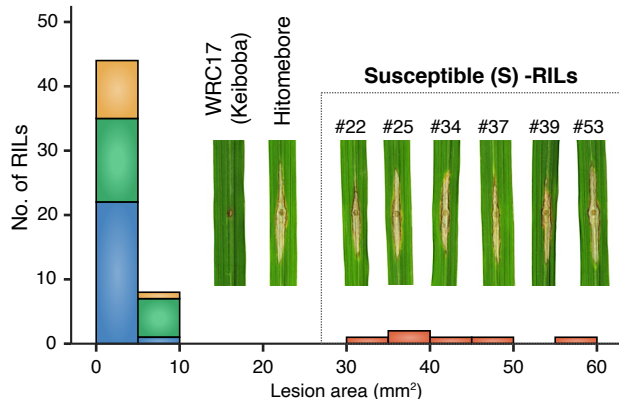
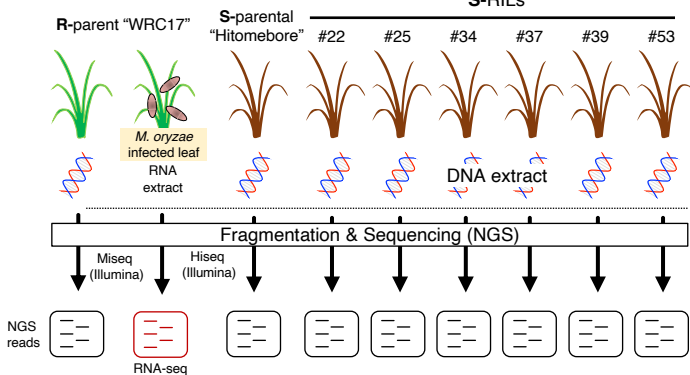


**(A) STEP1: Phenotyping of RILs**



**(B) STEP2: Whole genome sequencing of parental lines and susceptible RILs (S-RILs).**



**(C) STEP3: *De novo* assembly of R-parental line "WRC17" using "DISCOVAR" software.**

**(D) STEP4: Gene prediction of WRC17, the resistant parent, using RNA-seq data.**

Reference genome sequence of "WRC17" from STEP3

RNA-seq based Gene prediction

• Using "Hisat2" aligner and assembly of the transcript was performed by "StringTie"

Aligned RNA-seq read

Contig

Expressed genes

Gene A

Gene B

Gene C

**(E) STEP5: Mapping short reads of susceptible parent and RILs to the predicted genes of WRC17.**

