

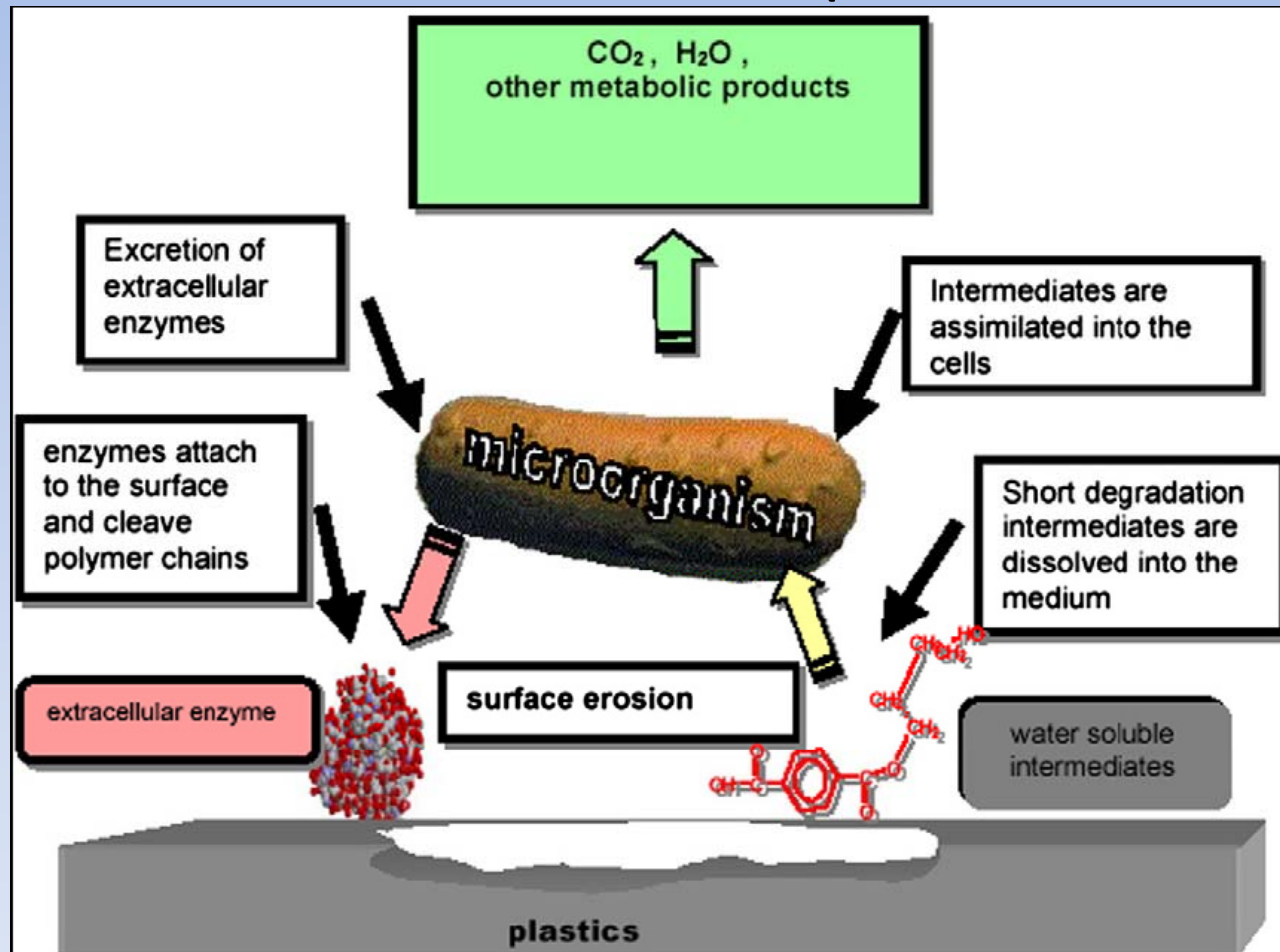
# Biological degradation of plastics

——周 颢 陆涵予  
豆佳宜 王优良

# Subject:

对多种芳香族聚合物（聚苯乙烯，聚苯基酰胺类）实现生物降解的“超级E.coli”

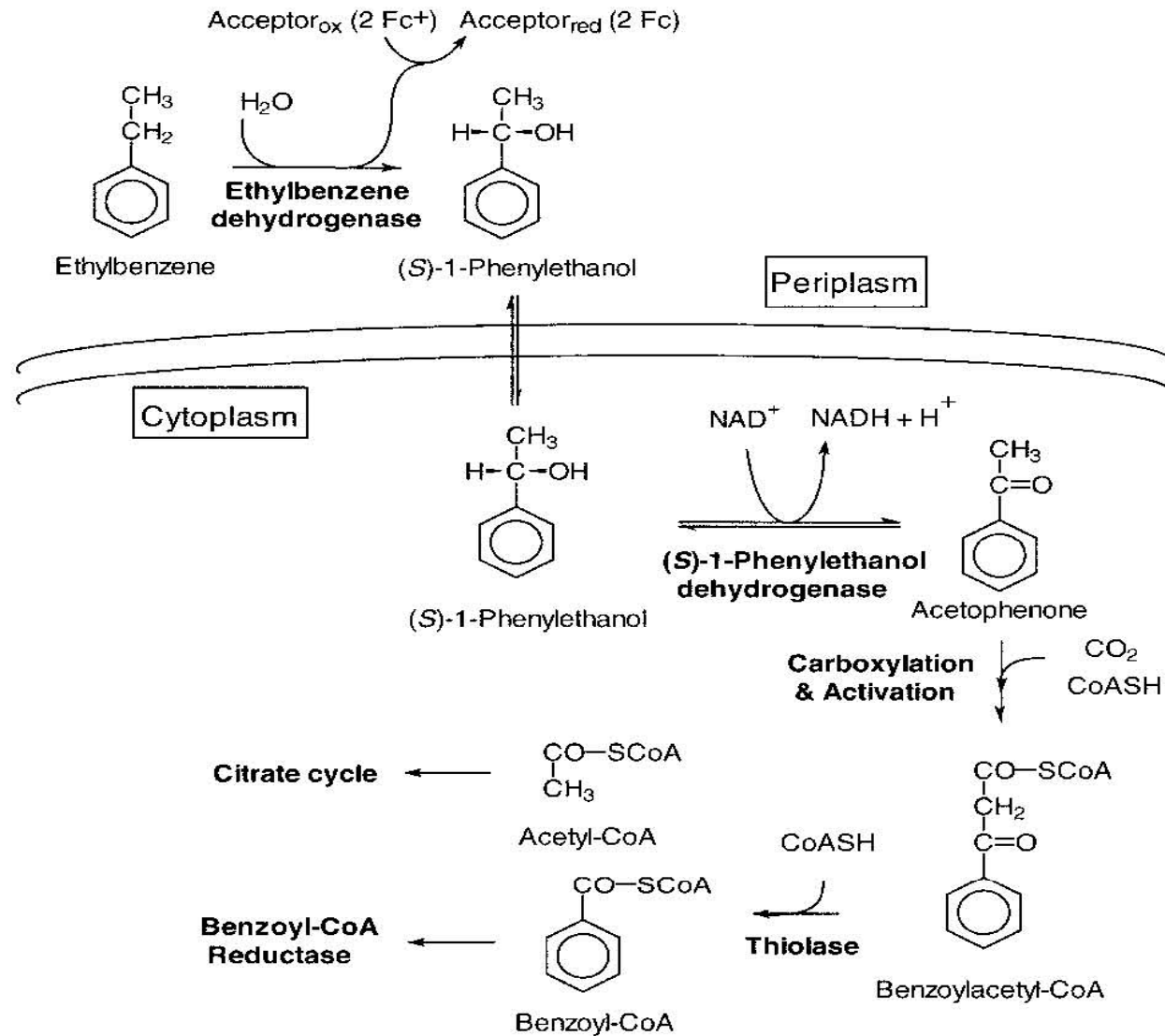
# General mechanism of plastic biodegradation under aerobic conditions (Mueller, 2003).



plastic → PS , PETE etc.

- BTEX is a known carcinogen and poses a risk to human health and other kinds of life
- it can nonspecifically break cell membrane integrity, increase permeability and lead to lysis
- 表面富集

# Biological battery



# Resource of gene sequence

- soil degraders:

Pseudomonas(Arengi et al. 2001), Rhodococcus (Kim et al. 2002;Taki et al. 2007), Marinobacter (from a brine soil, Nicholson and Fathepure 2004), Acinetobacter (Wang and Shao 2006), Alcaligenes, Brevibacterium, Nocardia, Bacillus, Bordetella, Arthrobacter, Bradyrhizobium, Acidovorax, Agrobacterium, Aquaspirillum, Variovorax and Stenotrophomonas (Hendrickx et al. 2006a, b).

- From sewage and fresh water  
Ralstonia(Kahng et al. 2000), Microbacterium (Cavalca et al. 2004), Mycobacterium (Cavalca et al. 2004), Azoarcus (Cavalca et al. 2004; Mohamed et al. 2001), Thauera (Yoshifumi et al.2004), Burkholderia (Johnson and Olsen 1997) and Sphingomonas (Fredrickson et al. 1995).
- in underground water and under anaerobic conditions  
(Chakraborty and Coates 2004; Hendrickx et al. 2005; Jahn et al. 2005; Botton and Parsons 2006)
- marine BTEX degradation  
Cycloclasticus (Wang et al. 1996) and Alcanivorax (Dutta and Harayama 2001)

# Example:

(Isolation, gene detection and solvent tolerance of benzene, toluene and xylene degrading bacteria from nearshore surface water and Pacific Ocean sediment. *Extremophiles* (2008) 12:335–342)

- The accession numbers of the isolates 16S rRNA gene from deep sea on GenBank are from DQ451096 to DQ451100; those from nearshore water are from EF683118 to EF683123. The toluene dioxygenase gene sequence from isolate LE9 and LUN2 were deposited as EF683124 and EF683125, respectively; those from isolate LB1, LJ2 LJ8, LE2, LE9 and LUN2 were assigned with accession No. as from EF683126 to EF683131.



**Table 1** BTX degrading bacteria isolated from nearshore water and deep-sea sediment

Isolates (MCCC No.)	Solvent <sup>a</sup>	Closest strain from NCBI	Identity by 16S rDNA (%)	Accession No. in GenBank
LB1 (1A00328)	Benzene	<i>Bacillus subtilis</i> strain MO5 (AY553098)	99	EF683118
LE2 (1A00331)	Xylene	<i>Rhodococcus rhodochrous</i> strain DSM43274T (X80624)	99	EF683121
LE9 (1A00290)	Xylene	<i>Pseudomonas stutzeri</i> 11C2 (AJ270452)	99	EF683122
LJ2 (1A03188)	Toluene	<i>Rhodococcus pyridinivorans</i> strain R04 (AF459741)	99	EF683119
LJ8 (1A00330)	Toluene	<i>Exiguobacterium gaibuli</i> strain TF-16(AY594264)	99	EF683120
LUN2 (1A00332)	Xylene	<i>Pseudomonas putida</i> (AF291048)	99	EF683123
JB5 (1A03189)	Toluene	<i>Bacillus mojavensis</i> (AB021191)	99	DQ451099
JB7 (1A00327)	Toluene	<i>Bacillus mojavensis</i> (AB021191)	99	DQ451100
EJB1 (1A03190)	Xylene	<i>Bacillus fusiformis</i> SW-89 (AY907676)	99	DQ451096
EJB5 (1A00324)	Xylene	<i>Bacillus fusiformis</i> SW-89 (AY907676)	99	DQ451097
EJB8 (1A03187)	Xylene	<i>Bacillus cereus</i> LRN (AY138275)	99	DQ451098

<sup>a</sup> The carbon source used in enrichment of BTX degrading bacterium

# System needed:

- 自身代谢（对BETX的耐受性）
- 识别与通路控制
- 休眠与激活
- 表面富集（苯环上的反应）
- extracellular depolymerases的分泌or膜表面  
面粘附

At least two categories of enzymes are actively involved in biological degradation of polymers: extracellular and intracellular depolymerases (Doi, 1990; Gu et al., 2000b)

# Analytical and computational techniques

- Masaji Watanabe, Analytical and computational techniques for exogenous depolymerization of xenobiotic polymers, *Mathematical Biosciences* 192 (2004) 19–37

$$\frac{dx}{dt} = -\alpha(M)x + \beta(M + L) \frac{M}{M + L} y.$$

# Standard testing methods

- Visual observations
- Weight loss measurements
- Changes in mechanical properties and molar mass
- CO<sub>2</sub> evolution/O<sub>2</sub> consumption (Hoffmann et al., 1997)
- Radiolabeling
- Clear-zone formation

# Puzzles:

- 通路控制系统normal?
- 表面富集?
- Effective biobrick?
- The length of the gene is quite long
  - all imported into a single cell?

**Thank you !**