

Table S1-1: Disease resistance QTL data for three different rice pathogens

QTL were mined from published databases, GRAMENE and Q-TARO (archive.gramene.org/ctl/, qtaro.abr.affrc.go.jp), as well as recent literature which the databases did not curate. Each QTL is labelled with a reference ID for the corresponding database, or a DOI for the publication from which it was extracted. Each QTL position was mapped to the rice reference genome (MSU v7.0 rice.plantbiology.msu.edu/). QTL flanking markers were mapped to the reference using the program vmatch (www.vmatch.de/). Resistant or susceptible parents are listed if known. Table is available in supplemental folder.

Table S1-2: Statistical enrichment test results for QTL density across the genome

Each chromosome was separated into 3Mb sections (bins) and the relative QTL density compared to the entire chromosome was calculated based on total possible nucleotides covered by QTL using the equation given in Figure 1-2. Each bin is named with the chromosome first, and the bin number second. Chromosomal coordinates are given for each bin, and the observed (bin frequency) and expected (chromosome frequency) values are given as a value out of 100. A Fisher exact test was performed with Benjamini-Hochberg P-value correction using a Q value=127 and FDR=0.05, no results were significant. Table is available in supplemental folder.

Table S3-1: Gene expression studies. Information on each experiment used in the defense response gene co-expression analysis. For each study, the treatment, rice variety used, tissue type, experimental conditions, expression data type (platform), and reference are given. Table is available in supplemental folder.

Table S3-2: DR-related Gene Ontology terms. Gene Ontology identifiers from the Plant GOSlim database (rice.plantbiology.msu.edu/index.shtml) that are deemed as related to the plant defense response. These terms were used for testing for enrichment in co-expression clusters. Table is available in supplemental folder.

Table S3-3: Functionally-Associated DR (FA-DR) genes. A list of genes that are functionally validated to be involved in the rice DR to pathogens. LocusID for the MSU7 Nipponbare reference genome is given. The disease the FA-DR gene is involved in as well as the method of validation are shown. The effect, positive (+) or negative (-), is shown, the reference for the gene, and annotation are given in the final columns. Table is available in supplemental folder.

Table S3-4: Co-expression clusters FA-DR gene enrichment tests. Each co-expressed gene cluster is labelled as a unique color name. The P-values given are a result of a Fisher Exact test based on the comparison of the number of FA-DR genes within the respective cluster or the rest of the genome. Only clusters with at least one FA-DR gene were tested. P-value correction was done using Benjamini-Hochberg (BH) procedure with a False Discovery Rate (FDR) of 0.05. Number of tests totaled to 36. One cluster, greenyellow, was found to be statistically enriched, and is named the “BS-DR” cluster for future analysis. Table is available in the supplemental folder.

Table S3-5: Co-expression clusters DR-GO term enrichment tests. Each co-expressed gene cluster is labelled as a unique color name. The P-values given are a result of a Fisher Exact test on each DR-GO term, counting the genes labelled with the respective DR-GO term within each respective cluster or the rest of the genome. DR-GO terms were only tested on the clusters that contained at least one gene labelled with the respective term. P-value correction was done using Benjamini-Hochberg (BH) procedure with a False Discovery Rate (FDR) of 0.05. Number of tests totaled to 1476. The row colored red is the last ranked DR-GO term which is less than the BH-corrected value. Table is available in the supplemental folder.

Table S3-6: Genes in BS-DR cluster. A list of the genes (including full annotations) found within the co-expressed BS-DR cluster. The MSU7 locus ID, representative gene model, chromosome and relative position, position on plus or minus strand are given. All genes are not transposable elements (is_TE = N). All are expressed and representative, meaning their transcripts have been validated, and the gene model is the model that encompasses all UTRs. Table is available in supplemental folder.

Table S3-7: DR gene families *OsPAL*, *OsOXO*, and *OsGLP8* within QTL. The QTL found to encompass each DR gene family member is listed. QTL were taken from databases Q-TARO, GRAMENE ((archive.gramene.org/qtl/), qtaro.abr.affrc.go.jp) and recent literature (DOI given). Table is available in supplemental folder.

Table S4-1: Functionally-associated DR genes that contain promoter CRMs. The FA-DR genes that harbored a particular CRM in their promoter that were found to be in at least one of the two rice varieties, IR64 and Nipponbare are given. If “None” is shown under either variety locus ID, there does not exist an ortholog in that variety. It is also specified whether or not the FA-DR gene is within the co-expressed BS-DR gene cluster. The functional annotation is given in the last column. Table is available in supplemental folder.