



Preface to Special Issue on *Sphingomonas*

The older readers amongst us may remember the mythical 'Schmoo' in the Li'l Abner comic strip. Schmoos were the perfect domesticated animals, pets and food sources. In this Special Issue we summarize the extraordinary metabolic capabilities of the sphingomonads, a group of Gram-negative bacteria that have been recognized as a discrete genus for only about 10 years. They might well be considered microbial Schmoos, in view of their capabilities to degrade a very wide variety of refractory environmental pollutants, and to carry out a variety of other biotechnologically useful activities, such as the biosynthesis of valuable biopolymers. Unfortunately, the sphingomonads are not perfect Schmoos, since members of the genus *Sphingomonas* have been found to be opportunistic pathogens, particularly by water-borne routes, to degrade copper pipes in water distribution systems, and to produce root infections in plants. On the other hand, some species can prevent phytopathogenic infections.

Sphingomonads are widely distributed in nature, and are found in various soils, in aqueous environments, and a number of species have been isolated from deep subsurface sediments. They are a phylogenetically tight group in the α -4 subclass of the Proteobacteria. They all contain a suite of 'signature' sphingolipid components. This signature is an 18 to 21-carbon straight-chain saturated, monounsaturated, and cyclopropane-containing dihydrosphingosine in a ceramide glycolipid containing uronic acid and amide-linked 2-hydroxy straight chain saturated fatty acids. This lipid totally replaces the lipopolysaccharide structure characteristic of conventional Gram-negative heterotrophic aerobes such as look-alike *Pseudomonas*, with which they were often confused until recently. In addition, sphingomonads contain an unusual benzoquinone with a side chain of 10 isoprenoid units (ubiquinone Q-10). Many are flagellated, and most contain a nostoxanthin carotenoid pigment. They do not contain detectable ester- or amide-linked 3-hydroxy fatty acids.

In this Special Issue, *Sphingomonas* chemotaxonomy is discussed by Busse *et al.*, their detection in the environment by Leung *et al.*, and in activated sludge by Neef and Kaemfer. Their distribution in marine environments is discussed by Caviccioli *et al.* The ecology, physiology and phylogeny of deep subsurface *Sphingomonas* isolates are discussed by Fredrickson *et al.* The biphenyl-degrading

organism first described in the early '70s and classified as a species of *Biejerinckia* is covered by Gibson, as are other aspects of polycyclic aromatic (PNA) compound metabolism. Kim and Zylstra present a functional analysis of the genes involved in aromatic hydrocarbon degradation by this organism, and Romine *et al.* discuss induction of aromatic catabolic activity in another *Sphingomonas* strain. Davison, Gillings *et al.* describe a red metabolite produced during biphenyl degradation. Various aspects of pentachlorophenol degradation and the organisms involved are discussed by Crawford and Ederer and by Colores and Schmidt. The degradation of diclofop herbicides is covered by Adkins *et al.*; phenoxyalkanoic acid herbicides by Kohler; chloro- and nitrophenols by Cassidy *et al.*; azo dyes by Coughlin *et al.*; 4-chlorobenzoic acid by Davison, Jardine and Karuso; chlorinated dibenzofurans by Wittich *et al.* and Keim *et al.*; lignins by Masai *et al.*; abietane triterpenoids by Mohn; hexachlorocyclohexane by Nagata *et al.*; naphthlene sulfonic acids by Stolz; and xenobiotic polymers by Kawai.

Kawahara presents the structure of the sphingolipids of sphingomonads, and their interactions with proteins are discussed by Wiese. The *Sphingomonas* cell envelope and transport are discussed by Momma *et al.* Dimorphism as related to biopolymer production is reviewed by Pollock and Armentrout, and *Sphingomonas* biopolymer rheology and uses are discussed by Shah and Ashtaputre.

The cardinal feature that defines the genus is the substitution of the uronic acid-containing ceramides in the outer cell membrane for the lipopolysaccharides (LPS) of the classical Gram-negative bacteria. Was this chemistry selected to make their association with plants more effective? Did they borrow genes from eukaryotes to form this eukaryote-like acidic carbohydrate surface as a part of their outer membrane rather than having an exopolysaccharide slime like the pseudomonads? And what other striking biodegradative capabilities await discovery? May the *Sphingomonas* Schmoos continue to amaze us!

The editors extend warm thanks to the reviewers for this issue, many of whom reviewed several manuscripts, for their excellent and thoughtful reviews.

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