Abstract. During morphogenesis of the Caenorhabditis elegans embryo, hypodermal (or epidermal) cells migrate to enclose the embryo in an epithelium and, subsequently, change shape coordinately to elongate the body (Priess, J.R., and D.I. Hirsh. 1986. Dev. Biol. 117:156–173; Williams-Masson, E.M., A.N. Malik, and J. Hardin. 1997. Development [Camb.]. 124:2889–2901). We have isolated mutants defective in morphogenesis that identify three genes required for both cell migration during body enclosure and cell shape change during body elongation. Analyses of hmp-1, hmp-2, and hmr-1 mutants suggest that products of these genes anchor contractile actin filament bundles at the adherens junctions between hypodermal cells and, thereby, transmit the force of bundle contraction into cell shape change. The protein products of all three genes localize to hypodermal adherens junctions in embryos. The sequences of the predicted HMP-1, HMP-2, and HMR-1 proteins are related to the cadherin family that mediate homotypic adhesion in the C. elegans embryo, but rather mediate specific aspects of morphogenetic cell shape change and cytoskeletal organization.

The morphology of the animal body and its tissues arise as embryonic cells change their shapes and/or positions (Mittenthal and Jacobson, 1990). Many of these changes are mediated by dynamic rearrangements of cytoskeletal components (Wessells et al., 1971). Cells can organize diverse patterns of microtubules and actin filaments, and movement of actin filaments by myosin proteins is thought to generate the force that drives many morphogenetic processes. An important step toward understanding the mechanical basis of morphogenesis is the identification and characterization of molecules that pattern the cytoskeleton and translate force into concerted cell movements.

For cells to change shape coordinately or move relative to each other, forces generated within an individual cell must be transmitted to adhesive junctions at the plasma membrane and exerted on neighboring cells or the extracellular matrix (Gumbiner, 1996). The best characterized cell-cell junction is the adherens junction. This type of junction usually forms a subapical, beltlike structure that mechanically links the lateral surfaces of adjacent epithelial cells. Adherens junctions contain transmembrane proteins of the cadherin family that mediate homotypic adhesion. Cadherins are thought to connect to the actin cytoskeleton indirectly through the proteins α-catenin and β-catenin. Catenin-cadherin complexes also are associated with sites of contact between blastomeres in vertebrate and invertebrate embryos. In Drosophila, mice, and Xenopus, gene inactivation of catenins or cadherins disrupts general cell adhesion and apicobasal polarity of blastomeres and epithelial cells (Heasman et al., 1994; Larue et al., 1994; Haegel et al., 1995; Cox et al., 1996; Müller and Wieschaus, 1996; Kafron et al., 1997; Torres et al., 1997). Thus, it has been difficult to define direct requirements for these proteins in cytoskeletal organization and morphogenesis, although there is evidence for specific roles in tracheal cell migration (Tanaka-Matakatsu et al., 1996) and axon outgrowth (Iwai et al., 1997) in Drosophila.

The Caenorhabditis elegans embryo provides a model system for studying how cells move and change shape to generate body and tissue morphologies. At hatching, the outermost cellular layer of the body consists of a monolayer of 85 epithelial cells called hypodermal cells that are linked together by adherens junctions (White, 1988). During embryogenesis, hypodermal cells are involved in two distinct processes that transform the initially ellipsoidal
mass of embryonic cells into a long, thin worm; these processes are called body enclosure and body elongation (Sulston et al., 1983; Priess and Hirsh, 1986; Williams-Masson et al., 1997). The hypodermal cells are born on the dorsal surface of the embryo. As the hypodermal cells develop adherens junction connections, they begin to spread as a sheet across the embryo until the contralateral edges of the sheet meet at the ventral midline. In the anterior of the embryo, ventral hypodermal cells on the periphery of the spreading sheet develop filopodial extensions that may function to draw the contralateral edges of the sheet together (Williams-Masson et al., 1997). In the posterior of the embryo, the contralateral edges appear to be drawn together by a purse-string–like contraction that completes the enclosure process (Williams-Masson et al., 1997). In several respects, these processes are similar to epithelial cell movements described in a variety of systems, such as wound healing in vertebrates (Martin and Lewis, 1992) and dorsal closure in Drosophila (Young et al., 1993).

At the completion of body enclosure in C. elegans, the apical surfaces of the hypodermal cells resemble rectangles that are elongated along the circumferential contour of the embryo’s body. These apical surfaces begin to change shape, constricting along the circumferential contour of the body and elongating along the anterior–posterior (longitudinal) axis. The coordinate changes in the shapes of the hypodermal cells appear to cause the body to decrease in circumference and to elongate about fourfold along its longitudinal axis (Sulston et al., 1983; Priess and Hirsh, 1986). Before body elongation, the apical cytoskeleton of each hypodermal cell reorganizes to form an array of parallel actin filament bundles oriented along the circumferential contour of the body (Priess and Hirsh, 1986; Costa et al., 1997). The parallel filament bundles bridge two opposing sides of each hypodermal cell, apparently connecting to the subapical adherens junction. Contraction of the filament bundles has been proposed as the force that elongates the embryo; the bundles become shorter and thicker during elongation, and drugs that disrupt actin filament organization prevent elongation. Apical constriction of cells has been shown in other systems to drive the invagination of epithelial sheets; because of the constriction of cells has been shown in other systems to drive the invagination of epithelial sheets; because of the constriction, cytoskeletal elements are required for the proper migration of hypodermal cells during body enclosure and for body elongation. We demonstrate that hmp-1, hmp-2, and hmr-1 can encode proteins related to α-catenin, β-catenin, and cadherin, respectively. We show that the protein products of these genes are required for the proper migration of hypodermal cells and that this coupling translates the force of bundle contraction into cell shape change.

Materials and Methods

C. elegans Strains

Bristol strain N2 was used as wild type. Listed below are the marker mutations and genetic deficiencies obtained from the C. elegans Genetic Stock Center (Bristol, England) and used in this study: Chromosome I: dpy-5 (e61), dpy-3, dpy-4, dpy-6, dpy-9, dpy-11, dpy-12, dpy-13, dpy-14, dpy-15, e244, sna-1 (e30), unc-42 (e270); and chromosome V: lin-11 (n566), unc-54 (e190), unc-75 (e950); chromosomes IV, HIM-3 (e1147); chromosome V: e244, sna-1 (e30), unc-42 (e270); and chromosome X: lin-2 (e1309). The hmp-1(zu202) allele was provided by Andreas Wissmann (University of Calgary, Calgary, Canada).

Genetics

Hmp alleles were isolated using the method described by Priess et al. (1987) with the following modifications for a nonclonal F2 mutagenesis screen: Individual F1 progeny were not separated, F2 embryos were screened by Nomarski microscopy while inside the carcass of their mothers, and recessive zygotic-lethal mutations were recovered through the heterozygous siblings in the carcass. Standard genetic complementation tests and mapping ordered the Hmp mutations into the following three complementation groups. hmp-1: zu242, zu244, zu278, zu234, zu236, zu239, zu402, zu403, zu404, zu406, and zu202; hmp-2: zu364; and hmr-1: zu248, zu389. To isolate germline mosaic animals, we constructed hmp-1 strains carrying a wild-type hmp-1 transgene on an extrachromosomal array. hmp-1 mutants that produced only inviable progeny were assumed to have spontaneously lost the extrachromosomal array from the germline. Germline mosaics were recovered for all three alleles tested (zu242, zu278, and zu202) at a frequency of 1–2%, and all produced embryos with the Hmr
phenotype. For the seven hmp-1 alleles tested (zu244, zu278, zu349, zu505, zu599, zu494, and zu02), transgenic animals that are not germline mosaic hmp-1 embryos produce progeny resulting from low or no maternal expression of the hmp-1 transgene, typical of transgenes generated by the method used here, and meiotic loss of the transgenic extrachromosomal array. Consistent with this hypothesis, many cleavage-stage embryos from the hmp-1 (zu278) V; zuEx5 strain show a lack of HMP-1 antiserum staining, as do many differentiating embryos. Thus we have used hmp-1 transgenic strains to examine the phenotype of loss of both maternal and zygotic hmp-1 activity in fixed, stained embryos.

Molecular Biology
We mapped hmp-1 between the cloned genes daf-11 and sma-1 on chromosome V. Germline transformation with genomic cosmid DNA from this region, provided by the C. elegans Genome Project, revealed that cosmID R13H4 completely rescued the hmp-1 mutant phenotype. Subcloning of this genomic DNA delimited the hmp-1 gene to a 7.6-kb fragment. We identified a cDNA (yK364) from the C. elegans cDNA Project (Y. Kohara, National Institute of Genetics, Mishima, Japan) that maps to the hmp-1 rescuing fragment. RNA-mediated interference (RNAi) was performed as described previously (Guo and Kemphues, 1995; Rocheleau et al., 1997); when RNA made from the yK364 cDNA clone was injected into wild-type gonads, the resulting embryos showed the HMP phenotype. We isolated and sequenced hmp-1 cDNA clones from cDNA libraries (provided by R. Barbacid and R. Waterston [Washington University, St. Louis, MO], J. Zhou, and J. Rothman [University of California, Santa Barbara, CA]) and from cDNA amplified by PCR. Together, these cDNAs span 3.2-kb and contain a single long open reading frame predicted to encode a protein of 927 amino acids. Genomic sequence of the cosmID R13H4, available from the C. elegans Genome Project under accession number ZM1579, agrees with our cDNA sequence and indicates that HMP-1 is encoded by eight exons included within the 7.6-kb rescuing fragment. The hmp-1 cDNA hybridizes to a single, ~3.0-kb mRNA species in RNA isolated from either embryonic or mixed larval and adult stages.

hmp-2 maps genetically to chromosome I.~1.5 map units to the left of the unc-93 gene. We found that the cDNA clone yK126e3, which was identified by the C. elegans cDNA Project (Y. Kohara) and shows homology to β-catenin/armadillo, maps near hmp-2 on the physical map constructed by the C. elegans Genome Project (yeast artificial chromosome clones Y2TH10, Y54E5, and Y53C6). Injection of RNA made from the cDNA clone into the gonads of wild-type worms generated embryos showing the hmp-2 mutant phenotype. We used the cDNA to isolate a 16.5-kb genomic DNA fragment from a phage library (Stratagene, La Jolla, CA). This genomic fragment displayed transgenic rescue of the hmp-2 mutant phenotype. Our complete cDNA sequence of hmp-2 reveals a 2.2-kb transcript containing a single long open reading frame that can encode a 678-amino acid protein. The sequence of our genomic clone and cosmids from the C. elegans Genome Project indicates that HMP-2 is encoded by five exons located on the transgenic rescuing fragment.

The hmr-1 gene maps 1.3 map units to the right of lin-11 on chromosome I. From the C. elegans Genome Project, we obtained a genomic cosmid clone (W02B9) that maps near this region and contains sequences homologous to classical cadherins. Germline transformation of this cosmid fully rescued all hmr-1 mutant phenotypes. We subcloned a 21.2-kb fragment of the cosmid that was injected only into the mother; related gene and found that this DNA fragment also exhibits transgenic rescue of hmr-1. Genomic DNA sequence from the C. elegans Genome Project and our sequence of hmr-1 partial cDNA clones suggest that the hmr-1 gene contains 10 exons that generate a 4.7-kb mRNA transcript and a 1.233-amino acid protein. Sequence data are available from GenBank/EMBL/DDJB under accession numbers AF016852 (hmp-1), AF016853 (hmp-2), and AF016854 (hmr-1).

Antibody Production and Morphological Analysis
To generate antisera against HMP-1, a plasmid construct designed to produce a glutathione S-transferase (GST)–HMP-1 fusion protein was made by subcloning a 0.8-kb cDNA fragment from the 3’ end of the hmp-1 transcript into the vector pGEX-4T2 (Pharmacia Biotech, Piscataway, NJ). Fusion protein was purified according to the instructions of Pharmacia Biotech. Rabbits were immunized with purified fusion protein by the University of Wisconsin Antibody Production Services Animal Care Unit. Immune serum was affinity purified against GST–HMP-1 fusion protein cross-linked to Artigel A resin (Sterogene Bioseparations, Inc., Carlbad, CA) according to the instructions of the manufacturer. To remove anti-GST antibodies, the process was repeated with a GST column. hmp-1 (zu278) mutant embryos lack detectable HMP-1 antiserum staining after the start of hypodermal enclosure, indicating that this antiserum specifically recognizes HMP-1 protein. Before hypodermal enclosure, hmp-1 (zu278) embryos appear to express HMP-1; this is presumably maternally supplied gene product.

For HMP-2 and HMR-1 antiseria, specific peptides were synthesized: NH2-terminal HMP-2 sequence DHDEVRTDSRIRSC and COOH-terminal HMR-1 sequence CAPYDELRIYDDRDN (by Quality Controlled Biochemicals Inc., Hopkinton, MA). Rabbits were immunized by the Fred Hutchinson Cancer Research Center Animal Care Facility. The HMP-2 and HMR-1 antiseria were affinity purified using BSA-coupled peptide attached to nitrocellulose membrane (ProBlott; Applied Biosystems, Inc., Foster City, CA) as described previously (Robinson et al., 1988). Specificity of the antiseria was tested on hmp-2(RNAi) and hmr-1(RNAi) embryos generated as described previously (Guo and Kemphues, 1995; Rocheleau et al., 1997) using the cDNAs yk126e3 and yk105b7 as templates for RNA. Immunostaining of embryos with affinity-purified HMP-1 antiserum, mAbMH27, and β-tubulin antibody (Boehringer-Mannheim Corp., Indianapolis, IN) was performed by both of the protocols described by Costa et al. (1997) with identical results. Staining with the affinity-purified HMP-2 and HMR-1 antiseria was as described by Albertson (1984). For double labeling, fluorescein- and either rhodamine- or Texas Red–conjugated secondary antibodies were used. Phalloidin staining was done according to Costa et al. (1997). Fluorescent images were obtained using either a confocal laser scanning microscope (model MRC1024 [laboratory of Judith Kimble, University of Wisconsin, Madison, WI] or MRC600; Bio-Rad Laboratories, Hercules, CA) or a Dage cooled CCD camera (Michigan City, IN) and DSP2000 processor. For Nomarski time-lapse videomicroscopy, embryos were mounted on agarose pads in M9 solution and sealed under a coverslip with Vaseline. Single focal plane recordings were made on a Panasonic (Bangkok) time-lapse video recorder using a Hammamatsu VE2000 camera (Bridgewater, NJ). Four-dimensional recordings were made as described by Draper et al. (1996).

Results
hmp-1, hmp-2, and hmr-1 Genes Are Required for Elongation of the Embryo
The wild-type C. elegans embryo increases fourfold in body length during morphogenesis (see Fig. 1 A). After standard ethylmethane sulfonate mutagenesis, we screened directly for mutant embryos that are defective in body elongation. We isolated 13 recessive, zygotic-lethal mutants that, in addition to failing to elongate properly, show abnormally bulged dorsal surfaces (Fig. 1 B). We call this novel phenotype Hmp (humpback); this phenotype contrasts with previously described elongation-defective Pat mutants that display bulges at variable positions (Williams and Waterston, 1994). The 13 Hmp mutants identify the genes hmp-1, hmp-2, and a third gene that we name hmr-1 for an additional phenotype described below.

We isolated 10 alleles of the gene hmp-1 and received another from A. Wissmann. All alleles show the same phenotype. Embryogenesis proceeds normally in hmp-1 mutants through the start of elongation. However elongation arrests at the 1.25× to 1.5× stage, and the mutant embryos retract to their original 1× length as abnormal bulges form on the dorsal side (Fig. 1 B). Although hmp-1 mutants have an early defect in elongation, cells appear to differentiate fully. For example, muscles, neurons, and pharyngeal cells in hmp-1 embryos express markers for terminal dif-
Differentiation (Fig. 1 D and data not shown). The hmp-1 mutants may completely lack hmp-1 gene activity, at least with respect to the zygotic requirement for elongation, since embryos homozygous for the hmp-1 deficiency ctDf1 show a similar Hmp phenotype (Fig. 1 C).

Our mutant screen identified a single allele of the hmp-2 gene. Approximately 40% (n = 251) of hmp-2 (zu364) mutant embryos appear indistinguishable from hmp-1 mutants. The other 60% of hmp-2 embryos elongate to variable extents with less bulging of the dorsal hypodermis than hmp-1 mutants (Fig. 1 E). About 1% of hmp-2 embryos hatch to form viable dumpy or lumpy larvae. Embryos hemizygous for hmp-2 (zu364) or homozygous for a hmp-2 deficiency (either eDf4 or eDf15), display variable Hmp phenotypes similar to hmp-2 homozygotes, suggesting hmp-2 (zu364) is a null allele (data not shown).

We isolated two alleles of the hmr-1 gene. For both mutations, ~2% (n = 450) of the homozygous embryos show a Hmp elongation phenotype identical to that of hmp-1 or hmp-2 mutants. However, in the remaining hmr-1 mutants the hypodermis fails to fully enclose the embryo. We call this phenotype Hmr (hammerhead; see Fig. 1 F). Hmr embryos, like Hmp embryos, show terminal differentiation of all tissues (data not shown). Before presenting further phenotypic characterization of Hmr and Hmp mutants, we describe here the cloning and molecular nature of the hmp-1, hmp-2, and hmr-1 genes.

hmp-1, hmp-2, and hmr-1 Encode Homologues of α-Catenin, β-Catenin/Armadillo, and Classical Cadherin

We cloned the hmp-1, hmp-2, and hmr-1 genes by positional cloning strategies using genetic mapping and transgenic rescue experiments (see Materials and Methods). For hmp-1, hmp-2, and hmr-1, we demonstrated that injection of in vitro-synthesized RNA into the gonads of wild-type adults produced Hmp or Hmr embryos (data not shown).

Sequence analysis of hmp-1 cDNAs revealed that hmp-1 can encode a protein, HMP-1, with 35–38% identity to α-catenins from vertebrates and invertebrates (Fig. 2 A). α-Catenin is a component of adherens junctions that appears to bind directly to F-actin (Rimm et al., 1995) and indirectly to classical cadherins (transmembrane cell adhesion proteins) through β-catenin (Pai et al., 1996). The homology extends throughout almost the entire length of HMP-1 and α-catenins, including putative binding domains for actin and β-catenin. However, the HMP-1 sequence is more diverged than that of previously isolated α-catenins, which show greater than 55% identity to each other.
The complete cDNA sequence of hmp-2 indicates that the predicted HMP-2 protein shows ~26% amino acid identity to β-catenin/Armadillo from vertebrates and invertebrates (Fig. 2B). This homology extends throughout the entire length of the proteins and includes the region of β-catenin/Armadillo that binds to α-catenin. HMP-2, like β-catenin, contains 13 imperfect repeats, called Arm repeats (Peifer and Wieschaus, 1990), of ~42 amino acids each that are arranged in tandem with an insertion between the 10th and 11th repeats. This arrangement is also found in plakoglobin, a component of both adherens and desmosome junctions; however, plakoglobin lacks a COOH-terminal hexapeptide conserved between HMP-2 and β-catenins.

Our sequence of hmr-1 partial cDNA clones and the sequence of the corresponding genomic region provided by the C. elegans Genome Project reveals that the predicted HMR-1 protein contains a putative signal peptide and a transmembrane domain (Fig. 2C, TM). The putative intracellular domain of HMR-1 shows 20–25% amino acid identity to the intracellular region of classical cadherins; this domain of classical cadherins binds to β-catenin/Armadillo (Pai et al., 1996). The putative extracellular portion of HMR-1 contains two and one-half repeats of an ~100-amino acid domain, called the EC repeat, believed to mediate homotypic binding (Shapiro et al., 1995). The HMR-1 extracellular domain also possesses a region of 733 amino acids (divided into segments called Fcc, C-rich1, LmA-G, and C-rich2) that is homologous to a region found in Drosophila N- and E-cadherin, but not in vertebrate cadherins (Iwai et al., 1997).

**Figure 2.** Sequence similarity of HMP-1, HMP-2, and HMR-1 proteins to catenins and cadherins. Schematic diagrams comparing the primary amino acid sequences of HMP-1 (A), HMP-2 (B), and HMR-1 (C) proteins from C. elegans with their Drosophila (labeled D) or vertebrate homologues. Domains that have been described for α-catenin, β-catenin, and classical cadherins are labeled. The percentage of amino acid identity with the corresponding regions of HMP-1, HMP-2, or HMR-1 is shown. (A) The β-catenin–binding domain identified in chicken αE-catenin (Nieset et al., 1997) appears to correspond to amino acids 92–143 in HMP-1. α-catenin seems to contain two F-actin-binding regions (Rimm et al., 1995). Although neither has been mapped extensively, the COOH-terminal region includes the portion homologous to the more precisely mapped actin-binding domain in the related protein vinculin (Menkel et al., 1994). This portion is depicted and corresponds to amino acids 690–817 of HMR-1. (B) The α-catenin–binding and cadherin-binding domains of Armadillo/β-catenin (Pai et al., 1996) are homologous to HMP-2 amino acids 19–84 and 146–397, respectively. (C) The β-catenin–binding domain identified in the intracellular region of DE-cadherin (Pai et al., 1996) corresponds to amino acids 1184–1223 of HMR-1. Arrows indicate predicted signal sequence cleavage sites. Bar, the length of 100 amino acids for all panels.

**Hmp Mutants Are Defective in Cell Shape Changes of the Dorsal Hypodermis**

The finding that the hmp-1, hmp-2, and hmr-1 genes can encode proteins related to α-catenin, β-catenin, and cadherin, respectively, suggests that mutants in the Hmp and Hmr classes might be defective in cellular adhesion or cytoskeletal function. We present here an analysis of the embryonic Hmp phenotype of hmp-1 mutants; similar results were obtained from experiments on hmp-2 and hmr-1 mutants expressing the Hmp phenotype. Living embryos were analyzed by videomicroscopy. Fixed embryos of various stages were analyzed by staining with phalloidin to detect actin filaments and by staining with the antibody mAbMH27 (Priess and Hirsh, 1986; Francis and Waterston, 1991; Podbielwicz and White, 1994). Immuno-electron microscopic studies have shown that mAbMH27 stains adherens junctions in the hypodermal cells, pharyngeal cells, and intestinal cells (Hall, D., personal communication).

Before body elongation commences, the body has a slight ventral flexure and the hypodermal cells are organized into distinct dorsal, lateral, and ventral rows (Fig. 3A). During body elongation, each hypodermal cell lengthens along the longitudinal axis of the body, and each cell shortens along the circumferential contour of the body (Fig. 3C; see also Priess and Hirsh, 1986). The dorsal and ventral sides of the body elongate at similar rates, and the body decreases in circumference uniformly. The nascent tail extends ventrally and then turns anteriorly toward the head; with further elongation, the body is contorted into a pretzel-like shape within the eggshell (Fig. 3C).

hmp-1 mutant embryos appear identical to wild-type embryos before body elongation (Fig. 3A). However, when elongation commences, only the ventral hypodermal cells elongate appreciably. The ventral flexure of the embryo disappears as the ventral hypodermal cells lengthen; the body straightens (Fig. 3B) and then develops a prominent dorsal flexure (Fig. 3D). During this process, the dorsal hypodermis appears to retract slightly in length and to

Costa et al. Catenin–Cadherin System in Caenorhabditis elegans 301
increase in circumference, forming the dorsal bulges characteristic of the Hmp class of mutants. Longitudinally oriented body wall muscles underlie the hypodermis (Fig. 4A) and contract in opposition to the direction of body elongation. To ask if inappropriate dorsal muscle contraction causes the dorsal retraction in hmp-1 mutants, we examined the development of embryos homozygous for the genetic deficiency ctDf1. This deficiency deletes both the hmp-1 gene and myo-3; the myo-3 gene encodes a body wall muscle myosin that is essential for muscle contraction. Videomicroscopy of ctDf1 homozygotes (n = 4) demonstrates that although these embryos have no visible muscle contractions, they show a pattern of dorsal retraction similar to that of hmp-1 mutants (Fig. 1C).

**Actin Filament Bundles in Hmp Mutants Detach from Adherens Junctions**

The cytoskeletal organization of wild-type hypodermal cells during body elongation has been described previously (Priess and Hirsh, 1986; Costa et al., 1997). Briefly, each hypodermal cell contains an array of actin filament bundles in its apical cortex; these bundles are oriented parallel to the circumferential contour of the body, and we refer to them as circumferential filament bundles (CFBs; see Fig. 8B). The CFBs appear to connect with the adherens junction that encircles each hypodermal cell (Figs. 4A and 8, A and B). Microtubules in the dorsal and ventral hypodermal cells are aligned parallel to the CFBs. However, few if any microtubules appear to contact the adherens junction; most instead terminate before, or run parallel to, the junction.

Before body elongation, the microtubules, CFBs, and adherens junctions in hmp-1 mutants and wild-type embryos appear identical (Figs. 4A and data not shown). As the hypodermal cells in hmp-1 mutants begin to change shape, the CFBs in the dorsal hypodermis separate from the adherens junctions (Figs. 4, C and D). The detached CFBs increase in thickness and retract several micrometers toward the dorsal midline (Figs. 4, C and D, and data not shown). These observations suggest that the CFBs in the dorsal hypodermis of hmp-1
embryos contract away from the adherens junction rather than draw together opposing sides of the cell. In contrast, the CFBs in the lateral and ventral hypodermal cells maintain their normal proximity to the adherens junctions (Fig. 4E). The organization of microtubules appears relatively normal in all hypodermal cells (Fig. 4F).

**hmp-1, hmp-2, and hmr-1 Are Required for Hypodermal Enclosure of the Embryo**

Most *hmr-1* mutant embryos show morphogenetic defects before the start of body elongation. In wild type, hypodermal cells are born on the dorsal side of the embryo and migrate ventrally to enclose the body. The hypodermal cells in *hmr-1* mutants initially are positioned normally (data not shown). However, the hypodermis in 98% (*n* = 450) of *hmr-1* mutants fails to fully enclose the anteroventral region of the embryo; we call this the Hmr phenotype (see Fig. 1F). Embryos that are deficient for both maternal and zygotic gene activity of *hmp-1* or *hmp-2* also exhibit the Hmr phenotype: All embryos produced by *hmp-1* germ-line mosaic animals show the Hmr phenotype (*n* = 100), as do all embryos from rare *hmp-2* homozygous mutants that survive to adulthood (*n* > 100). We have analyzed the cellular defects that prevent body enclosure in these embryos by four-dimensional Nomarski time-lapse videomicroscopy (data not shown) and by staining with mAbMH27 (Fig. 3F).
During body enclosure of the wild-type embryo, the left and right rows of ventral hypodermal cells migrate to the ventral midline (Williams-Masson et al., 1997). The two anterior-most ventral hypodermal cells on each side of the embryo, called the leading cells (Fig. 3 E, I and 2), are the first to begin moving and to reach the midline. Some ventral hypodermal cells form adherens junction with contralateral cells as their leading edges meet at the ventral midline, while others fuse together with contralateral cells.

In embryos from hmp-1 germline mosaic animals, the ventral hypodermal cells initiate ventral movement. However, the anterior three ventral hypodermal cells cease migration prematurely, stopping several micrometers from the ventral midline (Fig. 3 F and data not shown). In contrast, the other ventral hypodermal cells complete migration to the midline and either establish adherens junction contacts or fuse with contralateral cells (Fig. 3 F).

Circumferential contraction of the partially enclosed embryos seems to force internal cells out through the non-enclosed anterior region, forming the characteristic Hmr phenotype (see Fig. 1 F). Dorsal and lateral hypodermal cells contact neighboring cells along their entire margins; however, many embryos fixed after the start of elongation show ruptures at the ventral midline between contralateral pairs of posterior, ventral hypodermal cells (Fig. 3 F). In these Hmr embryos, as in Hmp embryos, the CFBs in the dorsal but not lateral or ventral hypodermis separate from the adherens junctions (Fig. 4 G and data not shown). Thus, both Hmr and Hmp embryos have similar cytoskeletal defects in the dorsal hypodermis. We note that the adherens junction antigen recognized by mAbMH27 is localized properly to the apical margins of hypodermal cells, indicating that at least some aspects of cell polarity and adherens junction structure remain in Hmr and Hmp embryos.

The HMP-1, HMP-2, and HMR-1 Proteins Localize to Adherens Junctions

To examine how the hmp and hmr gene products might interact with the actin cytoskeleton, we raised polyclonal antibodies against a HMP-1 fusion protein and against peptides specific for the predicted HMP-2 and HMR-1 proteins (see Materials and Methods). Specificity of each affinity-purified antiserum was tested on either mutants or mutant phenocopies generated by RNA-mediated interference (see Materials and Methods). We describe in detail the staining patterns observed with the HMP-1 antiserum; the HMP-2 and HMR-1 antisera gave very similar staining patterns at all stages of embryogenesis. The HMP-1 antiserum recognizes a single protein species of ~105-kD present in C. elegans extracts (data not shown).

Before morphogenesis and tissue differentiation, the HMP-1 antiserum stains all blastomeres of embryos (Fig. 5 A). HMP-1 antiserum prominently labels all regions of contact between blastomeres, in addition to showing diffuse cytoplasmic staining. At approximately the time adherens junctions begin to form in the hypodermis (Podbilewicz and White, 1994), HMP-1 protein accumulates to high levels along the apical margins of all hypodermal cells (Fig. 5 B; all hypodermal staining lies within a 1-µm focal plane near the cell surface). During migration of ventral hypodermal cells, HMP-1 antiserum staining is not detected at the leading edges of these cells (Fig. 5 C; these edges also lack mAbMH27 staining [Williams-Masson et al., 1997]). HMP-1 becomes localized to the ventral margins of these cells as they contact contralateral cells at the ventral midline (Fig. 5, C and D).

During body elongation, the HMP-1 antiserum stains predominantly the apical margins of all hypodermal, pha-

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**Figure 5.** Localization of HMP-1 protein before and during body enclosure of the embryo. Immunofluorescence micrographs of wild-type embryos stained for HMP-1 protein. (A) Four-cell stage embryo. HMP-1 protein is concentrated at the sites of contact between blastomeres (arrows). (B) Dorso-lateral view of an embryo at the onset of hypodermal enclosure showing HMP-1 accumulation at developing adherens junctions in hypodermal cells. Left and right rows of lateral hypodermal cells are labeled with asterisks as in Fig. 3; a hypodermal cell in the dorsal row is marked (+). (C) Ventrolateral view of an enclosing embryo; labeling as in Fig. 3 E. The arrow marks the unstained leading edge of a migrating ventral hypodermal cell. (D) Ventral view of an embryo at the end of hypodermal enclosure.
rygneal, and intestinal cells (Fig. 6, A and D), as does the mAbMH27 antiserum (Fig. 6 B). The staining of these two antisera appears to colocalize (Fig. 6 C), strongly suggesting that HMP-1 is a component of the adherens junctions. In later stages, staining appeared most prominent on the margins of the hypodermal cells that abut the two ends of the CFBs. For example, we observed intense staining in ventral hypodermal cells along the ventral midline (Fig. 6 D), but staining was faint or undetectable on lateral margins of the ventral cells (data not shown).

To test whether hmp-2 or hmr-1 gene activity is required to localize HMP-1 protein to adherens junctions, we stained hmp-2 and hmr-1 mutant embryos with the HMP-1 antiserum and with mAbMH27. Both mutants properly localize the adherens junction component recognized by mAbMH27 (Fig. 7 A). Although cytoplasmic HMP-1 is visible in these mutants, greatly reduced or undetectable levels of HMP-1 are associated with adherens junctions (Fig. 7 B, and data not shown). Similarly, mAbMH27 staining was apparent in hmr-1 mutant embryos (Fig. 7 C), but HMP-2 staining was not (Fig. 7 D). Thus hmr-1(+) activity appears to be required to localize both HMP-1 and HMP-2 to the adherens junction, and hmp-2 (+) activity is required to localize HMP-1. In contrast, neither hmr-1(+), hmp-1(+), nor hmp-2(+) activity appears to be necessary to localize the antigen recognized by MH27 to the adherens junction.

Discussion

A Catenin–Cadherin Complex at Cell Junctions in C. elegans

Our mutant screen identified three genes, hmp-1, hmp-2, and hmr-1, that are required for proper body enclosure and body elongation of C. elegans embryos. These two morphogenetic processes appear to be driven by shape changes in the hypodermal cells, and both processes are disrupted by inhibitors of actin filament function (Priess and Hirsh, 1986; Williams-Masson et al., 1997). Hypodermal cells in C. elegans have two prominent, actin-containing structures: a subapical adherens junction and an array of actin filament bundles that we call CFBs. Our phenotypic analysis of hmp-1, hmp-2, and hmr-1 mutants suggests that they are defective in body elongation because the CFBs in the dorsal hypodermal cells detach from adherens junctions.

The HMP-1, HMP-2, and HMR-1 proteins appear to be genuine members of the a-catenin, b-catenin, and classical cadherin families, respectively, although each is more diverged in primary structure than previously identified family members. More than 80% of the C. elegans genome has now been sequenced, and no genes that are more homologous have been identified. Catenins and cadherins are components of adherens junctions in other systems, and we have shown here that the HMP-1, HMP-2, and HMR-1 proteins appear to localize to adherens junctions in C. elegans embryos. Catenins and cadherins form a molecular complex and their binding sites for each other have been mapped (Pai et al., 1996; Nieset et al., 1997). Since there is a homologous region for each of these binding sites in HMP-1, HMP-2, or HMR-1, we suggest that these three C. elegans proteins may form an analogous complex (Fig. 7 C). In support of this model, we have shown that hmr-1(+) activity is required for proper localization of both HMP-1 and HMP-2 proteins and that hmp-2(+) activity is required for the proper localization of HMP-1.

Transmission of Forces Driving Embryo Elongation

The CFBs shorten and thicken as the hypodermal cells elongate in the orthogonal direction (Costa et al., 1997). This change in cytoskeletal morphology is consistent with,
but does not prove, the model that the CFBs are contractile, with contraction providing the force that changes the shape of individual hypodermal cells and, consequently, the shape of the embryo. For example, inhibitor studies demonstrate that actin is required not only to initiate body elongation but also to maintain the shape of the body during elongation (Priess and Hirsh, 1996). Thus, the CFBs could respond to, rather than cause, changes in hypodermal cell shape. We have shown here that the CFBs in the dorsal hypodermis of Hmp mutants shorten and thicken even after they have detached from the margins of the hypodermal cells, strongly suggesting that they are contractile. We thus propose that the HMP-1, HMP-2, and HMR-1 proteins normally anchor the CFBs to the adherens junction, allowing the force of CFB contraction to be transmitted into changes in cell shape.

The sequence similarity between HMP-1 and α-catenins suggests that HMP-1 may bind to, and bundle, actin filaments. HMP-1 might directly cross-link actin in the CFBs with actin filaments in the adherens junctions (Fig. 8C, upper cell). Alternatively, since adherens junctions may contain HMP-1 protein along their entire length, rather than localized only to points of contact with CFBs, accessory proteins might provide the actual links to the CFBs (Fig. 8C, lower cell).

The HMP-1, HMP-2, and HMR-1 proteins are present in the dorsal, lateral, and ventral hypodermal cells along the segments of the adherens junction that contact the CFBs. This localization pattern raises the question of why the CFBs detach from the adherens junctions only in the dorsal hypodermis cells. One possible explanation is that lateral and ventral hypodermal cells contain molecules that have redundant functions with HMP-1, HMP-2, and HMR-1. Currently, the C. elegans genomic and EST sequences reveal no genes other than hmr-1 that encode putative classical cadherins; several genes, including cdh-3 (Pettitt et al., 1996), are similar to cadherins only in the predicted extracellular domain. There is a second gene (corresponding to the CELK02251 EST) that shows significant homology to α-catenin. However, in preliminary antisense RNA experiments we find no evidence that this gene functions in hypodermal morphogenesis or substitutes for HMP-1 function (our unpublished results). A β-catenin–like gene, bar-1, has been shown to function in postembryonic development in C. elegans. However, null mutations in this gene have no embryonic phenotype (Eisenmann, D., personal communication). An additional β-catenin gene called wrm-1 has been shown to be required for a Wnt-like signal transduction pathway in the early embryo, but it is not known whether this gene has a cytoskeletal function (Rocheleau et al., 1997).

Another possibility is that the total mechanical stress on the CFB–adherens junction connections in the lateral and ventral hypodermal cells is less than on connections in the dorsal hypodermis. The force exerted on the connections from contraction of the CFBs within a cell might be similar for all hypodermal cells. However, these same connections must also withstand external stretching forces generated by CFBs contracting in neighboring cells (Fig. 8B). Part of the ability of a hypodermal cell to resist stretching likely derives from the sections of its adherens junction that are oriented parallel to the CFBs. In the dorsal hypodermis, there are relatively few such sections (see Figs. 3B and 8A). This is because the largest dorsal hypodermal “cell” is a multinucleate syncytium formed by the fusion of 23 individual cells. Before fusion, the 23 cells have 46 (two per cell) sections of adherens junction running parallel to the CFBs; after fusion there are only two such sections in the largest dorsal hypodermal cell. Thus, the CFB–adherens junction connections in the dorsal hypodermis may be stretched more forcefully and, consequently, break more easily than connections in the lateral or ventral hypodermal cells in Hmp mutants. It is worth noting that most of the cells in the C. elegans embryo are very small; the entire

![Figure 7. MH27, HMP-1, and HMP-2 localization in mutant embryos. (A and B) A single, terminal stage *hmp-2* mutant embryo is shown after staining with mAbMH27 (A) and with the anti–HMP-1 antiserum (B). (C and D) A single, terminal stage *hmr-1* (RNAi) embryo is shown after staining with mAbMH27 (C) and with the anti–HMP-2 antiserum (D). Asterisks label the same hypodermal cells indicated in Figs. 3 and 6.]
embryo is only 50 \( \mu \text{m} \) in length, which is comparable to the size of a single vertebrate fibroblast. Because of its size, the large dorsal hypodermal cell may be a particularly useful model for studying how vertebrate epithelial cells respond to cytoskeletal stress.

If each CFB in the \textit{C. elegans} hypodermis were attached to the adherens junction at its two ends but was otherwise free to move in the cytoplasm, breakage at one end might be expected to instantly relieve stress at the other end. Thus, a CFB might detach randomly from either side of the hypodermal cell but would not be expected to detach from both sides. Instead, we invariably detect detachment from both sides, and the CFBs appear to contract symmetrically toward the middle of the hypodermal cell surface. This observation suggests that the CFBs may also be linked to the apical cortex of a hypodermal cell. An interesting possibility is that the CFBs may be anchored to the hypodermal cell cortex at sites where body wall muscles contact the hypodermis. Beginning at about the 2X stage of elongation, hemidesmosomes form in the hypodermal cells in regions that overlie the body wall muscles (Hresko et al., 1994). It is possible that this intermediate filament system is linked to the CFBs. If such a connection was required to maintain the proper organization of the CFBs, it might explain why Pat mutants defective in body wall muscle function show incomplete body elongation.

**Cell Migrations Requiring a Catenin–Cadherin System**

In hmp-1, hmp-2, and hmr-1 mutants, the anterior three pairs of ventral hypodermal cells (the leading cells and G2/W) fail to complete ventral migration, resulting in the Hmr phenotype. In wild type embryogenesis, the leading cells are the first to extend ventrally, and only they project actin-rich filopodia from their leading edges (Williams-Masson et al., 1997). The normal migration behavior of G2/W has not been analyzed. Since initial migration of the leading cells does not appear to be affected in Hmr mutants, we speculate that HMP-1, HMP-2, and HMR-1 may function at the time filopodia from leading cells on either side of the embryo meet at the ventral midline. The HMP-1, HMP-2, and HMR-1 proteins appear to be absent from, or at very low levels in, the leading edge of migrating hypodermal cells. However, as hypodermal cells establish contact with contralateral cells and adherens junctions form, these proteins localize to the ventral midline. While HMP-1, HMP-2, and HMR-1 apparently are not required in general for adjacent cells to form adherens junctions (see below), they may act to stabilize fine filopodial contacts between contralateral pairs of ventral cells, and expand cell adhesion along these surfaces. This function may be analogous to the role of \textit{Drosophila} E-cadherin in adhesion of filopodia from migrating tracheal cells and expansion of the tracheal lumen (Tanaka-Matakatsu et al., 1996).

**Cell Contacts and Epithelial Tissue Integrity**

Perhaps as significant as the roles of hmp-1, hmp-2, and hmr-1 in specific morphogenetic processes is the apparent lack of requirement for these genes in cell adhesion, apical-basal polarity, and at least some aspects of adherens junction formation in the \textit{C. elegans} embryo. Gene inactivation of \textit{armadillo}/\( \beta \)-catenin in \textit{Drosophila} (Cox et al., 1996; Müller and Wieschaus, 1996), \( \alpha \)/E-catenin, E-cadherin, and \( \beta \)-catenin in mouse (Larue et al., 1994; Haegel et al., 1995; Torres et al., 1997), and EP-cadherin and \( \alpha \)-catenin in \textit{Xenopus} (Heasman et al., 1994; Kafron et al., 1997) demonstrate that some catenin–cadherin systems are essential for the integrity of embryonic epithelia.

The HMP-1, HMP-2, and HMR-1 proteins are present on the surfaces of all blastomeres in early embryos. Although aspects of body morphogenesis are abnormal in Hmp and Hmr mutants, tissue-specific cell associations and cell polarities are clearly visible. For example, during early embryogenesis, germ cell precursors apparently must adhere to the intestinal cell precursors to be brought into the body cavity during gastrulation. We find that germ cells are internalized correctly in hmp-1, hmp-2, and hmr-1 mutants. Also, if the hmp and hmr genes were essential for hypodermal cell adhesion, contraction of the CFBs might be expected to cause the rows of hypodermal cells to split apart from each other in the mutant embryos. Instead, we find that contacts between hypodermal cells generally remain intact. The only exception we observed was the sepa-
ration of some contralateral pairs of ventral hypodermal cells late in morphogenesis, which may result from incomplete body enclosure. Hypodermal cells clearly retain apical–basal polarity in Hmp and Hmr mutants since these cells secrete a cuticle on their apical surfaces and show subapical localization of the adherens junction antigen recognized by mAbMH27 antibody.

We do not believe the lack of additional defects in the Hmp or Hmr mutants is likely to be due to residual activities of the HMP or HMR proteins. hmp-1 (zu278) behaves genetically as a null mutation and produces no detectable HMP-1 protein, and embryos treated with RNA from the hmp-2 or hmr-1 genes do not produce detectable levels of the HMP-2 or HMR-1 proteins. Thus, if the HMP or HMR proteins have important, general roles in cell adhesion or cell polarity, other proteins must provide redundant functions. In any case, the absence of general cell adhesion defects in hmp-1, hmp-2, and hmr-1 mutants has allowed us to characterize specific functions for a presumptive catenin–cadherin system in cell shape changes, cell movement, and cytoskeletal integrity.

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