Proteases of the caspase family play a central role in the execution of programmed cell death in all metazoa examined. The Caenorhabditis elegans caspase CED-3 is essential for programmed cell death in this organism. Three additional C. elegans caspase-related genes, csp-1 (caspase homolog-1), which encodes the csp-1A, csp-1B, and csp-1C RNA species; csp-2, which encodes the csp-2A and csp-2B RNA species; and csp-3 are identified. Csp-1A, Csp-1B, Csp-2A, and Csp-2B proteins are similar in sequence to caspase proproteins. Csp-1C is similar only to large caspase subunits, and Csp-3 is similar only to small caspase subunits. Csp-1B can be activated to become a cysteine protease by processing at internal aspartate residues. Activated Csp-1B can cleave the Csp-1B, CED-3, and Csp-2B proproteins, and activated CED-3 can cleave the CED-3 and Csp-2B proproteins. Inhibitor and synthetic substrate studies further suggest that activated Csp-1B and activated CED-3 have different substrate specificities. These results suggest that C. elegans encodes several caspases that might act in proteolytic cascades to regulate processes such as programmed cell death.

Programmed cell death is a highly regulated process involving components conserved from nematodes to humans (1). The most downstream elements of this process described so far are proteases termed caspases (2). Caspases play a central role in programmed cell death and have also been implicated in the control of interleukin-1β production during inflammation in humans (3, 4) and oocyte maturation in Drosophila melanogaster (5).

Active caspases are formed by cleavage of a proprotein precursor at internal aspartate residues (2). These residues divide the proprotein into N-terminal, middle, and C-terminal domains. After proprotein processing, the middle and C-terminal domains associate to form the active enzyme (2–4, 6), a cysteine protease with a well conserved QAC/R/Q/G/G amino acid motif containing the active site cysteine. Active caspases cleave substrates following aspartate residues (2). However, not all aspartates can direct cleavage (3), suggesting that additional amino acid residues within a substrate are important in determining cleavage specificity.

The abbreviations used are: YAC, yeast artificial chromosome; PCR, polymerase chain reaction; RT-PCR, reverse transcriptase PCR; RACE, rapid amplification of cDNA ends; bp, base pair(s); kb, kilobase pair(s); AFC, 7-amino-4-trifluoromethyl-coumarin.

EXPERIMENTAL PROCEDURES

Northern, YAC’s Filter, and cDNA Library Hybridizations—Northern hybridization procedures followed those in Ref. 20. C. elegans total RNA was purified as described previously (17) from mixed stage wild-type strain N2 animals. Poly(A)+ RNA was isolated using the FastTrack kit (Invitrogen). YAC filter probing conditions were identical to those rec-
ommed for Southern blotting (20). The cDNA library used was constructed in a pBluescript-derived vector 2 (Stratagene) and was transformed into Escherichia coli DH5α bacteria. 1 × 10⁶ bacterial colonies were screened by hybridization (20) using probes specific for csp-1 or csp-2. The csp-1 probe was amplified from pAC1 using the primers SH161 (5′-ACGAGCCGCGAAGACTG-3′) and SH200 (5′-TAATACGGACGCTTTCGAG-3′). The csp-2/csp-3 probe was amplified from YAC Y479 using primers SH97 (5′-GCTTATCCAAATGGATTTCC-3′) and SH98 (5′-CTCATACTTGAGAATAACG-3′). Probes were labeled by random primer extension (20). Plasmids from hybridizing bacterial colonies were isolated by alkali lysis minipreps (20).

...erased the instructions of the manufacturer (Perkin-Elmer). 100 ng of genomic DNA was prepared as described previously (21). YAC DNA for...ers used were SH241 and SH239 (5′-GCTCACTTGAGAATAACG-3′) and SH136 (5′-ACGAGCCGCGAAGACTG-3′). The csp-3 genomic structure determination—C. elegans genomic DNA was prepared as described previously (21). YAC DNA for PCR was crudely isolated in a genomic DNA preparation of yeast harboring the YAC... expression data for the regulator of csp-1, primer pairs SH133/SH1134 and SH142/SH163 (5′-TCAACTGAGCGCTCCACTG-3′) were used to amplify DNA by PCR from YACs Y45F8 and Y73B6. Products of the expected sizes of 1 and 0.55 kb, respectively, were observed. RT-PCR was performed using the GeneAmp RT-PCR kit (Perkin-Elmer). Primers were used SH241 and SH239 (5′-CGTCGAGCTTGGAAAACTG-3′). Rapid amplification of cDNA ends (RACE) was performed using the 5′-RACE kit (Life Technologies, Inc.) using primer SH124 as the 3′-most primer and primer SH125 (5′-AACTGACATCACTTACTG-3′) as the adjacent 5′-primer.

...csp-1 Encodes at Least Three Distinct Transcripts—To identify new C. elegans caspases, translated genomic sequences compiled by the C. elegans genome sequencing project (24) were searched for similarities to the CED-3 caspase using the BLAST sequence comparison program (25). Two sequences with similarities to CED-3 were identified. One of these was located on YAC Y45E1, which contains DNA from the right arm of C. elegans chromosome II. To determine if this Y45E1 region was actively transcribed, a C. elegans cDNA library 2 was probed with 32P-labeled DNA amplified from Y45E1 by the PCR using primers SH161 and SH203. cDNAs of 1.8, 1.0, and 1.0 kb were isolated, and their sequences were determined (see “Experimental Procedures”; Fig. 1). The gene from which these cDNAs were derived was named csp-1 (caspase homolog-1), and the respective transcripts were named csp-1A, csp-1B, and csp-1C.

...comparison of the csp-1A cDNA sequence with the sequence of Y45E1 suggested that this cDNA was incomplete at its 5′-end and did not contain the full-length csp-1A open reading frame. To determine the location of the 5′-end of the csp-1A open reading frame, a 0.5-kb DNA fragment was amplified by RT-PCR using poly(A)+ C. elegans RNA, a primer located within the csp-1A cDNA, and a primer located upstream of the csp-1A cDNA 5′-end. Sequence determination of the 0.5-kb fragment revealed an open reading frame starting at position 173 of the csp-1A sequence (Fig. 1A, i) and preceded by an in frame stop codon. Transcripts csp-1A and csp-1C contained 8- and 6-hp sequences, respectively, identical to the C. elegans SL1 trans-spliced leader sequence (26) 41 bp upstream of their putative start codon, thus defining their 5′-ends. All three csp-1 transcripts contained poly(A) sequences at their 3′-ends. These results suggested that the full-length open reading frames of the csp-1A, csp-1B, and csp-1C mRNAs...
had been defined.

The genomic structure of csp-1 (Fig. 1A) was deduced by comparing the csp-1 RNA sequences with the sequence of Y48E1. The 3’ 932 bp (not including poly(A) sequences) of csp-1A, csp-1B, and csp-1C mRNAs were identical, with the exception of a G nucleotide insertion following position 463 of the csp-1C sequence (Fig. 1A, iii; see below).

To assess the relative abundance of the csp-1 transcripts, a Northern blot of mixed stage wild-type C. elegans poly(A)1 RNA was probed with the same probe used for the initial library screen. Two bands, one of 2.3 kb and one of 1.1 kb, were detected that correspond in size to csp-1A and to csp-1B and csp-1C, respectively. The 2.3-kb band was 5–10-fold less abundant than the 1.1-kb band, suggesting that csp-1A may be expressed at lower levels than csp-1B and csp-1C (data not shown).

As shown in Figs. 1B and 2, the putative proteins encoded by csp-1A and csp-1B showed extensive similarities to caspase proproteins. Amino acids 285–536 of CSP-1A and amino acids 17–269 of CSP-1B share 38% identity with amino acids 235–503 of CED-3. CSP-1A contains a putative N-terminal domain (amino acids 1–273; Fig. 1B) with no similarity to known sequences in current data bases. CSP-1B contains a short N-terminal domain of 5 amino acids (Fig. 1B).

CSP-1C is identical in its N-terminal 142 amino acids. Alternative splice-acceptor site selection in intron 2 of the csp-1C pre-mRNA results in the insertion of an extra G nucleotide at position 463 with respect to the csp-1B sequence (see Fig. 1B). This insertion results in an altered reading frame causing CSP-1C to terminate 7 amino acids downstream of amino acid 142 (see legend to Fig. 1B). Thus, CSP-1C appears to lack a C-terminal caspase domain, suggesting that it is unlikely to be an active enzyme.

Genomic Organization of csp-2 and csp-3—In addition to the csp-1 sequence described above, a sequence with similarity to ced-3 was also identified on the overlapping YACs, Y47H9 and Y53C10, which contain DNA from chromosome 1. To determine if this region was actively transcribed, a C. elegans cDNA library was probed with the same probe used for the initial library screen. Three cDNAs with lengths of 2.8, 1.1, and 0.7 kb were isolated. Sequence determination of these cDNAs revealed that the 0.7-kb cDNA was derived from YAC Y47H9. Nucleotides 1657–2743 of the 2.8-kb cDNA (Fig. 3A, i) were identical to nucleotides 1–1087 of the 1.1-kb cDNA.
Novel C. elegans Caspase Genes

Fig. 2. CSP-1A, CSP-2A, and CSP-3 are most similar to CED-3. Alignment of CSP-1A, CSP-2A, CSP-3, and CED-3 caspase proprotein sequences. Residues identical to CED-3 are highlighted. Numbers indicate amino acid positions. A bar indicates the conserved pentapeptide flanking the active site cysteine.

(Fig. 3A, ii), and the 3’ 603 nucleotides of both were similar to yet distinct from nucleotides 94–695 of the 0.7-kb cDNA (95% identity; Fig. 3A, iii). These results suggested that the 2.8- and 1.1-kb cDNAs were both derived from transcripts encoded by the same gene and that the 0.7-kb cDNA was derived from the transcript of a different gene. The gene encoding transcripts corresponding to the 2.8- and 1.1-kb cDNAs was named csp-2 (caspase homolog-2), and the respective transcripts were named csp-2A and csp-2B. The gene encoding the transcript corresponding to the 0.7-kb cDNA was named csp-3 (caspase homolog-3).

To determine the 5’-end of the csp-2A open reading frame, csp-2A cDNA 5’-ends were amplified from mixed stage wild-type RNA using RACE (see “Experimental Procedures”). Sequence determination of the resulting product suggested that the 5’-end of csp-2A was identical to that defined by the 2.8-kb cDNA (Fig. 3A, i). However, the possibility that a longer csp-2 transcript exists that was not detected in the cDNA library screen cannot be excluded. The 5’-end of the 1.1-kb csp-2B cDNA contained 8 bp of sequence identical to the C. elegans SL1 trans-spliced leader sequence (26), thus defining the 5’-end of the csp-2B transcript. The csp-3 cDNA contained an in frame stop codon 24 bp upstream of the first ATG start codon. Both csp-2 cDNAs as well as the csp-3 cDNA contained poly(A) sequences at their 3’-ends. These results suggested that the full-length open reading frames encoded by the csp-2A, csp-2B, and csp-3 mRNAs had been defined. A Northern blot of mixed stage wild-type C. elegans genomic DNA hybridized with the csp-2/csp-3-specific 32P-labeled DNA described above failed to re-veal hybridizing bands, suggesting that csp-2 and csp-3 are either expressed at low levels or only in a small number of cells.

To determine the genomic structure of csp-2, eight different primer pairs spanning the length of the csp-2A cDNA were used to amplify wild-type C. elegans genomic DNA (see “Experimental Procedures”). The exon and exon/intron sequences of amplified bands were determined by comparison with the csp-2A and csp-2B sequences. The genomic structure of csp-3 (Fig. 3A, iii) was determined by examining the sequence of the csp-3 cDNA with that of YAC Y47H9.

To determine the chromosomal location of csp-2, the same 32P-labeled DNA described above was used to probe a nitrocel-lulose filter spotted with an ordered array of C. elegans YACs (24). Hybridization was detected with the overlapping YACs Y47H9 and Y53C10 on chromosome I, which contain csp-3. In addition, hybridization was detected with the overlapping YACs Y48F8 and Y73B6 located on the left arm of chromosome IV (data not shown). These results suggested that csp-2 was located in the overlap region of YACs Y48F8 and Y73B6. To test this notion, DNA from these YACs was amplified by PCR using csp-2A-specific primers (see “Experimental Procedures”). Genomic DNA bands of the expected sizes were detected. These results confirmed that csp-2 was located in the overlap region of YACs Y48F8 and Y73B6 on chromosome IV.

The N-terminal Domain of CSP-2A Is Weakly Similar to E. coli Colicin E1—csp-2A and csp-2B encode proteins with similarities to caspase proproteins. The region of similarity is most similar to the corresponding region of the CED-3 proprotein. Specifically, there is 33% identity between amino acids 18–263 of the Csp-2B protein and amino acids 235–503 of CED-3. The sequence, VCCRG, containing the putative active site cysteine of CSP-2B and CSP-2B (Figs. 2 and 3B) is highly diverged from the consensus caspase sequence of QAC(R/Q/G)G (2).

The putative N-terminal domain of CSP-2B is only 7 amino acids long, suggesting that it is unlikely to interact with other proteins (Fig. 3B). However, the putative N-terminal domain of csp-2A is 571 amino acids long (Fig. 3B) and is weakly similar in sequence to E. coli colicin E1. Specifically, there is 27% identity between amino acids 104–201 of CSP-2A and amino acids 205–302 of colicin E1 (Fig. 3C). Colicin E1 is encoded by the ColE1 plasmid of E. coli and can kill bacterial cells by creating pores in the plasma membrane (27–30). The similarity between the N-terminal domain of CSP-2A and colicin E1 is restricted to the receptor-binding domain of this colicin (see “Discussion”).

The csp-3 transcript encodes a protein highly similar to the C-terminal domain of CSP-2A and CSP-2B (Fig. 3D). Amino acids 15–139 of CSP-3 are 92% identical to amino acids 705–826 of CSP-2A (Fig. 2). Since the CSP-3 open reading frame does not contain a middle caspase domain, it is unlikely that it encodes an active caspase.

CSP-1B Can Be Processed in E. coli—To determine if csp-1 could encode an active protease, the CSP-1B protein was stud-
ied, since the activated CSP-1A and activated CSP-1B caspases were likely to be identical. The CSP-1B protein was tagged at its C terminus with a FLAG peptide (amino acid sequence DYKDDDDK) and was expressed in *E. coli* (see “Experimental Procedures”). As shown in Fig. 4A, a Western blot of bacterial extracts from cells expressing CSP-1B-FLAG and probed with an anti-FLAG antibody revealed the presence of both the full-length 31-kDa wild-type CSP-1B-FLAG proprotein as well as a smaller 14-kDa protein. The 14-kDa protein was not detected when a CSP-1B-FLAG protein containing a C138S mutation in the putative catalytic cysteine residue was expressed in *E. coli* under identical conditions. These results suggested that the CSP-1B-FLAG proprotein could be specifically processed when expressed in bacteria. Similar processing has been shown for several other caspases (6).

To confirm that the CSP-1B-FLAG proprotein was processed in *E. coli*, extracts expressing the proprotein were passed over an anti-FLAG antibody column, and the bound proteins were eluted with FLAG peptide (see “Experimental Procedures”). The resulting eluate was run on a 15% SDS-polyacrylamide gel and stained with Coomassie Blue. As shown in Fig. 4B, three major bands were detected. The 31-kDa band corresponded in size to the CSP-1B-FLAG proprotein. To identify the 14- and 16-kDa proteins, their N-terminal sequences were determined (see “Experimental Procedures”). The N terminus of the 14-kDa protein contained the sequence GLPA, corresponding to...
Fig. 4. CSP-1B is processed in E. coli. A, Western analysis of E. coli extracts expressing either CSP-1B-FLAG or CSP-1B(C138S)-FLAG using a monoclonal anti-FLAG antibody (see “Results”). Band sizes are indicated. B, Coomassie Blue-stained gel of partially purified CSP-1B-FLAG. Sizes of major bands corresponding to full-length and processed CSP-1B-FLAG are indicated. The schematic diagram indicates the CSP-1B-FLAG proprotein, aspartate residues where processing was shown to take place, and predicted sizes of processed fragments. Black box indicates the pentapeptide surrounding the active site cysteine.

Amino acids 151–154 of CSP-1B (amino acids 419–422 of the CSP-1A sequence; Fig. 1B). The N terminus of the 16-kDa protein contained the sequence AKKS, corresponding to amino acids 6–9 of CSP-1B (amino acids 274–277 of the CSP-1A sequence; Fig. 1B). These results suggested that the CSP-1B proprotein was processed following aspartate 5 and aspartate 150. Furthermore, since the FLAG tag was located at the C-terminal end of the CSP-1B-FLAG proprotein, these results suggested that the 16-kDa CSP-1B protein could tightly associate with the 14-kDa FLAG-containing protein. Such processing at aspartate residues and tight association of the resulting subunits is characteristic of all known active caspases (2, 6).

CSP-2B Proprotein Is a Substrate of both Activated CSP-1B and Activated CED-3—The finding that C. elegans encodes at least two potentially active caspases in addition to CED-3 suggested that all of these proteases might cleave and activate each other as can occur in mammalian systems. To test this hypothesis, cleavage of the CSP-2B proprotein by activated CSP-1B or CED-3 was assessed. As shown in Fig. 5A, two different preparations of activated CSP-1B-FLAG could cleave the in vitro translated 32-kDa CSP-2B proprotein to generate two main cleavage products of 31 and 17 kDa (lanes 2 and 3). The 31-kDa band corresponded to the predicted C-terminal protein remaining after cleavage following aspartate 8 (aspartate 571 of the CSP-2A sequence; Fig. 3B). The N-terminal peptide released by such cleavage would have been too small to detect in the assay. The 17-kDa band corresponded to the predicted N-terminal protein remaining after cleavage following aspartate 149 (aspartate 712 of the CSP-2A sequence; Fig. 3B). The C-terminal portion of this protein may have not been detected, since it could potentially contain only two 35S-labeled methionine residues (compared with 5 methionines in the 17-kDa fragment), and cleavage at this second site was very inefficient. As shown in Fig. 5A, activated CED-3 tagged at the C terminus of its 15-kDa subunit with the FLAG peptide (see “Experimental Procedures”) could also cleave CSP-2B (lane 4). However, only one cleavage product, perhaps corresponding to cleavage at aspartate 8, could be detected.

To determine if activated CSP-1B-FLAG and CED-3-FLAG cleave CSP-2B following aspartate 8, the abilities of these enzymes to cleave a CSP-2B protein containing an aspartate-to-alanine mutation at position 8 was examined. As shown in Fig. 5B, no 31-kDa cleavage product was detected, suggesting that CSP-1B and CED-3 both cleave CSP-2B following aspartate 8.

CSP-2B cleavage by activated CSP-1B or CED-3 suggested that CSP-2B or CSP-2A processing could produce an active caspase. To test this idea, a CSP-2B-FLAG or CSP-2A-FLAG proprotein was expressed in E. coli as described above. Although full-length proteins were easily detected in E. coli extracts, specific processing was not detected under a variety of experimental conditions (data not shown). Furthermore, extracts expressing the CSP-2B-FLAG or CSP-2A-FLAG proteins did not cleave a variety of in vitro translated substrates (data not shown). These results suggested that processed CSP-2B and CSP-2A might not be active caspases. Consistent with this notion, these proteins contain divergent active site sequences that might not allow protease activity. Alternatively, the assay conditions used might not have been optimal to detect processing and activation.

Activated CSP-1B Can Cleave the CED-3 Proprotein—To determine whether activated CSP-1B could cleave other proteins, the ability of activated CSP-1B-FLAG to process the CED-3 proprotein was examined. As shown in Fig. 6A, wild-type activated CSP-1B-FLAG could process a 56-kDa in vitro translated CED-3 proprotein (lane 4). The sizes of the CED-3 proprotein cleavage products suggest that CSP-1B might cleave CED-3 at aspartates 144 and 374. These results suggest
Activated CED-3 and CSP-1B have different substrate specificities. A, 40 μg of partially purified activated CSP-1B-FLAG were incubated with in vitro translated 35S-labeled full-length CED-3 in the presence of inhibitors or buffer control (see “Experimental Procedures”). Final inhibitor concentrations were as follows: iodoacetic acid (lane 1), 5 mM; E-64 (lane 2), 0.2 mM; benzyloxycarbonyl-DEVD-fluoromethyl ketone (lane 3), 10 μM. Band sizes indicating full-length and cleavage fragments of CED-3 are shown. The schematic diagram indicates the CED-3 proprotein, aspartate residues where processing might take place, and predicted sizes of processed fragments. The black box indicates the pentapeptide surrounding the active site cysteine. B, same as A except that activated CED-3-FLAG was used as protease. Schematic diagram indicates the CED-3 proprotein, aspartate residues where processing was shown to take place (6), and predicted sizes of processed fragments. C, graph depicting cleavage of acetyl-DEVD-AFC by bacterial extracts containing CED-3-FLAG (filled circles), CSP-1B-FLAG (open circles), CED-3(C358S)-FLAG (◇), or CSP-1B(C138S)-FLAG (●). Released AFC was measured using a spectrofluorimeter. D, graph depicting cleavage of benzyloxycarbonyl-YVAD-AFC by bacterial extracts containing CSP-1B-FLAG (filled circles), CED-3-FLAG (○), CED-3(C358S)-FLAG (◇), or CSP-1B(C138S)-FLAG (●).
that activated CSP-1B is a caspase capable of processing the CED-3 proprotein, perhaps leading to CED-3 activation or inhibition.

Activated CSP-1B and CED-3 Have Different Substrate Specificities—As shown in Fig. 6, A and B, both activated CSP-1B-FLAG and activated CED-3-FLAG could cleave the CED-3 proprotein. However, whereas both proteases probably cleaved efficiently at aspartate 374 of the CED-3 proprotein, cleavage at other sites was enzyme-dependent. This result suggests that activated CSP-1B and CED-3 have different substrate specificities. To confirm this notion, the effect of protease inhibitors on activated CSP-1B and CED-3 activities was examined. The cysteine protease inhibitor iodoacetate acid (Sigma) blocked processing of the CED-3 proprotein by either activated CSP-1B-FLAG (Fig. 6A, lane 1) or CED-3-FLAG (Fig. 6B, lane 1). The cysteine protease inhibitor E-64 (Sigma) was unable to block activated CSP-1B-FLAG (Fig. 6A, lane 2) or CED-3-FLAG (Fig. 6B, lane 2) protease activity. Interestingly, the caspase peptide inhibitor benzyloxycarbonyl-DEVD-fluoromethyl ketone (Enzyme Systems Products) inhibited processing of the CED-3 proprotein by activated CED-3-FLAG (Fig. 6B, lane 3) but not by activated CSP-1B-FLAG (Fig. 6A, lane 3), suggesting that activated CSP-1B has a different substrate specificity from activated CED-3.

To further demonstrate the differing substrate specificities of activated CSP-1B and CED-3, their abilities to cleave synthetic caspase substrates were tested. As shown in Fig. 6C, activated CED-3, but not activated CSP-1B, could efficiently cleave the acetyl-DEVD-AFC substrate (Enzyme Systems Products). Conversely, the same preparations of activated CSP-1B, but not of activated CED-3, could cleave the benzoyloxycarbonyl-YVAD-AFC substrate (Fig. 6D). These observations further indicate that activated CSP-1B and CED-3 have different substrate specificities.

Activated CSP-1B but Not Activated CED-3 Can Cleave the CSP-1B Proprotein—Since both activated CED-3-FLAG and activated CSP-1B-FLAG can cleave the CED-3 proprotein, the ability of these proteases to cleave the CSP-1B proprotein was assessed. As shown in Fig. 7, two different preparations of activated CSP-1B-FLAG could process in vitro translated CSP-1B proprotein to generate two specific cleavage products of 14 and 16 kDa (lanes 2 and 3). These products corresponded in size to the CSP-1B middle and C-terminal caspase subunits (see Fig. 4). Interestingly, activated CED-3-FLAG could not process the in vitro translated CSP-1B proprotein (lane 4) although the same preparation of CED-3-FLAG protease could efficiently process the CED-3 proprotein (data not shown). These results suggest that CSP-1B could act upstream of CED-3 in a proteolytic cascade.

DISCUSSION

C. elegans Encodes Multiple Caspases—Many metazoans contain several caspases with different substrate specificities (6, 10). At least 11 caspases have been described in humans (12, 31), and at least three have been described in Drosophila melanogaster (32–34). In the nematode C. elegans, one caspase, CED-3, has been demonstrated to be important for the execution of the cell death program (15–17). Here it is shown that C. elegans expresses at least three different caspase-related genes, csp-1, csp-2, and csp-3, in addition to ced-3. Furthermore, the csp-1 and csp-2 genes express multiple transcripts encoding distinct caspase-related proteins. C. elegans thus possesses a repertoire of at least seven different caspase-related transcripts potentially encoding the CED-3, CSP-1A, CSP-1B, CSP-1C, CSP-2A, CSP-2B, and CSP-3 proteins.

CSP-1C and CSP-3 are similar only to the large and small catalytic domains of caspases, respectively, suggesting that they are unlikely to be active enzymes. However, such proteins might act in a dominant-negative fashion to inhibit the activities of activated CSP-1B and CSP-2B proteins, respectively. Alternatively, it has been previously shown that large and small subunits can be shared between different caspases (35). Thus, CSP-1C and CSP-3 might interact with subunits of activated CED-3, CSP-1B, or CSP-2B.

CSP-1A, CSP-1B, CSP-2A, and CSP-2B have divergent active site sequences. The activated CSP-1B caspase, for example, contains the sequence SACRG surrounding the active site cysteine (cysteine 138 of CSP-1B; Fig. 1B). This sequence differs from the consensus QAC(R/Q/G)G sequence present in most active caspases (2). Interestingly, the results presented here suggest that such sequence variation is still compatible with enzymatic activity. The CSP-2A and CSP-2B proteins contain the sequence VCCRG surrounding the putative active site cysteine (cysteine 137 of CSP-2B). Unlike CSP-1B, however, caspase activity could not be demonstrated for CSP-2B, suggesting that the sequence divergence in the CSP-2B active site may not be compatible with enzymatic activity.

C. elegans Caspases Have either Short or Long N-terminal Domains—CSP-1B and CSP-2B are caspase proproteins with short N-terminal domains. In mammals, such proteases (for example, caspase-3) are thought to be the most downstream effectors of programmed cell death (10) and are thought to be primarily regulated by cleavage by other caspases (2, 10). CSP-1A and CSP-2A are caspase proproteins with long N-terminal domains. In mammals and in C. elegans, such long N-terminal domains are thought to be important for binding to proteins that regulate caspase activation (7–9). Thus, C. elegans encodes the same classes of caspases seen in mammals, suggesting that interactions among C. elegans caspases might be similar to those among mammalian caspases.

Although the sequence of the N-terminal domain of CSP-1A is uninformative as to its potential function, the N-terminal domain of CSP-2A shows weak similarity to E. coli colicin E1. Colicins are plasmid-encoded bacterial proteins that are involved in killing of bacteria. Colicin E1 can insert into the plasma membranes of bacteria via specific receptors on the recipient bacterial membrane. Pore formation then kills the bacterial cell (27–30). The domain structure of colicin E1 has been roughly characterized and consists of an N-terminal re-
differentially cleaved synthetic caspase substrates. Thus, as in CSP-1B protease activity. Furthermore, CSP-1B and CED-3 ketone, which could inhibit CED-3 protease activity but not the caspase inhibitor benzyloxycarbonyl-DEVD-fluoromethyl activation may either activate or inhibit CED-3 and CSP-2B. Thus, CSP-1B proteins could process the CSP-1B, CED-3, and CSP-2B propro-
tially, it is possible that the N-terminal domain of CSP-2A does contain pore-forming sequences, in which case this domain could form pores in CSP-2A-expressing cells, hastening their demise. The possible lack of protease activity by CSP-2B and CSP-2A suggests that they could be similar to the mammalian FLIP/Caspase caspase that lacks a catalytic cysteine residue yet can still promote and prevent cell death (13, 14).

C. elegans Caspases Might Act in a Proteolytic Cascade—Although ced-3 has a clear role in programmed cell death, the roles of csp-1, csp-2, or csp-3 in this or other processes are unknown. csp-1, csp-2, and csp-3 might play a role in programmed cell death that is partially redundant with that of ced-3 or be involved in tissue-specific activation of ced-3. It is also possible that all four C. elegans caspase-related genes are involved in processes distinct from programmed cell death.

Several experiments described here suggest that the products of the ced-3, csp-1, and csp-2 genes may interact. Activated CSP-1B could process the CSP-1B, CSP-3, and CSP-2B proproteins in vitro, suggesting that cells containing activated CSP-1B might also contain cleaved CED-3 and CSP-2B. Thus, CSP-1B activation may either activate or inhibit CED-3 and CSP-2B.

Activated CED-3 did not cleave the CSP-1B proproteins, yet still processed the CED-3 and CSP-2B proproteins. These results suggest that active CED-3 and CSP-1B have different substrate specificities, a notion bolstered by experiments using the caspase inhibitor benzoylarginyl-DEVD-fluoromethyl ketone, which could inhibit CED-3 protease activity but not CSP-1B protease activity. Furthermore, CSP-1B and CED-3 differentially cleaved synthetic caspase substrates. Thus, as in mammals, C. elegans encodes caspases with differing substrate specificities.

The different target specificities of activated CSP-1B and CED-3 suggest that there might be a directionality in the interactions of CED-3, CSP-1B, and CSP-2B in vivo. Specifically, CSP-1B might activate or inhibit CED-3, which might, in combination with CSP-1B, activate or inhibit CSP-2B. All or parts of this cascade may be used in vivo to regulate caspase activation.

The finding that C. elegans encodes a number of different caspases suggests that this organism could be useful for understanding how caspases are regulated and how different caspases are targeted to different tasks, a problem currently poorly understood. Directed mutations in the csp-1, csp-2, and csp-3 genes should help to reveal the cellular roles played by each of these genes.

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