ICD-1/BTF3 antagonizes SKN-1-mediated endoderm specification in *Caenorhabditis elegans*

Chee Kiang Ewe[1], Yamila N Torres Cleuren[1,2], Geneva Alok[1] and Joel H Rothman[1§]

[1]Department of MCD Biology and Neuroscience Research Institute, University of California Santa Barbara, CA, USA
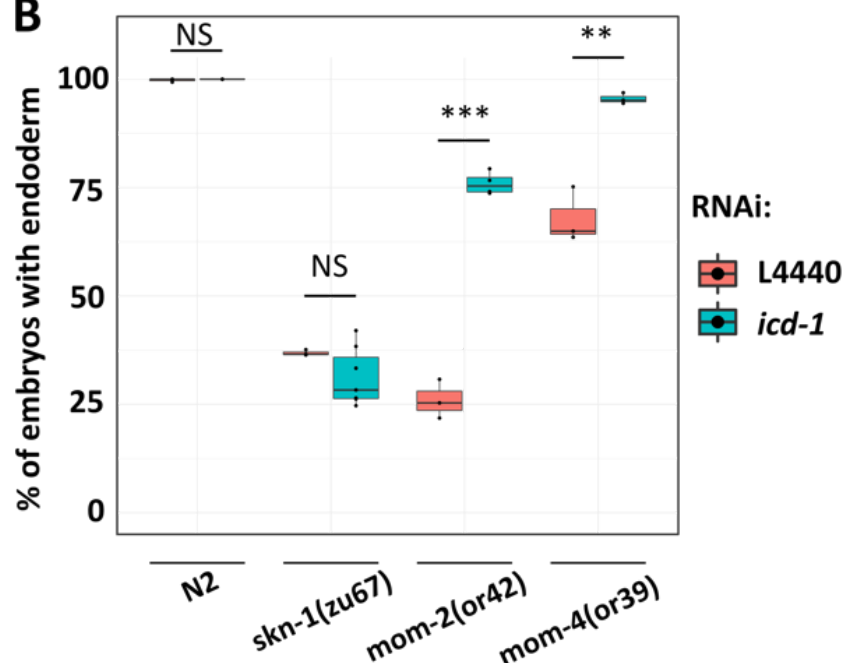
[2]School of Biological Sciences, University of Auckland, Auckland, New Zealand

[§]To whom correspondence should be addressed: joel.rothman@lifesci.ucsb.edu
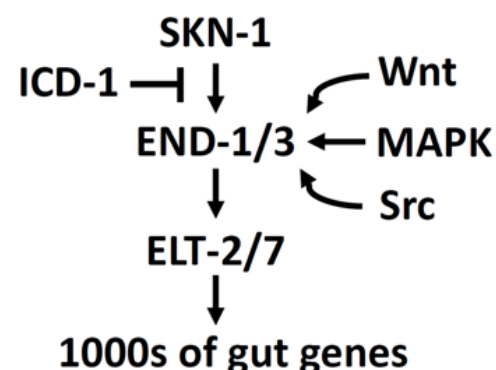
Figure 1: A) Amino acid sequence of ICD-1. The putative nuclear localization signal is highlighted in red. B) The effects of *icd-1* RNAi on N2, *skn-1(zu67)*, *mom-2(or42)*, and *mom-4(or39)* absence-of-endoderm phenotype. At least three replicates were performed per experiment with >200 embryos scored per experiment. Student t-test (NS p-value> 0.05, ** p-value ≤ 0.01, *** p-value ≤ 0.001). C) Hypothesized model of ICD-1 function in endoderm specification, positing that it antagonizes the SKN-1 input upstream of END-1/3.

Description

The entire *C. elegans* intestine is derived from a single endodermal progenitor cell (E), the posterior daughter arising from the asymmetric division of the EMS blastomere. During early embryonic development, maternally provided SKN-1/Nrf2 activates the mesendoderm gene regulatory network (GRN) in both E and its sister, MS. A triply redundant Wnt/MAPK/Src signaling system from the neighboring P_2 blastomere polarizes EMS, resulting in activation of E fate on the side contacting it. In MS, and in an unsignaled E cell, POP-1/Tcf represses expression of the redundant endoderm specifying factors, the END-1 and -3 GATA-type transcription factors. In a normal E cell, Wnt (initiated by the MOM-2/Wnt ligand) and MAPK signaling (through the MOM-4 MAPKKK) converge on POP-1 to convert it from a repressor to an activator of the *end* genes which, in collaboration with SKN-1, activates E cell fate (Thorpe *et al.* 1997; Maduro and Rothman 2002; McGhee 2007; Maduro 2017).

Basal transcription factor 3 (BTF3) facilitates transfer of nascent polypeptide chains into mitochondria and regulates transcription in plants and animals (Jamil *et al.* 2015). We previously found that the *C. elegans* BTF-3 orthologue, ICD-1, is required to prevent apoptosis: eliminating *icd-1* leads to increased cell death in embryos and larvae (Bloss *et al.* 2003). However, consistent with its potential function as a transcription factor, ICD-1 contains a putative nuclear localization signal in the N-terminus (Fig.1A) (Lange *et al.* 2007). Here, we report that ICD-1 performs a function in endoderm specification. We found that *icd-1* RNAi does not affect endoderm specification in a wild-type N2 background or the gut-less phenotype of *skn-1(-)* embryos. However, knockdown of *icd-1* strongly suppresses the absence of gut in *mom-2/Wnt(-)* embryos (*mom-2(or42)*: 26.0% ± s.d. 4.5% with gut *vs. mom-2(or42); icd-1(RNAi)*: 75.9% ± s.d. 2.6%). Similarly, depleting ICD-1 rescues the gut-less phenotype of *mom-4/Tak1(-)* embryos (*mom-4(or39)*: 67.9% ± s.d. 6.3% with gut *vs. mom-4(or39); icd-1(RNAi)*: 95.5% ± s.d. 1.2%) (Fig. 1B). Our findings suggest a model in which ICD-1 antagonizes the SKN-1 input, perhaps by preventing SKN-1 from binding to *end-1/3* promotors. This possibility is also consistent with the finding that competition between ICD-1 and SKN-1 is seen in the context of the unfolded protein response (UPR). SKN-1 binds to and activates *hsp-4*, which codes for an endoplasmic reticulum chaperone BiP (Glover-Cutter *et al.* 2013). Depleting ICD-1 results in upregulation of *hsp-4* and activation of the UPR (Arsenovic *et al.* 2012), suggesting that ICD-1 and SKN-1 perform opposing functions in other contexts. In this hypothesized model, ICD-1 may act to fine-tune developmental signals, thereby ensuring proper specification and differentiation of endoderm (Fig. 1C).

Reagents

Strains

JJ185 *dpy-13(e184) skn-1(zu67) IV; mDp1 (IV;f)*

JR3936 *dpy-13(e184) skn-1(zu67) IV/nT1 [qIs51] (IV;V)*

EU384 *dpy-11(e1180) mom-2(or42) V/nT1 [let-?(m435)] (IV;V).*

EU414 *unc-13(e1091) mom-4(or39)/hT2 I; +/hT2 [bli-4(e937) let-?(h661)] III.*

RNAi and quantification of endoderm specification

E. coli HT115 expressing *icd-1* dsRNA was obtained from the Ahringer RNAi library (Kamath *et al.* 2003). RNAi experiments for embryonic endoderm specification were performed as described (Torres Cleuren *et al.* 2019). In brief, bacteria were grown at 37°C in LB containing 50 µg/ml ampicillin. The overnight culture was then diluted 1:10. After 4 hours of incubation at 37°C, 1 mM of IPTG was added and 60 µl was seeded onto 35 mm agar plates containing 1 mM IPTG and 25 µg/ml carbenicillin. Seeded plates were allowed to dry overnight before use. 20-30 L4 or young adults were placed on the seeded RNAi plate. 24 hours later, they were transferred to a fresh RNAi plate and allowed to lay eggs for four hours. The adults were then removed, leaving the embryos to develop for an extra 5-7 hours. Embryos expressing birefringent gut granules were quantified and imaged on an agar pad using a Nikon Ti-E inverted microscope under dark field with polarized light (Clokey and Jacobson 1986; Hermann *et al.* 2005). All experiments were performed at 20°C.

References

Arsenovic P. T., A. T. Maldonado, V. D. Colleluori, and T. A. Bloss, 2012 Depletion of the C. elegans NAC engages the unfolded protein response, resulting in increased chaperone expression and apoptosis. PLoS One 7: e44038. DOI: 10.1371/journal.pone.0044038

Bloss T. A., E. S. Witze, and J. H. Rothman, 2003 Suppression of CED-3-independent apoptosis by mitochondrial βNAC in Caenorhabditis elegans. Nature 424: 1066–1071. DOI: 10.1038/nature01920

Clokey G. V, and L. A. Jacobson, 1986 The autofluorescent "lipofuscin granules" in the intestinal cells of Caenorhabditis elegans are secondary lysosomes. Mech. Ageing Dev. 35: 79–94. DOI: 10.1016/0047-6374(86)90068-0 | PMID: 3736133.

Glover-Cutter K. M., S. Lin, and T. K. Blackwell, 2013 Integration of the Unfolded Protein and Oxidative Stress Responses through SKN-1/Nrf, (D. A. Garsin, Ed.). PLoS Genet. 9: e1003701. DOI: 10.1371/journal.pgen.1003701

Hermann G. J., L. K. Schroeder, C. A. Hieb, A. M. Kershner, B. M. Rabbitts, et al., 2005 Genetic Analysis of Lysosomal Trafficking in Caenorhabditis elegans. Mol. Biol. Cell 16: 3273–3288. DOI: 10.1091/mbc.E05

Jamil M., W. Wang, M. Xu, and J. Tu, 2015 Exploring the roles of basal transcription factor 3 in eukaryotic growth and development. Biotechnol. Genet. Eng. Rev. 31: 21–45. DOI: 10.1080/02648725.2015.1080064

Kamath R. S., A. G. Fraser, Y. Dong, G. Poulin, R. Durbin, et al., 2003 Systematic functional analysis of the Caenorhabditis elegans genome using RNAi. Nature 421: 231–237. DOI: 10.1038/nature01278

Lange A., R. E. Mills, C. J. Lange, M. Stewart, S. E. Devine, et al., 2007 Classical nuclear localization signals: definition, function, and interaction with importin alpha. J. Biol. Chem. 282: 5101–5. DOI: 10.1074/jbc.R600026200

Maduro M. F., and J. H. Rothman, 2002 Making Worm Guts: The Gene Regulatory Network of the Caenorhabditis elegans Endoderm. Dev. Biol. 246: 68–85. DOI: 10.1006/DBIO.2002.0655

Maduro M. F., 2017 Gut development in C. elegans. Semin. Cell Dev. Biol. 66: 3–11. DOI: 10.1016/j.semcdb.2017.01.001

McGhee J., 2007 The C. elegans intestine. WormBook 1–36. https://doi.org/10.1895/wormbook.1.133.1 DOI: 10.1895/wormbook.1.133.1

Thorpe C. J., A. Schlesinger, J. C. Carter, and B. Bowerman, 1997 Wnt signaling polarizes an early C. elegans blastomere to distinguish endoderm from mesoderm. Cell 90: 695–705. DOI: 10.1016/s0092-8674(00)80530-9 | PMID: 9288749.

Torres Cleuren Y. N., C. K. Ewe, K. C. Chipman, E. R. Mears, C. G. Wood, et al., 2019 Extensive intraspecies cryptic variation in an ancient embryonic gene regulatory network. Elife 8. DOI: 10.7554/eLife.48220