

Supplementary Table S1. Microsatellite primers and concentrations.

NOTE: We used 2.0µl template DNA and Invitrogen Platinum *Taq* DNA Polymerase. As stated in the paper the annealing temperature was 56°C with a MgCl₂ concentration of 2.0 mM. The full amplification conditions were: 94°C for 3min; then 35 cycles of 94°C for 30sec, 56°C for 30sec, 72°C for 1min; then 72°C for 45min.

Primer	Dye label	5' tail (PT)	Sequence (5'-3')	µM
Pam010_F	VIC		GTGGCCTTGGTGAAGCAG	0.11
Pam010_R		GTTTCTT	CGCGCACTAGGTGCCAAATATC	
Pam017_F	6-FAM		CTGACTTTGTATGCATGTCCG	0.24
Pam017_R		GTTTCTT	GTTTGAGACCTCAGGGCAAG	
Pam021_F	PET		GATCTGACAATGACCACTTTACT	0.30
Pam021_R		GTTTCTT	CCTCTATAGGAATGCTGCTTTTG	
Pam025_F	6-FAM		CAAATAACATATGCACACATCAGC	0.21
Pam025_R		GTTTCTT	CTTCTCTGGCATGAATGTTTG	
Pam035_F	VIC		GGCTCGCTCTGGGCATTAC	0.06
Pam035_R		GTTTCTT	ACAACGTGAGCTATACCCGCC	
GJLKPX_F	NED		ACAGCAGGTGTCTATGATGGT	0.11
GJLKPX_R		GTTTCTT	TGGAAGCACTTCTGGCAATA	
GJSLB2_1_F	6-FAM		GAGGAGACAGGGGTGAAAAA	0.11
GJSLB2_1_R			TTCACACCCTCCTTCATCTACA	
GGOQ6A_F	NED		ACATGGACGTGCAGATAAAAA	0.27
GGOQ6A_R		GTTTCTT	ACTATCAGCAGCAATCTGTGTC	
GH00IK_F	PET		GCGGCGATAATAATGCAAAA	0.15
GH00IK_R		GTTTCTT	GATCCAGGAGCAAACAGCTC	

Supplementary Table S2. Summary of contemporary groups included in the analyses. (assessment date x tank): Numbers of sires and dams represented, number of full-sib (FS) families, and number of individual fish evaluated. Coding system consists of the date of the assessment fish followed by a 6-character code for the tank they occupied on the assessment date.

Contemporary Group	Sires	Dams	FS Families	Individuals
2009-04-15_NA001	7	2	14	239
2009-04-16_AA005	5	3	8	22
2009-04-16_NA003	7	3	14	145
2009-04-17_HA001	4	1	4	20
2009-04-17_NA005	7	7	20	349
2009-04-17_NA006	6	6	23	197
2009-05-14_AA004	6	5	14	31
2009-07-16_NA003	6	6	24	229
2009-07-16_NA005	7	7	21	287
2009-07-16_NA006	6	5	19	274
2009-07-17_NA001	10	6	21	225
2009-07-17_NA002	11	4	19	211
2009-08-10_AA001	5	4	11	20
2009-08-10_BA001	5	4	13	18
2009-09-10_NA001	13	7	34	270
2009-09-10_NA005	13	6	31	256
2009-09-10_NA006	13	7	35	272
2009-09-11_NA003	12	8	31	278
2009-09-11_NA004	6	6	24	248
2009-12-04_CA002	6	6	24	250
2009-12-09_CA004	13	7	34	270
2009-12-10_CA003	12	8	31	280
2009-12-11_CA005	13	6	31	257
2009-12-14_CA006	13	7	35	273
2010-04-23_CA003	13	6	28	159
2010-04-27_CA001	6	6	24	198
2010-04-28_CA002	8	6	22	128
2010-05-03_CA004	12	8	29	186
2010-05-05_CA005	13	6	32	175
2010-06-24_CA004	6	5	18	57
2011-02-15_NA001	5	3	11	276

Contemporary Group	Sires	Dams	FS Families	Individuals
2011-02-16_NA003	5	1	5	58
2011-02-17_BA006	4	1	4	22
2011-05-17_CA003	5	3	11	509
2011-05-19_CA004	5	6	19	572
2011-05-23_CA002	6	7	22	596
2011-05-24_NA002	8	6	36	726
2011-05-25_NA002	8	6	34	677
2011-08-04_CA004	6	7	22	595
2011-08-05_CA006	5	6	19	571
2011-08-10_CA005	5	3	11	487
2011-08-11_CA003	8	6	36	724
2011-08-12_CA002	8	6	34	673
2011-09-20_CA005	8	6	36	281
2011-09-21_CA001	6	7	22	141
2011-09-21_CA006	5	3	11	122
2011-09-22_CA003	8	6	34	212
2011-09-22_CA004	5	6	19	98
2011-11-22_CA004	13	12	52	171
2011-11-22_CA006	14	14	54	169
2011-11-23_CA001	13	13	55	165
2011-11-23_CA003	13	12	51	167
2011-11-24_CA002	13	13	57	177
2012-05-24_NA001	5	4	7	18
2012-05-24_NA002	7	4	10	26
2012-07-03_CA002	6	4	13	24
2012-07-03_CA004	6	4	12	19
2012-07-04_CA003	7	4	14	25
2012-07-04_CA005	7	4	13	25
2012-07-04_CA006	8	5	17	25
2012-07-13_NA003	4	2	5	56
2014-07-08_QA002	7	2	7	168
2014-07-08_QA003	4	3	7	56
2014-07-08_QA004	6	3	8	50
2014-07-08_QA008	5	4	11	57
2014-07-14_QA003	5	5	16	170

Contemporary Group	Sires	Dams	FS Families	Individuals
2014-07-14_QA004	6	4	17	171
2014-07-14_QA008	5	4	14	168
2014-09-19_QA002	7	2	7	168
2014-09-25_QA004	6	4	17	216
2014-09-30_QA003	5	5	16	223
2014-10-01_QA008	5	5	15	222
2014-11-27_QA002	5	5	15	112
2014-11-27_QA010	7	5	17	126
2014-11-27_QA011	6	4	14	93
2014-12-01_QA003	5	5	15	112
2014-12-01_QA007	5	4	14	112
2014-12-01_QA009	7	2	7	165
2014-12-02_QA004	5	4	13	113

Supplementary Table S3. Counts of occurrence of relationship coefficients in the A-matrix.

Relatedness Coefficient	Count
0	11,110,836
0.125	138,383
0.250	2,452,369
0.300	568
0.500	794,264
Total	14,496,420

Supplementary file S1. R code for ASReml-R analyses

The code below was used to estimate variance components and full-likelihood AIC and BIC using the `asreml()` and `asremlPlus()` packages.

Model terms:

- **ainv** = inverse of A matrix calculated from pedigree prior to analysis
- **mydata** = dataframe with columns for IDs, covariates and phenotypes
- **ID** = individual ID in pedigree as factor
- **IDpe** = second column equal to ID; required for PE effects due to bug in ASReml
- **fam** = full-sib family (sire x dam)
- **len** = phenotype: length at harvest
- **wt** = phenotype: weight at harvest
- **dph** = covariate: days-post-hatch (age in days as numeric)
- **cont_grp** = covariate: contemporary group (assessment x tank as factor)
- **X** = desired order for Legendre polynomials; **must be replaced w/ hard-coded integers**; seems impossible to use a variable name for this (e.g. `w/in` a for loop)

```
## Begin code #####

# load packages
library(asreml)
library(asremlPlus)

#####
# UNIVARIATE MODEL EXAMPLE
#####

# Phenotype = "phen"; Replace
# Dataset = "mydata"
# Legendre polynomial order = "X"; Replace
# Sections represent random effects structure for Models 1-4
# Comment out random statement and uncomments desired random effects
# to use different random effects (fam, PE)

Leg_univar <-
  asreml(
    fixed = phen ~
      cont_grp +
      leg(dph, X),

    # Models 1-4 RR structures
    random = ~ us(leg(dph, X)):vm(ID, ainv),

    ## Models 5-8 RR structures
    # random = ~ us(leg(dph, X)):fam +
    #           us(leg(dph, X)):vm(ID, ainv),

    ## Models 9-12 RR structures
    # random = ~ us(leg(dph, X)):fam +
    #           diag(leg(dph, X)):id(IDpe) +
    #           us(leg(dph, X)):vm(ID, ainv),

    ## Models 13-16 RR structures
    # random = ~ us(leg(dph, X)):fam +
    #           us(leg(dph, X)):id(IDpe) +
    #           us(leg(dph, X)):vm(ID, ainv),

    ## Models 17-21 RR structures
    # random = ~ us(leg(dph, X)):vm(ID, ainv) +
    #           us(leg(dph, X)):id(IDpe),

    ## Models 21-24 RR structures
    # random = ~ us(leg(dph, X)):vm(ID, ainv) +
    #           diag(leg(dph, X)):id(IDpe),
    residual = ~units,
    data = mydata,
    na.action = na.method(x = "include", y = "omit"),
    trace=T,
    extra=4,
    maxit = 10000)
```

```

# ESTIMATE AIC & BIC USING RESTRICTED LIKELIHOOD
Info_REML <- infoCriteria(Leg_univar,
  DF = NULL,
  bound.exclusions = c("F","B","S","C"),
  IClikelihood = "REML",
  fixedDF = NULL,
  varDF = NULL)

# ESTIMATE AIC & BIC USING FULL LIKELIHOOD
Info_FULL <- infoCriteria(Leg_univar,
  DF = NULL,
  bound.exclusions = c("F","B","S","C"),
  IClikelihood = "full",
  fixedDF = NULL,
  varDF = NULL)

#####
# BIVARIATE MODEL EXAMPLE
#####

# Only random genetic effect estimated based on univariate model selection
# Legendre order = 3 for fixed and direct genetic effects
# Phenotypes = "phen1" & "phen2"; Replace
# Dataset = "mydata"

Leg_bivar <- asreml(fixed = cbind(phen1, phen2) ~ trait +
  trait:cont_grp +
  trait:leg(dph, 3),

  random = ~ at(trait):us(leg(dph, 3)):vm(ID, ainv),
  residual = ~ id(units):us(trait),
  data = mydata,
  na.action = na.method(x = "include", y = "include"),
  trace=T,
  maxit=10000,
  extra=4,
  workspace="275gb")

# The order 3 Legendre bivariate model above estimates the following
# (c0)variance components with ASReml-R naming conventions
#
# NB: "order" in this table is actually "degree"

#
# VARIANCE COMPONENTS
#
# at(trait, phen1):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order0:order0 1
# at(trait, phen1):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order1:order0 2
# at(trait, phen1):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order1:order1 3
# at(trait, phen1):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order2:order0 4
# at(trait, phen1):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order2:order1 5
# at(trait, phen1):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order2:order2 6
# at(trait, phen1):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order3:order0 7
# at(trait, phen1):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order3:order1 8
# at(trait, phen1):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order3:order2 9
# at(trait, phen1):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order3:order3 10

# at(trait, phen2):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order0:order0 11
# at(trait, phen2):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order1:order0 12
# at(trait, phen2):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order1:order1 13
# at(trait, phen2):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order2:order0 14
# at(trait, phen2):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order2:order1 15
# at(trait, phen2):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order2:order2 16
# at(trait, phen2):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order3:order0 17
# at(trait, phen2):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order3:order1 18
# at(trait, phen2):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order3:order2 19
# at(trait, phen2):leg(dph, 3):vm(ANIMAL, ainv)!leg(dph, 3)_order3:order3 20

# units:trait!R 21
# units:trait!trait_phen1:phen1 22
# units:trait!trait_phen2:phen1 23
# units:trait!trait_phen2:phen2 24

```

Supplementary file S2. R functions for calculating standardized Legendre polynomials

```
#####
# Functions downloaded from
## http://morotalab.org/Mrode2005/rr/rr.html#section00020000000000000000
#####

## Function stdtime()
## Given time points covariate and order of fit for Legendre polynomials, return
## matrix 'M' containing the polynomials of standardized time. 'M' is order t
## (number of time points) by k (order of Legendre polynomials).

## Arguments
## t: a vector of time, age or dph
## n: order of polynomials
## tmax: max time (optional)
## tmin: min time (optional)

## Literature: Mrode, R.A. 2005. Linear Models for the Prediction of Animal Breeding Values. CAB
International, Oxon, UK.

## Author: Gota Morota <morota at wisc dot edu>
## Created: 31-Mar-2010
## Last-Modified: 2-Apr-2010
## License: GPLv3 or later

`stdtime` <-
function(t, n, tmax, tmin){
  if(missing(tmax)) {
    tmax <- t[which.max(t)]
  }
  if(missing(tmin)) {
    tmin <- t[which.min(t)]
  }

  N <- n+1
  M <- matrix(0, nrow=length(t), ncol=N)
  a <- -1 + 2*(t-tmin)/(tmax - tmin)
  M[,1] <- 1

  for (i in 2:N){
    M[,i] <- a^(i-1)
  }

  return(M)
}

## Function legendre()
## Return coefficient matrix (lambda) of n-th order Legendre polynomials

## Arguments
## n: order of polynomials
## gengler: logical value. If TRUE, Gengler's scaling (1999) will be applied.
## If not specified, TRUE is assumed.

## Literatures
## Mrode, R.A. 2005. Linear Models for the Prediction of Animal Breeding Values.
## CAB International, Oxon, UK.
## Gengler, N. et. al. 1999. Estimation of (Co)variance Function Coefficients for
## Test Day Yield with a Expectation-Maximization Restricted Maximum Likelihood
## Algorithm. Journal of Dairy Science. 82

## Author: Gota Morota <morota at wisc dot edu>
## Create: 31-Mar-2010
## Last-Modified: 2-Apr-2010
## License: GPLv3 or later

`legendre` <-
function(n, gengler){
  if (nargs()==1){
    gengler <- TRUE
  }

  if (gengler != TRUE & gengler != FALSE){
    gengler=TRUE
  }

  N <- n+1
```

```

L <- matrix(0,nrow=N, ncol=N)

for(i in (1:N)){
  if(i==1){
    L[i,i] <- 1
  }
  else if(i==2){
    L[i,i] <- 1
  }
  else {
    tmp <- L[i-1,]
    tmp2 <- as.numeric()
    tmp2 <- c(0,tmp[1:(N-1)])
    L[i,] <- (1/(i-2+1))*( (2*(i-2) + 1)*tmp2 -(i-2)*L[i-2,] )
  }
}

# Normalize
for (j in (1:N)){
  L[j,] <- (sqrt( (2*(j-1)+1)/2) )*L[j,]
}

# Gengler (1999)
if (gengler==TRUE){
  L <- sqrt(2)*L
}

return(L)
}

#####
# Application of above for this study
#####

# Get a vector of all dph values
dph <- sort(unique(dat_asreml$dph))
# Count the number of unique
dph_num <- length(dph)

# Create M, lambda and phi matrices for Legendres of order 1-3
M_1 <- stdtime(dph, 1)
M_2 <- stdtime(dph, 2)
M_3 <- stdtime(dph, 3)

lambda_1 <- legendre(1, gengler=FALSE)
lambda_2 <- legendre(2, gengler=FALSE)
lambda_3 <- legendre(3, gengler=FALSE)

phi_1 <- M_1 %**% t(lambda_1)
phi_2 <- M_2 %**% t(lambda_2)
phi_3 <- M_3 %**% t(lambda_3)

```