

A spurious *fln-2* mutation in a wide variety of commonly used *C. elegans* strains

Marina Kniazeva^{1,2}, Gary Ruvkun^{3,4§}

¹Molecular Biology , Massachusetts General Hospital, Boston, Massachusetts,

²Genetics, Harvard Medical School, Boston, Massachusetts

³Molecular Biology, Massachusetts General Hospital, Boston, Massachusetts, United States

⁴Genetics, Harvard Medical School

§To whom correspondence should be addressed: ruvkun@molbio.mgh.harvard.edu

Abstract

We describe a *fln-2* mutant allele present in many commonly used *Caenorhabditis elegans* strains. It is present in the *dpy-5(e907)* strain, ancestral to thousands of transgenic strains generated by the *C. elegans* Expression Project. This finding broadens the number of strains affected by the *fln-2* mutation, now impacting thousands of transgenic lines used in diverse studies. This expands on the previous identification of the *fln-2* mutation in a wild-type male stock strain used for outcrossing in genetic studies.

Figure 1. Background mutation shortens lifespan in *Pgpp-5::GFP* reporter strain.

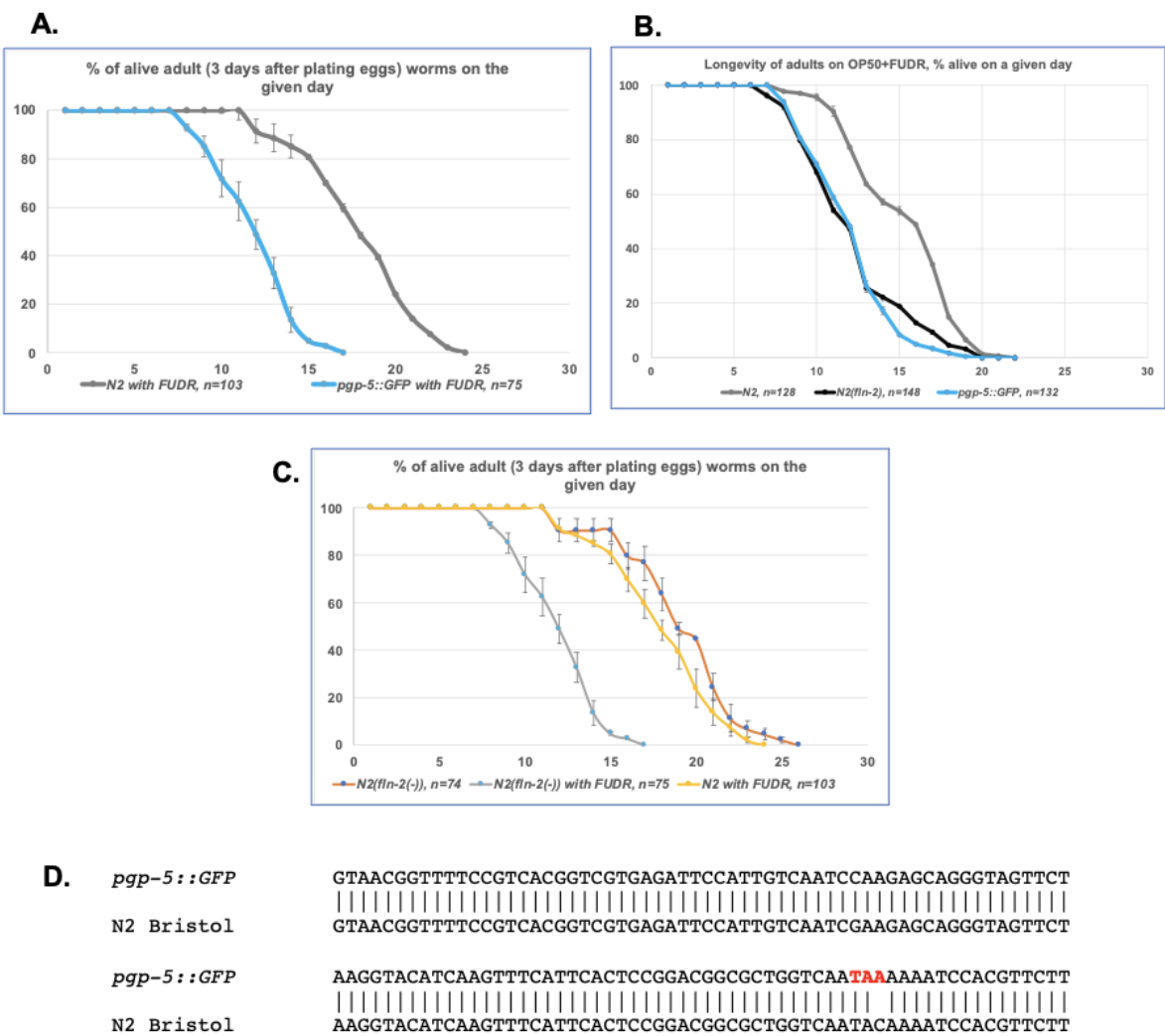


Figure 1. Background mutation shortens lifespan in *Pgpg-5::GFP* reporter strain:

1A. Animals carrying *pgp-5::GFP* have reduced life-span due to bursting in the experiments with FUDR-derived inhibition of proliferation.

1B. The life-span curve is similar in *pgp-5::GFP* strain and “*N2* male” strain carrying *fln-2* Y800* mutation.

1C. The *fln-2* mutant without FUDR treatment live as long as wild type *N2* treated with FUDR.

1D. DNA alignment of wild type *fln-2* in *N2* strain and *fln-2*(Y800*) in a strain constructed from a *pgp-5::GFP* reporter gene strain. The aligned DNA sequence refers to the *fln-2* locus (and specifically the Y800Stop mutation).

Description

We investigated *C. elegans* ZIP-2 transcription factor activation using a *pgp-5::GFP* reporter strain. During lifespan assays using FUDR (5-fluoro-2-deoxyuridine), a common method to prevent reproduction and simplify *C. elegans* aging studies, we observed a reduced lifespan and a prominent bursting (rupture) phenotype in this strain (Fig. 1A).

Filamins, like *FLN-2*, are crucial for organizing the actin cytoskeleton, a network essential for cellular structure, movement, shape changes, and intracellular transport. The *fln-2*(*ot611*) allele is a C-to-A mutation which causes a premature stop codon instead of the wild type tyrosine 800 (Y800*). This mutation was discovered in a “*N2* male stock” strain used for outcrossing mutants generated through mutagenesis. The strain was distributed from CGC, *Caenorhabditis* Genetic Center. Notably, in our experiments the bursting and lifespan kinetics in *pgp-5::GFP* strain closely mirrored those of *fln-2*(*ot611*) mutants (Fig 1B). The onset of rupture events occurred on day 8, with a daily rupture rate of 10-20% of the total population for the subsequent seven days, before dropping to approximately 1% for the remainder of the observation period in both strains. Our data show that *fln-2* mutant without FUDR treatment live as long as wt *N2* treated with FUDR (Fig. 1C)

Zhao et al. (Zhao et al., 2019) reported a *fln-2* Y800* mutation in variety of strains in their collection, finding it in approximately 50% of 50 tested strains, including those from the *C. elegans* Gene Knockout Project (gk and ok alleles, VC and RB prefix strains: 6/10 and 6/6) and the *C. elegans* Expression Project (s alleles: 9/9) (Consortium, 2012; Hunt-Newbury et al., 2007).

Sequencing of our *pgp-5::GFP* strain revealed the identical C-to-A mutation, mutating a TAC tyrosine codon to TAA stop (Fig. 1D).

Pedigree analysis of the *pgp-5::GFP* strain revealed its origin: a 300 bp *pgp-5* promoter fragment driving GFP expression, along with a rescuing *dpy-5*(+) gene, was injected into *dpy-5*(*e907*) *I* mutants, creating the *BC10030* strain (*C. elegans* Expression Project). Subsequent integration of the extrachromosomal array and outcrossing generated the *WE5172* strain (McKAY et al., 2003).

The *dpy-5*(*e907*) strain was originally chosen as a host for easy selection of array-carrying worms, as the co-injected *dpy-5*(+) construct rescues the *dpy-5* Dpy mutant phenotype to Non-Dpy. *dpy-5*(*e907*) itself was generated by ³²P irradiation of *N2* worms in the 1970s at the MRC Laboratory under the supervision of Sydney Brenner. Our sequencing of both *BC10030* and *WE5172* confirmed the presence of the Y800* mutation. Sequencing two other *dpy-5*(*e907*)-derived strains, *BC14247* and *BC10066* (unrelated to *pgp-5::GFP*), also revealed the *fln-2* mutation.

We conclude that the Y800* mutation was already present in the *N2* wild-type stock used to generate *dpy-5*(*e907*), probably in the “*N2* male stock” (Zhao et al., 2019).

Given that *dpy-5*(*e907*) served as the host strain for the creation of approximately 2,000 other *C. elegans* GFP expressing reporters, the potential for widespread dissemination of this mutation is significant.

Our combined data strongly indicate a prevalence of the *fln-2* mutation in strains circulating within the *C. elegans* research community. This finding highlights the importance of thorough strain characterization and careful interpretation of phenotypes, especially those related to cytoskeletal function, secretion, and lifespan.

Methods**Longevity assay:**

Gravid worms were bleached, and eggs were rinsed three times with M9 buffer. Eggs were then plated onto assay plates and incubated at 20°C for three days until worms reached adulthood.

Daily, the number of dead worms was counted. Lifespan was calculated in Excel as the number of live worms on each day, normalized to the total number of worms on each plate.

7/9/2025 - Open Access

The experiment was performed in triplicate for each strain. Average lifespan and standard error of the mean were plotted on the graphs.

Reagents

Nematode Growth Media (NGM containing bacto-peptone) (Brenner, 1974) agar plates with streptomycin.

2'-Deoxy-5-fluorouridine (FUDR, F0503, Sigma) stock 40 mM

PCR primers:

f1n-2F: GGTGTTTCGATTCTGGTCTGG

f1n-2R: ACATCGACGAGAAGACAACAC

Sequencing primer:

f1n-2SeqPCR: TGTACCCAGAAATTGACAAGATAC

Assay plate preparation for longevity assay: 170 µl of FUDR was mixed in 3 ml of [OP50-1](#) overnight culture and 200 µl were spotted on NGM agar plates (60 mm in diameter). Final FUDR concentration in agar was approximately 30 µM. Plates were let to dry at room temperature overnight.

Worm strains were provided by the [Caenorhabditis](#) Genetics Center, CGC:

[OP50-1](#) *E. coli*, streptomycin resistant CGC

[N2](#) Wild type, *C. elegans* CGC

[WE5172](#) *ajIs1* [*rCesC05A9.1::GFP* + *dpy-5(+)*] X CGC

[N2](#) male stock *f1n-2*(Y800*) CGC

[BC10030](#) *sEx864* [*rCesC05A9.1::GFP* + *pCeh361*] CGC

[BC14247](#) *sEx14247* [*rCes F42G4.3a::GFP* + *pCeh361*] CGC

[BC10066](#) *sEx900* [*rCesC15H9.6::GFP* + *pCeh361*] CGC

Acknowledgements: We thank WormBase for genome information and curation (Sternberg *et al.*, 2024) . Strains were provided by the CGC, Caenorhabditis Genetics Center, which is funded by NIH Office of Research Infrastructure Programs (P40 OD010440).

References

Brenner S. 1974. The genetics of *Caenorhabditis elegans*. *Genetics* 77(1): 71-94. PubMed ID: [4366476](#)

C. elegans Deletion Mutant Consortium. 2012. large-scale screening for targeted knockouts in the *Caenorhabditis elegans* genome. *G3 (Bethesda)* 2(11): 1415-25. PubMed ID: [23173093](#)

Hunt-Newbury R, Viveiros R, Johnsen R, Mah A, Anastas D, Fang L, et al., Moerman DG. 2007. High-throughput in vivo analysis of gene expression in *Caenorhabditis elegans*. *PLoS Biol* 5(9): e237. PubMed ID: [17850180](#)

McKay SJ, Johnsen R, Khattri J, Asano J, Baillie DL, Chan S, et al., Moerman DG. 2003. Gene expression profiling of cells, tissues, and developmental stages of the nematode *C. elegans*. *Cold Spring Harb Symp Quant Biol* 68: 159-69. PubMed ID: [15338614](#)

Sternberg PW, Van Auken K, Wang Q, Wright A, Yook K, Zarowiecki M, et al., Stein L. 2024. WormBase 2024: status and transitioning to Alliance infrastructure. *Genetics* 227(1): 10.1093/genetics/iyae050. PubMed ID: [38573366](#)

Zhao Y, Wang H, Poole RJ, Gems D. 2019. A *f1n-2* mutation affects lethal pathology and lifespan in *C. elegans*. *Nat Commun* 10(1): 5087. PubMed ID: [31704915](#)

Funding: This work was supported by the NIH National Institute on Aging R01AG16636 and R01AG043184 to GR.

Author Contributions: Marina Kniazeva: investigation, validation, writing - original draft. Gary Ruvkun: resources, supervision, writing - review editing.

Reviewed By: Anonymous

Nomenclature Validated By: Anonymous

WormBase Paper ID: WBPaper00068320

History: Received June 5, 2025 **Revision Received** July 3, 2025 **Accepted** July 9, 2025 **Published Online** July 9, 2025
Indexed July 23, 2025

Copyright: © 2025 by the authors. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International (CC BY 4.0) License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Citation: Kniazeva M, Ruvkun G. 2025. A spurious *fln-2* mutation in a wide variety of commonly used *C. elegans* strains. microPublication Biology. [10.17912/micropub.biology.001684](https://doi.org/10.17912/micropub.biology.001684)