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Mice models to study the tropism of *Neisseria* species

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### Background

The genus *Neisseria* is composed of species that live in symbiosis with their hosts. This relationship requires a stepwise adaptation which could be favored by their natural competence. This singularity has contributed to evolutionary events such as morphological transition, adaptation to different ecosystem and the emergence of pathogenic species. All these events are related to host-bacteria interactions and their study requires animal models. However, *Neisseria* have co-evolved with their host to become host specific. Therefore, can we mimic the different tropisms of *Neisseria* species in mice?

### Aim/Methods

The main objective is to determine the conditions for developing a mouse model for persistent *Neisseria* colonization. Unfortunately, due to their coevolution with their host, *Neisseria* species are not able to maintain or multiply in mice. By supplementing the mice with iron transporter proteins from the host, we can provide them with the nutrients they need to maintain themselves for several days in the mouse.

### Results

Previously, when we studied the tropism of bacteria in animal models, the experiments were very complicated. It required the use of many animals, the organs had to be crushed, diluted and inoculate on selective media. Finally, at the end of the experiment, we can miss the organ infected by the bacteria. Our solution to all these problems was to use strains genetically modified to produce a constitutive luminescent signal. So as long as the bacteria is alive it emits a signal that can be detected by the IVIS lumina III, so we could visualize the organs infected by *Neisseria* species and track them in real time in the same mouse. After supplementing the mice with iron transporter proteins, we were able to reproduce the tropism of meningococcus in the nasopharynx and eustachian tubes of mice. We were able to compare its tropism to *Neisseria muscoli*, a commensal species naturally present in the oral cavity of mice.

### Conclusions

We were able to reproduce and compare the tropism of meningococcus and *N.musculi* and use this model to identify genes potentially involved in the colonization and/or pathogenicity of this species. Upcoming, we wish to use these models to study other species of *Neisseria*.