Examining changes in antimicrobial expression in *Caenorhabditis elegans* exposed to *Elizabethkingia anophelis*

Sarah Grossen, Skylar List, Wesam Albayati, and Kristopher Schmidt
Department of Biology and Chemistry, Eastern Mennonite University, Harrisonburg VA

Abstract

Understanding how the immune system reacts to pathogens and subsequent mechanisms of infection are vital in developing therapeutic targets against pathogenic agents. *Elizabethkingia anophelis* is an aerobic, gram-negative bacteria that was first identified in 2011, and has since emerged in localized outbreaks in the Midwest (7,8). Given its recent discovery, its mechanism of infection in humans is still being elucidated. The innate immune systems of humans and C. elegans align closely with many conserved genetic pathways, allowing study of C. elegans to be a powerful model organism in understanding human innate immunity. In this study we used C. elegans to examine antimicrobial expression following exposure to *E. anophelis* and *E. coli* bacteria. Upon exposure to both *E. coli* and *E. anophelis*, antimicrobial expression in C. Elegans was measured through GFP fluorescence.

References

1.Dierking K *et al.* (2016) Antimicrobial effectors in the nematode Caenorhabditis elegans: an outgroup to the Arthropoda. *Philosophical transactions of the Royal Society of London.*
2.Estes K *et al.* (2010) bZIP transcription factor *zip-2* mediates an early response to *Pseudomonas aeruginosa* infection in *Caenorhabditis elegans*. *Proceedings of the National Academy of Sciences.*
3.Dunbar T *et al.* (2012) C. elegans detects pathogen-induced translational inhibition to activate immune signaling. *Cell host & microbe.*
4.Ewbank J (2006) Signaling in the immune response. *WormBook*.
5.Tepper R (2013) PQM-1 complements DAF-16 as a key transcriptional regulator of DAF-2-mediated development and longevity. *Cell*.
6.Shivers R *et al.* (2009) Tissue-specific activities of an immune signaling module regulate physiological responses to pathogenic and nutritional bacteria in C. elegans. *Cell host & microbe.*
7.Figueroa Castro, C *et al.* (2017) *Elizabethkingia anophelis*: Clinical Experience of an Academic Health System in Southeastern Wisconsin. *Open forum infectious diseases*.
8.About Elizabethkingia (2018) *Cdc.gov*
9.Rezai, P (2017) Microfluidic Systems to Study the Biology of Human Diseases and Identify Potential Therapeutic Targets in *Caenorhabditis elegans. Integrated Microsystems*.

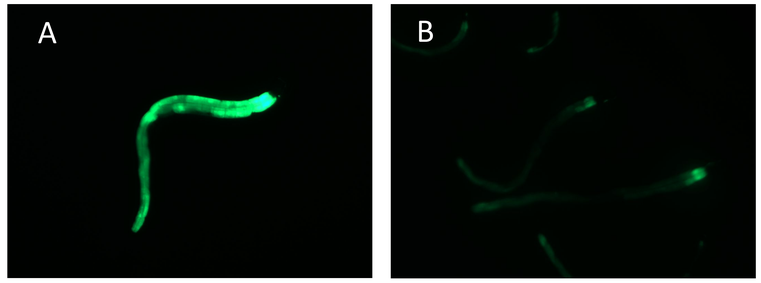

Figure 1. (A) Transgenic *C. elegans* containing reporting T24B8.5 expression after exposure to *E coli.* Fluorescence reflects stimulation of antimicrobial immune response. (B) Transgenic *C. elegans* reporting T24B8.5 expression after exposure to *E. anophelis*.

Figure 2. Larval stages of *C elegans*: embryo, L1, L2, L3, L4, adult. Antimicrobial immune response evaluated after bacterial exposure during embryonic and L1 stages. (9)

Introduction

- Antimicrobial proteins are expressed when exposure to pathogenic bacteria occurs. This is indicative of an innate immune response. (1)
- IRG-1 is part of the infection response gene class, acting as a general marker of infection and induced upon endotoxin driven translational inhibition in response to gram negative bacteria (2, 3).
- T24B8.5 is expressed in the intestine, encodes a toxin peptide released in response to stimulation of the innate immune system. (6)

Results

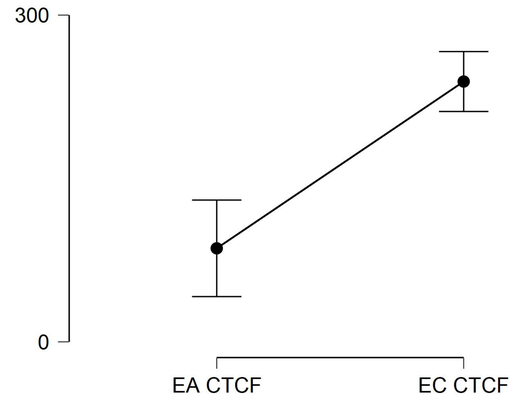

Figure 3. Difference in T24B8.5p expression indicated by fluorescence. p=0.017

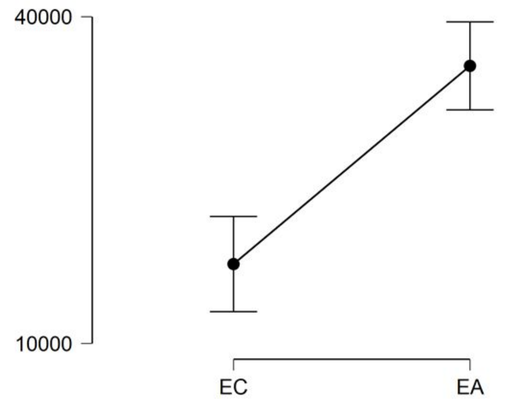

Figure 4: Difference in IRG-1 expression indicated by fluorescence. p=0.004

Conclusion

After exposure to both bacterial strains, expression of T24B8.5p showed greater increase in response to *E. coli* than *E. anophelis*, indicating suppressed immune activation of T24B8.5p encoded antimicrobial proteins in response to *E.anophelis.* The IRG-1 gene showed increased expression in response to *E. anophelis* rather than *E. coli*, displaying stronger innate immune activation of IRG-1 encoded antimicrobial proteins in response to *E. anophelis*.