Male parentage in dependent-lineage populations of the harvester ant *Pogonomyrmex barbatus*

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Abstract

We investigated the extent to which workers reproduce in a dependent-lineage population of the monogynous harvester ant Pogonomyrmex barbatus. Dependent-lineage populations contain two interbreeding, yet genetically distinct mitochondrial lineages, each associated with specific alleles at nuclear loci. Workers develop from matings between lineages, and queens develop from matings within lineages, so queens must mate with males of both lineages to produce daughter queens and workers. Males develop from unfertilized eggs and are haploid. Worker production of males could lead to male-mediated gene flow between the lineages if worker-produced males were reproductively capable. This could result in the loss of the dependent-lineage system, because its persistence depends on the maintenance of allelic differences between the lineages. To investigate the extent of worker reproduction in P. barbatus, we genotyped 19-20 males and workers from seven colonies, at seven microsatellite loci, and 1239 additional males at two microsatellite loci. Our methods were powerful enough to detect worker reproduction if workers produced more than 0.39% of males in the population. We detected no worker-produced males; all males appeared to be produced by queens. Thus, worker reproduction is sufficiently infrequent to have little impact on the dependent-lineage system. These results are consistent with predictions based on inclusive fitness theory because the effective queen mating frequency calculated from worker genotypes was 4.26, which is sufficiently high for workers to police those that attempt to reproduce.

Keywords: inclusive fitness, parentage, social insect, worker reproduction

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Introduction

Social insect societies are characterized by reproductive division of labour between queens and workers (Oster & Wilson 1978). However, workers of some species can produce unfertilized eggs that develop into haploid males (Charnov 1978). The lack of worker reproduction in colonies with a living queen has been explained by invoking inclusive fitness theory (Villesen & Boomsma 2003; Kronauer *et al.* 2006). However, the degree to which worker reproduction depends on nestmate relatedness remains controversial (Hammond & Keller 2004; Ratnieks *et al.* 2006). Worker reproduction is predicted not to occur when the population-wide effective mating frequency of queens is sufficiently

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high that workers are more related to the queen's sons than they would be to the sons of other workers (Hamilton 1972; Starr 1984; Ratnieks 1988). These circumstances could select for worker policing, worker aggression towards workers with developing ovaries (Monnin & Ratnieks 2001; Iwanishi *et al.* 2003) or selective removal of eggs laid by other workers (Ratnieks 1989; Foster & Ratnieks 2000, 2001; Halling *et al.* 2001; Oldroyd *et al.* 2001; Helanterä & Sundström 2005). Policing may also occur in the absence of relatedness-based conflict among colony members (Ratnieks 1988; Arevalo *et al.* 1998; Hartmann *et al.* 2003; Hammond & Keller 2004).

Inclusive fitness theory predicts that worker reproduction is absent or suppressed in harvester ants (genus *Pogonomyrmex*). Queens mate with many males in North American populations of this genus (Cole & Wiernasz 1999; Volny & Gordon 2002a; Gadau *et al.* 2003), which should result in low relatedness among nestmates, and no worker-produced

males. However, workers do have developed ovaries, and males have been observed in queenless laboratory colonies of *Pogonomyrmex badius* (Smith & Tschinkel 2006), and *Pogonomyrmex barbatus* (D.M. Gordon, personal observation). The extent to which workers realize their reproductive potential in natural populations remains unknown.

The evolution of worker reproduction within the harvester ant species complex that includes P. barbatus and its sister species Pogonomyrmex rugosus may be complicated by a newly discovered system of reproductive caste determination in some populations. In most ant species, the development of female eggs into either queens or workers is governed by environmental factors (Wheeler 1986, 1994). However, recent work has uncovered populations of *P. barbatus* in which reproductive caste is strongly associated with genotype. These dependent-lineage populations are widespread throughout the southwestern USA (Anderson et al. 2006; Schwander et al. 2007) and contain sets of two interbreeding but genetically distinct lineages (J1 and J2; Helms Cahan et al. 2002, 2004; Julian et al. 2002; Volny & Gordon 2002a; Helms Cahan & Keller 2003; Schwander et al. 2007). Lineages are cryptic and are characterized by distinct mitochondrial haplotypes, each associated with specific alleles at nuclear microsatellite loci (Helms Cahan & Keller 2003). Between-lineage matings result in the production of workers, and within-lineage matings result in the production of gynes; each lineage is unable to produce workers independently of the other (Helms Cahan et al. 2004). Thus, workers are heterozygous at the nuclear loci at which alleles are fixed within the lineages (Julian et al. 2002; Volny & Gordon 2002a; Helms Cahan & Keller 2003). Males develop from unfertilized eggs and are haploid.

Models that explain the maintenance of the dependentlineage system must explain both the persistence of genetically distinct lineages within populations, and the association of heterozygosity with workers and homozygosity with gynes. Helms Cahan & Keller (2003) proposed that the two lineages arose from historical hybridization events and in the process became fixed for incompatible alleles at interacting nuclear loci, so an interlineage combination of nuclear alleles is necessary to initiate worker development. Linksvayer et al. (2006) proposed that the system is the result of deleterious incompatibilities between nuclear and mitochondrial genomes in interlineage individuals that result in the development of workers. Under both models, worker reproduction could affect the stability of the dependent-lineage system (Linksvayer et al. 2006), because worker-produced males could have nuclear genomes with alleles of both lineages at different nuclear loci. If recombination occurs within workers, worker production of males could lead to male-mediated gene flow between the lineages. Moreover, if worker offspring were plentiful and reproductively capable, this could cause the dependentlineage system to collapse, because its persistence depends on the maintenance of allelic differences between the lineages. However, evidence suggests that little to no gene flow between the lineages has occurred (Helms Cahan & Keller 2003; Anderson *et al.* 2006), and the dependent-lineage system seems to be relatively ancient (Anderson *et al.* 2006). To investigate the maintenance of this system in harvester ants, we examined the extent to which workers produce males in a natural, dependent-lineage population of *P. barbatus*.

Materials and methods

Field site and colony collection

Specimens were collected from colonies within 8 km of our long-term study site in southeastern Arizona (Gordon & Kulig 1996). *Pogonomyrmex barbatus* colonies reproduce yearly, by producing winged males and females that fly to a mating aggregation. Male ants and workers were collected in July 2005 and 2006, before male ants had flown to the mating aggregation. One hundred and eighty-four nests were excavated with shovels. Twenty males and 19 or 20 workers were collected from seven nests, for a total of 279 individuals. Seven males each were collected from an additional 177 nests, for a total of 1239 individuals. All ants were stored in 95% ethanol until DNA extraction and analysis.

DNA extraction and microsatellite analysis

DNA was extracted from all males and workers by boiling heads in 250 μ L of a 5% Chelex (Bio-Rad) solution at 95 °C for 20 min. Samples were centrifuged and the supernatant was used as the template for polymerase chain reaction (PCR) amplification. Twenty males and 19 or 20 workers from seven colonies were genotyped at seven microsatellite loci using seven primer sets: L-18 (Foitzik *et al.* 1997), Myrt3 (Bourke *et al.* 1997), PO8 (Wiernasz *et al.* 2004), Pb5, Pb7, Pb8 (Volny & Gordon 2002b), and Pr-1 (Gadau *et al.* 2003), according to the procedure described in Helms Cahan & Keller (2003). The remaining 1239 males were genotyped at the microsatellite loci Myrt3 and Pr-1. PCR products were run on an ABI PRISM 3100 automated DNA sequencer (Applied Biosystems) using fluorescent dyes, and analysed using Genotyper software (Applied Biosystems).

Genetic analysis

The colonies we sampled are within the geographical range of the dependent-lineage system as documented in Anderson *et al.* (2006) and Schwander *et al.* (2006). We confirmed this by amplifying a 433-bp portion of the *cox*1 gene of 1 worker from 300 colonies on our long-term study site, as in Helms Cahan & Keller (2003), and performing restriction digests using enzymes that cut only one lineage, as in Helms

Cahan *et al.* (2006). This revealed two cryptic lineages in the geographical area sampled and allowed us to estimate the lineage ratio on the study site.

We assessed male parentage in *P. barbatus* in two ways. As is common in studies of worker reproduction (Dijkstra & Boomsma 2006; Kronauer *et al.* 2006), we reconstructed queen genotypes from worker genotypes and then compared male genotypes to queen genotypes, using the 20 males and 19–20 workers from seven colonies. Workers from the seven colonies were also used to estimate mating frequency. For the remaining 177 colonies, we also took advantage of allelic differences between the two lineages and assessed male parentage based only on male genotypes (see below). Additionally, we tested for linkage between loci using the 140 males sampled with workers, and the program genepop (Raymond & Rousset 1995).

Genotypes of colony queens were inferred from the genotypes of workers using the program MATESOFT, version 1.0 (Moilanen et al. 2003), which lists all possible queen genotypes and their respective probabilities. In cases where more than one queen genotype was possible, the most likely queen genotype was used in subsequent analyses. We used the program FSTAT to calculate background allele frequencies from worker genotypes. These allele frequencies were also used to estimate relatedness among workers within colonies as in Queller & Goodnight (1989), using the program spagedi (Hardy & Vekemans 2002). Mating frequency statistics were calculated using MATESOFT, and the estimated effective number of matings was corrected for sample size following Nielsen et al. (2003). The effective number of matings is the number of equally contributing mates that would result in the same average relatedness among the worker offspring. Lineage-specific nondetection errors for patrilines were calculated from allele frequencies generated from workers' fathers, as $\Pi_1^n(1-H_1)$, where H_i is the expected heterozygosity at the ith locus of n loci (Foster & Ratnieks 2001).

For the seven colonies from which we sampled both males and workers, the parentage of males was determined by comparing the multilocus genotypes of males with that of the inferred queen. All loci used were informative; the worker's maternal and paternal alleles differed. At an informative locus, there is a 50% chance that a worker-produced male receives an allele from his worker mother that is not shared by the queen (Foster & Ratnieks 2001). Males were considered to have been produced by workers if they carried an allele at any locus not compatible with the queen's genotype. The probability of detecting a worker-produced male (P_i) , the total number of assignable males (N_a) , and the probability of not sampling any worker-produced males were calculated as in Foster & Ratnieks (2001): the probability of detecting a workerproduced male was calculated for each nest as $\sum_{i=1}^{n} P_i (1 - 0.5^{li})$ where n is the number of patrilines, P_i is the proportional

representation of the ith patriline, and l_i is the number of informative loci analysed at the ith patriline. The total number of assignable males is (P_jN_j) where N_j is the number of males analysed for the jth nest. The probability of not sampling any worker-produced males was $(1-x)^{Na}$ where x is the hypothetical proportion of males that are produced by workers.

For the 177 colonies from which only males were sampled, we established parentage based on genotypes at two microsatellite loci diagnostic for lineage (Myrt3 and Pr-1). Workers are almost invariably heterozygous at these loci (Volny & Gordon 2002a; Helms Cahan & Keller 2003; Helms Cahan et al. 2006; Schwander et al. 2006). Queenproduced males have alleles corresponding to their mitochondrial lineage at all loci. However, worker-produced males could have a lineage-1 allele at one locus and a lineage-2 allele at the other locus. Also, if gueens produce all males, at most two alleles should be present among males from a given colony. Thus, we classified males as worker-produced if they had an interlineage genotype across nuclear loci, or more than two alleles were present at one locus among all the males from a given colony. For such males, the probability of detecting a worker-produced male as such is 0.5.

Results

We found no evidence of worker reproduction in *Pogonomyrmex barbatus*. For each colony, we detected no more than two alleles per locus among the males sampled. We detected only one allele at each locus for all males. All loci were unlinked and all males had multilocus genotypes with alleles from only one lineage. Thus, it appears that each male was queen-produced.

Queen genotypes inferred from males were in all cases consistent with queen genotypes inferred from workers. The power of detecting the correct queen genotype, calculated by MATESOFT, was greater than 0.99 for all colonies. Nondetection errors for patrilines were 5e10-4 for lineage 1 and 7e10-4 for lineage 2. Queen genotypes inferred from males were identical to the most probable queen genotype inferred from workers for six colonies. In one case (colony 5), worker genotypes indicated that the queen was heterozygous at locus PO8, although we found only one allele among all males from this colony. The probability of 20 males receiving only one of two queen alleles is very low (0.520). The five workers that possessed the allele not found among males could have been foreign, but we included these individuals because doing so did not change the outcome of our analysis. The probabilities of detecting a worker-produced male (P_i) for each colony from which we sampled 20 males and 19 or 20 workers ranged from 0.942 to 0.992 and the mean, weighted by the number of males analysed for each colony, was 0.985 (Table 1). P_i is 0.992 for

Table 1 Worker production of males was zero. Shown are measures demonstrating confidence in our ability to identify worker-produced males (WPM) for males from the seven colonies from which workers were sampled: the number (n) of males and workers analysed, the probability of detecting a worker's son (P_j) , and the percentage of WPM. The overall probability of detecting a worker-produced male (P_j) is the average over colonies weighted by the number of males analysed per colony

Colony	n males	n workers	$P_{\rm j}$	Percentage of WPM
1	20	20	0.992	0
2	20	20	0.992	0
3	20	20	0.992	0
4	20	20	0.942	0
5	20	19	0.992	0
6	20	20	0.992	0
7	20	20	0.992	0
Overall	140	139	0.985	0

six colonies because all seven loci were informative in all patrilines. In colony 4, P_j is lower because one workers' father had the same allele as the queen at one locus. For colonies from which we sampled both males and workers, the number of assignable males (N_a) was 138. For the remaining 177 colonies from which we sampled only males, the number of assignable males was 620, so the total number of assignable males was 758. We calculated the probability of not sampling any worker-produced males for $(1-x)^{Na} = 0.05$, and as in Kronauer *et al.* (2006). Therefore, for $N_a = 758$, the probability that we failed to detect a worker contribution more than 0.39% is less than 0.05.

The mean \pm standard error (SE) relatedness among workers was 0.35 ± 0.01 . Mating frequencies are given in Table 2. The mean \pm SE observed number of patrilines (K_{obs}) and sample size-corrected estimate of effective mating frequency (M_e) estimated by jackknifing over colonies were 4.71 ± 0.61 ($K_{\rm obs}$) and 3.58 ± 0.5 ($M_{\rm e}$). $K_{\rm obs}$ is lower than the total number of males with whom a queen mates, as it is an estimate only of the number of times a queen mates with a male of the opposite lineage. Also, it is possible that mating frequencies differ between the lineages. To test this, we computed average observed mating frequencies for each lineage and compared the number of patrilines of lineage 1 queens to lineage 2 queens for the seven colonies from which we sampled workers. The average number of patrilines found among lineage 1 is significantly higher than the number found among workers of lineage 2 (Tables 2, t-test, P < 0.03). This difference in patrilines among the lineages reflects the asymmetry in the lineage ratio. From the sample of 300 colonies, the ratio of lineage 1 to lineage 2 was 42:58, which is significantly different from 1:1 (chi-squared test; P < 0.05).

Table 2 Mating frequency statistics for matings between lineages in seven colonies. Shown are the lineages of colony queens, number of worker offspring analysed (n), the observed number of patrilines among workers $(K_{\rm obs})$, and the sample size-corrected estimate of queen effective mating frequency $(M_{\rm e})$. Mean number of patrilines $(K_{\rm obs})$, and mating frequency $(M_{\rm e}) \pm {\rm SE}$ were calculated by jackknifing over colonies

Colony	Lineage	n workers	K _{obs}	M_{e}
			ODS	
1	1	20	6	3.13
2	2	20	4	3.08
3	1	20	7	5.03
4	1	20	4	3.64
5	2	19	3	1.79
6	1	20	6	5.62
7	2	20	3	2.77
Overall		139	4.71 ± 0.5	3.58 ± 0.61

Discussion

Our results demonstrate that queens dominate male production in Pogonomyrmex barbatus. We detected no worker-produced males out of the 1379 analysed. The mechanisms underlying the absence of worker-produced males vary within the social insects, including direct policing by the queen in some species (Bego 1990; Saigo & Tsuchida 2004; Wenseleers et al. 2005). However, mature colonies of P. barbatus can contain over 10 000 workers (Gordon 1992), making it unlikely that direct restraint by the queen prevents the production or development of worker-produced males. Another possibility is that the lack of worker-produced males could be a result of the dependent-lineage system. Linksvayer et al. (2006) suggested that viability of males may depend on interactions between lineage-specific nuclear and mitochondrial gene products. Thus, the lack of worker-produced males could be the result of low viability of worker offspring. Polyandry is widespread throughout the genus Pogonomyrmex, so inclusive fitness theory predicts that worker-produced males are unlikely regardless of the mode of caste determination. It is also possible that workers do reproduce but no recombination occurs, or they discard the genome of one lineage. In this case, worker-produced males would be genetically identical to queen-produced males and would be undetectable by our molecular methods, but would not interfere with dependent-lineage dynamics.

Worker removal of worker-produced male eggs or aggression towards reproducing individuals may contribute to the observed lack of worker-derived offspring in *P. barbatus*. Workers often differ in their relatedness to queen-produced and worker-produced males (Wenseleers & Ratnieks 2006). An average effective mating frequency of 3.58, and low value of relatedness among workers within

colonies (0.35 \pm 0.01), is sufficient for workers to be more related to males produced by the queen than by their sisters, and to police one another. Mating frequencies may be similar throughout the genus Pogonomyrmex. Frequencies above 2.0, which would lead to low relatedness within colonies, have also been found in the harvester ants P. rugosus (Gadau et al. 2003), P. badius (Rheindt et al. 2004) and P. occidentalis (Wiernasz et al. 2004).

Our estimate of effective mating frequency is close to the previous estimate for *P. barbatus* (Volny & Gordon 2002a). Both estimates are based on data from worker genotypes, which provide an estimate only of the number of times the queen mated with males of the opposite lineage. Reproductive females in dependent-lineage populations of P. barbatus have fathers of the same lineage. If both lineages were equally represented in the population and queens mated randomly, or chose mates of both lineages based on their cuticular hydrocarbon profiles (Volny et al. 2006), the true average observed mating frequency would be doubled, or 9.42. However, an asymmetrical lineage ratio (Schwander et al. 2005) may result in differences in the number of patrilines represented among workers of each lineage. Lineage 2 is more frequent in the geographical area around our study site. For the seven colonies from which we sampled workers, the number of patrilines found among workers of lineage 1 was significantly higher than the number found among workers of lineage 2. Thus, the average observed mating frequency is between 4.71 and 9.42, and may be best estimated by adding the averages for each lineage: 9.08. Also, the ratio of patriline number for lineage 2 to lineage 1, 37:63, is not significantly different from the ratio of lineage 1:2 in our population (z-test for difference between population proportions; P = 0.47). These lineagespecific differences in patriline number among workers are consistent with random mating and indiscriminate use of sperm by queens (Schwander et al. 2005).

Our estimates of mating frequency in combination with the observed lack of worker-produced males have important implications for the maintenance of the dependentlineage system. Schwander et al. (2006) and Anderson et al. (2006) suggested that negative frequency-dependent selection acts on queens of the more frequent lineage at the mating flight; queens of the more frequent lineage have a lower change of mating with a male of the opposite lineage, producing workers, and establishing a colony. Thus, the factors most important to the persistence of the system are mating frequency and the lineage ratio. The probability that queens will mate only with males of the same lineage is the first term of the binomial expansion $[f(a) + f(b)]^n$, where f is lineage frequency, a and b represent both lineages, and n is the number of matings (Anderson et al. 2006). With an effective mating frequency of 6.9, and a lineage ratio of 42:58 in our population, 0.3% of lineage 1 queens and 2% of lineage 2 queens are be expected to be unable to produce workers. Given the assumption that both lineages produce an equal amount of reproductives, this sevenfold difference between the lineages in the probability of successful colony establishment could contribute to the maintenance of an asymmetrical lineage ratio through time.

To our knowledge, this is the first study documenting the lack of worker-produced males in the genus Pogonomyrmex. Inclusive fitness theory predicts their absence in other Pogonomyrmex species as well, given high mating frequencies within the genus. Indeed, the only documented evidence of worker reproduction in Pogonomyrmex is in queenless colonies of the Florida harvester ant P. badius (Smith & Tschinkel 2006) and P. barbatus (D.M. Gordon, personal observations). More work is needed to determine the mechanism underlying the lack of worker-produced males in P. barbatus, since workers have developed ovaries and laboratory colonies of P. barbatus have been observed to produce males after queen death. The extent to which workers produce males in queenless colonies in natural populations remains unknown. Our study was robust enough to detect worker-produced males if workers produced greater than 0.39% of the males among all colonies sampled. Thus, if it occurs, worker reproduction is sufficiently infrequent that it probably has little impact on colony or population-level processes in *P. barbatus*, particularly on the maintenance of the dependent-lineage system.

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