

**Comparative genomics of the conditionally dispensable chromosomes  
controlling plant infection in *Alternaria alternata* pathogens**

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**【Outline of survey】**

*Alternaria alternata* is one of the most cosmopolitan fungal species and generally saprophytic. However, this fungus contains seven variants (pathotypes), which produce host-specific toxins and cause necrotic diseases in different plants. Host-specific toxins produced by *A. alternata* are low-molecular weight secondary metabolites and critical determinants of host-specific pathogenicity. These pathotypes are fascinating case for studying intraspecific variation and evolution of pathogenicity in plant pathogenic fungi. We identified gene clusters required for host-specific toxin biosynthesis from five pathotypes of *A. alternata*. We also found that the toxin biosynthetic genes reside on conditionally dispensable (CD) chromosomes, which are small, dispensable for growth, in the genomes of the pathotypes. In this project, we will determine sequences of CD chromosomes from three pathotypes and compare their structure and function from the pathological and evolutionary viewpoints to elucidate the origin of CD chromosomes controlling plant infection in *A. alternata* pathogens.

**【Expected results】**

The CD chromosomes are unique genetic elements, which have been identified only from two plant pathogenic fungi, *A. alternata* and *Nectria haematococca*. Our recent data suggest that CD chromosomes of *A. alternata* also encode pathogenicity genes different in function from toxin biosynthetic genes. This project is expected to provide novel information concerning the evolution of pathogenicity in plant pathogenic fungi and also the diversity of genome structure and function in filamentous fungi.

**【References by the principal investigator】**

- Hatta, R., Ito, K., Hosaki, Y., Tanaka, T., Tanaka, A., Yamamoto, M., Akimitsu, K., and Tsuge, T. (2002). A conditionally dispensable chromosome controls host-specific pathogenicity in the fungal plant pathogen *Alternaria alternata*. *Genetics* 161: 59-70.
- Ito, K., Tanaka, T., Hatta, R., Yamamoto, M., Akimitsu, K., and Tsuge, T. (2004). Dissection of the host range of the fungal plant pathogen *Alternaria alternata* by modification of secondary metabolism. *Mol. Microbiol.* 52: 399-411.

**【Term of project】** FY2007—2011

**【Budget allocation】** 23,900,000 yen

(2007 direct cost)

**【Homepage address】**

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