., D. L. Fritz, D. M. Waag, J. M. Hartings, and G. P. Andrews. 2003. Biodefense-driven murine model of pneumonic melioidosis. *Infect. Immun.* **71**:584–587.
- Kast, P., and H. Hennecke. 1991. Amino acid substrate specificity of *Escherichia coli* phenylalanyl-tRNA synthetase altered by distinct mutations. *J. Mol. Biol.* **222**:99–124.
- Khan, S. R., D. V. Mavrodi, G. J. Jog, H. Suga, L. S. Thomashow, and S. K. Farrand. 2005. Activation of the *phz* operon of *Pseudomonas fluorescens* 2-79 requires the LuxR homolog PhzR, N-(3-OH-hexanoyl)-L-homoserine lactone produced by the LuxI homolog PhzI, and a *cis*-acting *phz* box. *J. Bacteriol.* **187**:6517–6527.
- Lee, J. H., Y. Lequette, and E. P. Greenberg. 2006. Activity of purified QscR, a *Pseudomonas aeruginosa* orphan quorum-sensing transcription factor. *Mol. Microbiol.* **59**:602–609.
- Lequette, Y., J. H. Lee, F. Ledgham, A. Lazdunski, and E. P. Greenberg. 2006. A distinct QscR regulon in the *Pseudomonas aeruginosa* quorum-sensing circuit. *J. Bacteriol.* **188**:3365–3370.
- Lertpatanasuwan, N., K. Sermisri, A. Pektaseam, S. Trakulsomboon, V. Thamlikitkul, and Y. Suputtamongkol. 1999. Arabinose-positive *Burkholderia pseudomallei* infection in humans: case report. *Clin. Infect. Dis.* **28**:927–928.
- Levy, A., A. J. Merritt, M. Aravena-Roman, M. M. Hodge, and T. J. Inglis. 2008. Expanded range of *Burkholderia* species in Australia. *Am. J. Trop. Med. Hyg.* **78**:599–604.
- Maniatis, T., E. F. Fritsch, and J. Sambrook. 1982. Molecular cloning: a laboratory manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.
- Moore, R. A., D. DeShazer, S. Reckseidler, A. Weissman, and D. E. Woods. 1999. Efflux-mediated aminoglycoside and macrolide resistance in *Burkholderia pseudomallei*. *Antimicrob. Agents Chemother.* **43**:465–470.
- Ong, C., C. H. Ooi, D. Wang, H. Chong, K. C. Ng, F. Rodrigues, M. A. Lee, and P. Tan. 2004. Patterns of large-scale genomic variation in virulent and avirulent *Burkholderia* species. *Genome Res.* **14**:2295–2307.
- Patankar, A. V., and J. E. Gonzalez. 2009. An orphan LuxR homolog of *Sinorhizobium meliloti* affects stress adaptation and competition for nodulation. *Appl. Environ. Microbiol.* **75**:946–955.
- Pearson, J. P., K. M. Gray, L. Passador, K. D. Tucker, A. Eberhard, B. H. Iglewski, and E. P. Greenberg. 1994. Structure of the autoinducer required for expression of *Pseudomonas aeruginosa* virulence genes. *Proc. Natl. Acad. Sci. USA* **91**:197–201.
- Pearson, J. P., E. C. Pesci, and B. H. Iglewski. 1997. Roles of *Pseudomonas aeruginosa* *las* and *rhl* quorum-sensing systems in control of elastase and rhamnolipid biosynthesis genes. *J. Bacteriol.* **179**:5756–5767.
- Pellock, B. J., M. Teplitski, R. P. Boonay, W. D. Bauer, and G. C. Walker. 2002. A LuxR homolog controls production of symbiotically active extracellular polysaccharide II by *Sinorhizobium meliloti*. *J. Bacteriol.* **184**:5067–5076.
- Puskas, A., E. P. Greenberg, S. Kaplan, and A. L. Schaefer. 1997. A quorum-sensing system in the free-living photosynthetic bacterium *Rhodospirillum rubrum*. *J. Bacteriol.* **179**:7530–7537.
- Raja, N. S., M. Z. Ahmed, and N. N. Singh. 2005. Melioidosis: an emerging infectious disease. *J. Postgrad. Med.* **51**:140–145.
- Redfield, R. J. 2002. Is quorum sensing a side effect of diffusion sensing? *Trends Microbiol.* **10**:365–370.
- Rotz, L. D., A. S. Khan, S. R. Lillibridge, S. M. Ostroff, and J. M. Hughes. 2002. Public health assessment of potential biological terrorism agents. *Emerg. Infect. Dis.* **8**:225–230.
- Sambrook, J. E., and D. W. Russel. 2001. Molecular cloning: a laboratory manual, 3rd ed. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.
- Schaefer, A. L., E. P. Greenberg, C. M. Oliver, Y. Oda, J. J. Huang, G. Bittan-Banin, C. M. Peres, S. Schmidt, K. Juhaszova, J. R. Sufrin, and C. S.

- Harwood. 2008. A new class of homoserine lactone quorum-sensing signals. *Nature* **454**:595–599.
48. Schaefer, A. L., E. P. Greenberg, and M. R. Parsek. 2001. Acylated homoserine lactone detection in *Pseudomonas aeruginosa* biofilms by radiolabel assay. *Methods Enzymol.* **336**:41–47.
49. Schaefer, A. L., T. A. Taylor, J. T. Beatty, and E. P. Greenberg. 2002. Long-chain acyl-homoserine lactone quorum-sensing regulation of *Rhodobacter capsulatus* gene transfer agent production. *J. Bacteriol.* **184**:6515–6521.
50. Schuster, M., C. P. Lostro, T. Ogi, and E. P. Greenberg. 2003. Identification, timing, and signal specificity of *Pseudomonas aeruginosa* quorum-controlled genes: a transcriptome analysis. *J. Bacteriol.* **185**:2066–2079.
51. Song, Y., C. Xie, Y. M. Ong, Y. H. Gan, and K. L. Chua. 2005. The BpsIR quorum-sensing system of *Burkholderia pseudomallei*. *J. Bacteriol.* **187**:785–790.
52. Studer, S. V., M. J. Mandel, and E. G. Ruby. 2008. AinS quorum sensing regulates the *Vibrio fischeri* acetate switch. *J. Bacteriol.* **190**:5915–5923.
53. Ulrich, R. L., D. Deshazer, E. E. Brueggemann, H. B. Hines, P. C. Oyston, and J. A. Jeddleloh. 2004. Role of quorum sensing in the pathogenicity of *Burkholderia pseudomallei*. *J. Med. Microbiol.* **53**:1053–1064.
54. Ulrich, R. L., D. Deshazer, H. B. Hines, and J. A. Jeddleloh. 2004. Quorum sensing: a transcriptional regulatory system involved in the pathogenicity of *Burkholderia mallei*. *Infect. Immun.* **72**:6589–6596.
55. Ulrich, R. L., H. B. Hines, N. Parthasarathy, and J. A. Jeddleloh. 2004. Mutational analysis and biochemical characterization of the *Burkholderia thailandensis* DW503 quorum-sensing network. *J. Bacteriol.* **186**:4350–4360.
56. Valade, E., F. M. Thibault, Y. P. Gauthier, M. Palencia, M. Y. Popoff, and D. R. Vidal. 2004. The PmlI-PmlR quorum-sensing system in *Burkholderia pseudomallei* plays a key role in virulence and modulates production of the MprA protease. *J. Bacteriol.* **186**:2288–2294.
57. Wagner, V. E., D. Bushnell, L. Passador, A. I. Brooks, and B. H. Iglewski. 2003. Microarray analysis of *Pseudomonas aeruginosa* quorum-sensing regulators: effects of growth phase and environment. *J. Bacteriol.* **185**:2080–2095.
58. Waters, C. M., and B. L. Bassler. 2005. Quorum sensing: cell-to-cell communication in bacteria. *Annu. Rev. Cell Dev. Biol.* **21**:319–346.
59. West, T. E., C. W. Frevert, H. D. Liggitt, and S. J. Skerrett. 2008. Inhalation of *Burkholderia thailandensis* results in lethal necrotizing pneumonia in mice: a surrogate model for pneumonic melioidosis. *Trans. R. Soc. Trop. Med. Hyg.* **102**:S119–S126.
60. Whitehead, N. A., A. M. Barnard, H. Slater, N. J. Simpson, and G. P. Salmond. 2001. Quorum-sensing in Gram-negative bacteria. *FEMS Microbiol. Rev.* **25**:365–404.
61. Whitlock, G. C., D. M. Estes, and A. G. Torres. 2007. Glanders: off to the races with *Burkholderia mallei*. *FEMS Microbiol. Lett.* **277**:115–122.
62. Yildiz, F. H., and G. K. Schoolnik. 1999. *Vibrio cholerae* O1 El Tor: identification of a gene cluster required for the rugose colony type, exopolysaccharide production, chlorine resistance, and biofilm formation. *Proc. Natl. Acad. Sci. USA* **96**:4028–4033.
63. Yu, Y., H. S. Kim, H. H. Chua, C. H. Lin, S. H. Sim, D. Lin, A. Derr, R. Engels, D. DeShazer, B. Birren, W. C. Nierman, and P. Tan. 2006. Genomic patterns of pathogen evolution revealed by comparison of *Burkholderia pseudomallei*, the causative agent of melioidosis, to avirulent *Burkholderia thailandensis*. *BMC Microbiol.* **6**:46.
64. Zhang, Z., and L. S. Pierson III. 2001. A second quorum-sensing system regulates cell surface properties but not phenazine antibiotic production in *Pseudomonas aureofaciens*. *Appl. Environ. Microbiol.* **67**:4305–4315.
65. Zhu, J., Y. Chai, Z. Zhong, S. Li, and S. C. Winans. 2003. *Agrobacterium* bioassay strain for ultrasensitive detection of *N*-acylhomoserine lactone-type quorum-sensing molecules: detection of autoinducers in *Mesorhizobium huakuii*. *Appl. Environ. Microbiol.* **69**:6949–6953.