

A Reverse Genetic Analysis of Components of the Toll Signaling Pathway in *Caenorhabditis elegans*

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In the original version of this article, we described a function for the single Toll-like receptor in the nematode *C. elegans*. In this study we also reported the characterization of a gene similar to the kinase IRAK, *pik-1* and failed to show any significant phenotype for a mutant *pik-1* strain. We subsequently determined that the strain supposed to be a homozygous *pik-1(nr2019)* mutant does not contain the predicted deletion. A new *pik-1* allele (*tm2167*) produced by the Japanese National Bioresource Project was kindly provided by the project's coordinator, S. Mitani. This mutant behaved in a very similar manner to the original strain. Thus *pik-1(tm2167)* mutants showed no visible phenotype, no alteration in the swelling phenotype to *Microbacterium nematophilum* (J. Hodgkin, personal communication), a wild-type resistance to *Pseudomonas aeruginosa* strain PA14, and a slightly decreased longevity both on *Serratia marcescens* and *Escherichia coli* strain OP50. Given these results, our original conclusions regarding *pik-1* are unchanged. Clearly, all further observations and conclusions in the paper are not affected by this revision. We thank Oliver Zugasti for performing survival assays and Jonathan Hodgkin for communicating unpublished results.

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