

## Functional Genomics of the Rice Blast Fungus

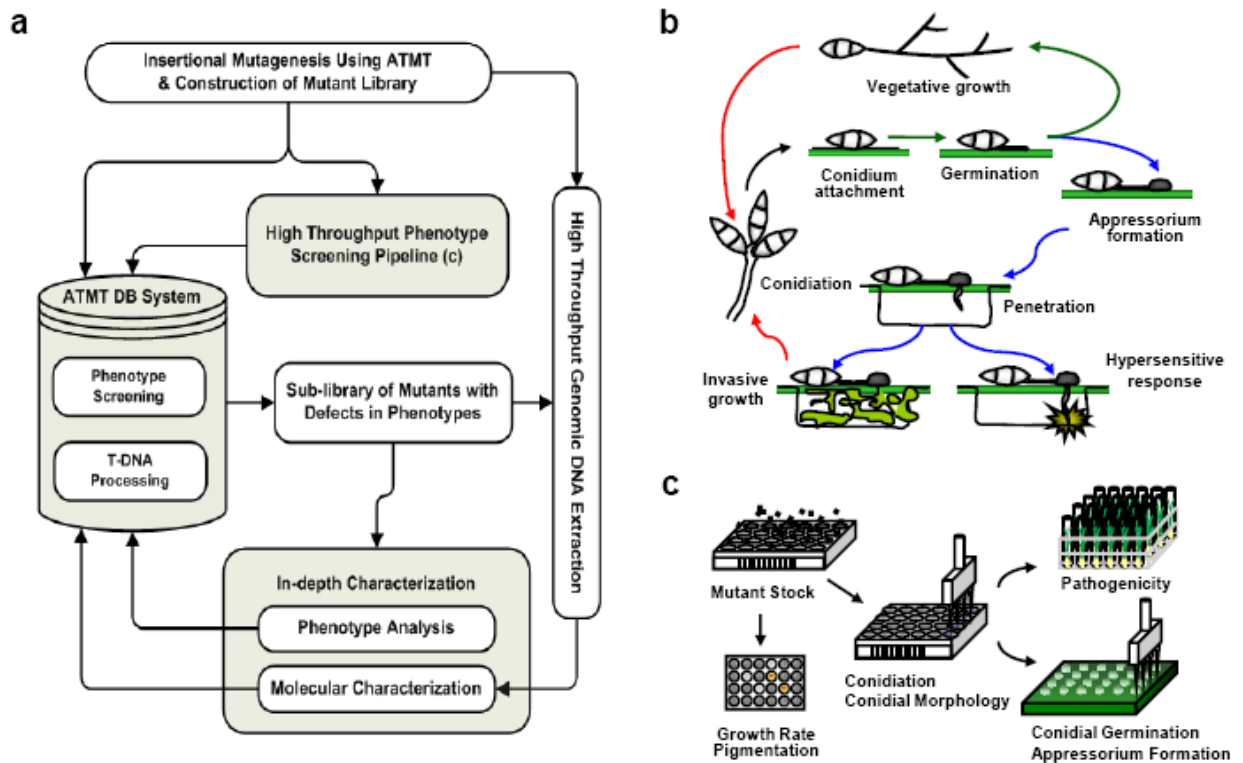
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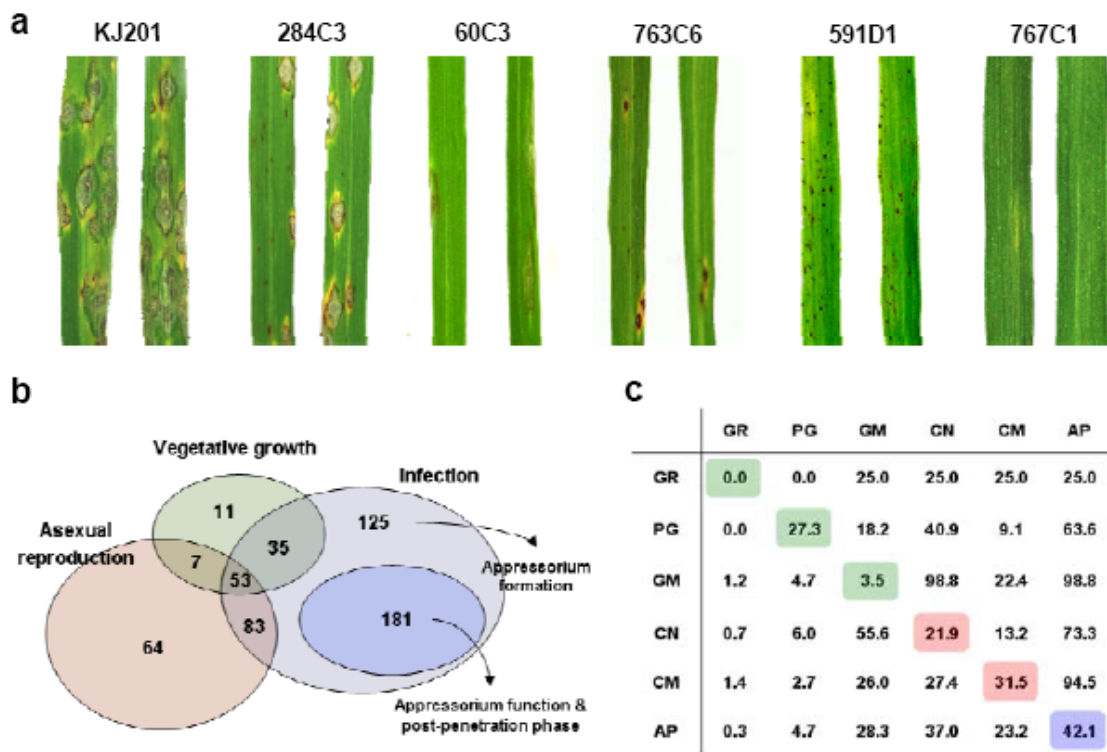
*Magnaporthe oryzae* is a causal agent of rice blast and considered as a model pathogen for studying plant-microbe interactions. This is due to not only economic significance of rice blast disease worldwide but genetic and molecular tractability of this fungal pathogen. Currently whole genome sequence of strain 70-15 is available in the public database. To decipher fungal pathogenicity factors at genome-wide level in this fungus, we initiated a large-scale insertional mutagenesis using *Agrobacterium tumefaciens*-mediated transformation (ATMT). This project includes (1) construction of transformants library (2) development of high throughput phenotype screening and DNA extraction systems, and (3) rescuing flanking sequences of T-DNA insertion from selected transformants. We generated over 21,000 transformants and screened for 7 phenotypes as a high throughput manner; conidiation, conidial morphology, conidial germination, appressorium formation, mycelial growth, pigmentation, and pathogenicity. Over 1,000 loss of virulence and development-defective mutants were obtained from ATMT mutant library. The T-DNA tagged sequences from the selected transformants are being rescued by TAIL-PCR and sequencing, and 1,100 unique loci are identified thus far. To verify phenotype changes by T-DNA insertion, crossing with a wild type and targeted gene knock-out are being applied. Distribution and integration patterns of T-DNA on fungal chromosomes are also analyzed. Furthermore, we developed the ATMT data management system to handle all phenomics and genomics data of these transformants. Current progress of this project will be presented.

### References

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Schematic diagram of high throughput screening system and life cycle in *Magnaporthe oryzae*



Composition and pairing analysis of phenotypes in pathogenicity-defective mutants