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Microbial comparative genomics provides insights into gene function, bacterial speciation and evolutionary relationships. In the August 14 [Proceedings of the National Academy of Sciences](#), Murray *et al.* describe an approach to explore genome diversity and relatedness in the absence of complete sequence information (*Proc Natl Acad Sci USA* 2001, **98**:9853-9858). They used sequence information from the *Shewanella oneidensis* strain MR-1 to construct DNA microarrays containing over 100 full-length open reading frames (ORFs). They then hybridized the arrays with genomic DNA from nine other *Shewanella* species to investigate differences. They observed a good correlation between hybridization values and the percentage sequence similarity for known genes. Hierarchical [clustering](#) revealed the relationships between bacterial profiles and indicated the phylogenetic distances. Most genes in [operons](#) had higher levels of relatedness, suggesting that such an approach could identify horizontally acquired genes. Microbial genomic hybridizations should provide insights into bacterial diversity and speciation, leading to a better understanding of the basis for genotypic and phenotypic differences.

References

1. *Proceedings of the National Academy of Sciences*, [<http://www.pnas.org>]
2. Cluster analysis and display of genome-wide expression patterns
3. Selfish operons: horizontal transfer may drive the evolution of gene clusters.