

## **Title: Observation of *C. elegans* dauer recovery in response to bacteria**

Preview for "Bubrig, L. T., et al. (2020). *Caenorhabditis elegans* dauers vary recovery in response to bacteria from natural habitat." bioRxiv: 2020.2004.2001.020693."

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### **Introduction**

Dauer diapause is the developmental arrested stage that shows a stress resistant and long-lived in response to harsh environmental conditions to survive and to maintain growth and reproduction in nematode *Caenorhabditis elegans*. *C. elegans* larva undergo dauer diapause after the second larval molt dependent upon population density, pheromone, food signal and temperature. Dauer larvae show distinct morphology, metabolism and behavior from other normal stages (Golden and Riddle, 1982, 1984). Signaling pathways and mechanisms regulate to enter dauer arrest are well-established: guanylyl cyclase pathway, TGF $\beta$ -like pathway, insulin-like pathway and steroid hormone pathway (Fielenbach and Antebi, 2008).

On the other hand, resuming the normal developmental process from dauer in favorable environmental conditions is also important for natural survival in *C. elegans*. Dauer recovery is triggered by bacterial food sources in experimental and natural conditions. However, there are little studies on whether dauer can choose favorable environmental conditions as external cues to resume normal growth and to avoid bad environmental conditions, for example, bacterial community composition (Samuel et al., 2016), and what factors affect the recovery of dauer diapause in *C. elegans*.

In a recent study, Bubrig, L. T., et al. (2020)., the authors investigated how four bacterial species from natural conditions influence recovery of dauer diapause and compared how three different genotype worm strains exhibit the recovery rate differently on different bacterial species.

### **Result**

To investigate whether the habitat (bacteria) and the species would affect worm's discerning recovery strategy, the authors exposed dauer worms to two kinds of bacteria for three hours, and collected and scored the worms based on their recovery status. They use three different geographically and genetically distinct worm strains to determine if there is intraspecific variation, N2, which is isolated in Bristol, CB4856, isolated in Hawaii, and JU1395, isolated in France recently in 2008. They used four ecologically-relevant bacterial species isolated from *C. elegans*' natural habitat, *E. coli*

OP50 and a control treatment with no food at all. Those four bacteria can be categorized into beneficial and detrimental. The beneficial bacteria support *C. elegans* population growth and do not activate its immune system, including *Raoultella sp.* JUb54 and *Providencia sp.* JUb39. The detrimental bacteria are pathogenic and cannot support *C. elegans* populations, including *Serratia sp.* JUb9 and *Pseudomonas sp.* BIGb0427. They total use 19,071 worms, and about 44% recovered from the dauer stage. The result showed that N2 has a total around 34% recovery rate, and has better recovery rate in *E. coli*, then beneficial bacteria. The detrimental bacteria has the worst recovery rate. CB4856 has a better recovery rate of 39.2% compared to N2. They also share the same trend of recovery rate in different bacteria strains, except CB4856 has a higher recovery rate in *Serratia sp.* JU1395 has the best recovery rate of 56.4% among all the strains. The recovery rate from high to low is beneficial bacteria, *E. coli*, then detrimental bacteria. However, in the group of *Serratia sp.* JU1395 also has a higher recovery rate. The batch differences are also big in each repeat. The author also did growth assay, which showed no difference in three worm strains. To explore which variables affected a worm's probability of recovering, they built a logistic regression model, where they used N2 and the control treatment as baselines. Odds ratios represent the fold-change in probability of recovering compared to the baseline. They claim their model showed a significant interaction between "Worm Strain" and "Treatment" because the odd ratios varied after multiplied by the adjustment odd ratio of worm strains. Last, they sequenced JU1395's genome. Genome comparisons showed that there are polymorphisms in some dauer-associated genes. Those genes might be important for studies related to worm-microbe interactions.

## Future Directions

*C. elegans* might have discerning strategy to colonize in the environment it preferred. On the other hand, there might be no fitness benefit to varying recovery in different habitats, which is an undiscerning strategy. In this paper, the authors showed that the behavioral strategies do not evolve in response to environmental pressures. However, the full understanding must take into account other factors. For example, bacteria may release odorants to specifically manipulate bacteriovore behavior.

In this study, several interesting on-going questions and experiments are unanswered. They remained the sequence comparison result between worm strains, which provided a good genetic tool/information for future study, despite they found polymorphism in JU1395's *daf-22*. They used one method to make dauer using starvation. Could differences have occurred in the results when using different methods to induce dauer formation, such as exogenous pheromone or high-density plating? (Karp, 2018) This question is also related to their polymorphism found in *daf-22*. They described *E. coli*

seeded Nematode Growth Medium (NGM) plates are used to induce dauer formation via starvation. Will the recovery rate change or be affected when they use the same or different bacterial strains before and after dauer diapause?

## References

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