# Supplementary Tables

**Table S1. Heritability for each trait in the two progeny populations.**



Dpi = Days post inoculation, SE = standard error.

**Table S2. Significant QTLs identified by simple interval QTL mapping for growth-related traits under oxidative stress.**

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Dpi = Days post inoculation, Chr = Chromosome, Var. = Variation explained.

**Table S3. Significant QTLs identified by simple interval QTL mapping for melanization-related traits under oxidative stress.**

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Dpi = Days post inoculation, Chr = Chromosome, Var. = Variation explained.

**Table S4. Significant QTLs identified by multiple QTLs model in mapping populations for growth-related traits under oxidative stress.**



Dpi = Days post inoculation, Chr = Chromosome, Var. = Variation explained. Interaction between QTLs is indicated with a colon. For example, chr7 : chr8 means an interaction was detected between the chromosome 7 QTL and the chromosome 8 QTL for the trait growth under control conditions at 12 dpi.

**Table S5. Significant QTLs identified by multiple QTL model in mapping populations for melanization-related traits under oxidative stress.**



Dpi = Days post inoculation, Chr = Chromosome, Var. = Variation explained, TE = Transposable element. Interaction between QTLs was indicated by colon.