



# Differential gene expression in a facultatively eusocial small carpenter bee (*Ceratina japonica*)

Wyatt A. Shell<sup>1</sup> & Sandra M. Rehan<sup>1,2</sup>

1) Department of Biological Sciences, University of New Hampshire

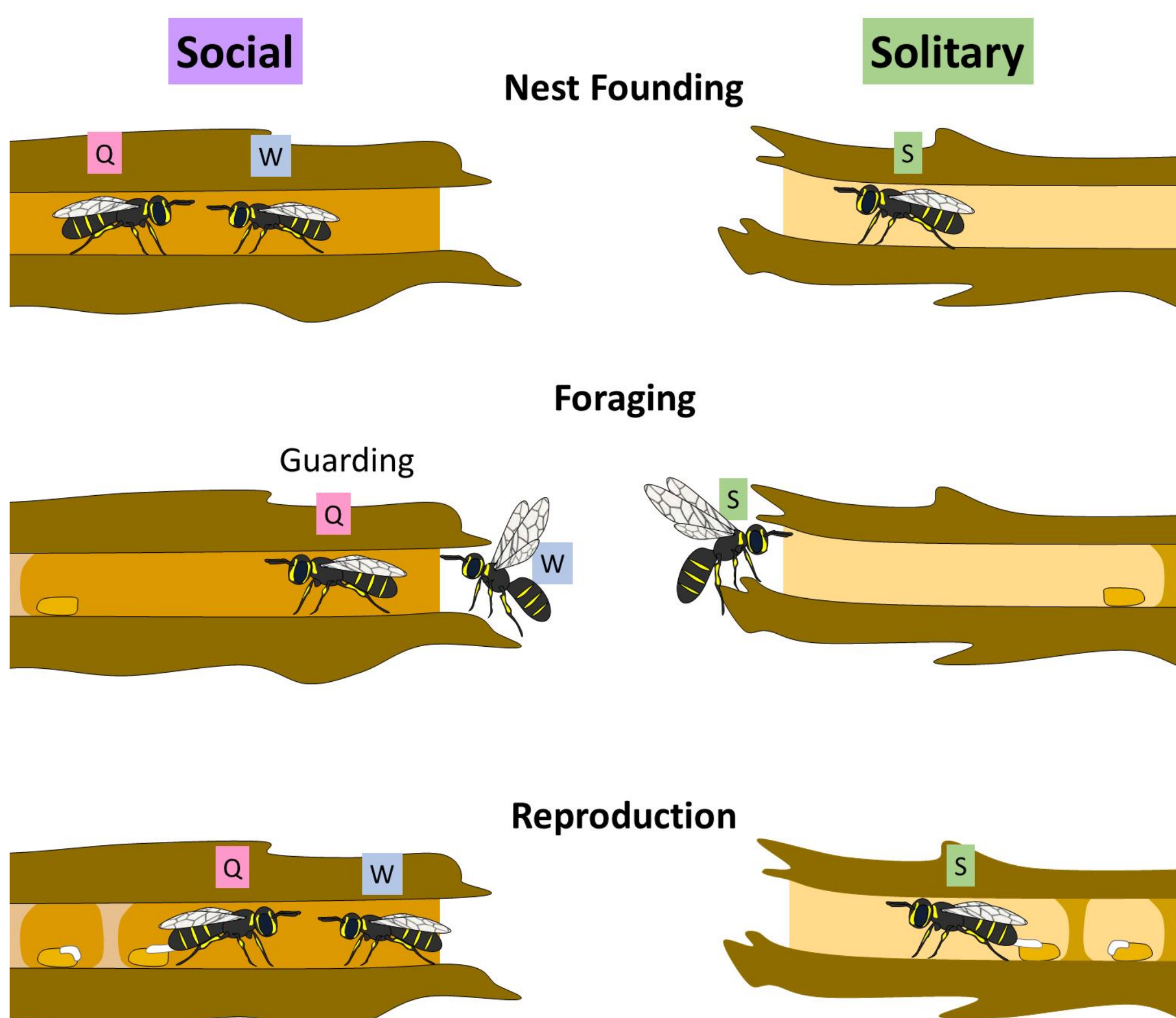
2) Department of Biology, York University, Toronto, Ontario, Canada

was2000@wildcats.unh.edu; sandra.rehan@gmail.com



## BACKGROUND

- Variations in developmental processes, and the timing and degree of gene expression are each theorized to underlie the evolution of complex insect sociality (Rehan and Toth 2015)
- Comparative genomics provides an opportunity to test the biological reality of these theories by exploring taxa thought to represent ancestral forms of closely related eusocial species (Shell and Rehan 2018)
- Ceratina japonica* is a facultatively eusocial small carpenter bee capable of forming both solitary and social nests in the same populations (Fig. 1)



**Figure 1.** Summary of *Ceratina japonica*'s major life history stages. Social nests are most often initiated in previously occupied burrows; solitary are often newly established. In social nests, the larger female assumes the focal reproductive role (queen), and the smaller forages and aids in guarding (worker). Solitary females perform all of these tasks alone.

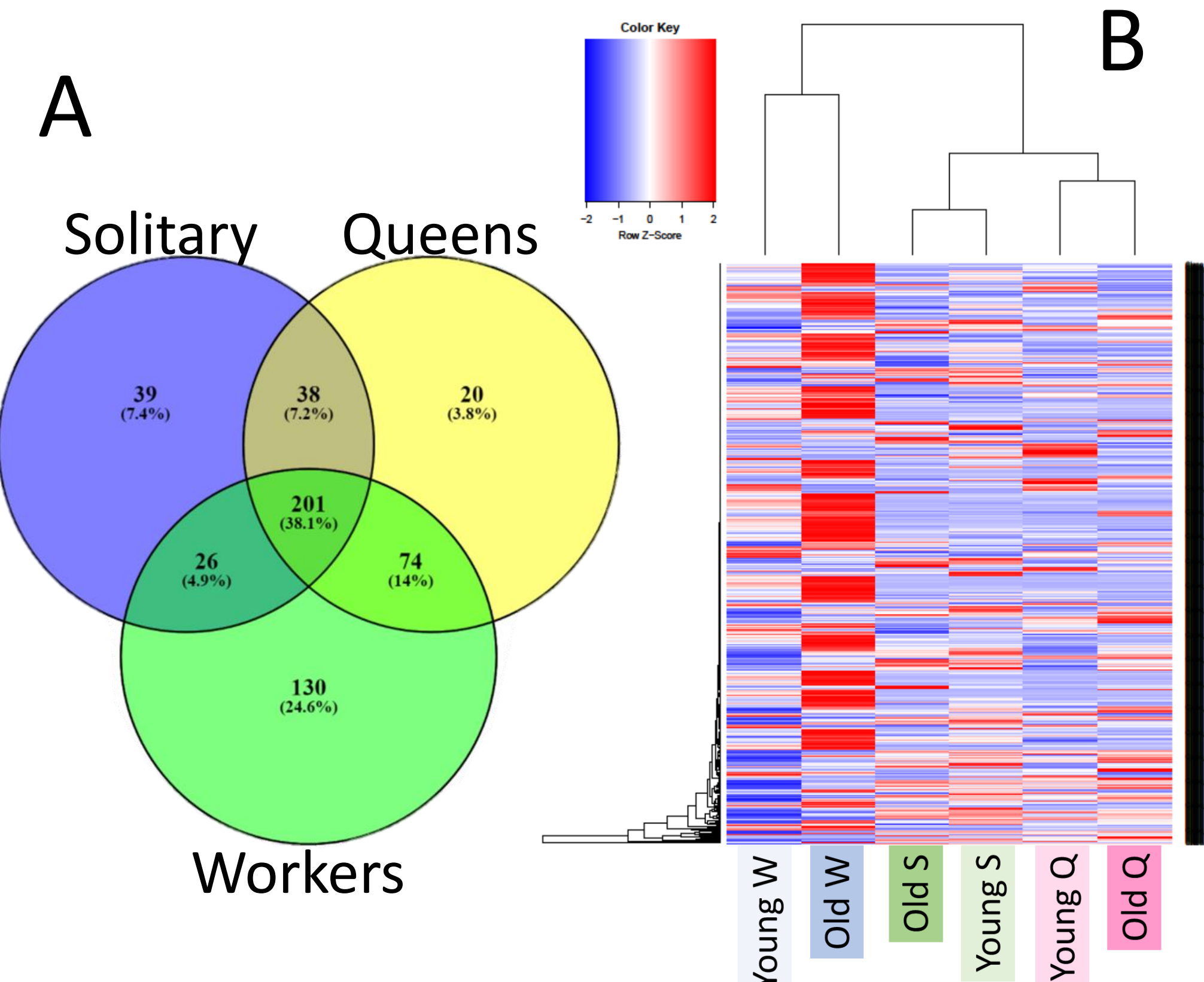
- Here, we use a newly sequenced genome and brain gene expression dataset to determine the molecular underpinnings of *C. japonica*'s facultative eusociality

## Research Aims

- Compare brain gene expression profiles of six phenotypic groups (i.e. old and young queens, workers, and solitary females) to assess variations in gene expression by role and age.
- Determine molecular mechanisms underlying sociality in *C. japonica*
- Compare molecular components identified within *C. japonica* to those of other social insects (e.g. honey bees; ants)

## SUMMARY

- 528 significant DEGs were identified among all categories (Fig. 2)

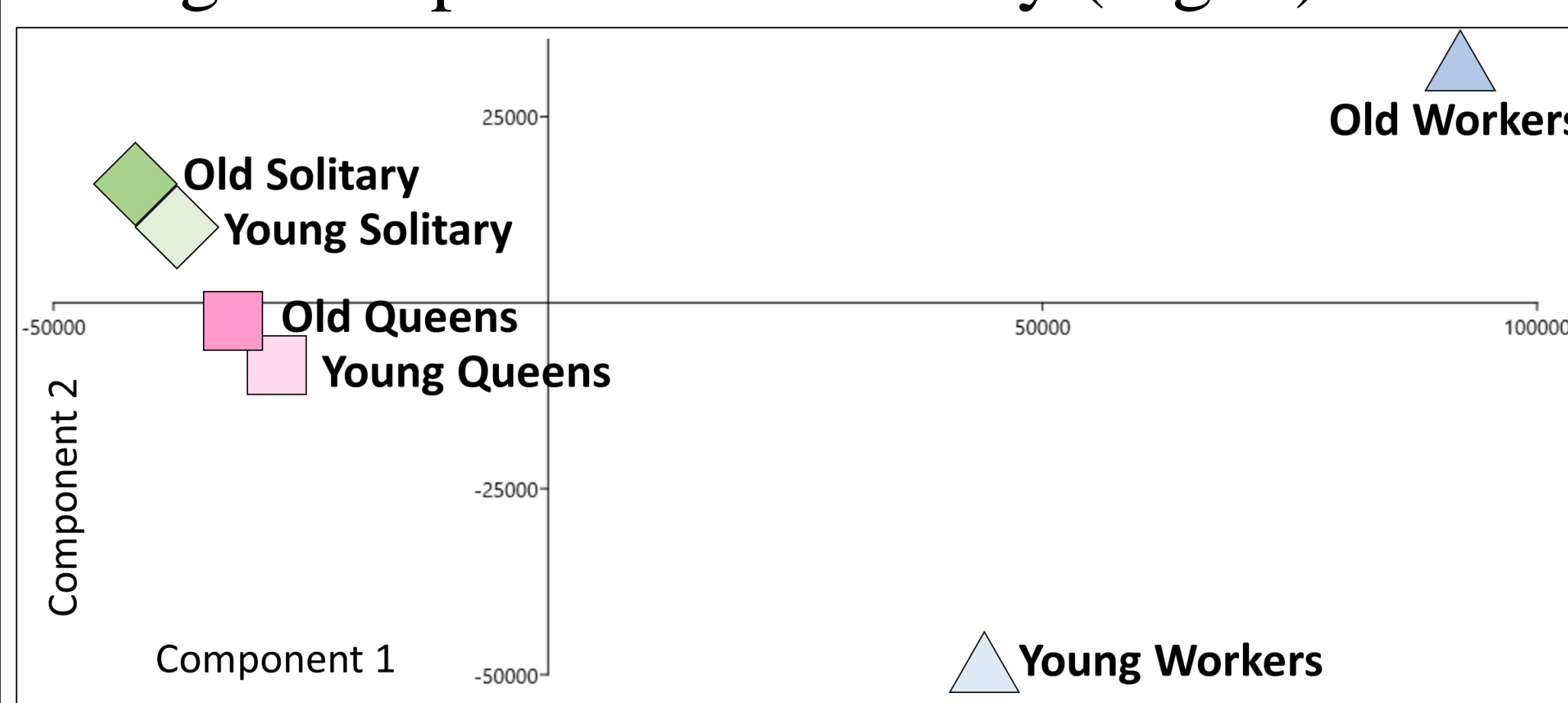


**Figure 2.** A) Venn diagram displaying all DEGs among caste groups; and B) Heat map displaying relative up (red) and down regulation (blue) of DEGs among all groups.

Brain gene expression profiles of *C. japonica* workers are highly distinct from queens and solitary females.

These caste differences in gene expression closely resemble patterns seen in advanced eusocial species (honey bees and fire ants) supporting the idea that obligate worker castes are more derived while queens are similar to ancestrally solitary species (Harpur et al. 2014).

- Principal component analysis (PCA) suggests reproductive status explains a large amount of gene expression variability (Fig. 3)



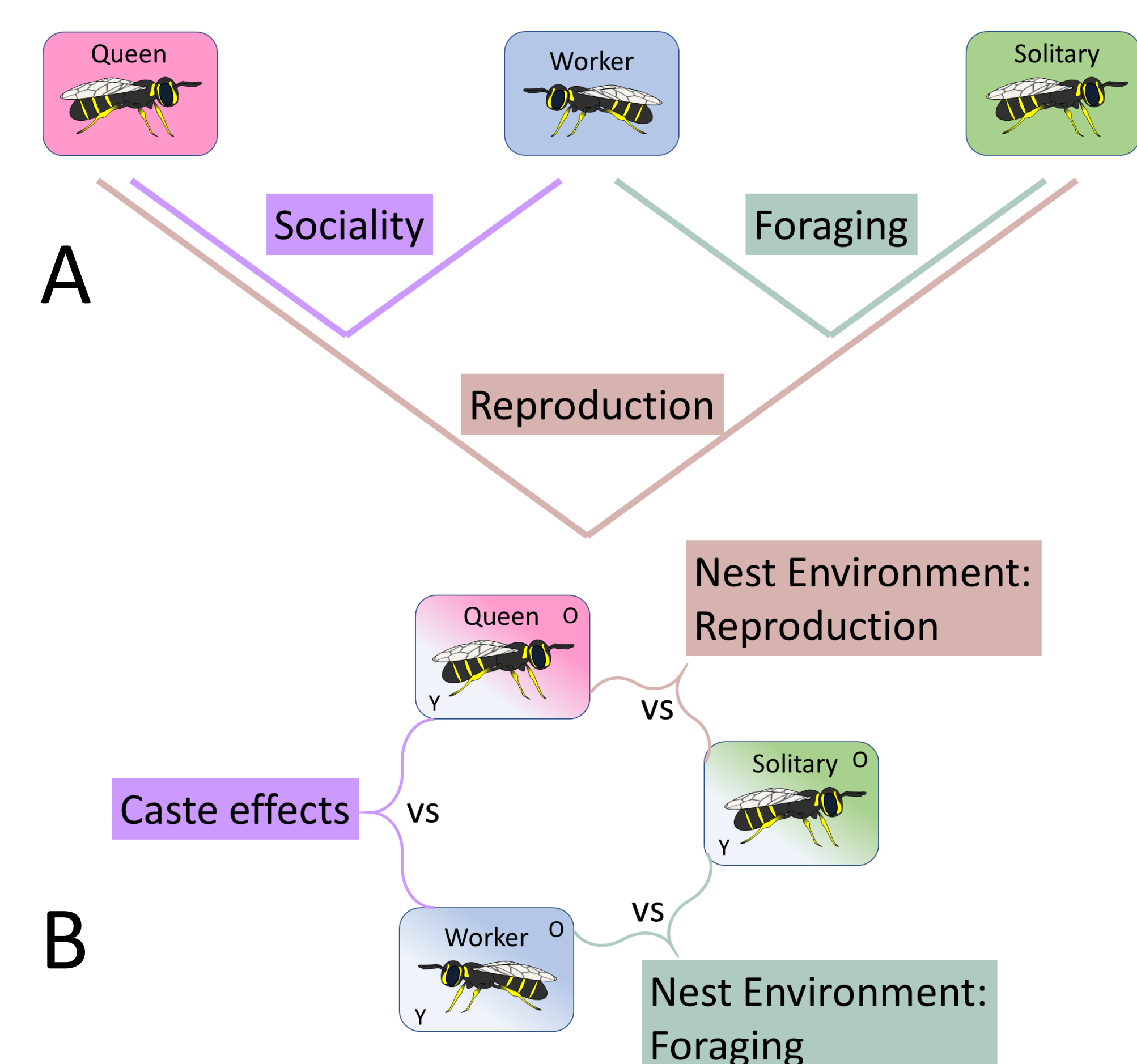
**Figure 3.** PCA handling DEG expression data across all caste and age categories. 94% of overall variability is explained by components 1 and 2.

## References Cited

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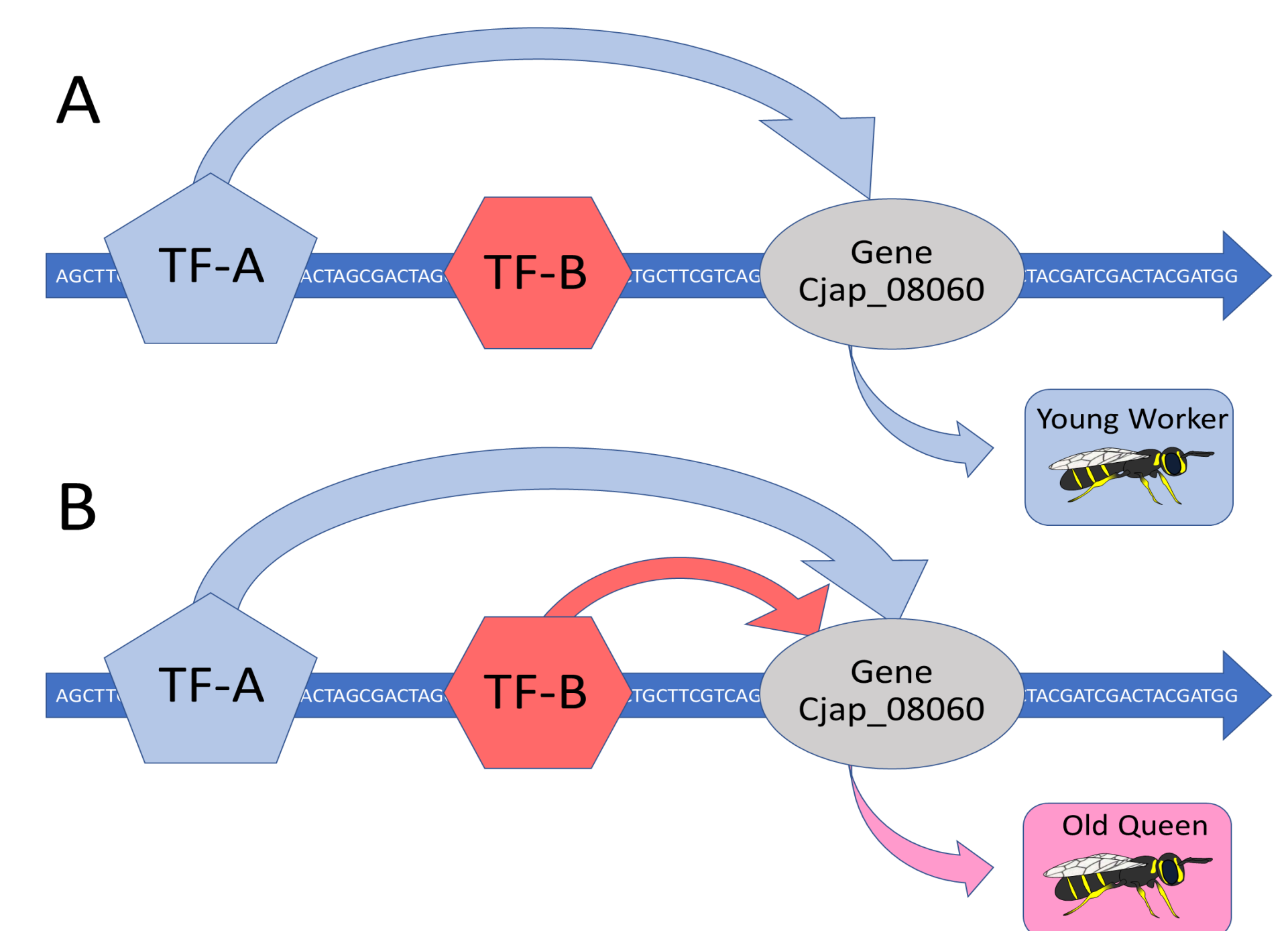
## METHODS

- Female *C. japonica* were collected from *Hydrangea sp.* from Sapporo, Japan
- Nest age was assessed by measuring wing wear; queen and worker caste identities were then determined by measuring individual body size and ovarian development
- RNA was extracted from the heads of 18 individuals representative of three old and three young social and solitary nests (6 queens, 6 workers, 6 solitary females total)
- DESeq was then run in R (v3.4.3) to determine DEGs among groups (Fig. 4)



**Figure 4.** Diagram of pairwise comparison categories used for differential gene expression analysis; A) major groups; B) minor groups (i.e. caste and age).

- The *C. japonica* genome was BLASTed against many other taxa to assess conservation of DEGs across phylogenies
- cis-Metalysis was then run to determine transcription factor (TF) binding site motif enrichment in regions flanking DEGs (Fig. 5)



**Figure 5.** Diagram of a DEG (Cjap\_08060) hypothetically regulated by two TFs; A) activation by TF A in young workers, B) activation by TFs A and B in old queens.

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University of New Hampshire