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SUPPLEMENTARY MATERIAL

Maternal effects in a wild songbird are environmentally plastic but only marginally alter the rate of adaptation

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This document contains the supplementary tables and figures associated with the main text, as well as an R script to simulate the individual-based model.

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Table S1. Results of the linear mixed-model ('animal model') analysis on clutch size in great tits at the Hoge Veluwe (1956–2013; n = 5394 observations from 3328 females).

Variable		Estimate	SE	F/χ^2 [a]	df	p
Fixed effects						
Age mother	1st-time breeder	9.24	0.05	40.96	1, 4260.6	< 0.0001
	older	9.53	0.05			
Laying date (centred)		-0.08	0.00	250.9	1, 5278.7	< 0.0001
Year of breeding	1956	9.54	1.19	23.57	57, 4755.4	< 0.0001
	1957	8.85	0.54			
	1958	9.95	0.74			
	1959	10.25	0.37			
	1960	9.98	0.33			
	1961	9.96	0.21			
	1962	10.43	0.44			
	1963	10.30	0.36			
	1964	11.07	0.32			
	1965	10.04	0.24			
	1966	10.37	0.22			
	1967	9.37	0.18			
	1968	9.89	0.16			
	1969	9.97	0.16			
	1970	10.09	0.17			
	1971	8.78	0.15			
	1972	9.36	0.15			
	1973	9.35	0.17			
	1974	8.91	0.17			
	1975	7.94	0.14			
	1976	8.35	0.15			
	1977	9.17	0.13			
	1978	9.99	0.17			
	1979	10.00	0.19			
	1980	10.15	0.16			
	1981	8.41	0.16			
	1982	8.26	0.16			
	1983	8.73	0.16			
	1984	7.98	0.15			
	1985	9.61	0.23			
	1986	10.61	0.18			
	1987	9.97	0.16			
	1988	7.40	0.14			
	1989	9.22	0.17			
	1990	9.47	0.17			
	1991	7.97	0.15			
	1992	10.01	0.16			
	1993	8.49	0.16			

1994	9.06	0.16			
1995	9.58	0.18			
1996	9.20	0.15			
1997	10.28	0.18			
1998	10.33	0.18			
1999	9.22	0.17			
2000	9.57	0.19			
2001	8.12	0.15			
2002	8.89	0.18			
2003	9.16	0.14			
2004	9.30	0.19			
2005	8.84	0.15			
2006	9.21	0.21			
2007	8.69	0.16			
2008	8.94	0.15			
2009	10.52	0.18			
2010	10.19	0.17			
2011	10.64	0.16			
2012	8.41	0.14			
2013	8.10	0.19			
Random effects[b]					
Female identity (permanent environment)	0.50	0.14	13.29	1	0.0003
Additive genetic effect	0.76	0.14	35.54	1	<0.0001
Nest box identity	0.05	0.02	10.22	1	0.0014
Mother identity (maternal effect)	0.16	0.11	2.19	1	0.14
Residual	1.80	0.06			

[a]Conditional Wald *F* tests were used to test significance of fixed effects; likelihood-ratio tests were used for random effects.

[b]Likelihood-ratio tests and parameter estimates based on models excluding non-significant term.

Table S2. Results of the linear mixed-effects model analysis on the effect of experimentally manipulated brood size on fledgling weight in great tits at the Hoge Veluwe (1983–1990; n = 2145 observations from 309 broods). Marginal and conditional R^2 of the final model (Nakagawa and Schielzeth 2013) were 0.25 and 0.59, respectively.

Variable		Estimate[b]	SE	F	df[c]	p
Fixed effects[a]						
Brood size		–0.10	0.02	102.79	1, 287.7	<0.0001
Year of breeding	1983	0.35	0.06	7.45	7, 233.6	<0.0001
	1984	0.49	0.05			
	1985	0.67	0.07			
	1986	0.81	0.05			
	1987	0.79	0.06			
	1988	0.53	0.06			
	1989	0.85	0.09			
	1990	0.62	0.07			
Brood size × year	BS:1983	–0.09	0.02	3.31	7, 260.7	0.0021
	BS:1984	–0.08	0.01			
	BS:1985	–0.06	0.02			
	BS:1986	–0.06	0.01			
	BS:1987	–0.05	0.01			
	BS:1988	–0.30	0.06			
	BS:1989	–0.07	0.03			
	BS:1990	–0.05	0.02			
Orginal clutch size				3.32	1, 288.6	0.07
Hatching date				0.42	1, 284.9	0.52
Random effects		Variance	SD			
Brood identity: mother identity		0.07	0.26			
Mother identity		0.04	0.21			
Residual		0.13	0.36			

[a]Fixed terms expressed in boldface appeared in the final model; continuous variables are centred around their mean for each year.

[b]Parameter estimates are on a logit scale and given only for significant terms.

[c]Denominator degrees of freedom estimated using Kenward–Roger approximation.

Table S3. Results of the mixed-effects logistic regression analysis on offspring recruitment probability in great tits at the Hoge Veluwe (1973–2013; n = 24320 observations from 3600 broods).

Variable	Estimate	SE	χ^2	df	p[a]
Fixed effects					
Intercept	–19.06	2.92			
Fledgling weight	1.62	0.33	171.33	1	0.0006
[Fledgling weight]^2	–0.04	0.01	20.74	1	0.0005
Random effects	Variance	SD			
Year of breeding	0.43	0.66			
Brood identity: year of breeding	0.32	0.57			

Note: area under ROC curve: 0.80 (95% CI: 0.79–0.81)

[a]*P*-values of the likelihood-ratio test were simulated using parametric bootstrapping with 2000 simulations

Table S4. Result of the linear mixed-effects analysis on centred clutch size (M_{CS_i}) estimating the environmentally plastic maternal effect in first-time breeding great tits at the Hoge Veluwe (1973–2013; n = 510).

Variable	Estimate	SE	F	df[b]	p	R^2 [c]
Fixed effects[a]						
Intercept	–0.25	0.06				
Fledgling weight	0.13	0.05	8.16	1, 498.6	0.0045	0.006
Breeding value	2.95	0.09	1007.39	1, 504.4	<0.0001	0.640
Random effects[d]	Variance	SD				
Year of breeding	0.01	0.12				
Residual	1.27	1.13				

[a]Fixed terms expressed in boldface appeared in the final model; fledgling weight was centred around its mean for each year.

[b]Denominator degrees of freedom estimated using the Kenward–Roger approximation.

[c]Marginal R^2 for fixed effects based on Nakagawa and Schielzeth (2013), termed M^2_{CS} for the maternal effect in Table 1 (main text); conditional R^2 of final model: 0.646.

[d]Brood of origin was left out to allow for comparison of relative clutch size among members of the whole population.

Table S5. Result of the linear mixed-effects analysis on centred clutch size (M_{CS_i}) estimating the fixed maternal effect in addition to the plastic maternal effect in first-time breeding great tits at the Hoge Veluwe (1973–2013; n = 510).

Variable	Estimate	SE	F	df[c]	p	R^2 [d]
Fixed effects[a]						
Intercept	–0.25	0.06				
Breeding value	3.17	0.10	1101.40	1, 504.6	<0.0001	0.692
Maternal clutch size (z_{CS_m})[b]	–0.21	0.03	42.83	1, 488.5	<0.0001	0.027
Fledgling weight (z_{FW_t})[b]	0.10	0.04	5.21	1, 497.7	0.0228	0.003
Population mean fledgling weight ($\bar{z}_{FW_t}$)			2.41	1, 23.8	0.13	
$z_{CS_m} \times \bar{z}_{FW_t}$			0.02	1, 422.6	0.90	
Random effects[e]	Variance	SD				
Year of breeding	0.02	0.14				
Residual	1.17	1.08				

[a]Fixed terms expressed in boldface appeared in the final model.

[b]Values were centred around the mean for each year.

[c]Denominator degrees of freedom estimated using the Kenward–Roger approximation.

[d]Marginal R^2 for fixed effects based on Nakagawa and Schielzeth (2013), termed M^2_{CS} for the maternal effect in Table 1 (main text); conditional R^2 of final model: 0.726.

[e]Brood of origin was left out to allow for comparison of relative clutch size among members of the whole population.

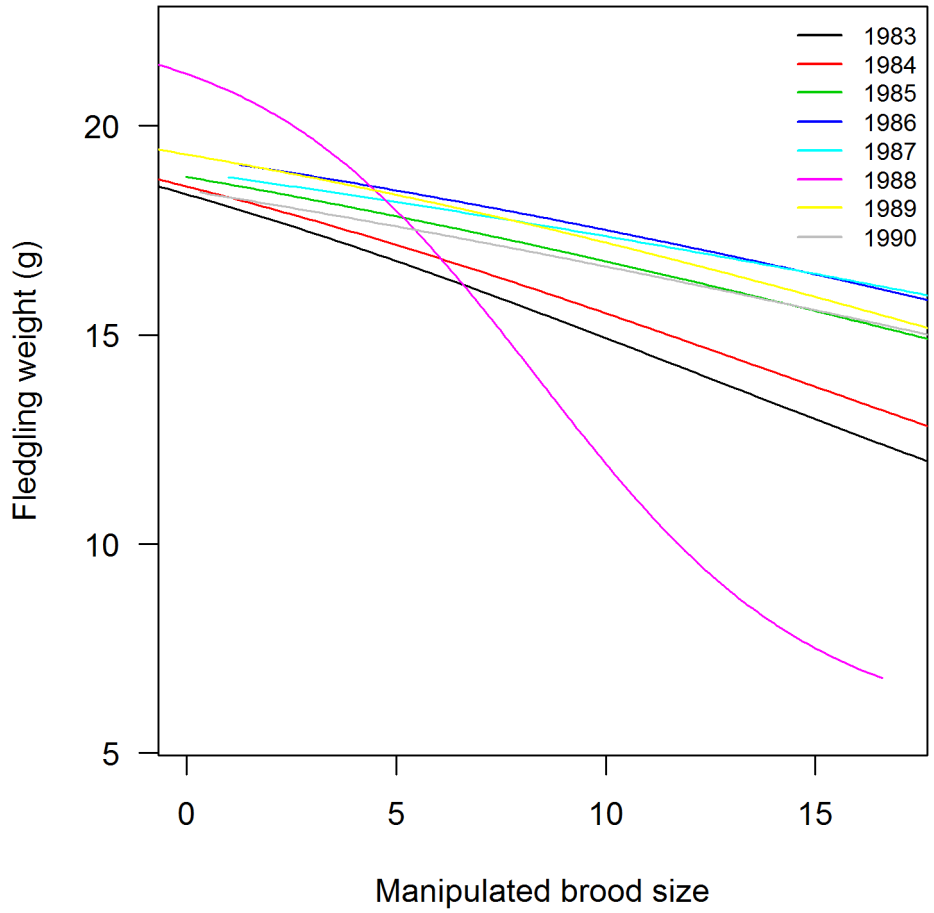


Fig. S1. Fledgling weight as a function of maternal clutch size, resulting from eight years of experimental brood size manipulations. Lines are back-transformed regression estimates from a linear mixed-effects model with a logit-transformed response variable.

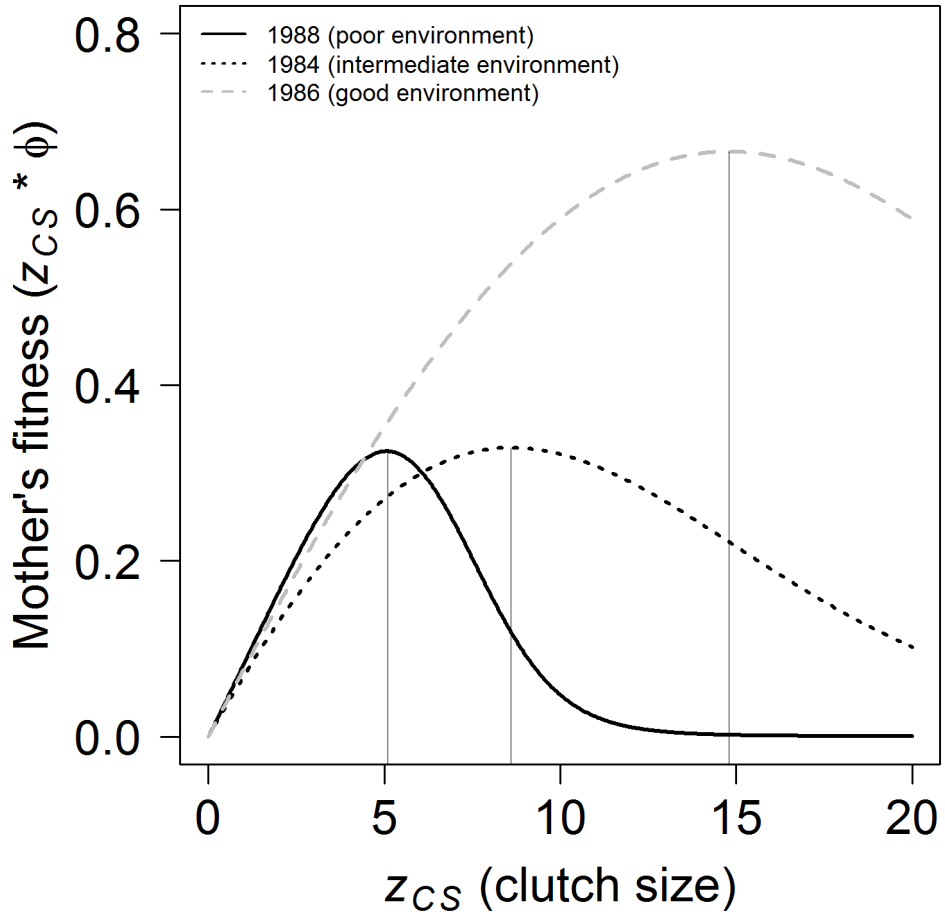


Fig. S2. Fitness curves associated with clutch size given different environments (solid line: poor environment; dashed line: intermediate environment, dotted line: good environment). Vertical lines denote the optimum phenotype for each environment.

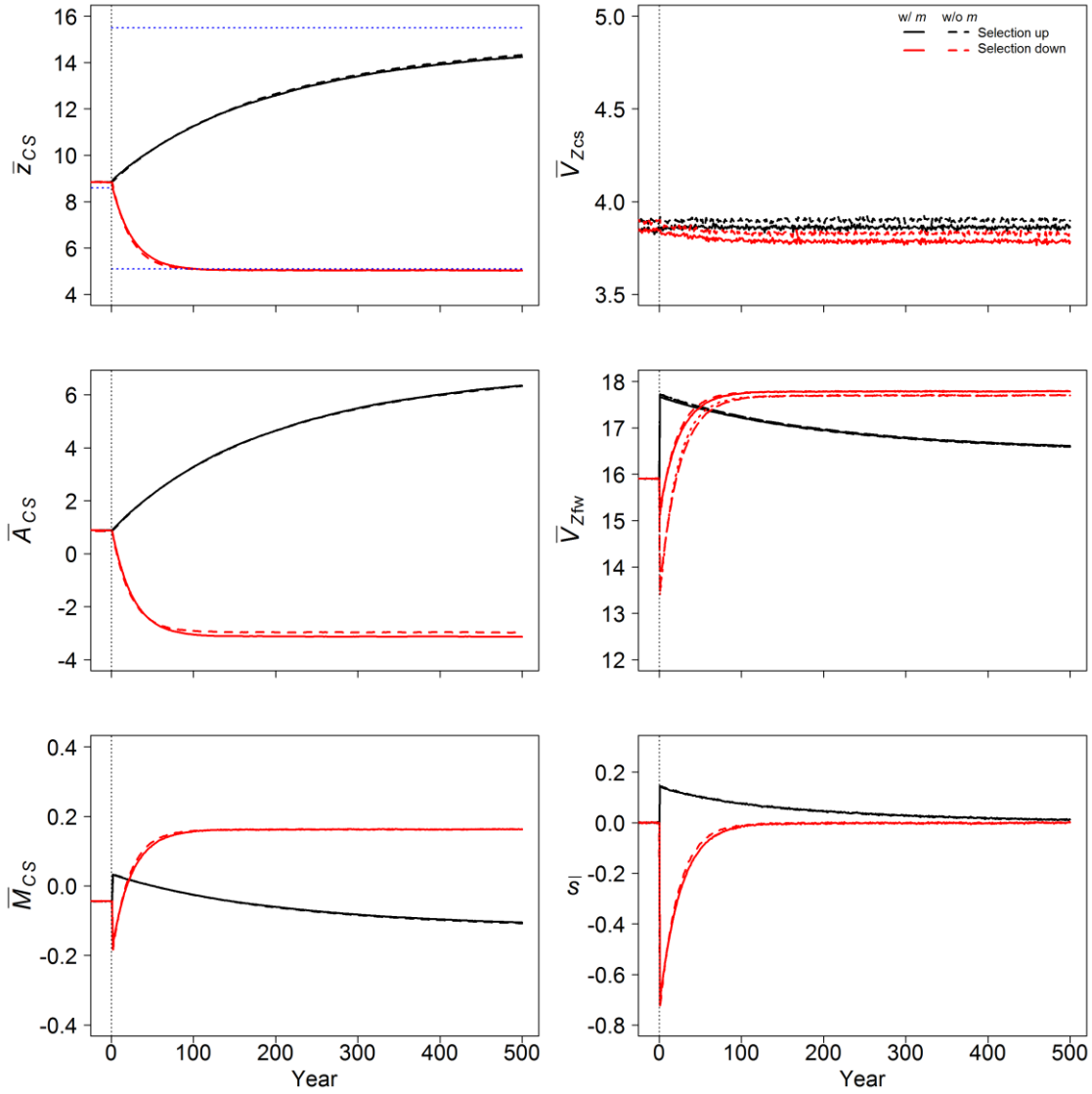


Fig. S3 (continued on next page). Environmentally plastic maternal effect-dependent (solid lines) or -independent (dashed lines) changes in mean phenotype $\bar{z}_{CS}$ (avian clutch size), genotype $\bar{A}_{CS}$, additive maternal component $\bar{M}_{CS}$, phenotypic variance $\bar{V}_{z_{CS}}$, fledgling mass $\bar{z}_{FW}$, and standardised selection differentials $\bar{s}$ over a time span of 500 years in an avian population modelled after the biology of the great tit at the Hoge Veluwe. The maternal effect is the effect of maternal clutch size on offspring clutch size via fledgling weight. The vertical line denotes the pre-burn-in period, after which selection moves from an intermediate clutch size to either a large (good environment) or small (poor environment) clutch; the blue dotted line in the $\bar{z}_{CS}$ panel denotes the 'optimal' phenotype, i.e. z at $W_{\max}$. In the $\bar{z}_{FW}$ panel, wide-dashed lines indicate fledgling weight before selection in presence of maternal effects (with solid lines indicating weight after selection), whereas dotted lines indicate weight before selection in absence of maternal effects (with narrow-dashed lines indicating weight after selection). Lines are the means of population averages over 1000 simulation runs. Input parameters are $\bar{V}_{z_{CS}}$ = 3.91, h^2_{CS} = 0.24, M^2_{CS} = 0.006, $m_p \approx$ –0.13, –0.04 or –0.03 (see main text and Table 1 for details).

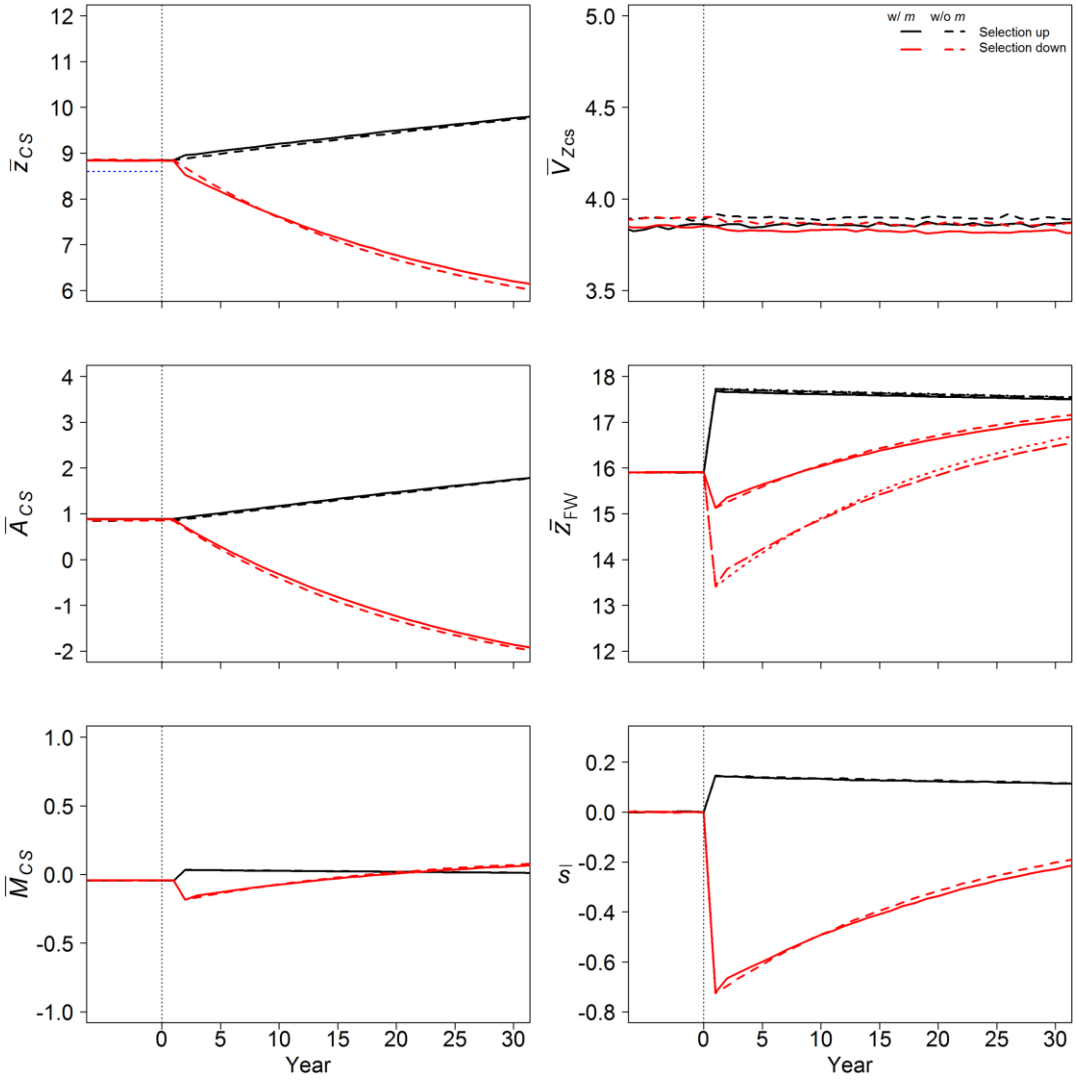


Fig. S3 (continued). Snapshot of the model simulation covering the first 30 years following the environmental shift.

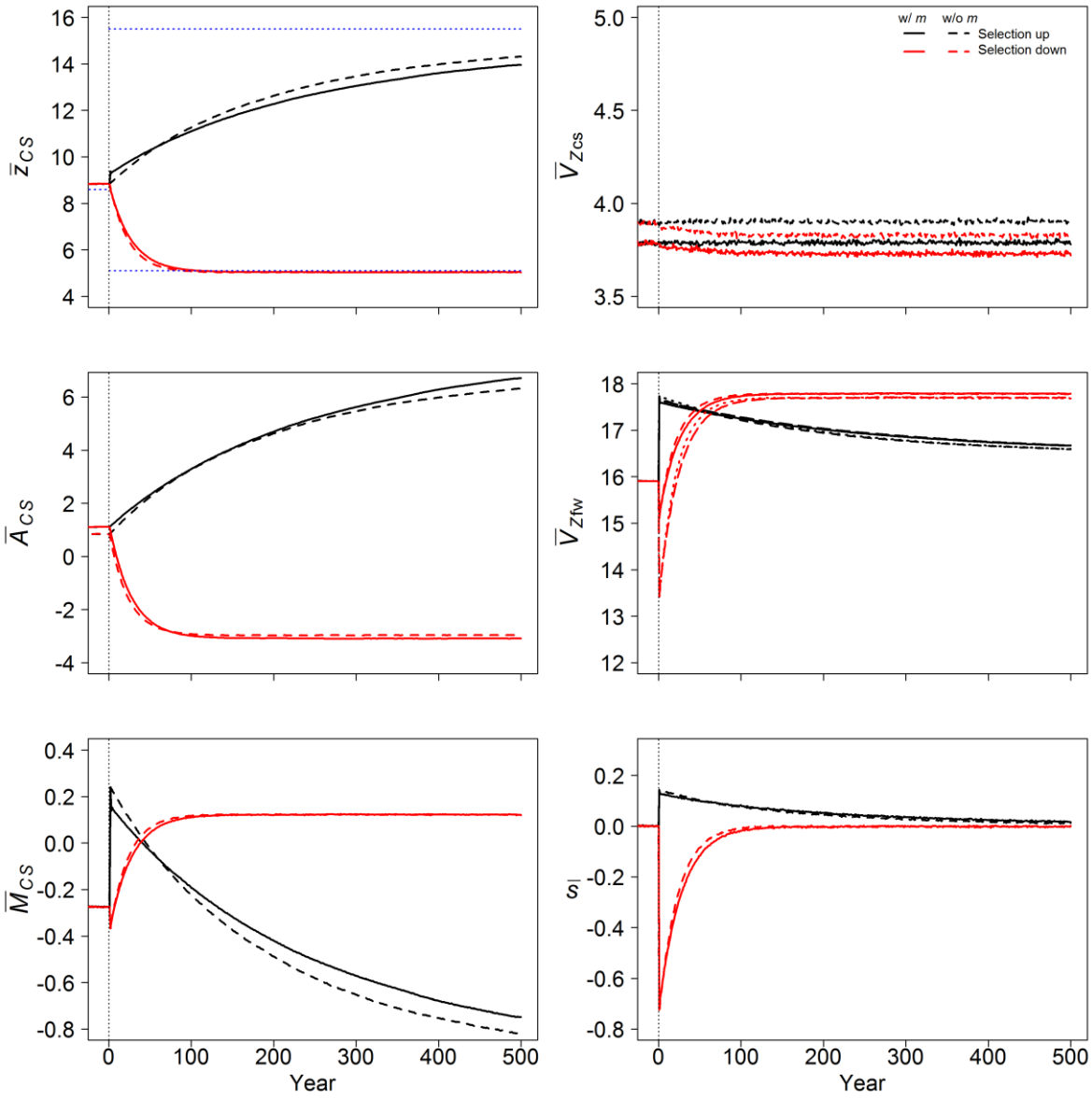


Fig. S4 (continued on next page). Fixed maternal effect-dependent (solid lines) or -independent (dashed lines) changes in mean phenotype $\bar{z}_{CS}$ (avian clutch size), genotype $\bar{A}_{CS}$, additive maternal component $\bar{M}_{CS}$, phenotypic variance $\bar{V}_{z_{CS}}$, fledgling mass $\bar{z}_{FW}$, and standardised selection differentials $\bar{s}$ over time span of 500 years in an avian population modelled after the biology of the great tit at the Hoge Veluwe. The maternal effect is the direct effect of maternal on offspring clutch size. The vertical line denotes the pre-burn-in period, after which selection moves from an intermediate clutch size to either a large (good environment) or small (poor environment) clutch; the blue dotted line in the $\bar{z}_{CS}$ panel denotes the 'optimal' phenotype, i.e. z at $W_{\max}$. In the $\bar{z}_{FW}$ panel, wide-dashed lines indicate fledgling weight before selection in the presence of maternal effects (with solid lines indicating weight after selection), whereas dotted lines indicate weight before selection in absence of maternal effects (with narrow-dashed lines indicating weight after selection). Lines are the means of population averages over 1000 simulation runs. Input parameters are $V_{z_{CS}}$ = 3.91, h^2_{CS} = 0.24, M^2_{CS} = 0.027, m_f = –0.21 (see main text and Table 1 for details).

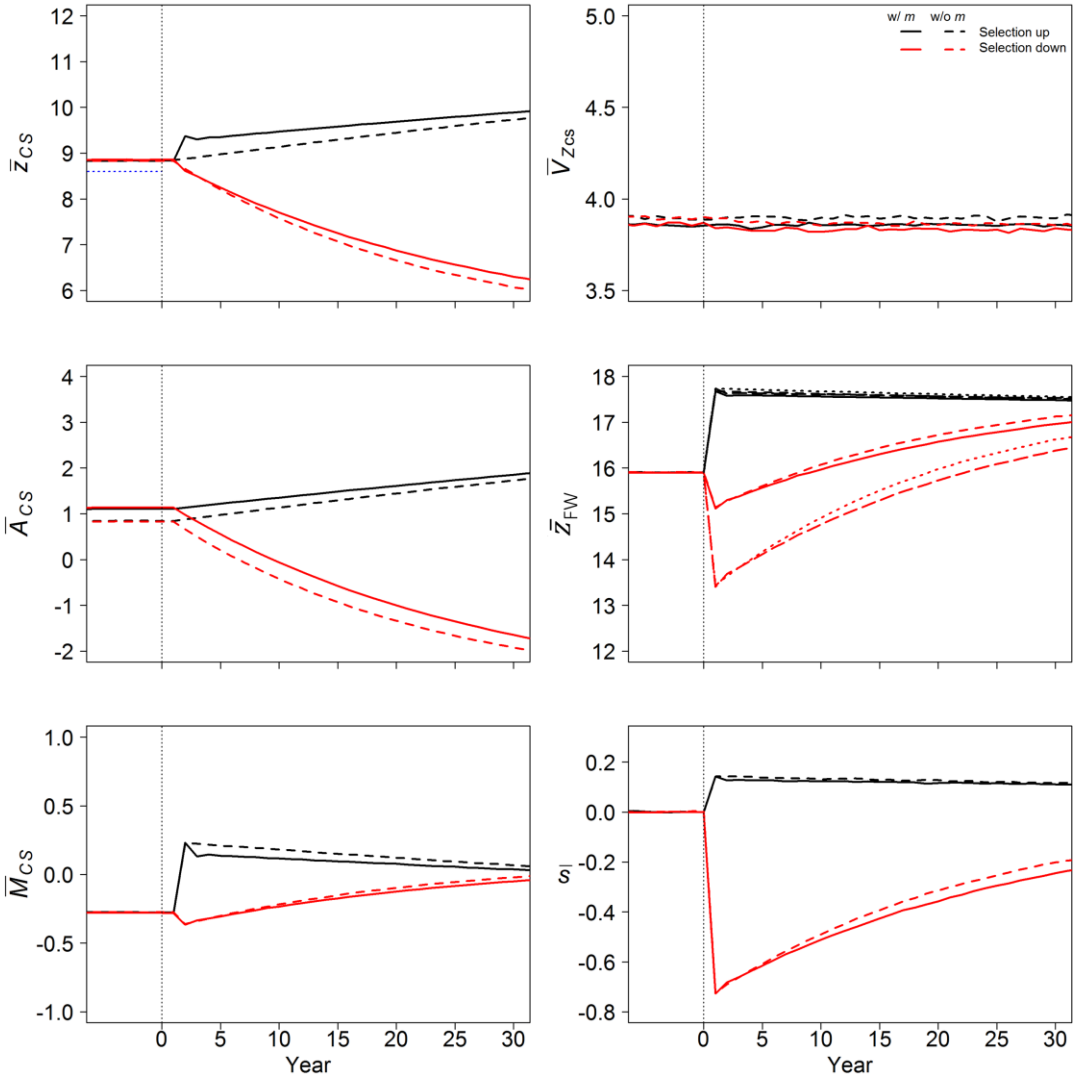


Fig. S4 (continued). Snapshot of the model simulation covering the first 30 years following the environmental shift.

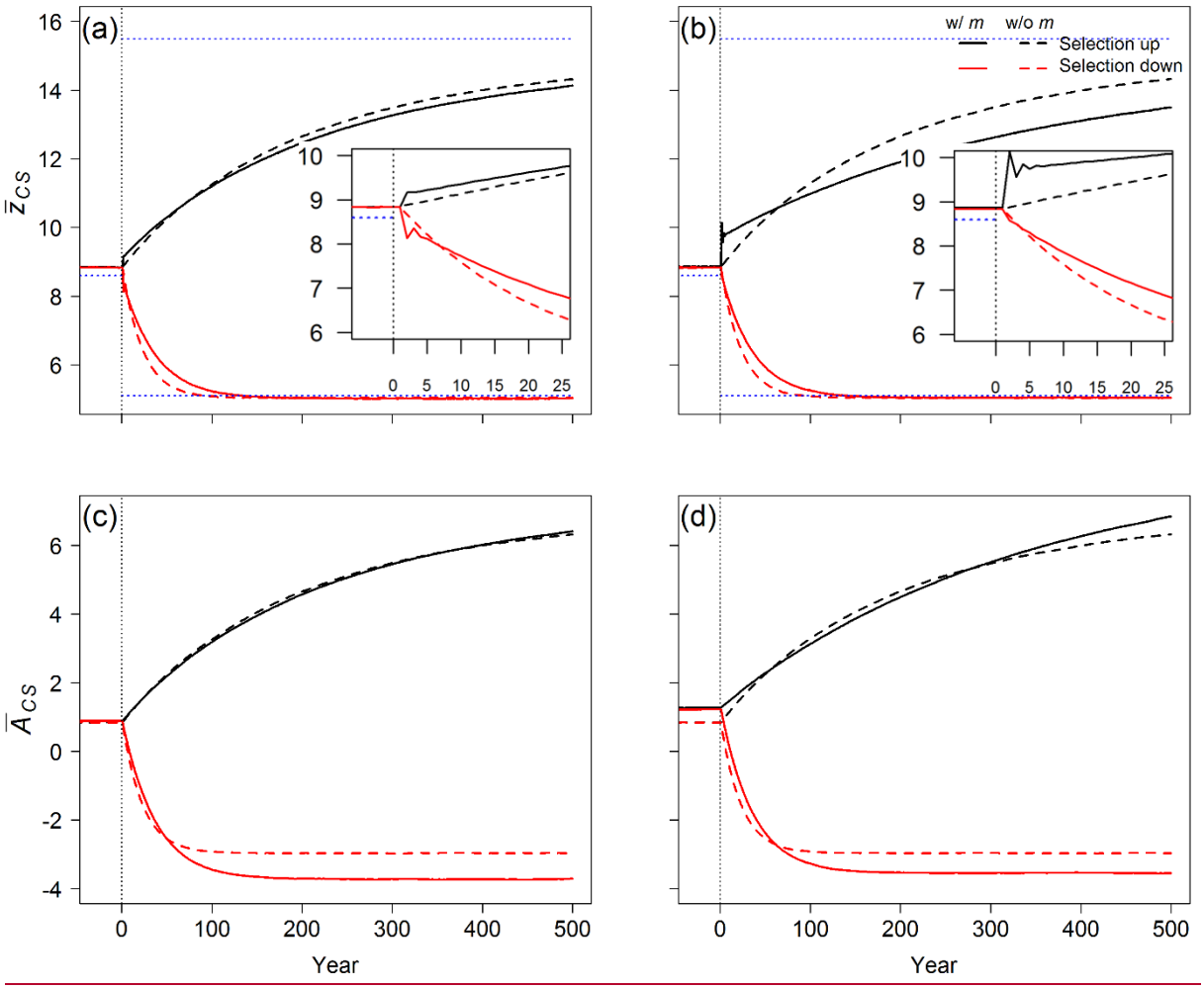


Fig. S5. Exaggerated maternal effects: predicted mean phenotypic (a, b) and genetic (c, d) change in avian clutch size (modelled after the great tit at the Hoge Veluwe) in response to selection when considering an exaggerated, environmentally plastic (i.e. via fledgling weight; a, c) or fixed (i.e. via maternal clutch size; b, d) maternal effect (solid lines), or no maternal effect at all (dashed lines). Phenotypic responses in the first 25 years are magnified in the insets in panels a and b. The vertical line denotes the pre-burn-in period, after which selection moves from an intermediate clutch size to either a large (good environment) or small (poor environment) clutch; the blue dotted lines in panels a and b denote the 'optimal' phenotype, i.e. z at W_{max}. Lines are the means of population averages over 1000 simulation runs. Input parameters are $V_{z_{CS}}$ = 3.91, h^2_{CS} = 0.24, M^2_{CS}= 0.006 (panel a and c) and 0.027 (panel b and d); $m_p \approx$ –0.52, –0.16 or –0.09, m_f = –0.5 (see main text and Table 1 for details).

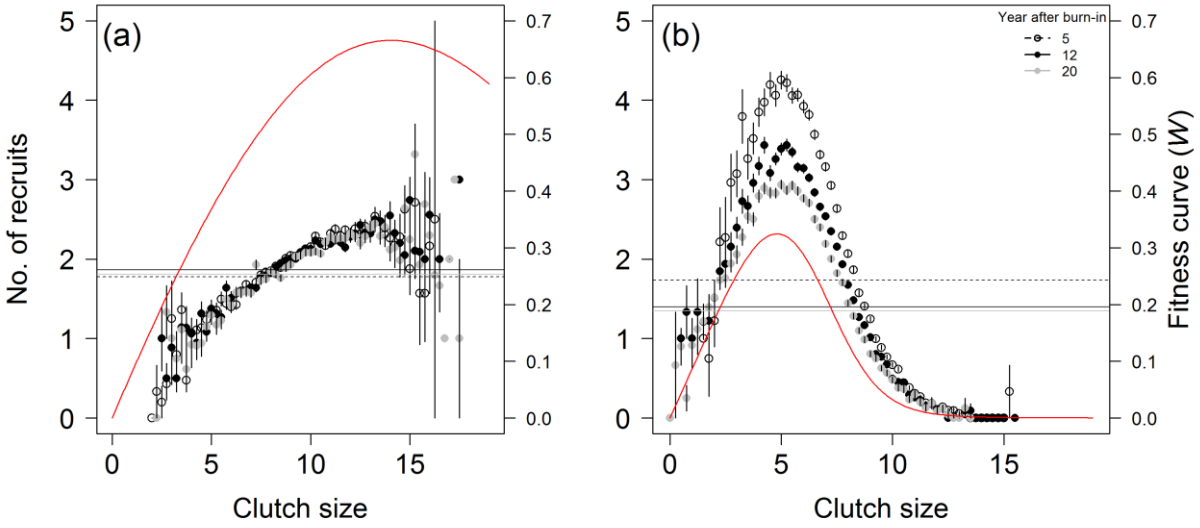


Fig. S6. The effect of maternal clutch size on fitness in a good (a) and poor (b) environment. Shown are the number of recruits (mean ± SE from 100 simulations; primary y axis) in three different generations following the environmental shift (year 5, 12, and 20), with the horizontal lines denoting the mean number of recruits associated with each year. Note that the heights of the 'curves' have no inherent meaning, as the total number of recruits was more or less equal in any given year. The red line denotes the fitness curves for the optimal trait value (eqn. 7 in main text; secondary y axis).

Reference

Nakagawa, S., and Schielzeth. 2013. A general and simple method for obtaining R^2 from generalized linear mixed-effects models. Methods in Ecology and Evolution 4:133–142.

Example R code for the individual-based model

```
#########################################################################################################################################################

###     Simple individual-based model roughly based on great tit life history.
###    NOTE: this particular script models the combined effect of fledgling weight & maternal clutch size on offspring clutch size

#########################################################################################################################################################

###     Basic parameters:

popsize1<- 500  # size of starting population
nyears  <- 1000 # simulate 1000 years
burnin  <- 500  # year number after which a new optimal phenotype kicks in
nsim    <- 1000  # repeat entire simulation 1000 times

Vz      <- 3.91         # phenotypic variance of 1st-clutch size HV dataset
h2      <- 0.24         # heritability from HV dataset
Va      <- Vz * h2      # additive genetic variance
r2.fw   <- 0.003        # proportion of Vz that is determined by plastic maternal effect (m_p)
r2.cs   <- 0.025        # proportion of Vz that is determined by fixed maternal effect (m_f)
Vm_p    <- Vz * r2.fw   # m_p variance
Vm_f    <- Vz * r2.cs   # m_f variance
switch  <- 1            # switches effect of m_f or m_p on and off



#########################################################################

###     Specific parameters:


## Fledgling weight as a function of the environment (on mean-centred fledgling weight; estimated from HV population):
weight.a.poor.cent.logit <- 0.53176028   # intercept of weight~phenotype relationship
weight.a.med.cent.logit <- 0.49121881    # (taken from 3 years with brood manipulations;
weight.a.good.cent.logit <-  0.80682573  # values in logit scale & based on centred CS)

weight.b.poor.cent.logit <- -0.30264491  # slopes, dito
weight.b.med.cent.logit <- -0.08348013
weight.b.good.cent.logit <- -0.05712750

## Entries for the logistic survival curve (on logit scale):
surv.a   <- -19.061352        # entries for logistic survival curve
surv.b   <-  1.620599
surv.c   <-  -0.039421

## Entries from maternal-effects model (on mean-centred fledgling weight; estimated from HV population):
m_p.a    <- -0.24749     # intercept of offsp.CS~fledweight relationship
m_p.b    <-0.09678       # slope of offsp.CS~fledweight relationship
```

```
m_p.c   <- 0.04303067   # mean breeding value (BLUPs)

## Entries from maternal-effects model (on mean-centred maternal clutch size; estimated from HV population):
m_f.a <- -0.24749       # intercept of offsp.CS~maternal.CS relationship
m_f.b <- -0.21          # slope of offsp.CS~maternal.CS relationship
m_f.c <- 0.05259404   # mean breeding value + mean centred fledgling weight


################################################################################
################################################################################

### Now initiate blank matrices for output:
sim               <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # number of simulation run
pop.size          <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # population size before breeding
pop.mean.phenotype<- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # mean phenotype before selection
pop.var.phenotype <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # variance in phenotype before selection
a.mean            <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # mean genotype
m_p.mean       <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # mean m_p component of phenotype (i.e. not the slope for m_p!)
m_f.mean       <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # mean m_f component of phenotype (i.e. not the slope for m_f!)
i.z               <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # standardised selection differential
pop.var.addgen    <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # population additive genetic variance
pop.var.m_p <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # population var. of maternal-effect (m_p) component (not slope)
pop.var.m_f <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # population var. of maternal-effect (m_f) component (not slope)
fw.before.sel     <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # fledgling weight before selection
fw.after.sel      <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # fledgling weight after selection
var.fw.bef.sel    <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # variation in fledgling weight before selection
var.fw.after.sel  <- matrix(NA,ncol=nyears,nrow=nsim, dimnames=list(1:nsim,1:nyears)) # variation in fledgling weight after selection


################################################################################
################################################################################

### SIMULATION STARTS HERE

ptm <- proc.time()              # get system time

for (Sim in 1:nsim) {           ### repeat whole simulation nreps times

  if(Sim/100==Sim%/%100) print(Sim)  # print 'sim' for every 100th simulation


  ### set up 'base' population
  a  <- rnorm(popsize1, 0, sqrt(Va))     # draw breeding values from a normal distribution with mean 0 and variance Va
  m_p  <- rnorm(popsize1, 0, sqrt(Vm_p)) # draw m_p component values from a normal distribution with mean 0 and variance Vm_p
  m_f <-  rnorm(popsize1, 0, sqrt(Vm_f)) # draw m_f component values from a normal distribution with mean 0 and variance Vm_f

  ### cycle over years
  for (year in 1:nyears)
  {
```

```
### store Population size, mean and variance of genotypes for elevation & slope and age structure
z <- 8 + a + switch*m_p + switch*m_f + rnorm(length(a), 0, sqrt(Vz-Va-switch*Vm_p-switch*Vm_f))
   # (create phenotypes by adding up a, m_p, m_f and residual)
z <- ifelse(z<0,0,z)  # avoid negative phenotypes (occurs very rarely)

sim[Sim,year]               <- Sim
pop.size[Sim,year]          <- length(a)
pop.mean.phenotype[Sim,year]<- mean(z, na.rm=T)
pop.var.phenotype[Sim,year] <- var(z, na.rm=T)
a.mean[Sim,year]            <- mean(a, na.rm=T)
m_p.mean[Sim,year]          <- mean(m_p, na.rm=T)
m_f.mean[Sim,year]          <- mean(m_f, na.rm=T)
pop.var.addgen[Sim,year]    <- var(a, na.rm=T)
pop.var.m_p[Sim,year]       <- var(m_p, na.rm=T)
pop.var.m_f[Sim,year]       <- var(m_f, na.rm=T)

### Random mating
ID <- 1:length(a)
npairs <- length(a)%/%2
father <- sample(ID,npairs,replace=F)
mother <- sample(ID[-father],npairs,replace=F)

### calculate midparent genotypes
a.fath <- a[match(father,ID)]
a.moth <- a[match(mother,ID)]
a.mid <- (a.moth+a.fath)/2

### calculate fledgling weight and number of surviving offspring
z.moth           <- z[match(mother,ID)] # phenotype (clutch size) of the mothers
z.moth.cent.med  <- z.moth - 8.447205   # centre around mean brood size in medium year
z.moth.cent.poor <- z.moth - 6.595556   # centre around mean brood size in poor year
z.moth.cent.good <- z.moth - 11.262443  # centre around mean brood size in good year

# IMPORTANT: switch from intermediate to either a good or poor year; adjust manually here:
if(year <= burnin) {ClutchSize <- z.moth.cent.med} else {ClutchSize <- z.moth.cent.poor} # switch from a medium to a poor or good year
Weight.a <- ifelse(year <= burnin, weight.a.med.cent.logit, weight.a.poor.cent.logit)    # switch from a medium to a poor or good year
Weight.b <- ifelse(year <= burnin, weight.b.med.cent.logit, weight.b.poor.cent.logit)    # switch from a medium to a poor or good year

fled.weight.logit <- Weight.a + ClutchSize * Weight.b
fled.weight <- (exp(fled.weight.logit)/(1+exp(fled.weight.logit))) * (22.5-5.5) + 5.5    # back-transformed weights

# Save mean fledgling weight and variance before selection:
fw.before.sel[Sim,year] <- mean(fled.weight)
var.fw.bef.sel[Sim,year] <- var(fled.weight)


surv.offsp.log <- surv.a + (surv.b * fled.weight) + surv.c * (fled.weight^2) # offspring survival
surv.offsp     <- 1/(1+exp(-surv.offsp.log))
```

```
    ### Calculate recruitment

    # calculate number of offspring that should be produced to keep population constant:
    mean.noffsp <- popsize1/npairs


    # Number of recruits produced:
    w1    <- surv.offsp * z.moth           # fitness based on phenotype
    w     <- w1 * (mean.noffsp/mean(w1))   # fitness rescaled to mean.noffsp required
    nrecr <- rpois(npairs,w)               # sample from a poisson distr. with mean = w (fitness)


    # Save mean fledgling weight and variance after selection:
    fw.after.sel[Sim,year] <- weighted.mean(fled.weight, nrecr)
    var.fw.after.sel       <- var(fled.weight[which(nrecr>0)])

    ### calculate breeding values and m component values of offspring

    # Breeding values:
    y     <- rnorm(sum(nrecr), 0, sqrt(Va*0.5)) # additive genetic deviates for offspring (to avoid shrinking of Va & add within-family var.)
    a     <- rep(a.mid, nrecr) + y              # replicate a.mid for every recruit to get their 'a'

    mean.wt.poor <- 16.22844     # mean fledgling weight in poor env (for centring purposes)
    mean.wt.med  <- 15.93413    # mean fledgling weight in med env (for centring purposes)
    mean.wt.good <- 17.10928    # mean fledgling weight in good env (for centring purposes)

    # maternal component values (IMPORTANT: switch manually here from med to either good or poor environment!):
    if(year <= burnin) {fledweight.centred <- fled.weight - mean.wt.med} else {fledweight.centred <- fled.weight - mean.wt.poor} #centred weights
    m_p <- m_p.a + m_p.b * rep(fledweight.centred, nrecr) + m_p.c
    m_f <- m_f.a + m_f.b * rep(ClutchSize, nrecr) + m_f.c


    ### calc. selection
    m.recr <- sum(nrecr)/npairs      # mean nr. of recruits per pair
    w      <- nrecr/m.recr           # recruits of pair i divided by mean
    # Save selection differential on phenotypes:
    i.z[Sim,year] <- cov(w, z.moth)/sd(z.moth)


  }   # end of loop over years

}   # SIMULATION ENDS HERE



### Storing data in dataframe 'res'

k1 <- data.frame(sim)
k1 <- stack(k1)
k1$year <- as.numeric(substr(as.character(k1$ind),2,nchar(as.character(k1$ind))))
```

```
res <- k1[,c(3,1)] ; names(res) <- c('year','sim')
k1 <- data.frame(pop.size)
k1 <- stack(k1)
res$pop.size <- k1$values
k1 <- data.frame(pop.mean.phenotype)
k1 <- stack(k1)
res$pop.mean.phenotype <- k1$values
k1 <- data.frame(pop.var.phenotype)
k1 <- stack(k1)
res$pop.var.phenotype <- k1$values
k1 <- data.frame(a.mean)
k1 <- stack(k1)
res$a.mean <- k1$values
k1 <- data.frame(m_p.mean)
k1 <- stack(k1)
res$m_p.mean <- k1$values
k1 <- data.frame(m_f.mean)
k1 <- stack(k1)
res$m_f.mean <- k1$values
k1 <- data.frame(i.z)
k1 <- stack(k1)
res$i.z <- k1$values
k1 <- data.frame(pop.var.addgen)
k1 <- stack(k1)
res$pop.var.addgen <- k1$values
k1 <- data.frame(fw.before.sel)
k1 <- stack(k1)
res$fw.before.sel <- k1$values
k1 <- data.frame(fw.after.sel)
k1 <- stack(k1)
res$fw.after.sel <- k1$values
k1 <- data.frame(var.fw.bef.sel)
k1 <- stack(k1)
res$var.fw.bef.sel <- k1$values
k1 <- data.frame(var.fw.after.sel)
k1 <- stack(k1)
res$var.fw.after.sel <- k1$values
k1 <- data.frame(pop.var.m_p)
k1 <- stack(k1)
res$pop.var.m_p <- k1$values
k1 <- data.frame(pop.var.m_f)
k1 <- stack(k1)
res$pop.var.m_F <- k1$values


proc.time() - ptm    # print run time
```