

Worm Nomenclature 101

By Cindy Voisine, updated 2019 by Renee Brielmann

Outline for *C. elegans* Nomenclature

- I. Lab Identification
- II. Gene Names
- III. Allele/Mutations
- IV. Transgenes
- V. Multiple Mutations in a Strain
- VI. Proteins/mRNA
- VII. Phenotypes
- VIII. Strains
- IX. Test

I. Lab Identification

Strain code for naming strains

Morimoto AM
Sydney Brenner CB
Bob Horvitz MT
Cynthia Kenyon CF

Allele code for mutations/transgenes

Morimoto *rm*
Sydney Brenner *e*
Bob Horvitz *n*
Cynthia Kenyon *mu*

II. Gene Names

Rule: - 3 or 4 letters, hyphen, number
- italicized
- lowercase
- *followed by linkage group (chromosome)

Example: *unc-54 I*
let-858 II

*These statements are recommendations not rules.

III. Allele/Mutations

- Rule:
- every mutation has a unique allele assignment
 - italicized letter(s) followed by arabic number
 - use gene name followed by allele in ()
 - *mutations that are temperature sensitive can be designated as *ts* following allele name
 - *wildtype alleles have + sign in ()
 - if deletion takes out more than one gene *Df*
 - knockout consortium allele codes are *ok*, *bc*, *tm*

Example: *unc-30(rm7)* *daf-16(mgDf50)*
unc-15(e1402ts) *dpy-5(+)*

IV. Transgenes

- Rule:
- Italicized name with allele (*rm*) prefix, *Ex* and a number
 - Integrated arrays are *Is*
 - MosSCI arrays are *Si*
 - *Can be followed by square brackets with genotypic or molecular information
 - *Reporter strains: transcriptional or translational fusions generally not defined; can have *p* for promoter; gene name followed by two colons and the reporter.

Example: *rmIs18[dpy-5(+)*unc-54p::GFP*]* I made up this strain.
vha-6::GFP
vha-6p::GFP

V. CRISPR

- Rule:
- gene name for location of CRISPR insertion followed by () containing an allele name
 - *Can be followed by brackets containing insertion information
 - *Can be followed by chromosome number.

Example: *lgg-1(rm17[lgg-1::mcherry]) II*.

This nomenclature denotes the endogenous *lgg-1* locus tagged with *mcherry*.

VI. Multiple Mutations in a Strain

Rule: - listed sequentially according to linkage
- different linkage groups separated by semicolon
- Heterozygotes: separate mutations on the two homologous chromosomes with a slash; can use + sign for wildtype

Example: *lin-12(n137) III; him-5(e147) V*
dpy-5(e61) unc-13(+)/dpy-5(+) unc-13 (e51) I

VII. Protein/RNA Names

Rule: For Protein, refer to gene name
- non-italicized and capitalized
- those with alternate splicing get letter
- mutant proteins are referred to by the change
For mRNA, refer to it as the protein's mRNA
For non-coding RNA, use gene name

Example: UNC-54 PQE-1(P79Q)
 PQE-1A UNC-54 mRNA levels
 PQE-1B *let-7* mRNA

VIII. Phenotypes

Rule: - non-italicized 3 or 4 letter abbreviation
which usually corresponds to a gene name
- first letter is capitalized
- when referring to wildtype call it non-
- RNAi phenotype use gene name with (*RNAi*)

Example: Unc non-Unc *mog-4(RNAi)*
 Dpy Daf
 Osm Muv

IX. Strain Names

- Rule:
- nonitalicized names consisting of 2 or 3 capital letters followed by a number
 - every cross requires a new strain name
 - back crossing does not (specify in database).
 - each independent extrachromosomal array line has a new strain name
 - each independent integrated array has a new strain name

Example: AM565
CF1057

X. TEST

- *daf-16* mutant number 86 from Cynthia Kenyon's lab. *daf-16* is on chromosome I
- Crossed to strain expressing a promoter fusion of *C12C8.1* to GFP marked with a *rol-6* dominant mutant with allele number 1006 from Henry Epstein's lab with an allele designation (*su*) integrated on chromosome II
- Inject an extrachromosomal array using HSF-1 tagged with RFP under its own promoter
- Generate 3 lines

Our strain data base last entry: AM702

Our last entry for arrays: *rmIs47* and *rmEx182*

What is/are the Strain Name(s?) and genotype(s)?

Answers: