



Editorial-Relation of Environment and Bacteria in Microbiology

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How bacterial cells sense environment cues is not well studied. Three kinds of histidine kinases were found as receptors to receive plant-associated or quorum sensing signals. Of these HKV gr S detects iron depletion by binding to ferric iron via an ExxE motif. RpfC binds diffusible signal factor (DSF) by its N terminal peptide and activates auto kinase activity through relaxation of autoinhibition, and PcrK specifically senses plant hormone cytokinin and elicits bacterial responses to oxidative stress. These HK's are critical sensors that regulate the virulence of a gram negative bacterium. *Xanthomonas campestris* pv *campestris*. Research progress on the signal perception of phytopathogenic bacterial HK's suggest that inter-kingdom signaling between host plants and pathogens control pathogenesis and can be used as a potential molecular target to protect plants from bacterial diseases [1].

Thorsdottir, et al. 2019 discussed the dual role of microglia in disease development, the beneficial functions crucial for bacterial clearing, and the destructive properties via triggering neuroinflammation, characterized by cytokine and chemokine release that leads to leucocyte trafficking through the brain vascular endothelium and breakdown of the blood-brain barrier integrity. Due to intrinsic complexity of microglia and lack of specific markers till now, the study of microglial response to bacterial pathogens has been challenging. New experimental models and techniques open up the possibility to accelerate progress in this field. They further reviewed existing models, discussing their possibilities and limitations and summarized the recent findings where bacterial virulence factors are identified to be important for the microglial purposes. Among the promising approaches are: modulators of microglia phenotype, switching toward anti-inflammatory and phagocytic functions, the use of nonbacterial antimicrobials,

presenting release of bacterial components into the neural milieu and consequent amplification of immune activation, and protection of the blood brain barrier integrity [2].

Although invasive meningococcal disease (IMD) in Europe has been declining in recent years, a rising incidence due to serogroup W (Men W), predominantly sequence type1 (ST-11), clonal complex 11 (cc11), was reported in some European countries. Thus Krone M carried out a retrospective observational study, where IMD surveillance data was collected from 2013-2017 by national reference laboratories and surveillance units from 13 European Countries and analyzed using descriptive statistics. They found that the overall incidence of IMD has been stable during the study period. Incidence of Men W IMD /10, 000 population (2013:0.03;2014:0.05;2015:0.08;2016:0.11;2017:0.11) and the proportion of this serogroup among all invasive cases (2013:5%; (116/2, 216); 2014:9% (161/1, 1, 761); 2015:13% (271, 2074); 2016:17% (388/2, 222); 2017:19% (393/2, 112) continuously increased. The most affected countries were England, the Netherlands, Switzerland and Sweden. Men W was more frequent in older age groups (≥ 45 years), while the proportion in children (< 15 yrs) was lower than in older age groups. Of the culture confirmed Men W IMD cases 80% (615/767) were caused by hypervirulent cc11. Thus during 2013-2017, an increase in Men W IMD, caused by Men W, cc11, was seen in majority of European countries. Given the unpredictable nature of meningococcal spread and the epidemiological potential of cc11, European countries may consider preventive strategies adaptive to their contexts [3].

Gantuya, et al. examined gastric mucosal microbiota in *Helicobacter pylori* (H. pylori-negative gastritis (HpN) compared to *Helicobacter pylori* (H. pylori-positive (HpP) and H. pylori-

negative non gastritis group (control). 11 subjects with HpN, 40 with HpP and 24 controls were studied. In endoscopy with gastric biopsies was done, Comparison groups were defined based on strictly histological criteria for the disease and *H. pylori* diagnosis. They used 16S rRNA gene amplicon sequencing to profile the gastric microbiota according to comparison groups. These results showed that the HpP group had significantly lower bacterial richness by the operational taxonomic unit (OUT) counts, and Shannon and Simpson indices as compared to HpN or controls. The linear discriminative analysis effect size analysis showed the enrichment of Firmicutes, Fusobacteria, Bacteroides and Actinobacteria at phylum level in the HpN group. In the age – adjusted multivariate analysis, *Streptococcus* sp. and *Haemophilus parainfluenzae* were at a significantly increased risk for HpN (odds ratio 18.9 and 12.3 respectively) based on abundance. *Treponema* sp was uniquely found in HpN based on occurrence. Thus concluding that *Streptococcus* sp, *Haemophilus parainfluenzae*, and *Treponema* sp are candidate pathogenic bacterial species for HpN. If these results get confirmed, they may have important implications [4].

A fundamental question in microbiology is how bacterial cells manage to coordinate gene expression with cell growth during adapting to various environmental conditions. Although the cellular responses to changing environments have been extensively studied using transcriptomic and proteomic approaches, it remains poorly understood regarding the molecular strategy enabling bacteria to manipulate the global gene expression patterns. The alarmone (p) ppGpp is a key secondary messenger involved in regulating various biochemical and physiological processes of bacterial cells. However despite of extensive studies of (p) ppGpp signaling is stringent response during the past 50 years, the connection between (p) ppGpp and exponential growth remains poorly understood, The recent work of Zhu., et al. demonstrated that (p) pp Gpp is strongly involved in regulating cell growth of *Escherichia coli* through balancing the cellular environment on metabolic proteins and ribosomes, highlighting itself as a magic governor of bacterial global resource allocation. This highlighted the current progress of the relation between (p) ppGpp and bacterial exponential growth. Two important future directions are i) to elucidate the cellular signal that triggers (p) ppGpp accumulation during poor growth conditions ii) investigate the relation between (p) ppGpp and exponential growth for bacterial species other than *E. coli* [5].

Antibiotic resistant genes (ARG's) are regarded as emerging environmental pollutants and pose a serious health risk to the human population. Integrons are genetic elements that are involved in the spread of ARG's amongst bacterial species. They also act as reservoirs of these resistance traits further contributing to the development of multidrug resistance in several water-borne pathogens like *Vibrio*, *Campylobacter*, *Salmonella*, *Shigella*, *Escherichia coli* and other opportunistic pathogens. These pathogens exhibit immense diversity in their resistance gene cassettes. The evolution of multiple novel and complex gene cassettes in integrons further suggests the selection and horizontal transfer of ARG's in multidrug resistance bacteria. Thus the detection and characterization of these integrons in water borne pathogens, especially in epidemic and pandemic strains, is of utmost importance. It will provide a framework in which health authorities can conduct improved surveillance of antibiotic resistance in our natural water bodies. Such a study will also be helpful in developing better strategies in the containment and cure of infections caused by these bacteria [6].

Phase –variable DNA methyl transferases control the expression of multiple genes via epigenetic mechanisms in a wide variety of bacterial species. These systems are called phase variations, for phase-variable regions, Phase variations regulate genes involved in pathogenesis, host adaptation and antibiotic resistance. Many human –adapted bacterial pathogens contain phase variations. These include leading causes of morbidity and mortality worldwide, such as non-typeable *Haemophilus influenzae*, *Streptococcus pneumoniae*, and *Neisseria* spp. Phase –variable methyl transferases and phase variations have also been discovered in environmental organisms and veterinary pathogens. The existence of many different examples suggests that phase variations have evolved multiple times as a contingency strategy in the bacterial domain, controlling phenotypes that are important in adapting to environmental change. Many of the organisms that contain phase variations have existing or emerging drug resistance. Vaccines may therefore represent the best and most cost effective way to prevent disease caused by these organisms. However many phase variations also control the expression of current and putative vaccine candidates; variable expression of antigens could lead to immune evasion, meaning that vaccines designed using these targets become ineffective. It is therefore essential to characterize phase variations in order to determine an organism's stably expressed antigenic repertoire, and rationally design broadly effective vaccines [7].

Mobile genetic element (MGE's) play critical roles in transferring ARG's among different microorganisms in the environment. Zhu L., et al. further aimed to explore the fate of MGE's during chicken manure (CM) and bovine manure (BM) composting to assess horizontal transfer risks of ARG's. The results showed that removal efficiency of MGE's during CM composting was significantly higher than during BM composting. Meanwhile, these potential host bacteria of MGE's were eliminated largely during CM composting. Meanwhile, these potential host bacterial communities are significantly influenced by pH, NH₄⁺, NO₃⁻ and total N, which can be used to regulate host bacterial communities to remove MGE's during composting. Projection pursuit regression further confirmed that composting can effectively reduce horizontal transfer risk of ARG's, especially for CM composting. These results identified the critical roles of host bacterial communities in MGE's removal during composting of different animal manures [8].

Bibliography

1. Wang FF and Qian W. "The roles of histidine kinases in sensing host plant and cell-cell communication signal in a phytopathogenic bacterium". *Philosophical Transactions of the Royal Society B: Biological Sciences* 374.1767 (2019): 20180311.
2. Thorsdottir S., et al. "The Role of Microglia in Bacterial Meningitis: Inflammatory Response, Experimental Models and New Neuroprotective Therapeutic Strategies". *Frontiers in Microbiology* 10 (2019): 576.
3. Krone M., et al. "Increase of invasive streptococcal serogroup W disease in Europe 2013-2017". *Eurosurveillance* 24.14 (2019).
4. Gantuya B., et al. "Gastric Microbiota in Helicobacter pylori-Negative and -Positive Gastritis Among High Incidence of Gastric Cancer Area". *Cancers (Basel)* 11.4 (2019).
5. Zhu M., et al. "(p) ppG pp: the magic governor of bacterial growth economy". *Current Genetics* (2019).
6. Kaushik M., et al. "Integrins and antibiotic resistance genes in water borne pathogens: threat detection and risk assessment". *Journal of Medical Microbiology* (2019).
7. Phillips ZN., et al. "Phase virions of bacterial pathogens –phase-variable epigenetic regulators evolving from restriction-modification systems". *Microbiology* (2019).
8. Zhu L., et al. "Host bacterial community of MGEs determines the risk of horizontal gene transfer during composting of different animal manures". *Environment Pollution* 250 (2019): 166-174.

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