

SPERM GENOTYPE PATTERNS IN NEWLY-MATED QUEENS OF THE RED IMPORTED FIRE ANT, *SOLENOPSIS INVICTA*

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Abstract

The breeding system of the Red Imported Fire Ant was examined by genotyping newly-mated queens and their stored sperm for a gene (the *Gp-9* locus) believed to code for a pheromone-binding protein affecting complex social behavior. Newly-mated queens were collected from a site in Florida with sympatric monogyne and polygyne colonies. Sperm storage patterns suggest that female alates mate disproportionately with males of their own social form.

Introduction

Our understanding of social insect organization and the forces that shape interactions fundamentally relies on our understanding of breeding systems and how these affect genetic structure and flow. The Red Imported Fire Ant has two social forms, monogyne and polygyne colonies. Previous studies estimating gene flow concluded that fertile polygyne males were too rare to contribute significantly to the gene pool of either social form where monogyne colonies occur in sympatry (Fig. 1; Ross and Shoemaker 1993; Shoemaker and Ross 1996). A recent study by Fritz et al. (2006) on sperm storage patterns in polygyne queens suggests queens may mate disproportionately and commonly with males of their own social form. This apparent mating bias was further elucidated in this study by examining sperm storage patterns in newly mated queens.

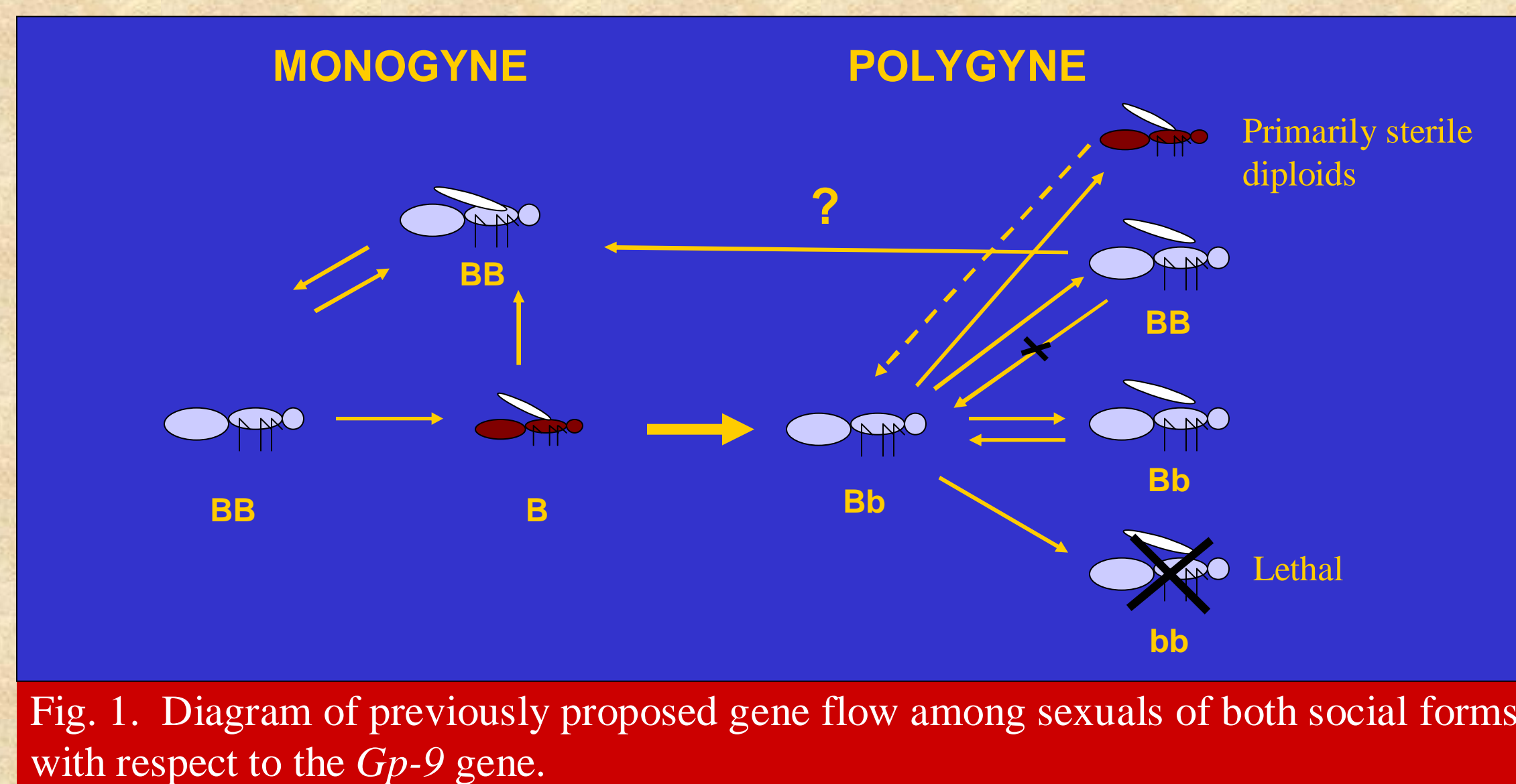


Fig. 1. Diagram of previously proposed gene flow among sexuals of both social forms with respect to the *Gp-9* gene.

Methods

Newly-mated queens were collected during a mating flight at a location in northcentral Florida shown previously to include a high frequency of polygyne colonies in sympatry with monogyne colonies. Newly-mated queens were genotyped, along with their stored sperm, for the *Gp-9* gene and compared to genotype frequencies of queens in polygyne colonies.

Results

The genotype of newly-mated queens included all three genotypes for the *Gp-9* gene: BB, Bb and bb (Fig. 2).

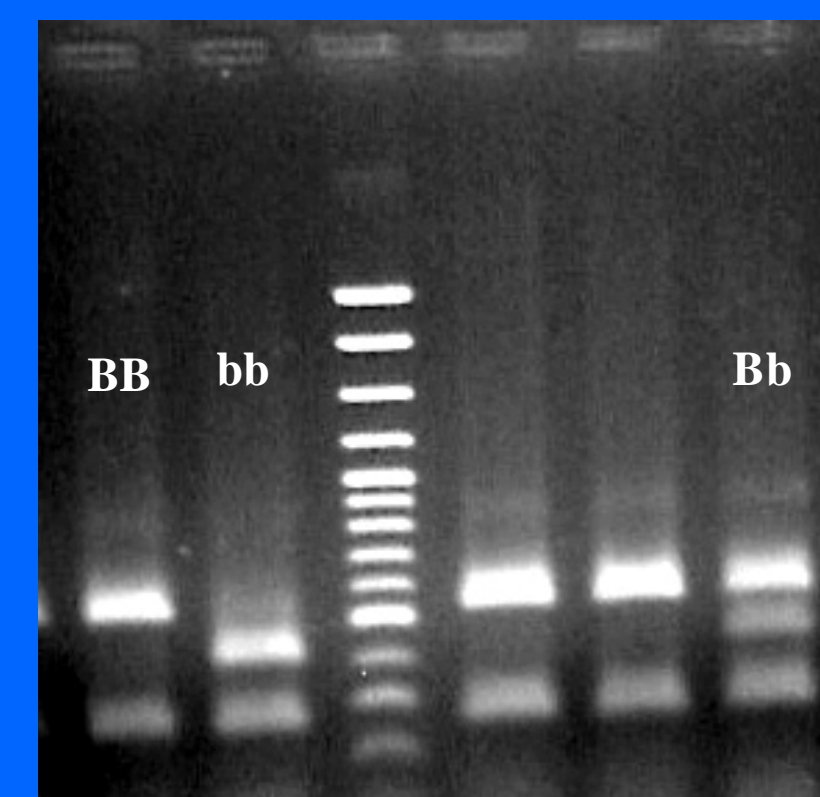


Fig. 2. Example band patterns of queen genotypes

Of those queens unambiguously originating from polygyne colonies (Bb and bb queens), approximately 85% were inseminated by males of their own social form. Similarly, queens originating primarily from monogyne colonies (BB queens) were significantly more likely to have sperm of the B genotype only (Fig. 3). No particular pattern was observed for the quantity of sperm contained in the spermathecae of queens from all three social forms.

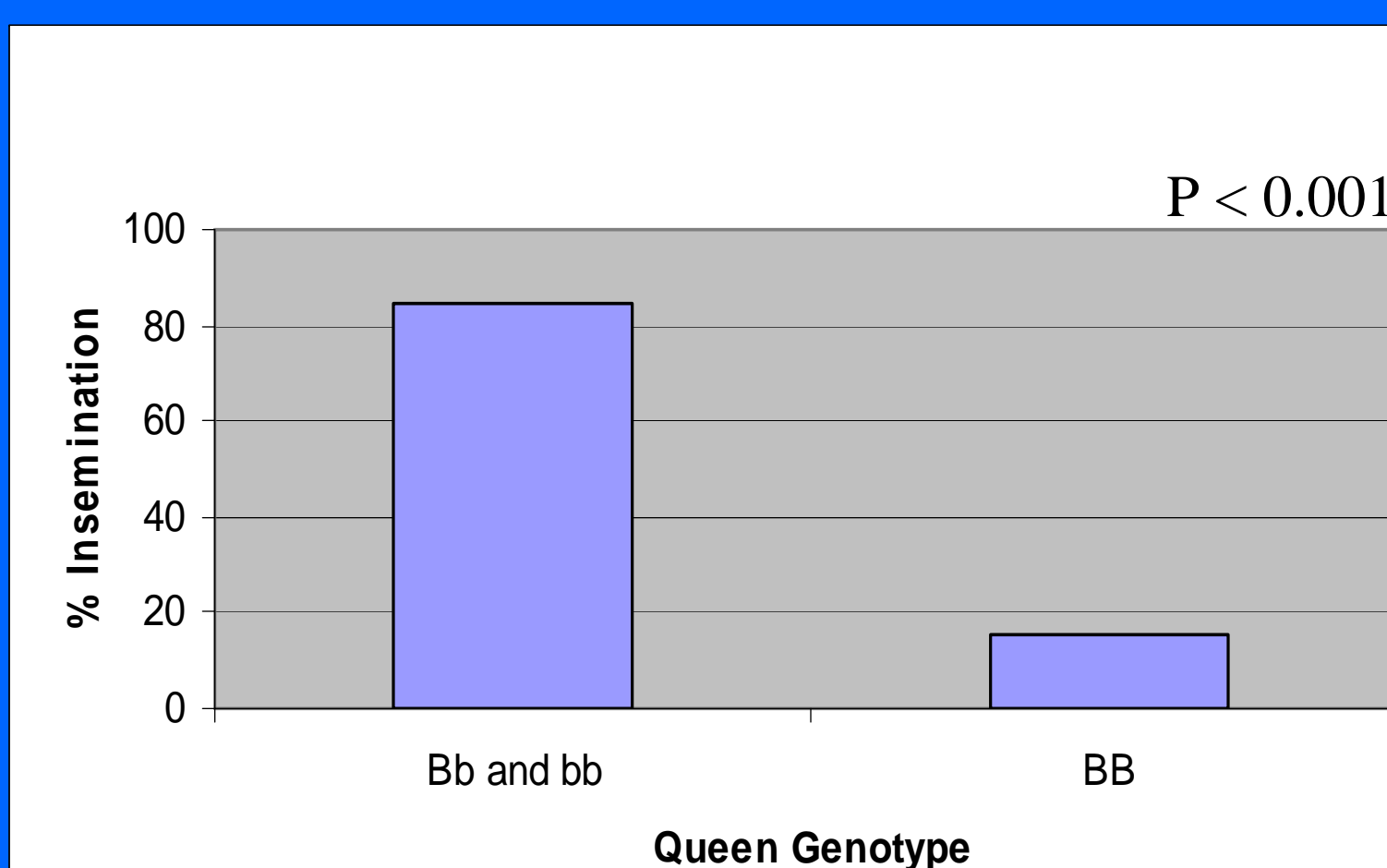


Fig. 3. Percent of queens inseminated by b males.

Though only one of the 15 queens with a b allele was a bb homozygote, this genotype was predicted to be rare (6%) based on the genotypes of female alates in polygyne colonies of this area. Six of 79 BB newly-mated queens had sperm with the b genotype, but the social form from which the latter queens originated was not determinable.

The percent insemination for queens from polygyne versus monogyne colonies was not significantly different (Fig. 4).

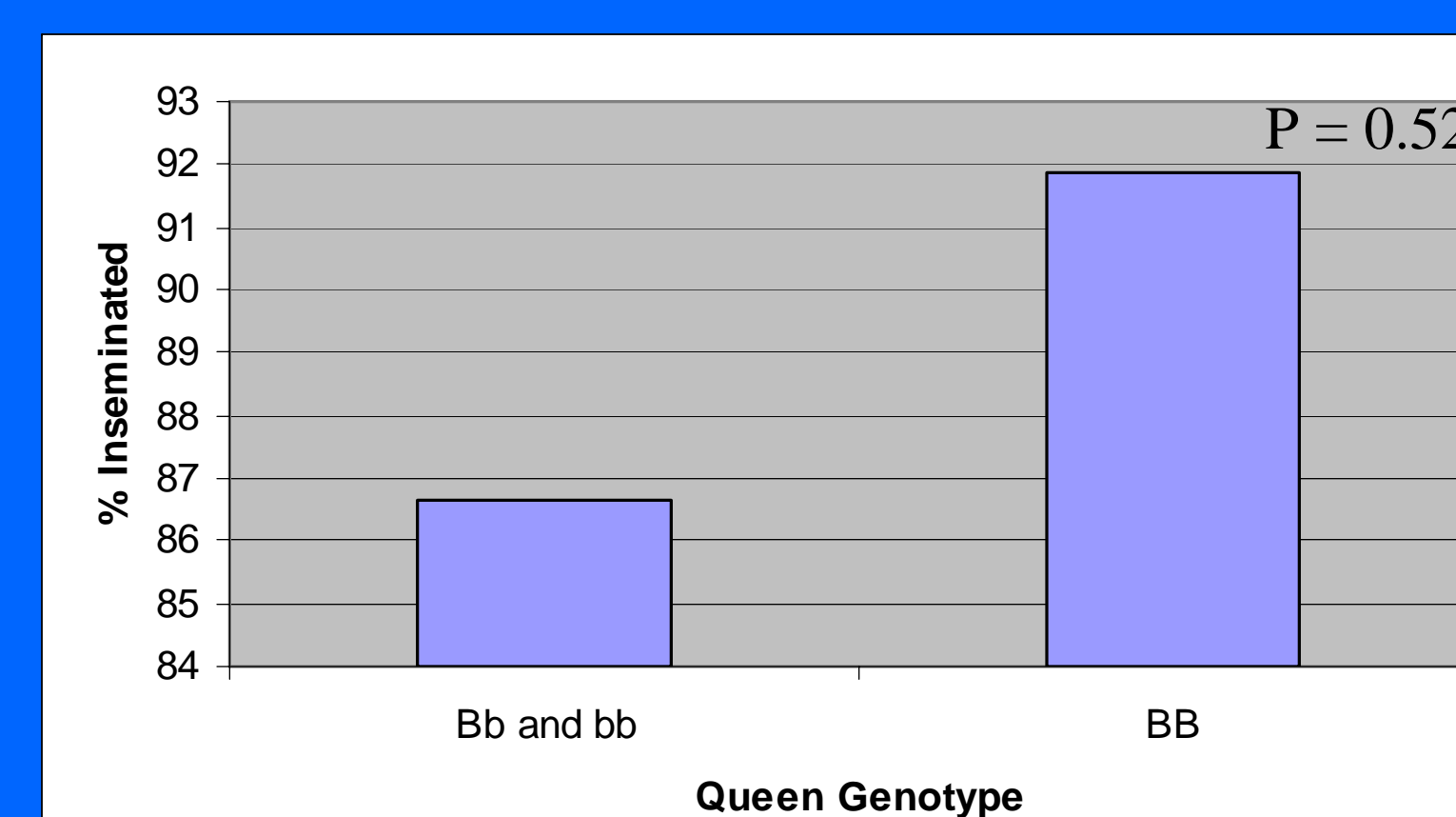


Fig. 4. Percent queens of two genotypes found inseminated

The percent insemination of newly-mated queens of the Bb and bb genotypes was also compared to that reported for queens (n = 226) in polygyne colonies from the same area; there was no significant difference (Fig. 5).

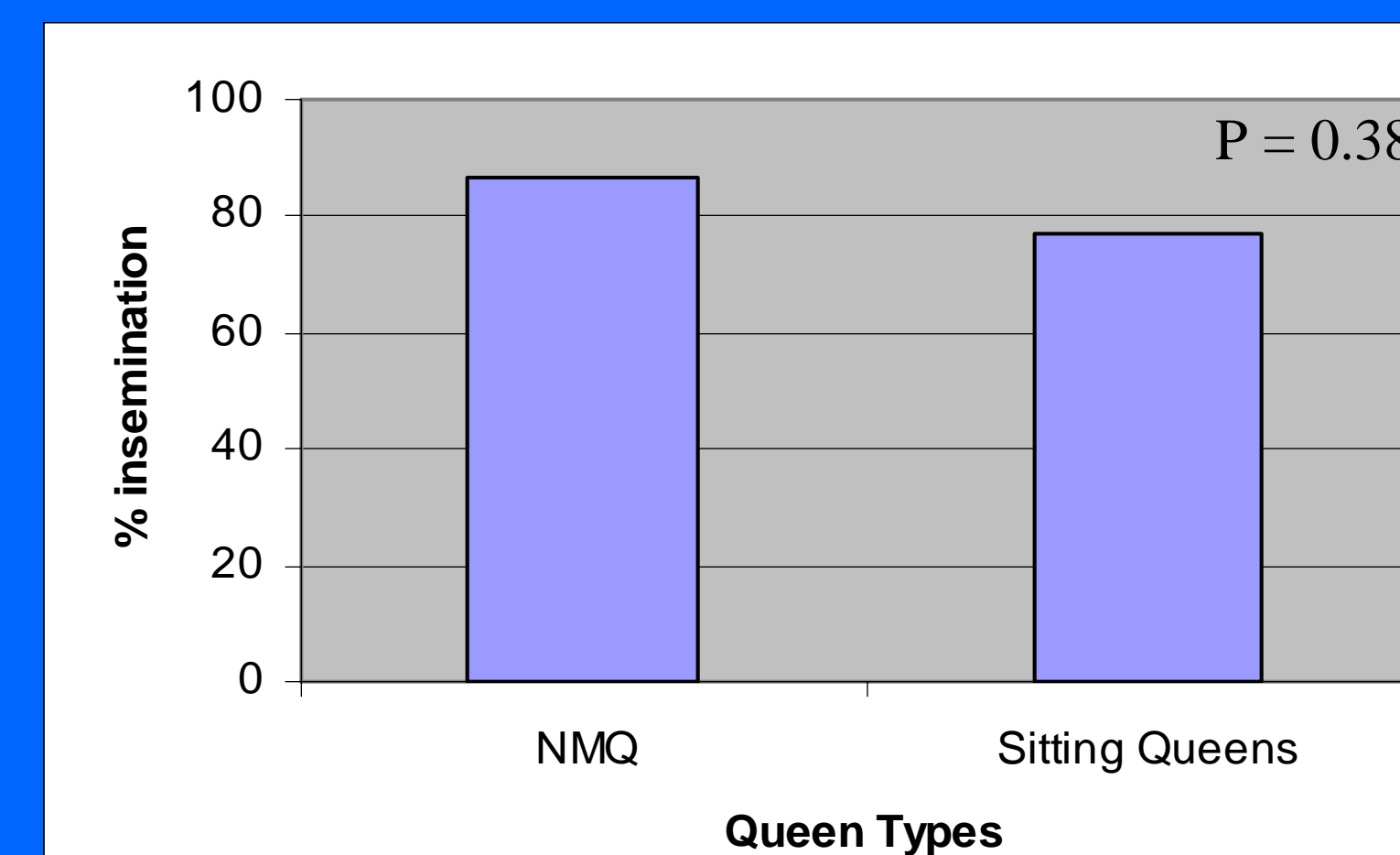


Fig. 5. Percent of queens inseminated from mating flights and in colonies.

A significantly smaller percent of queens sampled in colonies (n = 166) were found to be storing sperm with the b allele in comparison to newly-mated queens (n = 13) (Fig. 6).

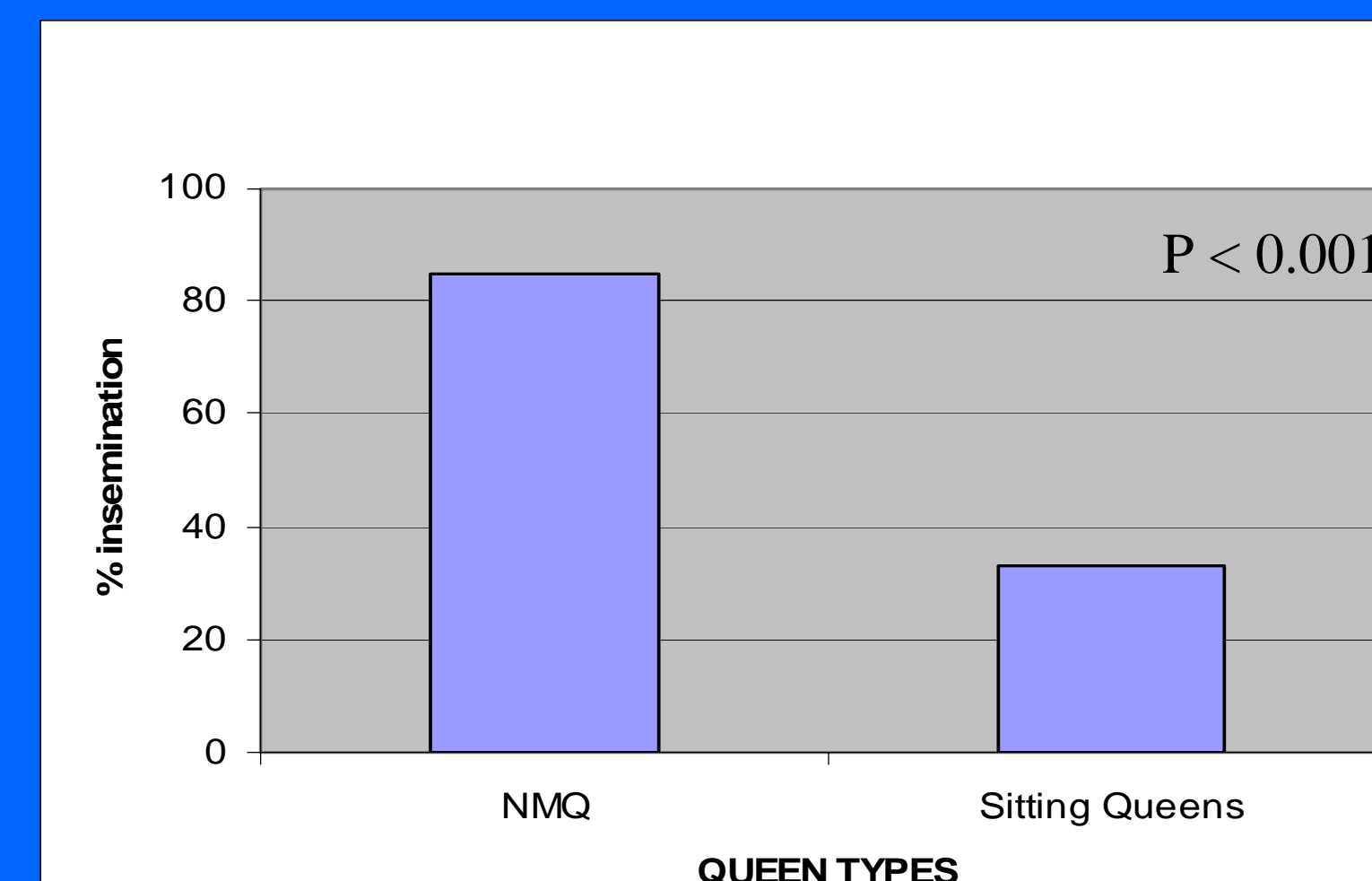


Fig. 6. Percent of queens inseminated by b males in mating flights and in colonies.

Conclusions

The vast majority of newly-mated queens collected in this study were of the BB genotype, indicating that the majority of sexuals participating in the mating flight originated from monogyne colonies. Since polygyne colonies produce a small fraction of males in comparison to monogyne colonies, and over 90% of polygyne males are thought to be sterile, it is noteworthy that most polygyne queens had spermathecae containing sperm with the b genotype. Furthermore, most BB queens had mated with males of the B genotype, a genotype corresponding to males from monogyne colonies. These results confirm a previous study (Fritz et al. 2006) suggesting that polygyne queens mate disproportionately with males of their own social form when in sympatry with monogyne colonies. Since all newly-mated queens were collected in the same area and at the same time, our results suggest that either mate choice or differences in the spatial distributions of sexuals from both social forms during mating flights favor copulations among individuals from the same social form. Data on queen dispersal by DeHeer et al. (1999) suggest that *Gp-9* genotypes may coincide with different mating flight spatial patterns.

If polygyne queens mate disproportionately with males of their own social form, fertile males should be a limiting factor in mating flights. Unexpectedly, insemination rates of BB queens were not significantly different from those of Bb and bb queens. It is possible, however, that some of the unmated BB queens originated from polygyne colonies and, therefore, explain this outcome.

The percent of queens in colonies with b sperm was significantly lower than that observed in newly mated queens. Our sample of newly-mated queens, however, represents a single sample and it is possible that the percent of newly-mated queens with b sperm might vary from mating flight to mating flight (e.g., depending on the mix of colonies participating in a particular flight during a particular day or time of year). The insemination pattern of queens in colonies also represents a single point in time and may vary as new queens are incorporated into the colony.

Previous studies have proposed that gene flow between both social forms is unidirectional and limited to the frequent copulation of monogyne males to polygyne queens (Ross and Shoemaker 1993, Shoemaker and Ross 1996). Our study suggests that even this avenue of gene flow may be under selection and further supports the incipient species status of this taxon. The apparent mating bias reported here, whatever its basis, further underscores the varied effects of one or a few closely linked genes on the breeding system of the Red Imported Fire Ant.

LITERATURE CITED

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