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Myths and misconceptions about C. elegans ecology and evolution

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C. elegans biologists show an admirable desire to understand all facets of the worm's biology, often wanting to relate their work to the context of *C. elegans* as a "real organism" that lives out in the wild world. However, some early perceptions about *C. elegans* biology are now known to be incorrect. Here we highlight four common misconceptions to, hopefully, eliminate the perpetuation of these myths.*C. elegans* is not a soil nematode: it is found in niches rich in decomposing organic matter. Despite old statements of *C. elegans* living in soil, no species of *Caenorhabditis* is found commonly in dirt – although *Caenorhabditis* are terrestrial when compared to marine nematodes. To understand why, it helps to think like a hungry worm. Like all species in the genus, *C. elegans* eats bacteria and some other microbes, and consequently *C. elegans* (and related species) occur in the wild with greatest prevalence in niches rich in decomposing organic matter that have abundant bacterial growth, such as rotting fruits, rotting flowers, and rotting plant stems. Compost bins are an analogous, human-constructed niche.

C. elegans and *C. briggsae* did not diverge 100 million years ago. The rapid generation time and somewhat higher mutation rate per generation of *Caenorhabditis* mean that sequence divergence accumulates faster per year than in many other organisms. Consequently, date estimates based on 'universal' molecular clock calibrations drastically overestimate divergence times of *C. elegans* with other organisms. The lack of a fossil record, the uncertainty in average generation turnover per year, and the extensive sequence divergence between *C. elegans* and its relatives all make it difficult to estimate accurately divergence times. However, best current estimates imply that *C. elegans* and *C. briggsae* diverged less than 30 million years ago (see Cutter 2015). Current published dates for the divergence of *C. elegans* and *Pristionchus pacificus* have no analytic support (Blaxter 2009).

N2 is not a "wild" genetic background, but is a strain adapted to the laboratory. Like all organisms reared for many generations in the lab, *C. elegans* N2 has adapted to the bench, perhaps aided by unintentional artificial selection. The genetic causes of several major lab adaptations are known in detail (*npr-1*, *glb-5*, *nath-10*), which exact numerous pleiotropic effects (Sterken et al. 2015). The domesticated

strain N2 may thus poorly predict the biology of wild strains for many traits, and epistasis may modify the phenotypic outcome of many mutations.

Selfing hermaphroditism (protandrous dioecy) is an unusual mode of reproduction in nematodes. Despite the famous experimental power of self-fertilization in *C. elegans*, its ancestors and 95% of the 52 known *Caenorhabditis species* reproduce by obligatory mating between males and females. Although a diversity of *C. elegans*' features reflect adaptation to a selfing lifestyle with few males (e.g. hermaphrodite resistance to mating, loss of sex-biased genes, small sperm), most traits shared with other *Caenorhabditis* require explanation in the evolutionary context of outbreeding ancestral species.

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