

Review

Medical properties, market potential, and microbial production of golden polyketide curcumin for food, biomedical, and cosmetic applications[☆]

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Curcumin, a potent plant polyketide in turmeric, has gained recognition for its outstanding health benefits, including anti-inflammatory, antioxidant, and anticancer effects. Classical turmeric farming, which is widely used to produce curcumin, is linked to deforestation, soil degradation, excessive water use, and reduced biodiversity. In recent years, the microbial synthesis of curcumin has been achieved and optimized through novel strategies, offering increased safety, improved sustainability, and the potential to revolutionize production. Here, we discuss recent breakthroughs in microbial engineering and fermentation techniques, as well as their capacity to increase the yield, purity, and cost-effectiveness of curcumin production. The utilization of microbial systems not only addresses supply chain limitations but also helps meet the growing demand for curcumin in various industries, including pharmaceuticals, foods, and cosmetics.

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Available online xxxx

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Introduction

Curcumin is the principal curcuminoid produced from the popular Indian spice turmeric (*Curcuma longa* L.), a member of the ginger family [1,2]. Chemically, the molecule contains two phenolic rings connected by a

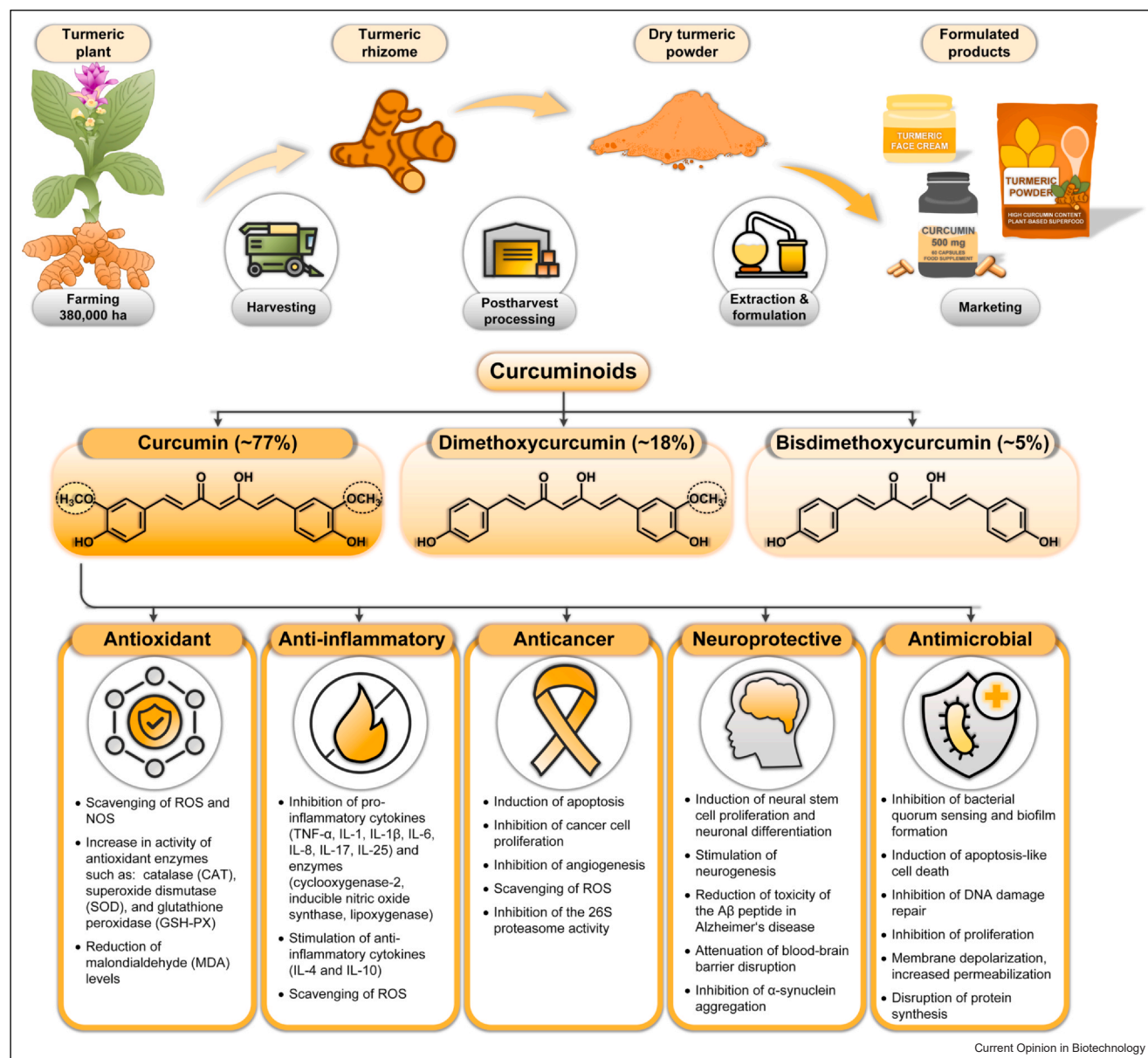
seven-carbon linker, which is responsible for the antioxidant properties of curcumin (Figure 1). Methoxy groups are attached to the rings, which contribute to the compound's solubility and influence its overall reactivity. As demonstrated by recent studies, curcumin has multiple benefits [3•]. In regard to human health, curcumin limits the growth of food pathogens [4], allows [3•] individuals to monitor food spoilage through color changes [5], and provides a bright yellow color to various foods [6,7]. In addition, numerous studies have reported that curcumin exhibits antioxidant [8], anti-inflammatory [9], anticancer [10], neuroprotective [11], and antimicrobial [12] effects (Figure 1).

Economically, curcumin has commercial value in the pharmaceutical, food, and cosmetics industries, as demonstrated by the US\$ 70 million in market value in 2022. The market is expected to more than double over the next 8 years, underlining that importance of curcumin will substantially increase (<https://www.gminsights.com/industry-analysis/curcumin-market>). Today, curcumin is almost exclusively obtained from turmeric plants through classical farming, followed by extraction and purification of the compound from the powdered turmeric rhizome (Figure 1). The global production of fresh turmeric rhizomes is estimated to reach 1.1 million metric tons per year, and India represents 80% of the global market [14]. Fresh rhizome contains 2–5% curcumin (depending on the growing season) [13], leading to an annual production volume of approximately 22,000–55,000 tons of curcumin.

The average yield of the spice is approximately 3.8 tons ha⁻¹, and 10% of the harvest must be stored as a seed material for the next farming season [15]. Unfortunately, turmeric farming raises environmental concerns, as the plants occupy valuable agricultural land (380 000 ha) and require intensive watering, which can lead to water scarcity in arid areas. Furthermore, these large monocultures can be infected by plant-parasitic nematodes [16], fungi [17], bacteria [18], and insects [19], necessitating massive use of pesticides and, inter alia, posing high risks of harvest loss.

[☆] Christoph Wittmann had no involvement in the peer review of the article and has no access to information regarding its peer review. Full responsibility for the editorial process of this article was delegated to Ken-ichi Yoshida.

Figure 1



From nature to applications: the curcumin value chain. Curcumin compounds are obtained from farmed turmeric plants and are extracted from the dried rhizome and formulation. Conventional extraction methods, such as solid–liquid and Soxhlet extraction [92], are easily performed but suffer from low efficiency, time exhaustion, and nonselectivity [20,93]. New methods that rely on ultrasound [94], electromagnetic waves [95], enzymes [96], supercritical fluids [97], pressurized liquids [98], and green solvents [99] offer more ecofriendly and efficient curcumin purification methods but remain in their infancy. Medically, curcumin is known to modulate various cellular pathways, and its mode of action has been intensively studied; curcumin molecules perform relevant interactions with transcription factors, proteins, cytokines, and inflammatory mediators, thereby providing protection against oxidation, inflammation, cancer, neurodegenerative diseases, and infections [100].

Curcumin can be chemically synthesized, but the yields are low; in addition, the products are contaminated with organic reagents, complicating their safe use in food and therapy [20].

Classical manufacturing involves obvious drawbacks, including the need for alternative routes that are more

efficient and sustainable. In this work, after updating the applications and market potential of curcumin, we review novel strategies that harness synthetic biology and systems metabolic engineering [21–23] to breed microbial cell factories for curcumin synthesis. Building upon our present knowledge of the underlying biochemistry and metabolic pathways involved, we showcase several

successful examples of curcumin synthesis in bacteria, fungi, and yeasts and anticipate a more sustainable future for curcumin manufacturing.

Market potential and applications of curcumin

Curcumin was awarded the generally regarded as safe (GRAS) status by the United States Food and Drug Administration and is used in various applications in the food, medical, and cosmetic industries (Figure 1). Extensive research efforts in recent years have led to tremendous growth in terms of market applications and commercial value of curcumin. In the food industry, curcumin is marketed as Natural Yellow 3, diferuloylmethane, CI 75300, or E100 [24]. Due to its pronounced yellow color, curcumin is a common dye for baked goods, dairy products, mustard, beverages, ice cream, and salad dressings [25]; thus, curcumin offers a beneficial replacement to synthetic yellow dyes that are unsafe [26]. Due to its pH-dependent color change [27], curcumin has been applied as a pH biosensor for monitoring food spoilage [28].

Owing to its antimicrobial and antioxidant activities, curcumin is also used to preserve green food [29] and has gained increasing attention for its ability to extend the shelf life of food [30]. Notably, when excited with visible light within 400 to 500 nm, curcumin is photoactivated and drives the formation of reactive oxygen species, such as singlet oxygen, superoxide anions, and hydroxyl radicals [31,32]. These factors, in turn, reduce the growth of prevalent food pathogens, including *Staphylococcus aureus* [33], *Listeria monocytogenes* [34], *Listeria innocua* [35], *Escherichia coli* O157:H7 [35], and *Salmonella typhimurium* [36], in fresh meat. Moreover, curcumin limits the growth of food-borne fungi, such as *Aspergillus flavus* in maize kernels [37], *Penicillium expansum* [38], and *Botrytis cinerea* in apples [39], and inactivates enzymes responsible for browning and deteriorating fruits [40,41].

Medically, curcumin has a range of health benefits and promotes well-being (Figure 1). Based on recent findings, curcumin suppresses cancer growth [10,42,43], protects against inflammation [9,44], and fights and prevents infectious and noninfectious diseases, including malaria, tuberculosis [45–47], diabetes [48,49], Alzheimer's disease [50,51], and Parkinson's disease [52,53]. Furthermore, curcumin actively supports wound healing [54,55] and helps achieve appropriate immune system modulation [56,57], leading to a wide range of therapeutic applications. As reported in the PubMed database, 268 clinical trials involving curcumin (February 2024) have been conducted since 2019 and have demonstrated the numerous health benefits of curcumin, highlighting the great potential of the compound. For example, oral administration of curcumin significantly reduced the progression of prostate-specific antigen, a biomarker for prostate cancer [58]; knee injury and

osteoarthritis outcome scores [59]; and serum levels of islet amyloid polypeptide, a hallmark of insulin resistance [60]. Therefore, curcumin exhibits anticancer, anti-inflammatory, and antidiabetic properties in humans.

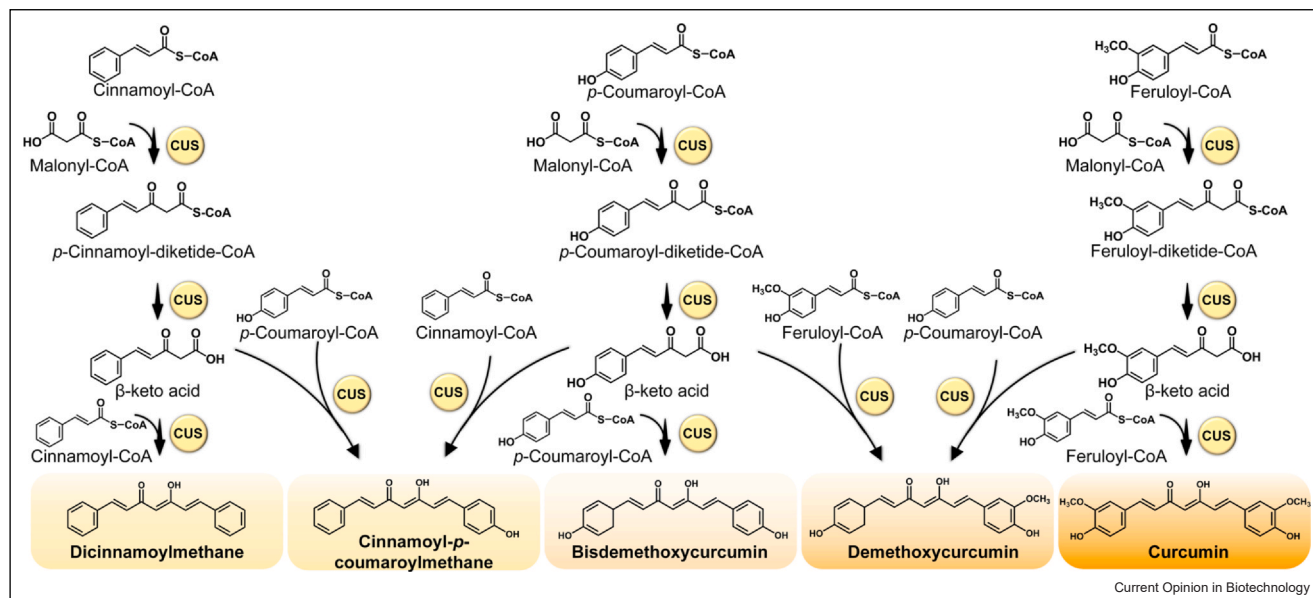
Biochemistry of curcumin synthesis in plants

As a polyketide, curcumin and its derivatives are synthesized from CoA thioesters, namely, one molecule of malonyl-CoA and two molecules of aromatic CoA [61•] (Figure 2). The latter compounds are formed by CoA-mediated activation of hydroxycinnamate intermediates of the phenylpropanoid pathway [62]; normally, this pathway supplies precursors for the biosynthesis of lignin, a major structural component of the cell wall in higher terrestrial plants [63,64], and other metabolites, such as flavonoids [65].

The biosynthetic route exhibits promiscuity and accepts different aromatic CoA thioesters. Curcumin is formed from two molecules of feruloyl-CoA, whereas partial or exclusive incorporation of *p*-coumaroyl-CoA results in the demethoxy analogs demethoxycurcumin and bisdemethoxycurcumin. The signature enzyme of the pathway is a type III polyketide synthase (PKS), which catalyzes the decarboxylative condensation of the aromatic CoA thioester with malonyl-CoA as the extender unit. CUS was originally discovered in rice (*Oryza sativa* L.), although the plant tissue does not contain curcuminoids *in vitro* [66] or *in vivo* [67]. Notably, *O*₃CUS exhibits differential affinities for cinnamoyl-CoA, *p*-coumaroyl-CoA, and feruloyl-CoA; in contrast, *O*₅CUS strongly prefers *p*-coumaroyl-CoA as a substrate, strongly impacting the curcuminoid spectrum [42].

Inspired by the findings for rice, researchers subsequently revealed the biosynthesis of curcuminoids in turmeric (*C. longa*), revealing a striking difference (Figure 3a). In turmeric, the following type III PKSs are collaboratively involved in the biosynthesis of curcuminoids: diketide-CoA synthase (DCS; BAH56225) and curcumin synthase (CURS) [68]. The DCS enzyme drives the formation of the diketide-CoA intermediate from malonyl-CoA and either *p*-coumaroyl-CoA or feruloyl-CoA. CURSs perform dual functions, as they catalyze the hydrolysis of diketide-CoA to β -keto acid and perform condensation with the second hydroxycinnamoyl-CoA thioester. Further studies of native curcuminoid pathways have revealed three different variants (CURS1, 2, and 3; BAH56226, BAH85780, and BAH85781, respectively) [69]. CURS1 exhibits a preference for feruloyl-CoA, although it accepts *p*-coumaroyl-CoA [68]; CURS2 exhibits a preference for feruloyl-CoA; and CURS3 exhibits similar affinities for feruloyl-CoA and *p*-coumaroyl-CoA [69]. In principle, differential expression of the three CURSs and

Figure 2



In vitro biosynthesis of curcumin and curcuminoid derivatives by curcuminoid synthase (CUS) from rice (*Oryza sativa*, *Os*). The gene *os07g17010*, encoding CUS from rice (*OsCUS*), was identified while researchers screened for putative type III PKS activity in rice. The enzyme catalyzes a three-step reaction from a phenylpropanoid-derived aromatic CoA thioester via diketide-CoA and β -keto acid intermediates to the corresponding curcuminoid molecule. Functional studies of a putative type III PKS, encoded in the rice genome, surprisingly revealed the synthesis of curcumin and bisdemethoxycurcumin, as well as related derivatives from CoA-based precursors [66] (Figure 2). Given its activity, the enzyme was named curcuminoid synthase (CUS). Rice-based enzymes (*OsCUS*s) function in a nontraditional 'head-to-head' fashion [101], thereby forming diketide-CoA. Subsequently, the intermediate is hydrolyzed to the corresponding β -ketoacid in a reaction catalyzed by the same enzyme [66]. In addition to other PKSs, *OsCUS* uses β -ketoacid as a second extender substrate and condenses the compound with another phenylpropanoid-derived CoA thioester [101]. In this manner, a single enzyme catalyzes the correspondingly 'one-pot' synthesis of curcuminoids [72]. *In vitro* feeding of malonyl-CoA and different aromatic CoA thioesters enabled the production of the natural curcuminoids curcumin, demethoxycurcumin, and bisdemethoxycurcumin; in addition, new, more unpolared derivatives were generated, such as dicinnamylmethane and cinnamoyl-*p*-coumaroylmethane. Regarding selectivity, *OsCUS* exhibits a preference for *p*-coumaroyl-CoA but also accepts cinnamoyl-CoA and feruloyl-CoA, enabling the synthesis of asymmetrical curcuminoids (demethoxycurcumin and cinnamoyl-*p*-coumaroylmethane). When *OsCUS* was subsequently expressed in *E. coli* BLR (DE3), it enabled the formation of all curcuminoids *in vivo*.

availability of the building blocks define the curcuminoid spectrum (Figure 3b) [44,69,70].

Upstream of the biosynthetic pathway, feruloyl-CoA and *p*-coumaroyl-CoA are derived from ferulate and *p*-coumarate, respectively, by the enzyme *p*-coumaroyl-CoA ligase (4CL) [61]. Ferulate is formed by the enzymatic modification of *p*-coumarate via caffeate as an intermediate [71••]. Notably, *p*-coumarate is synthesized directly via deamination of L-tyrosine or hydroxylation of cinnamate, which is produced by deamination of L-phenylalanine (Figure 3a) [72].

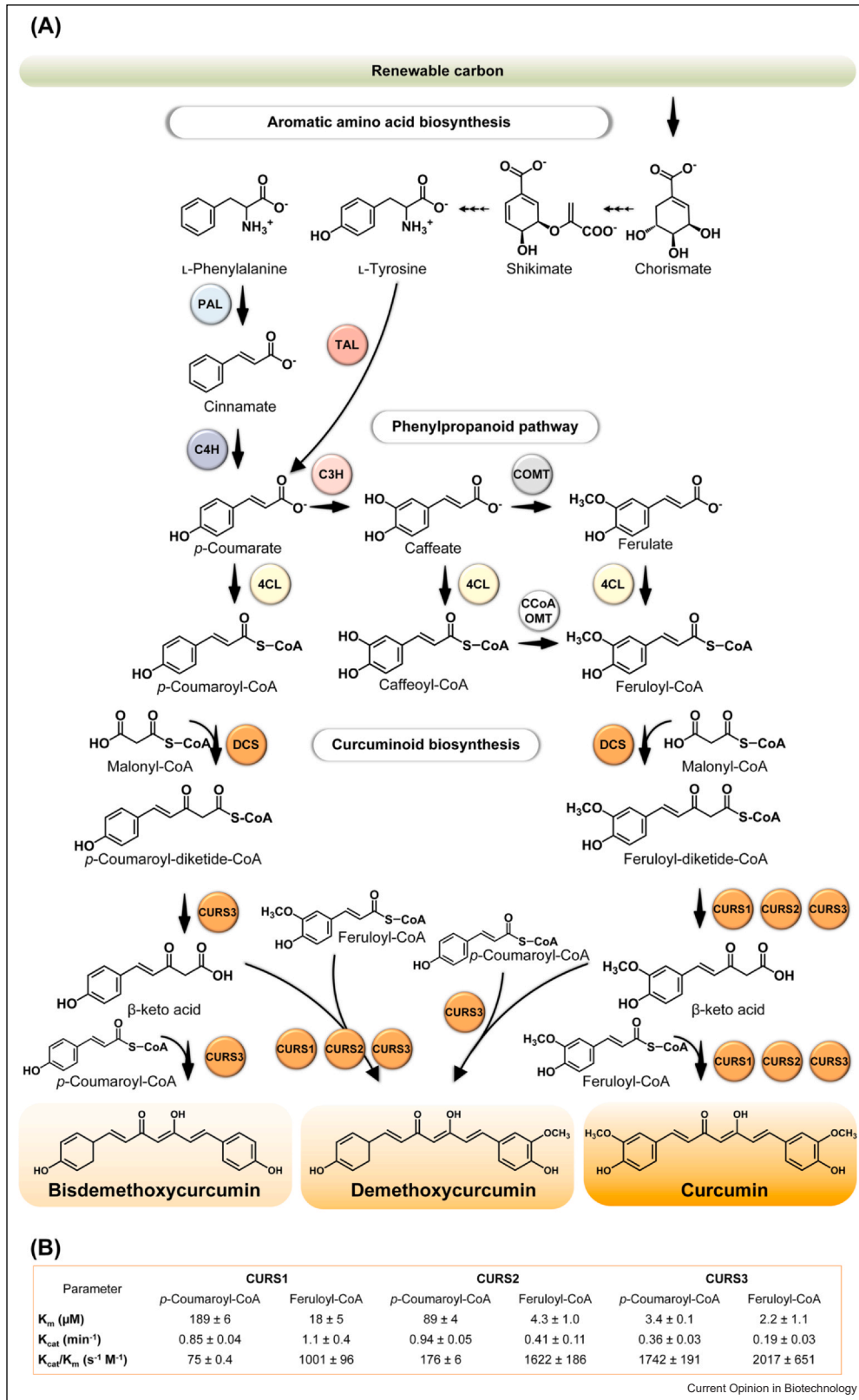
Briefly, *in vitro* studies of chalcone synthase from ginger (*Zingiber officinale* L.; GenBank: DQ486012.1) using feruloyl-CoA, *p*-coumaroyl-CoA, and cinnamoyl-CoA yielded curcumin, bisdemethoxycurcumin, and dicinnamylmethane, respectively [73] (Figure 2). However, further testing has not been performed with the enzyme [74].

Pioneering synthesis of curcumin in *Escherichia coli* using rice- and turmeric-based heterologous pathways

The identification of curcuminoid synthase activity in rice (*OsCUS*) and the demonstration of its functional operation *in vitro* [66,67] set the stage for heterologous curcumin production in microbes (Figure 4). To this end, *E. coli* BLR (DE3) was constructed with a plasmid-based heterologous pathway to convert the precursor ferulate into curcumin. The designed artificial biosynthesis-related gene cluster included four genes, including *os07g17010* from rice, which encodes *OsCUS*; *4cl1*, which encodes 4-coumarate-CoA ligase 1 (from *Lithospermum erythrorhizon*, purple gromwell); *accBC*; *dtsR1*, which encodes acetyl-CoA carboxylase subunit α ; and a homolog of the β subunit (from *Corynebacterium glutamicum*).

The recombinant *E. coli* BLR (DE3) strain that expresses these genes was tested in a two-step culture process. After large amounts of biomass were formed in

Figure 3



Metabolic pathways associated with the heterologous production of curcumin and related curcuminoids in microbes. The figure illustrates the native biosynthetic machinery from the turmeric plant (a) and the corresponding kinetic properties of the CURS1, CURS2, and CURS3 enzymes (b). The phenylpropanoid pathway is initiated by deamination of the aromatic amino acids L-phenylalanine and L-tyrosine by the enzymes PAL and TAL, yielding cinnamate and *p*-coumarate, respectively. Additionally, *p*-coumarate can be synthesized from L-phenylalanine via cinnamate by PAL and C4H. The final product of the phenylpropanoid pathway is ferulate, which is synthesized from *p*-coumarate via caffeate by C3H and COMT. The first committed reaction of the curcuminoid biosynthetic pathway is catalyzed by 4CL, which produces CoA-activated forms of phenylpropanoids. Subsequently, DCS elongates feruloyl-CoA or *p*-coumaroyl-CoA to form one acetate unit from malonyl-CoA, resulting in the formation of β -keto acids. Finally, CURS catalyzes the condensation of β -keto acids with one additional molecule of feruloyl-CoA or *p*-coumaroyl-CoA. Depending on the combination of starter and elongation units, curcumin, demethoxycurcumin, or bisdemethoxycurcumin can be produced. Abbreviations: C4H: cinnamate 4-hydroxylase; CCoAOMT: caffeoyl-CoA O-methyltransferase; CURS: curcumin synthase [70]; K_m : Michaelis–Menten constant; K_{cat} : turnover number; K_{cat}/K_m : catalytic efficiency.

complex nutrient broth, the cells were transferred to mineral media. The setup contained 40 g l⁻¹ glucose (as a growth substrate) and 1 mM ferulate (as a bio-transformation precursor). Within 60 hours, the recombinant strain formed 113 mg l⁻¹ of curcumin in a yield of 0.61 mol (mol ferulate)⁻¹ [67] (Figure 4). Subsequently, the artificial pathway was extended further expressing phenylalanine ammonia-lyase (PAL) from the yeast *Rhodotorula rubra*, which enabled isopropyl β -D-1-thiogalactopyranoside-inducible production from L-phenylalanine and L-tyrosine in the corresponding four-plasmid mutant (Figure 4). The same study produced curcumin from rice bran pitch, a ferulate-rich agricultural waste that is generated during rice milling [67].

Subsequently, the researchers induced the functional expression of the *dcs* and *curs1* genes from turmeric with *E. coli* K-12 using isopropyl β -D-1-thiogalactopyranoside-inducible medium- and high-copy-number plasmids [75] (Figure 4). Additionally, *4cl1* from tale cress (*Arabidopsis thaliana* (L.), Heyn.) was expressed on a low-copy-weight plasmid, and the three-plasmid host formed 69 mg l⁻¹ curcumin in a yield of 0.18 mol (mol ferulate)⁻¹. A two-stage process was used for production. Elevated levels of glucose (40 g l⁻¹) and ferulate (2 mM) were contained in the medium during the production phase. Additional studies suggested that the turmeric-based pathway, which consists of 4CL1 from *A. thaliana* and DCS and CURS1 from *C. longa* [75], exhibited greater efficiency than that of the rice-based pathway described previously, comprising 4CL from *L. erythrorhizon*, CUS, and the overexpression of acetyl-CoA carboxylase from *C. glutamicum* [67].

Strikingly, the chosen host substantially affected production (Figure 4). Recombinant *E. coli* BL21 (DE3) accumulated 301 mg l⁻¹ of curcumin in a ferulate-supplemented one-step process in terrific broth (TB), far more than the K-12 MG1655 (DE3) and K-12 JM109 (DE3) strains that expressed the same genes on the same vectors [76]. In contrast to the K-12 lineage, the BL21 (DE3) strain (as with other strains from the B lineage) lacks two major proteases, Lon and OmpT; thus, the strain can better express foreign proteins from cloned genes [77]. Furthermore, *E. coli* BL21 (DE3) exhibited a mutation in the *hdsB* gene, reducing plasmid degradation [78].

Furthermore, the host benefited from streamlined metabolism because it exhibited an increased capacity to re-metabolize secreted acetate; as a result, the host tolerated higher glucose levels and grew to higher cell concentrations than those of *E. coli* K-12 [79,80]. This metabolic property was linked to the upregulation of the tricarboxylic acid cycle and the glyoxylate shunt, which is involved in acetate metabolism, at the transcriptional level.

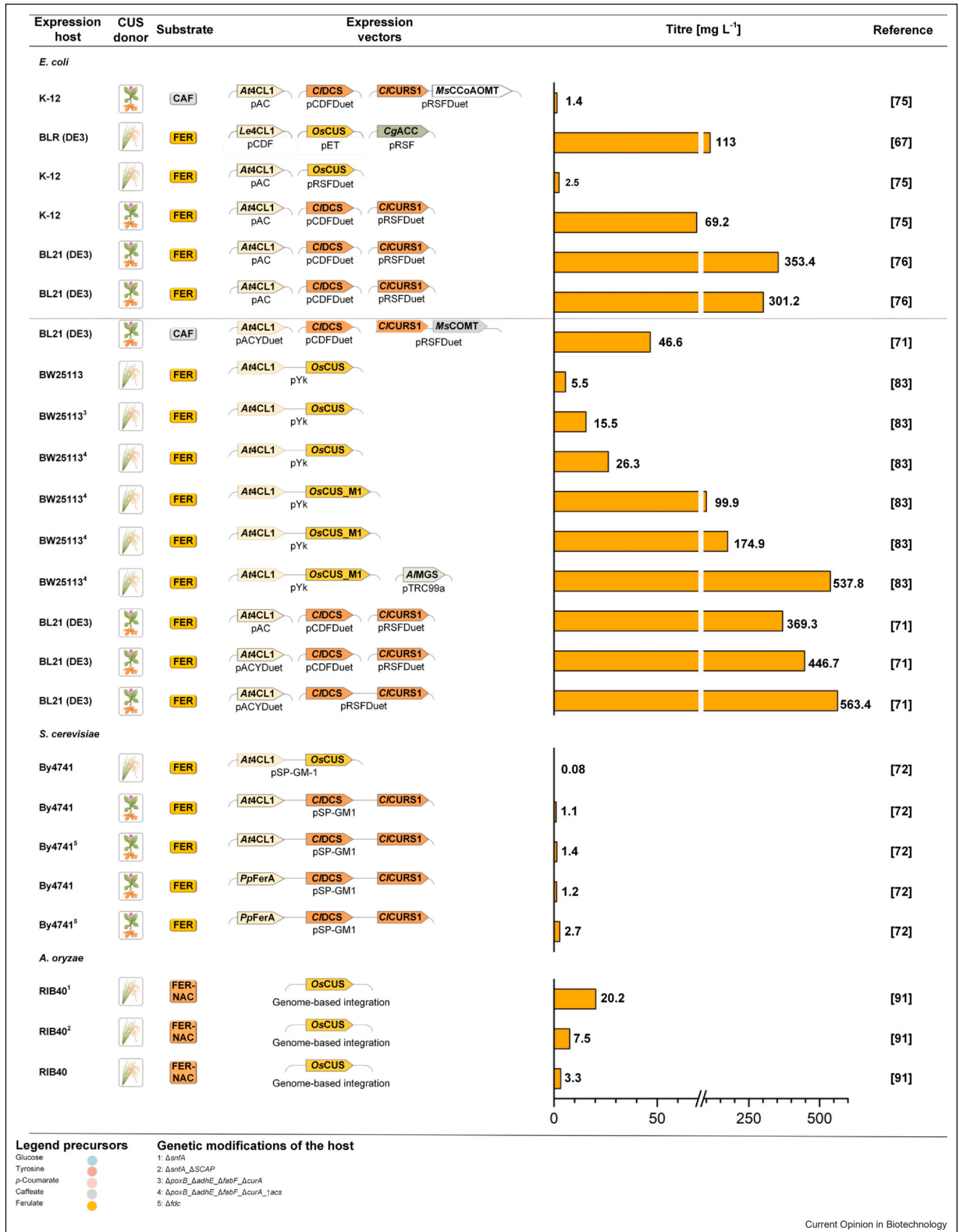
A range of medium tests were performed to explore the effects caused by nutrient availability and buffer capacity. This led to a two-step fermentation process (cell growth in Luria-Bertani (LB) and curcumin production in M9), which yielded 353 mg l⁻¹ curcumin at a yield of 0.95 mol (mol ferulate)⁻¹ [76] (Figure 4).

Furthermore, curcuminoids were synthesized from L-tyrosine via the caffeate pathway, although at substantially lower levels than those of the two-step fermentation [75] (Figure 4). This synthesis involved the utilization of tyrosine ammonia lyase (TAL) from the yeast *Rhodotorula glutinis* and 4-coumarate 3-hydroxylase (C3H) from the soil bacterium *Saccharothrix espanaensis* to produce caffeate from L-tyrosine. Subsequently, caffeoyl-CoA 3-O-methyltransferase (COMT) from lucerne (*Medicago sativa* L.) was employed to convert caffeoyl-CoA into feruloyl-CoA, a critical step in the production process.

Increased curcumin production in recombinant *Escherichia coli* using fine-tuned and extended biosynthetic pathways and novel coculture concepts

Research on microbial curcumin synthesis has intensified over the past 5 years. For example, in a range of studies, researchers explored new concepts to increase the production of curcumin in recombinant *E. coli* to a new level. Impressively, curcumin was generated from glucose through microbial *de novo* synthesis first time using the genomic expression of six genes in the tyrosine-overproducing derivative of *E. coli* C41; in this process, the need for antibiotics was eliminated [81••] (Figure 4). The biosynthetic genes were organized into two separate operons (modules). The ferulate-producing module (encompassing *tal* and *c3h* from *S. espanaensis* and *comt* from *M. sativa*) was integrated into the *bioC* locus of the host, while the curcumin-producing module

Figure 4



Overview of the microbial-based bioprocesses used to produce curcumin from caffeate, ferulate, and feruloyl-*N*-acetylcysteamine. The data are displayed regarding pioneering studies (above the dashed line) and recent work from the past 5 years (below the dashed line). From top to bottom the following hosts were used: *E. coli* K12 producing from *p*-coumarate (*P*-COU) and caffeate (CAF) via the turmeric pathway [75], *E. coli* BLR (DE3) producing from ferulate (FER) via the rice-based pathway [67], *E. coli* K12 from FER via the rice-based pathway and the turmeric pathway [75], *E. coli* BL21 (DE3) from FER via the turmeric route [76], *E. coli* BL21 (DE3) from CAF via the turmeric pathway [71], *E. coli* BW25113 from FER via the rice-based route [83••], *E. coli* BL21 (DE3) from FER via the turmeric route [71], *S. cerevisiae* By4741 from FER via the turmeric route [61], and *A. oryzae* RIB40 from FER-NAC via the rice-based pathway [91]. Given that curcumin production by *A. oryzae* was carried out on agar plate cultures [91], we estimated the achieved titer by assuming a volume of agar of 20 ml, which is routinely applied to grow such microbes. In established bioprocesses, curcumin is typically extracted from acidified whole-cell broth (pH = 3) using polar solvents, such as ethyl acetate, followed by drying. The recovered curcumin is subsequently resuspended in solvents, such as dimethyl sulfoxide [67], acetonitrile [71,75,76], and methanol [81,91], and analyzed via high-performance liquid chromatography via ultraviolet detection at 425 nm. Abbreviations: CAF: caffeate; FER: ferulate; FER-NAC: feruloyl-*N*-acetylcysteamine; CCoAOMT: caffeoyl-CoA *O*-methyltransferase; CUS: curcuminoid synthase; CURS: curcumin synthase; ACC: acetyl-CoA carboxylase; *Al*: *A. laidlawii*; *At*: *A. thaliana*; *Cl*: *C. longa*; *Ms*: *Medicago sativa*; *Nt*: *Nicotiana tabacum*; *Os*: *O. sativa*; *Pp*: *P. paucimobilis*; *Rg*: *R. glutinis*; *Se*: *S. espanaensis*; *Cg*: *C. glutamicum*. ¹: $\Delta snfA$; ²: $\Delta snfA \Delta SCAP$; ³: $\Delta poxB \Delta adhE \Delta fabF \Delta curA$; ⁴: $\Delta poxB \Delta adhE \Delta fabF \Delta curA$ 1acs; ⁵: Δfdc . For details about curcumin production from glucose, L-tyrosine, and *p*-coumarate, refer to Figure S1.

(containing the *4cl2* from *Nicotiana tabacum* L., *dcs* and *curs1* from *C. longa*) was inserted into the *lacZ* locus. Each gene was flanked by a ribosomal binding site and a T7 terminator sequence and expressed under the control of a viral T7 promoter. The authors were able to appropriately balance the expression levels [82] within the six-enzyme pathway by comprehensively screening a library that contained 5'-untranslated region sequence mutants obtained using multiplexed automated genome engineering. Among the variants generated, one mutant called 6M08rv exhibited a remarkable 38.2-fold improvement in curcumin production compared with that of the original parental strain. Notably, this improvement was achieved even though the calculated expression levels of two critical enzymes within the pathway (4CL and DCS) were significantly lower in 6M08rv than in the parental strain. Although the final curcumin titer (3.8 mg l⁻¹) was much lower than that obtained from ferulate-based processes, this approach is inspiring and provides an excellent starting point for creating streamlined *de novo* synthetic strains.

Following their previous work on *E. coli* BL21 (DE3), Rodrigues et al. systematically fine-tuned and extended the biosynthetic route to curcumin [71••] (Figure 4). Various plasmid combinations were tested, and the conversion of ferulate to feruloyl-CoA was optimized (module 1). Subsequently, the conversion of the latter compound into curcumin was evaluated (module 2). The best genetic layout included the combined expression of *dcs* and *curs1* from turmeric on a high-copy-number plasmid plus the expression of *4cl1* from *A. thaliana* from a low-copy-weight plasmid and the production of 563 mg l⁻¹ curcumin within 63 hours, which is the highest titer reported thus far. When both modules were combined in one single host, curcumin was obtained from L-tyrosine; however, the level attained was much lower (6.4 mg l⁻¹), suggesting that imbalances remain, and further engineering efforts are needed.

An interesting solution to this problem was provided in the same work [71••]. Using a novel approach, the

synthesis of curcumin was performed by two different producers (Figure 4). The strategy was based on a coculture in which one recombinant host carried synthetic module 1 to synthesize ferulate from L-tyrosine, whereas the second recombinant host expressed module 2 and used ferulate as a substrate to produce curcumin (Fig. S1).

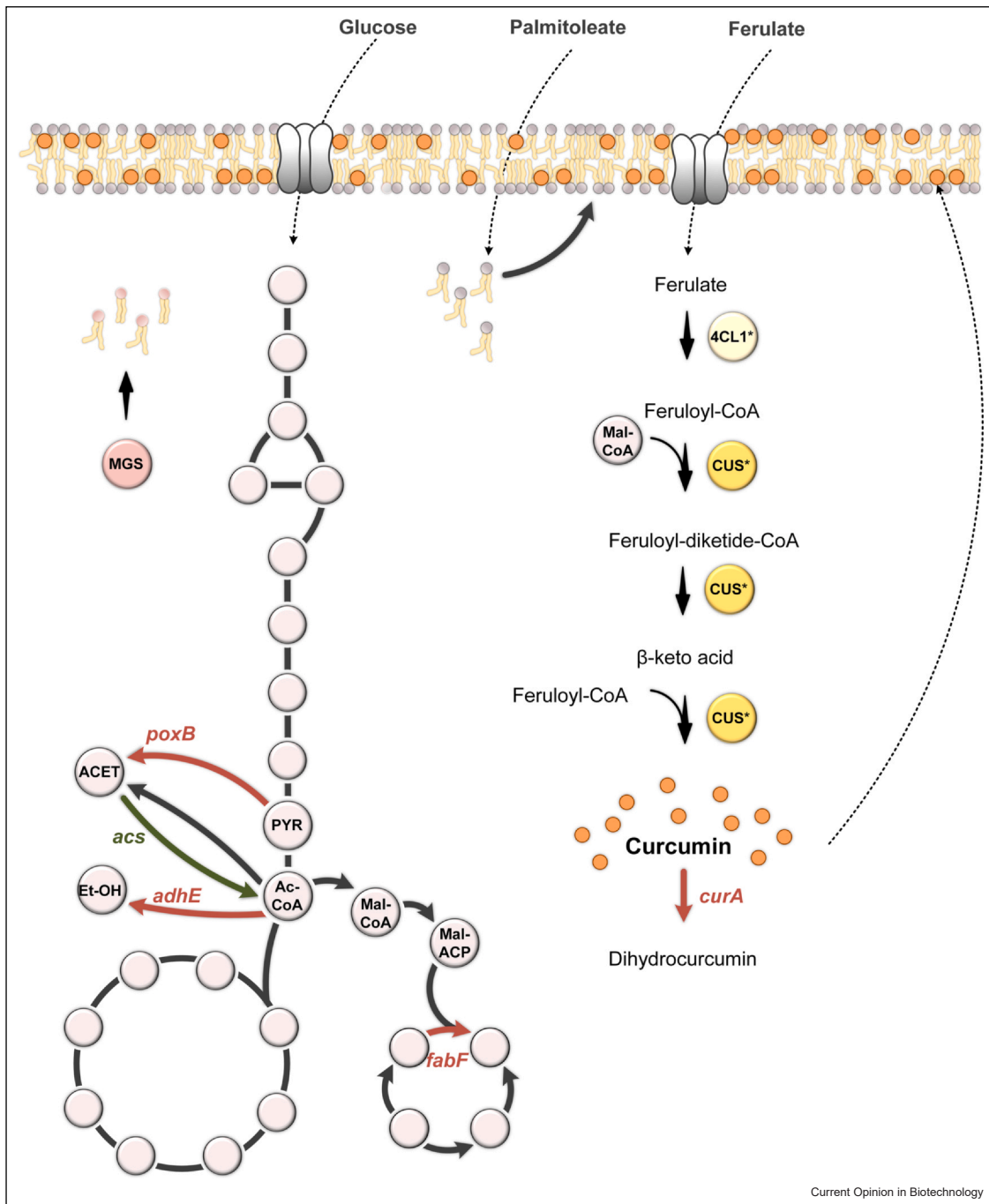
For this purpose, the first host expressed *tal* from *R. glutinis*, *c3h* from *S. espanaensis*, and *comt* from *A. thaliana*, while the second host expressed *4cl1* from *A. thaliana* as well as *dcs* and *curs1* from *C. longa*. In this manner, the number of heterologous genes in each strain was reduced from six to three, ultimately resulting in the formation of 15.9 mg l⁻¹ curcumin, the highest known titer of curcumin produced from L-tyrosine.

Increased membrane fluidity supports high-level production in *Escherichia coli* BW25113

Another study yielded a remarkable titer of 537 mg l⁻¹ and successfully expanded the panel of producers using *E. coli* BW25113 as a host [83••] (Figure 5). *E. coli* BW25113 is a derivative of *E. coli* K-12 that has become the parent strain for the single-gene deletion Keio collection and is extensively employed for systematic phenotypic surveys and synthetic biology efforts. This study utilized the rice-based route and ferulate as a biotransformation precursor. Another important finding of this work was that increasing membrane fluidity provided a beneficial effect on cell production cells, which reduced the toxic effects caused by the product.

Given its pronounced hydrophobic nature, curcumin may be anchored within the phospholipid bilayer, affecting its fluidity [84]. The exposure of *E. coli* to curcumin resulted in reduced membrane fluidity [83••]. Interestingly, this drawback could be partially reversed by pretreating the cells with unsaturated fatty acids, such as palmitoleate and oleate, which simultaneously promoted the production of curcumin [83••]. In contrast, adverse effects were observed when saturated fatty acids were added. The available knowledge was

Figure 5



System-level engineering of *E. coli* to produce curcumin. The comprehensive strategy used comprised (1) directed evolution and expression of the improved rice-based *cus* gene, (2) inactivation of *poxB*, *adhE*, *fabF*, and *curA*, (3) overexpression of acetyl-CoA-forming *acs*, (4) supplementation of unsaturated palmitoleate, and (5) enlargement of the membrane surface by overexpression of MGS from *A. laidlawii* [83••]. Abbreviations: ACET: acetate; Et-OH: ethanol; PYR: pyruvate; Ac-CoA: acetyl-CoA; Mal-CoA: malonyl-CoA; Mal-ACP: malonyl-ACP; CUS: curcuminoid synthase.

subsequently merged into a comprehensive strategy that involved the following methods: (1) performing directed evolution and expressing the improved rice-based *cus* gene; (2) inactivating pyruvate dehydrogenase (*poxB*), alcohol dehydrogenase (*adhE*), 3-oxoacyl-[acyl carrier protein] synthase 2 (*fabF*), and *curA* (curcumin reductase, which catalyzes the reduction of curcumin to dihydrocurcumin); (3) overexpressing acetyl-CoA synthase (*acs*), which results in the formation of acetyl-CoA; (4) adding unsaturated palmitoleate; and (5) enlarging the membrane surface and storage capacity of curcumin through overexpressing monoglucosyl-diacylglycerol synthase (MGS) from *Acholeplasma laidlawii* (Figure 5). After an incubation was performed with 4 mM ferulate as a biotransformation precursor in minimal medium, the titer of the metabolically engineered strain reached 537 mg l⁻¹. The accumulation of curcumin exerts toxic effects on the host, limiting overall production performance; this limitation is a relevant challenge in industrial bioproduction [85–87]. Here, membrane engineering may offer a valuable tool for overcoming storage bottlenecks.

Yeast and fungi fail as alternative hosts in the competitive production of curcumin

E. coli has become a prominent host for microbial curcumin production, similar to many other plant-based metabolites [88]. However, recent studies have aimed to implement alternative, GRAS microbes, which are attractive for addressing industrial markets in food, cosmetics, and medicine. Prominent candidates included *Aspergillus oryzae* [89] and *Saccharomyces cerevisiae* [90].

A metabolically engineered *A. oryzae* mutant that genomically expressed *cus* from rice but lacked the genes *snfA* and *SCAP* successfully formed curcumin when grown on MPY-based agar plates in the presence of feruloyl-*N*-acetylcysteamine, an analog of feruloyl-CoA [91•]. The strain accumulated 404.2 µg of curcumin per plate at a yield of 0.53 mol (mol feruloyl-*N*-acetylcysteamine)⁻¹. As no liquid cultures were performed, it was difficult to evaluate the achieved performance, but the general possibility of using fungi for production is interesting.

Additionally, heterologous synthesis of curcumin was recently established in baker's yeast through episomal expression of *dcs* and *curs1* from turmeric and *ferA*, which encodes feruloyl-CoA synthase enzyme (*ferA*), from *Pseudomonas paucimobilis* [61•]. Importantly, the native gene *fdc*, which encodes ferulate decarboxylase, was inactivated to prevent decarboxylation of ferulate to 4-vinylguaiaicol. The mutant formed 3 mg l⁻¹ of curcumin in a biotransformation setup from ferulate.

Conclusions

Recent efforts have led to microbial strains that produce the plant polyketide curcumin at the milligram scale

through streamlined heterologous pathways. Enabled by progress in recent years, a promising era in microbial curcumin production is near. However, much process optimization is needed to reach a viable curcumin fermentation industry. Several challenges must be addressed to unlock the full potential of microbial curcumin production and harness the benefits of curcumin for industry, health, and the environment. To improve economic factors, microbial strains and fermentation processes must be further optimized to attain higher curcumin yields and greater purity while minimizing byproducts and waste. In addition, downstream processing of curcumin, which is conventionally extracted from total cell broth using polar solvents, might be of interest for optimization. These achievements may be crucial for attaining scalable curcumin production with attractive carbon footprints and resource consumption levels. The inhibitory effects of curcumin reported thus far vary greatly. For *E. coli*, the minimum inhibitory concentration (MIC) ranges between 160 and 2000 µg ml⁻¹, depending on the strain and test conditions used [12,102,103]. For yeast, the MIC can even differ by more than 100-fold [12,103]. At this point, forming a clear conclusion about the extent to which strain limitations have been reached is difficult. More work is needed to clarify this topic. Notably, scientific and technical developments should accompany regulatory and safety considerations to ensure the quality and safety of microbial curcumin for consumer use. Therefore, regions that rely heavily on curcumin production for their livelihoods should receive equitable access to microbial curcumin technology.

CRedit authorship contribution statement

S. Beganovic: Conceptualization, Methodology, Validation, Formal analysis, Writing – original draft, Writing – review & editing. **C. Wittmann:** Conceptualization, Funding acquisition, Methodology, Validation, Formal analysis, Writing – original draft, Writing – review & editing, Funding acquisition.

Data Availability

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

Declaration of Competing Interest

Selma Beganovic and Christoph Wittmann declare that they have no competing interest.

Acknowledgements

The authors acknowledge financial support from the Leibniz ScienceCampus Living Therapeutic Materials (Saarbrücken, Germany).

Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.copbio.2024.103112.

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- of special interest
- of outstanding interest

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