MASTER'S THESIS

Characterization of hybrid incompatibilities between caenorhabditis briggsae and C. sp. 9

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Abstract

Hybrid incompatibility (HI) refers to lethality, sterility and other reduction in fitness of hybrid progeny between related species which has been frequently observed in different taxa. Its mechanism has been generalized as the consequence of conflicts between genomes of the related species that have been subject to independent evolution. HI plays a critical role in speciation by reducing or preventing exchange of the genetic materials between related species, gradually leading to reproductive isolation. According to the widely accepted Dobzhansky-Muller model, HI is produced by incompatible epistatic interactions between multiple genes that are independently diverged between the parental species. HI has been intensively studied especially in Drosophila species. A number of HI loci have been mapped in various species, several of which have been molecularly cloned. However, HI remains poorly understood in other taxa.

My thesis focuses on systematic characterization of HI between two sequenced nematode species, *C. briggsae* and *C. nigoni* (*C.* sp. 9). The former has long been established as a companion species of *C. elegans* for comparative study while the latter is a recently identified species that can mate with the former and produce viable and fertile hybrids in spite of their different reproduction modes, allowing one to genetically and molecularly characterize HI between nematode species for the first time. Such a study is impossible with model organism *C. elegans* as it cannot produce viable hybrids with any other nematode species. To facilitate genome-wide mapping of HI loci between the two nematode species, over 90 dominant visible GFP markers have been randomly integrated into *C. briggsae* chromosomes, permitting repeated backcrossing the marker-associated *C. briggsae* genomic fragments into an otherwise *C. nigoni* background and definitive mapping of HI loci. Genotyping of the introgressions has

been achieved by *C. briggsae* specific PCR, with primers as close as about half a million base pairs away from each other on average.

Using the cost-effective protocol for introgression and genotyping, a genome-wide HI map between the two species has been obtained based on characterization of approximately 100 independent introgression lines. A remarkable proportion of *C. nigoni* genome was found to be replaceable by that from *C. briggsae* as judged by the fact that these introgressions are viable as a homozygote. A few HI loci critical to male inviability and sterility have been narrowed down to small intervals on the X chromosome by contrasting genotypes and HI phenotypes of independent introgression strains. Strains containing these introgressions have been examined for their gonadal structures using fluorescence microscopy. Our study provides genome-wide landscape of HI between nematodes for the first time, allowing comparative studies of HI between nematode and other species.

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