

Modeling the dynamics and evolution of nitrogen assimilation in plant pathogenic *Pseudomonas*

Nutrient utilization profiles have long been used as taxonomic tools for identifying bacteria at a species and pathovar level, but relatively little research has been carried out into the biological and ecological context of nutrient utilization by plant-associated bacteria. Bacteria in the genus *Pseudomonas* form an ideal group in which to explore the evolution and ecology of nitrogen assimilation in plant-colonising microorganisms. They occupy a wide number of plant niches, are amenable to molecular genetic techniques and genome sequence data is available for at least nine strains with differing host plants and lifestyles. These include three strains of the plant pathogenic species *Pseudomonas syringae*, four strains of the non-pathogenic species *Pseudomonas fluorescens* and *Pseudomonas putida* and two strains of *Pseudomonas aeruginosa*, an opportunistic pathogen of animals and plants.

Current information regarding the structure and function of nitrogen assimilation pathways in *P. syringae* and *P. fluorescens* comes from three main sources: experimental analyses of N-source utilization *in vitro*, analyses of gene expression *in vivo* and *in vitro*, and genome sequence analyses of nitrogen assimilation genes. All these analyses indicate that plant pathogenic *P. syringae* possess a distinct array of nitrogen assimilation genes that set this species apart from other plant-colonising *Pseudomonas*. Genetic adaptation of N-assimilation genes takes three main forms: (1) gain of gene function through duplication, mutation and lateral transfer of nitrogen assimilation genes; (2) loss of gene function through mutations and deletions; (3) regulatory adaptation through gain, loss and mutation of transcriptional regulators, promoters and post-translational regulatory mechanisms. Current evidence indicates that we cannot explain the distribution, regulation and function of these pathways on the basis of nitrogen availability alone. Natural selection for specific patterns of nitrogen assimilation, for modulation of plant cell metabolism, and for evasion and suppression of host defense responses, along with evolutionary processes such as lateral gene transfer, genetic drift and genetic bottlenecks may all have played a role in the evolution and ecology of nitrogen assimilation mechanisms in plant pathogenic bacteria.

Comparative analyses of the composition, function and regulation of nitrogen assimilation genes and nitrogen assimilation activities in plant pathogenic *P. syringae* and non-pathogenic *P. fluorescens* strains can be used to construct and test models of the evolution and ecology of these bacteria. The results of this study will provide important insights into the metabolic evolution of pathogenic bacteria, and into the interaction of *Pseudomonas* with plant hosts, particularly when placed in the context of metabolomic, proteomic and transcriptomic data on plant nitrogen metabolism.

Aim: to model the regulation and function of nitrogen assimilation mechanisms in *Pseudomonas* and investigate the role of biotic and abiotic factors in the evolution of these mechanisms

Specific objectives

- 1) Predict and compare nitrogen assimilation and biosynthesis genes in *Pseudomonas* genomes
- 2) Predict and compare nitrogen regulators and regulator binding sites in *Pseudomonas* genomes
- 3) Construct and compare metabolic and regulatory models of nitrogen metabolism in plant pathogenic, animal pathogenic and non-pathogenic *Pseudomonas*
- 4) Evaluate evidence for the relative importance of natural selection by biotic and abiotic factors and for the action of other evolutionary processes in the evolution of nitrogen assimilation in *Pseudomonas*, integrating *in silico* predictions with physiological, metabolomic and transcriptomic data

Research will be carried out under the joint supervision of Dr. Gail Preston (Department of Plant Sciences) and Prof. Jotun Hein (Bioinformatics and Mathematical Genetics Group, Department of Statistics). The applicant will have the opportunity to interact with a dynamic community molecular geneticists, plant scientists, bioinformaticians, computer scientists and mathematicians. The background of the applicant could be in biology or the so called exact sciences (mathematics, statistics, chemistry, physics, computer science, ...), but the research would be highly interdisciplinary. Oxford University is one of the leading centres for bioinformatic and evolutionary research in the UK. For further information please contact hein@stats.ox.ac.uk or gail.preston@plant-sciences.oxford.ac.uk. The earliest starting date is October 1st 2005. Deadlines for applications are July 14th 2005