



On the road towards tailor-made rhamnolipids: current state and perspectives

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Abstract

Rhamnolipids are biosurfactants with an enormous potential to replace or complement classic surfactants in industrial applications. They consist of one or two L-rhamnose residues linked to one or two 3-hydroxyfatty acids of various chain lengths, which can also contain unsaturated carbon-carbon bonds, yielding a wide variety of different structures each with its specific physico-chemical properties. Since different applications of surfactants require specific tenside characteristics related to surface tension reduction, emulsification, and foaming etc., rhamnolipids represent a platform molecule which harbors an enormous potential to adopt tailor-made properties to meet a huge variety of demands of surfactants for food-, healthcare-, and biotechnological applications. We are here giving an overview on current technology to synthesize tailor-made rhamnolipids based on the biotechnological use of different enzymes responsible for rhamnolipid biosynthesis originating from different naturally rhamnolipid-producing microorganism. Furthermore, we present future strategies to determine the number of L-rhamnose and 3-hydroxyfatty acids as well as their specific chain lengths and unsaturations to produce customized rhamnolipids perfectly tuned for every application.

Keywords Rhamnolipids · Biosurfactant · *Pseudomonas* · *Burkholderia* · Biosynthesis pathway

Introduction

Biosurfactants possess outstanding characteristics compared to customary or “conventional” tensides, which are normally synthesized by chemical processes and mainly based on petrochemical and thus fossil resources. In contrast to their conventional counterparts, they are of almost exclusive microbiological origin, they are produced from renewable substrates, show lower toxicity, and are highly or even perfectly biocompatible and biodegradable (Desai and Banat 1997; Van Hamme et al. 2006; Hirata et al. 2009; Lima et al. 2011; Johann et al. 2016). In addition to their eco-friendly and sustainable characteristics,

examples exist which provide better foaming properties and—most important for a broad application potential—they especially have remarkable stabilities against extreme pH values, temperatures, and salt concentrations in contrast to many of the traditional surfactants (Pruthi and Cameotra 1997; Makkar and Cameotra 1998; Nitschke and Pastore 2006; Abdel-Mawgoud et al. 2008; Banat et al. 2010).

The term “biosurfactant” denominates a large variety of different molecules with extremely diverse chemical structures particularly produced by different microorganisms, e.g., the lipopeptide surfactin from *Bacillus subtilis* (Arima et al. 1968; Haddad et al. 2009; Dhali et al. 2017), the polymeric emulsan from *Acinetobacter calcoaceticus* (Rosenberg and Ron 1997; Johri et al. 2002; Chamanrokh et al. 2008), or more recently experiencing greater attention the class of glycolipids like mannosylerythritol lipids (MELs) from the genus *Pseudozyma* (Rau et al. 2005; Fukuoka et al. 2007; Saika et al. 2018), trehalose lipids from *Rhodococcus erythropolis* (Peng et al. 2007; Marqués et al. 2009; Luong et al. 2018), or sophorolipids produced by the yeasts of the genus *Candida* (Van Bogaert et al. 2011; Chandran and Das 2012; Konishi et al. 2018).

Furthermore, apart from aforementioned biosurfactants, another particular glycolipid is of considerable biotechnological

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interest and has therefore been intensively investigated in the past, which are designated the so-called rhamnolipids. Rhamnolipids (RL) were first described nearly 70 years ago by Jarvis and Johnson (1949) as an oily extract secreted by the human-pathogen *Pseudomonas aeruginosa*. As a molecule with surface-active properties, they possess the typical amphiphilic molecule character represented in this class of either one or two of the name giving L-rhamnose molecules as the hydrophilic part linked through a β -glycosidic bond to one or—in most molecules—two 3-hydroxyfatty acids as the hydrophobic part (Fig. 1; Soberón-Chávez et al. 2005). Since the nomenclature for different rhamnolipid species was inconsistent in the past and different congeners remained unconsidered, we here suggest novel terms and abbreviations to name (new) molecules more precisely but also very easily based on their number of rhamnose residues, their chain lengths, and by the fact whether they contain saturated or unsaturated fatty acids. Based on the number of L-rhamnose sugar residues, the rhamnolipids are classified into mono- and di-rhamnolipids and the number of fatty acids allows a further sub-classification

into so-called mono- and di-rhamno-di-lipids (mRdL and dRdL) with two and mono- and di-rhamno-mono-lipids (mRmL and dRmL), respectively, with only one fatty acid chain representing the four major native rhamnolipid species (Syldatk et al. 1985a; Abdel-Mawgoud et al. 2010). Within these species, various congeners have been identified varying in lengths of both 3-hydroxyfatty acid chains typically ranging from C_8 to C_{16} and being a characteristic “fingerprint” mainly depending on the genus of their bacterial producer. Thus, rhamnolipids possess a basic structural diversity, which can then be further expanded by introduction of one or more unsaturated carbon-carbon bonds in one of the fatty acids or in both of them (Abalos et al. 2001; Wittgens et al. 2018). Over the years of rhamnolipid research, more than 60 different congeners have been described featuring fundamentally different physicochemical properties and characteristics, which offers a unique potential to selectively use individual molecules in a variety of biotechnological and industrial applications (Abdel-Mawgoud et al. 2010; Chong and Li 2017).

The biosynthesis of rhamnolipids requires consecutive enzymatic reactions by using only two types of metabolites

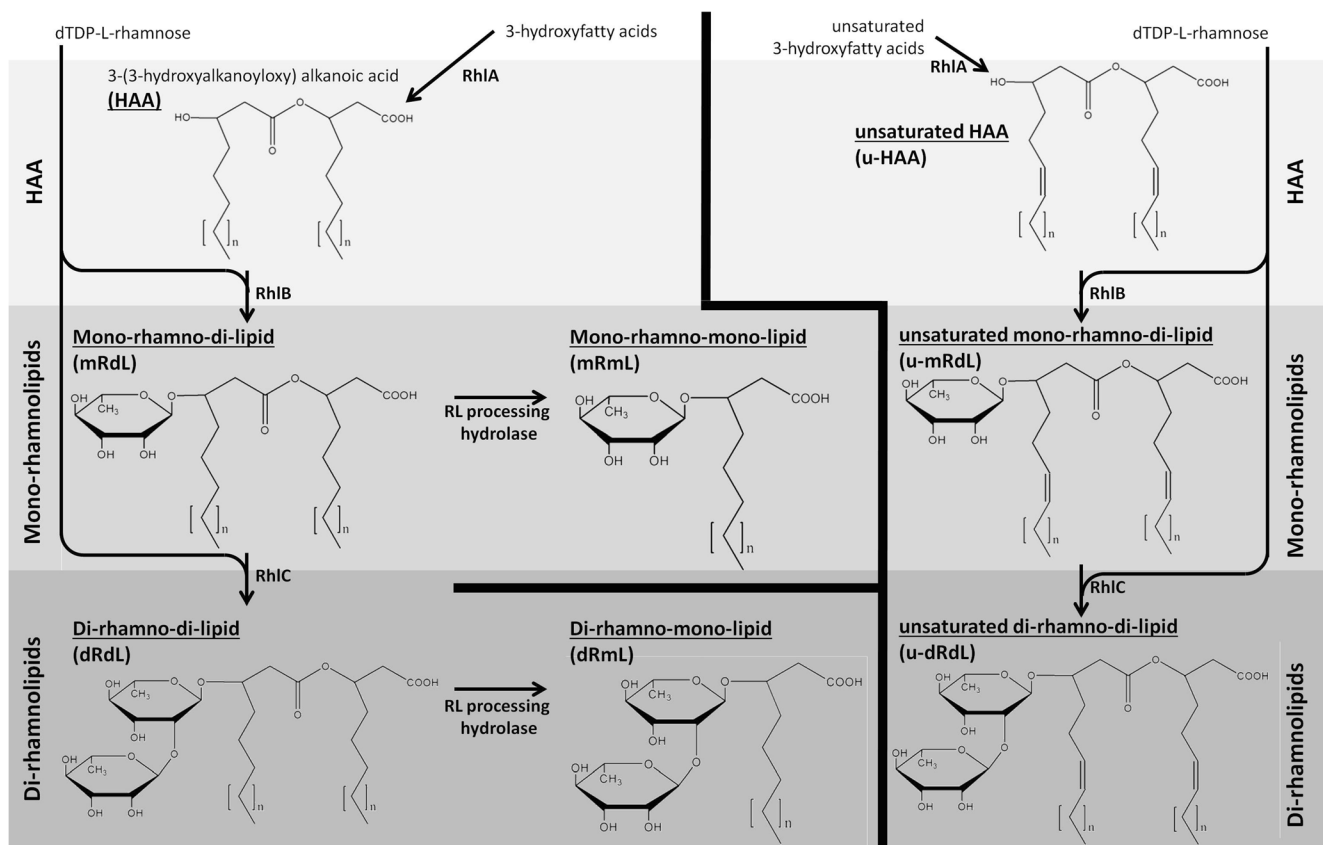


Fig. 1 Chemical structures and biosynthesis of rhamnolipids. The biosynthesis of rhamnolipids occurs in consecutive enzymatic reactions. RhIA synthesizes HAAs by esterification of two 3-hydroxyfatty acids. The rhamnosyltransferases RhIB and RhIC link an HAA molecule first with one and subsequently with a second dTDP-L-rhamnose to generate rhamnolipids. Based on the number of L-rhamnose residues, rhamnolipids are separated into mono- and di-rhamnolipids. Typical

rhamnolipid species containing two 3-hydroxyfatty acids (mono-rhamno-di-lipids and di-rhamno-di-lipids) can be processed by hydrolases to create mono-rhamno-mono-lipids and di-rhamno-mono-lipids containing only one fatty acid chain. Unsaturated HAAs and rhamnolipids are most probably synthesized by using unsaturated 3-hydroxyfatty acids. The fatty acids chain lengths of rhamnolipids typically vary between C_8 and C_{16}

originating from the central carbon metabolism (Fig. 1). Initially, the acyltransferase RhlA catalyzes the esterification of two 3-hydroxyacyl molecules and synthesizes 3-(3-hydroxyalkanoxyloxy)alcanoic acids (HAAs) as typical precursors. The origin of the 3-hydroxyfatty acids and whether they are bound to the acyl carrier protein (ACP) or to coenzyme A (CoA) are controversially discussed. Zhu and Rock (2008) described an *in vitro* HAA production using purified RhlA and 3-hydroxydecanoyl-ACP indicating a preference of RhlA for this intermediate from the fatty acid *de novo* synthesis (Rehm et al. 2001), whereas no HAA formation could be detected using 3-hydroxydecanoyl-CoA as substrate. However, Zhang et al. (2012) described an involvement of the β -oxidation in providing substrates for HAA biosynthesis depending on the used carbon source and they suggested a bypass route to recruit β -oxidation intermediates into the fatty acid *de novo* synthesis by an unknown β -ketoacyl-ACP synthase. Most recently, Abdel-Mawgoud et al. (2014) characterized 3-hydroxyacyl-CoA as the preferred substrate for HAA production using isotope-labeled carbon sources and *rhlYZ* mutant strains. RhlY and RhlZ are responsible for the conversion of *trans*-2-enoyl-CoA from the β -oxidation to *R*-3-hydroxyacyl-CoA. They also postulated a linkage between the fatty acid *de novo* synthesis and the β -oxidation to transfer ACP bound fatty acids to CoA as the central cofactor. The second key enzyme in rhamnolipid biosynthesis, the rhamnosyltransferase I (RhlB), synthesizes mono-rhamnolipids by linking a dTDP-L-rhamnose descending from glucose-6-phosphate (Olvera et al. 1999; Rahim et al. 2000) with an HAA molecule (Ochsner et al. 1994a; Wittgens et al. 2017). Finally, di-rhamnolipids are synthesized by the rhamnosyltransferase II (RhlC) by adding a second molecule of dTDP-L-rhamnose to the preformed mono-rhamnolipids (Rahim et al. 2001). The biosynthesis of mono-rhamno-mono-lipids and di-rhamno-mono-lipids representing a “processed” product lacking one of the fatty acid residues of a complete molecule most probably occurs by two specific but yet unknown α/β -hydrolases, which, taking into account the chain lengths of the substrate esters, reasonably have to be members of the esterase or even lipase family of hydrolases each dedicated to processing of one rhamnolipid species containing two fatty acid chains by removing the second 3-hydroxyacyl (Wittgens et al. 2017).

Different rhamnolipids can already be produced biotechnologically using recombinant genes or biosynthetic operons in the same host organism. Based on their structural diversity and the principle possibility to be targets of enzymatic modifications, rhamnolipids are developing into a platform molecule similar to the biologicals in the pharmaceutical industry. In the near future, processes will be available to produce tailor-made rhamnolipids and to freely choose their number of L-rhamnose sugars in combination with the amount of 3-hydroxyfatty acids, their chain lengths, and the degree of

saturation (or unsaturation) allowing to customize properties for any type of specific applications. In this overview, we describe current opportunities for the biosynthesis of specific rhamnolipids using different microbial producer strains and variations of *rhl*-genes and we discuss appearing future strategies including genetic enzyme evolution, optimization of selective purification technologies, and options for chemical and enzymatic modification of rhamnolipids, which may play promising roles to achieve real tailor-made rhamnolipids.

Rhamnolipids in industrial applications

Through the years, numerous applications were investigated and suggested, in which rhamnolipids can replace or complement “conventional” surfactants or which only become possible through the use of rhamnolipids. Traditional applications are especially their use in laundry or dishwashing detergents and cleaning agents (Nguyen and Sabatini 2011). Because of their abilities to form highly stable emulsions, they are also of great interest for applications in cosmetics and food (Klekner and Kosaric 1993; Velikonja and Kosaric 1993; Maier and Soberón-Chávez 2000; Nitschke and Costa 2007; Sinumvayo and Ishimwe 2015). Large-scale applications are the so called microbial enhanced oil recovery (MEOR), where the use of rhamnolipids can significantly increase the amount of recovered oil (Zhang and Zhang 1993; Wang et al. 2007; Al-Sulaimani et al. 2011; Sharma et al. 2018), and the bioremediation to remove crude oil, heavy metals, and other toxic compounds from contaminated soils and waters (Nguyen et al. 2008; Van Hamme and Urban 2009; Wang and Mulligan 2009; Liu et al. 2018). In the agriculture, rhamnolipids can be used as pesticides due to their antimicrobial properties or they increase the plants’ nutrient uptake (Stacey et al. 2008; Vatsa et al. 2010; Sha et al. 2011; Chen et al. 2017). Another large field of application is the pharmaceutical industry or biomedicine, where rhamnolipids can be used for example to improve the treatment against bacteria, viruses, and fungi or the wound healing (Irie et al. 2005; Remichkova et al. 2008; Stipcević et al. 2006; Piljac et al. 2008; Chen et al. 2017).

Generally, all these applications pose different requirements to the tenside properties relating to the reduction of surface tension, the ability to form highly stable aggregates, foaming, emulsifying, thickening, and solubilizing etc. These characteristics are strongly dependent on the chemical structure, in the case of rhamnolipids, on the numbers of L-rhamnose and 3-hydroxyfatty acids and the chain lengths, so that every rhamnolipid congener possesses different physicochemical and surface-active properties (Howe et al. 2006; Kłosowska-Chomiczewska et al. 2017).

However, all proposed applications so far are based on the usage of rhamnolipids from *P. aeruginosa* species comprising a mixture of mono- and primary di-rhamnolipids with various

congeners, since only rhamnolipids from this human-pathogen were available in larger quantities in the past. Therefore, an enlargement of the available rhamnolipid portfolio, which means the production of tailor-made rhamnolipids including specific species with defined chain lengths of their fatty acids, will be a great advantage and will open up unexpected fields of industrial applications for these remarkable biosurfactants.

Tailor-made rhamnolipids—today's and tomorrow's challenges

Rhamnolipid-producer strains and their specific chain length

The human-pathogen organism *Pseudomonas aeruginosa* is among the most potent and best characterized native rhamnolipid producer and able to yield titers of 40 g/L rhamnolipid in a bioreactor (Müller et al. 2010). One single publication reported rhamnolipid titers of more than 100 g/L by using the specific strain DSM7108 (Giani et al. 1997), but this record was never reproduced successfully (Müller et al. 2011). While *P. aeruginosa* typically synthesizes a heterogeneous mixture of various rhamnolipids species containing fatty acids with a predominant C₁₀ short chain length (sc-RL), bacteria from the genus *Burkholderia* produce long-chain rhamnolipids (lc-RL) with a predominant C₁₄ species. Among these bacteria are prominent human pathogens like *B. pseudomallei* (Häubler et al. 1998, 2003) or species like *B. plantarii* (Andrä et al. 2006; Hörmann et al. 2010) and *B. glumae* (Manso Pajaron et al. 1993; Costa et al. 2011), which are at least plant pathogens and for example cause wilt in many economically important crops and panicle blight in rice constituting an increasing global important problem (Jeong et al. 2003; Ham et al. 2011). However, there are also examples for naturally non or less pathogenic lc-RL producers like *B. thailandensis* (Dubeau et al. 2009; Funston et al. 2016; Elshikh et al. 2017) or *B. kururiensis* (Tavares et al. 2012). However, all *Burkholderia* species described so far failed to achieve productivities comparable with those of *P. aeruginosa* and the highest titer reported was about 1 to 3 g/L (Costa et al. 2011; Díaz De Rienzo et al. 2016; Funston et al. 2016).

Handling known pathogens or at least bacteria with a considerable but undefined pathogenic potential as it exists for “exotic” isolates represents another principle disadvantage of using wild-type organisms for the production of rhamnolipids at an industrial scale, since safety risks and very limited acceptance by customers prevent healthcare applications and the use in cosmetics and foods (Toribio et al. 2010; Müller and Hausmann 2011). Also, non-pathogenic rhamnolipid producer are a poor choice, since the rhamnolipid biosynthesis in all native producer strains is strongly

genetically regulated by a complex regulatory network consisting of the cell-density-dependent *quorum sensing* (Ochsner et al. 1994b; Ochsner and Reiser 1995; Pearson et al. 1997; Nickzad et al. 2015) and probably further signaling mechanisms (Wilhelm et al. 2007; Rosenau et al. 2010; Henkel et al. 2013), which severely hamper an easy and focused overproduction of rhamnolipids in wild-type strains (Toribio et al. 2010). As a consequence, tremendous efforts have been made to genetically optimize native rhamnolipid producers (Grosso-Becerra et al. 2016) or to establish heterologous production of rhamnolipids employing different host organism. The use of *Escherichia coli* proved to be rather limited, because it provides the dTDP-L-rhamnose as precursor for the rhamnolipid biosynthesis only in insufficient trace amounts (Cabrera-Valladares et al. 2006). More successful approaches were based on the use of *Pseudomonas fluorescence* or *Saccharomyces cerevisiae* (Ochsner et al. 1995; Bahia et al. 2018); however, currently, the most promising host is *Pseudomonas putida* (Ochsner et al. 1995; Cha et al. 2008; Wittgens et al. 2011; Cao et al. 2012; Tiso et al. 2016; Beuker et al. 2016a). This non-pathogenic and genetically perfectly accessible strain is meanwhile well established and recombinant strains can produce rhamnolipids at concentrations of up to 15 g/L (Beuker et al. 2016b). Using a heterologous host as a universal genetic and metabolic background further provides the principle opportunity to introduce synthetic and specific biosynthesis pathways for mono-rhamnolipids by expressing the *rhlAB* operon or a mixture of mono- and di-rhamnolipids by expressing a biosynthetic *rhlABC* operon from plasmid constructs allowing to freely choose and optimize appropriate expression levels for example by introducing libraries of synthetic promoters (Wittgens 2013). Furthermore, *P. putida* provides a powerful and flexible metabolic and physiological background allowing the specific biosynthesis of both, sc-RL by expressing genes originating from *P. aeruginosa* as well as of lc-RL using *rhl*-genes from *B. glumae* (Wittgens et al. 2018). Based on the possibility to produce rhamnolipids of different chain lengths in *P. putida* as a platform production strain, it is an attractive option to enlarge the portfolio of rhamnolipids by using synthetic enzymes of other bacterial species (Fig. 2). An interesting class which we want to call very short-chain rhamnolipids (vsc-RL) has been described for *Pseudomonas desmolyticum* containing a predominant species with C₆-C₈ fatty acids (Jadhav et al. 2011), while some thermophilic bacteria of the genus *Thermus* appear to be producers of rhamnolipids which represent extreme counterparts at the opposite scale with very long-chain lengths of rhamnolipids (vlc-RL) with fatty acids up to C₂₄ (Řezanka et al. 2011). Moreover, the increasing availability of microbial genome information allows identification of so far only putative rhamnolipid biosynthetic genes, which may easily be characterized for their products in the recombinant *P. putida* system without the need to establish

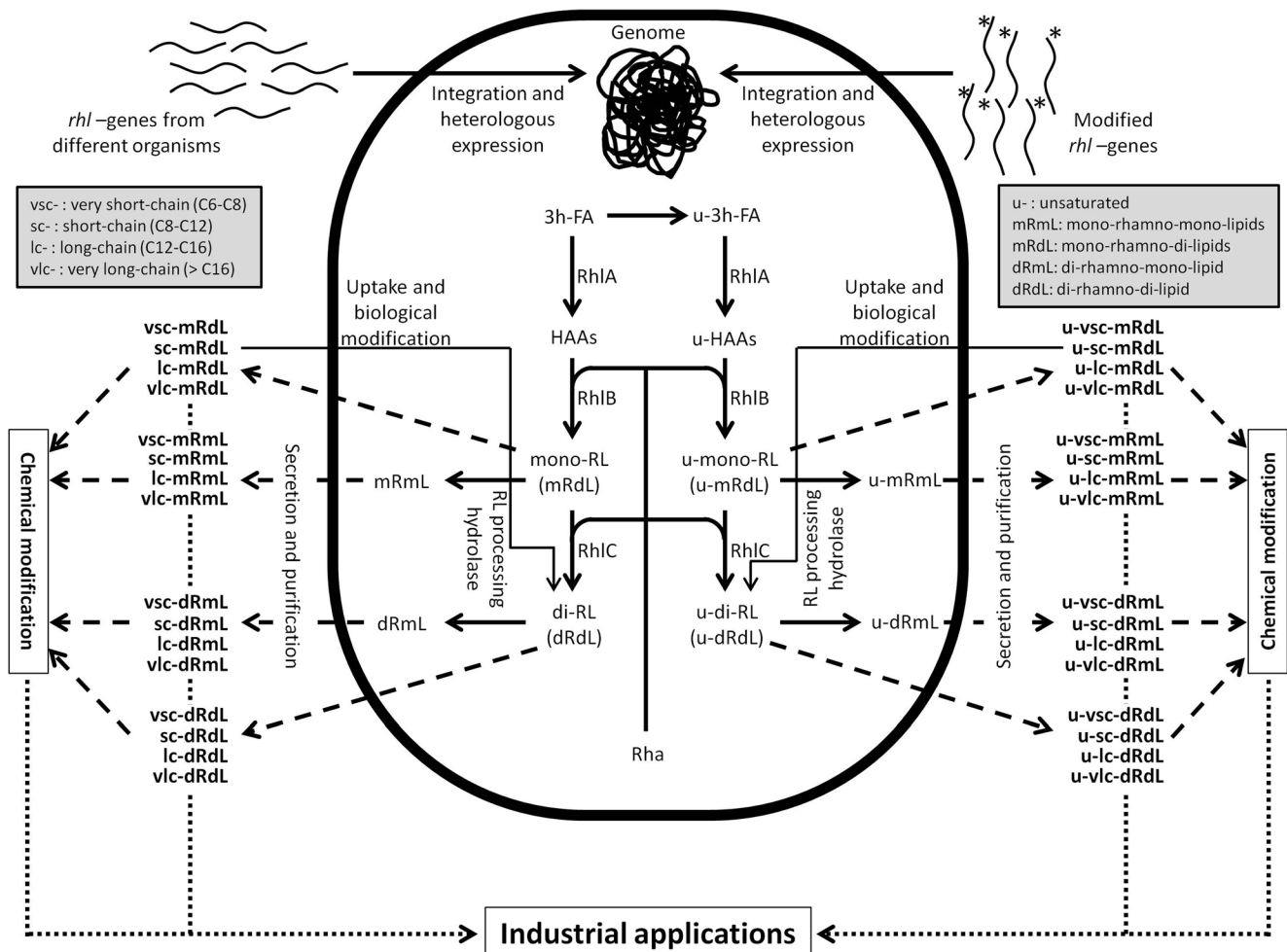


Fig. 2 Strategies for the production of tailor-made rhamnolipids. Native or modified *rhl*-genes from different organisms are introduced in various combinations to determine the numbers of rhamnose residues and the fatty acid chain lengths of the rhamnolipids (RL). Rhamnolipids are synthesized using dTDP-L-rhamnose (Rha) and 3-hydroxyfatty acids (3h-FA) for saturated or u-3h-FA for unsaturated rhamnolipids (u-RL). Mono- and di-rhamno-di-lipids (mRdL and dRdL) can be further processed by specific hydrolases to generate mono- and di-rhamno-mono-

lipids (mRmL and dRmL). Single congeners of very-short-chain (vsc-) to very-long-chain (vlc-) rhamnolipids can be obtained using optimized Rhl enzymes or can be enriched by purification after their secretion. All rhamnolipid congeners can be further customized by chemical modifications. The mRdL (native or chemical modified) can be taken up into the cell to undergo a biological modification by a subsequent conversion to di-RL. Therefore, numerous specialized rhamnolipids will be available for every industrial application

cultivation or optimization of growth conditions of the bacterial host to allow biochemical characterization of their products.

Enzyme design for specificity improvement

Current strategies for the production of rhamnolipids are based on the expression of unmodified wild-type *rhl*-genes and operons of them, which result in biosynthesis of heterogenic mixtures of various rhamnolipid species and congeners. A breakthrough, however, and therefore a more than desirable objective to obtain would be to establish tools to optimize rhamnolipid production towards more homogenous preparations already in the process and in the fermenter with ideally only one specific congener of rhamnolipids (i.e., defined chain lengths) being present in the culture medium. A

powerful technology to optimize biosynthetic enzymes and pathways is the genetic modification of the respective genes or operons by introducing random or semi-rational alterations into their DNA sequences using methods of the so-called directed or laboratory evolution (Arnold 1996; Martínez and Schwaneberg 2013; Packer and Liu 2015; Reetz 2016). For the biotechnology of rhamnolipids, the logical main target to optimize is RhIA, because this acyltransferase has been shown to be responsible for the chain length selectivity in the biosynthesis of HAA by dimerization of two 3-hydroxyfatty acids and thus RhIA defines the chain length of resulting rhamnolipids. In hybrid *rhlAB* operons with genes from *P. aeruginosa* and *B. glumae* exclusively, the origin of *rhlA* determined if the resulting rhamnolipids contained short-chain or long-chain 3-hydroxyfatty acids (Wittgens et al. 2018).

Optimization of the biosynthetic can in principle be done by mutagenesis in pure random approaches to introduce undirected DNA mutations or as more focused or directed approaches after bioinformatic identification and subsequent manipulation of important enzyme regions or domains, which are responsible for the selection and binding of fatty acids. Both approaches include the alternation of single amino acids or the replacement of entire domains to generate mutant variant or chimeric enzymes with parts originating from different organism. The aim of these efforts is to generate an acyltransferase, which has a much higher specificity for specific fatty acid chain lengths to enrich the desired single predominant rhamnolipid congeners to almost pure preparations already during the fermentation or to shift the specificity of the optimized biosynthetic pathway to a specific but so far uncommon or even unrealized chain length in rhamnolipids.

Rhamnolipid modifying enzymes

One further demand when talking about true tailor-made rhamnolipids and the development of molecules with presumably completely new physicochemical properties is to create an option allowing to freely define the number of fatty acid chains in the rhamnolipid molecule. Apart from the typical rhamnolipids containing two 3-hydroxyfatty acids (mono-rhamno-di-lipids and di-rhamno-di-lipids), also mono-rhamno-mono-lipids and di-rhamno-mono-lipids species have been described containing only a single fatty acid chain (Fig. 1; Syldatk et al. 1985b; Abdel-Mawgoud et al. 2010). Using resting cells of the strain *P. aeruginosa* DSM2874 or with naphthalene as the carbon source, the amount of mono-rhamno-mono-lipids and di-rhamno-mono-lipids could be increased up to almost 80% of total rhamnolipid amount (Syldatk et al. 1985a; Déziel et al. 1999). The formation of these rare rhamnolipid species has been reasoned to occur after the known route of rhamnolipid biosynthesis by the Rhl enzymes through removal of one fatty acid chain by a putative rhamnolipid processing hydrolase most probably belonging to the lipase/esterase enzyme family. The formation of mono-rhamno-mono-lipids and di-rhamno-mono-lipids does not occur as a side reaction by the rhamnosyltransferase I, since RhlB only utilize HAAs, but no single 3-hydroxyfatty acids for the biosynthesis of rhamnolipids, as it was shown in experiments with a single *rhlB* expressing strain and HAAs containing spend media (Wittgens et al. 2017). Due to the fact that this processing step appeared only for mono-rhamno-mono-lipids but not for di-rhamno-mono-lipids which could not be found in *P. putida* after heterologous expression of *rhl*-genes, it is reasonable to suspect that *P. putida* harbors only a mono-RL processing hydrolase, whereas *P. aeruginosa* has at least two of these enzymes, which process either mono-RL or di-RL (Wittgens et al. 2017, 2018). The identification of rhamnolipid processing hydrolases is currently carried out

by a systematic co-expression study with more than 40 candidate hydrolases identified in the genomes of *P. putida* and *P. aeruginosa* followed by characterization of their influence on single-chain rhamnolipid formation (Wittgens et al. unpublished). In the case of success, this would be a very easy way to add novel molecules to the portfolio of rhamnolipids and would probably also result in new applications for these novel surfactants (Fig. 2). The identification of further rhamnolipid modifying enzymes is also of importance, which may have similarities to the fungal naringinase from *Aspergillus* sp., which can remove the L-rhamnose residue from di- and mono-rhamnolipids and finally generates HAA and L-rhamnose (Trummeler et al. 2003). The L-rhamnose is of special interest as a fine chemical for cosmetics and food (Linhardt et al. 1989; Mixich et al. 1990; Giani et al. 1997), while HAAs as a molecule closely related to the rhamnolipids show surface-active properties itself and thus also could be interesting for industrial applications (Déziel et al. 2003).

Rhamnolipid congener enrichment via purification

Apart from strategies to increase the biosynthesis of specific rhamnolipid congeners, the production of tailor-made rhamnolipids can also be achieved during the downstream processing by enrichment of specific rhamnolipids using special purification conditions (Fig. 2). While common purification processes are targeted to recover as much rhamnolipids as possible depending on the desired purity (Mixich et al. 1997; Witek-Krowiak et al. 2011; Heyd et al. 2008; Müller et al. 2012), some technical opportunities were introduced for more specific rhamnolipid purifications. Manso Pajarron et al. (1993) used a crystallization process using n-hexane for a specific purification of the Rhl-Rhl-C₁₀-C₁₀ di-rhamnolipids. Most chromatographic separation processes from thin- or thick-layer chromatography to HPLC are generally used for the identification of single pure rhamnolipid species or congeners (Mata-Sandoval et al. 1999; Déziel et al. 2000; Monteiro et al. 2007; Behrens et al. 2016). However, Tiso et al. (2018) recently present a strategy for the purification of rhamnolipids using a liquid chromatography on a larger scale, which performs excellent especially for mono-rhamnolipids. During the elution process using an increasing amount of ethanol, various fractions containing the mono-rhamnolipid congeners Rha-C₈-C₁₀, Rha-C₁₀-C₁₀, Rha-C₁₀-C₁₂, and Rha-C₁₀-C_{12:1}, which successively exited the chromatography column, were collected. Some fractions contained one mono-rhamnolipid congener in almost pure quality, and others were highly enriched with a specific congener or contained mixtures of up to three of these congeners. Probably, this method can also be adapted for the enrichment of other rhamnolipid species and congeners, e.g., those with longer or single fatty acid chains.

Increased production of unsaturated rhamnolipids

Extending the repertoire of the fatty acids would create an enormous increase in rhamnolipid diversity. This includes mono- or polyunsaturated fatty acids which have been described in one or both fatty acids of the final molecule (Abalos et al. 2001; Abdel-Mawgoud et al. 2010; Wittgens et al. 2018). Since unsaturated fatty acids are known to be already present in the rhamnolipid precursors HAAs (Lépine et al. 2002; Déziel et al. 2003), it can be assumed that the unsaturated 3-hydroxyfatty acids serve as substrate for RhIA, too (Figs. 1 and 2). Subsequently, the resulting unsaturated HAAs (u-HAAs) are then—like their normal counterparts with saturated fatty acids—presumably used by the two rhamnosyltransferases RhIB and RhIC for the biosynthesis of unsaturated mono-rhamnolipids (u-mono-RL) and finally di-rhamnolipids (u-di-RL). Under standard cultivation conditions, unsaturated rhamnolipids represent only a minor fraction of total rhamnolipid congeners (Déziel et al. 1999; Haba et al. 2003; Costa et al. 2011), but it is to be expected that especially unsaturated rhamnolipids offer novel surfactant properties due to their unique structure in comparison to saturated rhamnolipids. Consequently, the intracellular amount of unsaturated 3-hydroxyfatty acids has to be increased to finally earn a higher amount of unsaturated rhamnolipids (u-RL). For realizing this idea, genetic and metabolic modifications could be done to ensure an improved expression of specific desaturases to shift the ratio between saturated and unsaturated 3-hydroxyfatty acids. The implementation of exceptional cultivation conditions and/or special feeding strategies may also contribute to increase the amount of available unsaturated fatty acids for the rhamnolipid production. Other possibilities to enrich the u-RL could be possibly achieved by an extensive enzyme optimization of RhIA to improve its specificity towards unsaturated 3-hydroxyfatty acids or by adapting the purification protocol to yield higher amounts of u-RL.

Chemical modification of rhamnolipids

Rhamnolipids can also be produced by chemical synthesis using the concept of hydrophobically assisted switching phase synthesis followed by further chemical modifications (Howe et al. 2006), which reveals totally artificial rhamnolipids containing a third rhamnose residue (tri-rhamnolipids) or a third 3-hydroxyfatty acid chain (mono- and di-rhamno-tri-lipids), uncommon C_4 or C_{18} fatty acids or an exchange of the carboxy against a hydroxy group at the C_1 atom of the former 3-hydroxyfatty acids. These changes in chemical structures effect a dramatic change in the physicochemical characteristics of the rhamnolipids with respect to the formation of aggregates, bioactivity, and fluidity (Howe et al. 2006). While an exclusive chemical synthesis is disproportionate complex and expensive, biological synthesis of rhamnolipids followed by a

chemical modification appears to be very attractive to generate highly customized rhamnolipids for specialized applications (Fig. 2). Except attaching further rhamnose or fatty acid moieties, such modifications could include the insertion or exchange of functional chemical groups to shift the ratio between the hydrophilic and hydrophobic molecule domain and could open up totally unexpected properties. Based on the findings that secreted HAAs and mono-RL can be taken up by the cell again and follow the biosynthesis route towards di-rhamnolipids, which was shown using HAA and mono-RL containing spend media (Wittgens et al. 2017), a chemical modification of these molecules followed by a subsequent biosynthesis of mono- and/or-di-rhamnolipids will be further possible.

Conclusion

Already today, the production of several rhamnolipid species and congeners is possible through the use of different producer strains or more preferable the heterologous expression of their responsible genes to achieve a mixture of either short-chain or long-chain rhamnolipids. By using variations of rhamnolipid synthesizing enzymes, the specific production of mono- and di-rhamnolipids is also possible.

The final steps towards real tailor-made rhamnolipids will be the identification of rhamnolipid processing enzymes for the targeted synthesis of mono- and di-rhamno-mono-lipids as well as an enzyme and purification optimization to enrich specific rhamnolipid congeners containing defined chain length and unsaturations. Further strategies include the enlargement of rhamnolipid portfolio with more chain lengths (vsc- and vlc-RL) and potential chemical modifications.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

Ethical approval This article does not contain any studies with animals performed by any of the authors.

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