EMBO
Workshop

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Abstracts Book

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40. The identification of intergenerational diapause-inducing bacteria from complex natural ecosystems.

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The state of diapause is a strategy used by many species to escape stress. For example, nematodes enter diapause as a defense mechanism against bacterial pathogens, a response that requires the RNAi machinery from hosts and sRNAs from the bacteria. These studies however, were done with laboratory-reared human pathogens but the impact of natural microbiota on diapause entry has not been studied. To address this question, we isolated a consortium of bacteria from the soil and fed them to *C. elegans* expressing a dauer specific fluorescent marker (*col-183::mCherry*). The mix of soil bacteria induced diapause in the second generation at a 5% rate, similar to pathogens and starvation. We isolated each bacterium from the consortium and sequenced their 16S ribosomal RNA, identifying them as *Comamonas koreensis, Chryseobacterium indologenes, Stenotrophomonas tumulicola,* and *Rhodococcus qingshegii.* Animals developed normally and did not avoid bacterial lawns. Dauer formation was only observed in the second generation of animals feeding on *R. qingshegii,* being 17% at 20°C and 29% at 25°C. The presence of other bacteria in the consortia seem to dilute but not eliminate the effect of *R. qingshegii* on dauer formation. These results suggest that dauer entry may be a common strategy found in natural ecosystems not necessarily in response to starvation but rather to the microbiota composition of the soil. Whether this is a heritable response, remains to be tested in the future.
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41. Bacterial diets are able to modulate life-history treats in *C. elegans* models of neurodegenerative diseases

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As life expectancy increase, age-related disorders, such us neurodegenerative diseases (ND), have become more prevalent. Moreover, conventional treatments only attenuate some of the symptoms, but fail to arrest or delaycharacteristic neuronal proteotoxicity that characterizes them.. Thus, new challenges emerge to science in order to understand molecular basis of these disorders. Lately, the gut-brain axis has gain attention and a close relation between gut microorganism and ND has been proposed. In this context,T the aim of our work was to evaluate the relevance of the microbiota in the development and progression of proteotoxic-based disorders, assessing the impact of six non-pathogenic bacterial diets on life-history traits in *C. elegans* models of neurodegenerative disordersND (vs standard OP50). In a first approach, we found 2 bacteria, *Escherichia coli* K12 and *E. coli* HB101, able to improve locomotion in liquid media, in worm's model of Parkinson disease (PD) at adult day 4, versus the traditional *E. coli* OP50. Moreover, an age-dependent locomotion improvement, between larva- L4 and adult day 4, was observed in solid media after feeding PD model´s worms with 4 different bacteria versus *E. coli* OP50. We also On the other hand, we obobserved an increase thatin the developmental timing of wild-type worms was increase when animals were grown in 4 bacteria versus *E. coli* OP50, but more interesting was the accelerated developmental rate selectively found in models of PD and Huntington disease feed with *E. coli* BL21 (DE3). We are currently evaluating aggregate numbers, lifespan and mitochondrial morphology among others. Our

results allowed us to identify bacteria with the ability to drive physiological outcomes and improve health status of *C. elegans* models of neurodegenerative diseases.

42. Spatio-temporal expression analysis of genes involved in the electron transport chain of Caenorhabditis elegans using machine learning.

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The electron transport chain is a key process in cellular energy production and is vital for the proper functioning of all organisms. In the nematode *C. elegans*, the genes involved in this process have been well characterized, but there is still much to learn about genes associated with of this process. In this study, we used a supervised machine learning approach to predict new genes associated with the electron transport chain in *C. elegans* using a RNA-seq dataset that includes single cell expression of the first three divisions of the development, 502 distinct cell lineages and 410 terminal cell types, and whole animal transcripts at each stage of the life cycle. We found that our approach was able to identify several new genes that were previously unknown to be involved in this process. These findings have significant implications for our understanding of the genetic regulation of the electron transport chain.