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## Functional analysis of the Rhodococcus equi genome

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Project in progress: Due in 2013 Prj: 753

## On-going project: an overview



The soil bacterium Rhodococcus equi is the causative agent of a severe respiratory disease of foals associated with a high case-fatality rate if antibiotic treatment is not rapidly administered. R. equi is recognised as a major cause of mortality in horses between 1 and 5 months of age, is endemic in many stud farms, and there is no vaccine to prevent the infection. We recently determined the complete nucleotide sequence of the R. equi genome (Pri712).

This project will focus on the functional characterisation of the genome by microarray transcriptomic profiling and mutant analysis to identify the mechanisms used by R. equi to cause infection and persist in the environment. The fundamental knowledge derived from these studies will help to identify targets for the rational design of attenuated live vaccines and therapies to treat R. equi infection, and to suggest interventions to limit the spread of the organism in the stud farms.