

## **Metagenomic Analysis of the Upper Respiratory Tract During *Bordetella bronchiseptica* Infection**

Metagenomics, a powerful sequencing technology that identifies all bacteria in a representative sample, has recently proven to be useful in medical microbiology. This technology can be applied to investigate how the quantity and variety of host microflora change within the host throughout infection, due to nutrient acquisition, spacial competition, and defensive microbe interactions. *Bordetella bronchiseptica* is a gram-negative respiratory pathogen that chronically infects the upper respiratory tract in a wide range of mammals and is known to displace host microflora in a way that is not well characterized. Here we proposed to define the changes in host microflora throughout a *B. bronchiseptica* infection in mice using a metagenomics approach. Microorganisms identified as affected by *B. bronchiseptica* will then be used to examine the nature of microbial interactions using *in vitro* and *in vivo* competition assays and microarray analysis to identify the response *B. bronchiseptica* to host microflora.