

Biobased *de novo* synthesis, upcycling, and recycling – the heartbeat toward a green and sustainable polyethylene terephthalate industry[☆]

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Polyethylene terephthalate (PET) has revolutionized the industrial sector because of its versatility, with its predominant uses in the textiles and packaging materials industries. Despite the various advantages of this polymer, its synthesis is, unfavorably, tightly intertwined with nonrenewable fossil resources. Additionally, given its widespread use, accumulating PET waste poses a significant environmental challenge. As a result, current research in the areas of biological recycling, upcycling, and *de novo* synthesis is intensifying. Biological recycling involves the use of micro-organisms or enzymes to breakdown PET into monomers, offering a sustainable alternative to traditional recycling. Upcycling transforms PET waste into value-added products, expanding its potential application range and promoting a circular economy. Moreover, studies of cascading biological and chemical processes driven by microbial cell factories have explored generating PET using renewable, biobased feedstocks such as lignin. These avenues of research promise to mitigate the environmental footprint of PET, underlining the importance of sustainable innovations in the industry.

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Introduction

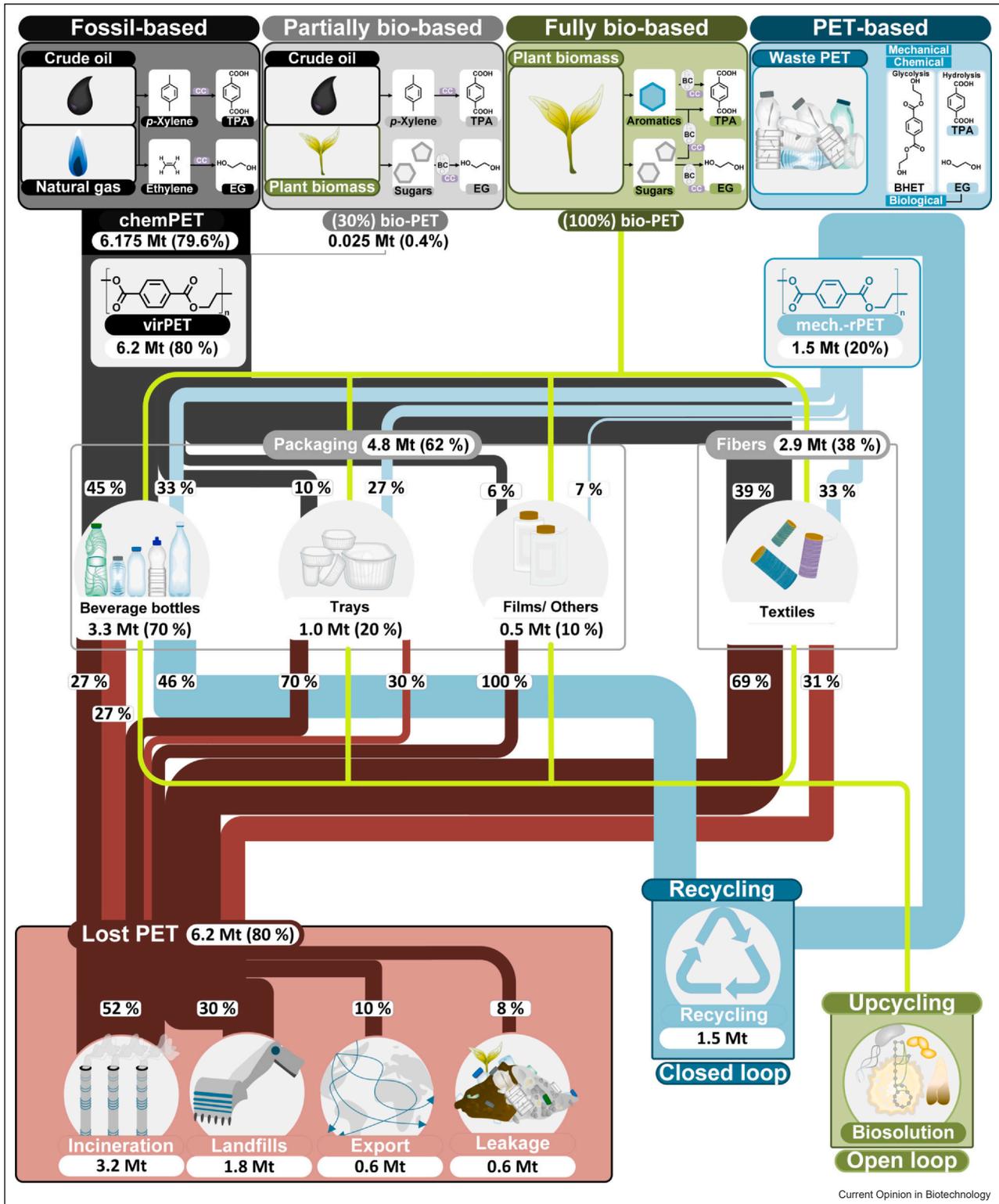
The synthetic polymer polyethylene terephthalate (PET) has a variety of uses in fibers, coatings, and packaging materials and thus plays a major role in our daily lives [1] (Figure 1). Considering its several advantageous properties [2], it is no surprise that the market volume for PET has burgeoned over the years, whereby current global production hovers near approximately 50 million metric tons annually [3].

The process of generating PET begins with two primary raw materials, purified (dimethyl)terephthalic acid (TPA) and ethylene glycol (EG), both of which are derived mainly via petrochemical routes (Figure 1) and undergo polycondensation [4,5]. TPA production starts with petroleum-derived *p*-xylene, which, in the most commonly used American Oil Company (AMOCO) process, undergoes liquid-phase oxidation with molecular oxygen as the oxidant, acetic acid as the solvent, and a catalytic system consisting of cobalt, manganese, and bromide ions [4,5]. EG is primarily obtained from ethylene via catalytic oxidation into ethylene oxide and subsequent hydrolysis [4]. Notably, conventional ethylene synthesis by steam cracking naphtha is not only energy intensive but also strongly contributes to global carbon emissions [6], ultimately influencing the environmental footprint of PET production.

However, both petrochemical-based PET-monomer synthesis [5,6] and the fate of postconsumer plastics (Figure 1) are reasons for the manifold environmental concerns [7,8]. An especially unfortunate side effect of the ubiquity of PET is its release into the environment, and the pervasive nature of certain plastics is known to be an urgent, enduring threat to terrestrial and marine ecosystems, as well as human society [8,9]. Additionally, even though the basic framework is ideal from a chemical viewpoint, recycled PET is often considered disadvantageous in terms of production costs, product quality, and energy consumption, limiting its re-entry into a new life cycle [1,2,7,10]. Thus, even in Europe,

[☆] Dedicated to Judith Becker (* 2.2. 1981, † 27.4.2021), a gifted metabolic engineer of sustainable cell factories and our cherished colleague and friend at the Institute of Systems Biotechnology of Saarland University.

Figure 1



Sourcing, application, and fate of European PET in numbers. The depicted data are taken from Ref. [11]. Monomers for PET synthesis can be derived from different sources, whereby the most common routes for TPA and EG production rely on fossil resources [4,84]. Synthetic routes for the green production of PET precursors largely rely on separated or integrated chemical catalysis (CC) and biocatalysis (BC) [84]. The available bio-PET contains 30% biomass (EG fraction) [4], whereby its given fraction of the available virgin PET takes into account the fact that 26.5% of bioplastics are produced in Europe and that the share of PET from the total global production of 2.22 million tons of plastics is 4.2% [85]. To date, the major fraction of PET has been lost (red), with light red bars indicating the percentage of PET that enters a sortation process but is not part of a further life cycle [11]. Regarding PET recycling (blue), novel developments [7] target an enhanced life cycle from waste PET to recycled PET with virgin-like characteristics (closed loop) [14]. Recent scientific advances in biobased solutions (green) for PET production and the upcycling of PET into various novel products (open loop [14]) could contribute to a sustainable PET industry.

which is generally known for high collection rates [2], the actual PET recycling rate is quite low, as only one-fifth of the available material enters a new life cycle, whereas the rest is ultimately lost without further usage [11] (Figure 1).

In terms of the increase in eco-consciousness worldwide, the magnitude of the PET waste problem underscores the urgent need for sustainable consumption practices, improved recycling technologies, and policies that promote a circular economy for plastics [1,12–15]. In this review, we highlight recent studies demonstrating how biotechnologically engineered cell factories can contribute not only to reviving postconsumer PET waste streams but also to the *de novo* synthesis of PET from green, alternative feedstocks. Based on these impressive achievements, green routes have the potential to drive the entire PET industry for the first time, but further advancements in the future are still needed.

Concepts and strategies for creating a biobased circular polyethylene terephthalate industry

The biobased valorization of postconsumer PET has a comparable start to that of other biotechnological feedstocks [16,17], with depolymerization [10] (Figure 2). Most of the available depolymerization methods are under constant development and result in specific product spectra [7]. Current studies rely either on separate chemical [18] or biobased [19] strategies or a combinatorial (tandem) approach [20] to transform PET polymers into suitable substrates for micro-organisms. However, micro-organisms have not had enough time to adapt to the environmental presence of man-made PET [19], and identifying microorganisms suitable as hosts or gene donors is essential for biobased PET valorization [21,22]. Therefore, the efficient coupling of (1) PET degradation strategies, (2) TPA and EG assimilation, and (3) production often requires other key biotechnological technologies, for example, adaptive laboratory evolution, in addition to genetic engineering [23] (Figure 2). Initiated by pioneering works [21], contemporary contributions (Table 1) have also demonstrated the potential of metabolically engineered cell factories for the open loop recycling or even upcycling of PET (monomers), hence allowing its conversion into new (and often value-added) products [14] (Figure 1). Similarly,

the metabolic layout of genetically engineered microbes may also be used for the production of PET precursors from alternative, renewable feedstocks, for example, lignin-based aromatics [24] and (hemi)cellulose-based sugars [25–27], which are chemically converted into biobased PET, thereby closing the circle (Figure 2).

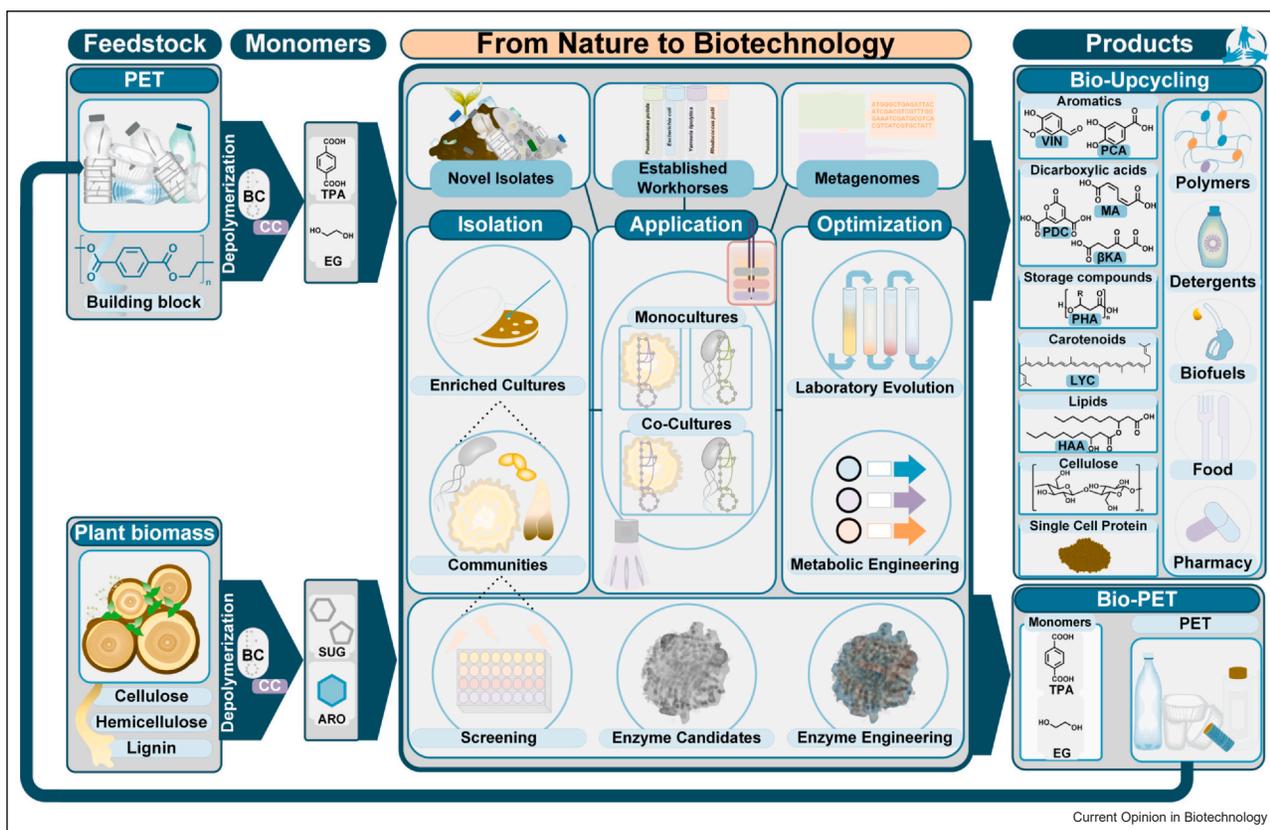
Microbes and hosts relevant to polyethylene terephthalate recycling and upcycling

PET was long considered nonbiodegradable [7]. However, since the initial discovery of PET depolymerization via the hydrolase TfH from the actinomycete *Thermobifida fusca* in 2005 [28], several enzymes with PET-degrading capabilities have been identified (Table 2) [29–31]. Additionally, the isolation of *Ideonella sakaiensis* 201-F6 from a PET-degrading microbial consortium capable of using PET as a major carbon and energy source [22] made the public aware of the potential for biobased PET degradation. Nevertheless, PET hydrolases are still rare, and identifying them requires extensive screening efforts [32] (Figure 2). Thus, more than 50% of the reported PET degraders have emerged from bacteria, particularly *Bacillus* sp., followed by fungi, including *Aspergillus* sp. [33]. Notably, the search for host strains benefits from the microbial variety in soils [33], whereby widespread PET pollution spurs mining efforts at contaminated sites on land [21] or in aquatic habitats [34].

Despite this clear variety, not all PET degraders are necessarily equally suitable for biobased PET recycling due to slow growth, for example, fungi [33], or the necessity to develop genetic engineering tools to unlock their potential [35]. Thus, so-far natural PET degraders are primarily used as donors for relevant enzymes, which are subsequently introduced into proven hosts, for example, *Escherichia coli* [36] and *Yarrowia lipolytica* [37]. In an attempt to bioremediate polluted seawater, key enzymes have also been introduced into marine micro-alga [38].

Remarkably, several bacteria associated with lignin valorization [16] also possess interesting properties as hosts for PET valorization. Known to withstand demanding and toxic conditions [10,39,40], *Pseudomonas putida* plays a vital role in the emerging field of PET valorization [20,41–43] (Table 1), and *Comamonas testosteroni* holds

Figure 2



The potential of using micro-organisms in a biobased PET industry. The use of PET as a feedstock for biotechnology requires its depolymerization via chemical catalysis (CC) and/or biocatalysis (BC) to afford the monomers TPA and EG [7]. For example, novel strains were isolated from PET-contaminated sites [21,22], and combined with established workhorses [20] and information gained from metagenomes [51], these strains serve as valuable sources for identifying the metabolic pathways and enzymes necessary for PET (monomer) metabolism. Hereby, key biotechnological methods, including adaptive laboratory evolution [23] and metabolic engineering [41], enable enhanced strain performance. Additionally, mining for novel enzymes has benefited from advanced screening strategies [55,103] complemented by biosensors [65] and improved enzyme candidates via protein engineering [49,59]. Monocultures [19] or cocultures [47,72,98] of streamlined cell factories may then be used for the upcycling of PET into various products [18–21,43,72,79–82,101]. Likewise, sugars [25–27] and aromatics [24] from plant biomass serve as substrates for the production of TPA and EG by metabolically engineered microbes, allowing the production of fully biobased PET. Abbreviations: ARO, aromatic compounds; EG, ethylene glycol; HAA, hydroxyalkanoxy-alkanoate; β KA, β -ketoadipic acid; LYC, lycopene; MA, *cis*, *cis*-muconic acid; PCA, protocatechuic acid; PDC, 2-pyrone-4,6-dicarboxylic acid; PHA, polyhydroxyalkanoates; SUG, sugar; VIN, vanillin.

the combined potential for the valorization of lignin- and PET-based aromatic monomers [44].

In addition to single-host strains (Table 1), PET valorization might also benefit from the employment of natural [45] and artificial [46,47] consortia, aiming at synergistic and co-operative PET degradation (Figure 2). This setup matches well with current research focusing on understanding the man-made plastisphere, which refers to the natural microbial communities that colonize plastic waste in terrestrial and aquatic ecosystems [48].

Novel enzymes for polyethylene terephthalate recycling

Compared with other plastics, the presence of ester bonds in PET facilitates the attack and subsequent degradation of PET by microbial enzymes, which have

great potential for use in environmental-benign PET recycling [1]. In addition to closed-loop recycling processes [49–51], these enzymes also play vital roles as starting points for microbial upcycling strategies [19,52] (Figure 1). Enzymes with the ability to modify or degrade PET include PETases (EC 3.1.1.101), cutinases (EC 3.1.1.74), lipases (EC 3.1.1.3), and carboxylesterases (EC 3.1.1.1), all of which share the common ability to hydrolyze carboxylic esters (EC 3.1.1) resulting in products with hydroxyl and carboxylic acid residues [7,29]. Additionally, MHETase (EC 3.1.1.102) [22] and the recently reported BHETase (EC number not yet assigned) [53] further breakdown the intermediate products mono-(2-hydroxyethyl) terephthalate (MHET) and bis-(2-hydroxyethyl)-terephthalate (BHET) into TPA and EG, altogether providing the optimal setup for further downstream microbial catabolism (Figure 3).

Table 1

Microbial upcycling of PET and PET-derived monomers. The following examples are categorized based on the strategy used for PET depolymerization, including chemical degradation (○), enzymatic hydrolysis by purified enzymes (●), or hydrolysis by enzymes produced by a cell factory (⊙). The strains were classified based on their natural genes for TPA (●) and EG (⊙) metabolism, as well as the application of metabolic engineering strategies for substrate assimilation or product formation (⊙).

Product	Strain designation	Substrate	Relevant carbon source for biosynthesis	Titer (g l ⁻¹)	Conversion	Method/scale	Reference
<i>Pseudomonas umsongensis</i> GO16	Wild type	PET ○	TPA	0.25 ^a	27% CDW	Batch, shake flask	[21]
PHA	Wild type	PET ○	TPA	2.61	30% CDW	Fed-batch, reactor	[97]
PHA	KS3	PET ● ^b	TPA_EG	0.15	7% CDW	Batch, reactor	[19]
HAA	KS3 pSB01	PET ● ^b	TPA	0.04	-	Batch, shake flasks	[19]
<i>Pseudomonas putida</i> GO19	Wild type	PET ○	TPA	0.25 ^a	23% CDW	Batch, shake flask	[21]
<i>Pseudomonas frederiksbergensis</i> GO23	Wild type	PET ○	TPA	0.26 ^a	24% CDW	Batch, shake flask	[21]
<i>Yarrowia lipolytica</i> and <i>Pseudomonas stutzeri</i>							
PHA	Po1fP _{Ylipo}	BHET ●	TPA	0.13 ^a	3.66% CDW	Batch, shake flask	[98]
PHA	TPA3P _{Pstutz}	TPA	TPA	-	11.56% CDW	Batch, shake flask	[98]
<i>Yarrowia lipolytica</i> IMUFRJ 50682	Wild type	EG	EG	32.67	74% mol mol ⁻¹	Batch, reactor	[83]
GLA	Wild type	EG	EG	0.22	45% mol mol ⁻¹ BHET ⁻¹	Fed-batch, shake flask	[20]
<i>Pseudomonas putida</i> KT2440	AW165	PET ○ ^b	BHET	15.1	76% mol mol ⁻¹ BHET ⁻¹	Fed-batch, reactor	[20]
β-KA	AW165	PET ● ^b	TPA_EG	5.61	100% mol mol ⁻¹ TPA ⁻¹	Fed-batch, shake flask	[43]
MA	tacRDL	PET ● ^b	TPA	-	32.2% CDW	Batch, shake flask	[75]
PHA	MFL185	EG	EG	4.73	-	Batch, shake flask	[47]
<i>Pseudomonas putida</i> EM42	Pp-T	PET ○	TPA	0.64	-	Fed-batch, shake flask	[47]
MA	Pp-E	PET ○	EG	0.75	48% CDW	Batch, Petri dish	[52]
PHA	Pp-T	PET ○	TPA	0.001	-	Fed-batch, shake flask	[80]
Pp-E	Pp-E	PET ○	EG	0.12	79% mol mol ⁻¹	Batch, shake flask	[81]
<i>Ideonella sakaiensis</i> 201-F6	Wild type	PET ●	TPA_EG	0.010	-	Batch, shake flask	[81]
PHA	Wild type	PET ○	TPA	0.43	81.4% mol mol ⁻¹	Batch, shake flask	[72]
<i>Rhodococcus jostii</i> PET	S6	PET ○	TPA_EG	0.46	92.5% mol mol ⁻¹	Batch, shake flask	[72]
Lycopene	S6	PET ○	TPA_EG	0.08	-	Batch, shake flask	[72]
<i>Escherichia coli</i>							
Vanillin	RARE_pVanX	TPA	TPA	0.38	85.4% mol mol ⁻¹	Batch, shake flask	[72]
Vanillin	RARE_pVanX	PET ●	TPA	0.24	41.6% mol mol ⁻¹	Batch, shake flask	[72]
PCA	PCA-1	PET ○	TPA	0.57	99% mol mol ⁻¹	Batch, shake flask	[18]
GAL	PCA-1	PET ○	TPA	-	-	-	-
PYG	HBH-2	PET ○	TPA	-	-	-	-
MA	CTL-1	PET ○	TPA	-	-	-	-
VNA	CH-1	PET ○	TPA	-	-	-	-
PDC	MA-1	PET ○	TPA	-	-	-	-
	PCA-1	PET ○	TPA	-	-	-	-
	OMT-2 ^{His}	PET ○	TPA	-	-	-	-

Table 1 (continued)

Product	Strain designation	Substrate	Relevant carbon source for biosynthesis	Titer (g l ⁻¹)	Conversion	Method/scale	Reference
CAT	PCA		●				
	PDC _{PCA}	PET ●	●	0.66	99.5% mol mol ⁻¹	Batch, shake flask	[99]
	pKE112TpnBaroY + pKM212TphAabc	PET ●	●				
Metal-organic frameworks	BL21 (DE3) pET21b-thermoPETase	PET ●	●	-	-	-	[100]
	Wild type	PET ○	●	0.80	98.6% mol mol ⁻¹	Batch, conical tubes	[72]
Gluconobacter oxydans	Wild type	PET ○	●	2.42	-	Batch, shake flask	[101]
	Taonella meyersensis WT-6	PET ○	●				
Bacterial cellulose	Wild type	PET ○	●				

GAL, gallic acid; GLA, glycolic acid; HAA, hydroxyalkanoxyloxy-alkanoates; MA, *cis, cis*-muconic acid; PCA, protocatechuic acid; PDC, 2-pyrone-4,6-dicarboxylic acid; PYG, pyrogallol; VNA, vanillic acid.

^a Estimated from the reference.

^b Improved by adaptive laboratory evolution or deregulating gene expression.

Among many other promising PETases, such as *Is*PETase from *I. sakaiensis* [22], the leaf-branch compost cutinase (LCC) [50] and the metagenomic polyester hydrolase PHL7 [51] are currently undergoing extensive optimization efforts (Table 2). Therefore, rational and structure-guided protein engineering targets, *inter alia*, at an enhanced thermostability over a broad temperature range and increased enzymatic activity [49,54–57]. Another interesting aspect is the broadening of the substrate spectrum of PETases to other polyesters [58]. Overall, protein crystal structures and bioinformatic tools have played pivotal roles in identifying specific amino acid chain mutations that can be used to modulate the desired enzyme features (Table 2). For example, the French company Carbios successfully developed the more efficient variant LCC^{ICCG} from the previously identified LCC cutinase [59]. They patented and industrialized the process under the term C-ZYME, claiming a 30% reduction in CO₂ emissions compared with conventional routes of PET waste management, for example, incineration [60] (Figure 1).

Additionally, other state-of-the-art strategies to enhance enzymatic PET depolymerization include (1) chimeric proteins of PETase and MHETase [61], (2) dual enzyme systems [62], and (3) the surface display of enzymes on microbial surfaces aided by a codisplay of hydrophobin, an adhesion protein facilitating adsorption to hydrophobic surfaces such as PET films [63] or by the addition of rhamnolipids [36]. The current successful application of bioinformatic tools and machine learning [49,57,64] complemented by biosensors [65] has already paved the way for overall accelerated enzyme discovery and improvement, thus facilitating the selection of suitable enzyme candidates via enzyme mining (Figure 2).

Metabolic pathways for the degradation of polyethylene terephthalate-based monomers

Notably, it has been known for several decades that different micro-organisms can metabolize the PET monomers TPA and EG; readers interested in these micro-organisms are referred to [15,66] for a more detailed overview of the underlying pathways, which in total provides a powerful basis for metabolic engineering (Figure 2). The aerobic TPA degradation pathway has been identified in different *Proteobacteria* [67–69] and the *Rhodococcus* genus [70,71] and generally follows the same pattern (Figure 3). Despite many similarities, including the genetic organization of the *tph* operon [15], the different cofactor preferences indicate the potential of certain adjustments for metabolic engineering [72]. Additionally, the downstream pathways involved in the degradation of protocatechuate, a key intermediate in aromatic degradation pathways, are quite diverse among host strains (Figure 3) [16], suggesting that the metabolic engineering of TPA

Table 2

Blockbuster enzymes for biological PET depolymerization.

Source	Name	Engineered variant	Substrate	Comment	Reference (s)
<i>Ideonella sakaiensis</i> 210 F6	IsPETase	IsPETase ^{S238F/W159H}	PET		[22,102]
			PET	Evolved from IsPETase	[58]
		ThermoPETase/IsPETase ^{TM/S121E/D186H/R280A}	PET	Evolved from IsPETase	[54]
		IsPETase ^{S121E/D186H/S242T/N246D}	PET	Evolved from IsPETase	[56]
		FAST-PETase	PET	Evolved from IsPETase	[49]
		HotPETase	PET	Evolved from IsPETase	[55]
		DuraPETase	PET	Evolved from IsPETase	[57]
		TS-PETase/IsPETase ^{R280A/S121E/D186H/N233C/S282C}	PET	Evolved from IsPETase	[103]
	Z1-PETase	PET	Evolved from IsPETase	[104]	
<i>Ideonella sakaiensis</i> 210 F6	IsMHETase		MHET		[22,102]
<i>Thermobifida fusca</i> DSM43793	TfH		PET		[28,105]
<i>Thermobifida fusca</i> KW3	TfC (TfCut1, TfCut2)		PET		[106,107]
<i>Thermobifida fusca</i> KW3	TfCa		MHET, BHET	Carboxyl esterase	[62]
		TfCa WA ^{I69W/V376A}	MHET, BHET	Evolved from TfCa	[62]
<i>Rhizobacter gummiphilus</i>	RgPETase		PET		[108]
<i>Brachybacterium ginsengisoli</i>	BgP		PET	Marine bacterium (deep sea)	[109]
<i>Streptomyces</i> sp. SM14	SM14est		PET	Marine bacterium	[110]
<i>Pseudomonas aestusnigri</i>	PE-H		PET	Marine bacterium	[111]
<i>Burkholderiales</i> bacterium	BbPETase		PET		[112]
		BbPETase ^{S335N/T338I/M363I/N365G}	PET		[112]
<i>Thermobifida cellulolytica</i>	Thc (Thc_Cut1, Thc_Cut2)		PET		[106,113]
<i>Humicola/Humilical</i>	HiC		PET	Fungal enzyme	[114]
<i>Thermomyces insolens</i>					
<i>Fusarium solani</i> f. sp. <i>pisi</i>	FsC		PET	Fungal enzyme	[114]
<i>Pseudomonas mendocina</i>	PmC		PET		[114]
<i>Bacillus subtilis</i>	Bs2Est		MHET, BHET	Carboxyl esterase	[99]
HR29	BhrPETase		PET		[115]
Leaf-branch compost metagenome	LCC		PET		[50,116]
		LCC ^{I1CCG}	PET		[50,59]
Compost metagenome	PHL7		PET		[51]
		PHL7 ^{L210T}	PET		[117]
Metagenome	PES-H1/PES-H2		PET	Polyester hydrolase	[118]
		PES-H1 ^{L92F/Q94Y}	PET		[118]
Metagenome	ChryBHETase		BHET	Carboxyl esterase	[53]
	BsEst		BHET	Carboxyl esterase	[53]

assimilates will largely benefit from recent developments in bacterial lignin upgrading [73].

Recent efforts have specifically focused on characterizing *P. putida* KT2440 in relation to EG metabolism. Starting from the initial insights from comparative proteomics with *Pseudomonas* strain JM37 [74], strain KT2440 was found to possess a *gcl* operon, providing the genomic setup for the glyoxylate carboligase (Gcl) pathway [75] (Figure 3). This pathway is naturally

repressed and must first be activated either by deletion of the specific transcriptional repressor GclR [23] or by constitutive overexpression [75], after which it could be allowed to grow on EG as the sole carbon and energy source. This pathway has also been identified in *Pseudomonas umsongensis* GO16 [69] and suggested for *I. sakaiensis* [76]; however, based on CO₂ release and the input of reducing equivalents metabolically, the use of this pathway is quite costly [77]. Establishing the β-hydroxyaspartate cycle from *Paracoccus denitrificans* as an

Figure 3

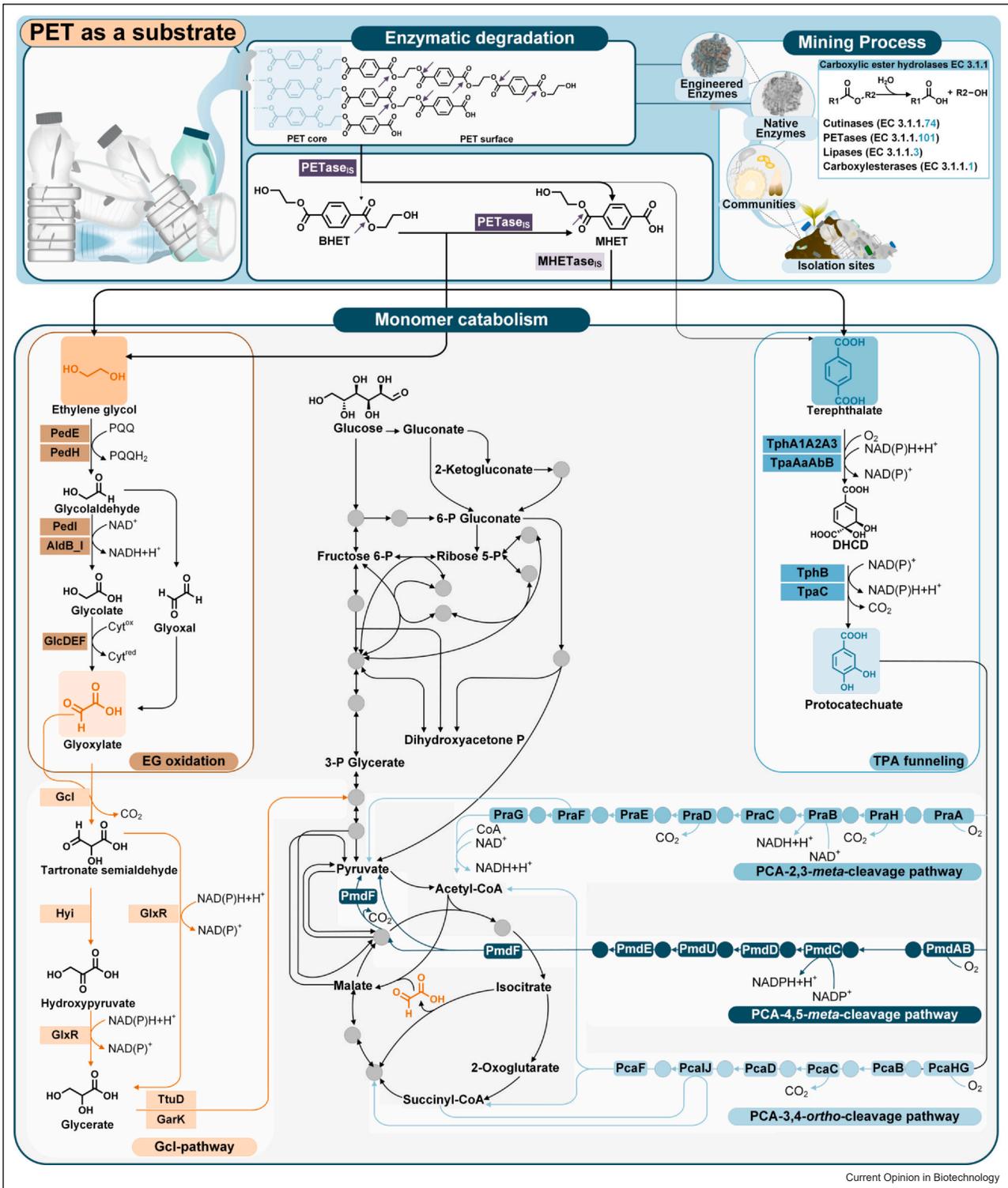
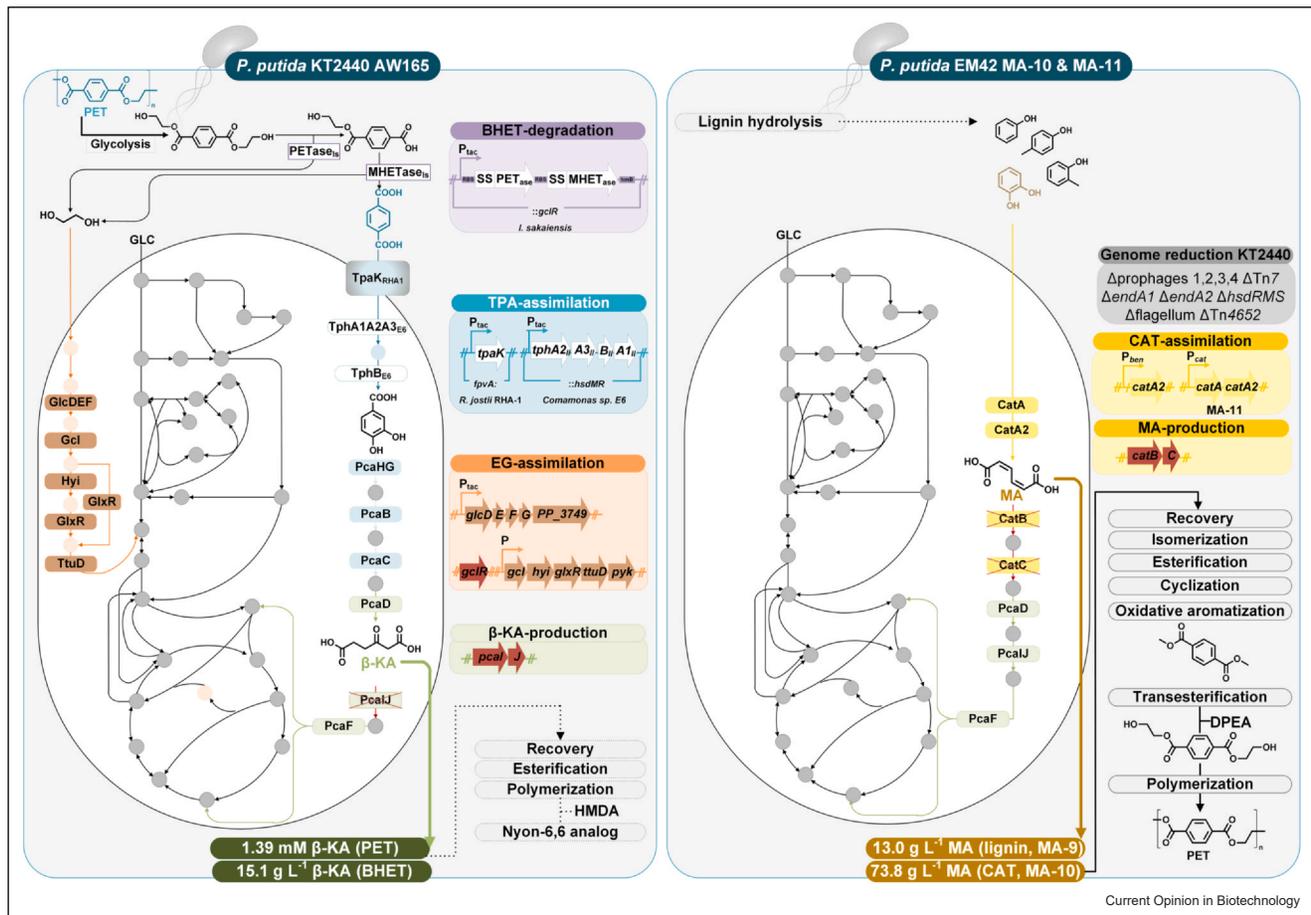


Figure 4



P. putida KT2440 as a case study for a biobased PET industry. **(a)** From PET to alternative polymers. *P. putida* KT2440 was streamlined for β-KA production from PET depolymerized by glycolysis. Strain AW165 is characterized by the following: (1) constitutive overexpression of genes involved in EG oxidation, (2) deletion of *gclR* for activation of the Gcl pathway, (3) expression of the *tphA2_{II}A3_{II}B_{II}A1_{II}* operon from *Comamonas* sp. E6 and *tpaK* from *R. jostii* for TPA catabolism and import, respectively, (4) expression of PETase and MHETase from *I. sakaiensis* for BHET hydrolysis, and (5) deletion of *pcaJ* for β-KA accumulation. The strain produced β-KA from PET, depolymerized using a combination of chemical and biological methods, which subsequently can be used to produce a nylon-6,6 analog [20]. **(b)** From lignin to PET. The genome-reduced *P. putida* KT2440 derivative EM42 was metabolically engineered for MA production by deleting the *catBC* genes, thereby generating the MA-10 strain. Additionally, strain MA-11 harbors a second copy of the native *catA2* gene, which is introduced downstream of *catA*, the major catechol-1,2-dioxygenase. The genetic setup of both strains enabled enhanced *cis,cis*-muconate production from the toxic lignin model compound CAT in comparison to the KT2440 strains without genome reduction in terms of productivity, titer, and yield. MA was recovered from the culture broth, followed by stepwise chemical conversion into BHET and final polymerization into PET [24]. Considering the results of previous works, a full value chain from lignin to PET is possible [40]. Color coding: deletions are highlighted in red, and native genes and enzymes are depicted in full color, whereas heterologous genes are shown in white with a colored frame. HMDA, hexamethylenediamine; DPEA, *N,N*-diisopropylethylamine.

been identified, allowing production from D-xylose [25,87–90], the downstream intermediate xylonic acid [91,92] or other pentose sugars [26] via the formation of glycolaldehyde, which is subsequently enzymatically reduced to EG (Figure 5). Alternative pathways start with glucose via L-serine as an intermediate [27,93], and, additionally, a novel biosynthetic pathway from acetate has been designed computationally [94].

Comparably fewer pathways are available for biobased *de novo* TPA production 15 (Figure 5). For instance, in a

metabolically engineered *E. coli* strain, the conversion of *p*-xylene was established by stepwise conversion with *p*-toluate as an intermediate [95]. In a subsequent study in which *P. putida* KT2440 was used as an alternative host, this approach was further improved, yielding a titer of 38.25 g l⁻¹ TPA [96]. In addition, Kohlstedt et al. demonstrated the feasibility of linking lignin-related aromatic degradation pathways with PET synthesis [24] (Figure 4b). The genome-reduced *P. putida* strain EM42 was equipped with genetic modifications relevant for the formation of catechol (CAT)-based *cis,cis*-muconate. The

PET as a product of coupled bio- and chemo-catalytic processes. Both representative sugars [119] and AROs [16] obtained from lignocellulosic biomass are interesting carbon sources for producing EG or the aromatic PET precursor TPA via metabolically engineered micro-organisms. From all the displayed routes, only EG production via the three-step conversion of ethanol has thus far reached commercial applicability for bio-PET production [84], profiting from recent developments in yeast-based ethanol production [120]. The depicted EG biosynthetic pathways start from D-xylulose [25,88–90], D-xylonic acid [91], other hemicellulose-derived pentoses [26], glucose [27,93], or acetate [94]. Additionally, AROs are suitable for direct TPA production from *p*-xylene [95] or for *cis,cis*-muconate production [24]. Toward fully biobased PET, both sugar-based EG and aromatic-derived (dimethyl)terephthalate may be used for BHET production, which subsequently undergoes polycondensation [4]. Enzymes: AceA: Isocitrate lyase; AldA: aldehyde dehydrogenase; Aldo-B: D-xylulose-1-phosphate aldolase; Adh: amino acid dehydrogenase; Agt: aminotransferase; Ald: alcohol dehydrogenase; AraA: L-arabinose isomerase; BetB: aldehyde dehydrogenase; BzdH: benzaldehyde dehydrogenase; CatA/CatA2: catechol-1,2-dioxygenase; CitDEF: citrate lyase; DTE: D-tagatose epimerase; FucA: L-fuculose phosphate aldolase; FucI: L-fucose isomerase; FucK: L-fuculokinase; FucO: lactaldehyde reductase; GcD: glucose dehydrogenase; GhrA: glyoxylate reductase; Mao: monoamine oxidase; Kdc: α -ketoacid decarboxylase; Khk-C: D-xylulose-1-kinase; Pdc: pyruvate decarboxylase; RhaA: L-rhamnose isomerase; RhaB: L-rhamnulokinase; RhaD: rhamnulose-1-phosphate aldolase; SerA: phosphoglycerate dehydrogenase; SerB: phosphoserine phosphatase; SerC: phosphoserine transaminase; Sdc: serine decarboxylase; TsaC: *p*-carboxybenzyl alcohol dehydrogenase; TsaD: *p*-carboxybenzaldehyde dehydrogenase; TsaMB: toluate methylmonooxygenase; Xmo: xylene monooxygenase; Xdh: D-xylulose dehydrogenase; XylA: xylose isomerase; XylB: xylose dehydrogenase; XylC: xylonolactonase; YjgB: aldehyde reductase; YjhG/YagF: D-xylonate dehydratase; YjhH/YagE: 2-keto 3-deoxy D-xylonate aldolase; YqhD: alcohol dehydrogenase.

purified product was subsequently chemically converted into dimethylterephthalate, which, after transesterification to generate BHET, was later used for PET production, paving the groundwork for a novel value chain from lignin to PET [24,40].

Conclusions

The global dependency on the all-around useful product PET faces two major issues arising from conventional fossil fuel-based production [5,6] and the limited possibilities of how to proceed with postconsumer PET in a manner that limits both material loss and environmental concerns [7,8]. Both challenges have been sizable drivers in recent years when establishing alternative routes for both PET synthesis [86] and its valorization [1]. As demonstrated by scientists worldwide, harnessing the outstanding variability and flexibility within natural microbial metabolic pathways is an enormous opportunity toward a sustainable PET industry [15,29,30,66], thereby contributing to the realization of the sustainable development goals of the United Nations [13]. However, biobased routes for PET production and valorization have played an almost nonexistent role in the PET industry thus far. Regarding the current landscape of PET usage (Figure 1), it has become clear that PET production and valorization require innovative approaches and solutions, in which micro-organisms and biotechnology will definitely play important roles.

Data Availability

No data were used for the research described in the article.

Declaration of Competing Interest

Michael Kohlstedt and Christoph Wittmann have filed patent applications on the use of lignin for bioproduction. Fabia Weiland declares that she has no competing interest.

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