

Supporting Information

This file contains the Supporting Information for the manuscript “*Patterns of paternity skew among polyandrous social insects: What can they tell us about the potential for sexual selection?*” by Rodolfo Jaffé, Francisco Garcia-Gonzalez, Susanne P. A. den Boer, Leigh W.

Simmons and Boris Baer. It includes:

Table S1

Figures S1 and S2

References

Table S1: Observed and effective paternity frequency (K_{obs} and m_e respectively), method and sample size (n) used to calculate m_e , paternity skew (S), queen number (QN) and colony size (CS) for 87 polyandrous species of social Hymenoptera. Arithmetic means over all studied colonies are shown for K_{obs} , n , QN and CS, while harmonic means are presented for m_e .

Species	K_{obs}	m_e^a	Method ^b	n^c	QN ^d	CS ^e	S^f	-95% CL ^g	+95% CL ^g	References
Family Apidae										
Subfamily Apinini										
<i>Apis andreniformis</i>	13.50	10.50	pn	60	1	4900	0.24*	-0.18	0.10	[1, 2]
<i>Apis cerana</i>	18.80	14.10	pn	74	1	6884	0.26*	-0.20	0.08	[1, 3]
<i>Apis dorsata</i>	54.90	44.20	pn	140	1	36630	0.2*	-0.30	-0.05	[1, 3]
<i>Apis florea</i>	11.60	7.90	pn	81	1	6271	0.35*	-0.11	0.10	[1, 3]
<i>Apis koschevnikovi</i>	16.20	13.30	pn	74	1	7000	0.19*	-0.17	0.09	[1, 2]
<i>Apis laboriosa</i>	34.40	18.28	pp	135	1	36630 ^h	0.48*	-0.17	0.03	[4, 5]
<i>Apis mellifera</i>	12.00	11.60	pn	61	1	19524	0.04 ^{ns}	-0.15	0.11	[1, 6, 7]
<i>Apis nigrocincta</i>	54.00	40.30	pn	159	1	6884 ⁱ	0.26*	-0.23	-0.02	[1, 5]
Subfamily Bombini										
<i>Bombus bimaculatus</i>	1.25	1.05	pp	8	1	60	0.79*	-0.33	0.67	[6, 8]
<i>Bombus citrinus</i>	2.50	1.76	pp	10	1	50	0.49*	-0.38	0.25	[8, 9]
<i>Bombus hypnorum</i>	1.87	1.18	pp,ps	23	1	29	0.79*	0.00	0.37	[3, 10, 11]
<i>Bombus impatiens</i>	1.55	1.04	pp	10	1	450	0.92*	-0.25	0.45	[6, 8, 12]
<i>Bombus mixtus</i>	4.00	3.57	ps	5	1	50	0.14 ^{ns}	0.14	0.14	[8, 9]
<i>Bombus ternarius</i>	2.00	2.04	pp	12	1	100	x	x	x	[6, 8]
Subfamily Meliponini										
<i>Melipona beecheii</i>	2.20	1.13	ps	10	1	1192.18	0.89*	0.03	0.41	[13-15]
<i>Scaptotrigona postica</i>	3.00	1.38	ps	25	1	10375	0.81*	0.00	0.30	[3, 13-15]

Species	K_{obs}	m_e^a	Method ^b	n^c	QN ^d	CS ^e	S^f	-95% CL ^g	+95% CL ^g	References
Family Halictidae										
Subfamily Halictini										
<i>Lasioglossum malachurum</i>	1.20	1.07	ps	5	1	33	0.66*	0.08	0.53	[16, 17]
Family Formicidae										
Subfamily Aenictinae										
<i>Aenictus dentatus</i>	19.00	25.90	pn	35	1	550000	x	x	x	[18]
<i>Aenictus laeviceps</i>	17.80	18.80	pn	46	1	100000	x	x	x	[18, 19]
Subfamily Dorylinae										
<i>Dorylus molestus</i> ^j	17.81	15.93	pn	35	1	15000000	0.11*	-0.53	-0.04	[19-21]
Subfamily Ecitoninae										
<i>Eciton burchellii</i>	14.70	11.82	pn	131	1	900000	0.21*	-0.08	0.07	[19, 22, 23]
<i>Neivamyrmex carolinensis</i>	1.86	1.43	pn	20	19	110000	0.5*	-0.10	0.35	[24-26]
<i>Neivamyrmex harrisi</i>	4.10	3.90	pn	21	1	550000	0.06 ^{ns}	-0.22	0.22	[18, 27]
<i>Neivamyrmex nigrescens</i>	14.90	12.77	pn	49	1	110000	0.15*	-0.26	0.09	[18, 25]
Subfamily Ectatomminae										
<i>Gnamptogenys striatula</i>	1.24	1.25	r	8	14	372	x	x	x	[28-30]
<i>Rhytidoponera sp. 12</i>	1.03	1.59	r	22	22	577	x	x	x	[31-33]
Subfamily Formicinae										
<i>Camponotus festinatus</i>	1.03	1.02	r	14	1.25	3000	x	x	x	[34, 35]
<i>Camponotus ligniperdus</i>	1.02	1.02	ps	13	2.9	5500	x	x	x	[36, 37]
<i>Cataglyphis cursor</i>	4.91	3.79	pn	28	1	752	0.29*	-0.16	0.21	[38, 39]
<i>Cataglyphis sabulosa</i>	2.54	2.30	pp	20	1	186	0.16 ^{ns}	-0.17	0.28	[40]
<i>Formica aquilonia</i>	1.94	1.48	pp	22	10	550000	0.49*	-0.10	0.29	[41-44]
<i>Formica candida</i> ^k	1.03	1.00	ps	10	2.4	5500	x	x	x	[42, 45]
<i>Formica exsecta</i>	1.46	1.25	pp, r	19	1	12179	0.47*	0.01	0.37	[3, 42, 46, 47]

Species	K_{obs}	m_e^a	Method ^b	n^c	QN ^d	CS ^e	S^f	-95% CL ^g	+95% CL ^g	References
<i>Formica fusca</i>	1.24	1.11	r	17	3.3	500	0.53*	0.00	0.40	[42, 48, 49]
<i>Formica paralugubris</i>	1.25	1.11	r	12	100	100000	0.56 ^{ns}	0.00	0.62	[50, 51]
<i>Formica podzolica</i>	1.07	1.10	r	8	4.5	22500	x	x	x	[52, 53]
<i>Formica pressilabris</i>	1.15	1.12	pp	11	2.5	12179 ^l	0.21 ^{ns}	-0.20	0.51	[42, 44, 46]
<i>Formica rufa</i>	1.48	1.47	r	18	1	65000	0.02 ^{ns}	0.00	0.33	[25, 42, 49, 54]
<i>Formica sanguinea</i>	1.08	1.31	pp	7	3.25	12900 ^m	x	x	x	[42, 44, 46]
<i>Formica truncorum</i>	1.45	1.43	r	20	7.39	12900	0.04 ^{ns}	0.00	0.40	[42, 46, 55, 56]
<i>Lasius niger</i>	1.53	1.22	pp	16	1	24247	0.57*	-0.14	0.33	[3, 57]
<i>Myrmecocystus mimicus</i>	1.30	1.15	r	25	1.62	97	0.49*	0.00	0.32	[58, 59]
<i>Oecophylla smaragdina</i>	1.70	1.32	pp	16	1.87	500000 ⁿ	0.54*	-0.14	0.33	[60]
<i>Plagiolepis pygmaea</i>	2.89	2.37	pn	29	23.6	2600	0.28*	-0.10	0.22	[61, 62]
<i>Proformica longiseta</i>	3.50	1.23	pp	35	3.4	480	0.91*	-0.11	0.17	[63, 64]
Subfamily Myrmicinae										
<i>Acromyrmex echinator</i>	9.30	5.30	pp	203	1.35	6344	0.48*	-0.04	0.05	[65-67]
<i>Acromyrmex insinuator</i>	1.15	1.09	pp	15	?	5500	0.4 ^{ns}	-0.14	0.48	[65, 68]
<i>Acromyrmex octospinosus</i>	6.10	3.93	pp	45	1	1000	0.43*	-0.15	0.14	[69, 70]
<i>Allomerus octoarticulatus</i>	1.24	1.14	pp	10	1.16	116 ^o	0.43 ^{ns}	-0.25	0.45	[71, 72]
<i>Atta colombica</i>	2.50	1.85	pn	10	1	2000000	0.43*	-0.27	0.29	[70, 73, 74]
<i>Atta sexdens</i>	2.70	2.60	pp	14	1	6500000	0.06 ^{ns}	-0.25	0.36	[25, 75]
<i>Cardiocondyla batesii</i>	1.49	3.42	pp	19	1	65	x	x	x	[76]
<i>Cardiocondyla elegans</i>	4.52	4.34	pp	11	1	204	0.05 ^{ns}	-0.71	0.10	[77]
<i>Crematogaster smithi</i>	1.25	1.02	pp	12	1	165	0.92*	-0.20	0.57	[3, 78]
<i>Leptothorax acervorum</i>	1.06	1.09	r	24	2.1	84	x	x	x	[3, 79]
<i>Leptothorax pergandei</i>	1.08	1.02	r	52	1	52	x	x	x	[80]
<i>Myrmica punctiventris</i>	1.54 ^p	1.04	r	10	1.38	64	0.92*	0.00	0.53	[3, 81, 82]

Species	K_{obs}	m_e^a	Method ^b	n^c	QN ^d	CS ^e	S^f	-95% CL ^g	+95% CL ^g	References
<i>Myrmica rubra</i>	1.17	1.22	pp	10	7.6	961	x	x	x	[83]
<i>Myrmica ruginodis</i>	1.20	1.08	r	10	2.5	600	0.6*	0.00	0.53	[84]
<i>Myrmica scabrinodis</i>	1.73	1.45	pp	20	1.37	217	0.38*	-0.11	0.35	[85, 86]
<i>Myrmica sulcinodis</i>	1.35	1.12	pp, r	12	8.6	120	0.65*	0.00	0.40	[25, 87]
<i>Pogonomyrmex badius</i>	11.00	7.02	pp	28	1	5246	0.4*	-0.47	0.08	[88-90]
<i>Pogonomyrmex barbatus</i>	4.71	3.16	pn	20	1	12358	0.42*	-0.24	0.26	[25, 91]
<i>Pogonomyrmex inermis</i>	9.20	6.49	pn	20	1	500	0.33*	-0.52	0.05	[88, 89, 92]
<i>Pogonomyrmex mendozani</i> ^q	11.67	11.38	pn	20	1	615	0.03*	-0.84	-0.07	[89, 92]
<i>Pogonomyrmex occidentalis</i>	6.29	5.98	pp	20	1	8800	0.06 ^{ns}	-0.42	0.18	[88, 93]
<i>Pogonomyrmex pima</i> ^r	1.30	1.17	pn	15	1.74	400	0.44*	-0.12	0.29	[88, 94]
<i>Pogonomyrmex rugosus</i>	6.07	4.02 ^s	ps	21	1	11447	0.4*	0.04	0.38	[88, 89, 95]
Subfamily Nothomyrmecinae										
<i>Nothomyrmecia macrops</i>	1.43	1.21	pp	19	1	60	0.52*	-0.11	0.31	[3, 96]
Subfamily Ponerinae										
<i>Pachycondyla inversa</i>	3.10	2.38	pn	19	2.29	40	0.34*	-0.22	0.25	[27, 97, 98]
<i>Pachycondyla villosa</i>	3.40	1.67	pn	25	2.37	17	0.72*	-0.16	0.23	[27, 98, 99]
Family Vespidae										
Subfamily Polistinae										
<i>Polistes annularis</i>	1.05	1.35	r	16	?	67 ^t	x	x	x	[100, 101]
Subfamily Vespinae										
<i>Dolichovespula arenaria</i>	1.43	1.13	ps	15	1	378	0.7*	0.01	0.36	[102, 103]
<i>Dolichovespula media</i>	1.18	1.08	ps	20	1	74	0.56*	0.00	0.40	[103, 104]
<i>Dolichovespula norwegica</i>	1.36	1.08	ps	20	1	59	0.78*	0.00	0.40	[103, 104]
<i>Dolichovespula saxonica</i>	1.70	1.35	ps	20	1	69	0.5*	0.00	0.40	[103, 104]
<i>Dolichovespula sylvestris</i>	1.36	1.15	ps	20	1	76	0.59*	0.00	0.40	[103, 104]

Species	K_{obs}	m_e^a	Method ^b	n^c	QN ^d	CS ^e	S^f	-95% CL ^g	+95% CL ^g	References
<i>Vespa affinis</i>	1.50	1.19	pn	20	1	135 ^u	0.61*	-0.10	0.35	[105, 106]
<i>Vespa crabro flavofasciata</i>	1.35	1.13	ps	20	1	125	0.63*	0.00	0.40	[103, 107]
<i>Vespa crabro gribodi</i>	1.43	1.11	ps	20	1	550	0.74*	0.00	0.40	[103, 108]
<i>Vespa mandarinia</i>	1.10	1.03	ps	20	1	221	0.74*	0.00	0.40	[103, 109]
<i>Vespa simillima</i>	1.53	1.33	ps	30	1	410	0.38*	0.00	0.28	[106, 110]
<i>Vespula germanica</i>	3.12	2.60	ps	27	1	1000	0.24 ^{ns}	0.01	0.31	[3, 111, 112]
<i>Vespula maculifrons</i>	5.64	4.96	pn	41	1	1000	0.15 ^{ns}	-0.13	0.15	[103, 113]
<i>Vespula rufa</i>	2.19	1.50	ps	25	1	57	0.58*	0.00	0.29	[103]
<i>Vespula squamosa</i>	7.25	5.58	pn	46	1	1000	0.27*	-0.16	0.14	[103, 113]
<i>Vespula vulgaris</i>	2.29	1.90	ps	20	1	1000	0.3 ^{ns}	0.01	0.36	[103, 114]

^a When raw data were not available m_e estimates were taken as reported in papers. ^b m_e was estimated from relatedness (r) or from pedigree analysis (p), and in the latter case it was based on the formulas given by Starr (1984)[115] (ps), Pamilo (1993)[41] (pp) or Nielsen et al. (2003)[116] (pn). ^c Mean number of workers analysed per colony. ^d Mean number of queens per colony. ^e Colony size expressed as mean worker population of a mature colony. Colony size is either a mean of values reported in one or multiple studies or an estimate of order of magnitude if data were unavailable. ^f Paternity Skew (S) estimated as $S=(K_{obs}-m_e)/(K_{obs}-1)$ according to Pamilo & Crozier (1996)[117]. Negative S values and S values from chiefly monoandrous species ($K_{obs} < 1.10$) are omitted (marked with an “x”, see methods for details). Cases where skew estimates were larger than the upper 95% confidence limit (CL) of the random S expectation are highlighted with *, while cases where S is within the 95% CL are highlighted by "ns". ^g Lower and upper 95% CL for random skew expectation obtained from simulations (see “Paternity skew analyses within species” section in methods). ^h Estimated to be similar in size as *A. dorsata*[5]. ⁱ Estimated to be similar in size as *A. cerana*[5]. ^j *Dorylus molestus* = *D. (Anomma) molestus*. ^k *Formica candida* = *F. transcaucasica*. ^l Estimated to be similar in same size as *F. exsecta*[44]. ^m Estimated to be similar in size as *F. truncorum*[44]. ⁿ Maximum estimate. ^o Estimate assuming one domatia can host three workers and an average domatia number per tree of 39. ^p Estimate assuming monogyny and double mating in all nests not consistent with one singly mated queen. ^q *P. pronotalis*. in Pol et al. (2008)[92] = *Pogonomyrmex mendozanus*, as described by Cuerdo & Claver (2009)[118]. ^r *Pogonomyrmex pima* = *P. (Epehebomyrmex) pima*. ^s Estimate based on monogynous colonies. ^t Estimate assuming the number of workers is 14% the number of cells, as in *P. gallicus*[119]. ^u Estimate assuming the number of workers is 12% the number of cells, as in *V. simillima*[106].

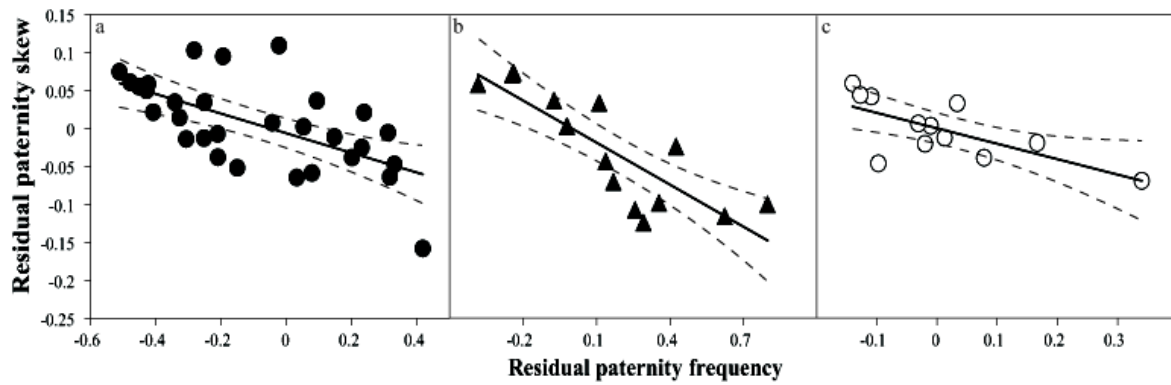


Figure S1: Relationship between paternity skew and paternity frequency in ants (a), bees (b) and wasps (c) after controlling for variation in colony size (only species showing significant skew values included, see Tables 2 and 3 for statistics and sample sizes). Residual values were obtained from simple regressions controlling for phylogenetic effects. Dashed lines represent 95% confidence limits for fitted values.

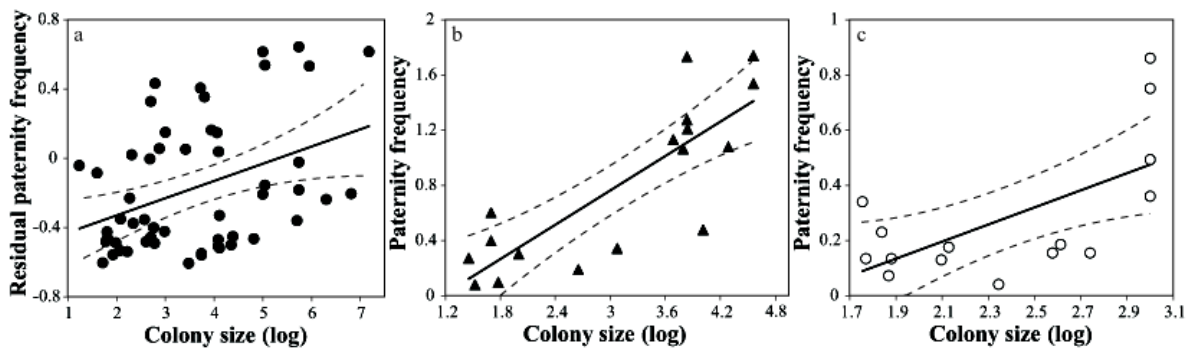


Figure S2: Relationship between paternity frequency and colony size in ants (a), bees (b) and wasps (c). Only species with a known queen number were included (see Tables 2 and 3 for statistics and sample sizes). Variation in queen number was controlled for only in ants, since all the bee and wasp species used had a single queen per colony. Residual values were obtained from a simple regression controlling for phylogenetic effects. Dashed lines represent 95% confidence limits for fitted values.

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