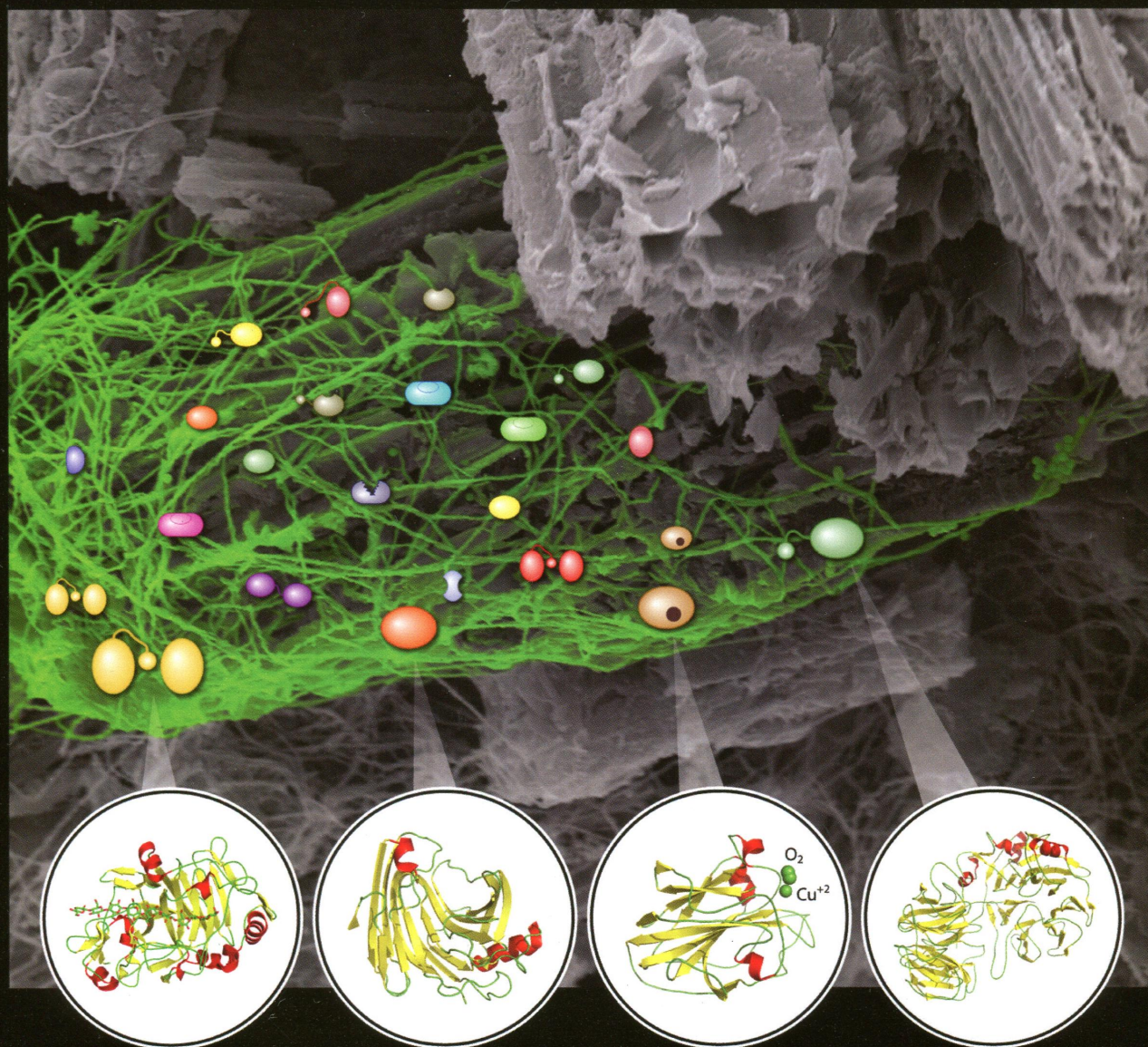


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REVIEWS

Evolutionary Ecology of the Marine *Roseobacter* Clade

573–587

Haiwei Luo, Mary Ann Moran

Summary: Members of the *Roseobacter* clade are equipped with a tremendous diversity of metabolic capabilities, which in part explains their success in so many different marine habitats. Ideas on how this diversity evolved and is maintained are reviewed, focusing on recent evolutionary studies exploring the timing and mechanisms of *Roseobacter* ecological diversification.

Genomics Review of Holocellulose Deconstruction by *Aspergilli*

588–613

Fernando Segato, André R. L. Damásio, Rosymar C. de Lucas, Fabio M. Squina, Rolf A. Prade

Summary: Biomass is constructed of dense recalcitrant polymeric materials: proteins, lignin, and holocellulose, a fraction constituting fibrous cellulose wrapped in hemicellulose-pectin. Bacteria and fungi are abundant in soil and forest floors, actively recycling biomass mainly by extracting sugars from holocellulose degradation. Here we review the genome-wide contents of seven *Aspergillus* species and unravel hundreds of gene models encoding holocellulose-degrading enzymes. Numerous apparent gene duplications followed functional evolution, grouping similar genes into smaller coherent functional families according to specialized structural features, domain organization, biochemical activity, and genus genome distribution. *Aspergilli* contain about 37 cellulase gene models, clustered in two mechanistic categories: 27 hydrolyze and 10 oxidize glycosidic bonds. Within the oxidative enzymes, we found two cellobiose dehydrogenases that produce oxygen radicals utilized by eight lytic polysaccharide monooxygenases that oxidize glycosidic linkages, breaking crystalline cellulose chains and making them accessible to hydrolytic enzymes. Among the hydrolases, six cellobiohydrolases with a tunnel-like structural fold embrace single crystalline cellulose chains and cooperate at nonreducing or reducing end termini, splitting off cellobiose. Five endoglucanases group into four structural families and interact randomly and internally with cellulose through an open cleft catalytic domain, and finally, seven extracellular β -glucosidases cleave cellobiose and related oligomers into glucose. *Aspergilli* contain, on average, 30 hemicellulase and 7 accessory gene models, distributed among 9 distinct functional categories: the backbone-attacking enzymes xylanase, mannosidase, arabinase, and xyloglucanase, the short-side-chain-removing enzymes xylan α -1,2-glucuronidase, arabinofuranosidase, and xylosidase, and the accessory enzymes acetyl xylan and feruloyl esterases.

Plant-Polysaccharide-Degrading Enzymes from Basidiomycetes

614–649

Johanna Rytioja, Kristiina Hildén, Jennifer Yuzon, Annele Hatakka, Ronald P. de Vries, Miia R. Mäkelä

Summary: Basidiomycete fungi subsist on various types of plant material in diverse environments, from living and dead trees and forest litter to crops and grasses and to decaying plant matter in soils. Due to the variation in their natural carbon sources, basidiomycetes have highly varied plant-polysaccharide-degrading capabilities. This topic is not as well studied for basidiomycetes as for ascomycete fungi, which are the main sources of knowledge on fungal plant polysaccharide degradation. Research on plant-biomass-decaying fungi has focused on isolating enzymes for current and future applications, such as for the production of fuels, the food industry, and waste treatment. More recently, genomic studies of basidiomycete fungi have provided a profound view of the plant-biomass-degrading potential of wood-rotting, litter-decomposing, plant-pathogenic, and ectomycorrhizal (ECM) basidiomycetes. This review summarizes the current knowledge on plant polysaccharide depolymerization by basidiomycete species from diverse habitats. In addition, these data are compared to those for the most broadly studied ascomycete genus, *Aspergillus*, to provide insight into specific features of basidiomycetes with respect to plant polysaccharide degradation.

Tuberculosis Vaccines and Prevention of Infection

650–671

Thomas R. Hawn, Tracey A. Day, Thomas J. Scriba, Mark Hatherill, Willem A. Hanekom, Thomas G. Evans, Gavin J. Churchyard, James G. Kublin, Linda-Gail Bekker, Steven G. Self

Summary: Tuberculosis (TB) is a leading cause of death worldwide despite the availability of effective chemotherapy for over 60 years. Although *Mycobacterium bovis* bacillus Calmette-Guérin (BCG) vaccination protects against active TB disease in some populations, its efficacy is suboptimal. Development of an effective TB vaccine is a top global priority that has been hampered by an incomplete understanding of protective immunity to TB. Thus far, preventing TB disease, rather than infection, has been the primary target for vaccine development. Several areas of research highlight the importance of including preinfection vaccines in the development pipeline. First, epidemiology and mathematical modeling studies indicate that a preinfection vaccine would have a high population-level impact for control of TB disease. Second, immunology studies support the rationale for targeting prevention of infection, with evidence that host responses may be more effective during acute infection than during chronic infection. Third, natural history studies indicate that resistance to TB infection occurs in a small percentage of the population. Fourth, case-control studies of BCG indicate that it may provide protection from infection. Fifth, prevention-of-infection trials would have smaller sample sizes and a shorter duration than disease prevention trials and would enable opportunities to search for correlates of immunity as well as serve as a criterion for selecting a vaccine product for testing in a larger TB disease prevention trial. Together, these points support expanding the focus of TB vaccine development efforts to include prevention of infection as a primary goal along with vaccines or other interventions that reduce the rate of transmission and reactivation.

Internal Sense of Direction: Sensing and Signaling from Cytoplasmic Chemoreceptors

672–684

Kieran D. Collins, Jesus Lacal, Karen M. Ottemann

Summary: Chemoreceptors sense environmental signals and drive chemotactic responses in *Bacteria* and *Archaea*. There are two main classes of chemoreceptors: integral inner membrane and soluble cytoplasmic proteins. The latter were identified more recently than integral membrane chemoreceptors and have been studied much less thoroughly. These cytoplasmic chemoreceptors are the subject of this review. Our analysis determined that 14% of bacterial and 43% of archaeal chemoreceptors are cytoplasmic, based on currently sequenced genomes. Cytoplasmic chemoreceptors appear to share the same key structural features as integral membrane chemoreceptors, including the formations of homodimers, trimers of dimers, and 12-nm hexagonal arrays within the cell. Cytoplasmic chemoreceptors exhibit varied subcellular locations, with some localizing to the poles and others appearing both cytoplasmic and polar. Some cytoplasmic chemoreceptors adopt more exotic locations, including the formations of exclusively internal clusters or moving dynamic clusters that coalesce at points of contact with other cells. Cytoplasmic chemoreceptors presumably sense signals within the cytoplasm and bear diverse signal input domains that are mostly N terminal to the domain that defines chemoreceptors, the so-called MA domain. Similar to the case for transmembrane receptors, our analysis suggests that the most common signal input domain is the PAS (Per-Arnt-Sim) domain, but a variety of other N-terminal domains exist. It is also common, however, for cytoplasmic chemoreceptors to have C-terminal domains that may function for signal input. The most common of these is the recently identified chemoreceptor zinc binding (CZB) domain, found in 8% of all cytoplasmic chemoreceptors. The widespread nature and diverse signal input domains suggest that these chemoreceptors can monitor a variety of cytoplasmically based signals, most of which remain to be determined.

Cover photograph (Copyright © 2014, American Society for Microbiology. All Rights Reserved): The scanning electron micrograph shows *Aspergillus nidulans* vegetative hyphae (highlighted green) growing on sorghum stover utilizing holocellulose as the primary carbon source. Graphic elements illustrate the vast number of enzymes designed for holocellulose digestion into sugars utilized to encourage vegetative growth. Structural models for cellulose glycoside hydrolase enzymes, cellobiohydrolase, endoglucanase, lytic polysaccharide monooxygenases, and xyloglucanobiohydrolase are shown in the forefront. Oklahoma State University graphic designer Mark Morgan created the cover graphic art image. (Scanning electron micrograph courtesy of S. Saykhedkar, A. Ray, and A. Mort.) (See related article on page 588.)