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Graef, F, Gordon, S and Lehr, C-M (2016) Anti-infectives in Drug Delivery-Overcoming the Gram-Negative Bacterial Cell Envelope. Current Topics in Microbiology and Immunology, 398. pp. 475-496. ISSN 0070-217X

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1 **Anti-Infectives in Drug Delivery – Overcoming** 2 **the Gram Negative Bacterial Cell Envelope**

3 **Florian Graef, Sarah Gordon and Claus-Michael Lehr**

4 **Abstract** Infectious diseases are becoming a major menace to the state of health
5 worldwide, with difficulties in effective treatment especially of nosocomial infec-
6 tions caused by Gram negative bacteria being increasingly reported. Inadequate
7 permeation of anti-infectives into or across the Gram negative bacterial cell enve-
8 lope, due to its intrinsic barrier function as well as barrier enhancement mediated
9 by resistance mechanisms, can be identified as one of the major reasons for insuf-
10 ficient therapeutic effects. Several *in vitro*, *in silico* and *in cellulo* models are cur-
11 rently employed to increase knowledge of anti-infective transport processes into or
12 across the bacterial cell envelope, however all such models exhibit drawbacks or
13 have limitations with respect to the information they are able to provide. Thus,
14 new approaches which allow for more comprehensive characterization of anti-
15 infective permeation processes (and as such, would be usable as screening meth-
16 ods in early drug discovery and development) are desperately needed. Further-
17 more, delivery methods or technologies capable of enhancing anti-infective per-
18 meation into or across the bacterial cell envelope are required. In this respect,
19 particle-based carrier systems have already been shown to provide the opportunity
20 to overcome compound related difficulties and allow for targeted delivery. In ad-
21 dition, formulations combining efflux pump inhibitors or antimicrobial peptides
22 with anti-infectives show promise in the restoration of antibiotic activity in re-
23 sistant bacterial strains. Despite considerable progress in this field however, the
24 design of carriers to specifically enhance transport across the bacterial envelope or
25 to target difficult to treat (e.g. intracellular) infections remains an urgently needed
26 area of improvement. What follows is a summary and evaluation of the state of the
27 art of both bacterial permeation models and advanced anti-infective formulation
28 strategies, together with an outlook for future directions in these fields.

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76 1. Introduction

77 The effective treatment of infectious diseases by means of anti-infective drug
78 therapies is currently associated with a significant and increasing level of difficul-
79 ty. The incidence of nosocomial infections caused in particular by pathogenic bac-
80 teria is an indicator of this problem. In Germany alone 400 000 – 600 000 hospi-
81 tal-acquired, bacterial infections occur per year; 7500 – 15 000 of such cases are
82 in fact lethal (Akademie der Wissenschaften and Deutsche Akademie der
83 Naturforscher 2013). These statistics are mainly due to the increasing incidence of
84 bacterial resistance to drug therapy, leading to a lack of sufficiently active anti-
85 infective treatment options. Gram negative bacteria are particularly problematic in
86 this respect: as an example, carbapenem-resistant-Enterobacteriaceae (CRE, for
87 abbreviations see Table 1) are capable of evading the action of almost all current-
88 ly-available antibiotics. This dire trend leads to the occurrence of nearly un-
89 treatable infections, with only two ‘last resort’ antibiotics available (tigecycline
90 and colistin) - neither of which are effective in every patient (McKenna 2013). We
91 are therefore faced with a major global challenge with respect to the successful
92 treatment of Gram negative bacterial infections (Wellington et al. 2013).

93
94 While resistance to anti-infective drug therapies is without doubt the primary
95 threat to effective infectious disease treatment, the evolution of resistance is com-
96 pounded by a number of additional factors. Firstly, the successful delivery of anti-
97 infectives to their site of action constitutes a challenging and complicated task,
98 even in the case of a wild type bacterium. This is due to the fact that the bacterial
99 cell envelope, especially that of Gram negative bacteria, works intrinsically as a
100 complex and significant biological barrier to the effective delivery of anti-
101 infective compounds and formulations (see section 2.1, Nelson et al. 2009). The
102 occurrence of several resistance mechanisms such as up-regulation of efflux pump
103 expression, down-regulation or alteration of the expression of transport and chan-
104 nel-forming proteins (e.g. porins) and the production of enzymes (e.g. β -
105 lactamase) within this envelope structure therefore acts to compound an already
106 existing problem for anti-infectives which must penetrate into or entirely through
107 the bacterial envelope in order to reach their site of action (Dever and Dermody
108 1991). As a further factor for consideration, from the so-called golden age of anti-
109 biotic discovery - lasting from the 1950s to the 1960s (Fischbach and Walsh 2009)
110 - until the introduction of the oxazolidinones in 2000, no new anti-infective class
111 was able to successfully reach the market. This low flow within the antibiotic de-
112 velopment pipeline continues today, meaning that the diminishing pool of effec-
113 tive therapies is not being replenished by newly-emerging treatment options.

114 The above described factors contributing towards the problematic nature of effec-
115 tive infection treatment can collectively be regarded as symptoms of a bacterial
116 bioavailability problem. Such a bioavailability issue draws attention to two signif-
117 icant necessities in the area of anti-infective research.

118 The first is the desperate need for new models and strategies to better investigate
 119 and characterize the trafficking of anti-infectives into or across the bacterial cell
 120 envelope, in order to increase collective knowledge of the envelope as a barrier
 121 which needs to be overcome. As a second need, novel anti-infective candidates
 122 with new modes of action are required, as are new delivery strategies which enable
 123 effective penetration into or across the Gram negative bacterial cell envelope.
 124 The current document will attempt to address aspects of both research needs, outlining
 125 the state of the art in each area as well as potential or actual future research
 126 directions. Specific emphasis will continue to be given to Gram negative bacteria
 127 as particularly problematic pathogens.
 128

129 **Table 1.** Abbreviations, in alphabetical order.

AMPs	Antimicrobial peptides
CRE	Carbapenem-resistant Enterobacteriaceae
DUV	Deep ultraviolet
EPIs	Efflux pump inhibitors
IM	Inner membrane
LB	Langmuir-Blodgett
LS	Langmuir-Schaefer
LPS	Lipopolysaccharides
MD	Molecular dynamics
MIC	Minimal inhibitory concentration
MRSA	Methicillin-resistant <i>Staphylococcus aureus</i>
OD	Optical density
OM	Outer membrane
OMPs	Outer membrane proteins
PaBN	Phenylalanin arginyl β -naphthylamine
PC	Phosphatidylcholine
PE	Phosphatidylethanolamine
PG	Phosphatidylglycerol
PL	Phospholipid
PS	Periplasmic space
QSARs	Quantitative structure-activity relationships
QSI	Quorum sensing inhibitor
RND	Resistance-nodulation-cell division
SLBs	Supported lipid bilayers
SLNs	Solid lipid nanoparticles

130

131

132 **2. The Gram Negative Bacterial Cell Envelope as a** 133 **Bioavailability Barrier to Anti-Infectives**

134 As already mentioned, the intrinsic structure of the Gram negative bacterial cell
135 envelope presents a significant barrier to the successful delivery of anti-infectives.
136 Therefore a brief overview of the major structural components of the cell enve-
137 lope, including details of envelope modifications responsible for the occurrence
138 and evolution of resistance, is first given here.
139
140

141 ***2.1 The Intrinsic Bacterial Barrier***

142
143 The Gram negative bacterial cell envelope can be divided into three major parts,
144 each of which constitutes a significant obstacle to anti-infective penetration (Fig-
145 ure 1). Starting from the bacterial cytoplasm and proceeding outwards, the inner
146 membrane (IM) represents the first layer of the envelope barrier. It consists of a
147 phospholipid (PL) bilayer mainly composed of phosphatidylethanolamine (PE),
148 phosphatidylglycerol (PG) and cardiolipin, with incorporated transmembrane pro-
149 teins and lipoproteins. The periplasmic space (PS) with the peptidoglycan cell wall
150 constitutes the second layer. Peptidoglycan, a polymer of repeating disaccharides,
151 is responsible for the maintenance of cell shape and structure. The surrounding ar-
152 ea is a highly viscous, aqueous compartment, densely packed with proteins
153 (Mullineaux et al. 2006). Furthermore defense mechanisms including enzymes
154 (e.g. β -lactamase) are also located within this space. The outer membrane (OM)
155 forms the third envelope sub-structure. The membrane itself is asymmetric in na-
156 ture, being subdivided into a PL- (mainly PE) containing inner leaflet, and an out-
157 er leaflet mainly consisting of lipopolysaccharide (LPS). LPS in turn is composed
158 of the so-called Lipid A, a phosphorylated glucosamine with six to seven acyl
159 chains which anchors LPS to the inner leaflet of the OM; a core oligosaccharide;
160 and the outermost portion of the molecule, the O-antigen. LPS acyl chains are
161 mainly saturated, which confers a gel-like structure on the molecule. Association
162 of gel-like LPS molecules within the outer leaflet is additionally strengthened by
163 the presence of divalent cations being present in the surrounding medium, which
164 neutralize the negative charge of LPS phosphate groups. This further contributes
165 to the formation of a viscous structure which limits the permeation of hydrophobic
166 compounds, including many anti-infectives and detergents. The OM also incorpo-
167 rates outer membrane proteins (OMPs) such as the porins (e.g. OmpF), which
168 span the entire OM. Porins allow for and control the passive diffusion of hydro-
169 philic compounds, for example β -lactam antibiotics, with a size limit for such
170 permeation of approximately 700 Dalton (Silhavy et al. 2010). The combination of

171 LPS and porins is therefore responsible for the strong permeability limiting prop-
 172 erties of the OM, which acts to restrict the permeation of hydrophobic as well as
 173 hydrophilic compounds.

174

175 In addition, efflux transporters, most commonly belonging to the resistance-
 176 nodulation-cell division (RND) superfamily, feature prominently within the cell
 177 envelope. Sub-structures of these transporters are present in each of the three ma-
 178 jor envelope subsections (for example AcrB-AcrA-TolC and MexB-MexA-OprM
 179 where subunits are located in the IM-PS-OM) meaning that the pump as a whole
 180 spans the entire envelope structure. Such efflux pumps are responsible for the ac-
 181 tive excretion of compounds (e.g. anti-infectives) in an energy-dependent manner
 182 (Kumar and Schweizer 2005).

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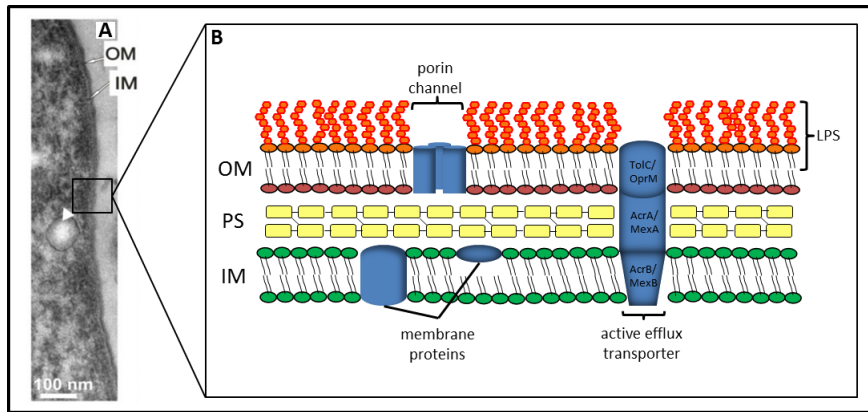
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197 **Fig. 1. Transmission electron microscopy image of the cell envelope of *Legionella dumoffii***
 198 **(A, adapted from Palusinska-Szys et al. 2012) and schematic overview of the Gram nega-**
 199 **tive bacterial cell envelope, highlighting the most important structural components (B): the**
 200 **inner membrane (IM) incorporating transmembrane and lipoproteins, the periplasmic**
 201 **space (PS) housing the peptidoglycan cell wall, and the asymmetric outer membrane (OM)**
 202 **with its lipopolysaccharide (LPS) outer leaflet and porins. The general structure of an ef-**
flux transporter is also shown.

203 **2.2 The Role of the Envelope in Mediating Resistance Mechanisms**

204 In principle we can differentiate between three major, antimicrobial resistance
205 strategies of bacteria: i) degradation of anti-infective compounds by bacterial en-
206 zymes, ii) protection of anti-infective targets by e.g. structural or expression modi-
207 fication, and, of most relevance to the current document, iii) alteration of the cell
208 envelope barrier function (Davin-Regli et al. 2008), which will here be further de-
209 scribed. Modifications to barrier properties result in an increased efflux in combi-
210 nation with a reduced uptake of anti-infectives, leading to inadequate intracellular
211 anti-infective levels. The increased efflux of anti-infectives occurs due to an over-
212 expression of efflux pumps (as mentioned above), which have a broad range of ac-
213 tion and as such, are able to mediate resistance to a variety of anti-infective classes
214 (Tenover 2006). Resistance in the context of reduced uptake arises due to bacterial
215 modification of OMP copy numbers or conformation, and/or alterations in LPS
216 structure. The expression of OMPs, in particular porins, can be down-regulated
217 within the OM structure, or can alternatively be completely abrogated (Nikaido
218 and Rosenberg 1981). The latter case is for example known from *Escherichia coli*
219 isolates, which are resistant against cefoxitin due to an absence of the major OmpF
220 porin channel (Tenover 2006). Furthermore, bacteria can modify the structure of
221 their porins as a strategy to prevent anti-infective entry. Such structural modifica-
222 tion can for example consist of a narrowing of the porin channel, which decreases
223 the permeation of larger, hydrophilic compounds (De et al. 2001). The structure of
224 LPS molecules can additionally be altered, in order to facilitate an increase in the
225 barrier properties of the OM. The most effective mechanism by which LPS altera-
226 tion leads to increased barrier function is via a reduction of negative net charge,
227 leading to a reduced permeation of cationic anti-infectives (Kumar and Schweizer
228 2005).

229 **2.3 Implications for Anti-Infective Drug Delivery**

230 Clearly, the unique structure of the Gram negative bacterial cell envelope, together
231 with the ability of bacteria to alter the structure and resulting functional activity of
232 various envelope components, creates a considerable hurdle to the cellular perme-
233 ation of anti-infectives. The development and application of models in order to fa-
234 cilitate an increased understanding of envelope permeation processes as well as
235 the investigation of new anti-infective delivery approaches are therefore intro-
236 duced and discussed below, as two research strategies required in order to address
237 the issue of inadequate anti-infective permeation.

238 **3. Strategies to Combat Intrinsic Difficulties/Bacterial** 239 **Resistance Mechanisms Related to Anti-Infective Transport**

240 ***3.1 Models for Characterization of Drug Transport Across the*** 241 ***Bacterial Cell Envelope***

242 As detailed above, the Gram negative bacterial cell envelope works as an effective
243 biological barrier to the successful delivery of anti-infectives to their target site.
244 The fundamental existing barrier properties of the envelope are also able to be fur-
245 ther increased through the up-regulation of resistance mechanisms. Therefore, in
246 addition to well-established and commonly used efficacy testing approaches, it is
247 of considerable interest to obtain a greater and more detailed level of knowledge
248 regarding rate, extent and mechanisms of the processes by which anti-infectives
249 permeate (actively or passively) across the envelope. Models which mimic the cell
250 envelope and so enable provision of such information can thus help to facilitate
251 the rational design of anti-infective agents, capable of overcoming intrinsic deliv-
252 ery difficulties/bacterial resistance mechanisms. Such models could additionally
253 contribute useful information to early anti-infective drug discovery processes. The
254 currently existing and employed models of the envelope structure, used in order to
255 provide permeation and transport information, will be described in the following
256 section. The needs which are unmet by these existing models will also be men-
257 tioned.

258 **3.1.1 Electrophysiology Studies**

259
260 Electrophysiological studies are applied to obtain information about the transport
261 of anti-infectives through single porins. The principle of electrophysiology is
262 based on the reconstitution of such channel forming proteins - mostly OmpF, as
263 the main porin responsible for the passive OM permeation of many anti-infectives
264 such as the β -lactams and quinolones - into planar lipid bilayers (Figure 2A). Such
265 bilayers mostly consist of phosphatidylcholine (PC), and are made for example by
266 bursting porin-containing proteoliposomes across an aperture within a solid sup-
267 port (Kreir et al. 2008). An external voltage is then applied across the aperture-
268 spanning membrane, which causes an ion flux through the inserted porin channel.
269 The strength of the resulting current allows for the provision of information re-
270 garding the channel structure and its functional properties in a variety of exper-
271 imental settings (e.g. ranges of salt concentration, pH). The technique is addition-
272 ally able to be automated (Mach et al. 2008a) and can be further optimized for
273 example by applying the porin-containing supported lipid bilayer system into glass
274 nanopipets (Gornall et al. 2011). In addition to providing information on porin

275 structure and function, anti-infective passage kinetics through the bilayer-
276 reconstituted porins can be studied by the use of high resolution ion-current fluctu-
277 ation analysis (Pages et al. 2008). In general, the permeation of anti-infective
278 compounds through porins is detected by a decrease in current due to an occlusion
279 of the porin channel by the permeating compound. Electrophysiological studies
280 therefore facilitate determination of the direct translocation of charged molecules
281 through porin channels. They additionally allow for evaluation of the interaction
282 of anti-infectives with the constriction zone of porins (the narrowest part of the
283 porin channel, which mediates the size-wise exclusion of molecule permeation
284 across the OM) in particular. The relative affinity of different anti-infective com-
285 pounds for specific porins can also be elucidated using electrophysiological stud-
286 ies – for example, enrofloxacin has been shown to have the strongest recorded af-
287 finity for OmpF. Combining the information obtained from electrophysiology
288 studies with molecular dynamic (MD) simulations enables the identification of the
289 specific anti-infective pathway across porin channels (Nestorovich et al. 2002;
290 Danelon et al. 2006; Mach et al. 2008b). This further contributes to understanding
291 the occurrence of porin structure-related resistance mechanisms. Again taking the
292 case of enrofloxacin, a relatively simple modification to the OmpF channel (a sin-
293 gle-point mutation in the constriction zone) has been shown by such a combina-
294 tion electrophysiology-MD approach to lead to a drastic decrease in anti-infective
295 translocation (Mahendran et al. 2010).

296 **3.1.2 Liposome Based Assays**

297
298 Assays utilizing liposomes as artificial membrane models are also employed to in-
299 vestigate permeabilization effects of anti-infectives, as well as the extent of anti-
300 infective permeation into such model membranes. The existing liposome-based
301 approaches can be basically differentiated into two major categories. On one hand
302 the so-called liposome swelling assays or leakage studies must be mentioned.
303 These approaches are based on uni- or multilamellar vesicles made of a single PL
304 species (e.g. PC, PE) with or without incorporated porins (Nikaido and Rosenberg
305 1983), PL mixtures, or PL-LPS (rough (without O-antigen) or smooth LPS (with
306 O-antigen)) mixtures, utilized in an attempt to mimic the OM components. Poly-
307 mers or fluorescent dyes are further incorporated into the central aqueous com-
308 partment or within the bilayers of such liposomes. This provides for an indirect
309 detection method for permeation of the analyzed anti-infective, by means of track-
310 ing changes in optical density (OD), or via fluorescence analysis. As an example
311 of such a setup, the anti-infective of interest is mixed with polymer-containing
312 liposome dispersions (which often also have inserted porins) under isosmotic con-
313 ditions. If the anti-infective is not able to penetrate into the vesicles, the measured
314 OD will remain unaltered. If however the anti-infective compound is able to per-
315 meate into the liposomes, a swelling of the vesicles occurs due to an influx of wa-
316 ter, caused by the presence of an osmotic gradient as mediated by the permeating

317 anti-infective compound. Anti-infective permeation and liposome swelling can
318 ultimately result in bursting of the liposomes, leading to a release of the incorpo-
319 rated polymer, which is then detectable as a decrease in OD (Figure 2B). Lipo-
320 some swelling or leakage assays also facilitate study of direct membrane
321 disrupting effects of proteins (e.g. lamB or surfactant protein A) and antimicrobial
322 peptides (AMPs, e.g. aurein 1.2) on artificial membrane systems (Luckey and
323 Nikaido 1980; Kuzmenko et al. 2006; Fernandez et al. 2012; Fernandez et al.
324 2013). Of considerable current interest with respect to such assays is the use of
325 liposomes which imitate more closely Gram negative bacterial membrane compo-
326 sitions. In this respect, liposomes made of LPS or PL-LPS mixtures as a more re-
327 alistic OM mimic are also often used for swelling or leakage studies, or to investi-
328 gate PL-LPS interactions within the model membrane. Such studies could help to
329 improve understanding of the OM organization or modulation of the OM during
330 the development of resistance mechanisms (D'Errico et al. 2009; Kubiak et al.
331 2011).

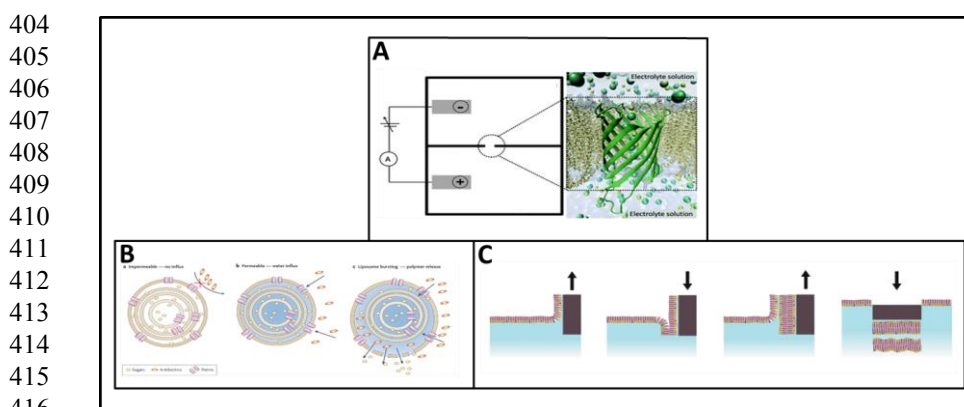
332
333 On the other hand, liposomes can be used to study the accumulation and uptake of
334 anti-infective compounds in liposomal membranes by direct analysis of anti-
335 infectives themselves. In this respect, anti-infectives of interest, which are either
336 auto-fluorescent or fluorescently labeled, are incubated with liposomes. The rela-
337 tion between anti-infective structural characteristics/modifications and interaction
338 with the artificial liposomal membrane can then be studied, as can anti-infective
339 uptake into such model membranes. This is achieved by determining the accumu-
340 lation of anti-infectives within the lipid membrane or their uptake into the vesi-
341 cles, analyzed via nucleic magnetic resonance spectroscopy or fluorescence mi-
342 croscopy (Rodrigues et al. 2003; Ries et al. 2015).

343 **3.1.3 Langmuir Trough Based Approaches**

344
345 Mono- and/or bilayers prepared from PL and/or LPS in various combinations are
346 also employed as models in anti-infective research. Such approaches facilitate in-
347 vestigation of the organization and interactions within artificial membrane systems
348 and, with respect to permeation, study of the influence of antimicrobial proteins or
349 peptides in particular on membrane integrity. In general, these experimental set-
350 ups were originally developed to study interactions within mammalian-mimicking
351 membrane structures, or interaction of external entities with such structures. Imita-
352 tion of the double bilayer nature of the Gram negative bacterial envelope, as well
353 as the OM, with particular emphasis being placed on its structural components and
354 asymmetric nature, is however of considerable interest in the current application
355 of such approaches.

356
357 Preparation of lipid monolayers on the surface of water or buffer is achieved by
358 using a Langmuir film balance or trough, whereas lipid bilayers are mostly pre-

359 pared as supported lipid bilayers (SLBs) on silicon - less often mica or gold - sur-
360 faces as solid supports. SLBs in turn can be prepared from lipid vesicles which are
361 fused onto the solid support, via Langmuir-Blodgett (LB) or a combination of LB
362 and Langmuir-Schaefer (LS) deposition techniques (Peetla et al. 2009). An ad-
363 vancement of SLBs resulting in the production of more bacteriomimetic models is
364 represented by the additional incorporation of floating lipid bilayers. Production of
365 such a model involves combining three vertical LB depositions with one horizon-
366 tal LS deposition (Figure 2C), resulting in the formation of a lipid bilayer which
367 floats at a distance of 2-3 nm from the supported lipid bilayer (Charitat et al. 1999;
368 Fragneto et al. 2012). Langmuir-derived lipid bilayers are often prepared from PC
369 or PC-PG mixtures (in order to mimic the negative charge of bacterial mem-
370 branes) and used to study the membrane insertion potential of AMPs, as well as
371 their disordering and transmembrane pore forming abilities. Results show a higher
372 affinity and disruptive effect on models composed of negatively charged PLs
373 (Fernandez et al. 2012; Fernandez et al. 2013). Langmuir-produced monolayers
374 made of PG with or without incorporated OmpF have also been used to investigate
375 the interaction of antibacterial proteins such as colicins with the OM, as well as
376 their pathway across the OM (Clifton et al. 2012). As mentioned above, many
377 such Langmuir-based models additionally take the impact of LPS as the major
378 OM structural component into account. In one instance, stable Langmuir mono-
379 layers were prepared at the air-liquid interface using rough strain LPS. Such a
380 model provided valuable information about LPS structure at the air-liquid inter-
381 face, and therefore constitutes a further step to a more accurate model of the OM
382 (Le Brun et al. 2013). In a further approach, a realistic mimic of the OM structure
383 was prepared by combining a PC bilayer deposited via LB on a solid support (rep-
384 resenting the inner OM leaflet) with an overlying rough strain LPS bilayer (outer
385 OM leaflet), introduced via LS deposition. This model successfully mimics the
386 asymmetric nature of the OM, and was first employed to describe the molecular
387 mechanisms of the well-known OM destabilization effect occurring as a result of
388 the removal of divalent cations from surrounding media (Clifton et al. 2015).
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417 **Fig. 2. Schematic overview of *in vitro* approaches to produce bacterial membrane models,**
 418 **for the characterization of drug transport. (A) The experimental setup for electrophysiology**
 419 **studies to investigate anti-infective transport through porins, incorporated in planar li-**
 420 **pid bilayers (adapted from Modi et al. 2012 with permission from The Royal Society of**
 421 **Chemistry);(B) the principle of a liposome swelling assay, employed to assess permeabiliza-**
 422 **tion processes mediated by anti-infective compounds (reprinted from Pages et al. 2008 by**
 423 **permission from Macmillan Publishers Ltd: [Nature Reviews Microbiology] Pages et al.**
 424 **2008, copyright 2008); (C) the Langmuir-based preparation procedure for preparing float-**
 425 **ing lipid bilayers (from Fragneto et al. 2012, with kind permission from Springer Sci-**
 426 **ence+Business Media) is additionally depicted .**

427 **3.1.4 *In Silico* Methods**

428
429 Besides the so-far described *in vitro* models, *in silico* approaches are also utilized
 430 to investigate the impact and interaction of various lipid species within simulated
 431 bilayers (which in turn may have a bearing on anti-infective permeability). They
 432 are furthermore applied to inform the development of membrane models which
 433 more closely and accurately reflect the structure and components of the IM and
 434 OM. *In silico* approaches may also be employed to determine the affinity and/or
 435 translocation of anti-infectives with or across porin channels, as alluded to previ-
 436 ously (see 3.1.1). They may additionally be used to screen compounds for anti-
 437 infective activity based on quantitative structure-activity relationships (QSARs),
 438 defined via topological descriptors (numerical values correlating chemical proper-
 439 ties with biological activity (Mayers 2009)) and physicochemical parameters. In
 440 one example, MD simulations have been used to mimic the IM – consisting of PE
 441 and PG in a 3:1 ratio, closely reflecting the *in cellulo* composition – in order to
 442 evaluate intra-bilayer PL interactions. Conducted simulations showed that interac-
 443 tions between these specific PLs are mainly based on H-bond formation and chief-
 444 ly occur between PE and PG, less often between only PE molecules and almost
 445 never between PG molecules alone. As a consequence, the presence of PG within
 446 the membrane leads to a decrease in PE headgroup protrusion and a reduced mo-

447 tion along the artificial membrane; this results in an enhanced membrane stability,
448 leading to a strengthening of the IM permeation barrier (Murzyn et al. 2005; Zhao
449 et al. 2008). *In silico* studies which even more accurately reflect the PL composi-
450 tion of the IM have also been conducted. As a first step bilayers consisting of CL
451 alone were simulated, to determine its biophysical role within membranes via
452 evaluation of its charge-dependent lipid packing (Lemmin et al. 2013). Further,
453 IM models which additionally include heterogeneous lipids, exhibiting different
454 acyl chain lengths and cyclopropane rings, can be considered as yet further im-
455 provements towards an accurate IM mimic (Pandit and Klauda 2012).

456
457 The OM has also been simulated in various *in silico* studies, starting with models
458 consisting of LPS alone and followed by simulations using a combination of a PL
459 inner leaflet and LPS outer leaflet to more accurately reflect the asymmetric OM
460 structure. These models have largely been used to study properties such as interac-
461 tions between LPS molecules in the OM, the stabilization effect of divalent cations
462 on the membrane structure (and resulting barrier properties), the effect of elec-
463 troporation on the barrier function of protein-free, asymmetric membrane
464 structures and the impact of OM enzymes as well as proteins on membrane integ-
465 rity (Lins and Straatsma 2001; Wu et al. 2014; Piggot et al. 2011). Simulations of
466 the OM as well as the IM have additionally been employed to study the interaction
467 of AMPs with such artificial systems, highlighting the way in which AMPs are
468 able to pass through and disrupt the bacterial envelope – firstly due to a self-
469 promoted uptake across the OM, and subsequently as a result of disruption of the
470 IM via the formation of micelle-like aggregates (Berglund et al. 2015). MD simu-
471 lations have further been used to determine the molecular and rate-limiting inter-
472 actions occurring during anti-infective permeation through porins on an atomic
473 scale. Such studies allow for a better understanding of the translocation pathway
474 and estimated permeation time of anti-infective compounds, as well as the way in
475 which modifications in the porin channel constriction zone can affect and reduce
476 anti-infective permeation (Mach et al. 2008b; Mahendran et al. 2010; Singh et al.
477 2012; Hajjar et al. 2010). *In silico* screening has furthermore been employed to de-
478 fine QSARs of anti-infectives by evaluating the impact of physicochemical prop-
479 erties such as lipophilicity and molecular weight on anti-infective activity (O’Shea
480 and Moser 2008; Cronin et al. 2002). The definition of topological descriptors to-
481 gether with the performance of linear discriminant analysis further enable the at-
482 tainment of discriminant functions, which allow for differentiation between active
483 and non-active anti-infectives. Such functions can subsequently be applied to
484 screen compound libraries for new lead structures showing promising anti-
485 infective activity. (Murcia-Soler et al. 2003; Murcia-Soler et al. 2004).

486

487

488 3.1.5 *In Cellulo* Approaches

489

490 *In cellulo* approaches which give information about permeability processes by fa-
491 cilitating the determination of intra-bacterial accumulated anti-infectives are of
492 enormous interest, as such approaches of course constitute the most accurate rep-
493 resentation of the envelope structure. Within the scope of these approaches, a large
494 number of bacteria are usually incubated with the anti-infective compound of in-
495 terest. This is followed by washing to remove remaining extracellular and/or ad-
496 herent compound, lysis of the bacterial cells and subsequent quantification of the
497 amount of intracellular drug. LC-MS/MS methods are generally employed in order
498 to quantify what often proves to be a very low level of anti-infective comp-
499 ound. Such quantification methods are also frequently applied to examine the
500 permeation of various different anti-infectives tested on distinct bacterial strains
501 (Cai et al. 2009; Davis et al. 2014). As such an approach is possibly error-prone
502 due to the potential for inadequate removal of extracellular/adherent anti-infective,
503 as well as the population-based rather than single-cell nature of the quantification
504 process, approaches with direct single-cell resolution based on deep ultraviolet
505 (DUV) fluorescence or the combination of a DUV fluorescence microscope with a
506 synchrotron beamline have been employed. These approaches allow for quantify-
507 ing fluorescent or fluorescently-labeled compounds, and for example have been
508 used to compare anti-infective uptake in wildtype and mutant/resistant bacterial
509 strains (Pages et al. 2013; Kascakova et al. 2012). It must be mentioned here how-
510 ever that such an approach is still limited to an ‘inside/outside’ distinction of anti-
511 infective location, and determination of anti-infective permeation with any higher
512 degree of spatial resolution remains extremely difficult.

513 3.1.6 Shortcomings of Existing Models and Future Directions

514

515 The current modeling approaches discussed in this section help to get a better un-
516 derstanding of permeation processes across various sub-structures of the Gram
517 negative bacterial cell envelope. However, drawbacks and unmet needs can be
518 mentioned for each of the above categories of models available to date. As a gen-
519 eral comment, the *in vitro* and *in silico* modeling approaches described here most-
520 ly focus on producing or simulating structures which approximate either the IM or
521 OM, and not the cell envelope as a whole – or, in the small number of cases where
522 the overall envelope structure is approximated, the resulting model is often tai-
523 lored to the examination of intra-membrane interactions or causes of membrane
524 disruption. In addition, many such models consist of a phospholipid composition
525 which deviates from that found *in cellulo*, and, while it has been mentioned that
526 attempts are made in some cases to represent the asymmetric structure of the OM
527 in models of this membrane component, many models still neglect to feature this
528 important aspect. Furthermore, due to considerable difficulties associated with

529 scale and resolution, the vast majority of models to date allow for a qualitative
530 prediction of anti-infective permeation and transport, rather than for quantification
531 of such processes. *In cellulo* approaches where multiple planktonic cells rather
532 than single cells are used have proven very useful in order to provide detailed and
533 in some cases, quantitative insights into permeation processes; however, as men-
534 tioned, such methods generally rely on an average permeation within a bacterial
535 population to draw conclusions regarding single cell permeation. Furthermore,
536 current *in cellulo* approaches do not allow for evaluation of the specific extent of
537 anti-infective permeation into the envelope structure. Hence, models which mimic
538 the overall envelope in terms of their PL composition and structure, which are de-
539 signed to explicitly investigate and quantify transport and permeation processes,
540 and which are able to discriminate between active and passive permeation of anti-
541 infective compounds and delivery systems in both a spatially- and kinetically- re-
542 solved manner are desperately needed.
543

544 ***3.2 Improving Bacterial Bioavailability using Advanced Delivery*** 545 ***Strategies***

546 In addition to employment and development of bacterial permeation models, a di-
547 rect research focus is also placed on anti-infective therapies themselves in an at-
548 tempt to overcome the cell envelope structure, achieve an increase in intra-
549 bacterial drug concentrations, and, in doing so, improve bioavailability in bacteria.
550 In this respect, the search for new anti-infective drug candidates as well as the in-
551 vestigation of alternative approaches to antibiotic therapy continues, as presented
552 and discussed in detail elsewhere. Additional strategies, such as the re-formulation
553 of currently available anti-infectives with permeation-enhancing excipients or the
554 application of advanced carrier systems, also represent promising research direc-
555 tions. Such strategies are particularly valuable in instances where bacterial bioa-
556 vailability issues cannot be directly resolved by the introduction of new molecules,
557 or through modification of existing anti-infective structures using medicinal chem-
558 istry approaches. As such, a number of currently investigated advanced formula-
559 tion strategies are presented below.

560 **3.2.1 Efflux Pump Inhibitors**

561
562 As mentioned in section 2.1, efflux in wild-type as well as drug resistant Gram
563 negative bacteria is mainly mediated by the RND superfamily of efflux transport-
564 ers. The use of formulations incorporating efflux pump inhibitors (EPIs) which are
565 able to interact with such pumps, decreasing anti-infective efflux and subsequently

566 leading to higher intracellular drug levels, therefore represents a useful strategy to
567 restore anti-infective potency. The inhibition of pumps as mediated by EPIs can be
568 described as occurring by two major modes of action. One can be classified as
569 biological, in which EPIs act to decrease the expression of the pumps themselves
570 by inhibiting transcription or translation via antisense oligonucleotides. A pharma-
571 cological mechanism represents the second mode of action, in which EPIs operate
572 through direct interaction with the pump affinity site, acting for example to col-
573 lapse the efflux energy or to competitively or non-competitively inhibit the efflux
574 process (Van Bambeke et al. 2010). EPIs can be further differentiated into inhibi-
575 tors with a narrow spectrum of activity, being used as diagnostic tools to detect ac-
576 tive efflux, or inhibitors with a broad spectrum of action, which could be poten-
577 tially useful in clinical settings. The further ability of EPIs to restore the activity of
578 simultaneously applied anti-infectives (being visible for example in a decrease of
579 minimum inhibitory concentration (MIC)) makes them an even more promising
580 approach as a means to increase anti-infective bacterial bioavailability. Examples
581 of known EPIs include analogues or lead structures of tetracyclines or fluoroquin-
582 olones, arylpiperidine and phenothiazine derivatives as well as peptidomimetics
583 (Pages and Amaral 2009). Peptidomimetics with phenylalanine arginyl β -
584 naphthylamine (PA β N) as lead compound represent the first efflux inhibiting
585 group which showed an effective blocking of fluoroquinolone efflux in a RND
586 over-expressing strain of *Pseudomonas aeruginosa* (Renau et al. 2002). Currently,
587 EPIs are used primarily as *in vitro* screening tools; their potential use in the clinic
588 is still under investigation due to the existence of several challenging factors. The
589 primary obstacle to the use of EPIs in a clinical setting is that of toxicity - most of
590 the known EPIs to date need to be used in high concentrations, which may lead to
591 possible toxic effects. Their use in combination with anti-infectives also demands
592 the absence of interactions between the EPI and the anti-infective compound, as
593 well as comparability in their pharmacokinetic profiles.

594 **3.2.2 Antimicrobial Peptides**

595
596 The use of the previously mentioned AMPs, either alone or especially in synergis-
597 tic combinations with conventional anti-infectives, represents a further strategy to
598 overcome anti-infective bioavailability problems by enhancing their transport
599 across the bacterial cell envelope. AMPs can be further used as stimuli for the in-
600 nate immune system, or as endotoxin-neutralizing agents (Gordon et al. 2005).
601 AMPs in themselves are generally small cationic peptides which can be derived
602 from humans, bacteria, or even viruses (Yount and Yeaman 2004). Their mode of
603 action as bioavailability-potentiating agents is primarily based on the initiation of
604 bacterial membrane perturbation, an effect mainly mediated by electrostatic inter-
605 actions between the positively charged peptide and the negatively charged LPS of
606 the OM. Such interactions lead to a destabilization of the OM by displacing pre-
607 sent divalent cations, which facilitates penetration of AMPs and any other associ-

608 ated compounds through the OM structure. Following this self-promoted uptake
609 through the OM, the further association of AMPs with the outer leaflet of the IM
610 followed by the formation of micelle-like aggregates finally leads to a rupture of
611 the bacterial envelope. This allows either for bacterial killing, or for an even fur-
612 ther enhanced uptake of the simultaneously administered anti-infective. A non-
613 destructive action of AMPs, facilitated by binding to DNA or RNA, is also further
614 described (Hancock 1997; Hancock and Chapple 1999). Several studies report the
615 potentiating effect of AMP–anti-infective combinations, resulting in an increased
616 anti-infective activity even in hard to treat bacterial strains and biofilm forming
617 species. In this respect, the synergistic effect of AMPs together with a wide range
618 of anti-infectives with different modes of action could be demonstrated by the ef-
619 fective treatment of *Clostridium difficile* (Nuding et al. 2014). Furthermore, com-
620 binations of AMPs with anti-infectives have shown to result in an increased activi-
621 ty against the biofilm formation of Methicillin Resistant *Staphylococcus aureus*
622 (MRSA), and have demonstrated a successful inhibition of *Pseudomonas fluo-*
623 *rescens* (Mataraci and Dosler 2012; Naghmouchi et al. 2012). Hence, AMPs rep-
624 resent a promising approach to improve anti-infective bioavailability in Gram
625 negative as well as Gram positive bacteria, as well as in particularly problematic
626 bacterial infections involving biofilm formation. Several clinical trials, especially
627 for topical application of AMPs to human subjects, are ongoing, but are associated
628 with several challenges. In addition to the potential for toxic effects which could
629 for example result from non-specific membrane disruption, the fast degradation
630 and short half-life of AMPs constitute the main obstacles to generalized use (Park
631 et al. 2011). The incorporation of AMPs into particulate carrier systems could po-
632 tentially help to reduce or overcome these difficulties – such approaches are fur-
633 ther discussed below.

634 3.2.3 Nanoparticulate Drug Carriers (“Nanopharmaceuticals”)

635
636 Anti-infectives as free drugs may show low water-solubility, unfavorable pharma-
637 cokinetics, side effects or stability problems (Xiong et al. 2014) – all factors which
638 intrinsically create problems for penetration into and effective action within bacte-
639 ria. The incorporation of anti-infectives into carrier systems, such as liposomes,
640 polymeric nanoparticles, solid lipid nanoparticles (SLNs) or dendrimers may help
641 to reduce the impact of such characteristics, and as such presents several ad-
642 vantages compared to the use of free anti-infectives. In light of their typical size
643 range, these carriers are nowadays also regarded as nanomaterials or nanoparti-
644 cles, and with respect to their specific application also referred to as nanomedi-
645 cines or nanopharmaceuticals.

646
647 The incorporation of anti-infectives into nanoparticulate carrier systems may al-
648 low for a high drug loading in some cases, facilitating an increase in effective drug
649 solubility; a masking of undesirable drug effects; a tailoring of anti-infective

650 pharmacokinetics; or a directly increased permeability. Modifications for example
651 to the particle surface may allow for further improvements, such as a targeted de-
652 livery. One of the first examples of a nanoparticulate anti-infective formulation
653 which was granted access to the market is a liposomal formulation of amphotericin
654 B – this formulation remains widely used in clinical settings due to the exhibi-
655 tion of many of the above mentioned advantages (Walsh et al. 1998). Polymeric
656 nanoparticles are also extensively investigated as carriers for anti-infective drugs
657 in several labs around the globe. The protective function of particulate carriers and
658 the possibility for co-loading is also a considerable advantage with respect to de-
659 livery of readily-degraded compounds like AMPs. The possibility to incorporate
660 more than one anti-infective compound into particulate carriers, or to combine anti-
661 infective loaded carriers with particles of known antimicrobial substances like
662 gold or silver, constitutes a further advantage to the use of such delivery systems
663 (Huh and Kwon 2011). Significant progress in the development of nanotechnology-
664 based approaches specifically to treat bacterial infections has been made in re-
665 cent years, leading to the existence of several sophisticated carrier systems. For
666 example, Trojan horse systems made of nanoparticles tagged with folic acid have
667 been shown to mediate an increased activity of the incorporated anti-infective
668 vancomycin in resistant *Staphylococcus aureus* (Chakraborty et al. 2012). The
669 linkage of penicillin G to surface functionalized silica nanoparticles has also
670 shown a restored anti-infective activity even in formerly resistant MRSA (Wang et
671 al. 2014).

672
673 Infection-activated delivery systems are another promising approach, being for
674 example composed of chitosan-modified gold nanoparticles which are attached to
675 liposomes or polymeric triple-layered nanogels. Substances like toxins or enzymes
676 which are present in the local environment of a bacterial infection work as a trig-
677 ger for release of carrier-incorporated anti-infective, allowing for the reduction of
678 potential side effects resulting from systemic anti-infective administration as well
679 as the achievement of high local drug concentrations at the site of infection
680 (Pornpattananankul et al. 2011; Xiong et al. 2012). Anionic liposomes have also
681 been successfully used to incorporate and deliver plasmid DNA and antisense oli-
682 gonucleotides into inner bacterial compartments in order to inhibit gene expres-
683 sion in resistant strains (Meng et al. 2009; Fillion et al. 2001). Recently, an SLN-
684 based formulation was successfully used to incorporate and deliver high amounts
685 of a novel quorum sensing inhibitor (QSI), which act as anti-virulence factors by
686 interfering with bacterial cell-cell communication via action on intracellular tar-
687 gets (Miller and Bassler 2001). SLNs with incorporated QSI showed a prolonged
688 release, mucus penetrating ability and an effective delivery to the pulmonary re-
689 gion, as well as an enhanced anti-virulence activity against *Pseudomonas aeru-*
690 *ginosa* as compared to the compound alone (Nafee et al. 2014). As these examples
691 illustrate, innovative delivery strategies (along with the search for and optimiza-
692 tion of novel anti-infective targets and compounds) offer the potential for over-
693 coming bacterial absorption problems.

694 3.2.4 Evaluation of Current Status and Future Directions

695
696 The combination of EPIs and AMPs with conventional or even new anti-infectives
697 may result in a reduction of undesirable intrinsic anti-infective properties as well
698 as an increased bacterial permeation, leading to higher intracellular drug levels
699 and so an enhanced bacterial bioavailability. Furthermore, carrier systems are able
700 to provide a means of circumventing compound related difficulties, such as unfav-
701 orable pharmacokinetics, and to achieve high intracellular drug levels. In this
702 manner such advanced formulation strategies may act to increase the bioavailabil-
703 ity of anti-infectives, and for this reason continue to be employed and developed.
704 The treatment of intracellular infections as well as the specific development of
705 permeability enhancing carriers constitutes an important direction of future appli-
706 cations.

707 4. Conclusion and Outlook

708 This paper has aimed to give an overview of current difficulties in the treatment of
709 infectious diseases, in particular those caused by Gram negative bacteria. In this
710 respect, the significant bioavailability problems of anti-infective compounds - de-
711 fined as an inadequate delivery to their (mainly intra-bacterial) sites of action -
712 largely stem from the complex nature of the cell envelope and its formidable bar-
713 rier function. This barrier function may be even further enhanced by the evolution
714 of resistance mechanisms. Numerous models - *in vitro*, *in silico* as well as *in cellu-*
715 *lo* in nature - may be used in order to increase understanding of permeation pro-
716 cesses into or across the envelope, as well as to enable evaluation of how the cell
717 envelope in its entirety or as its individual sub-structures acts as a permeation lim-
718 iting factor. However, a paucity of quantitative approaches which accurately mim-
719 ic the overall envelope structure has to be mentioned, meaning that obtained in-
720 formation may lack comprehensiveness. Therefore, new permeation models which
721 more accurately represent the various structural components of the Gram negative
722 bacterial cell envelope, and which are further able to provide quantitative, kinet-
723 ically- and spatially-resolved permeation data are desperately needed. Such mod-
724 els would also ideally allow for discrimination between active and passive
725 transport processes, and would be applicable as high throughput screening meth-
726 ods in early drug discovery. With respect to anti-infective compounds themselves,
727 the combination of EPIs or AMPs with conventional anti-infectives presents a
728 promising strategy in overcoming bacterial bioavailability problems, enabling the
729 restoration of anti-infective activity even in resistant strains. Particulate delivery
730 systems may similarly facilitate an increase in anti-infective bioavailability, by
731 acting to overcome drawbacks related to the free drug itself; such carrier systems
732 may additionally facilitate a targeted delivery of anti-infectives. Anti-infective
733 formulations which are designed to particularly increase the permeation or

734 transport of anti-infectives into or across the bacterial cell envelope, or to treat
735 particularly problematic bacteria (such as those which reside within mammalian
736 cells) are still urgently needed however, and would constitute a further significant
737 improvement in anti-infective therapy.
738

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