Identification of oda6 as a Chlamydomonas Dynein Mutant by Rescue with the Wild-type Gene

David R. Mitchell and Yong Kang

Department of Anatomy and Cell Biology, State University of New York Health Science Center, Syracuse, New York 13210

Abstract. We find that two Chlamydomonas outer arm dynein assembly loci, oda6 and oda9, are located on the left arm of linkage group XII, in the vicinity of the previously mapped locus for a 70,000 Mr dynein intermediate chain protein. Restriction fragment length polymorphism mapping indicates that this dynein gene is very closely linked to the oda6 locus. A cDNA clone encoding the 70,000 Mr protein was isolated, sequenced, and used to select genomic clones spanning the corresponding locus from both wild-type and oda6 libraries. When wild-type clones were introduced into cells containing an oda6 allele, the mutant phenotype was rescued, while no rescue was observed after transformation with oda6 clones. Genetic analysis further revealed that newly introduced gene copies were responsible for the rescued phenotype and thus confirms that ODA6 encodes the 70,000 Mr dynein intermediate chain protein. The inability of oda6 mutants to assemble any major outer arm dynein subunits shows that this protein is essential for assembly of stable outer dynein arms. This is the first use of transformation with a wild-type gene to identify the product of a Chlamydomonas mutant.

Materials and Methods

Chlamydomonas Strains and Genetics

Chlamydomonas stocks were maintained by standard methods (Harris, 1988). The outer row of dynein arms in Chlamydomonas is composed of three ∼400-kD heavy chains (alpha, beta, and gamma), two intermediate chains (80 and 70 kD), and at least eight light chains (10–30 kD) (Pfister et al., 1982; Piperno and Luck, 1979). A wide variety of mutations affecting flagellar structure and function have been isolated in this organism, including mutations at 12 loci that prevent formation of functional outer row dynein arms (Mitchell and Rosenbaum, 1985; Kamiya, 1988). All but one of these loci were identified on the basis of alleles that block the transport of dynein subunits into the flagellar compartment and/or prevent their assembly onto flagellar doublet microtubules, so that all three outer arm heavy chain subunits are missing from gels of flagellar proteins (outer arm dynein assembly, or oda mutants). The one exception, sup-pf1, was first identified as a suppressor of radial spoke and central pair defects in which the beta dynein chain has an altered electrophoretic mobility (Huang et al., 1982). Restriction fragment length polymorphism (RFLP) analysis has confirmed that sup-pf1 is linked to the beta dynein gene (Ranum et al., 1988) and genetic analysis shows that sup-pf1 is allelic to assembly mutant oda4 (Luck and Piperno, 1989). The other eleven loci, whose gene products have not yet been identified, could potentially encode either additional key structural components of the complex or factors involved in dynein synthesis and/or assembly. Here we use genetic mapping and complementation with a genomic clone to identify one of these mutations, oda6, as a defect in the 70-kD intermediate chain gene.

1. Abbreviation used in this paper: RFLP, restriction fragment length polymorphism.
1989) on minimal medium I of Sager and Granick (1955). Strains SID2, glnl, and corl were obtained from Dr. P. A. LeFeuvre (University of Minnesota), strain 13% was obtained from Dr. J. L. Rosenbaum (Yale University), and strains oda6-95, oda9-141, and idal-98 were generously provided by Dr. R. Kamiya (Nagoya University). Double mutant strain oda6-95, idal-98 (designated as oda6, idal throughout this publication) was constructed in our laboratory. Genetic crosses were performed by standard procedures, except that zygotes were germinated on medium solidified with 1.5% Gel Gro (ICN Biochemicals, Inc., Irvine, CA) rather than agar, and tetrad were dissected with the aid of a micromanipulator (Allen Benignini Inc., Tempe, AZ). Map distances were calculated as \((NPD + 0.5T)/(PD + NPD + T)\) (Gowans, 1965).

**RFLP Mapping**

For RFLP mapping, oda mutants were crossed to wild-type strain SID2 (Gross et al., 1988). Tetrad were dissected, and the products were scored by light microscopic observation as either fast swimming (wild type) or slow swimming (oda). DNA was isolated by the method of Weeks et al., 1986, digested with SalI, separated on agarose gels, and blotted to Nytran (Schleicher & Schuell) following standard methods (Sambrook et al., 1989). Blots were probed with cDNA clone c70-16 (see below) labeled using a random prime kit from Boehringer Mannheim Biochemicals (Indianapolis, IN) and 32P-dCTP. For most of the tetrad used in RFLP linkage studies, to minimize the required number of DNA samples, only DNA from the two slow-swimming or the two fast-swimming products were used for Southern blotting.

**Selection of cDNA and Genomic Clones**

cDNA clones were selected from a lambda gtl cDNA library (provided by Dr. S. Adair, Tufts University) constructed from wild-type strain NO-gamete mRNA, by hybridization with genomic clone Dal (Williams et al., 1986). To obtain large genomic clones, the insert from lambda gtl cDNA clone L70-16 was subcloned into pBluescript KS+ and used to screen an EMBL4 genomic library (provided by J. Rosenbaum, Yale University) prepared from Sau 3A-digested DNA isolated from strain 137c-7. A single EMBL4 clone, E70B2, was used for further study.

To clone the oda6-95 ICT0 gene, a library of reduced complexity was constructed from oda6-95 DNA. DNA was digested with SacI, EcoRI, BamHI, and HindIII and run on a 1% agarose gel, and fragments of ~6.2 kb were electroeluted, ethanol precipitated, and cloned into the SacI site of pBluescript KS (–). This library was transformed into E. coli DH5a MCR (Gibco-BRL Laboratories, Grand Island, NY), and colony lifts were probed with cDNA insert c70-16. Several positives were selected and analyzed by restriction mapping, and clone pBoda6-c7 was chosen for further use.

**Sequence Analysis**

Overlapping deletions of insert c70-16 in pBluescript KS+ (Strategene Cloning Systems, La Jolla, CA) were generated in both insert orientations by high fidelity PCR amplification using an Erase-a-base kit from Promega Biotec (Madison, WI). Single-stranded sequencing templates were prepared from each sample by superinfection with R408 helper phage (Kidd et al., 1986) and sequenced with an Sequenase kit from United States Biochemical Corp. (Cleveland, OH). Sequences were assembled and analyzed using the GCG sequence analysis software programs, and the predicted amino acid sequence was compared with sequences from the Genbank (release 64.0) and National Biomedical Research Foundation (release 250) databases.

**Transformation**

Strains oda6, idal and oda9, idal were used as recipients for transformation. Vegetative cells were grown to \(1 \times 10^6\) cells/ml in acetate-supplemented medium (medium II of Sager and Granick, 1953) and harvested by centrifugation, and cell walls were removed by two successive 30-min incubations in filter-sterilized gametic cell wall lysozyme (Harris, 1989). Spheroplasts were prepared from Sau 3A-digested DNA isolated from strain 137c+. A single DNA clones were selected from a lambda gt11 cDNA library (provided by J. Rosenbaum, Yale University) and each of the two fast-swimming (oda) and slow-swimming (oda) products were used for Southern blotting.

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For initial experiments reported in Table II, 2 \(\times 10^6\) cells were used in each experiment, and cells were diluted with medium I and aliquoted into 60 tubes, each containing 1 \(\times 10^6\) cells and 4 ml medium I. After 1 wk under constant illumination, tubes were examined daily for the appearance of motile cells. For further analysis, single motile clones were selected from six different tubes.

For later experiments comparing wild-type clone pGTOS and oda6-95 clone pBoda6-c7, the number of cells per transformation was reduced to 5 \(\times 10^6\) and cells were distributed among 5 tubes rather than 60. Other aspects of the transformation and screening were not altered.

**Frequency Determination**

Beat frequency determinations were made on individual free-swimming cells suspended in a 20-µl sample between a glass slide and a cover slip supported along two edges with petroleum jelly. Cells were observed under dark-field illumination on a Zeiss Axioskop microscope, with stroboscopic illumination from a xenon flash tube powered by a Chadwick-Helmuth Strobebox model 8440 frequency generator and power supply. Beat frequencies were determined by recording the strobe frequency required to create a "still" waveform image. Results were averaged from measurements on 15 cells per sample.

**Results**

**Genetic Mapping**

Genomic clones Dal and Da2, which encode part of the 70,000 M, outer arm dynein intermediate chain, were previously selected by screening a lambda gtl expression library with an mAb (Williams et al., 1986). One of these clones, Dal, was recently used to genetically map this intermediate chain gene to linkage group XII by RFLP analysis (Ranum et al., 1988). Recombination frequencies between Dal and each of the two Chlamydomonas beta tubulin genes, as well as between Dal and the centromere, placed the 70,000 M, intermediate chain (ICT0) gene ~22 map units from the centromere on the left arm of XII. While no motility mutant loci have been precisely mapped to this region, Kamiya (1988) determined that two oda loci, oda6 and oda9, are linked to a centromere marker on linkage group XII (pf27). To determine whether either of these oda mutations

![Diagram](https://via.placeholder.com/150)

Table I. Genetic Mapping of oda6 and oda9 on L.G. XII

<table>
<thead>
<tr>
<th>Experiment</th>
<th>Cross</th>
<th>Loci</th>
<th>P/N/T</th>
<th>Distance</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>oda9 x gln1</td>
<td>24:0:8</td>
<td>12.5</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>idal x corl</td>
<td>15:1:24</td>
<td>32.5</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>idal x oda6</td>
<td>76:0:52</td>
<td>20.3</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>idal x oda9</td>
<td>19:0:74</td>
<td>39.8</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>oda9, gln1 x cor1</td>
<td>16:0:16</td>
<td>25.0</td>
<td></td>
</tr>
</tbody>
</table>

Genetic map distances of several loci on linkage group XII calculated from five crosses were used to construct the map shown at top. The dashed line indicates uncertainty in the location of ICT0 determined by Ranum et al., 1988. Data from each cross is summarized in the table as tetrad ratios, where P = parental ditype, N = nonparental ditype, and T = tetratype.

1. Data from Ranum et al., 1988.
3. Distance calculated as \((n + 0.5T)/(P + N + T) \times 100\).
could be allelic to the IC70 gene, we first mapped them relative to three other linkage group XII markers, gln1, cor1, and idal. As shown in Table I, both oda6 and oda9 map on XII left, with oda9 proximal to oda6. The data of Ranum et al. (1988) place the IC70 locus in the region of both assembly loci.

Further tests of linkage were performed by crossing oda6 and oda9 strains with wild-type strain SID2, which displays many RFLPs with respect to the lab strain, 137c, that is used as the background for most mutational analysis. Meiotic products (tetrads) were dissected and scored for motility phenotype (both oda6 and oda9 cells swim at approximately half of the wild-type speed) and for inheritance of a SalI restriction site polymorphism at the IC70 locus. Lanes 1 and 2 of Fig. 1 show the pattern of hybridization of IC70 cDNA clone pBC70-16 (see below) to DNA isolated from each parental strain and digested with SalI, and demonstrate the presence of a clear polymorphism detectable with this enzyme. The RFLP patterns of progeny from an oda6 × SID2 tetrad are shown in lanes 3–6. Motility phenotypes of these progeny, indicated at the bottom of each lane, show that in this tetrad the IC70 RFLP pattern has not recombined with the oda6 mutation. Southern blots from an additional 13 tetrads revealed no recombinants between IC70 and oda6, indicating linkage to within three map units, while similar blots from an oda9 cross produced two recombinants among four tetrads (data not shown).

Selection of IC70 cDNA Clones and Sequence Analysis

To determine whether oda6 could be a mutation in the IC70 gene, we wished to test the ability of a full-length IC70 clone to complement the oda6 mutation by transformation. Since preliminary evidence suggested that our available genomic IC70 clone, Dal, represented only a partial gene fragment, we first selected cDNA clones that could be used to map the complete transcription unit. An amplified lambda gt1 cDNA library was screened with Dal, and five positives were selected. Lc70-13 contained a 2.1-kb insert, while Lc70-16 and four other apparently identical clones contained 2.6-kb inserts (Fig. 2A). Since the Lc70-16 insert hybridizes to a single 2.6-kb mRNA (Fig. 2B), we judged it to be close to full length. This insert was subcloned in both orientations into pBluescript KS+, nested deletions were generated by the Henikoff exonuclease III procedure (Henikoff, 1987), and both strands were sequenced.

Sequence analysis of c70-16 revealed a 2,603-bp insert containing a single large open reading frame of 1,701 nt, beginning with an ATG at nt 313 and ending with a TAA stop codon at nt 2,014 (Fig. 3). Near the 3' end of the insert is a perfect copy of the putative Chlamydomonas polyadenylation signal, TGTAAT, followed by 14 nt and a short poly A tract. While there are several ATG codons near the 5' end of the insert, only the ATG at position 313 is followed by a long open reading frame, and codon usage for this ORF adheres to the codon bias typical of both flagellar (Williams et al., 1989) and nonflagellar (Goldschmidt-Clermont and Rahire, 1986) Chlamydomonas genes, with only 2.8% of the codons containing A residues in the third position. Furthermore, the predicted amino acid sequence between residues 332 and 350 is identical to the directly determined sequence of a cyanogen bromide fragment of the 70,000 M, dynein protein (personal communication, S. King and G. Witman, Worcester Foundation). A search of the NBRF and EMBL databases revealed no obvious homologies with previously reported sequences.
The predicted amino acid sequence is shown beginning at the presumed translational start at nt 313. The 110-nt open reading frame terminates with TAA and is followed by a 590 nt 3' untranslated region. A single stop codon of the putative myodona-linked adenylon s, TGTAA, is near the 3' end and has been underlined. These sequence data are available from EMBL/GenBank/DDBJ under accession number X55382.

The predicted 567 a.a. sequence encodes a 63,400 Mr protein with a pI of 5.2, while the native IC70 protein has an Mr of 68,000-73,000 and a pI of ~5.9, as estimated from two-dimensional gel electrophoresis of flagellar protein fractions (Williams et al., 1986; Piperno and Luck, 1979). We previously demonstrated that in vitro translation in a reticulocyte lysate of mRNA hybrid selected with IC70 clone Dal generates a protein of identical charge and size to the endogenous flagellar protein, not the smaller and more acidic gene product predicted from the eDNA sequence (Williams et al., 1986). While additional sequence analysis of independently isolated eDNA or genomic clones will be required to rule out a possible eDNA cloning artifact, our data suggest that the IC70 protein may run anomalously on two-dimensional gels. Similar discrepancies between predicted and observed gel mobility characteristics have been reported for a Chlamydomonas flagellar radial spoke protein (Williams et al., 1989).

Selection of Wild-type IC70 Genomic Clones

An EMBL4 genomic library was screened with c70-16, and several overlapping or identical inserts were selected. EMBL4 clone E70B2 was selected for further use because restriction maps indicated that it extends for several kilobases both 5' and 3' of the transcription unit (Fig. 4). A 6.2-kb Sac-I fragment that also spans the IC70 coding region was subcloned from E70B2 into the SacI site of plasmid vector pGEM2 to create pG70S. Both E70B2 and pG70S were used in the transformation experiments described below.

To determine gene copy number, Southern blots of DNA from EMBL4 clone d0-16. The predicted amino acid sequence is shown beginning at the presumed translational start at nt 313. The 110-nt open reading frame terminates with TAA and is followed by a 590 nt 3' untranslated region. A single stop codon of the putative myodona-linked adenylon s, TGTAA, is near the 3' end and has been underlined. These sequence data are available from EMBL/GenBank/DDBJ under accession number X55382.
isolated from wild-type cells were probed with cDNA clone c70-16. As shown in Fig. 5, this clone hybridized to a single band in five of six digests. Two bands appear only after c70-16. As shown in Fig. 5, this clone hybridized to a single band in five of six digests. Two bands appear only after digestion by SalI, which is consistent with the location of a band in five of six digests. Two bands appear only after digestion by SalI, which is consistent with the location of a SalI site within the clone used as hybridization probe. These results demonstrate that the IC70 locus previously mapped to a SalI site within the clone used as hybridization probe. These results demonstrate that the IC70 locus previously mapped to a SalI site within the clone used as hybridization probe.

Transformation

Double mutant strains containing an outer dynein arm assembly mutation (either oda6 or oda9) and an inner dynein arm assembly mutation (idal) were constructed as backgrounds for selecting transformants. Strains containing only idal are easily distinguished from strains containing only oda mutations on the basis of flagellar beat frequency, which is wild type (∼60 Hz) in idal, but reduced to ∼24 Hz in oda strains (Brokaw and Kamiya, 1987). While each mutation alone causes a reduction in swimming speed to ∼50% of the wild-type value, the two mutations in combination result in complete flagellar paralysis (Kamiya et al., 1989). Complementation or reversion of the oda6 mutation should therefore rescue paralyzed double mutants back to a motile phenotype characteristic of cells containing idal alone. To test this screen, double mutants were suspended in liquid medium either with or without prior exposure to a mutagenizing dose of ultraviolet irradiation. The results indicated that motile revertants could be selected at an efficiency of 10⁻⁶ by this screen after UV mutagenesis, while spontaneous reversion rates of both the oda6-95 and idal-98 alleles were <10⁻⁸ (data not shown).

For transformation, double mutant strains oda6,idal and oda9,idal were treated with gametic autolysis to remove cell walls, and spheroplasts were transformed by the glass bead method of Kindle (1990). After transformation, cells were distributed into 60 tubes, each containing ∼3 × 10⁶ cells in 4 ml of minimal medium. Tubes were visually examined after a 2-wk incubation, and single clones were isolated from tubes containing motile cells. As summarized in Table II, transformation of oda6,idal with either the complete 17-kb lambda clone E70B2 or 6-kb subclone pG70S resulted in the appearance of motile cells, while no motile cells were recovered after transformation of oda9,idal, or after transformation of oda6,idal with vector alone. Assuming the distribution of motile cells among the 60 tubes follows a Poisson distribution, where P₀ (the probability that a tube contains 0 swimmers) is related to u (the average number of swimmers per tube) by the formula P₀ = e⁻ᵘ, then in the experiment of Table II, E70B2 generated 60 swimmers (if u = 1, P₀ × 60 tubes = 22 tubes with no swimmers), while pG70S generated a minimum of 300 swimmers (if u = 5, P₀ × 60 tubes = 0.4 tubes with no swimmers).

In every case tested, motile clones displayed the slow swimming speed and near wild-type beat frequency typical of the idal phenotype, consistent with complementation, reversion, or suppression of oda6-95. Swimming phenotype was initially scored by visual discrimination of “vibrational” swimming, indicative of low flagellar beat frequency, vs. “smooth” swimming, associated with a higher beat frequency. Direct measurement then confirmed that the beat frequency of a randomly selected transformant (51 ± 3 Hz, n = 15) was not statistically different from that of idal-98 (52 ± 3 Hz) or of four other transformants. In contrast, the beat frequency of an oda6-95 strain under the same conditions was 28 ± 2 Hz, while that of wild-type strain 137c was 58 ± 3 Hz.

Five putative pG70S transformants were tested for the presence of extra gene copies by Southern blot analysis. Since XbaI cuts once within the fragment used as probe, Southern blots of XbaI + EcoRI digests should reveal two bands for every gene copy. As shown in Fig. 6, the endogenous gene (lane WT) is cut by EcoRI + XbaI into fragments of ∼25 kb (A) and 5.4 kb (B), while all five transformants

Table II. Transformation with IC70 Clones

<table>
<thead>
<tr>
<th>DNA (insert)</th>
<th>Recipient strain</th>
<th>Tubes with swimmers (#080/60 tubes)</th>
</tr>
</thead>
<tbody>
<tr>
<td>pGEM (vector)</td>
<td>oda6, idal</td>
<td>0</td>
</tr>
<tr>
<td>E70B2 (17 kb)</td>
<td>oda6, idal</td>
<td>38</td>
</tr>
<tr>
<td>pG70S (6 kb)</td>
<td>oda6, idal</td>
<td>60</td>
</tr>
<tr>
<td>pG70S (6 kb)</td>
<td>oda9, idal</td>
<td>0</td>
</tr>
</tbody>
</table>

The indicated recipient strains were transformed as described in Materials and Methods with either 12 μg (E70B2) or 8 μg (pGEM, pG70S) of DNA.
(lanes 1–5) contain additional IC70-specific sequences. Integration of intact pG70S should result in new bands of 4.3 kb (C) and 1.9 (D); other bands presumably result from rearrangements or from integration of fragments of pG70S. The observed patterns suggest the presence of two to four additional IC70 gene copies in each transformant examined.

Further evidence that the introduced gene copies can complement oda6 was obtained from genetic analysis of transformants. Since transformation of *Chlamydomonas* by the presently available methods results primarily or exclusively in integration by nonhomologous rather than site-specific recombination (Kindle et al., 1989; Diener et al., 1990), introduced gene copies should be integrated at random locations and should segregate away from the original oda6-95 mutation during meiosis. If introduced genes are complementing the original mutation, then some meiotic products will display the mutant phenotype. If an intragenic reversion has eliminated the original mutation, it will not be uncovered in a backcross, while if an extragenic suppressor has been generated, it will segregate from the original mutation but will not cosegregate with introduced gene copies. Six pG70S transformants including the five analyzed in Fig. 6 were crossed with an *ODA6, ida1-98* strain, and in every case paralyzed progeny were obtained, indicating that the original oda6-95 allele was still present in the transformed cells (Table III). Furthermore, in products from a cross of transformant #3 with an oda6-95, *Ida1* strain, the introduced pG70S sequences cosegregate with the *ODA4*+ phenotype (Fig. 7), confirming that pG70S is complementing the oda6-95 mutation.

**Table III. Backcross of pG70S Transformants**

<table>
<thead>
<tr>
<th>Transformant</th>
<th>4:0</th>
<th>3:1</th>
<th>2:2</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>5</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>3</td>
<td>0</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>4</td>
<td>0</td>
<td>5</td>
<td>0</td>
</tr>
<tr>
<td>5</td>
<td>2</td>
<td>6</td>
<td>0</td>
</tr>
<tr>
<td>6</td>
<td>2</td>
<td>5</td>
<td>1</td>
</tr>
</tbody>
</table>

Six putative transformants (oda6, *ida1*, pG70-n) were crossed with ida1, and tetrad products of each cross were scored as motile or paralyzed. The appearance of paralyzed products among the progeny of all six crosses indicates that motility of putative transformants is not due to intragenic reversion of the oda6 mutation.

**Transformation with an oda6 IC70 Clone**

When wild-type and oda6-95 alleles of the IC70 locus were compared by probing genomic Southern blots with pG70S, no differences in restriction fragment size were observed (not shown). To eliminate the possibility that oda6 was closely linked but not allelic to IC70, and was merely complemented by overexpression of the nearby IC70 gene, we cloned the IC70 gene from oda6 cells and tested its ability to complement the mutation. If oda6 were not an IC70 mutation, overexpression of the IC70 allele cloned from oda6 cells should also rescue the mutation. A plasmid mini-library of ~6.2 kb SacI fragments was prepared from DNA isolated from an oda6-95 strain, and clone pBoda6-c7 was selected. No differences were observed in the location of restriction sites in the pBoda6-c7 and pG70S inserts when 10 enzymes known to cut the wild-type gene were used.

In two separate experiments, 5 × 10⁷ *oda6, ida1* cells were transformed with 5 μg of either pG70S or pBoda6-c7 and distributed into five tubes. Each time, swimming cells were observed in all five tubes containing cells transformed with pG70S after 5–7 d, while no swimming cells were observed in tubes containing cells transformed with pBoda6-c7.

**Discussion**

Because flagellar motility depends on the coordinate action of a large number of components, it has been an obvious target of mutational analysis. Flagellar mutations have been described that selectively disrupt assembly of part or all of the central pair complex, radial spokes, inner dynein arms, outer dynein arms, basal bodies, and even structures within the doublet microtubules (reviewed in Dutcher and Lux, 1989). Primarily by electrophoretic analysis of flagellar proteins from intragenic pseudorevertants and temporary dikaryons, the gene products of many of these mutations have been identified (Luck et al., 1977), but for reasons that are not clearly understood, these methods have not been successfully applied to mutations that disrupt outer arm dynein assembly. Gene products have thus far been identified only for oda4, which encodes the beta-heavy chain (Huang et al., 1982; Luck and Piperno, 1989), and for oda6 (this study).
We previously selected and characterized a genomic clone, Dal, encoding part of the *Chlamydomonas* 70-kD dynein intermediate chain (Williams et al., 1986), and this clone was used by Ranum et al. (1988) to map the corresponding genetic locus to a region of the left arm of linkage group XII, ~22 map units distal to the centromere. Mutations affecting outer dynein arms are absent from published maps of the corresponding interval of linkage group XII (and of linkage group XIII, which may not actually be a separate linkage group from XII; Dutcher et al., 1991). We have now mapped two oda loci, *oda6* and *oda9*, to this general region, and have determined their locations relative to the IC70 gene.

RFLP analysis with cDNA clone pBc70-16 and the two *oda* loci on linkage group XIII revealed that IC70 had recombined with *oda9*, but not with *oda6*. Only 14 tetrads from the cross between *oda6* and SID2 were examined, so that linkage better than three map units could not be proven, but since further RFLP analysis could merely reduce the possible interval between IC70 and *oda6* without proving identity, we turned to other methods to extend this analysis. Southern blots indicated that *Chlamydomonas* contains only a single copy of the IC70 gene, eliminating the possibility that *oda6* and IC70 could be closely related genes resulting from a recent gene duplication. To further rule out the remote possibility that *oda6* represented a mutation in a closely-linked, unrelated gene, and not in the IC70 structural gene, we cloned full-length copies of the wild-type and *oda6*-95 IC70 genes and tested their ability to complement the *oda6* mutation by transformation.

A 17-kb genomic fragment spanning the wild-type IC70 locus, as well as a 6-kb SacI subclone of the wild-type gene, were each capable of complementing the *oda6* mutation when introduced into *oda6*,*idal* cells by glass bead-mediated transformation. Transformation events that successfully complemented the *oda6* mutation were selected directly by screening for motile cells, and in all cases examined, motile clones contained one or more newly introduced gene copies. Proof that introduced gene copies were responsible for loss of the mutant phenotype included genetic crosses in which the new wild-type locus cosegregated with the introduced sequences. Additional crosses in which the original mutant locus was uncovered indicated that swimming cells were not spontaneous revertants of *oda6*-95.

Similar transformation experiments with the *oda6*-95 IC70 gene failed to complement the mutation, indicating that the *oda6*-95 mutation resides within the 6.2-kb SacI fragment used in these experiments. Preliminary transformation experiments with chimeric genes suggest that the *oda6*-95 defect is located in the 5'-half of the IC70 transcription unit (Y. Kang and D. Mitchell, unpublished observations), but further molecular analysis will be needed to determine the exact nature of this mutation.

This is, to our knowledge, the first report of a full-length sequence for any dynein protein, so the apparent lack of homology with other sequences is perhaps not unexpected. Cross-reactivity of antibodies against this *Chlamydomonas* protein with outer arm dynein proteins of similar size in sea urchin and trout spermatozoa (King et al., 1990) indicates that at least portions of the primary structure have been conserved across a considerable evolutionary distance. Whether this conservation extends to intermediate chains of flagellar inner row dynein arms or cytoplasmic dyneins is a question of considerable interest that must await further study.

The 70-kD intermediate chain is clearly needed for assembly of other outer arm dynein proteins, since none of the major outer arm dynein subunits is present in flagella isolated from cells containing either of two *oda6* alleles (Kamiya, 1988). The precise reason for lack of outer arm assembly in these mutants has not been determined. If attachment of outer arm complexes to doublet microtubules is directly mediated by the 70-kD intermediate chain, then its absence or alteration would necessarily prevent other proteins from assembling, and would result in an oda phenotype. Models of dynein morphology based both on electron microscopic images of extracted dynein particles and on biochemical dissociation experiments place a heterodimer of the 70- and 80-kD intermediate chains at the “base” of the tripartite *Chlamydomonas* outer arm dynein (King et al., 1990; Mitchell and Rosenbaum, 1986; King and Witman, 1990), but unfortunately, although the data show that intermediate chains are at one end of the extracted dynein complex, the relationship between the morphology of dyneins in vitro and in situ remains poorly understood. Electron microscopic analysis of in situ dyneins both in wild-type cells (Goodenough and Heuser, 1984) and in alpha heavy chain assembly mutant *oda11* (Sakakibara et al., 1991), suggests that globular heavy chain head domains are located closer to the site of force generation on the B subfiber than to the structural attachment site on the A subfiber, but an exact location of intermediate chains within the in situ outer arm remains to be determined.

An alternative hypothesis to explain the assembly phenotype of *oda6* would be that dynein proteins normally associate into complexes in the cytoplasm and attach to outer doublets as complete outer arm units, in which case the functional absence of any member of the complex could prevent...
an entire unit from assembling. This idea is supported by the observation that mutations at all of the other oda loci, with the exception of oda1, result in similar assembly defects. It also provides an explanation for the inability of mutations at some of these loci to complement mutations at other oda loci in temporary diploids (Kamiya, 1988), since the normal proteins contributed by each haploid cell would be sequestered into incomplete complexes and hence be unable to associate into a functional dynein arm. Further knowledge of the gene products of other oda loci, and of the location of dynein polypeptides within the in situ outer arm structure, should begin to resolve these questions.

The ability to use transformation with a wild-type gene to identify the gene product of a Chlamydomonas mutation, as reported here, demonstrates the expanding repertoire of techniques available for molecular and genetic analyses of cellular processes in this organism. It should now be possible to use complementation with a genomic library to clone the remaining oda loci and to determine whether they encode additional known dynein subunits, previously unidentified structural components of the flagellum essential to dynein assembly, or proteins that act in nonstructural roles to aid in the assembly process. Analysis of the functions of individual dynein subunits in force generation should then be amenable to dissection through transformation of null mutants with in vitro-mutagenized genes.

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