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Sommario/riassunto	<p>The most common quorum sensing (QS) system in Gram-negative bacteria occurs via N-acyl homoserine lactone (AHLs) signals. An archetypical system consists of a LuxI-family protein synthesizing the AHL signal which binds at quorum concentrations to the cognate LuxR-family transcription factors which then control gene expression by binding to specific sequences in target gene promoters. QS LuxR-family proteins are approximately 250 amino acids long and made up of two domains; at the N-terminus there is an autoinducer-binding domain whereas the C-terminus contains a DNA-binding helix-turn-helix (HTH) domain. QS LuxRs display surprisingly low similarities (18-25%) even if they respond to structurally similar AHLs. 95% of LuxRs share 9 highly conserved amino acid residues; six of these are hydrophobic or aromatic and form the cavity of the AHL-binding domain and the remaining three are in the HTH domain. With only very few exceptions, the luxI/R cognate genes of AHL QS systems are located adjacent to each other. The sequencing of many bacterial genomes has revealed that many proteobacteria also possess LuxRs that do not have a cognate LuxI protein associated with them. These LuxRs have been called orphans and more recently solos. LuxR solos are widespread in proteobacterial species that possess a canonical complete AHL QS system as well as in species that do not. In many cases more than one LuxR solo is present in a bacterial genome. Scientists are beginning to investigate these solos. Are solos</p>

responding to AHL signals? If present in a bacterium which possesses a canonical AHL QS system are solos an integral part of the regulatory circuit? Are LuxR solos eavesdropping on AHLs produced by neighboring bacteria? Have they evolved to respond to different signals instead of AHLs, and are these signals endogenously produced or exogenously provided? Are they involved in interkingdom signaling by responding to eukaryotic signals? Recent studies have revealed that LuxR solos are involved in several mechanisms of cell-cell communication in bacteria implicating them in bacterial intraspecies and interspecies communication as well as in interkingdom signaling by responding to molecules produced by eukaryotes. LuxR solos are likely to become major players in signaling since they are widespread among proteobacterial genomes and because initial studies highlight their different roles in bacterial communication. This Research Topic allows scientists studying or interested in LuxR solos to report their data and/or express their hypotheses and thoughts on this important and currently understudied family of signaling proteins.

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