Supplemental Figures

Figure S1

Linkage disequilibrium decay in simulated chromosomes.

These curves represent the LD decay as a function of the physical distance, assuming a Human-like chromosome (top) or an Arabidopsis-like chromosome (bottom); that is assuming 1 cM equals 1 Mbp or 0.25 Mbp in human and *A. thaliana*, respectively (Nordborg *et al*, 2002). LD is measured with r^2. Black curves represent 1 000 simulations, and the red curve is the average of 1 000 simulations at a given physical distance. The one-half LD decay (i.e. the physical distance at which r^2 reaches half the maximum r^2 value between two SNPs) ranges from 27 to 37 kbp for Arabidopsis-like chromosomes, and from 7 to 9 kbp for Human-like chromosomes.

Figure S2

Major QTL detection power by *p-value – based* tests (EMMAX method) and methods based on aggregation of *p-values* (Local Score, LHiSA and LandScape).

Strictly the same legend as in Figure 3, except that in this figure the two simulated QTL heritability values were 0.20 (top row) and 0.4 (bottom row). In these cases, power curves were calculated at the QTL position and on windows of +/- 10 kbp, +/- 50 kbp or +/- 100 kbp on both sides of the QTL position. LHiSA power curves were compared to power curves of the other methods on windows which were the closest to the mean interval size given by LHiSA; that is 66 071 bp and 135 697 bp, for QTL heritability values of 0.20 and 0.40, respectively.

Figure S3

A kinship matrix based on a genome-wide SNP sampling, which implies population structure and heterogeneous relatedness among accessions of *Medicago truncatula*.

This heatmap describes a hierarchical clustering of pairwise genetic similarities (Identity By State) between accessions of the *M. truncatula* collection, estimated by using a genome-wide dataset of 5 328 852 SNPs with a minor allele frequency of 5%. The kinship matrix clearly implies population structure (FW = Far West population, C = Circum population; see (Bonhomme *et al*, 2014)) and within-population heterogeneous relatedness in the *M. truncatula* collection.

Figure S4

Magnification of the region on chromosome 3 encompassing an F-box protein coding gene (Medtr3g011020), previously identified as the main QDR locus in response to isolate ATCC 201684 in the GWAS of PC1 parameter which used the *M. truncatula* genome version Mt3.5 (Bonhomme *et al*, 2014).

Black points correspond to SNPs. The blue curve corresponds to the Lindley process. The red line indicates the position of the F-box protein coding gene (Medtr3g011020). The horizontal black and blue dotted lines indicate the significance threshold for *p-value*–based tests (10^{-6}) and for the local score (13.92).

Supplemental Tables

Table S1

List of the candidate QDR loci identified using the local score analysis (ξ = 2, chromosome-wide FWER of 20%) from GWAS of QDR to five different *A. euteiches* isolates.

The column "phenotype" indicates whether QDR was assessed using either the PC1 parameter (Bonhomme *et al*, 2014) or the RRI parameter (Pilet-Nayel *et al*, 2009). The column

"Aphanomyces_isolate" indicates with which *A. euteiches* isolate the *M. truncatula* collection was infected. The column "chromosome" indicates on which chromosome each QDR locus was identified. The columns "begin_int" and "end_int" indicate the physical position of the beginning and end of the QTL interval detected by the local score approach. The column "maximum_Lindley" indicates the maximum value of the local score within the interval size of each region. The column "SNP_int" indicates the number of SNPs within the detected intervals. The column "minimum_p-value" indicates the lowest SNP-based p-value provided by EMMAX within the detected interval. The column "closest_gene_model(s)" corresponds to the *Medicago truncatula* gene model identifier(s) (Mt4 genome version) found within each detected interval. The column "gene_model(s)_position" indicates the physical positions of the gene model(s) on Mt4 genome version. The column "gene_annotation" shows the functional annotation of each candidate gene according to the Mt4 genome version (http://www.medicagogenome.org/). The column "local_score_quantile_0.8" indicates the value of the 80% quantile used as significance threshold for each chromosome in each GWAS. Candidate QDR loci highlighted in darkbrown, brown, green and blue correspond to loci which are common to (i) all *A. euteiches* pea isolates (i.e. pathotype I and III), (ii) *A. euteiches* pea isolates from pathotype I, (iii) *A. euteiches* alfalfa isolates and (iv) *A. euteiches* pea and alfalfa isolates.

Supplemental Files

File S1

This file contains Root Rot Index (RRI) adjusted mean for each accession, obtained following infection with *A. euteiches* isolates ATCC 201684, RB84, Ae109, MF-1, and NC-1, plus the

PC1 values obtained following infection with isolate ATCC 201684 (Bonhomme *et al*, 2014). These values were used as phenotypic data in the GWAS of *M. truncatula* QDR to *A. euteiches*.