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EDITORIAL

Common Themes Amid Diversity

As reflected in the related Articles and News stories in this special issue on frontiers in microbiology, microbes, despite their diversity, use a common set of strategies to sense and respond to environmental cues. These strategies allow adaptation to different ecological niches, be they the intestine of a human, a plant leaf, the light organ of a squid, or the rocky depths of the Earth (see the News story on deep life, p. 703). There are, however, variations on these themes that constantly provide surprises and require new interpretations.

By identifying bacterial genes that are expressed only in a given environment or are essential for growth in a given environment, investigators are trying new ways to prevent infectious diseases of plants and vertebrates, as well as environmental hazards such as biocorrosion (see Strauss and Falkow, p. 707). Microbes have evolved different strategies to benefit or eliminate one another. The ability of related bacteria to cross-talk by secreting autoinducers such as acylated homoserine lactones is one example of community sensing. Similar autoinducers regulate the density-dependent expression of tissue-damaging enzymes when Pseudomonads infect lung tissue. Bacterial competition through interference is an old observation that is getting a new twist from the discovery of secreted peptides that prevent bacteria unrelated to the secreters from responding appropriately to the environment.

Bacterial sensing of extracellular cues is often handled by two-component sensory transduction systems, which allow animal and plant pathogens to adapt to microenvironments in the host and undergo a successful pathogenic cycle. The exact molecular mechanisms leading to the autophosphorylation of the histidine kinase components of these sensors are just beginning to be unraveled. Two-component regulatory systems also trigger developmental events in bacteria, as described by Shapiro and Losick (p. 712). These developmental systems illustrate how differential positioning of proteins within a cell creates the asymmetry that drives development. The fascinating task that lies ahead is to find out how a protein within an individual bacterium is targeted to a defined region. Protein asymmetries within bacteria are also important for bacterial spread within and between host cells, through polymerization of actin at only one of the two bacterial poles, which leads to intracellular motility (see Finlay and Cossart, p. 718).

Many bacterial species readily interact with inanimate or animate surfaces, forming highly adapted communities. Interactions between bacterial pathogens and host cells trigger signaling events in each partner, the basics of which are surprisingly similar in plant and animal pathogens, as described by Baker *et al.* (p. 726) and Finlay and Cossart. One approach, commonly used by Gram-negative bacteria, is to deliver effector proteins into the cytosol of the host cell through specialized secretion systems. These systems are highly conserved between species and were probably obtained by horizontal gene transfer from a common ancestor. However, the effector proteins that the bacteria choose to send out through these systems differ among pathogens. For example, *Shigella* and *Salmonella* deliver proteins that stimulate their uptake into host cells, but *Yersinia* introduces target proteins that prevent its internalization. Interestingly, plant cellular defense responses against microbes may be analogous to the innate immunity found in vertebrates and insects. In all three cases, microbial products trigger a nonspecific response that involves ligand binding, which results in nuclear translocation of transcriptional factors that initiate defense. Bacterial effector proteins that directly interfere with transcriptional factors will surely be found soon.

Although we have a much-improved understanding of microbial phylogeny (see the News profile of Carl Woese, p. 699), only a small fraction of the biosphere's total microbial gene pool is known, as described by Pace (p. 734). As the genomes of more microbes are sequenced, the identification of conserved genes will yield information about how they cause disease. Above all, the increased number of sequenced microbial genomes will provide information about potentially useful microbes and about the enzymes and metabolic activities that sustain life on Earth in all of its niches (see the News stories on extremophile biotechnology, p. 705).

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