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# Anti-quorum Sensing, Anti-bacterial, and Immunomodulatory Properties of *Panax ginseng*

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## ABSTRACT

The increased emergence of multi-drug and pandrug resistant bacteria necessitates the identification of new therapies. Although antibiotics are used to treat infections, the novel antibiotic discovery rate lags behind development of resistance. Antibiotics in clinical use combat infection through bactericidal or bacteriostatic action, which allows for selection of resistant strains. To impede or avoid resistance, treatments targeting microbial cell pathways critical for virulence and pathogenicity, but not essential for viability are being explored. One such signaling pathway is quorum sensing (QS) which regulates virulence factor expression in many pathogenic bacteria. Interference with this signaling pathway results in attenuation of pathogenicity and allows the host immune response system to eradicate the infection. Natural products have long been a rich source of antibiotic scaffolds as well as inhibitors of QS. *Panax ginseng* has been used as an herbal panacea for thousands of years, yet its ability to inhibit bacterial growth and QS is only beginning to be characterized. This review provides a brief outline of the microbial infection process, an overview of quorum sensing, an introduction to the use of natural products as alternative therapies, and a synopsis of the current literature describing the anti-bacterial and anti-QS activities of *Panax ginseng*.

Keywords: anti-quorum sensing, alternative therapy, Panax ginseng, Pseudomonas aeruginosa, virulence factor

Abbreviations:  $3OHC_4HSL$ , *N*-(3-hydroxybutanoyl) homoserine lactone;  $3OC_{12}$ -HSL, *N*-3-oxo-dodecanoyl homoserine lactone;  $3OC_6HSL$ , *N*-3-(oxo-hexanoyl)-homoserine lactone; AI, autoinducer; AIP, autoinducing peptide; C<sub>4</sub>-HSL, butyryl homoserine lactone; CF, cystic fibrosis; DPD, 4,5-dihydroxy-2,3-pentadione; HHQ, 2-heptyl-4(1H)-quinolone; HSL, N-acylhomoserine lactone; IL, interleukin; MDR, multi-drug resistant; MIC, minimum inhibitory concentration; PQS, *Pseudomonas* quinolone signal; QS, quorum sensing

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# INTRODUCTION

The continuous use and abuse of antibiotics selects for resistant strains of bacteria. Consequently, the problem of antibiotic resistance has been growing at an alarming rate in recent years. Of the 2 million patients that acquire noso-comial infections, it was estimated 90,000 will die as a result and more than 70% will be infected by multi-drug resistant bacteria requiring more than one antibiotic for treatment (National Institutes of Health, NIAID 2006). Thus, there is an urgent need for novel antibiotics.

The rate of finding new antibiotics has slowed by 56% in the past 20 years as evidenced by the number of drugs approved by the FDA (Fischbach and Walsh 2009). Inefficient screening and the great cost and time required to

bring a new antibiotic to market are part of the reason for this decreasing trend in the development of novel antibiotics. To effectively eradicate infections, either novel antimicrobials or alternative therapies are needed. These can be synthesized in the laboratory, derived from natural products, or a combination of both. The study of ethnobotany has led to the identification of many botanical sources with antimicrobial activity at a rate greater than random screening (Khafagi and Dewedar 2000). The focus of this review is the potential therapeutic use of extracts and compounds from *Panax ginseng*, which has been used since ancient times as a "cure-all." *P. ginseng* has been shown to affect Gram positive and Gram negative bacteria growth and pathogenicity both directly and indirectly as detailed in this review. Brief summaries of the infection process and quo-

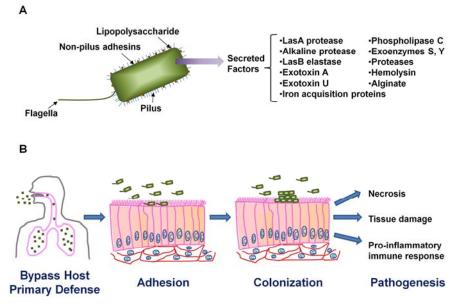


Fig. 1 *Pseudomonas aeruginosa* infection. (A) *Pseudomonas aeruginosa* structures and factors important for virulence (B) *Pseudomonas aeruginosa* infection process: bypass of host primary defense, adhesion, colonization and host effects.

rum sensing (QS) are provided as background to fully appreciate the effects of ginseng on microbial pathogenesis.

### AN OVERVIEW OF THE INFECTION PROCESS

Bacteria, are relatively simple in structure, yet have evolved complex metabolisms which allow them to inhabit diverse environments, one of which is the human body. Although many are commensal or avirulent, invasion of primarily sterile sites in the body by opportunistic and pathogenic bacteria may cause disease. For this to occur, bacteria must enter the host, adhere and colonize the site, acquire nourishment, and evade host defenses. Different bacteria use methods unique to their species to invade tissues and disseminate through the body while dealing with local and systemic inflammatory responses. For the purpose of this review, which focuses on the ability of *P. ginseng* to inhibit bacterial growth and virulence, only the infection process for *Pseudomonas aeruginosa*, a common ubiquitous, opportunistic pathogen, will be detailed.

Individuals most often infected by P. aeruginosa are burn victims (Tredget et al. 2004), those receiving mechanical ventilation (Garau and Gomez 2003; Cao et al. 2004), immunocompromised individuals, including those with AIDS or neutropenia (Obritsch et al. 2005), and those afflicted with compromised lung function, such as individuals with diffuse panbronchiolitis (Homma et al. 1983) or cystic fibrosis (CF) (Phair et al. 1970; Mearns et al. 1972; Hoiby 1974; Frederiksen et al. 1999). P. aeruginosa has become quite successful in establishing infection due to its intrinsic antibiotic resistance, low outer membrane permeability, presence of multidrug efflux pumps, hypermutability and ability to form biofilms. Fifty percent of hospitalized patients are colonized by *P. aeruginosa* (Pollack 2000). Initial infection is acute, however, in chronic infections, as in the case of individuals with CF, P. aeruginosa infection results in host lung damage and eventual mortality (Hoiby et al. 1977).

*P. aeruginosa* that initially infect the host are planktonic, motile cells that produce and secrete numerous toxins and virulence factors necessary for establishing and maintaining an infection (**Fig. 1**). After successfully passing the host's primary line of defense, the next step in the infection process is adhesion via binding to any of several different glycoproteins (**Fig. 1**). *P. aeruginosa* accomplishes this by producing virulence factors that help compromise the host defenses, including the AprA alkaline protease (Duong *et al.* 1992), protease IV/PrpL (Wilderman *et al.* 2001), LasB elastase (Bever and Iglewski 1988), LasA staphylolytic protease (Goldberg and Ohman 1987; Toder et al. 1991), phospholipase C (Liu 1966), pyocyanin (Stewart-Tull and Armstrong 1972), pyoverdin (Ankenbauer et al. 1985), rhamnolipids (Burger et al. 1962; Edwards and Hayashi 1965), exotoxin A (Liu 1973; Liu and Hsieh 1973; Liu et al. 1973), lipopolysaccharide (LPS) (Homma and Suzuki 1961; Homma et al. 1963) and exoenzymes S and U (Iglewski et al. 1978; Finck-Barbancon et al. 1997). These enable multiple stages of the infection process including host tissue damage, cellular necrosis, and pro-inflammatory immune response. Many of these virulence factors must be secreted by Pseudomonas aeruginosa to exert their action on the host. To secrete the extracellular products, P. aeruginosa makes use of six different secretion systems (Ma et al. 2003; Saier 2006). All of these affect virulence by facilitating transport of the aforementioned virulence factors (Wretlind and Pavlovskis 1984; Lindgren and Wretlind 1987; Yahr et al. 1996; Yahr et al. 1997; Duong et al. 2001; Ochsner et al. 2002; Mougous et al. 2006; Hood et al. 2010).

Biofilm formation also plays a pivotal role in colonization (Costerton *et al.* 1999; Drenkard 2003). This occurs when dense aggregates of cells adhere to surfaces and become embedded in a matrix consisting of extracellular DNA, proteins and polysaccharides such as alginate, Pel (pellicle formation) and Psl (polysaccharide synthesis locus) (Evans and Linker 1973; Friedman and Kolter 2004a, 2004b). Biofilm formation is associated with increased antibiotic resistance as well as chronic *P. aeruginosa* infections (Nickel *et al.* 1985a, 1985b; Nichols *et al.* 1989; Drenkard 2003).

Thus the *P. aeruginosa* infection process, like that of all pathogenic bacteria, is multilayered and complex. Underlying virtually every step of this process, adherence, colonization, virulence factor production, secretion and biofilm formation, is the ability of the bacteria to communicate with members of its own species and others to coordinate the infection process and improve the chance of success. This is accomplished through a signaling pathway called quorum sensing (QS).

### **OVERVIEW OF QUORUM SENSING**

QS is a type of communication process bacteria use to coordinate and synchronize their behavior (Nealson and Hastings 1979; Fuqua *et al.* 1996). In QS, bacteria synthesize and secrete chemical signals that alter the transcriptional program in a cell density dependent manner (Nealson *et al.*  A: Communication

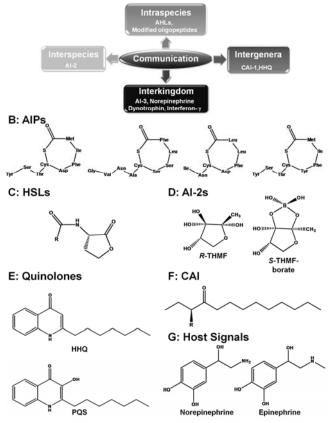


Fig. 2 Communication pathways affecting microbial virulence and structures of the most well characterized quoromones. (A) Summary of communication types; (B) Structures of AIP-I – IV (from left to right); (C) HSL structure. The R group can vary as indicated in Table 1. (D) Structures AI-2 from *Salmonella* (left) and *Vibrio* (right). (E) Structure of the quinolonoes HHQ and PQS. (F) Generic structure of CAI-I. R may be a hydroxyl group (CAI-1) or an amino group (Amino-CAI-1). (G) Structures of norepinephrine (left) and epinephrine (right). (B-F) adapted from (Ng and Bassler 2009).

1970). Although first discovered in the bioluminescent bacteria *Vibrio fischeri* (Kempner and Hanson 1968; Nealson *et al.* 1970; Eberhard 1972), QS systems have been identified in many bacteria and, in addition to bioluminescence, affect various cellular processes including conjugation, sporulation, biofilm formation, virulence factor production and secretion (**Table 1**).

The QS signals are also called autoinducers or quoromones. Specifically, quoromones identified in Gram positive bacteria include linear, modified, and cyclic peptides and  $\gamma$ -butyrolactones, and 4,5-dihydroxy-2,3-pentandione (DPD) derivatives (autoinducer 2 (AI-2)) (Havarstein et al. 1995; Ji et al. 1995; Solomon et al. 1996; Surette and Bassler 1998; Surette et al. 1999; Miller et al. 2004). Gram negative bacteria have been shown to use N-acylhomoserine lactones (HSLs), 2-alkyl-4-quinolones, fatty acid methyl esters, long-chain fatty acid derivatives, peptides, γ-butyrolactones, furanones, AI-2 and autoinducer 3 (AI-3) as indicators of population density. These signals may serve to communicate with members of the same species, (intraspecies), different species (interspecies), different genera (intergenera) or between the bacteria and the host (interkingdom) (Fig. 2A). A comprehensive review of QS is beyond the scope of this review, thus only one or two examples of each will be discussed.

# Gram negative bacteria intraspecies communication

The major paradigm of intraspecies QS system in Gram

negative bacteria, including P. aeruginosa, is the LuxI/ LuxR system. The LuxI/R QS system was first identified in V. fischeri as a regulator of bioluminescence through activation of the luciferase luxICDABEG operon (Eberhard et al. 1981; Engebrecht et al. 1983; Engebrecht and Silverman 1984, 1987; Swartzman et al. 1990). The "I" and "R" proteins are at the heart of this type of QS, encoding the quoromone synthase and cytoplasmic receptor/transcriptional activator, respectively. The quoromone involved in the LuxI/R QS system is an HSL (Fig. 2C). HSLs contain a homoserine lactone (HSL) ring and an acyl side chain (Eberhard et al. 1981; Engebrecht and Silverman 1984, 1987). The side chain varies between four and 18 carbons in length and may contain a modification, primarily at the C<sub>3</sub> position depending upon the species (Table 1). The LuxI protein synthesizes the HSL by transfer of a fatty acid chain from an acylated carrier protein to S-adenosyl methionine creating HSL and 5'-methylthioadenosine (Schaefer et al. 1996). The HSL is transported into and out of the cell by diffusion (Kaplan and Greenberg 1985).

As the population density increases, the intracellular concentration of HSL increases due to diffusion into the cell. Inside the cell, HSL binds the LuxR protein (Urbanowski *et al.* 2004). The stable ligand-bound LuxR binds and activates gene expression (Urbanowski *et al.* 2004).

QS signaling is so vital to the bacteria that often they have more than one LuxI/R system or utilize the LuxI/R system with other QS systems (Waters and Bassler 2005). For example, *P. aeruginosa*, utilizes two LuxI/R based systems, the Las and the Rhl systems, and also synthesizes 2heptyl-3-hydroxy-4(1*H*)-quinolone (*Pseudomonas* quinolone signal or PQS), which is part of an additional regulatory circuit of the Las and Rhl pathways (reviewed in Williams and Camara (2009)).

# Gram positive bacteria intraspecies communication

In Gram positive bacteria, the chemical signal is often a modified oligopeptide (Solomon *et al.* 1996) or autoinducing peptide (AIP) as is the case for *Staphylococcus aureus* (Ji *et al.* 1995) (**Fig. 2B**). Transport of these across the membrane usually requires special transporters and peptide modifications such as processing and/or cyclization. Extracellular accumulation of these signaling oligopeptides results in activation of a two-component signaling system which results in altered gene expression (reviewed in Novick and Geisinger (2008)).

# Interspecies communication – the LuxS-based system

The LuxS system is a form of interspecies communication; it is widespread and both Gram negative and Gram positive bacteria synthesize and respond to this class of quoromone; termed AI-2 (reviewed in Ng and Bassler (2009)). This phenomenon was first observed in the marine bacteria *Vibrio harveyi* (Greenberg *et al.* 1979).

*V. harveyi* synthesizes and recognizes three types of quoromones (Henke and Bassler 2004). One is an intraspecies communication molecule; the *N*-(3-hydroxybutanoyl) HSL (3OHC<sub>4</sub>-HSL) (Cao and Meighen 1989; Bassler *et al.* 1993). A second has been proposed to be an intergenera signal, CAI-1, which has not yet been purified from *V. harveyi*, but was identified as (*S*)-3-hydroxytridecan-4-one in *Vibrio cholerae* (Higgins *et al.* 2007) (**Fig. 2F**). The third is the interspecies signal AI-2 (Surette *et al.* 1999; Schauder *et al.* 2001; Chen *et al.* 2002) (**Fig. 2D**).

AI-2 is used by both Gram negative and positive bacteria, and is often referred to as a universal signal. Even bacteria, such as *P. aeruginosa*, that do not synthesize AI-2, can detect AI-2 in the environment and alter gene expression accordingly, further emphasizing its role as a universal signal (Duan *et al.* 2003; Duan and Surette 2007; Rezzonico and Duffy 2008). Synthesis of AI-2 begins with LuxS con-

Bacteria	Gene	Autoinducer molecule (AI)*	Virulence Factor	Reference
Aeromonas hydrophila	ahyI/ahyR	C <sub>4</sub> -HSL	Type VI secretion system, biofilm and metalloprotease production	Khajanchi et al. 2009
4eromonas salmonicida	asal/asaR	C <sub>4</sub> -HSL and C <sub>6</sub> -HSL	Virulence factors	Rasch et al. 2007
Agrobacterium tumefaciens	traI/traR	3OC <sub>8</sub> -HSL and C <sub>6</sub> -HSL	Ti plasmid conjugation	Zhang et al. 1993
	1.5	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~		Hwang et al. 1994
Brucella melitensis	vbjR	C <sub>12</sub> -HSL	Virulence factor production	Weeks et al. 2010
Burkholderia cenocepacia	cepI/R	C <sub>6</sub> -HSL and C <sub>8</sub> -HSL	Virulence factor, protease, chitinase, siderophore, biofilm and AidA production and swarming motility	Lewenza <i>et al.</i> 1999; Sokol <i>et al.</i> 2000; Huber <i>et al.</i> 2001; Lewenza and Sokol 2001; Aguilar <i>et al.</i> 2003
		HHQ	Colony morphology and elastase production	Diggle et al. 2006a
	bcam 0581	BDSF	Virulence factor, motility, biofilm formation, metalloprotease, lipase, lipase chaperone and siderophore expression, and <i>Candida albicans</i> morphology	Boon <i>et al.</i> 2008; Deng <i>et al.</i> 2009; Ryan <i>et al.</i> 2009
Burkholderia mallei	bmaI1/R1 bmaI3/R3	C <sub>8</sub> -HSL and 3OC <sub>8</sub> -HSL C <sub>8</sub> -HSL, OC <sub>8</sub> -HSL and C <sub>10</sub> - HSL	Virulence factor Virulence factor	Ulrich <i>et al.</i> 2004b Ulrich <i>et al.</i> 2004b
	bmaR4	IIGL	Virulence factor	Ulrich <i>et al.</i> 2004b
Burkholderia pseudomallei	bmaR5 pml11/R1	C <sub>8</sub> -HSL, C <sub>10</sub> -HSL, and	Virulence factor Virulence factor, MprA protease	Ulrich <i>et al.</i> 2004b Ulrich <i>et al.</i> 2004a; Valade <i>et al.</i>
	bpmI2/R2	3OHC <sub>8</sub> -HSL C <sub>8</sub> -HSL, C <sub>10</sub> -HSL, and 3OHC <sub>8</sub> -HSL	production and colonization Virulence factor and colonization	2004 Ulrich <i>et al.</i> 2004a
	bpmI3/R3	C <sub>8</sub> -HSL, C <sub>10</sub> -HSL, and 3OHC <sub>8</sub> -HSL		
	bpmR4 bpmR5			
	hhqA/E	HHQ	Colony morphology, elastase production	Diggle et al. 2006b
Burkholderia vietnamiensis G4	cepI/R	C <sub>6</sub> -HSL and C <sub>8</sub> -HSL		Lutter <i>et al.</i> 2001; Conway and Greenberg 2002; Malott and Sokol 2007
	bviI/R	C <sub>6</sub> -HSL, C <sub>8</sub> -HSL, C <sub>10</sub> -HSL, C <sub>12</sub> -HSL and 3OC <sub>10</sub> -HSL		Lutter <i>et al.</i> 2001; Malott and Sokol 2007
Chromo-bacterium violaceum	cviI/cviR	C <sub>6</sub> -HSL	Biofilm formation and virulence factors	McClean et al. 1997
Erwinia carotovora subsp. betavasculorum	ecbI/ecbR	3OC <sub>6</sub> -HSL	Antibiotic and exoenzymes	Costa and Loper 1997
<i>Erwinia carotovora</i> subsp. <i>carotovora</i> 71	hslI/hslR	3OC <sub>6</sub> -HSL	Exoenzymes	Chatterjee et al. 1995
<i>Erwinia carotovora</i> subsp. <i>carotovora</i> GS101	carI/carR	3OC <sub>6</sub> -HSL	Carbapenems and exoenzymes	Pirhonen <i>et al.</i> 1993; Swift <i>et al.</i> 1993
<i>Erwinia carotovora</i> subsp. <i>carotovora</i> SCC3193	expI/expR1,expR2	3OC <sub>8</sub> -HSL and 3OC <sub>6</sub> -HSL	Virulence factors and exoenzyme	Pirhonen et al. 1993; Chatterjee et al. 2005; Sjoblom et al. 2006
Klebsiella pneumoniae		AI-2	Biofilm formation	Balestrino et al. 2005
Pantoea agglomerans pv.	pagI/pagR	C <sub>6</sub> -HSL	Gall development	Chalupowicz et al. 2008
'gypsophilae' Pantoea stewartii subsp. Stewartii (formerly Erwinia	easI/esaR	3OC <sub>6</sub> -HSL	EPS and virulence factors	Beck von Bodman and Farrand 1995
stewartii) Pseudomonas aeruginosa	lasI/lasR	3OC <sub>12</sub> -HSL	Alkaline protease, pyocyanin, hydrogen cyanide, lectins, and elastase	Gambello and Iglewski 1991; Pearson <i>et al.</i> 1994; Brint and Ohman 1995; Latifi <i>et al.</i> 1995; Ochsner and Reiser 1995; Winson
	rhll/rhlR	C <sub>4</sub> -HSL	Induces LasB and Rhll expression	<i>et al.</i> 1995 Brint and Ohman 1995; Latifi <i>et al.</i> 1995; Ochsner and Reiser 1995; Pearson <i>et al.</i> 1997; Winzer <i>et al.</i> 2000
	qscR	3OC <sub>12</sub> -HSL	Represses virulence factor expression	Lequette <i>et al.</i> 2006
	pqs	HHQ	Virulence factors	Pesci et al. 1999
Pseudomonas aureofaciens	phzI/phzR	C <sub>6</sub> -HSL	Virulence factors and biofilm	Pierson et al. 1994; Wood and
30-84	csaI/R	Unknown	production Colonization, exoprotease production, and suppression of mucoid phenotype	Pierson 1996 Zhang and Pierson 2001

Bacteria	Gene	Autoinducer molecule (AI)*	Virulence Factor	Reference
Pseudomonas fluorescens 2P24	pcoI/R	3OC <sub>8</sub> -HSL	Biofilm formation and wheat rhizosphere colonization	Wei and Zhang 2006
Pseudomonas fuscovaginae	pfsI/R	C10-HSL and C12-HSL	Virulence factors	Mattiuzzo et al. 2011
	pfvI/R	3OC10-HSL and 3OC12-HSL	Virulence factors	Mattiuzzo et al. 2011
Pseudomonas putida PCL1445	ppuI/R	3OC <sub>6</sub> -HSL, 3OC <sub>8</sub> -HSL, 3OC <sub>10</sub> -HSL and 3OC <sub>12</sub> -HSL	Biofilm architecture	Dubern et al. 2006
Pseudomonas syringae pv. 'syringae'	ahlI/ahlR	C <sub>8</sub> -HSL	Antibiotic production	Quinones et al. 2004; Quinones et al. 2005
Pseudomonas syringae pv. 'tabaci'	psyI/psyR	3OC <sub>6</sub> -HSL	Biofilm formation and virulence factors	Shaw et al. 1997
Ralstonia solanacearum	solI/solR	C <sub>6</sub> -HSL and C <sub>8</sub> -HSL	Unknown	Flavier et al. 1997
	phc	3-OH PAME	Production of EPS and exoenzyme synthesis	Brumbley et al. 1993; Flavier et al. 1997
Rhodobacter sphaeroides	cerI/cerR	C <sub>14</sub> -HSL	Phenazine antibiotic production	Puskas et al. 1997; Kirwan et al. 2006
Serratia liquefaciens	swrI/swrR	C <sub>4</sub> -HSL and C <sub>6</sub> -HSL	Swarming motility	Eberl et al. 1996
Vibrio anguillarum	vanI/vanR	3OC <sub>12</sub> -HSL	Unknown	Milton <i>et al.</i> 1997; Croxatto <i>et al.</i> 2002
	vanM/vanN	C <sub>6</sub> -HSL and 3OHC <sub>6</sub> -HSL	Extracellular protease, pigment and biofilm formation	Milton et al. 2001
	vanS/vanQ	AI-2	Extracellular protease, pigment and biofilm formation	Croxatto et al. 2004
Vibrio cholerae	luxP/luxQ	AI-2	Biofilm and virulence factor production repression	Miller et al. 2002
	cqsS/cqsA	CAI-1, amino-CAI-1		Miller <i>et al.</i> 2002; Higgins <i>et al.</i> 2007; Kelly <i>et al.</i> 2009
Vibrio fischeri	luxI/luxR	3OC <sub>6</sub> -HSL	Bioluminescence	Eberhard et al. 1981
	ainS/R	C <sub>8</sub> -HSL		Gilson et al. 1995
	luxS/luxP, luxQ	AI-2		Chen et al. 2002
Vibrio harveyi	luxM/luxN	3OHC <sub>4</sub> -HSL	Bioluminescence. metalloprotease, siderophore, and	Lilley and Bassler 2000; Mok <i>et al.</i> 2003
	luxS/luxP, luxQ	AI-2	exopolysaccharide production	Surette <i>et al.</i> 1999; Schauder <i>et al.</i> 2001; Chen <i>et al.</i> 2002
	cqsA/cqsS	CAI-1		Henke and Bassler 2004
Vibrio parahaemo-lyticus	opaI/	Unknown	Haemolysin and protease	McCarter 1998; Henke and
	opaR		production, opacity, regulation of TTSS	Bassler 2004
Vibrio salmonicida	luxI/luxR1, luxR2	3OC <sub>6</sub> HSL	Virulence factors	Nelson et al. 2007
Vibrio vulnificus	luxS/luxP, luxQ	AI-2	Virulence factors	Kim et al. 2003
Xanthomonas campestris	rpfC/rpfG	11CH <sub>3</sub> C <sub>12</sub> -HSL	Virulence factors	Torres <i>et al.</i> 2007; He and Zhang 2008
Yersinia pestis	yepI/yepR	C <sub>8</sub> -HSL, 3OC <sub>6</sub> -HSL and C <sub>6</sub> - HSL	Virulence factors	Atkinson et al. 1999; Gelhaus et al. 2009
Yersinia pseudo-tuberculosis	ypsI/ypsR ytbI/ytbR	C <sub>6</sub> -HSL, 3OC <sub>6</sub> HSL, 3OC <sub>7</sub> -HSL, C <sub>8</sub> -HSL, 3OHC <sub>8</sub> - HSL, 3OC <sub>12</sub> -HSL	Aggregation and motility	Atkinson <i>et al.</i> 1999; Ortori <i>et al.</i> 2007

\*Abbreviations used, AI-2, furanosyl borate diester; BDSF, *cis*-2-dodecenoic acid; CAI-1, Cholera autoinducer: HSL, homoserine lactone; C<sub>4</sub>-HSL, *N*-butanoyl-L-HSL; 30HC<sub>4</sub>-HSL, *N*-3-hydroxybutanoyl-L-HSL; C<sub>6</sub>-HSL, *N*-hexanoyl-L-HSL; 30C<sub>6</sub>-HSL, *N*-3-oxo-hexanoyl-HSL; 30HC<sub>6</sub>-HSL, *N*-3-hydroxybutanoyl-L-HSL; 30C<sub>7</sub>-HSL, *N*-3-oxo-septanoyl-L-HSL; C<sub>8</sub>-HSL, *N*-octanoyl-L-HSL; 30C<sub>8</sub>-HSL, *N*-3-oxo-octanoyl-L-HSL; 30C<sub>10</sub>-HSL, *N*-3-oxodecanoyl-L-HSL; 30C<sub>10</sub>-HSL, *N*-3-oxodecanoyl-L-HSL; 30C<sub>12</sub>-HSL, 50C<sub>12</sub>-HSL, 50C<sub>12</sub>-HSL

verting ribose-homocysteine into homocysteine and DPD (Schauder *et al.* 2001). Spontaneous rearrangement of DPD results in the formation of different AI-2 compounds, depending upon the environmental chemistry (Miller *et al.* 2004). One of the most well characterized pathways is that of *V. harveyi*, which utilizes a furanosyl borate diester, (2S,4S)-2-methyl-2,3,3,4-tetrahydroxytetrahydrofuran borate (**Fig. 2D**, right panel) (Chen *et al.* 2002). Salmonella enteric serovar Typhimurium and Escherichia coli use (2R,4S)-2-methyl-2,3,3,4-tetrahydroxytetrahydrofuran (**Fig. 2D**, left panel) (Chen *et al.* 2002; Miller *et al.* 2004).

### Interkingdom signaling

The infection process is complex and bacteria have evolved to coordinate this process not only with members of their own species and kingdom, but also with other kingdoms capable of co-infecting the host and the host itself. This is accomplished by signaling that feeds into the QS systems.

The microbial intestinal flora present in the healthy human gut, produce another autoinducer termed autoinducer  $\overline{3}$  (AI-3), which regulates the operons within the locus for enterocyte effacement (LEE operons) and flagella genes in enterohemorrhagic E. coli (Sperandio et al. 2003). The LEE operons encode the proteins involved in Type 3 secretion systems and adhesion (Elliott et al. 1998). AI-3 is detected by a two component system, QseBC, which also recognizes norepinephrine and epinephrine (Fig. 2G) (Sperandio et al. 2003; Clarke et al. 2006; Kendall et al. 2007; Reading et al. 2007). It has been proposed that this may be a mechanism the bacteria use to sense that it is in the gut (reviewed in Moreira and Sperandio (2010)). The synthesis and chemical structure of AI-3 remains to be elucidated. The detection pathway has been shown to be present in numerous Gram negative bacteria; however, its role in commensal organisms needs further characterization.

### Pseudomonas aeruginosa QS

The QS systems in *P. aeruginosa* are well characterized, most likely because of their importance in virulence. *P. aeruginosa* exhibits intraspecies, interspecies and interkingdom signaling. As described above, *P. aeruginosa* can respond to, but not synthesize AI-2 (Duan *et al.* 2003; Duan and Surette 2007).

*P. aeruginosa* synthesizes and detects two HSLs, N-3oxo-dodecanoyl homoserine lactone ( $3OC_{12}$ -HSL) and butyryl homoserine lactone ( $C_4$ -HSL) which bind LasR and RhIR, respectively (reviewed in Fuqua *et al.* (1996)). These complexes directly or indirectly regulate transcription of more than 10% percent of the *P. aeruginosa* genome (Schuster and Greenberg 2006). These two pathways in part appear hierarchical, with the Las system upstream from the RhI system, although the RhI pathway can be activated during stationary phase in the absence of Las signaling (Latifi *et al.* 1996; Pesci *et al.* 1997; Dekimpe and Déziel 2009).

A third receptor, QscR (quorum-sensing-control repressor), has also been identified in *P. aeruginosa* (Chugani *et al.* 2001). QscR was initially shown to antagonize Las and Rhl signaling and *qscR* mutants were hypervirulent (Chugani *et al.* 2001). Microarray studies show that the QscR regulon is distinct, but partially overlaps that of LasR and RhIR (Lequette *et al.* 2006). QscR has a relatively relaxed specificity, leading to the suggestion that QscR may respond to HSLs produced by other bacteria present in a mixed infection (Lequette *et al.* 2006; Oinuma and Greenberg 2011).

Recently, LasR-, RhlR-, and QscR-independent N-decanoyl-homoserine lactone (C10-HSL) signaling was observed in P. aeruginosa (Chugani and Greenberg 2010). Receptorindependent, C<sub>10</sub>-HSL-dependent gene regulation requires anthranilate produced by the kynurenine pathway (Chugani and Greenberg 2010). Under the experimental conditions used, the kynurenine pathway is the main source of anthranilate used for PQS synthesis (Farrow and Pesci 2007), the signaling molecule used in the third QS pathway (Pesci et *al.* 1999; McKnight *et al.* 2000), suggesting another layer of control. Synthesis of PQS (**Fig. 2E**) is accomplished through condensation reactions of anthranilate and β-keto-(do)decanoate (Bredenbruch et al. 2005). The genes responsible, pqsA, pqsB, pqsC, and pqsD, part of the pqsABCDE operon, also synthesize over 50 2-alkyl-4-quinolones (Lepine et al. 2004; Bredenbruch et al. 2005). Many of these are in low quantities and their physiological function is unknown (Déziel *et al.* 2004). One of these, however, is the immedi-ate precursor of PQS, 2-heptyl-4(1*H*)-quinolone (HHQ) (**Fig. 2E**) (Déziel *et al.* 2004). The *pqsABCDE* operon is conserved in Burkholderia pseudomallei, Burkholderia thailandensis, and Burkholderia cenocepacia (Diggle et al. 2006b). These organisms synthesize HHQ, not PQS, and thus, HHQ has been proposed to be an intergenera signaling molecule. Expression of the pqsABCDE operon is also regulated by interkingdom signaling, as it has been shown to be activated by mammalian interferon-gamma (IFN- $\gamma$ ) and dynorphin (Wu et al. 2005; Zaborina et al. 2007). PgsE is important for host-pathogen adaptation (Rampioni et al. 2010)

The presence of many different QS systems serves as a testament to the idea that QS serves an important role in bacteria. By coordinating their behavior and only turning on specific genes, such as those for virulence, at high cell density, the bacteria are able to achieve their goal successfully and establish infection.

### ANTIBIOTIC RESISTENCE

The discovery of penicillin by Alexander Fleming in the 1920's heralded the golden age of antibiotics (Fleming 1929; Kong *et al.* 2010). At the time, many believed that the discovery of these antibiotics would eradicate infectious disease. Of course, concomitant with the use of antibiotics

was the appearance of resistant strains. Interestingly, penicillin resistance was central in Fleming's seminal paper (Fleming 1929).

Today, emerging antibiotic resistance in three groups of pathogens is of particular public health concern: methicillin-resistant S. aureus (MRSA), multidrug resistant (MDR) and extensively drug-resistant (XDR) Mycobacterium tuberculosis, and pandrug-resistant (PDR) and MDR Gram negative bacteria (Weigel et al. 2003; Falagas et al. 2005; Klevens et al. 2007). MRSA was first isolated in the United States in 1968 (Barrett et al. 1968). It is estimated that invasive MRSA led to 18,650 in-hospital deaths in the US in 2005 (Klevens et al. 2007). MRSA is treated with vancomycin. Fortunately, only a handful of vancomycin resistant S. aureus strains have been reported, nine in the US (Finks et al. 2009). In 2008, there were an estimated 11.1 million people with M. tuberculosis and 1.8 million M. tuberculosis-related deaths (World Health Organization 2010). It is also estimated that 3.6% of all M. tuberculosis infections are MDR and in some sections of the former Soviet Union, as many as 28.3% of all new tuberculosis cases were with MDR with 10% of these being XDR bacteria (World Health Organization 2010). Recent reviews have addressed the increased occurrence of MDR and PDR Gram negative pathogens: Acinetobacter baumannii, Klebsiella pneumoniae, E. coli, and P. aeruginosa (Giske et al. 2008; Fischbach and Walsh 2009; Pfeifer et al. 2010). This increase not only results in greater mortality rates, but also a heavier economic burden (Giske et al. 2008). Unfortunately, the development of novel antibiotics is not keeping pace with the emergence of MDR and PDR Gram negative pathogens. This is adding to the inherent resistance of these organisms. For example, the rate of ceftazidime resistance for *P. aeru*ginosa increased by 22% from 1997 to 2001 (Solomon et al. 2003). For especially pernicious infections caused by P. aeruginosa, more than one antibiotic is needed for eradication.

### ALTERNATIVE THERAPIES

Alternative therapies are another avenue for treatment. Since ancient times, people have used natural products to treat infection. Antimicrobial activities have been identified in plants from every continent including Antarctica (for example: Romero *et al.* 2005; Ivanova *et al.* 2007; Oliveira *et al.* 2007; McGaw *et al.* 2008; Goncalves *et al.* 2009; Ahameethunisa and Hopper 2010). The antimicrobial properties of essential oils are also well established (Edris 2007; Alviano and Alviano 2009). Several classes of plant compounds, including phenols, polyphenols, phenolic acid, quinones, flavonoids, flavones, flavonols, tannins, coumarins, and polyacetylenes were found to be antimicrobial (Toda *et al.* 1992; King and Tempesta 1994; Perrett *et al.* 1995; Fernandez *et al.* 1996; Avato *et al.* 1997; Peres *et al.* 1997).

Besides possessing antibacterial properties, herbal remedies can also target QS. By targeting QS, an infective property of the bacteria, one can potentially impede the rate of resistance and infection. Halogenated furanones, synthesized by Delisea pulchra, were the first natural products to exhibit anti-QS effect by competitively binding to LuxR (Manefield et al. 1999, 2002). Evidence suggests that these compounds may also inhibit AI-2 signaling (Ren et al. 2001). Six south Florida medicinal plants, Conocarpus erectus, Bucida buceras, Callistemon viminalis, Quercus virginiana, Tetrazygia bicolor and Chamaesyce hypericifolia, were shown to inhibit QS in Chromobacterium violaceum, Agrobacterium tumefaciens and P. aeruginosa (Adonizio et al. 2006, 2008a). Aqueous extracts from three of these, C. erectus, B. buceras, and C. viminalis, significantly reduced the levels of pyoverdin, LasA protease, LasB elastase and biofilm formation (Adonizio et al. 2008a). Use of reporter constructs and HSL quantification suggested that C. erectus and B. buceras extracts inhibited both 3OC<sub>12</sub>-HSL and C<sub>4</sub>-HSL expression while C. viminalis extracts specifically inhibited  $3OC_{12}$ -HSL expression (Adonizio *et al.* 2008a). Further testing of these three extracts in a *Caenor-habditis elegans* model system demonstrated that they inhibited *P. aeruginosa* gut infection death and toxin-dependent mortality in 60% and 50-90% of the worms, respectively, without host cytotoxic effects (Adonizio *et al.* 2008b).

Garlic extracts have also been shown to inhibit QS. In DNA microarray experiments, addition of garlic extracts down-regulated 92 QS-regulated P. aeruginosa genes (Rasmussen et al. 2005). The exact mechanism of anti-QS action is unknown but believed to act upon either the I or R protein since the mRNA levels of the key QS players were unaffected (Rasmussen et al. 2005). Further experiments demonstrated a synergistic effect of garlic and tobramycin on P. aeruginosa biofilms in mice lungs (Bjarnsholt et al. 2005). Garlic altered the biofilm structure, increasing the bacteria's sensitivity to tobramycin, thus enhancing bacterial clearance from the lung (Bjarnsholt et al. 2005; Rasmussen et al. 2005). Garlic also has antibacterial effects (Tessema et al. 2006). Moving from a mouse model to human, a recent study was conducted analyzing the effect of garlic in patients with cystic fibrosis (Smyth et al. 2010). This is the first study conducted using an anti-QS agent in humans. Levels of HSLs were used as a marker for anti-QS; however, only 3OC<sub>12</sub>-HSL was detected. Overall, it was reported there was no significant difference between garlictreated patients and their placebo counterparts. This may be attributed to small sample sizes (Smyth et al. 2010).

Other plants have been researched for their anti-infective properties based on their traditional use. One, *P. ginseng*, is the main focus of this review.

#### Panax ginseng

Ginseng has a long history of medicinal use, especially in China, Japan and Korea, and is highly valued. Used for rejuvenation of the body, it is considered an adaptogen, able to bolster the body's immune system during times of stress (Brekhman and Dardymov 1969). It is also believed to improve stamina and concentration (Petkov *et al.* 1994). In addition, it is believed to maintain homeostatic balance of the body. This is probably due to a wide range of chemicals found in the plant.

The Latin name for Asian ginseng is P. ginseng. The term "ginseng" is derived from the Chinese phonetic pronunciation of ginseng, which is rén shēn, or "the image of man," because of the roots' anthropomorphic resemblance to the human body. Ginseng belongs to the genus Panax, derived from the Greek word for cure all, "panacea," because it was believed to be a universal remedy. There are about 11 species of the genus Panax. All are characterized by the presence of ginsenosides. Besides P. ginseng, American ginseng (Panax quinquefolius) is also used in herbal medicine and extensively researched. In addition, Tienchi or Sanchi (Panax notoginseng), Japanese ginseng (Panax japonicus), and Vietnamese ginseng (Panax vietnamensis) are also widely grown and used as folk remedies (Yun 2001). While some compounds are shared by many of the Panax species, some are only found in one. These distinctions are useful in determining purity of ginseng preparations. For example, the ginsenoside Rf, is found in P. ginseng but not in P. quinquefolius (Li et al. 2000).

*P. ginseng* is typically found in the cooler regions of the Northern Hemisphere. Often reaching a height of six to 18 inches, the slow growing perennial plant has one to three umbels of 15 to 30 flowers and bears a round, small-sized, red berry (Fleming 1998). Roots are often harvested at four to six years of age. Roots are yellowish white and contain a primary root divided into rootlets and root hairs. Depending on the time of harvest and processing of the root, it can be called either white or red ginseng (Yun 2001). White ginseng is when the peeled root has been dried in the sun and retains a white color. Red ginseng refers to the steaming and boiling of the root resulting in the titular color. Both types

of ginseng yield different kinds of compounds because of the processing method employed, causing partial hydrolysis of esters and glycosides (Blumenthal 2003).

Several bioactive compounds have been identified in P. ginseng, including polysaccharides, polyenes, flavonoids, volatile oils and ginsenosides (Hou 1977). Of these, the ginsenosides are perhaps the best characterized. Ginsenosides or saponins contain four ring hydrophobic steroid-like structures with attached sugars which may be a glucose, maltose, fructose, galactose, pentose, or methylpentose (Liu and Xiao 1992; Coates 2005). It is in the variation, number, and position of the sugar group that account for each ginsenosides' unique physiological effect on the body. To date, 38 ginsenosides have been isolated from *P. ginseng*, far exceeding the number of ginsenosides found in any other species (Choi 2008). Ginsenosides have been divided into groups based on their structure. Most ginsenosides belong to one of two main groups, protopanaxadiols (PPD) and protopanaxatriols (PPT), which differ at the  $C_6$  position (Leung and Wong 2010). There are also rare ginsenosides, such as oleanane (Leung and Wong 2010). Ginsenoside content varies depending upon the age of the plant and season at the time of harvest, the part of the plant used, and how the plant material is processed (preserved and extracted) (Liberti and Der Marderosian 1978). Interestingly, the ratio of ginsenosides can determine physiological effect (Jin et al. 1999).

Due to the complex chemical composition of ginseng, many different physiological effects have been noted to be consistent with its use as a panacea. The literature is vast, thus the reader is referred to several recent reviews summarizing ginseng's immune system modulatory, anti-cancer and cytotoxic, neuroprotective, memory and learning stimulatory, antihyperglycemic, aphrodisiac and cardiovascular effects (Radad *et al.* 2006; Choi 2008; Christensen 2009; Jia *et al.* 2009; Lee *et al.* 2009b). This chapter focuses on the antimicrobial effects of *P. ginseng* extracts and components. Three mechanisms of microbial inhibition have been attributed to *P. ginseng:* inhibition of infection via immune system modulation, direct antibacterial activity, or inhibition of virulence factor production.

To better understand how P. ginseng affects the immune system response to microbial infection, a brief summary of the immune system focusing on aspects affected by ginseng is warranted. The initial response is detection of the pathogen by the innate immune system. This occurs by recognition of pathogen-associated molecular patterns (PAMPs) by its cognate Toll-like receptor (TLR) (Janeway 1989; Medzhitov et al. 1997; Uematsu and Akira 2008). PAMP binding to TLRs activates a signaling pathway that requires the adapter protein, myeloid differentiation primary response gene 88 (MyD88) (Lord et al. 1990; Medzhitov et al. 1998). Depending upon which TLR is conducting the signal, different cytokines are secreted which in turn activate the adaptive immune response (Medzhitov and Janeway 1999). This includes differentiation of CD4 cells into various T helper (Th) cell lineages including Th1, Th2, and Th17 (reviewed in Zhu et al. 2010). The Th1 response is required to clear intracellular pathogens, the Th2 response is important for extracellular pathogens, and the Th17 response targets Gram negative bacteria, fungi and select protozoa (reviewed in Fietta and Delsante 2009)). In a Th1 response, secretion of IFN- $\gamma$ , interleukin-2 (IL-2), and tumor necrosis factor alpha (TNF- $\alpha$ ) (Mosmann *et al.* 1986; Killar *et al.* 1987) leads to macrophage activation and cellular immunity (Meltzer et al. 1982). Interleukin 12 (IL-12) is important for the Th1 response because it induces IFN-y and TNF production, natural killer cell and T-cell proliferation and CD-4 to Th1 cell differentiation (Trinchieri et al. 1992). A Th2 response results in humoral immunity through secretion of interleukin 4 (IL-4), interleukin 5 (IL-5), and interleukin 13 (IL-13) (Mosmann et al. 1986; Killar et al. 1987) which in turn suppress macrophage activation and stimulate IgE production, as well as eosinophil and mast cell activation (reviewed in Deo et al. 2010). If the pathogen enters macrophages, a Th2 response would cause extensive tissue damage without affecting the pathogen, while the inflammation caused by the Th1 response would not be as damaging and would likely slow disease progression due to increased pathogen clearance. *P. aeruginosa* infection promotes a Th2 response, in part by production of 3OC<sub>12</sub>-HSL (Telford *et al.* 1998).

P. ginseng has long been known to have immunomodulatory activities (reviewed in Spelman et al. 2006). Modulation of the immune system by P. ginseng also enhances bacterial clearance (Song et al. 1997a). Crude aqueous extracts administered subcutaneously to a P. aeruginosa infected chronic pneumonia rat model system resulted in less severe lung pathology and a reduction in numbers of mast cells in lung foci, total immunoglobulin (IgG) levels and bacterial load with respect to infected animals treated with cortisone or saline instead of ginseng (Song et al. 1997a). The polymorphonuclear cell oxidative burst response and serum IgG2 levels were increased compared to the untreated or uninfected controls (Song et al. 1998). Interestingly, similar results were also observed in athymic rats (Song et al. 1997b). Together, these data suggest that ginseng activates innate immunity, enhances the Th1 response and down-regulates the Th2 response (Song et al. 1997a, 1997b, 1998). These studies did not measure cytokines.

Cytokines were measured in studies using a commercial preparation of ginseng, Gerimax ginseng, on the same P. aeruginosa rat model infection system (Song et al. 2002). Daily ginseng treatment resulted in decreased serum IgM and lung IL-4 levels seven days post infection. By day 21, lung IgĂ, IFN-γ, IL-4 and TNF-α and serum IgG2a responses were increased and lung pathology and P. aeruginosa colony forming units were reduced (Song et al. 2002). This is suggestive that ginseng promotes a shift from a Th2 to Th1 response. An *in vitro* assay showed that addition of Gerimax ginseng aqueous extracts in the presence of LPS and IFN- $\gamma$  to peripheral blood mononuclear cells increased IL-12 production by at least 5% compared to control, further suggesting that ginseng can stimulate the Th1 response (Larsen et al. 2004). Experiments with P. ginseng using a mouse chronic P. aeruginosa infection model also corroborate this effect, IFN- $\gamma$  and TNF- $\alpha$  levels as well as IFN- $\gamma$ /IL-4 ratio were higher and IL-4 levels were lower in the ginseng-treated animals relative to the control group (Song et al. 2003). As before, there was a milder lung pathology and increased bacterial clearance (Song et al. 2003).

Although it is possible that the aqueous P. ginseng extract affected P. aeruginosa clearance only by modulating the immune system, recent studies have shown that it directly inhibits P. aeruginosa QS (Song et al. 2010). Addition of ginseng extract to PAO1 cultures resulted in decreased 3OC12-HSL and C4-HSL production, LasA and LasB activity, without affecting growth. Since 3OC<sub>12</sub>-HSL stimulates the Th2 response, and ginseng promotes the Th1 response over that of Th2, it is possible that this is accomplished at least in part through QS inhibition. In agreement with this, aqueous P. ginseng extracts reduced biofilm formation and disrupted pre-formed biofilms in P. aeruginosa (Wu et al. 2011). Twitching and swimming motility were enhanced while swarming was also reduced (Wu et al. 2011). Biofilm formation and swarming are both QS-dependent (Davies et al. 1998, Kohler et al. 2000). Recently, an acetone:water extract of P. notoginseng flowers were shown to have antibacterial and anti-QS activity against C. violaceum and inhibit swarming in P. aeruginosa (Koh and Tham 2011).

Thus, ginseng seems to offer promise as an anti-*Pseudomonas* therapeutic agent, however, more investigation is needed. As previously stated, overproduction of alginate and conversion to a mucoid phenotype by *P. aeruginosa* leads to poor patient prognosis. Addition of aqueous ginseng extract to a well-characterized mucoid variant of PAO1 stimulated alginate production, yet reduced biofilm formation *in vitro* (Song *et al.* 2010; Wu *et al.* 2011). This may be explained by the observation that alginate production promotes formation of three-dimensional biofilms, while reducing biofilm formation in a solid-surface assay (Hay *et al.* 2009). Thus, additional studies must be performed to determine the suitability and conditions of ginseng use in treatment of acute and chronic *P. aeruginosa* infections. Also, since these observations were made using a crude extract, it is possible that different compounds are responsible for the different activities. Purification, characterization and identification of the active compounds may facilitate the development of therapeutics with different modes of action.

Purified components of *P. ginseng* also modulate the immune system to facilitate bacterial clearance (Lim et al. 2002; Ahn et al. 2006a). Ginsan is an acidic polysaccharide present in the ethanol insoluble aqueous fraction that consists of  $\alpha(1\rightarrow 6)$  glucopyranoside and  $\beta(2\rightarrow 6)$  fructofuranoside (Lee et al. 1997; Ahn et al. 2006a, 2006b). Ginsan does not have a direct antibacterial effect on S. aureus in vitro (Lim et al. 2002; Ahn et al. 2006b), but has an anti-septicaemic effect in mice infected with S. aureus (Lim et al. 2002). Pretreatment of mice with ginsan protected the animals from death due to S. aureus infection (Lim et al. 2002; Ahn et al. 2006a). Increased bacterial clearance was observed that may be due to a reduced early acute inflammatory response and enhanced macrophage activation (Lim et al. 2002; Ahn et al. 2006a). Ginsan did increase the in vitro phagocytic activity of macrophages (Ahn et al. 2006b). To further analyze if ginsan was acting through macrophages in vivo, mice were treated with the anti-cancer drug etoposide, which depletes macrophages (Ahn et al. 2006b). Etoposide treatment and ginsan lowered bacterial levels and increased survival rates compared to mice treated with just etoposide, suggesting that the anti-bacterial activity was not through ginsan acting on macrophages (Ahn et al. 2006b), however, it is possible that the etoposide did not completely deplete the macrophages.

Ginsan may act by down-regulating inflammatory cytokines. In sepsis, Toll-like receptor and MyD88 are also key players in the inflammatory response as they detect PAMPs and transduce the signal to induce expression of relevant genes and certain cytokines (Peck-Palmer et al. 2008). In vivo, pretreatment of mice with ginsan prior to infection with  $\bar{S}$ . aureus, resulted in decreased levels of IL-1 $\beta$ , IL-6, TNF- $\alpha$ , IFN- $\gamma$ , IL-12 and IL-18 (Ahn *et al.* 2006b), which are usually elevated in sepsis. Ginsan treatment decreased levels of Toll-like receptor and MyD88 in mouse peritoneal macrophages treated with heat-killed S. aureus in vitro (Ahn et al. 2006b). By activating macrophages and downregulating inflammatory cytokines, ginsan is able to impart a protective effect on mice. Ginsan treatment combined with vancomycin administration enhances survival in this mouse septic model system (Lim et al. 2002).

Besides being a biological response modifier, acidic polysaccharides purified from P. ginseng display anti-adhesive activities (Belogortseva et al. 2000; Lee et al. 2004a, 2004b, 2006, 2009a). The structures of these are not as well characterized as ginsan, however, these polysaccharides are pectin-like and are rich in uronic acid, with the majority being galacturonic acid (Lee et al. 2009a). These effectively inhibit adhesion of the gut pathogen, Helicobacter pylori, the oral pathogens Porphytomonas gingivalis and Actinobacillus actinomycetemcomitans, and the skin pathogens Propionibacterium acnes and S. aureus (Lee et al. 2004b, 2006, 2009a). Interestingly, these polysaccharides did not affect adhesion of the commensal bacteria Staphylococcus epidermidis, E. coli, Lactobacillus acidophilus and Bifidobacterium bifidum (Lee et al. 2006, 2009a). The polysaccharides did not affect growth of either the mammalian cells or the bacteria (Lee et al. 2006, 2009a). These properties of only targeting pathogenic bacteria without harming the natural flora or the host cells make these compounds potential therapeutics.

Polyacetylenes have also been isolated from *P. ginseng* (Fujimoto and Satoh 1988; Matsunaga *et al.* 1989; Fujimoto *et al.* 1990). One of these, panaxytriol, inhibits growth of *H.* 

**Table 2** Summary of anti-microbial effects of Panax ginseng.

Panax ginseng component	Target organism	Effect	Reference
Aqueous extract	P. aeruginosa	Immunoclearance	Song et al. 1997a
-		Shift to Th1 response	Song et al. 1997a, 1997b, 1998
		QS inhibition	Song et al. 2010
		Reduced biofilm formation	Wu et al. 2011
		Reduced swarming, enhanced motility	Wu et al. 2011
Ginsan	S. aureus	Reduced acute inflammatory response, enhanced	Lin et al. 2002, Ahn et al.
		macrophage activation, anti-septicaemic effect	2006a
		Enhanced macrophage phagocytic in vitro activity	Ahn et al. 2006b
Uronic acid-rich	H. pylori, P. gingivalis, S. aureus, P.	Adhesion inhibition	Lee et al. 2004b, 2006, 2009a
polysaccharides	acnes, A. acitinomycetemcomitans		
Panaxytriol	H. pylori	Growth inhibition	Bae et al. 2001
Ginsenosides	S. aureus, S. epidermis, S. typhimuriaum, V. vulnificus	Growth inhibition	Sung and Lee 2008

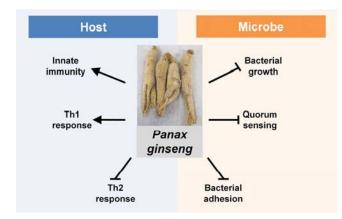


Fig. 3 Summary of *Panax ginseng* activities affecting microbial growth and pathogenesis.

*pylori* (Bae *et al.* 2001). Panaxytriol is also a cell cycle inhibitor, arresting a mouse lymphoma cell line, P388D1 at G2/M (Kim *et al.* 2002). To date, there is limited literature on the anti-bacterial activity of *P. ginseng* derived polyacetylenes, although polyacetylenes isolated from other sources have been demonstrated to affect microbial growth (Lechner *et al.* 2004; Schinkovitz *et al.* 2008).

Ginsenosides have also been identified as having antibacterial and immunomodulatory activities. A ginsenoside fraction purified from P. ginseng containing Rb<sub>1</sub>, Rb<sub>2</sub>, Rc, Rd, Re, Rf, Rg<sub>1</sub>, Rg<sub>2</sub>, Rg<sub>3</sub>, Rh<sub>2</sub> inhibited growth at a minimum inhibitory concentration (MIC) of 100 µg/ml of S. aureus, S. epidermidis, Salmonella typhimurium, and Vibrio vulnificus (Sung and Lee 2008). The ginsenosides were not as effective as the positive controls, nisin (MIC against the Gram positive bacteria, 40 µg/ml) and propionic acid (MIC against Gram negative bacteria, 50 µg/ml). The ginsenosides exhibited a synergistic effect with kanamycin and cefotaxime against MRSA (Sung and Lee 2008). The exact mechanism for this effect is unknown but since ginsenosides are amphipathic they may interact with the cell membrane and allow entry of the antibiotic into the cell. In agreement with perturbation of the cell membrane by the ginsenosides, addition of the ginsenosides to calcein-encapsulated large unilamellar vesicles resulted in a dose-dependent leakage of dye (Sung and Lee 2008). Mitogen-induced lymphocyte proliferation was reduced by treatment with  $Rb_2$ , Re and  $Rg_1$ , but not  $Rb_1$  (Cho *et al.* 2002). A caveat to these results is that the ginsenosides used were purified from P. ginseng and the fraction may contain other compounds, although the fractions shown to have immunomodulatory effects were >95% pure.

#### CONCLUSION

In summary, ginseng contains immunomodulatory, antimicrobial and anti-QS compounds that may be useful in treatment of bacterial infections (**Fig. 3, Table 2**). While some active compounds have been isolated and characterized, limited studies have been performed and the main compounds responsible for the anti-*Pseudomonas* immune system modulation and anti-QS effect remain to be purified. Once the bioactive compound(s) have been isolated they can be characterized for their effects alone and in combination with other effective compounds and antibiotics *in vitro* and in animal models. These studies will pave the way for ginseng use as an anti-infective therapeutic.

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