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Supplemental Information

Ecology, Not the Genetics
of Sex Determination, Determines
Who Helps in Eusocial Populations

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# **Supplemental Data:**

Figure S1: Relates to figure 3 and 4. Phylogenetic relationships among social lineages. Branch lengths are proportional to time.

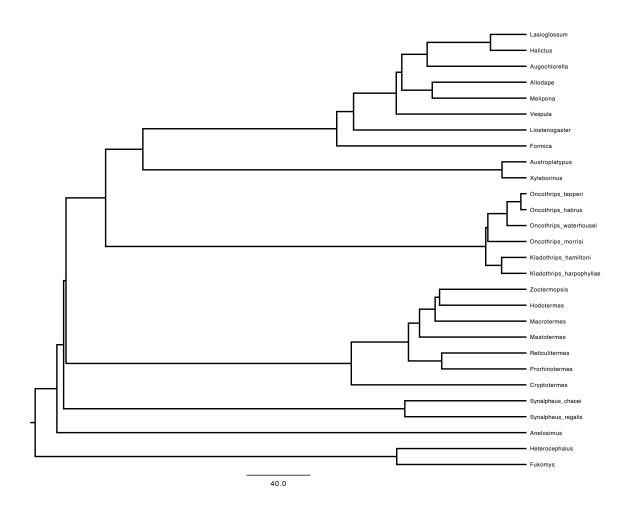


Figure S2: Relates to figure 4 and table S2. Proportion of eusocial origins with female/unbiased helpers (based on table S2). Data uncorrected for phylogeny.

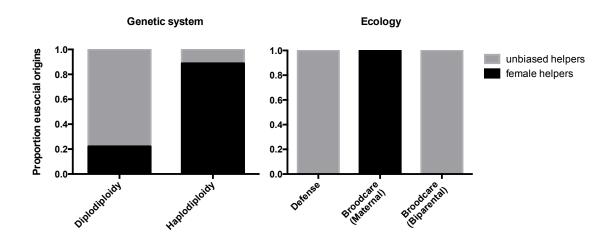


Figure S3: Relates to figure 2. Illustration of life-for-life relatedness for male or female helpers toward either offspring or siblings for haplodiploid and diplodiploid taxa. The pink ant represents a female while the blue ant represents a male.

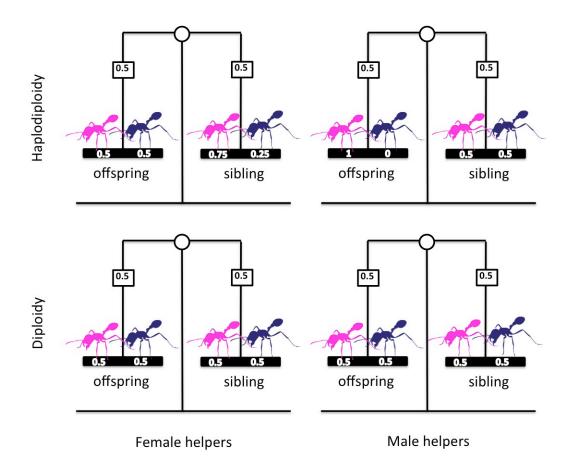


Table S1: Relates to figure 3 and 4. Genbank Accession numbers for DNA sequences used in phylogenetic analysis.

Taxon	Ef1a	168	Cytb	COI	LWO	285	185	Wingless	<b>12S</b>
Allodape	NA	NA	JN564695.1	JN564689.1	NA	NA	NA	NA	NA
Anelosimus	NA	JX977513.1	NA	JX977273.1	NA	JX977391.1	EF050203.1	NA	NA
Augochlorella	NA	NA	NA	JX546143.1	AY227935.1	JQ279154.1	AY995647.1	AY222572.1	NA
Austroplatypus	NA	NA	NA	FJ867832.1	NA	JN544546.1	NA	NA	NA
Cryptotermes	NA	HQ215842.1	AF189122.1	EU253840.1	NA	FJ806528.1	FJ806329.1	FJ706793.1	FJ805969.1
Formica	JQ519673.1	FR865871.1	JX170891.1	JX829423.1	FJ824464.1	FJ407396.1	FJ824197.1	AY233599.1	NA
Fukomys	NA	NA	AY425867.1	NA	NA	NA	NA	NA	AF012213.1
Halictus	EF601166.1	NA	NA	JX833115.1	JQ861245.1	JQ279228.1	AY995651.1	JQ266713.1	NA
Heterocephalus	NA	NC_015112.1	NC_015112.1	NA	NA	JH165919.1	NA	NA	NC_015112.1
Hodotermes	NA	NA	EU253913.1	JN615371.1	NA	JN615328.1	FJ806328.1	NA	FJ805968.1
Kladothrips hamiltoni	NA	AF386659.1	NA	U93515.1	NA	NA	NA	AF386728.1	NA
Kladothrips harpophyllae	NA	AF386664.1	NA	U93514.1	NA	NA	NA	NA	NA
Lasioglossum	NA	NA	NA	JX831587.1	JQ342159.1	JQ279184.1	GU320090.1	JQ266745.1	NA
Liostenogaster	NA	AF066939.1	NA	GU596840.1	NA	GU596730.1	EF190726.1	NA	GU596568.1
Macrotermes	NA	JX050221.1	JX501185.1	JF923342.1	NA	JQ957912.1	FJ806334.1	NA	JX050221.1
Mastotermes	EU414693.2	NC_018120.1	NC_018120.1	JN615367.1	NA	DQ441950.1	FJ806331.1	FJ802921.1	NC_018120.1
Melipona	EU163257.1	NC_004529.1	NC_004529.1	JN315139.1	AF344607.1	EU049745.1	HQ651726.1	GU245576.1	NC_004529.1
Oncothrips habrus	NA	DQ246465.1	NA	AY920992.1	NA	NA	NA	DQ246503.1	NA
Oncothrips morrisi	NA	AF386660.1	NA	U93532.1	NA	NA	NA	AF386729.1	NA
Oncothrips tepperi	NA	U93545.1	NA	U93527.1	NA	NA	NA	AF386731.1	NA
Oncothrips waterhousei	NA	AF386673.1	NA	AY920991.1	NA	NA	NA	NA	NA
Prorhinotermes	NA	EU253752.1	EU253925.1	EU253849.1	NA	EU253672.1	EU253791.1	NA	EU253713.1
Reticulitermes	AB602838.1	GU070788.1	JX501149.1	JQ431093.1	NA	JQ431133.1	JQ972694.1	NA	FJ805972.1
Synalpheus chacei	NA	HQ435440.1	NA	HQ435381.1	NA	NA	NA	NA	NA
Synalpheus regalis	NA	HQ435474.1	NA	HQ435406.1	NA	NA	NA	NA	NA
Vespula	NA	AY206804.2	NA	JX832523.1	NA	AF142527.1	AF142515.1	DQ353143.1	GU596560.1
Xyleborinus	AF259876.1	NA	NA	AB588938.1	NA	HM099727.1	AJ850038.1	NA	AF259835.1
Zootermopsis	NA	NC_018123.1	NC_018123.1	JN615368.1	NA	JN615325.1	EU253799.1	NA	NC_018123.1

Table S2: Relates to figure 3 and 4. Data included in the comparative analysis (including references). We were forced to exclude one of the Hymenopteran origins (Microstigma) because of a lack of sequence data. The representative taxon is the one for which we collected sequence data, life history data is extrapolated across larger taxonomic groups. Further justification for the assignments for some taxonomic groups is provided below. Taxa with an asterisk behind their name were excluded from the second analyses that followed the stricter "Crespi-Boomsma" definition of eusociality.

Order	Origin	Representative taxon	Genetic system	Helper sex	Helper task	Sister group	Ancestral care
Hymeoptera	1 [S1, S2]	Formica fusca	haplodiploidy [S1, S3]	female [S3]	broodcare [S3-5]	Solitary wasps [S4-7]	maternal [S2, S6, S7]
Hymeoptera	2 [S1, S2]	Vespula germanica	haplodiploidy [S1, S6]	female [S6]	broodcare [S4-6]	Solitary wasps [S4-7]	maternal [S2, S6, S7]
Hymeoptera	3 [S1, S2]	Liostenogaster	haplodiploidy [S1, S8]	female [S8, S9]	broodcare [S4, S5, S9]	Solitary wasps [S4-7]	maternal [S2, S6, S7]
		flavolineata					
Hymeoptera	4 [S1, S2]	Melipona subnitida	haplodiploidy [S1, S9]	female [S9]	broodcare [S4, S5, S9]	Solitary bees [S4, S5, S9]	maternal [S2, S9]
Hymeoptera	5 [S1, S2]	Allodape punctata	haplodiploidy [S1, S9]	female [S9]	broodcare [S4, S5, S9]	Solitary bees [S4, S5, S9]	maternal [S2, S9]
Hymeoptera	6 [S1, S2]	Lasioglossum rowheri	haplodiploidy [S1, S9]	female [S9]	broodcare [S4, S5, S9]	Solitary bees [S4, S5, S9]	maternal [S2, S9]
Hymeoptera	7 [S1, S2]	Halictus marginatus	haplodiploidy [S1, S9]	female [S9]	broodcare [S4, S5, S9]	Solitary bees [S4, S5, S9]	maternal [S2, S9]
Hymeoptera	8 [S1, S2]	Augochlorella striata	haplodiploidy [S1, S9]	female [S9]	broodcare [S4, S5, S9]	Solitary bees [S4, S5, S9]	maternal [S9, S10]
Rodentia	1	Heterocephalus glaber*	diplodiploidy [S9, S10]	both [S9]	broodcare [S9, S10]	Bathyergidae [S10, S11]	biparental [S10, S11]
Rodentia	2	Fukomys damarensis*	diplodiploidy [S9, S10]	both [S9]	broodcare [S9, S10]	Bathyergidae [S10, S11]	biparental [S11, S12]
Thysanoptera	1	Kladothrips hamiltoni	haplodiploidy [S12, S13]	both [S12, S13]	defense [S13, S14]	NA	NA
Coleoptera	1	Austroplatypus	diplodiploidy [S14-16]	female [S15,	broodcare [S15, S16]	Platypodinae [S16]	maternal [S16, S17]
		incompertus		S16]			
Coleoptera	2	Xyleborinus saxesnii*	haplodiploidy [S17]	female [S17]	broodcare [S17, S18]	Xyleborini [S16, S18]	maternal [S16, S19]
Decapoda	1 [S19, S20]	Synalpheus chacei*	diplodiploidy [S20]	both [S20]	defense [S19, S20]	NA	NA
Decapoda	2 [S19, S20]	Synalpheus regalis*	diplodiploidy [S20]	both [S20]	defense [S20, S21]	NA	NA
Araneae	1	Anelosimus eximius	diplodiploidy [S21]	female [S21]	broodcare [S21, S22]	subsocial <i>Anelosimus</i> [S16, S22]	maternal [S16, S22- S24]
Isoptera	1 [S23-25]	Macrotermes	diplodiploidy [S25]	both [S25, S26]	broodcare [S24, S27]	Cryptocercidae [S28, S29]	biparental [S23, S24,
	0 (000 05)	subhyalinus	II I II I I I I I I I I I I I I I I I	[505 606]			S28]
Isoptera	2 [S23-25]	Mastotermes darwiniensis	diplodiploidy [S25]	both [S25, S26]	broodcare [S24, S27]	Cryptocercidae [S28, S29]	biparental [S23, S24, S28]
Isoptera	3 [S23-25]	Cryptotermes secundus	diplodiploidy [S25]	both [S25, S26]	defense [S24, S27]	Cryptocercidae [S28, S29]	biparental [S23, S24, S28]
Isoptera	4 [S23-25]	Prorhinotermes	diplodiploidy [S25]	both [S25, S26]	defense [S24, S27]	Cryptocercidae [S28, S29]	biparental [S23, S24,
Icontoro	5 [S23-25]	simplex Reticulitermes flavipes	diplodiploidy [S25]	both [S25, S26]	broodcare [S24, S27]	Cryptocercidae [S28, S29]	S28] biparental [S23, S24,
Isoptera	5 [323-25]	Reticuliterines havipes	dipiodipiolay [525]	DOUT [325, 326]	broodcare [524, 527]	Cryptocerciade [528, 529]	S28]
Isoptera	6 [S23-25]	Zootermopsis	diplodiploidy [S25]	both [S25, S26]	defense [S24, S27]	Cryptocercidae [S28, S29]	biparental [S23, S24,
Isoptera	7 [S23-25]	nevadensis Hodotermes mossambicus	diplodiploidy [S25]	both [S25, S26]	broodcare [S24, S27]	Cryptocercidae [S28, S29]	S28] biparental [S13, S28, S30]

Table S3: Relates to figure 3 and 4. All available estimates of helper sex ratios in eusocial societies, including information on helper task.

Order	family	species	Colony sex ratio	Worker sex ration	Male helping (1= defense, 2= alloparental care)	Alloparental care (1=provisioning, 2=egg care, 3= transport)	Further comments
Araneae	Theridiidae	Anelosimus eximius	0.08-0.15 [S31]	-	none [S31]	present (1) [S25, S31]	
Coleoptera	Curculionidae	Austroplatypus incompertus	0.5 [S15, S16]	0 (female only) [S15]	none [S15]	present (1,2) [S15, S17]	
Coleoptera	Curculionidae	Xyleborinus saxesnii	0.05-0.12 [S17]	-	none [S17, S32]	present (1,2)	males occasionally allogroom, but this is considered courtship behaviour
Decapoda	Alpheidae	Synalpheus chacei	0.5 [S20, S32]	-	1 [S20]	absent [S20, S32]	
Decapoda	Alpheidae	Synalpheus regalis	0.5 [S20, S32]	-	1 [S20]	absent [S20, S31]	
Hymeoptera	-	All eusocial species	variable	0 (female only)	none (see comment)	in all species studied [S1,S2,S3]	Only a single species shows male cooperative behaviour; the ant Cardiocondyla where males were observed to carry larva
Isoptera	Hodotermitidae	Anacanthotermes ahngerianus		male biased (soldiers+workers) [S33]	yes	present [S24, S27]	
Isoptera	Hodotermitidae	Hodotermes mossambicus		male biased (soldiers) [S33]	yes	present [S24, S27]	
Isoptera	Kalotermitidae	Cryptotermes domesticus	0.5	0.5 (soldiers)	1	absent [S24, S27]	
Isoptera	Kalotermitidae	Cryptotermes secundus	0.5	0.2 (soldiers)	1	absent [S24, S27]	
Isoptera	Kalotermitidae	Incisitermes schwarzi	-	0.55 (0.61) [S33]	1	absent [S24, S27]	
Isoptera	Kalotermitidae	Neotermes connexus	fem biased	fem biased (soldiers) [S33]	1	absent [S24, S27]	
Isoptera	Rhinotermitidae	Coptotermes lacteus		fem biased (soldiers) [S33]	1	absent [S24, S27]	
Isoptera	Rhinotermitidae	Prorhinotermes simplex	0.5 [S25, S34]	0.5 (soldier) [S34, S35]	1+2	absent [S24, S27]	
Isoptera	Rhinotermitidae	Reticulitermes flavipes	≈ 0.5 [S35, S36]	≈ 0.5 [S35, S36]	1+2	present [S24, S27]	
Isoptera	Rhinotermitidae	Reticulitermes kanmonensis		≈ 0.4 [S25, S36]	1+2	present [S24, S27]	
Isoptera	Rhinotermitidae	Reticulitermes speratus		0.5 [S36]	1+2	present [S24, S27]	
Isoptera	Rhinotermitidae	Reticulitermes virginicus		female only [S36]	1+2	present [S24, S27]	
Isoptera	Rhinotermitidae	Schedorhinotermes Iamanianus		female biased (soldiers+pseudoworkers) [S33]	1+2	present [S24, S27]	
Isoptera	Termitidae	Amitermes evuncifer		unbiased (soldiers) [S33]	1+2	present [S24, S27]	
Isoptera	Termitidae	Constrictotermes cyphergaster		male biased (soldiers+workers) [S37]	1+2	present [S24, S27]	
Isoptera	Termitidae	Cornitermes walkeri		male biased (soldiers+workers) [S33]	1+2	present [S24, S27]	
Isoptera	Termitidae	Macrotermitinae		fem biased (soldiers) [S33]	1+2	present [S24, S27]	
Isoptera	Termitidae	Mastotermes darwiniensis	≈ 0.5 [S25, S34, S38]		1+2	present [S24, S27]	
Isoptera	Termitidae	Microcerotermes		fem biased (soldiers) [S33]	1+2	present [S24, S27]	
		fuscotibialis					
Isoptera	Termitidae	Nasutitermes arborum		male biased (soldiers) [S33]	1+2	present [S24, S27]	
Isoptera	Termitidae	Rhynchotermes perarmatus		male biased (workers) + fem biased (soldiers) [S33]	1+2	present (1,2,3)	
Isoptera	Termitidae	Sphaerotermes		male biased (soldiers) [S33]	1+2	present (1,2,3)	

		sphaerothorax					
Isoptera	Termitidae	Termes hospes		fem biased (soldiers) [S33]	1+2	present (1,2,3)	
Isoptera	Termitidae	Trinervitermes spp.		fem biased (workers) + male biased (soldiers) [S33]	yes	present (1,2,3)	
Isoptera	Termopsidae,	sp.		unbiased (soldiers) [S33]			
Rodentia	Bathyergidae	Fukomys damarensis	0.59 [S39, S40], 0.22- 0.29 [S39, S41]	-	1+2 [S30, S41]	present (3)	
Rodentia	Bathyergidae	Heterocephalus glaber	slight male bias [S42]	-	1+2 [S40, S42]	present (1,3)	
Thysanoptera	Phlaeothripidae	Kladothrips hamiltoni	0.94 (dispersers) [S30]	0.45 (soldiers) [S30, S43]	1 [S15, S16, S43]	absent	
Thysanoptera	Phlaeothripidae	Oncothrips habrus	0.49 (dispersers) [S30]	0.89 (soldiers) [S30, S43]	1 [S30, S43]	absent	High % soldier reproduction, biased soldier SR due to LMC
Thysanoptera	Phlaeothripidae	Oncothrips morrisi	0.69 (dispersers) [S30]	0.69 (soldiers) [S30]			High % soldier reproduction, biased soldier SR due to LMC
Thysanoptera	Phlaeothripidae	Oncothrips tepperi	0.89 (dispersers) [S30]	0.89 (soldiers) [S30, S43]	1 [S30, S43]	absent	High % soldier reproduction, biased soldier SR due to LMC
Thysanoptera	Phlaeothripidae	Oncothrips waterhousei	0.49 (dispersers) [S30]	0.88 (soldiers) [S30, S43]	1 [S30, S43]	absent	High % soldier reproduction, biased soldier SR due to LMC

Table S4: Relates to figure 4. Full summary table comparative analysis. The intercepts shows the estimate for diploid taxa with helpers that preform broodcare and a ancestral biparental care system. All other fixed effects are displayed a s the difference from the intercept. We also estimated the phylogenetic signal (the binary equivalent to Pagel's lamda), which was 0.11 (CI95%: 0.002-0.47).

Posterior	95% Credibility	Effective	рМСМС
mean	interval	samples	
-5.32	-10.871.08	1201	0.004**
9.51	2.04 - 10.2	1000	0.001**
-3.50	-11.21 - 3.58	1000	0.382
2.63	-3.41 - 9.77	1392	0.416
1.29	0.01 - 3.87	1000	
	mean -5.32 9.51 -3.50 2.63	mean interval  -5.32 -10.871.08  9.51 2.04 - 10.2  -3.50 -11.21 - 3.58  2.63 -3.41 - 9.77	mean         interval         samples           -5.32         -10.871.08         1201           9.51         2.04 - 10.2         1000           -3.50         -11.21 - 3.58         1000           2.63         -3.41 - 9.77         1392

Table S5: Relates to figure 4. Full summary table comparative analysis for the restricted model that excludes those taxa considered "cooperative breeders" by Crespi and Yanega [S44, S45] (indicated with an asterisks in table S2). The intercepts shows the estimate for diploid taxa with helpers that preform broodcare and a ancestral biparental care system. All other fixed effects are displayed a s the difference from the intercept. We also estimated the phylogenetic signal (the binary equivalent to Pagel's lamda), which was 0.14 (CI95%: 0.003-0.67).

	Posterior	95% Credibility	Effective	рМСМС
	mean	interval	samples	
FIXED EFFECTS				
Intercept (broodcare.biparental	-4.97	-10.400.046	1049	0.032*
+diploidy)				
broodcare.maternal	9.24	2.88 - 16.13	1000	<0.001**
Defense	-3.41	-11.14 - 4.36	1000	0.430
haplodiploidy	2.21	-4.11 – 9.04	1000	0.504
RANDOM EFFECTS				
phylogeny	2.15	0.011 - 8.79	1000	

Table S6: Relates to figure 2. Consanguinities of family members under diploidy and haplodiploidy, assuming outbreeding.

Actor	Consang	Consanguinity						
	Self	Daughter	Son	Sister	Brother			
Diploidy								
Female	1/2	1/4	1/4	1/4	1/4			
Male	1/2	1/4	1/4	1/4	1/4			
Haplodiploid	ly .							
Female	1/2	1/4	1/2	3/8	1/4			
Male	1	1/2	0	1/4	1/2			

## **Supplemental Experimental Procedures:**

### Assignment of helper sex ratio and helper task

#### Helper sex ratio

In general, we consider the helper sex ratio female only if more than 90% of helpers are female (sex ratio of 0.1) or if males have never been observed performing cooperative behaviours. In some species, there are only colony-level estimates of the sex ratio, in which case we use these estimates. In some taxa, both worker and reproductives sex ratios are highly skewed, in which case we assign female-biased helping only when the sex ratio of the helpers is more female-biased than that of the reproductives. The only exception to these rules are for determining the assignments for the thrips and the termites. Soldier sex ratio in both groups appears to be variable, yet in both cases this variation has appeared after the origin of eusociality. In thrips male soldier are present in all species studied but the sex ratio of soldiers is biased (in comparison to the reproductives) in a few of the more derived species, this bias is absent however in the most ancestral eusocial taxa and can be understood in terms of worker reproduction and local mate competition [S13, S30, S33, S46]. Likewise although several termites have a biased soldier caste this again appears to be a derived state [S33, S42, S46] not present either at the origin of eusociality or at the origins of a true worker caste. Therefore for both thrips and the primitive and advanced termites we have assigned the helper sex ratio as unbiased.

#### Helper task

Helpers in eusocial societies often engage in both broodcare and defense. However the importance of these two types of behaviours at the origin of eusociality differ (referred to as fortress defense vs. life insurance, Crespi, Queller). For example soldiers appeared at the origin of eusociality in thrips and termites, and primitive termites and thrips do not dispay alloparental broodcare, while all eusocial Hymenoptera provide some form of alloparental care. We expect alloparental care to be sex-linked if there is a pre-existing bias toward maternal care, while we do not expect such bias for defensive tasks. We have therefore divided the eusocial taxa in those that 1) *never* provide broodcare and those that 2) *do* provide some form of broodcare (evolving either from maternal or paternal care). We recognize three different behaviors as alloparental care: (1) direct provisioning of the young; (2) care for the eggs; and (3) transport of eggs and young. We indicate the presence of these behaviours in table S3

#### R Code and prior used for the analysis in the MCMCglmm package [S44]

```
library(MCMCglmm)
eus<-read.table("/Users/lauraross/eusoc_analysis_dataframe.txt",header=T)</pre>
tree1300.eus <- read.tree("/Users/lauraross/eusocial_1300.trees")</pre>
INtree.eus<- inverseA(tree1300.eus[[1]], nodes="TIPS")</pre>
gelmanprior < -list(B=list(mu=c(0,0,0,0),V=gelman.prior(\sim ecology+genetic.sys, data=eus,
scale=1+1+pi^2/3), R=list(V=1,fix=1), G=list(G1=list(V=diaq(1)*0.1, nu=1))
mphylMCMC.start<-MCMCglmm(helper.sex~ecology+genetic.sys, random=~animal, data=eus,</pre>
ginverse=list(animal=INtree.eus$Ainv), family="categorical", prior=gelmanprior,
pl=TRUE, slice=TRUE, nitt=1000, thin=1, burnin=0)
mphylMCMC<-mphylMCMC.start</pre>
for(i in 1:1300){
INtree.eus<- inverseA(tree1300.eus[[i]],nodes="TIPS")</pre>
start<-list(Liab=mphylMCMC$Liab[1,], R=1, G=list(G1=mphylMCMC$VCV[1,1]))</pre>
mphylMCMC<-MCMCqlmm(helper.sex~ecology+genetic.sys, random=~animal, data=eus,</pre>
family="categorical", prior=gelmanprior,
ginverse=list(animal=INtree.eus$Ainv), pl=TRUE,slice=TRUE, nitt=1000, thin=1,
burnin=999, start=start, verbose=FALSE)
if(i>300){
mphylMCMC.start$VCV[i-300,]<-mphylMCMC$VCV[1,]</pre>
mphylMCMC.start$Sol[i-300,]<-mphylMCMC$Sol[1,]</pre>
mphylMCMC.start$Liab[i-300,]<-mphylMCMC$Liab[1,]</pre>
}
print(i)
summary(mphylMCMC.start)
hist(mphylMCMC.start$Liab)
hist(mphylMCMC.start$VCV[,1]/(rowSums(mphylMCMC.start$VCV)+pi^2/3))
mean(mphylMCMC.start$VCV\[,1]/(rowSums(mphylMCMC.start$VCV)+pi^2/3))
HPDinterval(mphylMCMC.start$VCV[,1]/(rowSums(mphylMCMC.start$VCV)+pi^2/3))
write.table(predict(mphylMCMC.start, interval = "confidence"),"/Users/lauraross/
eusoc_analysis_predictions.csv",sep = ",")
```

**Analysis notes:** We marginalized over the posterior distribution of trees by sampling a tree from the posterior at iteration t, running the MCMC comparative analysis for 1000 iterations and saving

the last MCMC sample. The values of the latent variables and variance components were passed as starting values to the analysis at iteration t+1 for which a new tree from the posterior sample was taken. The process was repeated for 1300 iterations (i.e. t=1300) disposing the first 300 iterations as burnin. If the posterior distribution of the tree topology is variable then it is not clear how the latent variables at ancestral nodes from tree t should map onto the latent variables at ancestral nodes from tree t+1 when defining the starting value.

Given that the introduction of latent variables at ancestral nodes was a computational trick in order to exploit algorithms for solving sparse—linear systems rather than a necessity for valid inference, we ran models in which the parameter space was not augmented with the ancestral states and the only latent variables were associated with extant taxa which could be defined consistently between trees. For large phylogenies this may prove to be too slow, in which case 1000 independent MCMC analyses (one for each tree) could be performed, although the number of iterations per tree would probably have to be increased with a suitable burnin period to ensure that the posterior distribution of the comparative analysis parameters is adequately sampled.

#### Theory: Why doesn't the genetics of sex determination matter?

Inclusive fitness is gained by sending copies of one's genes into future generations. Hence, an actor values a recipient according to how well the recipient transmits copies of the actor's genes to future generations [S47]. This is the product of two quantities: their consanguinity (p), i.e. the extent to which the actor and recipient share genes in common; and the recipient's reproductive value (v), i.e. the extent to which they transmit their own genes to future generations [S48-50]. The consanguinities for diploid and haplodiploid family members are summarized in Table S6. The reproductive values are  $v_{\varphi} = 1/(1-z)$  for females and  $v_{\vartheta} = 1/z$  for males under diploidy, and  $v_{\varphi} = 2/(1-z)$  for females and  $v_{\vartheta} = 1/z$  for males under haplodiploidy, where z is the population sex ratio (proportion male).

Thus, in a diploid population, a female who raises b extra siblings at a cost of c to her own reproduction increases her inclusive fitness by an amount  $b \times (z \times p_{\text{Bro}|\mathbb{Q}} \times v_{\mathcal{O}} + (1-z) \times p_{\text{Sis}|\mathbb{Q}} \times v_{\mathbb{Q}}) - c \times (z \times p_{\text{Son}|\mathbb{Q}} \times v_{\mathcal{O}} + (1-z) \times p_{\text{Dau}|\mathbb{Q}} \times v_{\mathbb{Q}})$ , which is positive if  $c/b < \frac{1}{2}$ . For a male, the calculation is  $b \times (z \times p_{\text{Bro}|\mathbb{Q}} \times v_{\mathcal{O}} + (1-z) \times p_{\text{Sis}|\mathbb{Q}} \times v_{\mathbb{Q}}) - c \times (z \times p_{\text{Son}|\mathbb{Q}} \times v_{\mathcal{O}} + (1-z) \times p_{\text{Dau}|\mathbb{Q}} \times v_{\mathbb{Q}})$ , which is also positive if  $c/b < \frac{1}{2}$ . In a haplodiploid population, the calculation for a female is  $b \times (z \times p_{\text{Bro}|\mathbb{Q}} \times v_{\mathcal{O}} + (1-z) \times p_{\text{Sis}|\mathbb{Q}} \times v_{\mathbb{Q}}) - c \times (z \times p_{\text{Son}|\mathbb{Q}} \times v_{\mathcal{O}} + (1-z) \times p_{\text{Dau}|\mathbb{Q}} \times v_{\mathbb{Q}})$ , yielding exactly the same condition  $c/b < \frac{1}{2}$ . And for a male the calculation is  $b \times (z \times p_{\text{Bro}|\mathbb{Q}} \times v_{\mathbb{Q}}) - c \times (z \times p_{\text{Son}|\mathbb{Q}} \times v_{\mathbb{Q}}) + (1-z) \times p_{\text{Sis}|\mathbb{Q}} \times v_{\mathbb{Q}})$ , which also yields the condition  $c/b < \frac{1}{2}$ . Hence, the genetics of sex determination neither predisposes haplodiploid versus diploids to eusociality nor predisposes females versus males to altruistic helping in haplodiploid societies [S1, S51-55].

The above argument has been framed in terms of consanguinity and reproductive value. However, the concept of life-for-life relatedness, which combines these quantities into a single measure of value, is more commonly encountered in the social insect literature. Life-for-life relatednesses are recovered by multiplying the consanguinity of actor and recipient by the recipient's reproductive value, and dividing by the product of the actor's consanguinity to self and the actor's own reproductive value. For example, this recovers the familiar  $\frac{3}{4}$  relatedness between haplodiploid sisters:  $R_{\text{Sis}|\diamondsuit} = (p_{\text{Sis}|\diamondsuit} \times v_{\diamondsuit})/(p_{\text{Sel}|\diamondsuit} \times v_{\diamondsuit}) = \frac{3}{4}$ . Assuming an even sex ratio, the other consanguinities are:  $R_{\text{Bro}|\diamondsuit} = (p_{\text{Sis}|\diamondsuit} \times v_{\diamondsuit})/(p_{\text{Sel}|\diamondsuit} \times v_{\diamondsuit}) = \frac{3}{4}$ .  $R_{\text{Sis}|\diamondsuit} = \frac{1}{2}$ ,  $R_{\text{Bro}|\diamondsuit} = \frac{1}{2}$ ,  $R_{\text{Bon}|\diamondsuit} = \frac{1}{2}$ , and the above argument framed in terms of consanguinity and reproductive value reveals that this result continues to hold even when sex ratios are biased.

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