



**HAL**  
open science

# Endocrine microbiology: A transdisciplinary approach of the human physiology

Marc G.J. Feuilleley, Olivier Lesouhaitier

## ► To cite this version:

Marc G.J. Feuilleley, Olivier Lesouhaitier. Endocrine microbiology: A transdisciplinary approach of the human physiology. *Current Opinion in Endocrine and Metabolic Research*, 2025, 38, pp.100570. <10.1016/j.coemr.2025.100570>. <hal-05552122>

**HAL Id: hal-05552122**

**<https://hal.science/hal-05552122v1>**

Submitted on 13 Mar 2026

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons CC BY-NC-ND 4.0 - Attribution - Non-commercial use - No Derivative Works - International License

## **Endocrine Microbiology : A transdisciplinary approach of the human physiology**

Marc G.J. Feuilloy and Olivier Lesouhaitier

« Endocrine Microbiology » is the term used by Mark Lyte to designate the study of the effects of hormones, neurohormones and cytokines on microorganisms, and particularly bacteria, and subsequently the effect of hormone like-molecules produced by bacteria on eukaryotic cells [1]. This concept was faced to high psychological resistance, essentially due to the scientific distance between endocrinology and microbiology which are generally taught in independent cursus. Then, microbiologists have usually a limited knowledge of human physiology and endocrinologists rarely know that bacteria are complex organisms capable to communicate through a multitude of mechanisms. Recent developments in this field illustrate the importance of studying the interactions between mammals and bacteria using signaling molecules. For example, hepcidin, a hormone produced by the liver and involved in iron homeostasis, was identified 20 years ago as a potent antibacterial agent against certain bacterial species [2]

As explained in the present issue by A. Lukmann *et al.* and M. Boujnane *et al.* in their articles on the effects of catecholamines on bacteria, this is well illustrated by the first observation of the impact of epinephrine on bacterial growth in 1930 that was initially attributed to an unknown effect on the human physiology, then to an activity of catecholamines as secondary siderophores (which is actually essential at high concentrations), before being finally recognized as a direct action through specific bacterial sensors. Bacteria are present in many different regions of the human body where they organize as communities designated as microbiota, in intimate interaction with the host physiology. The best known, and more studied, is the intestinal microbiota which is now considered as a real organ with its mean  $10^{14}$  microorganisms for a total mass estimated to 1.5 kg and catecholamines have been particularly investigated in this context. However, host-bacteria communication is not operating in a single sense. Indeed, bacteria can also produce biogenic amines and metabolites, such as phenylacetyl acid, which can interfere with the human physiology through activation of adrenergic receptors and this phenomenon can have important clinical consequences in gut. It is important to note that close to their role in iron captation (Perraud *et al.*, 2022), the exposition of numerous bacterial species to

catecholamines modifies the pathogenicity of the bacteria, as Boujnane *et al.*, exposed in their review, and today this side effect is not taken into account in therapy using drugs that modified catecholamines release in patients. The skin microbiota is the second of the human body. Cutaneous bacteria, such as *Cutibacterium* (former *Propionibacterium*) *acnes*, have been shown to also respond to epinephrine and norepinephrine providing a potential explanation to the link between stress and acne. As reviewed by Feuilloley *et al.*, other bacterial species are capable of detecting skin neurohormones such as Substance P and Calcitonin-Gen Related Peptide, two neuropeptides known for their key role in skin neurogen inflammation (inflammation generated in the absence of exogenous stimulation by the local release from nerve terminals). These observations were leading to a new vision of neurogenic inflammation including the cutaneous microbiota in a regulatory loop since, as in the gut, skin associated bacteria are synthesizing molecules such as histamine, glutamine or GABA which can be detected by eukaryotic receptors and probably molecules such as ClpB a structural bacterial analog of  $\alpha$ -melanocyte stimulating hormone ( $\alpha$ MSH), whose systemic activity has been deeply investigated [4]. Skin is presenting specific niches, such as the hair follicle, where bacteria are exposed to hormones and neurotransmitters released in at the level of the bulge, a structure particularly rich in capillary vessels and nerve terminals. That can explain the sensitivity of bacteria such as *C. acnes*, *Staphylococcus aureus* and *Staphylococcus epidermidis* to atrial natriuretic peptide (ANP) and C-type natriuretic peptide. Natriuretic peptides have a central role in another microbiota, the respiratory tract microbiota, as detailed by Lesouhaitier *et al.* Bacteria are rarely living as planktonic cells but generally as aggregates or biofilms in which they organize in a complex extracellular matrix similar to a conjunctive tissue. In lungs, biofilm formation by opportunistic pathogens, such as *Pseudomonas aeruginosa*, *Acinetobacter baumani* or *S. aureus*, causes a shift in the severity of pathologies including cystic fibrosis and chronic obstructive pulmonary disease (COPD). Natriuretic peptides play a key role by controlling the switch between the planktonic and biofilms behaviors of *Pseudomonas aeruginosa* and probably other species, Since bacteria embedded in a biofilm are much less sensitive to antibiotics, this observation offers a new strategy for disrupting biofilms, thus helping antibiotics to eliminate bacteria. Insulin is another example of the central role of endocrine microbiology in host-bacteria interactions. Hence, as described by Gursoy *et al.*, type 1 diabetes has a direct impact on the oral microbiota resulting from a dysbiosis in the oral microbiota, which ultimately favors

dental carries and periodontitis. However, the exact role of insulin on bacteria needs more investigation since it has been reported a positive effect of this hormone on the host infected by the pathogen *Burkholderia pseudomallei*, a bacterium responsible for melioidosis in immunocompromised patients [5]. The list of human hormones now identified for having an impact on bacterial physiology is long, and it is not limited to biogenic amines and peptides. Indeed, as demonstrated in the vaginal environment, estradiol is essential for adhesion and biosurfactant production by *Lactobacillus crispatus* [6]. This observation could explain the disappearance of this bacterium essential for vaginal homeostasis after menopause and the subsequent problems frequently encountered by women. As explained by Zommiti and Feuilleley, a real sex-hormones – gut microbiota axis should also exist, based on interplay between estrogens, androgens and their metabolites with the intestinal microbiota.

Endocrine microbiology is a recent science that remains particularly complex to investigate. Besides the problems linked to all transdisciplinary researches, the extreme variability of bacteria, even within a same species, their rapid phenotypic adaptation to different environments and their capacity to evolve through DNA exchanges is adding to the difficulty. Moreover, although bacteria can respond to a large diversity of human hormones, they actually only express a small number of real specific sensors. Probably because of the limited size of their genome, they developed another strategy based on the expression of multifunctional proteins. Some of the molecules, designated as “moonlighting proteins”, have both enzymatic or chaperone functions in the cytoplasm and sensor functions after export to the bacterial surface. This process probably involves structure rearrangements, multimerization and epigenetic modifications but these proteins are particularly hard to investigate and until now cannot be predicted. As discussed by Gannesen *et al.*, open questions are multiples in endocrine microbiology, but that makes of it a particularly dynamic and attractive research topic where almost everything remains to do.

## References

1. Lyte M.: **Microbial endocrinology and infectious disease in the 21st century.** *Trends Microbiol* 2004, **12**:14-20.
2. Park CH *et al.*: **Hepcidin, a urinary antimicrobial peptide synthesized in the liver.** *J Biol Chem* 2001, **276**:7806-7810.

3. Perraud Q *et al.*: **Opportunistic use of catecholamine neurotransmitters as siderophores to access iron by *Pseudomonas aeruginosa***. *Environ Microbiol* 2022 **24**:878-893.
4. Dominique M *et al.*: **Effects of bacterial CLPB protein fragments on food intake and PYY secretion**. *Nutrients* 2021, **13**:2223.
5. Woods DE *et al.*: **Interaction of insulin with *Pseudomonas pseudomallei***. *Infect Immun* 1993, **61**: 4045-4050.
6. Clabaut M *et al.*: **Variability of the response of human vaginal *Lactobacillus crispatus* to 17 $\beta$ -estradiol**. *Sci Rep* 2021, **11**:11533.