**moc-6/MOCS2A is necessary for molybdenum cofactor synthesis in C. elegans**

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**Abstract**

Molybdenum cofactor (Moco) is an essential prosthetic group that mediates the activity of 4 animal oxidases and is required for viability. Humans with mutations in the genes encoding Moco-biosynthetic enzymes suffer from Moco deficiency, a neonatal lethal inborn error of metabolism. *Caenorhabditis elegans* has recently emerged as a useful and tractable genetic discovery engine for Moco biology. Here, we identify and characterize K10D2.7/moc-6, the *C. elegans* ortholog of human MOCS2A, a sulfur-carrier protein essential for Moco synthesis. Using CRISPR/Cas9 gene editing, we generate 3 null mutations in K10D2.7/moc-6 and with these alleles genetically demonstrate that K10D2.7/moc-6 is necessary for endogenous Moco synthesis in *C. elegans*.

![Image](https://example.com/image1.png)

**Figure 1. moc-6 is required for C. elegans Moco synthesis:** (A) Amino acid alignment between human MOCS2A and *C. elegans* K10D2.7/MOC-6. Shaded amino acids (*) are identical. Strong (:) and weak (.) amino acid similarity are also displayed. (B) Nucleotide sequence for the wild type K10D2.7/moc-6 locus is displayed as are the sequences for newly generated K10D2.7/moc-6 deletions rae295, rae296, and rae297. Guide RNAs were designed targeting the 2 K10D2.7/moc-6
sequences displayed in red. The 2 corresponding PAM sites are displayed in blue. (C) Wild-type, rae295, rae296, and rae297 animals were cultured from synchronized L1 larvae for 72 hours on wild-type (Moco producing) and ΔmoaA mutant (Moco deficient) E. coli. Animal length was determined for each condition. (D) moc-6(rae296), cth-2(mg599); moc-6(rae296), and moc-6(rae296); cdo-1(mg622) mutant animals were cultured from synchronized L1 larvae for 72 hours on wild-type (Moco producing) and ΔmoaA mutant (Moco deficient) E. coli. Animal length was determined for each condition. For panels C and D, box plots display the median, upper, and lower quartiles, and whiskers indicate minimum and maximum data points. Sample size (n) is displayed for each experiment. *, indicates a statistically significant difference (p<0.01, unpaired t-test) in C. elegans growth on ΔmoaA E. coli when compared to corresponding growth on wild-type E. coli. (E) Hatching rates for wild-type and mutant C. elegans was determined. Moco+ diet indicates that mothers were cultured on wild-type E. coli while Moco- indicates that mothers were shifted to ΔmoaA mutant E. coli at the L4 stage of development, depriving animals of dietary Moco during reproductive adulthood. n is the number of embryos scored for hatching for each genotype and condition. * (red), indicates a statistically significant difference (p<0.01, Chi-square test) in the hatching rates of the progeny of C. elegans mothers fed ΔmoaA E. coli when compared to the corresponding hatching rate when fed wild-type E. coli. * (black), indicates a statistically significant difference (p<0.01, Chi-square test) in hatching rates of the progeny of cth-2(mg599); moc-6(rae296) and moc-6(rae296); cdo-1(mg622) double mutant C. elegans mothers fed ΔmoaA E. coli when compared to moc-6(rae296) single mutant mothers fed ΔmoaA E. coli.

Description

The nematode C. elegans has recently emerged as a tractable system for genetic discovery in Moco biology (Warnhoff and Ruvkun 2019; Warnhoff et al. 2021). In C. elegans, endogenous Moco biosynthesis is not required for growth, development, and reproduction. C. elegans mutants defective in Moco biosynthesis are viable because they acquire and use Moco from their bacterial diet (Warnhoff and Ruvkun 2019; Warnhoff et al. 2021). Thus, C. elegans has 2 redundant pathways for maintaining cellular Moco: endogenous synthesis and dietary acquisition. C. elegans is the only known animal for which Moco biosynthesis is dispensable.

The human MOCS2A enzyme is required for Moco synthesis (Schwarz et al. 2009). MOCS2A is a small sulfur-carrier protein that is necessary for the conversion of cyclic pyranopterin monophosphate to molybdopterin. This reaction is the second step in the linear synthesis pathway of Moco from guanosine triphosphate (Schwarz et al. 2009). Loss-of-function mutations in MOCS2A cause human Moco deficiency, a rare and lethal inborn error of metabolism (Johnson et al. 2001). However, the C. elegans orthologue of MOCS2A has not been molecularly identified or genetically studied. Using amino acid sequence analysis, we determined that the C. elegans K10D2.7 genomic locus encodes a protein with high amino acid similarity and identity to human MOCS2A (Fig. 1A) (Altschul et al. 1990). To determine the role K10D2.7 plays in Moco biosynthesis, we used CRISPR/Cas9 to engineer 3 independent deletions of K10D2.7 (Fig. 1B) (Cho et al. 2013; Ghanta and Mello 2020). These K10D2.7 deletion alleles (rae295, rae296, and rae297) are likely null mutations because they eliminate >80% of the K10D2.7 coding sequence. As we have shown for other C. elegans mutations in Moco biosynthetic machinery, the K10D2.7 deletion alleles rae295, rae296, or rae297 cause no defects when animals are cultured under standard laboratory conditions feeding on wild-type E. coli which also synthesizes Moco. To determine if K10D2.7 is necessary for endogenous Moco synthesis, we cultured wild-type, rae295, rae296, and rae297 mutant animals on wild-type and ΔmoaA E. coli, a mutant bacterial strain that is unable to synthesize Moco. rae295, rae296, and rae297 mutant animals grew well on wild-type (Moco producing) E. coli but displayed a completely penetrant developmental arrest when cultured on ΔmoaA (Moco deficient) mutant E. coli (Fig. 1C). In contrast to K10D2.7 mutant animals, wild-type C. elegans grow well on wild-type or ΔmoaA mutant E. coli, although we observed a subtle, but statistically significant, reduction in the growth of wild-type animals on ΔmoaA mutant E. coli (Fig. 1C). By eliminating Moco from the diet, we revealed the defect in endogenous Moco synthesis caused by the rae295, rae296, and rae297 mutations. We conclude that K10D2.7 is required for C. elegans Moco synthesis and name this gene moc-6 (Molybdenum Cofactor biosynthesis).

Moco deficiency in C. elegans also results in embryonic lethality when maternal animals are deprived of both endogenous and exogenous sources of Moco during reproductive adulthood (Warnhoff and Ruvkun 2019). moc-6 mutant C. elegans mothers were fed wild-type E. coli until the L4 stage of development, one stage prior to reproductive adulthood. These moc-6 mutant L4 mothers were then shifted onto wild-type or ΔmoaA mutant E. coli and the hatching rate of their progeny was determined. When moc-6 mutant animals were shifted to a Moco deficient diet, 0% of their embryos hatched (Fig. 1E). In contrast, 100% of moc-6 mutant embryos hatched when their mothers were fed wild-type E. coli. Hatching rates of wild-type embryos were not affected by the maternal diet (Fig. 1E). We conclude that maternal dietary Moco is sufficient to support the required Moco-dependent enzymes for embryonic development. Whether dietary Moco is acting maternally or embryonically to support embryonic development remains to be determined.
Previous genetic studies of the *C. elegans* Moco biosynthetic pathway demonstrated that Moco is required for the detoxification of sulfites produced by the sulfur amino acid metabolism pathway governed by cystathionase (*cth-2*) and cysteine dioxygenase (*cdo-1*). The activities of *cth-2* and *cdo-1* are required for the developmental arrest that occurs when *C. elegans* are defective in Moco synthesis and lack dietary Moco (Warnhoff and Ruvkun 2019). Loss-of-function/null mutations in *cth-2* or *cdo-1* suppress the developmental arrest displayed by *moc* mutant *C. elegans* grown on Moco-deficient *E. coli* (Warnhoff and Ruvkun 2019). To determine if the developmental arrest of *moc* mutant *C. elegans* was also dependent upon *cth-2* and *cdo-1*, we engineered *cth-2; moc-6* and *moc-6; cdo-1* double mutant animals and assessed their growth on wild-type and ΔmoaA mutant *E. coli*. In contrast to *moc-6* single mutant animals, *cth-2; moc-6* and *moc-6; cdo-1* double mutant animals grew well on both wild-type and ΔmoaA mutant *E. coli* (Fig. 1D). *cth-2* and *cdo-1* single mutant animals grow well on both wild-type and ΔmoaA mutant *E. coli* (Warnhoff and Ruvkun 2019). Furthermore, mutations in *cth-2* or *cdo-1* suppressed the embryogenesis defects displayed by *moc-6* mutant mothers fed on Moco-deficient *E. coli* (Fig. 1E). Although, we find that *moc-6; cdo-1* double mutant embryos derived from mothers fed ΔmoaA mutant *E. coli* do not hatch at the same rate as wild type. Further studies are required to account for this observation. Together, these data demonstrate that *cth-2* and *cdo-1* inhibit normal development when Moco is deficient due to loss of both *moc-6* and dietary Moco. CTH-2 and CDO-1 act in a catabolic pathway to produce sulfite from the sulfur amino acids methionine and cysteine. Sulfites are extremely toxic during Moco deficiency due to inactivity of the Moco-requiring sulfite oxidase enzyme, SUOX-1. Loss of *cth-2* or *cdo-1* prevents the metabolic production of sulfites, alleviates the cellular stress caused by inactive SUOX-1 (concomitant with Moco deficiency), and permits growth, development, and reproduction (Warnhoff and Ruvkun 2019). The mechanism by which sulfite promotes larval arrest and death remains enigmatic in both our *C. elegans* models and in human patients suffering from Moco deficiency.

This study demonstrates that *moc-6* is required for endogenous *C. elegans* Moco biosynthesis and amino acid sequence analyses strongly suggest that *moc-6* is orthologous to human MOCS2A.

**Methods**

Request a detailed protocol

Animal cultivation:

*C. elegans* strains were cultured using established protocols (Brenner 1974). Briefly, animals were cultured at 20°C on nematode growth media (NGM) seeded with wild-type *E. coli* (BW25113) unless otherwise noted. The wild-type *C. elegans* strain was Bristol N2. All *C. elegans* and *E. coli* strains used in this work are listed in the Reagents table.

Engineering deletions of *moc-6*/K10D2.7 using CRISPR/Cas9:

Genome engineering using CRISPR/Cas9 technology was performed using established techniques (Cho et al. 2013; Ghanta and Mello 2020). Briefly, 2 guide RNAs were designed and synthesized (IDT) that targeted the K10D2.7 locus (Fig. 1B). Cas9 (IDT) guide RNA ribonucleoprotein complexes were directly injected into the *C. elegans* germline (Cho et al. 2013). Newly induced deletions were identified in the offspring of injected animals using a PCR-based screening approach. The DNA primers used to screen for new deletions were: 5’-ggggatgggacatctca-3’ and 5’-tccctattttgcaccctttg-3’. We were able to isolate and homozygoze 3 independent deletions of K10D2.7; *rae295*, *rae296*, and *rae297* (Fig. 1B).

*C. elegans* growth assays:

*C. elegans* were synchronized at the first stage of larval development (L1). L1 animals were cultured on NGM seeded with wild-type or ΔmoaA mutant *E. coli*. Animals were cultured for 72 hours at 20°C and live animals were imaged using an SMZ25 stereomicroscope (Nikon) equipped with an ORCA-Flash4.0 camera (Hamamatsu). Images were captured using NIS-Elements software (Nikon) and processed using ImageJ. Animal length was measured from the tip of the head to the end of the tail. GraphPad Prism software was used to perform statistical tests as well as calculations of median, upper, and lower quartiles.

Quantification of embryo hatching:

To determine the hatching rate of wild-type and mutant *C. elegans*, we performed synchronized egg lays using young adult animals. Embryos were scored for hatching 12-24 hours after being laid. To test the effect of maternal dietary Moco on embryo hatching, mothers were initially grown on wild-type *E. coli* to the L4 stage of development and were shifted onto either wild-type or ΔmoaA mutant *E. coli*. Shifted L4 animals developed overnight into young adults on their respective *E. coli* diets and their progeny were assayed for their ability to hatch.

**Reagents**
| Organism   | Strain     | Genotype                    | Source       |
|------------|------------|-----------------------------|--------------|
| C. elegans | N2         | Wild type                   | CGC          |
| C. elegans | USD954     | moc-6(rae295) III           | This work    |
| C. elegans | USD955     | moc-6(rae296) III           | This work    |
| C. elegans | USD956     | moc-6(rae297) III           | This work    |
| C. elegans | GR2257     | cth-2(mg599) II             | CGC          |
| C. elegans | GR2260     | cdo-1(mg622) X              | CGC          |
| C. elegans | USD959     | moc-6(rae296) III; cdo-1(mg622) X | This work |
| C. elegans | USD960     | cth-2(mg599) II; moc-6(rae296) III | This work |
| E. coli    | BW25113    | Wild type                   | NIG          |
| E. coli    | JW0764-2   | ΔmoaA753::kan               | NIG          |

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References

Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990. Basic local alignment search tool. J Mol Biol 215: 403-10. PMID: 2231712.

Brenner S. 1974. The genetics of *Caenorhabditis elegans*. Genetics 77: 71-94. PMID: 436476.

Cho SW, Lee J, Carroll D, Kim JS, Lee J. 2013. Heritable gene knockout in *Caenorhabditis elegans* by direct injection of Cas9-sgRNA ribonucleoproteins. Genetics 195: 1177-80. PMID: 23979576.

Ghanta KS, Mello CC. 2020. Melting dsDNA Donor Molecules Greatly Improves Precision Genome Editing in *Caenorhabditis elegans*. Genetics 216: 643-650. PMID: 32963112.

Johnson JL, Coyne KE, Rajagopalan KV, Van Hove JL, Mackay M, Pitt J, Boneh A. 2001. Molybdopterin synthase mutations in a mild case of molybdenum cofactor deficiency. Am J Med Genet 104: 169-73. PMID: 11746050.

Schwarz G, Mendel RR, Ribbe MW. 2009. Molybdenum cofactors, enzymes and pathways. Nature 460: 839-47. PMID: 19675644.

Warnhoff K, Hercher TW, Mendel RR, Ruvkun G. 2021. Protein-bound molybdenum cofactor is bioavailable and rescues molybdenum cofactor-deficient *C. elegans*. Genes Dev 35: 212-217. PMID: 33446569.

Warnhoff K, Ruvkun G. 2019. Molybdenum cofactor transfer from bacteria to nematode mediates sulfite detoxification. Nat Chem Biol 15: 480-488. PMID: 30911177.

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