This is the README file.

Environment (location) names

M0405: NICS (average of 2004 and 2005)
T2008: NIAS
K2009: FRERC (average of two replicates)
F0612: WARC (average of 2006–2012)
M2004, M2005: NICS in 2004 and 2005
KE2009, KL2009: Two replicates at FRERC
F2006–F2012: WARC in 2006–2012

We used M0405, T2008, K2009, and F0612 for the NSE and OLM analyses.
The followings are the explanations of the presented files.

Source codes

File name: main.c
File name: header.h
These files are the C source codes of the program for the nonlinear structural equation (NSE) and the ordinary linear model (OLM) which is named as "mta05". This can be compiled on Linux by typing "gcc main.c -o mta05 -lm" or on Mac by typing "gcc main.c -o mta05".

R scripts and data

File name: RealDataAnalysis.R
File name: RealDataAnalysis.RData
This script was used for the real data analysis.

File name: SimulateDatasets.R
This script was used to simulate data sets from the real data analysis results.
File name: ReadSimulationResults.R
File name: SimulationResults_[*Simulation scheme*]_[*Environment*].RData
These files contain the results of simulation analysis. The analysis results were output by the C program as text files, read by R, and saved as RData objects. *Simulation scheme* is either of nonlinear, linear0, or linear1.2.

File name: SummarizeSimulationResults.R
This script was used to summarize the simulation results.

Phenotypic records

File name: [*Environment name*]_DHCL.txt

These files contain the phenotypic values of DH and CL at each environment. The first half values are the DH and the last half values are the CL values. The order of the cultivars is the same as that in Supplementary Material. The 59th and 73th cultivars were not evaluated at NIAS. Thus the number of cultivars is 108 at NIAS.

Genetic relationship matrix

File name: iA_110x3102.txt

This file contains the inverse of the genetic relationship matrix between the 110 cultivars. The markers used in Onogi et al. 2015 (Theor Appl Genet 128:41–53) and the function A.mat in the rrBLUP package were used for calculation. The order of the cultivars is the same as that in Supplementary Material.

Identity matrix

File name: IdentityMatrix.txt

This contains the 2 x 2 identity matrix which was used when the non-informative prior was used for the residual covariance of NSE.

Major gene genotypes

File name: MajorGenes_N108_Nr1_10_13.txt

File name: MajorGenes_N110_Nr1_10_13.txt

These files contain the intercepts and the major gene genotypes copied from the Supplementary Material. The first 10 columns were for DH and the last 13 columns were for CL. "MajorGenes_N108_Nr1_10_13.txt" was used at NIAS. "MajorGenes_N110_Nr1_10_13.txt" was used at NICS, FRERC, and WARC.

Major gene names

File name: MajorGeneNames.txt

This contains the names of the major gene polymorphisms.

Design matrix

File name: Z108.txt

This file contains the design matrix that relates the relationship matrix with the phenotypic values. This was only used for the NIAS data.

A file to specify the structural equation model

File name: Model3.txt

This file specifies the position of the recursive effects between the traits and the modeling schemes of the

recursive effects. The first and second columns (rows) indicate DH and CL, respectively. The number (3) in position [2, 1] means that DH influences CL, and 3 means that B-spline is used to model the causal influence. When 1 is entered, the influence is modeled as a linear trend. See the source code for the explanation of 2.

Scale parameters of the inverse Wishart distributions

File name: [*Environment name*]_DHCL_Halfcov.txt

These files contain the scale parameters of the inverse Wishart distributions which were used as the prior distributions of the genetic and residual covariances of NSE and OLM. These files were created by RealDataAnalysis.R.

Parameter files of NSE

File name: [*Environment name*]_DHCL_se.txt

These files contain the parameter values required by mta05 when NSE is executed. These files were created by RealDataAnalysis.R.

File name: [*Environment name*]_DHCL_se_nir.txt

These files contain the parameter values required by mta05 when NSE is executed using the non-informative prior distributions of the residual covariance.

Parameter files of OLM

File name: [*Environment name*]_DHCL_lm.txt

These files contain the parameter values required by the mta05 program when OLM is executed. These files were created by RealDataAnalysis.R.

Phenotypic covariance and correlation between the traits

File name: PhenotypicCovariance.txt

This file contains the phenotypic covariance and correlation between DH and CL. This file was created by RealDataAnalysis.R.

Results of NSE

File name: mta05_[*Environment name*]_DHCL_se_[*Inferred parameter*].txt

These files contain the results of the NSE analyses. "*Inferred parameters*" are explained in the followings.

Inferred parameters

B: "Fixed" effects. The file contains the number of MCMC samples × the number of the fixed effects matrix. The order of the fixed effects is same as that of MajorGenes_N110_Nr1_10_13.txt.

G: Genetic covariance. The file contains the number of MCMC samples × 4 matrix. The first and last columns contain the variance of DH and CL, and the second and the third contain the covariance.

R: Residual covariance. The file contains the number of MCMC samples × 4 matrix. The first and last columns contain the variance of DH and CL, and the second and the third contain the covariance.

U: Polygenic effects. The file contains the number of MCMC samples × (2 × number of the lines). The first half columns contain the effects on DH and the last half columns contain the effects on CL. The order of the polygenic effects is same as that of iA_110x3102.txt.

Basis1: The values returned by the basis functions (ϕ_m^4). The file contains the number of the basis functions (8) × the number of the lines matrix. The order of the lines is same as that of [*Environment name*]_DHCL.txt.

Criterion: This file contains DIC and WAIC calculated by the program.

Lambda1: Phenotypic influence calculated by $\sum_{m=0}^{M} P_m \phi_m^4 \left(y_{i,DH} \right)$. The file contains the number of MCMC samples × number of the lines matrix. The order of the lines is same as that of [*Environment name*]_DHCL.txt.

LogLikelihood: The file contains the number of MCMC samples × number of the lines matrix. Log likelihood was calculated for each line at each MCMC sample. The order of the lines is same as that of [*Environment name*]_DHCL.txt.

Pi1: Weight of the basis functions (P_m). The file contains the number of MCMC samples × the number of the basis functions (8) matrix.

parameters: Parameter values used for the analysis.

File name: mta05_[*Environment name*]_DHCL_se_nir_[*Inferred parameter*].txt

These files contain the results of the NSE analyses based on the non-informative priors of the residual covariance.

Results of OLM

File name: mta05_[*Environment name*]_DHCL_lm_[*Inferred parameter*].txt

These files contain the results of the OLM analyses

Summary of the real data analysis

File name: SummaryReal.txt

File name: SummaryReal.nir.txt

These files contain the summary of the real data analysis. These files were created by RealDataAnalysis.R. The column names of these files are explained in the followings.

varG: Genetic variance

covG: Genetic covariance

varR: Residual variance

covR: Residual covariance

mean: Posterior mean

sd: Posterior standard deviation

se: Estimates by NSE

lm: Estimates by OLM

deltaWAIC: (WAIC of NSE) − (WAIC of OLM)

CorWithG0–7: Correlation of MCMC samples between the genetic covariance and the weight parameters of the 1–8th basis functions

CorWithR0–7: Correlation of MCMC samples between the residual covariance and the weight parameters of the 1–8th basis functions