
Genome-wide identification of plant host invasion traits in *Agrobacterium tumefaciens* using transposon-sequencing

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Abstract

Ecological niche construction, which ensures a preferred access to resource, represents a recurrent strategy evolved by pathogens and symbionts. Identifying metabolic pathways involved in the exploitation of resource and evaluating their involvement in the fitness of microbes colonizing their host represent an important issue in ecology and evolution. In this work we used transposon-sequencing (Tn-seq) for identifying the fitness genes in the niche-constructing pathogen *Agrobacterium tumefaciens* when it is exploiting plant host. Tn-seq combines both transposon insertional mutagenesis and massively parallel sequencing of the transposon insertion sites. We will present two approaches:

1/ using metabolomics, we determined the enriched plant metabolites in the ecological niche which is constructed and exploited by the pathogen, and then we used transcriptomics and Tn-seq for identifying the fitness genes that are important for exploiting these metabolites;

2/ using Tn-seq, we directly determined the fitness genes that are important for exploiting the constructed niche on plant host.

These two complementary approaches will be discussed. This work also highlights the advantage and limits of Tn-seq to decipher the microbial genetic determinants that are involved in ecological niche exploitation on plant host.

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