

Comparative and functional analysis of *Magnaporthe grisea* KJ201 genome

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Magnaporthe grisea is a causal fungus of the rice blast, the most destructive disease on rice worldwide. This fungus has been intensively studied as a model pathogen in plant-pathogen interactions. Recently, the genome sequence of *M. grisea* 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. grisea* Korean strain KJ201 was launched. We constructed fosmid library with a copy number controllable pCC1 vector. 5X genome coverage of fosmids will be end-sequenced, and anchored on genome sequence of the strain 70-15. Currently, 3,000 end-reads of fosmid clones are aligned to the sequences of strain 70-15. With following criteria for match regions: matching length longer than 90 % of reads length, matching score larger than 50, and matching percentage larger than 95 %, about 65 % genome coverage was achieved and coverage plot is presented for each chromosome. For better alignment, an in-house python-based sequence analyzing program, Match_manager, was developed and Cross_match (<http://www.phrap.org/>) was integrated as a key analyzer. In the next step, shot-gun sequencing of fosmid clones will be followed in conjunction with comparative genomic hybridization between two strains. Our sequencing strategy would provide an alternative genome sequencing with the limited resources for comparative genomic analysis

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