



**Background of participants**

The PhD students should have a background in environmental, medical or evolutionary microbiology combined with interest for ecology

**Responsible**

Dr. Niels Bohse Hendriksen

**Administration**

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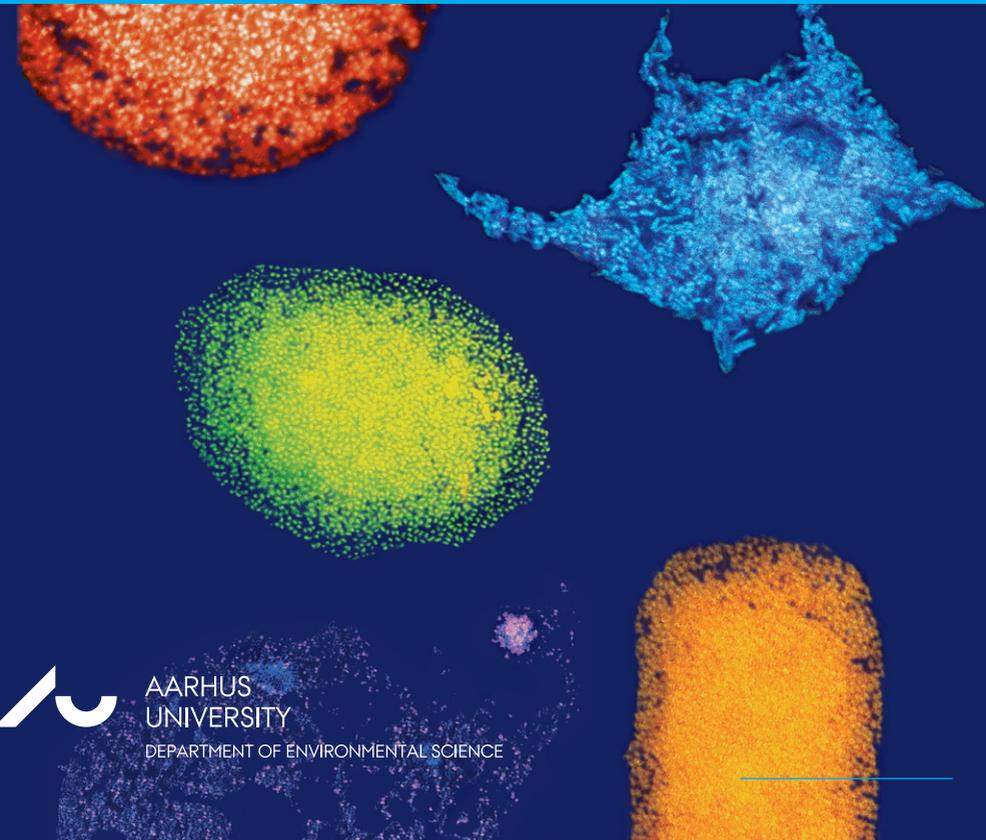
**More information**

<http://thegoodbadanduglybacteria.dmu.dk>

# THE GOOD, THE BAD AND THE UGLY BACTERIA

OCTOBER 9<sup>TH</sup> – 15<sup>TH</sup> 2011

AT AARHUS UNIVERSITY, ROSKILDE; DENMARK



## The good, the bad and the ugly bacteria

Microbes have dominated life on Earth for most of its 4.5 billion-year history. Their contribution to the biosphere is enormous and their impacts can be felt on every scale – from subtle human infections to the cycling of elements critical for maintaining life on the planet.

Traditionally, microbiologists have focussed on either the detrimental or the positive features of specific microbes, i.e. their pathogenicity towards humans or their applicability as probiotics, degraders of hazardous waste, biological pesticides etc.

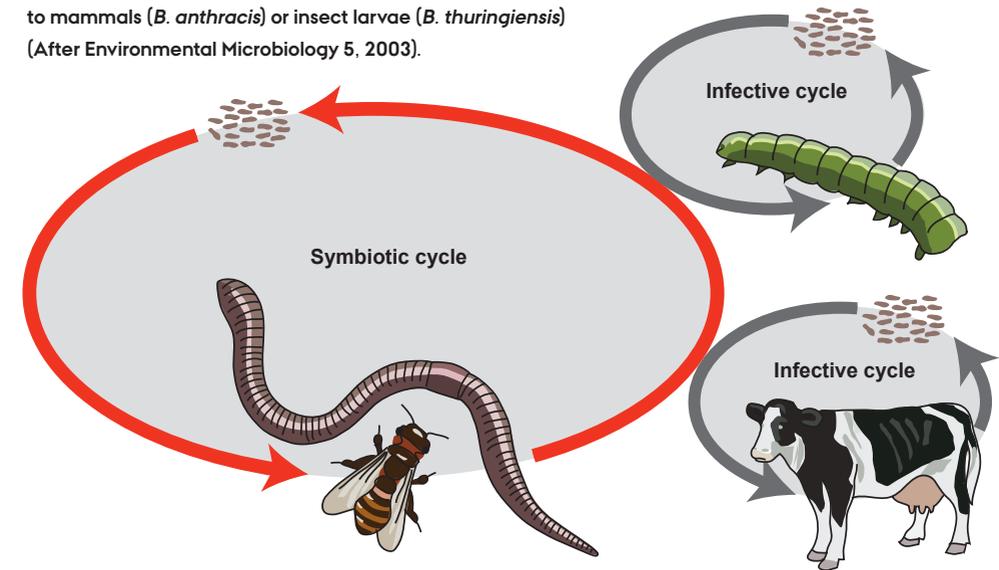
It has, however, become apparent that this narrow view on microorganisms often prevents an understanding on how bacteria evolve and interact with their environment, and that even among closely related bacteria one may find a commensal *Dr. Jekyll* and a pathogenic *Mr. Hyde*.

Many of the microorganisms normally associated with humans are primarily occurring in the outer environment. Here they not only survive, they also multiply and adapt. The awareness, that virulence genes may also be common in non-pathogenic environmental microorganisms has suggested that these traits may be used by the environmental bacteria for survival and growth in the non-host environments. Thus, the “global human virulome” does not only consist of genes in known human pathogens but also include genes found in diverse non-pathogenic environmental bacteria.

As an illustration of closely related bacteria that contain both good and ugly bacteria is the *Bacillus cereus* group. Among these bacteria one finds the ugly highly virulent *B. anthracis*, causing anthrax, and the good *B. thuringiensis* that can be applied as microbial pest control agent instead of chemical pesticides.

The scope of this PhD course is to challenge the concepts of the ‘good’, the ‘bad’ and the ‘ugly’ bacteria in the context of their natural occurrence in the environment, their interactions with other organisms, and how these interactions may have influenced the evolution of the bacteria. Bacteria of relevance for environmental, medical and food microbiology will be used. Introductory morning lectures will provide the general background from selected examples as the starting point for the discussions and the exercises. The participants will also do practical laboratory exercises and get introduced to a number of useful methods for investigating the good, the bad and the ugly bacteria *in situ*, *in vitro* and *in vivo*. Methods will include isolation and identification procedures, different PCR-based techniques, models for investigation of pathogenicity, and PC-based procedures for investigating phylogeny at gene and protein level.

Figure: Lifecycles proposed for *Bacillus cereus* group members: A frequent symbiotic cycle associated to invertebrates and a more infrequent infective cycle associated to mammals (*B. anthracis*) or insect larvae (*B. thuringiensis*) (After Environmental Microbiology 5, 2003).



**This course will include lectures by international and national experts on the following topics**

- What is the characteristics of the good, the bad and the ugly bacteria
- Microorganisms in the environment – the good, the bad and the ugly
- Microorganisms related to humans – the good, the bad and the ugly
- The interactions of microorganisms in communities – importance for health
- The evolution of bacteria – with emphasis of pathogenic traits
- The exposure of humans to microorganisms through food and other pathways
- Risk assessment of microorganisms to be used for human activities

**Laboratory exercises will include**

- How to study specific bacteria or specific genes directly in the environment and in humans
- How to identify and isolate specific bacteria with interesting favourable functions
- How to study potential pathogenicity using molecular techniques
- How to study potential pathogenicity by the use of cell, invertebrate and mammal-models
- How to study the phylogeny of bacteria