

## Genome wide analysis of rice blast pathogen, *Magnaporthe oryzae*, in Korea

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*Magnaporthe oryzae* is a causal pathogen of the rice blast, the most destructive disease of rice worldwide. This ascomycete fungus has been intensively studied as a model organism in plant-pathogen interactions. Recently, the genome sequence of *M. oryzae* 70-15 was published by International Rice Blast Consortium. This led us to investigate comparative and functional analysis of this pathogen at genome-wide level. As a first step, sequencing project of *M. oryzae* Korean strain KJ201 was launched to face practical interests on diversity of plant pathogens. We constructed a fosmid library with a copy number controllable pCC1 vector. Over 13,000 end reads from 6637 fosmid clones were generated and anchored on genome sequence of the strain 70-15. Currently, 9,793 end reads, in which 2,684 clones with both ends and 1,757 clones with one end matched, are aligned to the sequence of strain 70-15. In the next step, shotgun sequencing of fosmid clones was conducted for fine scale comparative analysis of chromosome 7 that is well defined in genome sequencing of 70-15. Totally 119 fosmid clones were pooled in region and analyzed. For reasonable intra-species comparison in genome of *M. oryzae*, two strains, KJ201 and Guy11, were chosen for whole genome shotgun sequencing analysis with GS454 FLX system. About 8X genome coverage sequences were obtained for each strain and being merged for comparative analysis. Genome information of other strains is being also available from China and Japanese research groups and could be joined together for extended comparative analysis and the results give more detail in genome diversity in species level.