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GENETIC ANALYSIS OF POLYCYCLIC AROMATIC HYDROCARBON DEGRADATION

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Naphthalene (two rings), phenanthrene (three rings), and pyrene (four rings) have been used as model compounds to analyze the microbial metabolism of polycyclic aromatic hydrocarbons at the biochemical and molecular level. The *nah* genes for the initial steps in the degradation of naphthalene and related compounds have been cloned and sequenced from many different *Pseudomonas* strains. The sequenced regions share more than 90% identity to the analogous sequences from the well-studied *P. putida* NCIB 9816. However, the presence of a single, highly homologous group of genes for the degradation of simple polycyclic aromatic hydrocarbons does not reflect the true metabolic diversity and evolutionary potential of microorganisms. We have been analyzing genes for polycyclic aromatic hydrocarbon degradation that show extensive divergence from those isolated from the *Pseudomonas* strains. For instance, *Comamonas testosteroni* GZ39 contains genes for naphthalene and phenanthrene degradation that are very different from those found in *Pseudomonas* species not only in their gene sequence but in their organization. *C. testosteroni* GZ42 contains genes for naphthalene and phenanthrene degradation that are related to those found in *Pseudomonas* species but metabolize the polycyclic compounds via a different downstream pathway. *Sphingomonas yanoikuyae* B1 is able to degrade toluene, *m*-xylene, *p*-xylene, biphenyl, naphthalene, and phenanthrene. The nucleotide sequence of a 40 kilobase pair region that codes for the degradation of aromatic compounds shows that at least six operons are involved and that the genes for the metabolism of both monocyclic and polycyclic compounds are intertwined. The genes for dioxygenase enzymes involved in pyrene degradation have also been cloned and sequenced from *Mycobacterium* sp. strain PYO1 and potentially represent a new class of dioxygenase enzymes.