

A CaMK cascade activates CRE-mediated transcription in neurons of *Caenorhabditis elegans*

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Calcium (Ca²⁺) signals regulate a diverse set of cellular responses, from proliferation to muscular contraction and neuro-endocrine secretion. The ubiquitous Ca²⁺ sensor, calmodulin (CaM), translates changes in local intracellular Ca²⁺ concentrations into changes in enzyme activities. Among its targets, the Ca²⁺/CaM-dependent protein kinases I and IV (CaMKs) are capable of transducing intraneuronal signals, and these kinases are implicated in neuronal gene regulation that mediates synaptic plasticity in mammals. Recently, the cyclic AMP response element binding protein (CREB) has been proposed as a target for a CaMK cascade involving not only CaMKI or CaMKIV, but also an upstream kinase kinase that is also CaM regulated (CaMKK). Here, we report that all components of this pathway are coexpressed in head neurons of *Caenorhabditis elegans*. Utilizing a transgenic approach to visualize CREB-dependent transcription *in vivo*, we show that this CaMK cascade regulates CRE-mediated transcription in a subset of head neurons in living nematodes.

INTRODUCTION

It is clear from overexpression studies that calcium/calmodulin (Ca²⁺/CaM)-dependent protein kinases (CaMKs) can influence the phosphorylation state and transcriptional transactivating activity of the cyclic AMP response element binding protein (CREB; Sun *et al.*, 1994; Bito *et al.*, 1996), but thus far the only evidence that CREB might be a target of a CaMK *in vivo* comes from the demonstration that CaMKIV-null mice exhibit reduced

CREB phosphorylation in a subset of cells that includes neurons of the central nervous system (Ho *et al.*, 2000; Ribar *et al.*, 2000). Furthermore, although the components of a CaMK cascade (a CaMK kinase, CaMKK, and a CaMKI or CaMKIV) have been identified and characterized in several organisms, as yet there is no evidence that these constituents act as a cascade *in vivo* or that such a cascade has physiologic consequences. Recent studies identified sole *Caenorhabditis elegans* homologs of each of the putative cascade components, CaMKK (*ckk-1*; Tokumitsu *et al.*, 1999) and CaMKI (*cmk-1*; Eto *et al.*, 1999), and established that, *in vitro*, CKK-1 could activate CMK-1 through phosphorylation of Thr179. In addition, it was demonstrated that *C. elegans* kinases heterologously expressed in COS-7 cells promoted phosphorylation of mammalian CREB and CRE-dependent transcription (Eto *et al.*, 1999). Those results suggested that CREB could be a target of a *C. elegans* CaMK cascade analogous to the presumptive mammalian CaMKK/CaMKIV cascade. Here, we identify the *C. elegans* homolog of CREB (*crh-1*) and demonstrate that a CaMKK/CaMK/CREB cascade functions in neurons in living nematodes.

RESULTS AND DISCUSSION

To isolate a CREB homolog in *C. elegans*, we screened a cDNA library using as a probe a *C. elegans* cDNA project clone (yk217f19) that showed high homology to the C-terminal coding region of mouse CREB (encoding residues 296–337). A cDNA containing an open reading frame (ORF) predicted to encode a

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protein of 306 amino acids was isolated; the sequence shared ~50% primary sequence identity with vertebrate CREBs (Gonzalez *et al.*, 1989; Meyer and Habener, 1992; Sakaguchi *et al.*, 1999). Importantly, both a kinase inducible domain (KID, residues 5–50) containing a putative activation phosphorylation site (Arg-Arg-Pro-Ser29, homologous to Ser133 in mammalian CREB), and a basic and leucine zipper domain (bZIP, residues 243–304, required for dimerization and DNA binding) are particularly well conserved (80 and 95% identity, respectively; Figure 1A). Several splice variants identified by 5'-RACE (rapid amplification of cDNA ends) incorporate small changes into the N-terminus without altering the integrity of the KID and bZIP domains and/or overall homology. However, none of these variants is identical to the predicted ORFs in this region, Y41C4A.4a and Y41C4A.4b. A survey of the *C. elegans* genome found at least 19 bZIP-containing genes (Ruvkun and Hobert, 1998), but *crh-1* is unique in encoding both bZIP and KID motifs, indicating that it is the only CREB family gene in *C. elegans*.

Through screening a library of mutagenized nematodes, we identified a strain, YT3 *crh-1(tz2)*, carrying a deletion of 979 nucleotides (54730–55708 in Y41C4A; from the last exon 7 to the 3' UTR of *crh-1*) that eliminates 38 amino acids at the C-terminus of the bZIP region (Glu268-Met306). RT-PCR showed that both N2 and *crh-1(tz2)* expressed mRNA until exon 6 of *crh-1*, but *crh-1(tz2)* does not express full-length mRNA for *crh-1* (Figure 1B). Western blot analysis using anti-phospho-CREB antibody revealed that the N2 strain contains the expected immunoreactive 40 kDa band, whereas the 40 kDa band was not detected in *crh-1(tz2)* (Figure 1C), indicating that *crh-1(tz2)* could not produce functional CRH-1 proteins.

To confirm that the *crh-1* gene product can be phosphorylated by the *C. elegans* CaMK, recombinant His-tagged CRH-1 β was purified from bacteria and used as a substrate for *in vitro* kinase assays. As shown in Figure 2A, CRH-1 β is weakly phosphorylated by CMK-1 alone, but the phosphate incorporation is markedly enhanced by the activation of CMK-1 with CKK-1, as assessed either by ³²P-incorporation or by immunoreactivity with anti-phospho-Ser133 of mammalian CREB. This is consistent with previous observations that CKK-1 activates CMK-1 via phosphorylation of Thr179 and thereby decreases CMK-1's *K_m* value for peptide substrates (Eto *et al.*, 1999; Hook *et al.*, 1999). Mutation of CRH-1 β Ser29 to Ala completely abolished its phosphorylation by activated CMK-1, indicating that this site is the only CMK-1 phosphorylated residue.

That phosphorylation of CRH-1 β by the CaMK cascade is capable of activating transcription was shown using the GAL4-luciferase reporter assay system. The cDNA sequence encoding the transactivation domain of CRH-1 β (1–242, lacking the bZIP domain) was fused to the DNA-binding domain of GAL4 and transfected into COS-7 cells along with a 5 × Gal luciferase reporter gene and various combinations of CMK-1 and CKK-1 expression plasmids (Figure 2B). Ionomycin-induced CRH-1 β -dependent transcription was significantly enhanced by coexpression of wild-type CMK-1, in comparison with a kinase-inactive CMK-1 mutant, *cmk-1(K52A)*. Co-transfection of *ckk-1* with wild-type *cmk-1* further stimulated transcriptional activity 3- to 4-fold, an effect that was not apparent when the activation loop mutant of *cmk-1*, Thr179Ala, was substituted for wild-type *cmk-1* in the assay. Furthermore, the kinases' effects were abolished by using the Ser29Ala mutant of CRH-1 β , indicating that phosphorylation

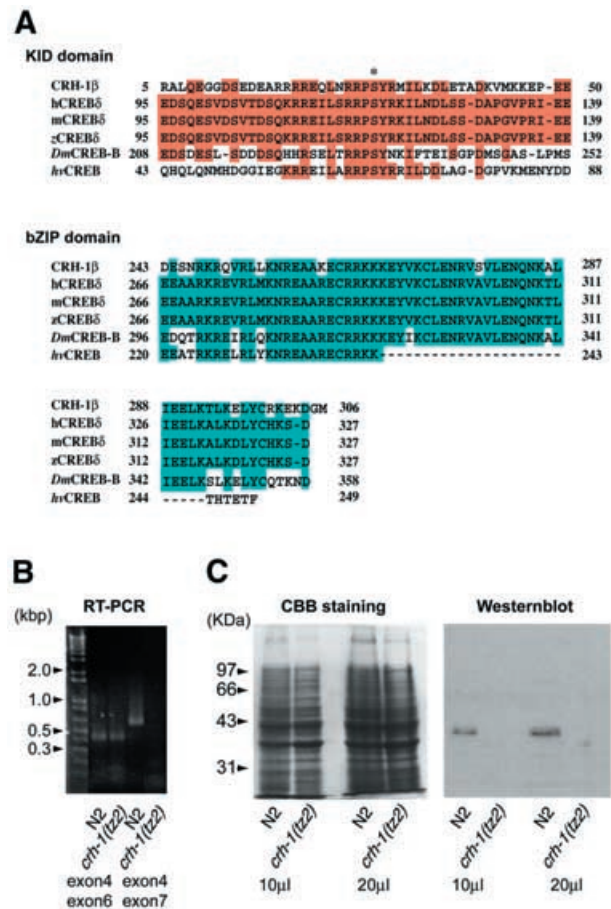


Fig. 1. CREB homolog of *C. elegans* (*crh-1*). (A) An amino acid sequence alignment of KID and bZIP domains of the CREB family from *C. elegans* (CRH-1 β), human (hCREB), mouse (mCREB), zebra finch (zCREB), *Drosophila* (*DmCREB2-a*) and hydra (*hvCREB*). Shading indicates identical amino acids. The asterisk indicates the putative phosphorylated Ser residue of each CREB family member. (B) Analysis of RT-PCR in N2 and *crh-1(tz2)* worms. cDNAs were amplified with primers from exons 4 and 6 (left) and 4 and 7 (right), respectively. Exon 7 is deleted in *crh-1(tz2)* strain. (C) Analysis of CRH-1 phosphorylation in N2 and *crh-1(tz2)* worms. Worm extracts (10 and 20 μ l) were prepared with SDS-PAGE sample buffer and subjected to western blot analysis using anti-phospho-CREB antibody. CBB, Coomassie Brilliant Blue.

of this Ser is required for CRH-1 β -dependent transcription. Taken together, these results indicate that Ca²⁺ mobilization activates the *C. elegans* CaMK cascade, which leads to phosphorylation and activation of CRH-1 in transfected cells.

We evaluated the expression patterns of the *ckk-1*, *cmk-1* and *crh-1* genes to establish that the presumptive cascade members are appropriately located to function as a signaling pathway in *C. elegans*. For each of the kinases, several kilobases of genomic sequence upstream of each coding region was used to promote GFP expression in transgenic nematodes. Adult hermaphrodites carrying a *ckk-1::GFP* fusion gene express GFP primarily in head and tail neurons and vulval muscles (Figure 3, top). Nematodes carrying the analogous *cmk-1* vector exhibit strong fluorescence in numerous neurons and weak expression in vulval muscle cells (Figure 3, middle). *crh-1* mRNA expression was sufficiently robust that we visualized its distribution by whole-mount *in situ*

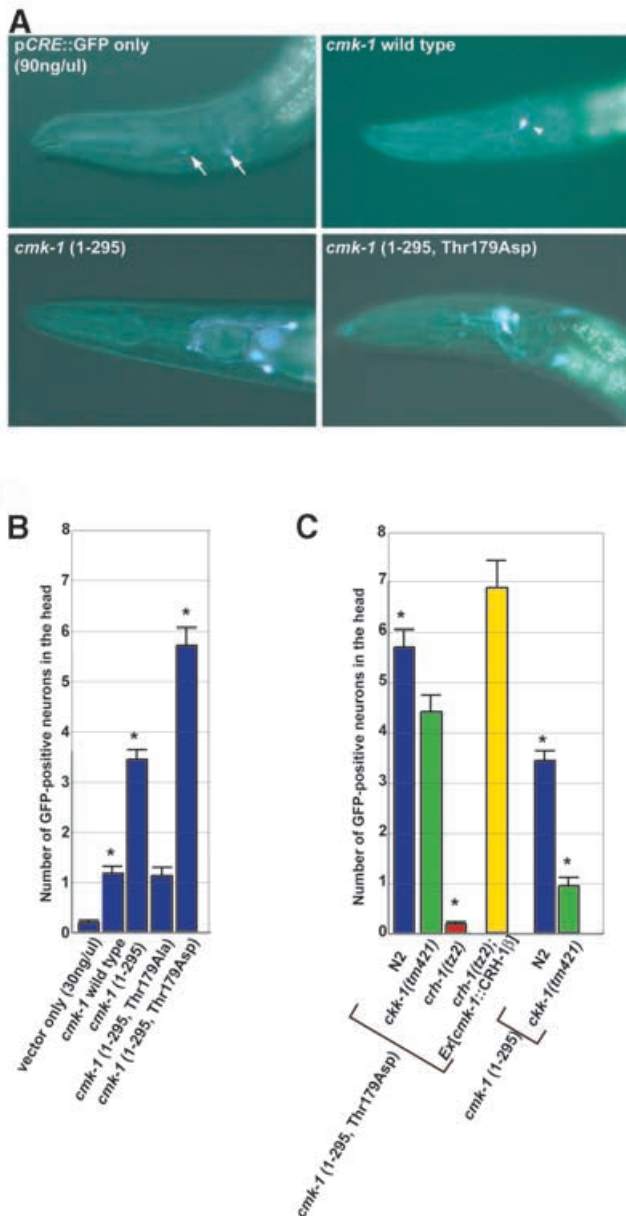


Fig. 4. Monitoring CRE-dependent transcription in living nematodes. (A) GFP fluorescence of a transgenic worm carrying only pCRE::GFP (90 ng/μl), wild-type, Ca²⁺/CaM-independent (1–295) or constitutively active forms of *cmk-1* (1–295, Thr179Asp). Arrows indicate the expression seen in neurons when a large amount of pCRE::GFP was injected. The arrowhead indicates the typical asymmetrical expression often seen in pharynx neurons when wild-type *cmk-1* was injected. (B) Comparison of the number of fluorescent neurons in transgenic animals carrying only pCRE::GFP (30 ng/μl), wild-type, Ca²⁺/CaM-independent (1–295), unphosphorylated (1–295, Thr179Ala) or constitutively active (1–295, Thr179Asp) form of *cmk-1* in wild-type animals. (C) Effect of *crh-1* and *cck-1* genes for the enhanced expression induced by the constitutively active (1–295, Thr179Asp) or Ca²⁺-independent (1–295) forms of *cmk-1*. Error bars equal SEM. The *p*-value (asterisks, <0.0001) in (B) indicates a significant difference in CRE-GFP inducible activity between the wild-type and various forms of *cmk-1*. The *p*-value (asterisks, <0.0001) in (C) indicates a significant difference of fluorescence between N2 and either the *crh-1* or the *cck-1* mutant.

neurons, the upstream kinase is expressed in only a subset of the other mammalian and *C. elegans* cell types that express a CaMK. This seems extravagant if phosphorylation by CaMKK is absolutely necessary for the activation of CaMK and suggests that there may be kinases other than CaMKK that are capable of activating CaMKI/CaMKIV (Soderling 1999). Alternatively, activation loop phosphorylation of the CaMK may not be required for its activity towards all substrates, as is indicated by *in vitro* peptide phosphorylation analyses (Hook *et al.*, 1999). The *cck-1*-deficient nematode should provide an ideal system in which to further discern the biochemical requirements for localized CaMK function.

Although our genetic analyses using pCRE::GFP demonstrate that the cascade activates the transcription of CRE-sequence-dependent genes through CRH-1, the physiological function of this cascade has not been assessed yet. Pathway components are coexpressed only in sensory neurons and interneurons in the head, suggesting that the CaMK cascade may regulate nematodes' responses to environmental stimuli. Actually, *crh-1*-deficient worms looked normal and fertile; however, they grew slightly slower than the wild type (data not shown). In addition, our preliminary observation suggested that *crh-1(tz2)* worms have some behavioral defects. For example, they are slightly clumpy and tend to burrow into the agar plate even in food-rich conditions (data not shown), indicating that *crh-1*-deficient worms have some defects in sensing and/or integrating the stimuli from circumstances. However, we could not find any structural abnormalities in the sensory neurons visualized by the retrograde labeling with DiQ (data not shown). Several mutations in *C. elegans* genes whose mammalian homologs interact with CaMKK/CaMK/CREB signaling in biochemical and transfection experiments (CaMKII and ras/MAPK/MAPKK; Sun *et al.*, 1994; Enslin *et al.*, 1996) have developmental and behavioral phenotypes associated with dysfunction of these same neurons (CaMKII, *unc-43*; ras, *let-60*; MAPKKs, *sek-1*, *nsy-1*; Reiner *et al.*, 1999; Sagasti *et al.*, 2001; Hirotsu *et al.*, 2000; Tanaka-Hino *et al.*, 2002). The relative contributions of these pathways and the CaMK cascade in transducing Ca²⁺ signals in various contexts are unknown. Our genetic model system provides an opportunity to assess functional outcomes dependent on physiological interactions between the CaMK cascade and these other biochemical pathways and establishes a precedent for applying this direct *in vivo* approach to map endogenous signaling networks.

METHODS

Transgenic strains generation and analysis. Germline transformation was carried out as described previously (Mello *et al.*, 1991; Mitani 1995). Host strains were either *lin-15(n765ts)*, *crh-1(tz2)*, *cck-1(tm421)* or wild-type N2. The *lin-15* clone pJMZ (10–50 ng/μl; Clark *et al.*, 1994) was used as a co-injection marker for *lin-15(n765ts)*. Transgenic lines were identified by rescue of the multivulva phenotype at 20°C. For the other mutant and wild-type strains, plasmid pRF4 (Rol) was used as a co-injection marker. All test DNA was injected at 30–100 ng/μl, except the pCRE::GFP plasmid, which was co-injected with *cmk-1* plasmids at concentrations <30 ng/μl to minimize background fluorescence. A minimum of three independent lines were selected and analyzed for each DNA pool. Chromosomal integrated lines

Y. Kimura et al.

carrying pCRE::GFP; pCRE::GFP and *cmk-1::CMK-1(T179D)*; *cmk-1::GFP*; *ckk-1::GFP* were established by UV crosslinking (Stratalinker1800, Stratagene) at a dose of 300 J/m², then backcrossed twice before use.

Supplementary data. Supplementary data are available at *EMBO reports* Online.

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