

Development of gut-restricted antibiofilm peptides to target gastrointestinal biofilms

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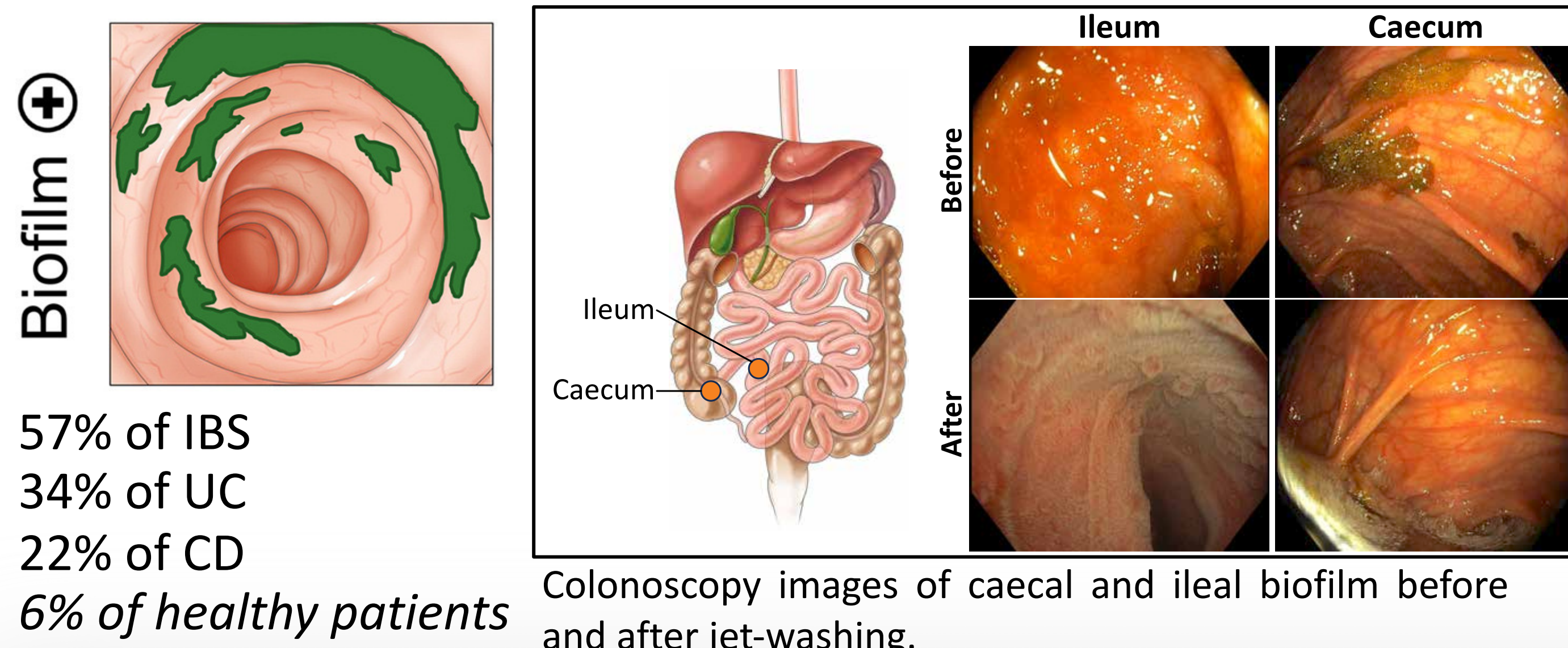
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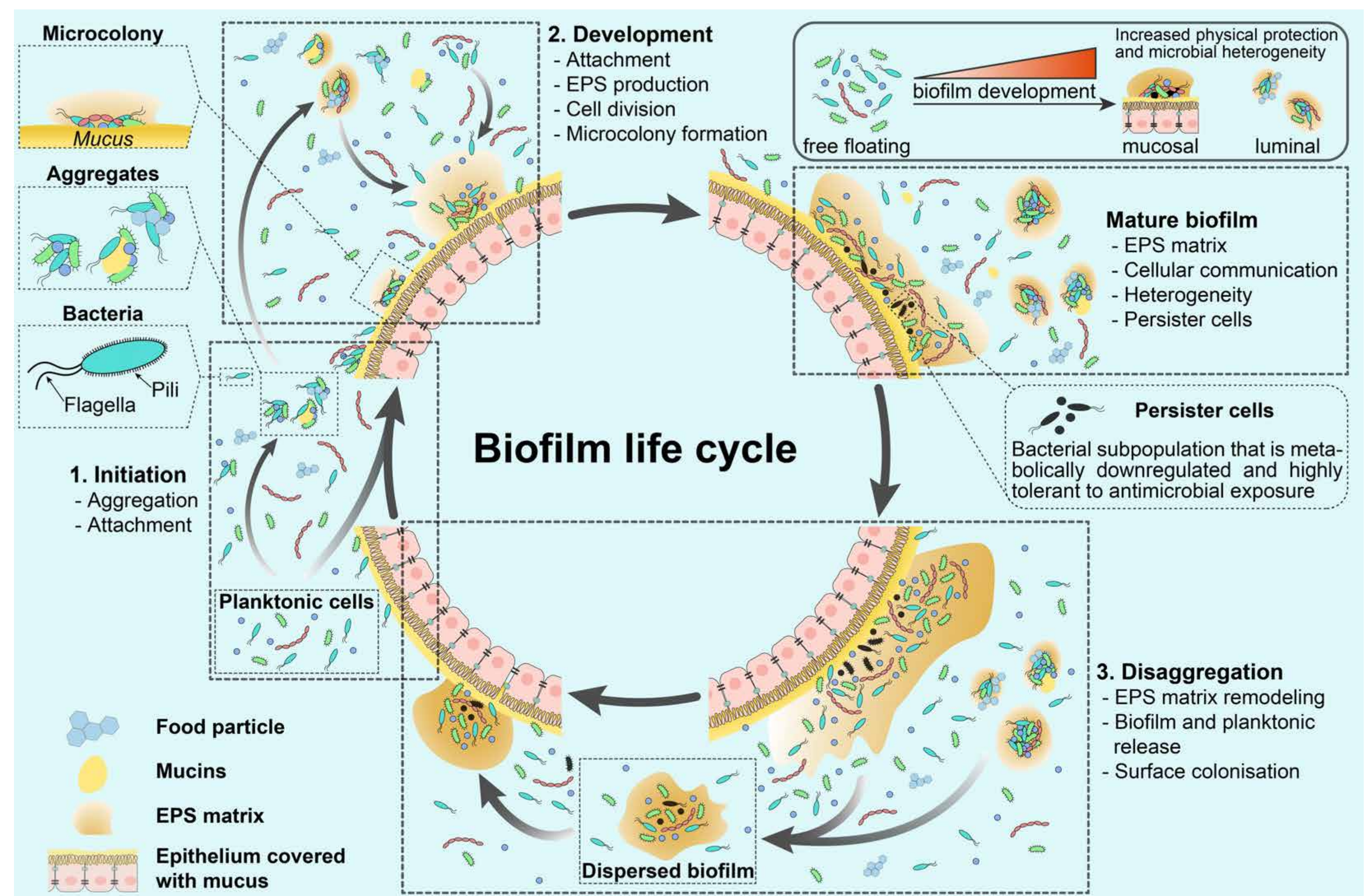
Introduction

Inflammatory bowel diseases (IBD) and irritable bowel syndrome (IBS) are gastrointestinal (GI) disorders that together affect 10–15% of the Western population. A recent study identified mucosal biofilms in 57% of IBS, 34% of ulcerative colitis (UC) and 22% of Crohn's disease (CD) patients compared with 6% in the control group.^[1] No drug is on the market that selectively targets biofilms and conventional antibiotics are mostly ineffective, leaving jet-washing during endoscopy the only way to remove gut biofilms.

This work explores the potential of antimicrobial peptides (AMP) as antibiofilm agents and investigates chemical strategies to improve potency and gut-stability. Gut-stable antibiofilm peptides are promising therapeutic candidates to target mucosal biofilms in patients with GI disorders, as their large size prevents systemic uptake and reduces side effects by keeping them gut-restricted when orally administered.



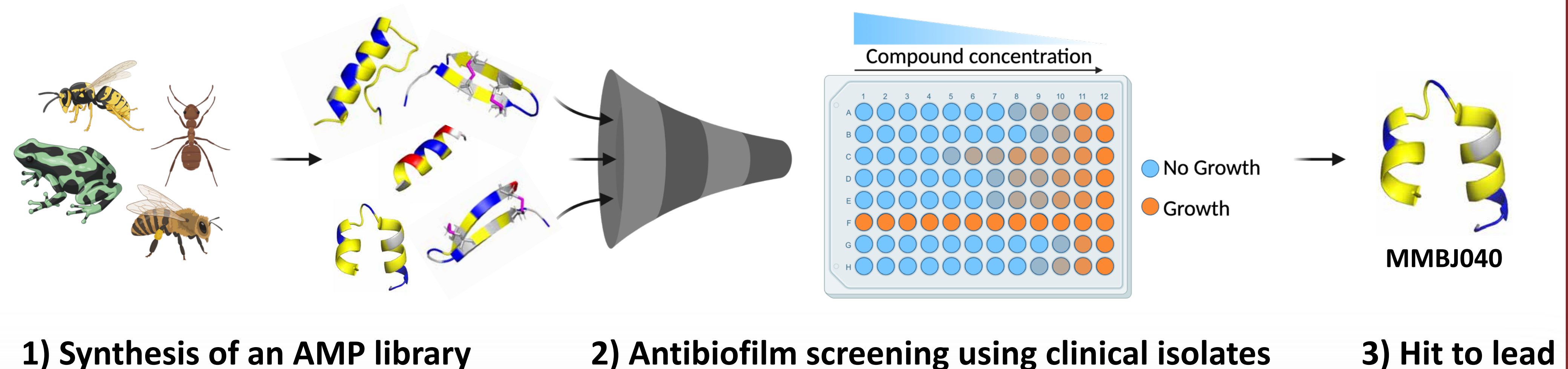
Therapeutic target



The biofilm life cycle. The four stages of the biofilm life cycle are: initial adhesion, early development, biofilm maturation and biofilm dispersal. Therapeutic approaches focus on these stages of the biofilm life cycle, aiming to (i) inhibit bacterial surface adhesion, (ii) inhibit biofilm formation, and (iii) eradicate mature biofilms.

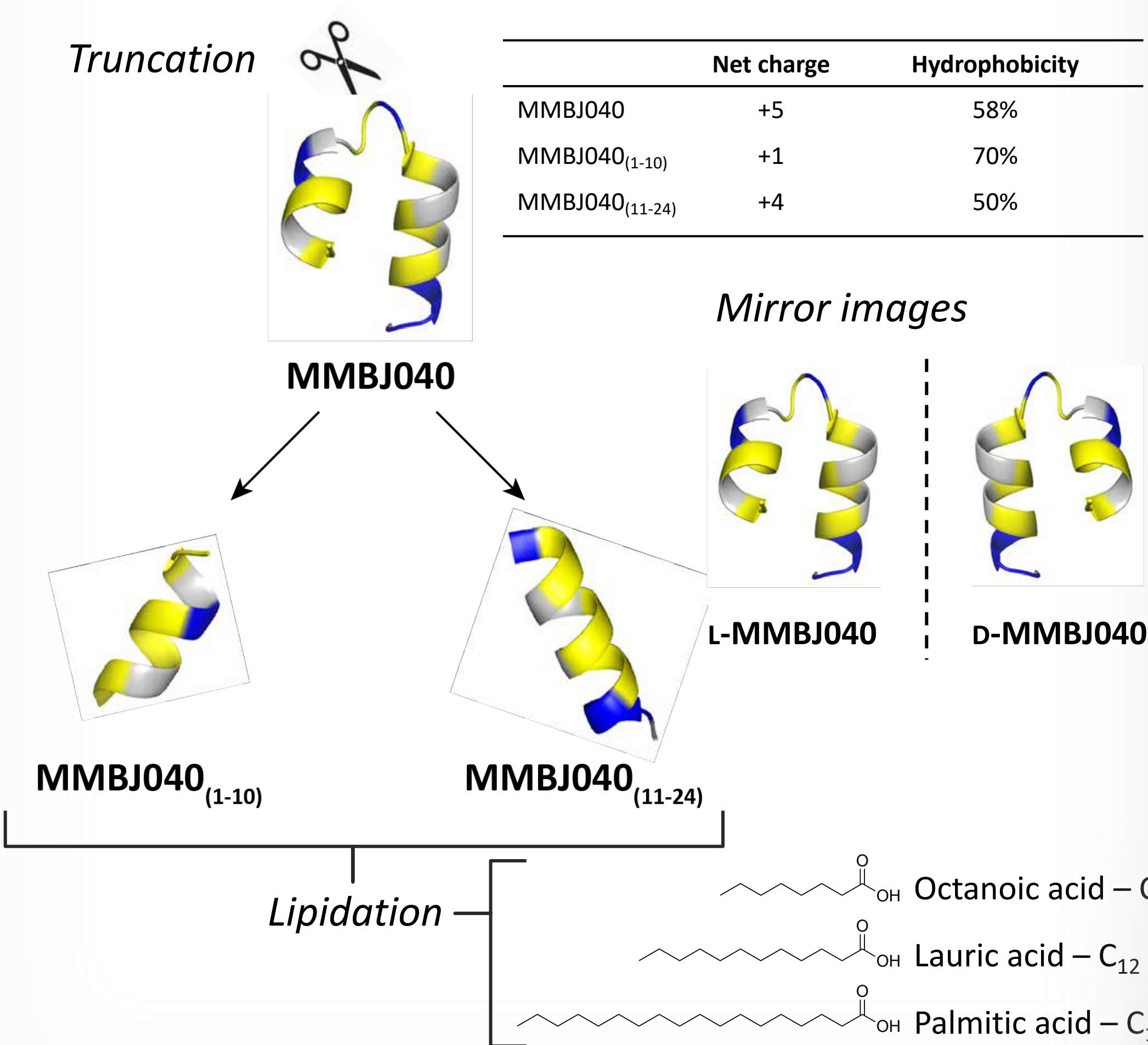
Approach

We have chemically synthesized a medium-size AMP compound library (>40 peptides), including peptides produced by ants, bees, frogs, and wasps. By screening of our library we identified 16 hits with promising antibiofilm activity. Out of these hits, we selected MMBJ040 to conduct a systematic structure-activity relationship (SAR) using diverse medicinal chemistry approaches.

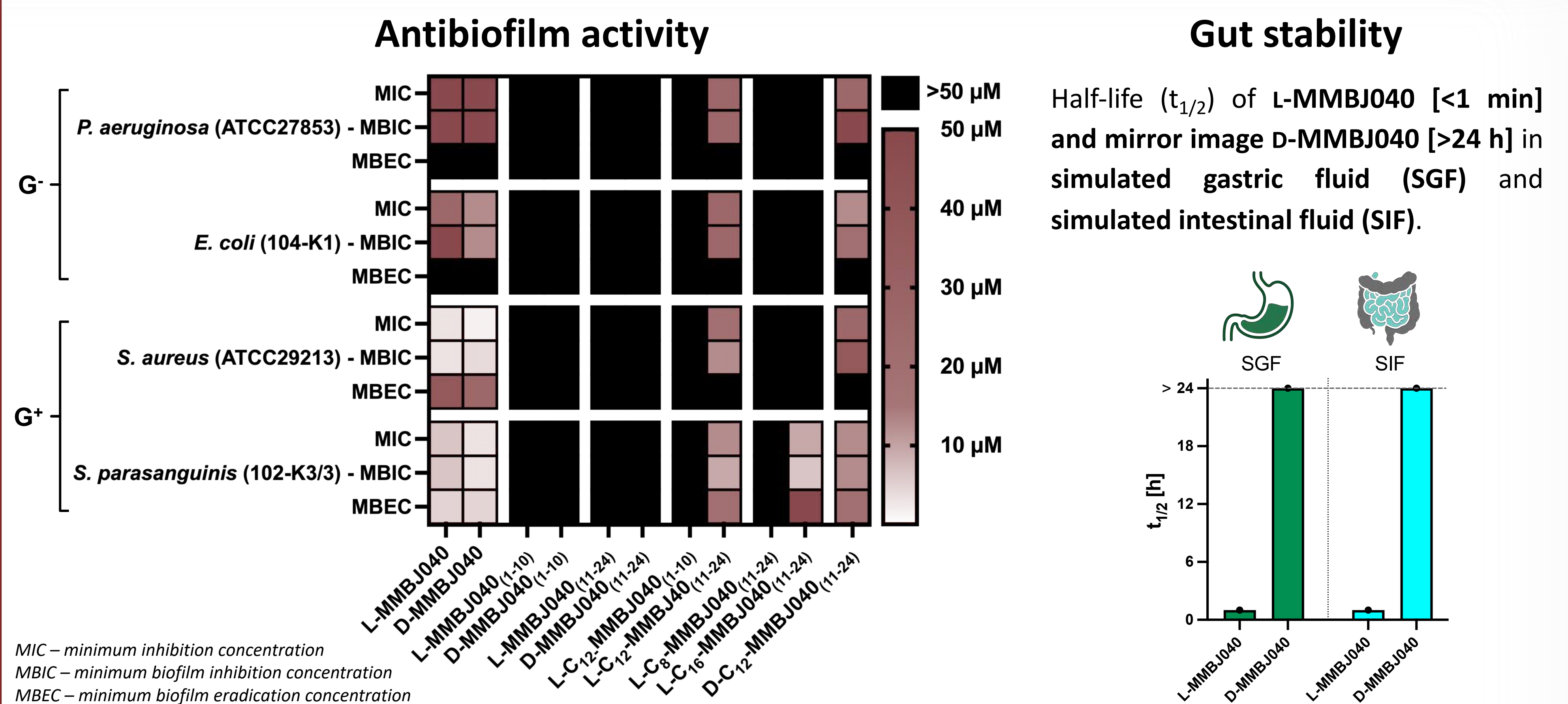


Study design

We applied Chemical strategies such as truncation, lipidation and the establishment of mirror images and evaluated the minimum inhibition concentration (MIC), minimum biofilm inhibition concentration (MBIC), and minimum biofilm eradication concentration (MBEC) using two clinical isolates from biofilm-positive patients (*Streptococcus parasanguinis* (Gram-positive (G⁺)) and *Escherichia coli* (Gram-negative (G⁻))) and two biofilm-forming type strains (*Staphylococcus aureus* (G⁺) and *Pseudomonas aeruginosa* (G⁻)). Further, we determined the gut stability of our best-performing candidates using simulated gastric fluid (SGF) and simulated intestinal fluid (SIF) assays.



Results



Truncation: Our MMBJ040 SAR exploration revealed that the two truncated α -helical domains MMBJ040₍₁₋₁₀₎ and MMBJ040₍₁₁₋₂₄₎ had no antimicrobial or antibiofilm activity. **Lipidation:** The lipidation of MMBJ040₍₁₁₋₂₄₎ reestablished antimicrobial activity but did not increase the antibiofilm activity, and C₁₂ fatty acid conjugation led to the best result; lipidation of MMBJ040₍₁₋₁₀₎ did not display antimicrobial activity. **Mirror images:** All-D versions of active all-L parent peptides were also active. D-MMBJ040 has the most potent antibiofilm activity.

In conclusion, we developed the gut-stable peptide D-MMBJ040 with potent antibiofilm activity against G⁺ biofilm-forming bacteria. Moreover, we identified that fatty acid substitution of hydrophobic domains in antimicrobial peptides could serve as an attractive approach to lower the production costs of antimicrobials.

Acknowledgement

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