The cellular slime mold *Dictyostelium discoideum* is an attractive system for studying the roles of microtubule-based motility in cell development and differentiation. In this work, we report the first molecular characterization of kinesin-related proteins (KRPs) in *Dictyostelium*.* A PCR-based strategy was used to isolate DNA fragments encoding six KRPs, several of which are induced during the developmental program that is initiated by starvation. The complete sequence of one such developmentally regulated KRP (designated K7) was determined and found to be a novel member of the kinesin superfamily. The motor domain of K7 is most similar to that of conventional kinesin, but unlike conventional kinesin, K7 is not predicted to have an extensive α-helical coiled-coil domain. The nonmotor domain is unusual and is rich in Asn, Gln, and Thr residues; similar sequences are found in other developmentally regulated genes in *Dictyostelium*. K7, expressed in *Escherichia coli*, supports plus end-directed microtubule motility in vitro at a speed of 0.14 μm/s, indicating that it is a bona fide motor protein. The K7 motor is found only in developing cells and reaches a peak level of expression between 12 and 16 h after starvation. By immunofluorescence microscopy, K7 localizes to a membranous perinuclear structure. To examine K7 function, we prepared a null cell line but found that these cells show no gross developmental abnormalities. However, when cultivated in the presence of wild-type cells, the K7-null cells are mostly absent from the prestalk zone of the slug. This result suggests that in a population composed largely of wild-type cells, the absence of the K7 motor protein interferes either with the ability of the cells to localize to the prestalk zone or to differentiate into prestalk cells.

**INTRODUCTION**

Since the prototype kinesin was purified from squid axoplasm (Lasek and Brady, 1985; Schroer *et al.*, 1985; Vale *et al.*, 1985), dozens of related proteins (here referred to as kinesins or kinesin-related proteins [KRPs]) have been identified in organisms ranging from fungi to mammals (Moore and Endow, 1996). KRPs share a conserved mechanochemical motor domain responsible for ATP hydrolysis and microtubule binding. Outside of the 350-amino acid-long motor domain, KRPs show great sequence diversity, but regions predicted to mediate homodimerization via formation of coiled-coil structures are often present (Goldstein, 1993). Sequence diversity among KRPs outside of the motor domain is thought to play a key role in their functional diversity by specifying which proteins and cargo associate with the motor (Goldstein, 1993). Kinesins have been shown to drive the movement of vesicles in fast axonal transport (Hall and Hedgecock, 1991; Hurd and Saxton, 1996; Hurd *et al.*, 1996), the movement of vesicles between the Golgi...
and the ER (Lippincott-Schwartz and Cole, 1995; Lippincott-Schwartz et al., 1995), and the movement of other organelles, including secretory vesicles, lysosomes, mitochondria, and nuclei (Hirokawa, 1996; Lopez, 1996; Cottingham and Hoyt, 1997; DeZwaan, et al., 1997; Pereira et al., 1997). Kinesins have also been shown to be involved in the organization, assembly, and operation of the mitotic spindle (Barton and Goldstein, 1996; Walczak and Mitchison, 1996) as well as in the function of the kinetochores, which connect chromosomes to microtubules (Brown et al., 1996).

Several studies have also implicated kinesins in developmental processes. Microtubules are known to be necessary for the proper localization of Vg1 RNA in Xenopus oocytes (Yisraeli et al., 1990), and it has been proposed that microtubule-based motors are involved in this and other cases of RNA localization (for review, see Wilhelm and Vale, 1993). A role in development has been demonstrated for the kinesin-related protein Xklp1 in Xenopus, which is required for both spindle assembly and for the aggregation of germ plasm in early Xenopus embryos (Robb et al., 1996). In Drosophila, COS2 is a distant kinesin relative, which is thought to tether a signaling complex consisting of the fused kinase and the cubitus interruptus transcription factor to microtubules (Robbins, et al., 1997; Sisson, et al., 1997). The access of the complex to the nucleus is in turn believed to be regulated by the hedgehog gene product, which may reverse the binding of COS2 to microtubules.

Dictyostelium has many advantages as a model system for the study of the cytoskeleton (for reviews, see Schleicher and Noegel, 1992; Schleicher et al., 1995) and developmental processes (for reviews, see Firtel, 1996; Loomis, 1996). Like yeast, it offers the possibility of combining biochemical and genetic approaches, but in addition, it shows a full spectrum of cellular functions, including chemotaxis and multicellular development. Dictyostelium has been used extensively in the study of actin-based myosin motors (Novak et al., 1996; Jung et al., 1996; Temesvari et al., 1996; Wessels et al., 1996). Work on microtubule-based motors has included the characterization of cytoplasmic dynein (Koonce and McIntosh, 1990; Koonce et al., 1992, 1994) and the purification of a protein with the properties of a kinesin motor from vegetative cells (McCaffrey and Vale, 1989). The following is the first report on the molecular biology of kinesin motors in this organism.

Here, we describe the identification of six KRP s, several of which are induced during the Dictyostelium developmental program. One motor (termed K7) was extensively characterized; its complete sequence, developmental expression pattern, motor activity, intracellular localization, and null phenotype are reported in this work. K7 is a novel plus end-directed kinesin motor with an unusual structure in the nonmotor domain. Transcription is developmentally regulated, and the protein localizes to what appears to be a membranous perinuclear structure. In pure culture, the mutant null cells show no obvious phenotype. However, when mixed with wild-type cells, the K7-null cells are absent from the prestalk zone of the slug. This result reveals a developmental defect in an environment where mutant and wild-type cells are both present.

MATERIALS AND METHODS

Cloning of Dictyostelium KRPs

Fully degenerate oligonucleotides (kindly provided by Dr. Mark Rose, Princeton University, Princeton, NJ) corresponding to the highly conserved kinesin peptides IFAYGQT and LVDLAGSE (Stewart et al., 1991) were used to prime a PCR using genomic Dictyostelium DNA as a template. Two PCR products (K2 and K4) were cloned and used as probes to screen a cDNA λ gt11 library (Clontech, Palo Alto, CA) made from cells that had been starved for 4 h (developmental time points are referred to as hours after starvation, e.g., “T4”). Two KRP cDNAs were isolated using each probe: K6 and K8 using K2, and K3 and K7 using K4. Southern and Northern blots were hybridized at 65°C in phosphate buffer (250 mM NaPO4, 250 mM NaCl, 10% wt/vol PEG 8000, 1 mM EDTA, pH 7.2) as described (Amasino, 1986).

The entire 3.7-kb K7 insert was sequenced, and it was found to be a mixed clone of two unrelated cDNAs: one end of the insert encodes a KRP, whereas the other end encodes a protein with a high degree of homology to the mitochondrial ribosomal protein S14. This insert is thought to be the product of a cloning artifact. The breakpoint between the two parts of the insert was located in a region containing repeats of the trinucleotide AAC (nucleotides 2640–2700).

To find additional cDNAs encoding K7, a λ-Zap cDNA library made from T8–T12 cells (kindly provided by Dr. R. Firtel, University of California, San Diego, CA) was screened using the fragment of the original insert corresponding to the KRP and ending at an EcoRV site upstream of the breakpoint. A cDNA was obtained that spanned the breakpoint in the original K7 clone but still appeared to terminate prematurely. The final piece of the K7 3′ end was obtained by RT-PCR using a primer based on the 3′ end of the K-Zap clone. Total RNA was extracted from T12 cells (RNAeasy kit; Qiagen, Santa Clarita, CA) and used as a template for RT-PCR (3′-Amplitaq FINDER rapid amplification of cDNA ends 3′-RT-PCR kit; Clontech, Palo Alto, CA) which yielded a product corresponding to the 3′ end of the K7 transcript. Percent identity between protein sequences was calculated using the program Bestfit of the Wisconsin Package (Genetics Computer Group, Madison, WI). Multiple sequence alignment was done with the program Pileup (Genetics Computer Group). Coiled-coil predictions were made using the worldwide web version of the program Paircoil (Berger et al., 1995) available at http://ostrich.lcs.mit.edu/cgi-bin/score.

Gene Disruption

The K7 gene was disrupted following a previously described strategy (de Hostos et al., 1993) designed to replace the endogenous copy of the gene with a modified copy interrupted by an antibiotic resistance cassette. Using the first 2 kb of the K7 cDNA as a template, 5′ and 3′ end fragments (corresponding to nucleotides 32–1073 and 1502–2723, respectively) containing appropriate restriction sites were generated by PCR and subcloned. A cassette conferring ampicillin resistance (kindly provided by Dr. H. Adachi, University of Tokyo, Tokyo, Japan; Adachi et al., 1994) was cloned between the two K7 fragments to complete the gene disruption construct. Plasmid DNA was digested to release the gene disruption construct.
Expression of K7-GFP in E. coli

The same K7 fragment that was used for the generation of a K7/MBP antigen (residues 1–520) was cloned into the EcoRI site of the histidine tag expression vector pET23a (Novagen, Madison, WI). The coding sequence of the _Aequorea victoria_ green fluorescent protein (S65T GFP mutant; Heim et al., 1995) was cloned into the HindII and _XhoI_ sites of the vector. GFP was included in the construct to make the fusion protein suitable for future single-molecule fluorescence experiments (see Pierce et al., 1997); the green color of the fusion protein also serves as a convenient marker during purification. BL21(DE3) _E. coli_ cells transformed with the expression construct were grown to an OD600 of 1–2 at 37°C in low-salt TPM medium (amounts per liter: 20 g tryptone, 15 g yeast extract, 4 g NaCl, 2 g Na2HPO4, 1 g NaH2PO4, 2 g glucose, 0.1 g ampicillin, pH 7.0). Cultures were cooled to 23°C, induced by the addition of 0.2 mM isopropyl-1-thio-β-D-galactopyranoside, and grown for an additional 14 h at 23°C. Cells were harvested by centrifugation and stored at −80°C. Cell pellets from 1 l of culture were thawed and resuspended in 25 ml of lysis buffer (50 mM NaPO4, pH 8.0, 250 mM NaCl, 20 mM imidazole, 250 mM NaCl, 1 mM MgCl2, 0.5 mM ATP, 10 mM β-mercaptoethanol [β-ME] containing leupeptin (1 μg/ml), pepstatin (1 μg/ml), chymostatin (1 μg/ml), aprotinin (1 μg/ml), and 0.25 μg/ml Pefabloc (Boehringer Mannheim, Indianapolis, IN) and disrupted in a French press. The lysate was clarified by centrifugation for 30 min at 28,000 × g, and the supernatant was incubated with Ni-nitrotriacetic acid resin (QIAGEN) for 1 h at 4°C (1.5 ml bed volume of resin per 50 ml of supernatant). The mixture was then transferred to a disposable column, and the resin was washed with 50 ml of 50 mM NaPO4 (pH 6), 250 mM NaCl, 1 mM MgCl2, 0.1 mM ATP, and 10 mM β-ME. K7-GFP was eluted with 50 mM NaPO4, 500 mM imidazole, 250 mM NaCl, 1 mM MgCl2, 0.1 mM ATP, and 10 mM β-ME (pH 7.2). The peak fractions were then diluted 20-fold into column buffer [25 mM Na-piperazine-N,N'-bis(2-ethanesulfonic acid) pH 6.8, 2 mM MgCl2, 1 mM EGTA, 1 mM ATP, and 0.1 mM ATP] and further purified by FPLC chromatography on a mono-Q column (Pharmacia, Piscataway, NJ) using a 20-ml 0–1.0 M NaCl gradient in column buffer. K7-GFP eluted as a sharp band centered at 290 mM NaCl.

In Vitro Motility Assay

Polarity-marked microtubules were prepared and an in vitro motility assay was performed essentially as described (Howard and Hyman, 1993), except that microtubules were added in BRB12 buffer [12 mM K-Na-piperazine-N,N'-bis(2-ethanesulfonic acid) pH 6.8, 2 mM MgCl2, 1 mM EGTA, 1 mM ATP containing 2 μg/ml casein and 20 μM taxol (Molecular Probes, Eugene, OR) and a coupled enzyme oxygen scavenger system (Harada et al., 1990). Recombinant motor protein eluted from the mono-Q purification step was loaded directly into a flow cell and allowed to bind to the glass surface. Microtubules were introduced into the chamber and imaged with a Zeiss Axioshot microscope. Images were obtained using a silicon intensifier target camera (Hamamatsu Photonics, Bridgewater, NJ) and recorded to sVHS tape. Individual frames were grabbed from the video using an Apple Power Macintosh running Adobe Premiere. Velocities declined on prolonged illumination when using fluorescent microtubules; therefore velocity measurements reported were performed using unlabeled microtubules imaged by differential interference contrast and contrast enhanced using an Argus 20 image processor (Hamamatsu).

Preparation of Dictyostelium Membranes

Cells were starved in suspension culture for 12 h at a density of 1 × 10⁷ cells/ml of phosphate buffer. Crude membranes were prepared essentially as described (Goodloe-Holland and Luna, 1987). The cells were resuspended in lysis buffer supplemented with a protease inhibitor mix (Complete, Boehringer Mannheim) and 1 mM DTT.
Figure 1.

<table>
<thead>
<tr>
<th>K2</th>
<th>Regulation</th>
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The cells were broken by passage though a BioNeb cell disrupter (Glas-Col, Terre Haute, IN) at 150 psi of N₂. The homogenate was centrifuged for 20 min at 38,000 × g to obtain a supernatant and crude membrane pellet. Protein samples containing 1 × 10⁶ cell equivalents were subjected to SDS-PAGE (Laemmlli, 1970) through 8% gels and Western blotting.

Construction of a GFP Marker for the ER

The coding sequence of the GFP S65T mutant was modified using PCR by the addition to its 3’ end of codons coding for the yeast ER retention signal HDEL (Pelham et al., 1988) and cloned into the KpnI and XbaI sites of the vector pDXA-3H (Manstein et al., 1995), which carries the marker neo and expresses cloned inserts under the control of the constitutive actin-15 promoter. To provide a translational start site and a leader peptide, a DNA fragment encoding the first 38 amino acids of contact site A (Noegel et al., 1986) was amplified by PCR from a cDNA library (de Hostos, unpublished results) made in the vector λ-YES (Ellèdige et al., 1991) and cloned into HindIII and KpnI sites upstream of the modified GFP. The construct was cotransformed by electroporation (de Hostos et al., 1993) into AX2 cells with the pREP helper plasmid (Manstein et al., 1995), and transformants were selected and maintained in DD-broth (termed K2 and K4) were then used as probes to screen a cDNA library made from cells in early development (4 h of starvation or T4). In this manner, two different KRP cDNAs were isolated with each probe: K6 and K8 using the K2 probe, and K3 and K7 using the K4 probe. The cDNAs isolated ranged in size from 300 to 3.7 kb. No additional cDNAs corresponding to K2 and K4 were isolated in this screen.

The predicted amino acid sequences of all of the fragments obtained are shown in Figure 1A. Codon usage in the predicted reading frames of all fragments showed the pronounced bias toward A/T-rich codons, which is characteristic of Dictyostelium coding sequences. In addition, all of the DNA fragments isolated except K2 have been found to hybridize to YAC clones of Dictyostelium DNA (A. Kuspa, personal communication). A nearly full-length cDNA corresponding to K2, however, has been isolated (Mayorga and de Hostos, unpublished data) by screening a development phase cDNA library (kindly provided by S. Liu and A. Kuspa, Baylor College of Medicine, Houston, TX). The various KRP fragments were used to probe Northern blots of RNA from vegetative and T8 cells; the summary of these experiments is shown in Figure 1B. No hybridization was detectable with the K3 probe but the presence of K3 sequences in the Dictyostelium genome has been confirmed by high-stringency hybridization to YACs and Southern blotting of digested Dictyostelium DNA. Taken together, these results indicate that all of the KRP-coding fragments isolated represent genuine Dictyostelium sequences and are not derived from contaminating sources.

All of the other probes except K8 hybridized to transcripts that were significantly enriched in RNA from T8 cells. The signal obtained from hybridization to the K4 and K6 probes was particularly weak, indicating a very low level of expression at this stage of development. The developmental regulation of K2 and K4 provides a possible explanation for why corresponding cDNAs were not identified in screening the cDNA library, which is made from cells at an early stage of development (T4). K8 was found to be expressed constitutively and but showed a small induction in developing cells.

The amino acid sequences deduced from the various DNA fragments show similarities to KRP s from a variety of kinesin subfamilies. The K2 fragment shows strong homology to a family of C-terminal kinesins (KatA–KatC) from the plant Arabidopsis thaliana (Mitsui et al., 1993, 1994). The sequence of the nearly full-length K2 cDNA has confirmed the C-terminal location of the K2 motor domain (Mayorga and de Hostos, unpublished data), which has 52% identity with the motor domain of KatA (Mitsui et al., 1993; Liu et al., 1996). The K8 sequence is...
unusual in that it contains a segment ~67 residues long, which has no counterpart in other kinesins. This segment is located in a region that corresponds to a surface loop (L10) in the crystal structure of kinesin motor domains (Kull et al., 1996; Sablin et al., 1996), but its function is unknown.

K7 Is an Unusual Kinesin-related Protein

One of the developmentally regulated kinesin-related genes was chosen for further study. The complete 4.2-kb K7 cDNA sequence was assembled from three separate fragments and found to encode a ~140 kDa protein that represents a novel member of the kinesin superfamily. The derived sequence is shown in Figure 2. The K7 motor domain shows the highest degree of similarity to conventional kinesin from Neurospora (32% identity; Steinberg and Schliwa, 1995) and other members of the conventional kinesin family (e.g., human kinesin heavy chain; Navone et al., 1992). However, the sequence outside of the motor domain does not show any amino acid similarity with conventional kinesin or any other member of the kinesin superfamily. Thus, the sequence data indicate that K7 is a novel kinesin superfamily member that does not clearly belong to any identified kinesin subfamily.

The nonmotor domain of K7 is unusual in several respects. First, unlike conventional kinesin and several other types of kinesin motors, K7 is predicted to adopt a coiled-coil conformation in two relatively
short segments that are widely separated from one another (Figure 2, double underlined). Based on a structure prediction using the program Paircoil (Berger et al., 1995), the nonmotor domain (beginning approximately after residue 350) can be divided into a central non-α helical core (residues 424-1089) that has 22 scattered Pro residues, flanked by two segments predicted to have a largely coiled-coil conformation (residues 390–423 and 1090–1218). The nonhelical central domain of K7 is also different from any other known kinesin in that it contains clustered repeats of Asn, Thr, or Gln residues (Figure 2, italicized). Most of the poly-Gln repeats and many of the residues in the clusters of Asn and Thr are encoded by the trinucleotide AAC in the alternate reading frames CAA, AAC, and ACA, respectively. The significance of the nucleotide repeats and the amino acid clusters is not known, but similar repeats have been identified in other developmentally regulated genes in *Dictyostelium* (Shaw et al., 1989). The structures adopted by these repeat elements are unknown.

Figure 3 shows a K7 Northern blot of RNA extracted from cells at different times after development was induced by starvation. A transcript of ~4.2 kb is detectable in developing cells, with the highest levels detectable between 12 and 16 h of development. During this time window, wild-type cells are between the finger and slug stages of development (Soll, 1987). An additional band of ~4 kb is also detectable in these blots and shows approximately the same pattern of expression as the major 4.2-kb transcript, except at T0, when only the 4-kb band is seen. The nature of the 4-kb band is unknown, but it could represent a degradation product of the main 4.2-kb transcript or an alternatively processed transcript of the K7 gene.

**K7 Is a Plus End–directed Motor**

A fragment of K7 encoding residues 1–520 was cloned in frame with the sequence of the GFP into a histidine tag pET expression vector. The fragment of K7 expressed includes the first putative coiled-coil domain and the beginning of the non-α-helical domain of the protein. Expressed fragments consisting of the first 448 amino acids of *Drosophila* kinesin heavy chain have been shown to form stable dimers and to have the same speed, directionality, and microtubule tracking properties of full-length kinesins (Stewart, et al., 1993; Berliner, et al., 1995). Thus it is likely that the K7 fragment will have motor properties very similar to those of the full-length motor.

The recombinant fusion protein was purified and tested in an in vitro motility assay using polarity-labeled microtubules that contain a highly fluorescent segment marking the microtubule minus end (Howard and Hyman, 1993). The recombinant K7 fusion protein supported the movement of the microtubules with their brighter minus ends leading (Figure 4), demonstrating that K7 is a plus end–directed motor. The labeled microtubules moved at a speed of $0.14 \pm 0.02 \mu m/s (n = 23)$, which is approximately half the speed ($0.32 \mu m/s$) of human kinesin heavy chain (K560) fused to GFP under similar conditions (Case et al., 1997). Thus, K7 is a bona fide microtubule motor protein.

**K7 Shows Perinuclear Localization**

Antiserum was raised against K7 residues 1–520, which were to fused to the C terminus of the MBP. The crude anti-K7/MBP antiserum reacted strongly with a protein band present only in extracts from developing cells but also showed significant reactivity against various proteins in both vegetative and developing cells. This background reactivity was reduced significantly, but not completely, by preadsorption of the antiserum with nitrocellulose filters previously soaked in a crude lysate of the *Dictyostelium* K7-null strain (see below) and of *E. coli* expressing MBP. A Western blot in Figure 5A shows that the anti-K7/MBP antiserum reacts strongly against a ~140 kDa protein in cells starved for 12 h (T12) cells but not in vegetative cells (T0) or in starved cells in which the K7 gene had been knocked out (KO; see below). These results are consistent with the size of the protein predicted by the K7 cDNA sequence as well as with the mRNA expression pattern of K7 in vegetative and starved cells (Figure 3). In addition to the prominent 140-kDa band, the antiserum reacts weakly with a band of ~116 kDa that is present in all three lanes, as well as other minor components.

Using the above antiserum, the subcellular localization of K7 was determined by immunofluorescence microscopy (Figure 6). In developing cells, K7 was...
detected in what appears to be a membranous and in some cases vesiculated (Figure 6a) structure around the nucleus. The overall pattern is distinct from that reported for the Golgi apparatus of Dictyostelium (Weiner, et al., 1993) but is similar to that expected for the nuclear envelope. To determine whether the structure labeled could be the nuclear envelope, antibodies against mammalian nuclear pore proteins (Snow et al., 1987) and against the ER-resident protein Kar2p (BiP homolog) from yeast (Ng and Walter, 1996) were tested but did not label Dictyostelium cells.

To generate a tag for the nuclear envelope, we modified the GFP (GFP S65T mutant; Heim et al., 1995) so that it would be targeted to the ER–nuclear envelope membrane complex. This was accomplished by introducing an N-terminal signal sequence derived from the contact site A cell adhesion glycoprotein (Noegel et al., 1986) and a C-terminal sequence encoding the peptide HDEL, which functions as the ER retention signal in yeast (Pelham et al., 1988) and other lower eukaryotes. Cells transformed with the GFP-ER construct showed a fluorescence pattern consistent with a distribution within the ER and nuclear envelope membrane system (Figure 6d). Green fluorescent vesicles can be prepared from these cells. These results strongly suggest that the peptide HDEL functions as an ER retention signal in Dictyostelium. Figure 6d also shows that the perinuclear portion of the fluorescence in the GFP-ER–expressing cells is similar to the labeling pattern of K7 in the same cells. This similarity is consistent with our hypothesis that the membranous structure labeled by the anti-K7/MBP antiserum is either the nuclear envelope or a membranous structure close to the nucleus.

To determine whether K7 is associated with a membrane fraction, Dictyostelium cells were broken, and soluble and sedimentable fractions were prepared. The Western blot in Figure 5b shows that the majority of K7 is soluble and not enriched in a crude membrane pellet where nuclei are expected. Residual K7 is stripped by further purification of the pellet fraction by washing with buffer and centrifugation through a sucrose gradient. These results indicate that K7 is released into a soluble fraction after cell lysis and is not tightly associated with a membrane fraction under these conditions. Similarly, although membrane staining patterns have been described for conventional kinesin (Hollenbeck, 1989; Lippincott-Schwartz et al., 1995; Lin et al., 1996), the majority of this motor is in the soluble fraction after cell lysis (Hollenbeck, 1989; Niclas et al., 1994).

**Disruption of the K7 Gene**

A gene disruption construct was made by inserting a cassette conferring resistance to blasticidin (Adachi et al., 1994) between PCR-generated fragments from the first 2 kb of the original K7 cDNA. Clones of cells in which the K7 gene had been inactivated were found at a high frequency (>80%). In RNA from two KO cell lines after 12 h of development (T12), neither the main 4.2-kb transcript nor the minor 4-kb band was detectable (Figure 7A). In these cells, K7 was also not detectable by immunoblotting (Figure 5A) or immunofluorescence (Figure 6c). Disruption of the K7 gene in these cell lines was confirmed by Southern blotting; a single fragment was detected, which was 1 kb greater in size compared the fragment detected in DNA from wild-type cells (Figure 7B). This size shift is expected from a...
gene replacement event. The K7-null cells grew well and appeared normal in morphology during vegetative growth. In the course of development, the null cells formed fingers, slugs, and fruiting bodies with a normal appearance.

To determine whether the K7-null cells are at some disadvantage when developing together with wild-type cells, mixing experiments with fluorescently labeled tracer cells (Knecht and Shelden, 1995; Xu et al., 1996) were conducted. K7-null and wild-type AX2 cells were labeled by incubation with a cell-tracking dye and added as 5% of a mixture with unlabeled AX2 cells. The mixtures were plated on phosphate plates and photographed after 12 h of development. Figure 8 shows that the distribution of labeled AX2 cells is uniform throughout the body of the slugs, but labeled K7-null cells are mostly absent from the front of the slug. The anterior portion of the slug contains prestalk cells that go on to form the stalk of the Dictyostelium fruiting body. Similar results were obtained when K7-null cells were detected histochemically after transformation with a plasmid containing a constitutively expressed lacZ gene. These results suggest that the absence of the K7 motor protein impairs the ability of the mutant cells to localize properly in the slug or affects the developmental fate of the mutant cells in a population composed largely of wild-type cells.

DISCUSSION

In this study, we report the characterization of a novel plus end–directed kinesin motor protein (K7) that plays a role in Dictyostelium development. The sequence of the K7 motor domain is most homologous to that of conventional kinesin, but the unusual sequence of the nonmotor domain indicates that K7 does not belong to an existing kinesin subfamily. The most intriguing element in the nonmotor domain of K7 is a large (∼74 kDa) nonhelical region that is rich in Pro and characterized by clusters of either Asn, Gln, or Thr residues. These clusters are mostly encoded by repeats of the trinucleotide CAA. Similar repeats have been found in a diverse group of developmentally regulated proteins in Dictyostelium (Shaw et al., 1989), but their significance is unknown. It will be interesting to explore whether the function of these repeats is important at the RNA or at the protein level; the K7-null strain will be useful in addressing this question.

K7-null cells demonstrate a conditional developmental defect. In pure cultures, K7-null cells appear to develop normally. However, when mutant cells are mixed with wild-type cells, the K7-null cells are mostly absent from the prestalk region of the slug. In a wild-type slug, the front 20% of the body con-
Figure 6. Immunofluorescence localization of K7. In a–c, the frames on the left are images of cells stained with DAPI, which reveals the nuclei. The frames on the right show that the anti-K7/MBP antiserum labels a membranous perinuclear structure. In a, what appear to be vesiculations of the nuclear envelope are brightly labeled by the antiserum. The frames in b show cells that were streaming toward an
sists primarily of prestalk cells (Jermyn, et al., 1996). The absence of K7-null cells from the front of the slug suggests that K7-null cells have a problem in the localization or differentiation of prestalk cells in the mixed aggregate. This finding also demonstrates the importance of conducting mixing experiments to uncover subtle phenotypic differences in Dictyostelium gene KO cell lines.

There are two possible explanations for the aberrant localization of K7-null cells in the mixed aggregate. The first possibility is that K7-null cells have a defect in motility that makes it more difficult for them to crawl in the aggregate and reach the appropriate position in the body of a slug. However, if the cells have such a defect, it appears to manifest itself only when the mutant cells must compete with wild-type cells for position within the slug. Myosin II mutants display an inability to penetrate aggregating streams when these are composed mostly of wild-type cells. This results in their exclusion from fruiting bodies and is thought to be caused by impaired motility and a weakened cell cortex (Knecht and Shelden, 1995; Xu et al., 1996). To address the possibility that the K7-null cells have a problem in motility within the wild-type slug, it will be informative to trace the paths of labeled cells within the slug by time-lapse confocal microscopy as was done for the myosin II mutants (Knecht and Shelden, 1995; Xu et al., 1996).

The other possible explanation for the K7-null phenotype is that these cells do not differentiate properly into prestalk cells in the mixed aggregate. However, K7-null cells in pure culture seem to form prestalk and prespore cells in normal proportions, so if a defect in cell determination exists, it must only be manifested in the mixed population. To determine whether K7-null cells simply do not become prestalk cells in the mixed aggregate, the expression of prestalk-specific genes can be tested using reporter gene constructs (Bichler and Weijer, 1994; Jermyn, et al., 1996). In addition, experiments should be conducted to determine whether isolated K7-null cells have a defect in cell fate determination (Gomer and Firtel, 1987).

Immunolocalization results suggest that K7 is associated with a membranous perinuclear structure, which could be the ER–nuclear envelope complex of membranes. This type of tight perinuclear envelope localization with little associated staining of vesicles, the Golgi, or the ER is intriguing and has not been reported previously for a kinesin motor. Immunoelectron microscopy should clarify the subcellular localization of K7 and its relation to the nuclear envelope.
This information will help formulate a better model for the function of this motor protein.

In this study, we have also identified five KRPs other than K7. Based on the homology of these sequences to other motor proteins, Dictyostelium appears to have representatives of several KRP subfamilies, as well as unique kinesins. With the availability of these probes, it will be possible to characterize a broad range of kinesin-based functions in Dictyostelium.

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REFERENCES


A Developmentally Regulated Kinesin


