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CONTENTS/SUMMARIES

- Role of Receptors in *Bacillus thuringiensis* Crystal Toxin Activity.** Craig R. Pigott and David J. Ellar. 255–281

Summary: Bacillus thuringiensis produces crystalline protein inclusions with insecticidal or nematocidal properties. These crystal (Cry) proteins determine a particular strain's toxicity profile. Transgenic crops expressing one or more recombinant Cry toxins have become agriculturally important. Individual Cry toxins are usually toxic to only a few species within an order, and receptors on midgut epithelial cells have been shown to be critical determinants of Cry specificity. The best characterized of these receptors have been identified for lepidopterans, and two major receptor classes have emerged: the aminopeptidase N (APN) receptors and the cadherin-like receptors. Currently, 38 different APNs have been reported for 12 different lepidopterans. Each APN belongs to one of five groups that have unique structural features and Cry-binding properties. While 17 different APNs have been reported to bind to Cry toxins, only 2 have been shown to mediate toxin susceptibility in vivo. In contrast, several cadherin-like proteins bind to Cry toxins and confer toxin susceptibility in vitro, and disruption of the cadherin gene has been associated with toxin resistance. Nonetheless, only a small subset of the lepidopteran-specific Cry toxins has been shown to interact with cadherin-like proteins. This review analyzes the interactions between Cry toxins and their receptors, focusing on the identification and validation of receptors, the molecular basis for receptor recognition, the role of the receptor in resistant insects, and proposed models to explain the sequence of events at the cell surface by which receptor binding leads to cell death.

- A Biochemical Guide to Yeast Adhesins: Glycoproteins for Social and Antisocial Occasions.** Anne M. Dranginis, Jason M. Rauceo, Juan E. Coronado, and Peter N. Lipke 282–294

*Summary: Fungi are nonmotile eukaryotes that rely on their adhesins for selective interaction with the environment and with other fungal cells. Glycosylphosphatidylinositol (GPI)-cross-linked adhesins have essential roles in mating, colony morphology, host-pathogen interactions, and biofilm formation. We review the structure and binding properties of cell wall-bound adhesins of ascomycetous yeasts and relate them to their effects on cellular interactions, with particular emphasis on the agglutinins and flocculins of *Saccharomyces* and the Als proteins of *Candida*. These glycoproteins share common structural motifs tailored to surface activity and biological function. After being secreted to the outer face of the plasma membrane, they are covalently anchored in the wall through modified GPI anchors, with their binding domains elevated beyond the wall surface on highly glycosylated extended stalks. N-terminal globular domains bind peptide or sugar ligands, with between millimolar and nanomolar affinities. These affinities and the high density of adhesins and ligands at the cell surface determine microscopic and macroscopic characteristics of cell-cell associations. Central domains often include Thr-*

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rich tandemly repeated sequences that are highly glycosylated. These domains potentiate cell-to-cell binding, but the molecular mechanism of such an association is not yet clear. These repeats also mediate recombination between repeats and between genes. The high levels of recombination and epigenetic regulation are sources of variation which enable the population to continually exploit new niches and resources.

Sponge-Associated Microorganisms: Evolution, Ecology, and Biotechnological Potential. Michael W. Taylor, Regina Radax, Doris Steger, and Michael Wagner 295–347

Summary: Marine sponges often contain diverse and abundant microbial communities, including bacteria, archaea, microalgae, and fungi. In some cases, these microbial associates comprise as much as 40% of the sponge volume and can contribute significantly to host metabolism (e.g., via photosynthesis or nitrogen fixation). We review in detail the diversity of microbes associated with sponges, including extensive 16S rRNA-based phylogenetic analyses which support the previously suggested existence of a sponge-specific microbiota. These analyses provide a suitable vantage point from which to consider the potential evolutionary and ecological ramifications of these widespread, sponge-specific microorganisms. Subsequently, we examine the ecology of sponge-microbe associations, including the establishment and maintenance of these sometimes intimate partnerships, the varied nature of the interactions (ranging from mutualism to host-pathogen relationships), and the broad-scale patterns of symbiont distribution. The ecological and evolutionary importance of sponge-microbe associations is mirrored by their enormous biotechnological potential: marine sponges are among the animal kingdom's most prolific producers of bioactive metabolites, and in at least some cases, the compounds are of microbial rather than sponge origin. We review the status of this important field, outlining the various approaches (e.g., cultivation, cell separation, and metagenomics) which have been employed to access the chemical wealth of sponge-microbe associations.

Environmental Sensing and Signal Transduction Pathways Regulating Morphopathogenic Determinants of *Candida albicans*. Subhrajit Biswas, Patrick Van Dijck, and Asis Datta 348–376

Summary: *Candida albicans* is an opportunistic fungal pathogen that is found in the normal gastrointestinal flora of most healthy humans. However, under certain environmental conditions, it can become a life-threatening pathogen. The shift from commensal organism to pathogen is often correlated with the capacity to undergo morphogenesis. Indeed, under certain conditions, including growth at ambient temperature, the presence of serum or N-acetylglucosamine, neutral pH, and nutrient starvation, *C. albicans* can undergo reversible transitions from the yeast form to the mycelial form. This morphological plasticity reflects the interplay of various signal transduction pathways, either stimulating or repressing hyphal formation. In this review, we provide an overview of the different sensing and signaling pathways involved in the morphogenesis and pathogenesis of *C. albicans*. Where appropriate, we compare the analogous pathways/genes in *Saccharomyces cerevisiae* in an attempt to highlight the evolution of the different components of the two organisms. The downstream components of these pathways, some of which may be interesting antifungal targets, are also discussed.

***Listeria monocytogenes* Surface Proteins: from Genome Predictions to Function.** H el ene Bierne and Pascale Cossart 377–397

Summary: The genome of the human food-borne pathogen *Listeria monocytogenes* is predicted to encode a high number of surface proteins. This abundance likely reflects the ability of this bacterium to survive in diverse environments, including soil, food, and the human host. This review focuses on the various mechanisms by which listerial proteins are attached at the bacterial surface and their many functions, including peptidoglycan metabolism, protein processing, adhesion to host cells, and invasion of host tissues. Extensive *in silico* analysis of the domains or motifs present in these mosaic proteins reveals that diverse structural features allow the surface proteome to interact with diverse bacterial or host components. This diversity offers new clues about the molecular bases of *Listeria* pathogenesis.

Viral Proteomics. Karen L. Maxwell and Lori Frappier 398–411

Summary: Viruses have long been studied not only for their pathology and associated disease but also as model systems for molecular processes and as tools for identifying important cellular regulatory proteins and pathways. Recent advances in mass spectrometry methods coupled with the development of proteomic approaches have greatly facilitated the detection of virion components, protein interactions in infected cells, and virally induced changes in the cellular proteome, resulting in a more comprehensive understanding of viral infection. In addition, a rapidly increasing number of high-resolution structures for viral proteins have provided valuable information on the mechanism of action of these proteins as well as aided in the design and understanding of specific inhibitors that could be used in antiviral therapies. In this paper, we discuss proteomic studies conducted on all eukaryotic viruses and bacteriophages, covering virion composition, viral protein structures, virus-virus and virus-host protein interactions, and changes in the cellular proteome upon viral infection.