

The queen-worker olfactory interaction in the fire ant *Solenopsis invicta*

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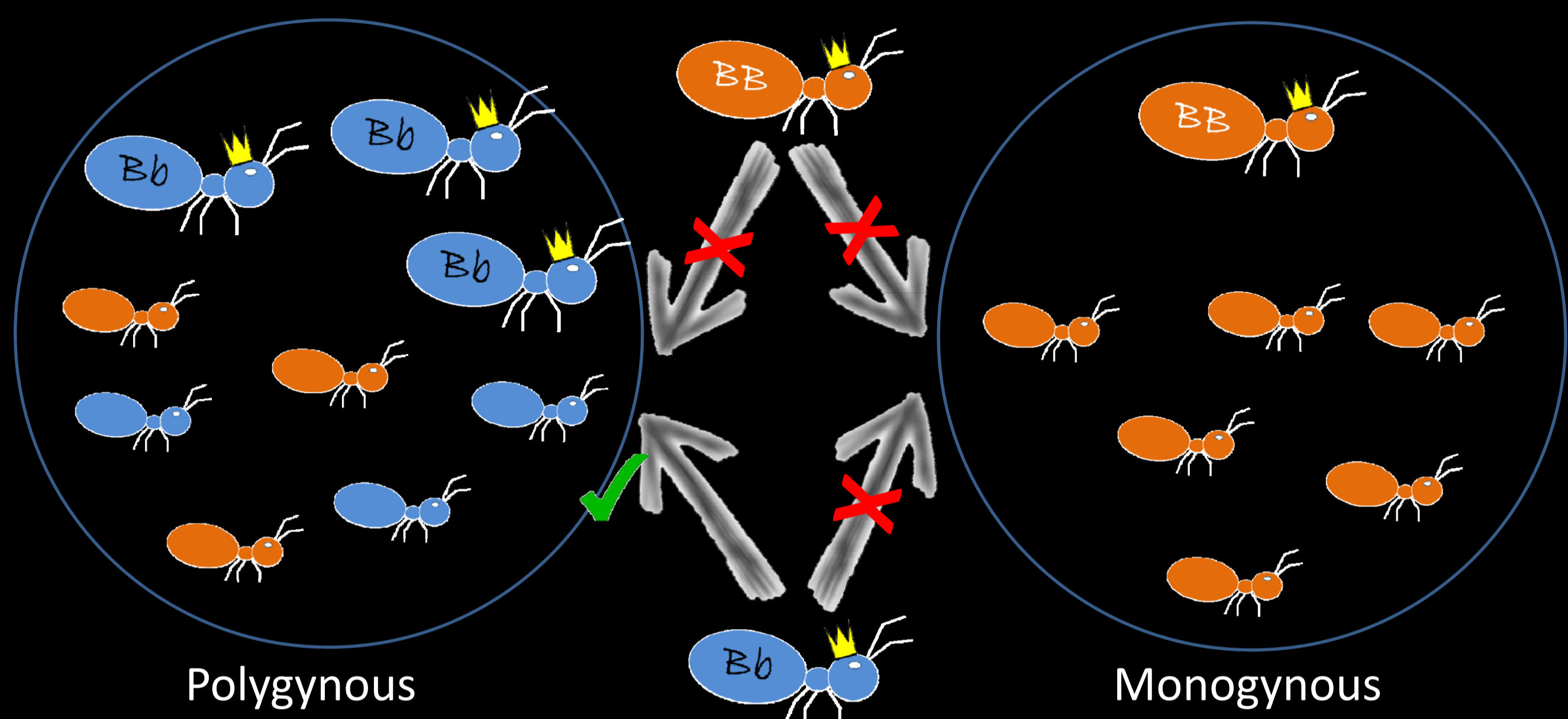
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Abstract

The two types of social organization, monogyny and polygyny, in the fire ant (*Solenopsis invicta*) are known to be fully associated with a single gene *Gp-9*. In contrast to the genetic homogeneity of all individuals in monogyne colonies (all *Gp-9BB* genotype), queens of polygyne colonies have the *Gp-9Bb* genotype while their workers have either the *Gp-9BB* or the *Gp-9Bb* genotype. Recently, the *Gp-9* gene has been found to be a part of a big supergene. Although the supergene holds the potential for explaining the many characteristics associated with social form in fire ant, the precise relationships between genes and phenotypes are still unclear. One of the interesting fire ant behaviors is the ability of *Gp-9Bb* workers to distinguish and accept only *Gp-9Bb* queens into polygyne colonies based on odor cues. We are using a transcriptomics approach to determine what gene products expressed in workers may be responsible for sensing the queen odors. We are currently profiling gene expression in the antennae and brains of different castes and genotypes of the two social forms by using Real Time qPCR, microarrays and Illumina RNA sequencing. Here we will present our preliminary results and analyses.

Introduction



How do polygyne workers distinguish BB queens and Bb queens?

Background

Proportion of *Bb* workers > *BB* workers surrounding introduced *BB* queens

Number of workers of each *Gp-9* genotype surrounding attacked, *Gp-9^{BB}* queens and non-attacked, *Gp-9^{Bb}* queens

| Worker <i>Gp-9</i> genotype | Queen <i>Gp-9</i> genotype | |
|--------------------------------|-------------------------------|-----------------------------|
| | <i>BB</i> (attacked) | <i>Bb</i> (non-attacked) |
| <i>BB</i> | 50 (0.213) | 81 (0.344) |
| <i>Bb</i> | 184 (0.783) | 147 (0.626) |
| <i>bb</i> | 1 (0.004) | 7 (0.030) |
| Total | 235 | 235 |

(1998, Keller and Ross)

BB and *Bb* have differences in cuticular hydrocarbons (CHCs) and expression level of genes associated with odor

Queen Worker

Desaturase locus 009049 (2013, Nipitwattanaphon et al.)

| Compound | Reproductive queens | |
|---|-----------------------|-----------------------|
| | <i>BB^b</i> | <i>Bb^b</i> |
| Hydrocarbons | | |
| Unsaturated | | |
| [3] ^β x-heptacosene (C _{27:1}) | – | 2.5±1.0 |
| [18] x,y-nonacosadiene (C _{29:2}) | – | 2.6±0.5 |
| [19] x-nonacosene (C _{29:1}) | 0.1±0.2 (3) | 4.4±1.4 |
| [23] x,y-hentriacontadiene (C _{31:2}) | 0.5±0.3 (11) | 6.0±1.7 |
| [24] x-hentriacontene (C _{31:1}) | 0.2±0.2 (8) | 2.3±1.0 |

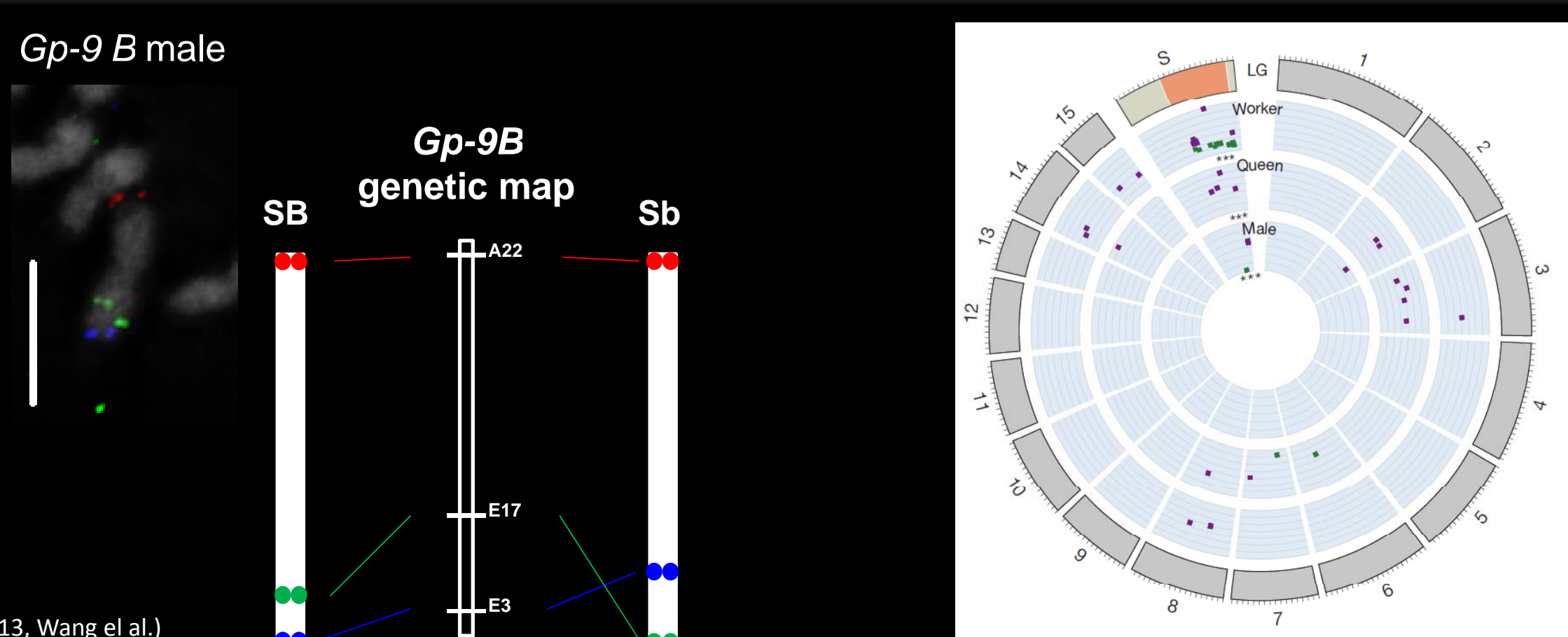
(2011, Elyahu et al.)

Olfactory putative gene product

| Gene | Fold different (<i>Bb</i> : <i>BB</i> workers) |
|------|---|
| OBP1 | 0.49 |
| OBP2 | 1.69 |
| CSP | 0.54 |

(2008, Wang et al.)

The supergene on the social chromosome (linkage group (LG) 16) likely explains many of the differences between colony organizations and individual genotypes

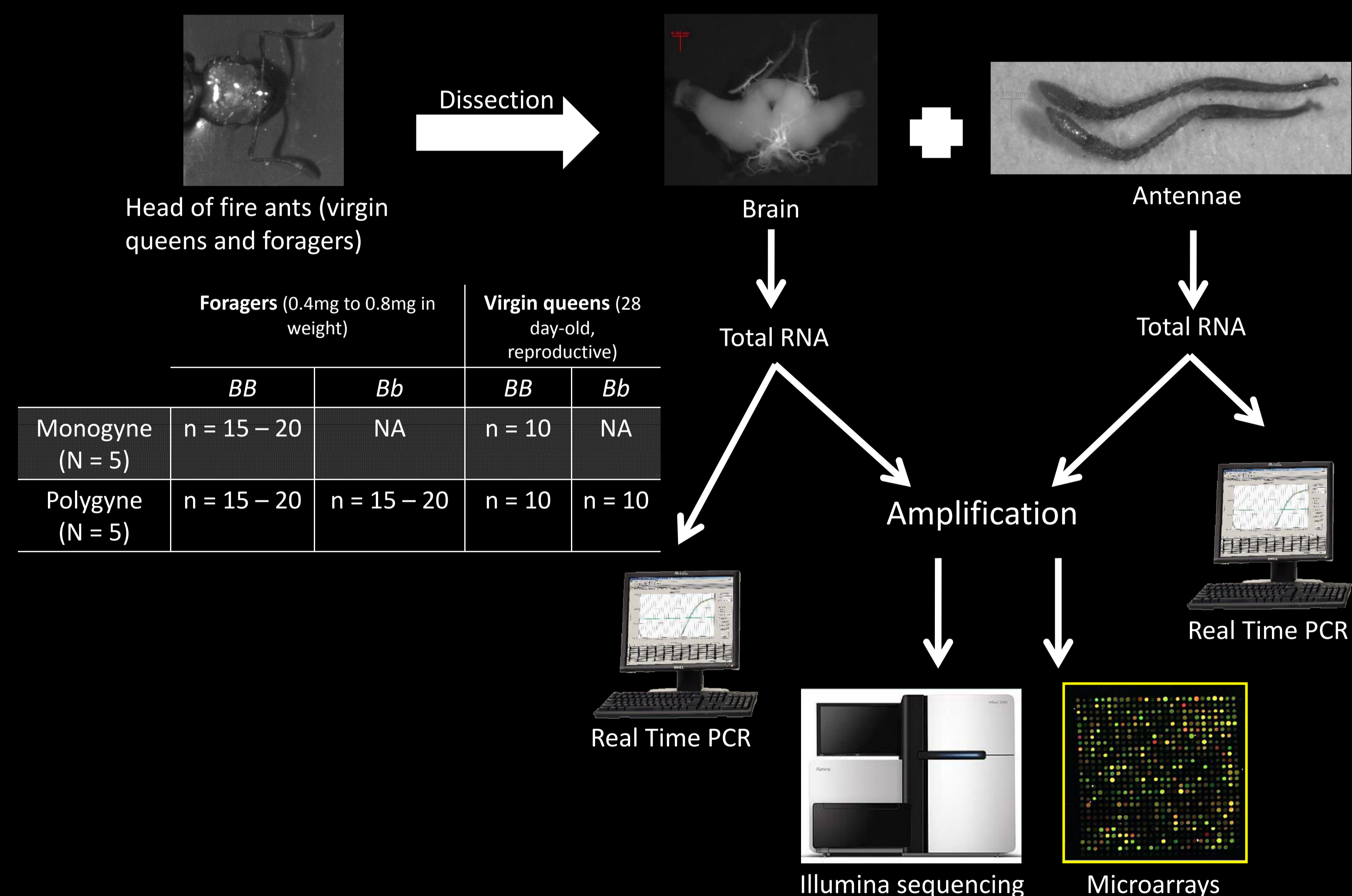


Material & Method

Hypothesis

Genes responsible for sensing queen odors are expressed differently between *BB* and *Bb* workers

Approach → Transcriptomics approach using qPCR, microarrays, and Illumina sequencing



Preliminary results

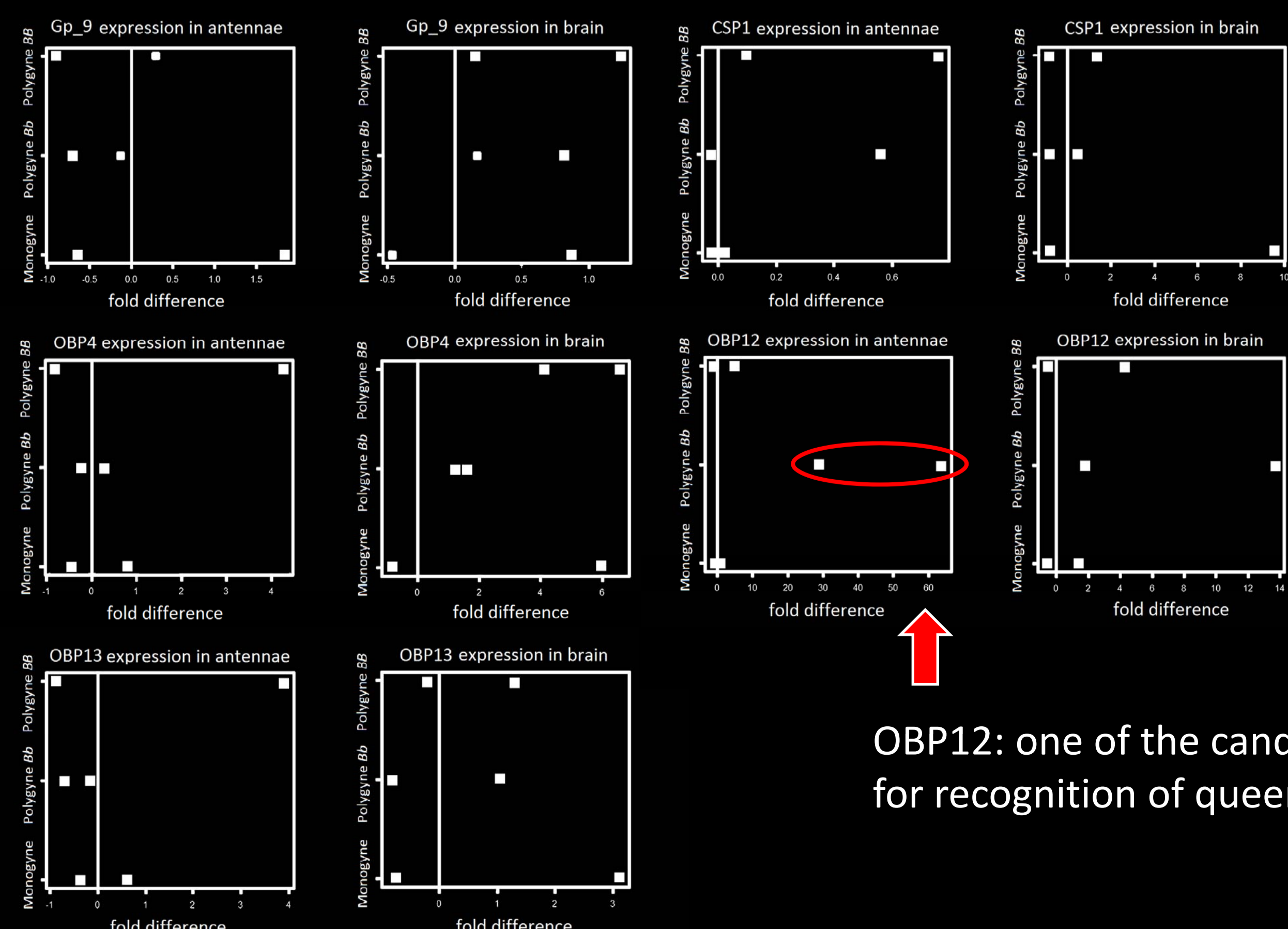
Expectation: Candidate genes could be different in

- (1) Amino acid sequence
- (2) Gene expression level
- (3) Tissue of expression
- (4) Etc.

With qPCR results, we focus on the difference in gene expression level

Foragers (0.4mg to 0.8mg in weight)

| | <i>BB</i> | <i>Bb</i> |
|------------------|-----------|-----------|
| Monogyne (N = 2) | n = 17 | NA |
| Polygyne (N = 2) | n = 17 | n = 17 |



OBP12: one of the candidate genes for recognition of queens odor