Wild-type *Caenorhabditis elegans* Isolates Exhibit Distinct Gene Expression Profiles in Response to Microbial Infection

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The nematode *Caenorhabditis elegans* serves as a model system to study innate immunity against microbial pathogens. *C. elegans* have been collected from around the world, where they have presumably adapted to regional microbial ecologies. Here we use survival assays and RNA-sequencing to better understand how two isolates from disparate climates respond to pathogenic bacteria. We found that, relative to N2 (originally isolated in Bristol, UK), CB4856 (isolated in Hawaii), was more susceptible to the Gram-positive pathogen, *Staphylococcus epidermidis*, but equally susceptible to *Staphylococcus aureus* as well as two Gram-negative pathogens, *Providencia rettgeri* and *Pseudomonas aeruginosa*. Transcriptome analysis of infected worms found gene expression profiles to be considerably different in an isolate-specific and pathogen-specific manner. We utilized geneset enrichment analysis to categorize differential gene expression in response to *S. epidermidis*. In N2, genes that encoded detoxification enzymes and extracellular matrix proteins were significantly enriched, while in CB4856, genes that encoded detoxification enzymes, C-type lectins, and lipid metabolism proteins were enriched, suggesting these isolates have different responses to the pathogen, despite being the same species. Finally, to examine changes in transcriptional networks post-infection, we cross-referenced our list of differentially expressed genes with a list of *C. elegans* transcription factors. In total, 22 transcription factors were differentially expressed between N2 and CB4856 worms following *S. epidermidis* infection, 13 of which were members of the nuclear hormone receptor family. Overall, discerning gene expression signatures in an isolate-by-pathogen manner can help us better understand the different possibilities for the evolution of immune responses within organisms.