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CONTENTS/SUMMARIES

- Evolution of the Chaperone/Usher Assembly Pathway: Fimbrial Classification Goes Greek.** Sean-Paul Nuccio and Andreas J. Bäumlner 551–575

Summary: Many Proteobacteria use the chaperone/usher pathway to assemble proteinaceous filaments on the bacterial surface. These filaments can curl into fimbrial or nonfimbrial surface structures (e.g., a capsule or spore coat). This article reviews the phylogeny of operons belonging to the chaperone/usher assembly class to explore the utility of establishing a scheme for subdividing them into clades of phylogenetically related gene clusters. Based on usher amino acid sequence comparisons, our analysis shows that the chaperone/usher assembly class is subdivided into six major phylogenetic clades, which we have termed α -, β -, γ -, κ -, π -, and σ -fimbriae. Members of each clade share related operon structures and encode fimbrial subunits with similar protein domains. The proposed classification system offers a simple and convenient method for assigning newly discovered chaperone/usher systems to one of the six major phylogenetic groups.

- Function, Structure, and Evolution of the RubisCO-Like Proteins and Their RubisCO Homologs.** F. Robert Tabita, Thomas E. Hanson, Huiying Li, Sriram Satagopan, Jaya Singh, and Sum Chan 576–599

Summary: About 30 years have now passed since it was discovered that microbes synthesize RubisCO molecules that differ from the typical plant paradigm. RubisCOs of forms I, II, and III catalyze CO₂ fixation reactions, albeit for potentially different physiological purposes, while the RubisCO-like protein (RLP) (form IV RubisCO) has evolved, thus far at least, to catalyze reactions that are important for sulfur metabolism. RubisCO is the major global CO₂ fixation catalyst, and RLP is a somewhat related protein, exemplified by the fact that some of the latter proteins, along with RubisCO, catalyze similar enolization reactions as a part of their respective catalytic mechanisms. RLP in some organisms catalyzes a key reaction of a methionine salvage pathway, while in green sulfur bacteria, RLP plays a role in oxidative thiosulfate metabolism. In many organisms, the function of RLP is unknown. Indeed, there now appear to be at least six different clades of RLP molecules found in nature. Consideration of the many RubisCO (forms I, II, and III) and RLP (form IV) sequences in sequence databases has subsequently led to a coherent picture of how these proteins may have evolved, with a form III RubisCO arising from the Methanomicrobia as the most likely ultimate source of all RubisCO and RLP lineages. In addition, structure-function analyses of RLP and RubisCO have provided information as to how the active sites of these proteins have evolved for their specific functions.

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The Autodisplay Story, from Discovery to Biotechnical and Biomedical Applications. Joachim Jose and Thomas F. Meyer

600–619

*Summary: Among the pathways used by gram-negative bacteria for protein secretion, the autotransporter pathway represents a solution of impressive simplicity. Proteins are transported, independent of their nature as recombinant or native passengers, as long as the coding nucleotide sequence is inserted in frame between those of an N-terminal signal peptide and a C-terminal domain, referred to as the β -barrel of the outer membrane translocation unit. The immunoglobulin A1 (IgA1) protease from *Neisseria gonorrhoeae* was the first identified member of the autotransporter family of secreted proteins. The IgA1 protease was employed in initial experiments investigating autotransporter-mediated surface display of recombinant proteins and to investigate structural and functional requirements. Various other autotransporter proteins have since been described, and the autodisplay system was developed on the basis of the natural *Escherichia coli* autotransporter protein AIDA-I (adhesin involved in diffuse adherence). Autodisplay has been used for the surface display of random peptide libraries to successfully screen for novel enzyme inhibitors. The autodisplay system was also used for the surface display of functional enzymes, including esterases, oxidoreductases, and electron transfer proteins. Whole *E. coli* cells displaying enzymes have been utilized to efficiently synthesize industrially important rare organic compounds with specific chirality. Autodisplay of epitopes on the surfaces of attenuated *Salmonella* carriers has also provided a novel way to induce immune protection after oral vaccination. This review summarizes the structural and functional features of the autodisplay system, illustrating its discovery and most recent applications. Autodisplay facilitates the export of more than 100,000 recombinant molecules per single cell and permits the oligomerization of subunits on the cell surface as well as the incorporation of inorganic prosthetic groups after transport of apoproteins onto the bacterial surface without disturbing bacterial integrity or viability. We discuss future biotechnical and biomedical applications in the light of these achievements.*

Lipid Intermediates in the Biosynthesis of Bacterial Peptidoglycan. Jean van Heijenoort

620–635

*Summary: This review is an attempt to bring together and critically evaluate the now-abundant but dispersed data concerning the lipid intermediates of the biosynthesis of bacterial peptidoglycan. Lipid I, lipid II, and their modified forms play a key role not only as the specific link between the intracellular synthesis of the peptidoglycan monomer unit and the extracytoplasmic polymerization reactions but also in the attachment of proteins to the bacterial cell wall and in the mechanisms of action of antibiotics with which they form specific complexes. The survey deals first with their detection, purification, structure, and preparation by chemical and enzymatic methods. The recent important advances in the study of transferases *MraY* and *MurG*, responsible for the formation of lipids I and II, are reported. Various modifications undergone by lipids I and II are described, especially those occurring in gram-positive organisms. The following section concerns the cellular location of the lipid intermediates and the translocation of lipid II across the cytoplasmic membrane. The great efforts made since 2000 in the study of the glycosyltransferases catalyzing the glycan chain formation with lipid II or analogues are analyzed in detail. Finally, examples of antibiotics forming complexes with the lipid intermediates are presented.*

Manipulation of Rab GTPase Function by Intracellular Bacterial Pathogens. John H. Brumell and Marci A. Scidmore

636–652

Summary: Intracellular bacterial pathogens have evolved highly specialized mechanisms to enter and survive within their eukaryotic hosts. In order to do this, bacterial pathogens need to avoid host cell degradation and obtain nutrients and biosynthetic precursors, as well as evade detection by the host immune system. To create an intracellular niche that is favorable for replication, some intracellular pathogens inhibit the maturation of the phagosome or exit the endocytic pathway by modifying the identity of their phagosome through the exploitation of host cell trafficking pathways. In eukaryotic cells, organelle identity is determined, in part, by the composition of active Rab GTPases on the membranes of each organelle. This review describes our current understanding of how selected bacterial pathogens regulate host trafficking pathways

by the selective inclusion or retention of Rab GTPases on membranes of the vacuoles that they occupy in host cells during infection.

Interspecies Interactions within Oral Microbial Communities. Howard K. Kuramitsu, Xuesong He, Renate Lux, Maxwell H. Anderson, and Wenyuan Shi

653–670

Summary: While reductionism has greatly advanced microbiology in the past 400 years, assembly of smaller pieces just could not explain the whole! Modern microbiologists are learning “system thinking” and “holism.” Such an approach is changing our understanding of microbial physiology and our ability to diagnose/treat microbial infections. This review uses oral microbial communities as a focal point to describe this new trend. With the common name “dental plaque,” oral microbial communities are some of the most complex microbial floras in the human body, consisting of more than 700 different bacterial species. For a very long time, oral microbiologists endeavored to use reductionism to identify the key genes or key pathogens responsible for oral microbial pathogenesis. The limitations of reductionism forced scientists to begin adopting new strategies using emerging concepts such as interspecies interaction, microbial community, biofilms, polymicrobial disease, etc. These new research directions indicate that the whole is much more than the simple sum of its parts, since the interactions between different parts resulted in many new physiological functions which cannot be observed with individual components. This review describes some of these interesting interspecies-interaction scenarios.