

SUPPLEMENTARY INFORMATION

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## Supplementary model code

The code used to implement analyses presented in SI tables 1-10 was as follows:

### *SI Table 1*

i) Without phylogeny

Prior: `list(R=list(V=1,nu=0.002))`

Model: `MCMCglmm(cbind(number of relatives, number of non-relatives) ~ log(extra-pair paternity+1), family = "multinomial2", nitt=600000, burnin=100000, thin=100)`

ii) With phylogeny

Prior: `list(R=list(V=1,nu=0.002), G=list(G1=list(V=1, nu=0.002))`

Model: `MCMCglmm((cbind(number of relatives, number of non-relatives) ~ log(extra-pair paternity+1), random = ~animal, pedigree=tree, family = "multinomial2", nitt=600000, burnin=100000, thin=100)`

### *SI Table 2 & 11*

i) Without phylogeny

Prior: `list(R=list(V=1,nu=0.002))`

Model: `MCMCglmm(cbind(extra-pair offspring, within-pair offspring) ~ Cooperation, family = "multinomial2", nitt=600000, burnin=100000, thin=100)`

ii) With phylogeny

Prior: `list(R=list(V=1,nu=0.002), G=list(G1=list(V=1, nu=0.002))`

Model: `MCMCglmm(cbind(extra-pair offspring, within-pair offspring) ~ Cooperation, random = ~animal, pedigree=tree, family = "multinomial2", nitt=600000, burnin=100000, thin=100)`

### *SI Table 3*

i) Without phylogeny

Prior: `list(R=list(V=1,nu=0.002))`

Model: `MCMCglmm(cbind(% extra-pair offspring, 100-% extra-pair offspring) ~ Cooperation, family = "multinomial2", nitt=600000, burnin=100000, thin=100)`

ii) With phylogeny

Prior: `list(R=list(V=1,nu=0.002), G=list(G1=list(V=1, nu=0.002))`

Model: `MCMCglmm(cbind(% extra-pair offspring, 100-% extra-pair offspring) ~ Cooperation, random = ~animal, pedigree=tree, family = "multinomial2", nitt=600000, burnin=100000, thin=100)`

*SI Table 4*

Prior: list(R = list(V = diag(2), nu=1.002, fix=2), G = list(G1=list(V = diag(2), nu =1.002)))

Model: MCMCglmm(cbind(cbind(extra-pair offspring, within-pair offspring), Probability of Cooperation) ~ trait-1, random = ~us(trait):species, rcov = ~us(trait):units, family = c("multinomial2", "categorical"), nitt=7100000, burnin=100000, thin=1000)

*SI Table 5 & 12*

Prior: list(R = list(V = diag(2), nu=1.002, fix=2), G = list(G1=list(V = diag(2), nu =1.002)))

Model: MCMCglmm(cbind(cbind(extra-pair offspring, within-pair offspring), Probability of Cooperation) ~ trait-1, random = ~us(trait):animal, rcov = ~us(trait):units, pedigree=tree, family = c("multinomial2", "categorical"), nitt=7100000, burnin=100000, thin=1000)

*SI Table 7 & 14*

Prior: list(R=list(V=1,nu=0.002), G=list(G1=list(V=1, nu=0.002))

Model: MCMCglmm(cbind(extra-pair offspring, within-pair offspring) ~ Cooperation category, random = ~animal, pedigree=tree, family = "multinomial2", nitt=600000, burnin=100000, thin=100)

*SI Table 8*

## i) Without phylogeny

Prior: list(R=list(V=1,nu=0.002))

Model: MCMCglmm(Z transformed rkin ~ extra-pair paternity+extra-pair paternity<sup>2</sup>, mev=measurement error variance, family = "gaussian", nitt=600000, burnin=100000, thin=100)

## ii) With phylogeny

Prior: list(R=list(V=1,nu=0.002), G=list(G1=list(V=1, nu=0.002))

Model: MCMCglmm(Z transformed rkin ~ extra-pair paternity+extra-pair paternity<sup>2</sup>, random = ~animal, mev=measurement error variance, pedigree=tree, family = "multinomial2", nitt=600000, burnin=100000, thin=100)

*SI Table 9*

## i) Without phylogeny

Prior: list(R=list(V=1,nu=0.002))

































































































































































































