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Sommario/riassunto	Many biodegradation pathways, both aerobic and anaerobic, have already been characterised, and the phylogenetic relationships among catabolic genes within them have been studied. However, new biodegradation activities and their coding genes are continuously being reported, including those involved in the catabolism of emerging contaminants and those generally regarded as non-biodegradable. Gene regulation is also an important issue for the efficient biodegradation of contaminants. Specific induction by the substrate and over-imposed global regulatory networks adjust the expression of the biodegradation genes to meet bacterial physiological needs. New biodegradation pathways can be assembled in a particular strain or in a bacterial consortium by recruiting biodegradation genes from different origins through horizontal gene transfer. The abundance and diversity of biodegradation genes, analysed by either genomic or metagenomic approaches, constitute valuable indicators of the biodegradation potential of a particular environmental niche. This knowledge paves the way to systems metabolic engineering approaches to valorise biowaste for the production of value-added products.