Mikologia Lekarska 2010, 17 (2): 108-112

www.cornetis.com.pl
ISSN 1232-986X

Multispecies microbial communities. Part I: quorum sensing signaling in bacterial and mixed bacterial-fungal communities

Wielogatunkowe populacje drobnoustrojów. Część I: *quorum sensing* w bakteryjnych i mieszanych bakteryjno-grzybiczych populacjach

Zulma Rocío Suárez-Moreno[1], Ádám Kerényi[2], Sándor Pongor[1], Vittorio Venturi[1]

[1] International Centre for Genetic Engineering and Biotechnology, Trieste, Italy
[2] Biological Research Center of the Hungarian Academy of Sciences, Szeged, Hungary

ADDRESS FOR CORRESPONDENCE: Sandor Pongor
Protein Structure and Bioinformatics, International Centre for Genetic Engineering & Biotechnology,
Padriciano 99,34149,Trieste, Italy, tel.: +39 040 375 73 00; fax: +39 040 226 555; e-mail: pongor@icgeb.org
Vittorio Venturi
Bacteriology Group, International Centre for Genetic Engineering & Biotechnology,
Padriciano 99, 34149 Trieste, Italy, tel.: +39 04 03 757 319; fax: +39 04 02 265 55; e-mail: venturi@icgeb.org

ABSTRACT The discovery that many bacterial species coordinate their behavior when they form a group has revolutionized bacteriology in the 1990s. According to this mechanism, termed "quorum sensing", bacteria produce chemical signals which are either secreted or released into the external environment. Since the external signal concentration is tightly correlated with population density, any concentration-dependent response by the individual cells will result in a density dependent community behavior. This fundamental mechanism has been shown now in a variety of bacterium species and interesting parallel mechanisms were found in more distant organisms. This essay gives an overview of bacterial quorum sensing and its applications to bacterial-fungal interactions.

KEY WORDS: quorum sensing

STRESZCZENIE Odkrycie faktu, że wiele gatunków bakterii koordynuje wzajemnie swoje zachowania, stanowiło przełom w bakteriologii lat 90. ubiegłego stulecia. W mechanizmie określanym jako *quorum sensing* bakterie wytwarzają oraz wydzielają lub uwalniają do środowiska zewnętrznego chemiczne substancje przekaźnikowe. Stężenie w środowisku zewnętrznym substancji przekaźnikowych jest ściśle skorelowane z gęstością populacji, tak więc odpowiedź poszczególnych komórek będzie zależała od zachowania całej populacji. Ten bardzo istotny mechanizm został wykazany u różnych gatunków bakterii, a analogiczne mechanizmy zostały opisane także w przypadku innych organizmów. Niniejsza praca koncentruje się na opisie bateryjnych zachowań typu *quorum sensing* i podobnych reakcji w stosunkach bakteryjno-grzybiczych.

SŁOWA KLUCZOWE: *quorum sensing*

Introduction

The discovery of chemical communication among bacteria in the 1990s has fundamentally changed the traditional view that pictures bacteria as single-celled organisms living in isolation. In the last fifteen years it has become increasingly evident that bacteria have the potential to establish highly complex communities. In fact, most bacteria are able to monitor their population density by producing and detecting small molecular weight signaling compounds (also called autoinducers) in a process which has been termed "quorum sensing" (QS) (1). Since the original reports and discoveries, the field has substantially expanded, and recent genomic analyses confirmed that in addition to known QS systems, there is substantial cross talk between various species as many bacteria may respond to a variety of known and unknown signals (Subramoni and Venturi, 2009; Ryan and Dow, 2008). As of today, bacterial signalling can be integrated into a larger context of interspecies signaling that plays role in a range of quite distant fields such as host parasite interactions, plant-bacterium interactions etc (2-4). Bacterial-fungal communities occupy a special place in this picture since bacteria very often accompany a variety of the known fungal infections. This essay gives a brief overview of bacterial quorum sensing and some of the known cases of bacteria-fungal interactions.

Quorum sensing in bacteria

Quorum sensing (QS) is a cell-cell communication process in which bacteria use the production and detection of autoinducers, to monitor cell population density and make a coordinated response. When the autoinducer reaches a critical level, the population responds through the coordinated expression of specific target genes (1). This synchronous response of bacterial populations, confers them a form of multicellularity and enables them to adapt and survive continually to changing environments by coupling individual cell responses to population-wide alterations (5).

The fundamental steps involved in the response to fluctuations in cell number are comparable in all QS systems. In a canonical system, the autoinducer molecules are passively released or actively secreted outside of the cells. As the number of cells in a population increases, the extracellular signal concentration likewise increases and when it accumulates above the minimal threshold level required for detection, cognate receptors bind the autoinducers and

trigger signal transduction cascades that result in population-wide changes in the gene expression (fig. 1).

Thus far the most studied autoinducers are the *N*-acylhomoserine lactones, however other examples of compounds involved in bacterial quorum sensing are: oligopeptides, Autoinducer type-2 (AI-2), quinolones and a molecule termed 'diffusible signal factor (DSF) (tab. I).

Acyl homoserine lactones (AHLs) are believed thus far to be the major class of autoinducer signals used by Gram-negative bacteria. These molecules have a conserved homoserine lactone ring

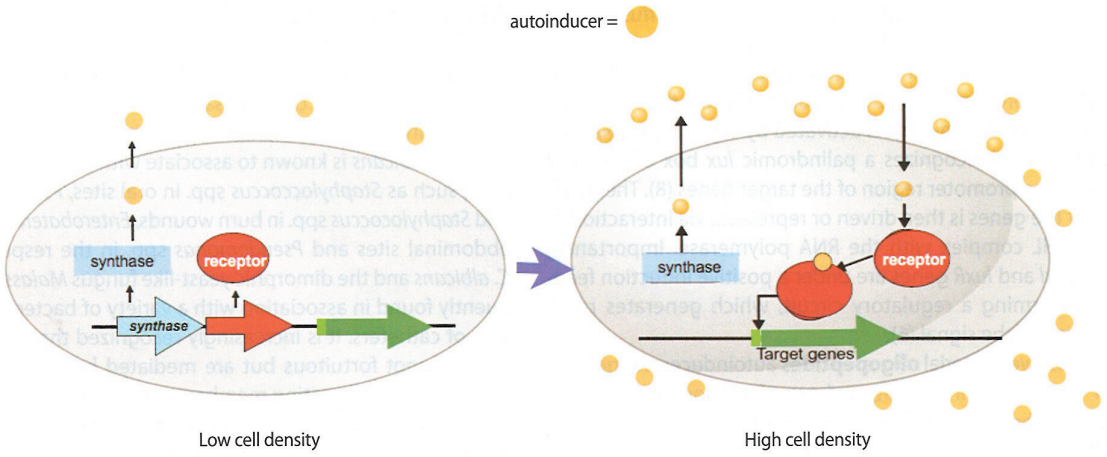


Fig. 1. The canonical scheme of bacterial quorum sensing regulation.
Ryc. 1. Schemat bakteryjnej regulacji *quorum sensing*

Table I: Examples of QS signaling molecules
Tabela I: Przykłady substsncji przekaźnikowych w QS

Compound & structure *Związek i struktura*	**Example of producer organisms** *Przykłady organizmów wytwarzających*	**Qs system** *System qs*	**Ref** *Poz. lit.*
N-acyl homoserine lactones	*Agrobacterium tumefaciens* *Pseudomonas aeruginosa* *Burkholderia cepacia* *Pantoea stewarti* *Vibrio fisheri*	TraIR LasIR, RhlIR CepIR EsaIR LuxIR	(9) (10, 11) (12) (13) (14)
DSF Diffusible signal factor	*Xanthomonas campestris* pv. *campestris* Chemical analogs also found in: *Xylella fastidiosa* *Stenotrophomonas maltophilia*	Rpf system	(15) (16) (17)
Gram Positive Oligopeptides Cyclic: ComX ADPITRQWGD CSP EMRLSKFFRDFILQRKK AIP-1 YSTCDFIM AIP-2 GVNACSSLF AIP-3 INCDFLL AIP-4 YSTCYFIM	 *Staphylococcus aureus* *B.subtilis* *S. pneumoniae*	 AgrC/AgrA ComP/ComA ComD/ComE	 (18) (19) (20)
Autoinducer Type 2 AI-2 *Vibrios Salmonella*	 *Vibrio harveyi* *Vibrio cholerae* *Salmonella thypimurium*	 LuxS/LuxPQ LuxS/LuxPQ LuxS/LsrB	(21) (22) (23)
PQS Pseudomonas Quinolone Signal	*Pseudomonas aeruginosa*	PqsABCDE-R	(24)

with an acyl side chain, which may vary from 3 to 18 carbons. The length and saturation level of the acyl chain coupled to the presence or absence of oxo or hydroxyl substitutions at the C3 position of the acyl chain provide variation and specificity for quorum sensing communication in mixed bacterial populations. The homoserine lactone ring imparts hydrophilic character on the molecule, while the length, substitution and saturation modulate their hydrophobicity (6). All AHLs are believed to be able to freely diffuse across the cell envelope; however efflux pumps may actively export some longer chain AHLs (7). In an AHL-QS circuit, AHLs are synthesized by a LuxI-type protein and at critical concentration, the AHL binds a LuxR-type protein, which gets activated by exposing a DNA binding domain that recognizes a palindromic *lux* box *cis*-element localized in the promoter region of the target genes (8). The transcription of the genes is then driven or repressed, via interaction of the LuxR-AHL complex with the RNA polymerase. Importantly, often the *luxI* and *luxR* genes are under a positive induction feedback loop forming a regulatory circuit, which generates rapid amplification of the signal (6).

Gram positive bacterial **oligopeptides** autoinducers range from 5 to 34 aminoacids in length, and are often postranslationally modified by the incorporation of lactone and thiolactone rings, lanthionines and isoprenyl groups. Due to their hydrophobicity, oligopeptide release requires specialized transporters, and two-component signalling proteins located in the membrane then mediate its perception with signal transduction occurring by a phosporylation cascade (25). Different oligopeptide autoinducers contain subtle variations, which confer signalling specificity because of the discriminatory properties of their cognate receptors. Some examples are ComX and CSF of *Bacillus subtillis*, CSP from *S. pneumoniae*, and the four types of AIP (Autoinducer Peptide) from *S. aureus* (18-20).

The **Autoinducer 2 (AI-2)** is found both in other Gram negative and Gram-positive bacteria and is thought to enable interspecies communication (26, 27). The LuxM protein is responsible of the synthesis of the AI-2 precursor, DPD (4,5-hydroxy-2,3-pentanedione), which cyclises spontaneously to give rise to several related **furanones** that are believed to be in equilibrium. Importantly in *V. harveyi*, AI-2 contains boron, while the AI-2 active form in *Salmonella* does not (tab. I). Different species of bacteria may recognize distinct DPD moieties, which allows bacteria to respond to their own DPD and also to those produced by other bacteria (23). In *V. harveyi*, the AI-2 circuit also integrates with other intercellular signalling systems resulting in a complex and timely regulation of bioluminescence (28). In other species it also control functions such virulence factor production, motility and biofilm formation (29).

The **diffusible signal factor** (DSF) was first identified in *Xanthomonas campestris*, but is also produced by other species including *X. oryzae, Xylella fastidiosa* and *Stenotrophomonas maltophilia*. DSF is an unsaturated fatty acid (cis-11-methyl-2-dodecenoic acid), and is synthesized by RpfF protein, a two-component system is then responsible for DSF perception. All these gene products are encoded by the *rpf* cluster (15, 30). The *rpf*/DSF system controls diverse functions including virulence factor systems, aggregative behaviour and biofilm formation. A similar molecule was also recently reported in *Burkholderia* spp. (BDSF) and its role in interspecies communication is currently under investigation (31).

One of the *Pseudomonas* autoinducers is known as ***Pseudomonas* quinolone signal** (PQS) which is a 2-heptyl-3hydroxy-4 quinolone (24) .This molecule is synthesized from anthranilate via the action of *pqsA-D* and *pqsH* gene products. Together with other QS circuits in *P. aeruginosa*, PQS functions to control a battery of genes required for virulence and biofilm formation (32). Examples of other autoinducers are the CAI-1 of *V. cholera* and *V. harveyi*, bradyoxetin from *Bradirhizobium japonicum* and the diketopiperazines from *Pseudomonas* spp. and *Proteus mirabilis* (5).

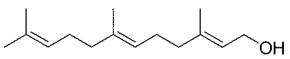
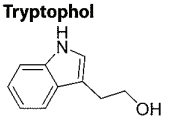
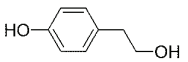
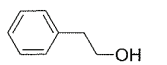
Fungal and bacterial-fungal interactions

Consortia of bacteria and fungi are abundant in the human body and are the source of serious medical problems (2-4). *Candida albicans* is a benign commensal of the human body which can however induce serious infections in immunocompromised individuals. *C. albicans* is known to associate with a large variety of bacteria, such as *Staphyloccoccus* spp. in oral sites, *Pseudomonas* spp. and *Staphylococcus* spp. in burn wounds, *Enterobateriaceae* in intra-abdominal sites and *Pseudomonas* spp. in the respiratory tract. *C. albicans* and the dimorphic yeast-like fungus *Malassezia*, are frequently found in association with a variety of bacteria on the surface of catheters. It is increasingly recognized that these associations are not fortuitous but are mediated by specific molecular signals actively recruiting members of the cellular community.

C. albicans can exist in the form of budding yeast, filamenting hyphae or pseudohyphae, and can also form poysaccharide-matrix-enclosed biofilm communities. The corresponding transitions are regulated by various exogenous and endogenous signals. Farnesol produced by *C. albicans* cells represses filamentation in a cell-density dependent manner; interestingly, this was the first fungal QS system identified (33). Tyrosol is another QS molecule produced by *C. albicans* that is able to specifically shorten the lag phase of growth in a low-density culture without affecting the exponential growth phase (35). Phenylethanol and tryptophol induce pseudohyphal growth in *S. cerevisiae* in a cell density-dependent way. Many of the known fungal signaling molecules are volatile so they can travel between distant, sessile cells and/or communities (tab. II).

C. albicans and *P. aeruginosa* are frequently found in the same niche and interact in a variety of ways. *P. aeruginosa* is able to form biofilms on the hyphae of *C. albicans* and can kill the hyphae by

Table II: Examples of fungal signaling molecules
Tabela II: Przykłady grzybiczych substancji przekaźnikowych

Compound & structure *Związek i struktura*	**Example of producer organisms** *Przykłady organizmów wytwarzających*	**Ref** *Poz. lit.*
Farnesol 	*C. albicans*	(33) (34)
Tryptophol 	*C. albicans* *S. cerevisiae*	(35)
Tyrosol 	*C. albicans* *S. cerevisiae*	(35)
Phenlethanol 	*C. albicans* *S. Cerevisiae*	(35)

producing phenazines (36) and phospholipase C (37). On the other hand, yeast-form *C. albicans* cells and *P. aeruginosa* can also form mixed biofilms in which the two species interact by signals. AHL signals of *P. aeruginosa* inhibit the hyphal growth of *C. albicans* so *P. aeruginosa* apparently keeps *C. albicans* cells in the yeast form suitable for mixed biofilm formation. On the other hand, farnesol and other unidentified factors of *C. albicans* influence QS in *P. aeruginosa* (36, 38).

One of the notorious problems of studying microbial consortia is the lack of simple and straightforward model systems. Animal models are frequently used, for instance intravenous or intraperitoneal injection of mice with *Candida albicans* and *Escherichia coli* has been used to study polymicrobial bacteraemia or peritonitis, respectively (39, 40). Burn wound and subcutaneous-infection models have been used to study mixed infections with *Candida* spp. and *Pseudomonas aeruginosa* (41-43). Mammalian models for polymicrobial interactions have also been developed, including a model of vaginal candidiasis (44).

Conclusions

In this essay we focused on the fundamental principles of bacterial quorum sensing and its potential applications of bacterial-fungal communications. The unifying view emerging from recent studies is that the various signalling molecules sequestered by microbes may create a variety of chemical milieus allowing the formation of stable microbial communities. Thus far, QS bacterial communities are the best known examples, we can expect that a variety of other unicellular organisms can also form mixed microbial communities such as bacterial-fungal associations as observed in various pathological conditions. Understanding the signaling mechanism stabilizing microbial communities may be crucially important for designing better prevention and control strategies.

Acknowledgements

ZRSM and ÁK are PhD students at the ICGEB PhD program in Molecular biology and at the Biology PhD Program of the University of Szeged, Hungary, respectively. The work at BRC Szeged was partly supported by a grant no TAMOP-4.2.2-08/1/2008-008 from the Hungarian National Office for Research and Technology (NKTH).

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Received: 2010.05.05. Approved: 2010.05.07.

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