Abstract. The Drosophila Glued gene product shares sequence homology with the p150 component of vertebrate dynactin. Dynactin is a multiprotein complex that stimulates cytoplasmic dynein-mediated vesicle motility in vitro. In this report, we present biochemical, cytological, and genetic evidence that demonstrates a functional similarity between the Drosophila Glued complex and vertebrate dynactin. We show that, similar to the vertebrate homologues in dynactin, the Glued polypeptides are components of a 20S complex. Our biochemical studies further reveal differential expression of the Glued polypeptides, all of which copurify as microtubule-associated proteins. In our analysis of the Glued polypeptides encoded by the dominant mutation, Glued1, we identify a truncated polypeptide that fails to assemble into the wild-type 20S complex, but retains the ability to copurify with microtubules. The spatial and temporal distribution of the Glued complex during oogenesis is shown by immunocytochemistry methods to be identical to the pattern previously described for cytoplasmic dynein. Significantly, the pattern of Glued distribution in oogenesis is dependent on dynein function, as well as several other gene products known to be required for proper dynein localization. In genetic complementation studies, we find that certain mutations in the cytoplasmic dynein heavy chain gene Dhc64C act as dominant suppressors or enhancers of the rough eye phenotype of the dominant Glued1 mutation. Furthermore, we show that a mutation that was previously isolated as a suppressor of the Glued1 mutation is an allele of Dhc64C. Together with the observed dependency of Glued localization on dynein function, these genetic interactions demonstrate a functional association between the Drosophila dynein motor and Glued complexes.
ACT5~ and Saccharomyces cerevisiae (Clark and Meyer, 1994; Muhua et al., 1994) have provided molecular and genetic evidence for the existence of dynactin-related subunits in these organisms, as well as their involvement in a common cellular process together with cytoplasmic dynein. In N. crassa, the isolation of suppressors of a mutation in the cot-I locus, which encodes a cAMP-dependent protein kinase (Yarden et al., 1992), identified a number of loci including the genes encoding the cytoplasmic dynein heavy chain gene and/or the Arp-1 homologue ACT5/ACT3, results in defects in mitotic spindle orientation and nuclear migration (Eschel et al., 1993; Li et al., 1993; Clark and Meyer, 1994; Muhua et al., 1994). Despite this evidence for similar phenotypes produced by mutations in the dynein heavy chain gene and genes encoding apparent dynactin-related subunits, the nature of the interaction between dynein and dynactin in vivo remains to be determined.

The Drosophila Glued gene shares significant homology with the gene encoding the p150 subunit of the dynactin complex in rat and chicken (Swaroop et al., 1987; Gill et al., 1991; Holzbaur et al., 1991). The Glued locus was initially identified by the spontaneous mutation, Glued1 (Gl1), which results in a dominant rough eye phenotype in adult flies (Plough and Ives, 1935). In heterozygotes the Gl1 mutation causes a severe disruption in the organization of the retina and in the retinal projections to the optic lobe (Meyerowitz and Kankel, 1978). In homozygous animals the Gl1 mutation is recessive lethal, demonstrating that the Glued gene is also essential for normal development in Drosophila. Screens for revertants of the dominant rough eye phenotype of Gl1 recovered additional recessive lethal mutations at the Glued locus (Harte and Kankel, 1982). In addition to late embryonic and larval lethal phenotypes, several of these new Glued alleles displayed a temperature-sensitive maternal effect, suggesting that Glued is required not only for proper nervous system and eye development, but during the early development of the egg or embryo (Harte and Kankel, 1982). In mosaic analyses using a null mutation of Glued, somatic clones of homozygous Glued mutant tissue were not recovered, suggesting that the Glued gene product has an essential function within the cell. Alternatively, Glued might be required for the successful differentiation and incorporation of particular cell types into developing tissues (Harte and Kankel, 1982).

The Drosophila Glued gene is expressed throughout development (Swaroop et al., 1986), consistent with the genetic data suggesting that Glued has an essential role in Drosophila development (Harte and Kankel, 1982). The molecular characterization of the dominant Gl1 mutation revealed the insertion of a transposon into the Glued coding sequence, resulting in the production of a truncated message that could potentially encode a truncated polypeptide (Swaroop et al., 1985). The dominant nature of the Gl1 mutation suggests that the truncated Glued transcript encodes a protein product that acts as a "poison" to disrupt the function of the wild-type polypeptide.

We previously cloned Dhc64C, a gene encoding a Drosophila cytoplasmic dynein heavy chain (Li et al., 1994), and subsequently isolated recessive lethal mutations in the gene (Gepner, J., M.-g. Li, S. Ludmann, K. Boylan, M. McGrail, and T. S. Hays, manuscript in preparation). In addition to the recessive lethality, we have noticed additional phenotypes in adult flies that are doubly heterozygous for certain combinations of the dynein mutations. These phenotypes include female sterility, male sterility, bristle defects, and a rough eye phenotype similar to that observed in flies that contain the dominant Gl1 mutation (Gepner, J., manuscript in preparation). The Dhc64C mutations provide tools to analyze the regulation and function of the dynein motor. In this report, we use mutations in both the dynein heavy chain and Glued genes to investigate the interaction between the Drosophila cytoplasmic dynein motor and the dynactin-related Glued complex. We identify and characterize the Glued polypeptides as components of a 20S complex similar to vertebrate dynactin and present cell biological and genetic observations that indicate the physical and functional interaction of the Glued and dynein motor complexes.

Materials and Methods

Fly Stocks and Genetic Analyses

The Dhc64C mutations used in this study were isolated by a standard F2 screen for recessive lethal mutations under the deficiency Df(3L)10H (46B10-12; 64C5-9) which removes the chromosomal region containing the dynein gene. The third chromosome deficiency Df(3L)10H was provided by J. Garbe (University of California, Berkeley). For the purposes of the studies described here, the identity of the dynein mutations is established by the rescue of the recessive lethal phenotype of the dynein mutations by an X-linked element insert containing a genomic copy of the Dhc64C transcription unit (designated P(Dhc+); see Table III). Molecular clones containing the intact Dhc64C transcription unit were previously reported (Li et al., 1994). A detailed description of the isolation and phenotypic characterization of the dynein mutations will be reported elsewhere (see also McGrail, M. J., Gepner, M.-g. Li, S. Ludmann, K. Boylan, S. Iyadurai, and T. S. Hays, 1994. Mol. Biol. Cell Abstracts. S:131a).

The stocks Gl1 Sb, Df(3L)Gl1~12, and Su(Gl)102 were provided by Dr. Douglas Kankel, Yale University, and are described in Harte and Kankel (1982). The alleles egalitarian55, Bicaudal-D52, capuccino55, and spin9 were provided by Dr. Trudi Schüpbach, Princeton University, and are described in Manseau and Schtipbach (1989), Suter et al. (1989), and Schüpbach and Weischaus (1991). The second chromosome deficiency Df(2L)TW19, which removes the Bicaudal-D gene, was obtained from Dr. Ruth Steward, Rutgers University, and is described in Steward et al. (1987).

For the analysis of cytoplasmic dynein and Glued localization in the female-sterile combination of dynein alleles Dhc64C6/Dhc64C6, virgin females of the genotype Dhc64C6/TM6B, D Hu were crossed with males of the genotype Dhc64C6/TM6B, D H, and female progeny that were wild type for the dominant marker mutations Dichaete (D, outstretched wings) and Humeral (Hu, extra hairs on the shoulder) were selected. In the analysis of cytoplasmic dynein and Glued localization in the Bicaudal-D52 mutant, Bicaudal-D52/Df(2L)TW19 females were recovered from the cross Bicaudal-D52/Cyo X Df(2L)TW19/Cyo. Markers and other chromosomes used are described in Lindsey and Zimm (1992).

Analysis of the genetic interactions between the Dhc64C alleles and the Gl1 mutation was performed by crossing heterozygous virgin females from the stock Gl1 Sb/TM6B, D H with heterozygous males of the following genotypes: Df(3L)10H/TM6B, D Huc; Dhc64C~6/TM6B, D Huc; Dhc64C~4/TM6B, D Huc; Dhc64C~10/TM6B, D Huc; Dhc64C~16/TM6B, D Huc. In the progeny, flies

1. Abbreviation used in this paper: Gl1, Glued1.
heterozygous for the Glu mutation and the dynein mutation were identified by the presence of adults which show the dominant bristle phenotype caused by the Sb (Subbrel, short blunt bristles) mutation, but were wild type for the dominant wing and bristle phenotypes of the Dichaete (D) and Humeral (Hu) mutations. To examine the effect of an additional copy of the wild-type Dhc64C gene in flies heterozygous for the Glu mutation and the dynein alleles Dhc64C/A or Dhc64C/C, an X chromosome bearing the wild-type Dhc64C transgene was separately crossed into the Dhc64C/A and Dhc64C/C backgrounds and stocked. Males of the genotype P(Dhc+)Y; Dhc64C+/TM6B, D Hu and P(Dhc+)Y; Dhc64C+/TM6B, D Hu were crossed to virgin Glu Sb/TM6B, D Hu females. All of the female progeny from this cross carry one X chromosome bearing the Dhc64C transgene P(Dhc+).

Complementation analyses between the Su(GF)102 mutation and the Dhc64C mutations were performed by crossing heterozygous Su(GF)102/TM6B, D Hu virgin females with males heterozygous for the deficiency Df(3L)1OH or the appropriate Dhc64C allele, and TM6B, D Hu. The critical class was scored by the absence of the TM6B, D Hu third chromosome balancer dominant marker mutations Dichaete (D) and Humeral (Hu) in adult progeny.

To test the ability of the dyeine transgene to rescue the lethality of Su(GF)102 in combination with Df(3L)1OH and the Dhc64C alleles Dhc64C/A, Dhc64C/C, and Dhc64C/C, the following crosses were performed: heterozygous w, P(Dhc+ w)Y; Su(GF)102/TM6B males were crossed with heterozygous, virgin w/w; Df(3L)1OH/TM6B, w/w; Dhc64C/C/ TM6B, w/w; Dhc64C/C/TM6B or w/w; Dhc64C/C/TM6B females. Rescue of the critical class (Su(GF)102/mutant) was scored by the presence of w- Dichaete "Humeral" adults in the progeny from each cross. Because the wild-type dyeine transgene is carried on the X chromosome and is contributed by the male, only female progeny inherit the wild-type dyeine transgene and should be rescued. The absence of male progeny that carry the dyeine mutations but lack the paternally derived X-linked wild-type dyeine transgene demonstrates that the rescue of lethality in the female progeny is due to the presence of the dyeine transgene.

RNA Blot Analyses
Total RNA was isolated from ovaries and testes, staged collections of embryos, larvae, pupae, and heads, as described previously (Li et al., 1994). 25 µg total RNA was run on a 7.5% agarose-formaldehyde denaturing gel, and blotting, hybridization, and washing conditions were as described previously (Li et al., 1994). A 1.8-kb BamHI fragment from the Glued cDNA (Swaroop et al., 1987), provided by Dr. Alan Garen, Yale University, was used to prepare a DNA probe labeled with [32P]dATP using random hexamer primers (Pharmacia LKB Biotechnology Inc., Piscataway, NJ). A probe derived from the RP49 gene (Vaslet et al., 1980) was used to monitor loading and to verify integrity of the RNA.

Antibody Production and Purification
An anti-Glu rat polyclonal serum was prepared using a bacterially expressed Glued fusion protein. A 1.8-kb BamHI fragment of the Glued cDNA, provided by Dr. Alan Garen, which encodes the ~600 COOH-terminal residues of the Glued open reading frame (Swaroop et al., 1987), was cloned in frame into the expression vector pGEX1 (Smith and Johnson, 1988) and expressed in the bacterial strain HB101. Inclusion bodies containing the glutathione S-transferase-Glued fusion protein were prepared as described (Li et al., 1994) and fractionated by SDS-PAGE. Gel slices corresponding to the glutathione-S-transferase-Glued fusion protein were excised and used to elicit a polyclonal serum in rat according to the supplier’s instructions. The affinity-purified antibodies were stored in PBS containing 1 mg/ml BSA.

Microtubule-associated Protein Preparations
Ovaries from well-fed 3-d-old wild-type Oregon R females and heterozygous Glu/TM6B females were dissected in EBR buffer (130 mM NaCl, 5 mM KCl, 2 mM CaCl2, 10 mM Hepes, pH 6.9), placed on ice until 100 µl of ovaries were obtained, quick frozen in liquid nitrogen, and stored at −80°C until use. Heads and embryos were collected from the wild-type Oregon R and the Glu/TM6B stocks, quick frozen in liquid nitrogen, and stored at −80°C until use. Microtubule-associated proteins from each tissue were prepared as described previously (Hays et al., 1994). Briefly, ~1 ml packed ovaries, 6 ml packed heads, or 15 ml packed embryos, were rinsed three times in PMEG buffer (100 mM Pipes, pH 6.9, 5 mM MgOAc, 5 mM EGTA, 0.1 mM EDTA, 0.5 mM DTT, 0.9 M glycerol) plus protease inhibitors (10 µg/ml aprotinin, 1 µg/ml leupeptin, 1 µg/ml pepstatin, 0.1 µg/ml each of soybean trypsin inhibitor, n-tosyl L-arginine methyl ester, and benzamidine). Tissues were homogenized on ice in a glass homogenizer in 1.5 vols PMEG plus protease inhibitors. The homogenate was spun at 125,000 g for 40 min at 4°C, and the supernatant was further fractionated by centrifugation through a 10% (w/v) sucrose cushion into 10% (w/v) sucrose and 0.1% (w/v) PEG 4000. The 10% (w/v) sucrose fraction was further fractionated by centrifugation through a 40% (w/v) sucrose cushion to load the insoluble pellet at the bottom of the tube. All subsequent steps were carried out at 4°C. Microtubules were assembled in the high-speed supernatant by the addition of GTP to 1.0 mM and taxol to 20 µM, plus 20 µM cytochalasin B and D to inhibit assembly of filamentous actin. After 15 min incubation with gentle rocking, endogenous ATP was depleted from the extract by the addition of hexokinase and glucose to final concentrations of 10 mM and 100 mM, respectively, and the extract incubated further for 45 min. The extract was undilayed with a 1/4 vol 15% sucrose cushion and centrifuged at 37,000 g for 30 min in a rotor (SW50.1; Beckman Instruments, Inc., Fullerton, CA) to pellet microtubules and microtubule-associated proteins. The microtubule pellet was washed once by resuspension in PMEG plus taxol and recentrifuged. The microtubule pellet was extracted with PMEG containing 10 mM Mg-ATP and 20 µM taxol, and recentrifuged at 37,000 g for 15 min in an SW50.1 rotor plus adapters for 5 × 41 mm open-topped ultracentrifuge tubes (Beckman Instruments, Inc.).

Sucrose Density Gradient Centrifugation
1 mg total protein of a high-speed extract (125,000 g) from ovary homogenates, and 2 mg total protein of a high-speed extract from embryo and head homogenates, were sedimented through 11.5 ml 5-20% sucrose gradients prepared in PMEG buffer plus protease inhibitors as described previously (Hays et al., 1994). The gradients were spun at 4°C in a rotor (SW40; Beckman Instruments, Inc.) for 16 h at 230,000 g, and then collected into 0.5-ml fractions. The sedimentation standards thyroglobulin (19S), catalase (11S), and cytochrome (2S) (Sigma Chemical Co., St. Louis, MO) were run in parallel on a separate gradient.

Immunoblotting
SDS-PAGE and immunoblotting were carried out as described by Laemmli (1970) and Towbin et al. (1979). Proteins were electrophoresed on 0.75 mm, 7.5% polyacrylamide slab gels prepared with a 1:100 ratio of acrylamide/bis-acrylamide, and proteins were stained with Coomassie brilliant blue or electroblotted to PVDF membrane (Millipore Corp., Burlington, MA). Blots were probed with the affinity-purified anti-Glu antibody diluted 1:100, or the affinity-purified anti-dynein heavy chain antibody PEPI (Li et al., 1994) diluted 1:500, in PBS/0.05% Tween-20 containing 0.2% 1-Block (Tropix, Bedford, MA). Alkaline phosphatase-conjugated secondary antibodies were diluted in the same. Blots were developed with NBT and BCIP (Sigma Chemical Co.) in alkaline phosphatase buffer (100 mM NaCl, 5 mM MgCl2, 100 mM Tris, pH 9.5), or with a nonradioactive chemiluminescence detection system (Tropix) according to the supplier’s instructions. Images of gels were captured on an IRIS Indigo Video board installed on a Silicon Graphics R3000 Indigo workstation (Silicon Graphics Computer Systems, Mountain View, CA). Images of blots were obtained from blots and x-ray films scanned into a Macintosh Power PC 8100 (Apple Computer Corp., Cupertino, CA) with a flat bed scanner (ScanJet IIC; Hewlett Packard, Corvalis, OR) using Adobe Photoshop 3.0 software (Adobe System Inc., Mountain View, CA). Hardcopy image prints were produced on a dye sublimation printer (Phaser IISDX; Tektronix, Inc., Beaverton, OR).

Immunolocalization
Ovaries were dissected, fixed, and prepared for immunocytochemistry as described previously (Li et al., 1994). Briefly, ovaries were dissected from 2-3-d-old females in EBR and fixed for 5 min in 100 µl devitellinizing buffer/600 µl heptane using the method of Cooley et al. (1992). Devitellinizing buffer = 1 vol buffer B1/1 vol 36% formaldehyde/4 vol H2O. Buffer B contains 100 mM KH2PO4/NaHPO4, pH 6.8, 450 mM KCl, 150 mM NaCl, and 20 mM MgCl2/6H2O. After fixation, ovaries were rinsed three times in PBS, rinsed three times in PBS 0.1% Triton-X-100 (PBT), and washed for

McGrail et al. Glued and Cytoplasmic Dynein Interaction in Drosophila 413
1–2 h in PBT with gentle rocking. The ovarioles were then teased apart, washed for 1–2 h on a rotating wheel (Cole-Farmer Instrument Co., Chicago, IL), and blocked in PBT containing 1% BSA for 1–2 h at room temperature. The ovarioles were double labeled with the affinity-purified rabbit anti-dynein antibody PEP1 (Li et al., 1994) diluted 1:5 or 1:50, and the affinity-purified rat anti-Glued antibody diluted 1:5. The anti-dynein and anti-Glued antibodies were detected with anti-rabbit FITC-conjugated (Boehringer Mannheim Biochemicals, Indianapolis, IN) and anti-rat Texas red-conjugated (Jackson Immunoresearch Laboratories, West Grove, PA) secondary antibodies, respectively. Antibody incubations were performed overnight at 4°C. The secondary antibodies were used at a final dilution of 1:100 after preabsorbing against fixed embryos at a dilution of 1:10. All antibodies were diluted in PBS/0.1% Triton X-100 containing 1% BSA. Ovarioles were mounted in a solution of PBS/90% glycerol containing 1 mg/ml p-phenylenediamine (Sigma Chem. Co.), and examined on a diaphot (Nikon Inc. Instrument Group, Melville, NY) microscope with a confocal imaging system (MRC-600; Bio-Rad Laboratories, Hercules, CA), using a 60×1.4 planapochromat lens.

**SEM Analysis**

Drosophila heads were dehydrated in an ethanol series as described (Carthew and Rubin, 1990) and prepared for scanning electron microscopy by critical point drying and coating with gold-palladium. Images were recorded on film (type 55; Polaroid Corp., Technical Imaging Products, Cambridge, MA).

**Results**

**Drosophila Glued Gene Product Is a Component of a 20S Complex**

To initiate our analysis of the *Drosophila* Glued gene, we characterized the expression profile of Glued during development. Our results, like those reported by Swaroop et al. (1986), show that the Glued transcript is expressed throughout embryonic development. Our analysis also shows that Glued is expressed in heads, testes, and ovaries of adult flies (Fig. 1a). The developmental profile of the Glued gene is highly similar to that of the cytoplasmic dynein heavy chain gene, Dhc64C (Li et al., 1994). Both the Glued and Dhc64C transcripts are abundantly expressed in the ovaries of adults, and are present at high levels in 0–2-h embryos (Fig. 1a, and Li et al., 1994). The high level of Glued transcript present in 0–2-h embryos indicates that, like Dhc64C, there is a substantial maternal contribution of Glued in the early embryo.

The polypeptides encoded by the Glued gene exhibit biochemical characteristics similar to those of the homologous vertebrate gene products. As shown in Fig. 1b, we used an affinity-purified rat polyclonal serum specific for the *Drosophila* Glued polypeptides (see Materials and Methods) to determine whether the polypeptides were components of a multiprotein complex. Analysis of *Drosophila* ovariocyte cytosol by sucrose density gradient centrifugation revealed that a doublet of polypeptides of ~145/160-kD are recognized by the Glued antibody, and sediment in the ~20S fraction of the sucrose gradient (Fig. 1b, bottom). The apparent molecular weights of the Glued polypeptides and their sedimentation as a 20S particle are similar to the characteristics of the homologous p150 subunits in vertebrate dynactin (Gill et al., 1991; Schroer and Sheetz, 1991; Paschal et al., 1993). In comparison, the cytoplasmic dynein complex in ovariocyte extracts sediments at a lower S-value as detected by antibodies that recognize the heavy chain polypeptide (Fig. 1b, top). The *Drosophila* Glued polypeptides, like the homologous vertebrate polypeptides, also exhibit an ATP-sensitive microtubule association. In the absence of endogenous nucleotide, the Glued polypeptides are detected in microtubule protein prepared from ovariocyte extracts (Fig. 1c, lane 5'). The Glued polypeptides are enriched in the fraction of proteins released from taxol-stabilized microtubules by extraction with 10 mM ATP (Fig. 1c, lane 8'). These results show that the *Drosophila* Glued gene and the related vertebrate genes encode polypeptides with similar biochemical properties.

**Glued and Cytoplasmic Dynein Colocalize Throughout Drosophila Oogenesis**

The *Drosophila* ovariocyte consists of ~15 ovariocytes, each of which contains a series of egg chambers of increasing developmental age (for reviews on *Drosophila* oogenesis, see King, 1970; Spradling, 1993). The egg chamber is formed at the tip of the ovariocyte in the germarium, where the stem cells reside. Oogenesis begins with a stem cell division, which produces a cytokinesis that will then undergo four rounds of cell division with incomplete cytokinesis to produce a cyst of 16 cells that remain connected by intercellular bridges called ring canals. As the 16-cell cluster moves posteriorly through the germarium, one of the 16 cells is specified to become the oocyte, while the other 15 adopt the fate of nurse cells. Somatically derived follicle cells migrate around the 16-cell cluster, eventually enveloping the cluster as it buds off the germarium to form the stage 1 follicle, or egg chamber. As the egg chamber matures, the nurse cells supply the oocyte with the materials required for growth. Ultimately, during stages 10B-11 the nurse cells transfer their entire cytoplasmic content into the oocyte and subsequently degenerate as formation of the mature egg is completed.

We have previously reported that during *Drosophila* oogenesis cytoplasmic dynein accumulates in the presumptive oocyte in region 2b of the germarium, and is asymmetrically localized to the posterior pole of the oocyte during stage 9 of oogenesis (Li et al., 1994). The temporal and spatial pattern of dynein distribution during oogenesis provides an excellent opportunity to examine the association of the Glued complex and cytoplasmic dynein. We compared the distribution of the dynein and Glued polypeptides during oogenesis by immunocytochemical double labeling of ovaries with the affinity-purified anti-Glued antibody and the affinity-purified anti-dynein antibody PEP1 (Li et al., 1994). The pattern of Glued localization is indistinguishable from that of cytoplasmic dynein (Fig. 2a–d). Glued is initially evenly distributed throughout all cells in the anterior of the germarium (Fig. 2c, arrowhead), then accumulates in the single cell destined to become the oocyte in region 2b of the germarium (Fig. 2c, arrow). Similar to the cytoplasmic dynein heavy chain, the Glued polypeptides remain enriched in the oocyte as the egg chamber matures and later during stage 9 become localized to the posterior pole of the oocyte (Fig. 2b and d, arrowheads).

**Glued Localization in Oogenesis Requires Cytoplasmic Dynein**

To address whether the colocalization of dynein and Glued
in oogenesis reflects an association of the dynein and Glued complexes, we asked whether Glued localization is dependent on the function of cytoplasmic dynein. To do this, we made use of mutations in the cytoplasmic dynein heavy chain gene that disrupt the localization of dynein during oogenesis. flies that are doubly heterozygous for the mutations Dhc64C66 and Dhc64C612 are female sterile (data not shown). In ovaries derived from these sterile females, the dynein heavy chain does not accumulate at the posterior pole of the oocyte in stages 9 and 10 egg chambers, but is mislocalized in a punctate pattern at the anterior margin of the oocyte (arrows, Fig. 2, e and f). In addition, dynein is frequently concentrated in patches within the cytoplasm of the nurse cells (arrowheads, Fig. 2, e and f). In this mutant combination of Dhc64C alleles the posterior localization of the Glued polypeptides is similarly dis-
Figure 2. The Glued polypeptides colocalize with cytoplasmic dynein during oogenesis and have the same genetic requirements for localization. (a–d) Double-label immunolocalization of cytoplasmic dynein (a and b) and Glued (c and d) in ovaries from wild-type Oregon R females. The Glued polypeptides are evenly distributed in the mitotically active cells in the anterior of the germarium (arrowhead, c) and are differentially localized to the pro-oocyte (arrow, c) coincident with cytoplasmic dynein (arrow, a; Li et al., 1994). The Glued polypeptides remain enriched in the oocyte as the egg chamber matures during its passage down the ovariole. Later in oogenesis, like cytoplasmic dynein (arrowhead, b; Li et al., 1994), the Glued polypeptides are asymmetrically localized to the posterior pole of the oocyte in the stage 9 egg chamber (arrowhead, d). (e–h) Double-label immunolocalization of cytoplasmic dynein (e and f) and Glued (g and h) in stages 9 and 10 egg chambers from heteroallelic Dhc64C6/6/Dhc64C5/12 females. (e and f) In egg chambers from Dhc64C6/6/Dhc64C5/12 females, dynein is not localized to the posterior pole of the stage 9 and stage 10 oocyte. Instead, dynein is mislocalized in a punctate pattern at the anterior margin of the oocyte (arrows, e and f), and in bright patches within the nurse cell cytoplasm (arrowheads, e and f). (g and h) Like cytoplasmic dynein, localization of the Glued polypeptides to the posterior pole of the oocyte is disrupted in the Dhc64C6/6/Dhc64C5/12 mutant egg chambers. Glued is mislocalized with dynein to the anterior margin of the oocyte (arrows, g and f).
h) and to bright patches within the nurse cell cytoplasm (arrowheads, g and h). (i–l) Glued localization, like cytoplasmic dynein (Li et al., 1994), requires the genes egalitarian, Bicaudal-D, cappuccino, and spire. The Glued polypeptides are not enriched in a single cell in egg chambers from egalitarianWUS;egalitarianWUS, Bicaudal-D;RP48, or spire;RP48 females. In cappuccino;spire females, the Glued polypeptides are not asymmetrically localized to the posterior pole of the stage 9 oocyte. The localization of Glued to the oocyte through stage 8 of oogenesis is completely normal in cappuccino;spire mutants (data not shown). In all panels, anterior is at left. Magnification is identical in panels a–d, e–h, and i–l. Bars shown in d and l, 100 μm; bar in h, 50 μm.

Glued and Cytoplasmic Dynein Localization Exhibit Similar Genetic Requirements in Oogenesis

To examine further the association of dynein and Glued in vivo, we asked whether mutations in other genes that disrupt the localization of dynein during oogenesis also affect the distribution of the Glued polypeptides. We have previously shown that mutations in the genes Bicaudal-D (Bic-D) and egalitarian (egl) disrupt the accumulation of dynein to the presumptive oocyte (Li et al., 1994). Loss-of-function mutations in either of these genes prevent oocyte differentiation and result in egg chambers containing 16 cells that develop as nurse cells (Suter et al., 1989; Schüpbach and Weischaus, 1991). Like the cytoplasmic dynein heavy chain polypeptide, the Glued polypeptides fail to accumulate in a single cell in egg chambers derived from females homozygous mutant for the eglWUS mutation, or hemizygous for the Bic-DRP48 mutation (Fig. 2, i and k).

We also examined the effect of mutations in cappuccino (capu) and spire (Schüpbach and Weischaus, 1991) on the accumulation of Glued during oogenesis. The capu and spire genes are required for both dorsoventral and anteroposterior axis formation during oogenesis. Mutations in these two maternal effect loci cause a disruption in the accumulation of the posterior group gene products, staufen protein and oskar mRNA, to the posterior pole of the oocyte (Manseau and Schüpbach, 1989). We have previously shown that both the capu and spire gene products are also required for the enrichment of cytoplasmic dynein at the posterior pole of stage 9 oocytes (Li et al., 1994). As shown in Fig. 2, we observe a similar disruption of Glued accumulation in the posterior pole of oocytes derived from females that are homozygous mutant for either capuBERT or spireRP48 (Fig. 2, j and l). The observations that the Glued and cytoplasmic dynein heavy chain polypeptides exhibit similar genetic requirements for their proper localization during oogenesis is consistent with the physical association of the two complexes.

A Dominant Mutation in the Glued Gene, GI1, Encodes a Truncated Polypeptide that Associates with Microtubules

The dominant mutation in the Glued locus, GI1, was previously shown to be caused by the insertion of a transposable element in the 3′ coding sequence of the Glued gene (Swaroop et al., 1985). Analysis of Glued expression in heterozygous GI1/+ flies revealed, in addition to the wild-type Glued transcript, a truncated message presumably caused by premature termination of transcription due to the inserted transposon (Swaroop et al., 1985). Like other Glued alleles, the GI1 mutation is a recessive lethal mutation and homozygous animals die in late embryogenesis or early larval stages of development (Plough and Ives, 1935; Harte and Kankel, 1982). In addition, the GI1 mutation produces a dominant rough eye phenotype in heterozygous adults (Plough and Ives, 1935). This dominant phenotype was shown to be dosage dependent. The addition of small chromosomal duplications carrying extra copies of the wild-type Glued gene into heterozygous GI1/+ flies rendered the severity of the eye phenotype less extreme in a dosage-sensitive manner (Harte and Kankel, 1982). The dosage dependence of the eye phenotype, together with the molecular nature of the lesion, suggests that the GI1 mutation encodes a truncated polypeptide that acts as a poison product. In support of this model, we have identified the truncated protein product encoded by the GI1 mutation and examined the association of the truncated polypeptide with microtubules and the Glued complex.

To identify the product of the GI1 mutation, we compared the Glued polypeptides in microtubule-associated proteins prepared from wild-type versus heterozygous GI1/+ tissues. These studies provided a number of new findings. First, the pattern of Glued polypeptide species encoded by the wild-type Glued gene is tissue dependent. The simplest pattern is observed in extracts from adult heads, in which the predominant species of Glued polypeptide is a single band which migrates at ~160 kD on SDS-PAGE (upper arrow, Fig. 3 a, lane marked head, +/+). This species is larger than the predicted molecular mass of 148 kD based on the cDNA sequence (Swaroop et al., 1987). An additional lower molecular mass species of ~145 kD is present in minor amounts (lower arrow, Fig. 3 a, lane marked head, +/+). In contrast, the 145-kD species in ovaries appears more abundant than the 160-kD form (Fig. 3 a, lane marked ovary, +/+). In embryos, the 160-kD and 145-kD species are present in relatively equal amounts (Fig. 3 a, lane marked embryo, +/+). In all three tissues, a third species that migrates at ~135 kD is present in minor amounts (arrowhead, Fig. 3 a). The presence of a single Glued transcript in each of these tissues suggests that the multiple Glued polypeptides may arise from the posttranslational modification of a single wild-type product, as opposed to different products resulting from alternative splicing. Second, each of the wild-type Glued gene species sediments with microtubules (Fig. 3 b, lanes marked +/+ and is enriched in microtubule-associated proteins eluted with ATP (Fig. 3 b, lanes marked +/+). A dominant portion of the Glued polypeptides in each tissue re-
main unbound in the supernatant after microtubule sedimentation (Fig. 3 a, lanes marked +/+), similar to the behavior described for the dynactin complex from chicken (Gill et al., 1991).

The analysis of microtubule-associated protein preparations from heterozygous GlU/+ tissues reveals a truncated Glued polypeptide of ~130 kD in addition to the wild-type polypeptides. The truncated polypeptide is most easily distinguished in the samples derived from head extracts, in which the truncated polypeptide is most abundant (asterisks, Fig. 3 a–c, lanes marked GlU/+). In comparison to wild type, the additional polypeptide present in GlU/+ extracts migrates slightly faster than the smallest wild-type species of ~135 kD. The presence of this additional polypeptide in extracts from heterozygous GlU/+ tissues indicates that the ~130-kD polypeptide represents the truncated polypeptide encoded by the GlU mutation. The variation in the amount of the mutant Glued polypeptide between ovaries, embryos, and heads may reflect variability in the expression of the Glued gene, or in the stability of the truncated Glued product, in these different tissues. Like the wild-type Glued polypeptides, the ~130-kD Glued polypeptide sediments with microtubules (asterisks, Fig 3 b, lanes marked GlU/+), and is enriched in the ATP-eluted microtubule-associated proteins (asterisks, Fig. 3 c, lanes marked GlU/+). This result suggests that the COOH-terminal ~20 kD of the wild-type Glued polypeptide is not strictly required for the ability of Glued to sediment with microtubules.

To examine further the behavior of the mutant Glued polypeptide, we analyzed the sedimentation of the truncated polypeptide on sucrose density gradients. Extracts from wild-type and heterozygous GlU/+ tissues were fractionated and analyzed by SDS-PAGE and immunoblotting with the affinity-purified Glued antibody. In wild-type head extracts the predominant 160-kD Glued polypeptide sediments in the 20S fraction of the gradient, similar to the sedimentation profile of the major 145/160-kD doublet of Glued polypeptides present in wild-type ovaries (see Fig. 1 b) and embryos (data not shown). In head extracts from GlU/+ flies, the truncated Glued polypeptide of ~130 kD sediments at ~6–7S (asterisk, Fig. 3 d), while the 160-kD wild-type Glued polypeptide remains in the 20S fraction of the gradient (arrow, Fig. 3 d). A similar result was obtained from the fractionation of extracts from GlU/+ embryos (data not shown). The distinct sedimentation values of the wild-type and mutant Glued polypeptides indicate that the truncated Glued product does not associate with
the wild-type polypeptide in an ~20S complex. Based on the predicted molecular mass of ~130 kD for the truncated polypeptide, its sedimentation behavior suggests that the mutant Glued polypeptide may be present in the cytoplasm as a monomer. However, our experiments do not exclude the possible association of the truncated Glued protein with other component polypeptides of the Glued complex.

Mutations in Dhc64C Display a Rough Eye Phenotype Similar to the Gl1 Mutation

The Drosophila adult eye is composed of ~800 ommatidia arranged in a precise hexagonal pattern (Fig. 4, a and a'; for a review on Drosophila eye development, see Dickson and Hafen, 1993). Each of the ommatidia, or unit eyes, is made up of ~20 cells, including eight photoreceptor cells, four cone cells which secrete the lens material, several pigment and associated cells, and a single hair cell. The ordered array of ommatidia in the adult eye arises from a precise spatial and temporal sequence of cell divisions, cell shape changes, and cell signaling events during the differentiation of the eye imaginal disc epithelium in the third larval instar.

We have identified several heteroallelic combinations of Dhc64C mutations that produce viable adults displaying a rough eye phenotype. For example, as shown in Fig. 4 (b and b'), the heteroallellic combination of Dhc64C alleles Dhc64C3-31/Dhc64C8-10 disrupts the shape, size, and organization of the ommatidia within the eye. This eye phenotype is similar to that observed for the dominant Gl1 mutation (Plough and Ives, 1935; Meyerowitz and Kankel, 1978; Harte and Kankel, 1982) (Fig. 4, c and c'). The Gl1 rough eye phenotype is apparently due to the failure to complete and/or maintain the differentiation of clusters of neuronal precursor cells within the developing retinal epithelium during the third larval instar (Renfranz and Benzer, 1989). The similarity between the rough eye phenotypes of heteroallelic combinations of Dhc64C mutations and the dominant Gl1 mutant suggests that the dynein and Glued complexes are components of a common cellular pathway involved in the development of the adult eye.

Mutations in Dhc64C Act To Suppress or Enhance the Rough Eye Phenotype of Gl1

To obtain more direct evidence that dynein and Glued interact in vivo, we asked whether mutations in the Dhc64C gene could act to modify the rough eye phenotype of the dominant mutation Gl1. In the analysis of flies doubly heterozygous for a Dhc64C allele and the Gl1 mutation, we have found that certain Dhc64C alleles act as dominant suppressors of the Gl1 rough eye phenotype, while other Dhc64C alleles act as dominant enhancers of the Gl1 phenotype (Table I and Fig. 4). For example, in flies doubly heterozygous for the Dhc64C8-6 allele and the Gl1 mutation, the rough eye phenotype is largely suppressed except in the most posterior portion of the eye (Fig. 4 e), and the shape and packing of ommatidia is very similar to that observed in wild-type flies (Fig. 4 e'). In contrast, the Dhc64C8-6 and Dhc64C8-10 alleles enhance the rough eye phenotype of Gl1; the eyes are significantly smaller (Fig. 4 g) and the remaining ommatidia are more severely disrupted than those observed in flies carrying only the Gl1 mutation (Fig. 4 g'). The specificity of these genetic interactions is demonstrated by the observation that a deficiency that removes the Dhc64C gene, Df(3L)10H, in heterozygous combination with Gl1 does not alter the Gl1 rough eye phenotype (Fig. 4 f and f'; Table I). Moreover, the Dhc64C alleles do not display a phenotype in combination with a deletion that entirely removes the Glued gene, Gl1-R2 (Table I; Harte and Kankel, 1982), or with other recessive lethal alleles of Glued (data not shown). The observed allele specificity indicates that the dominant genetic interactions depend on the presence of the mutant dynein and Glued gene products.

To gain insight into the nature of the interaction between the enhancer alleles of Dhc64C and Gl1, we examined the effect of an additional copy of the wild-type Dhc64C gene on the enhancement of the Gl1 rough eye phenotype by the Dhc64C8-6 and Dhc64C8-10 alleles. The appropriate crosses were conducted to introduce a wild-type Dhc64C transgene carried on the X chromosome into flies that were also doubly heterozygous for the Gl1 mutation and the Dhc64C8-6 or Dhc64C8-10 allele. The increased dosage of wild-type dynein heavy chain resulted in the reversal of the enhanced rough eye phenotype (Table I and Fig. 4 h). The shape, size, and alignment of the ommatidia were less disrupted (Fig. 4 h') and more nearly resembled the original Gl1 rough-eyed phenotype. This result demonstrates that the activity of the wild-type Dhc64C gene product can functionally compete with the product of the Dhc64C enhancer allele. We conclude that the genetic interaction observed between the Dhc64C and Glued mutations reflects the normal interaction of the dynein and Glued complexes in vivo, rather than an aberrant (neomorphic) activity associated with the mutant polypeptides.

A Previously Isolated Suppressor of Gl1, Su(GI)102, Is a Dhc64C Allele

Our observations that certain known Dhc64C mutations interact with Gl1 suggested that mutations originally isolated as suppressors of Gl1 might identify additional Dhc64C alleles. One candidate was the Su(GI)102 mutation (Harte and Kankel, 1982), which was previously recovered in a screen for EMS-induced revertants of the Gl1 rough-eyed phenotype (Fig. 4, d and d'). The Su(GI)102 mutation is recessive lethal and maps within the interval between roughoid and hairy on the left arm of chromosome three (Harte and Kankel, 1982). Significantly, this interval includes the deficiency Df(3L)10H which removes the Dhc64C gene. To examine whether the Su(GI)102 mutation is an allele of Dhc64C, we performed a number of complementation tests. We found that Su(GI)102 is lethal in combination with the deficiency Df(3L)10H, as shown by the absence of progeny of the genotype Su(GI)102/Df(3L)10H in the cross between heterozygous Su(GI)102/TM3 and Df(3L)10H/TM6 flies (Table II, column labeled Critical Class). This result shows that the Su(GI)102 mutation lies within the region uncovered by the deficiency. Similar crosses were performed between the Su(GI)102 mutation and each of the Dhc64C alleles, and show that Su(GI)102 is lethal in combination with all but two of the Dhc64C alleles that we had isolated (Table II, column la-
Figure 4. Low (a–h) and high (a′–h′) magnification SEM micrographs documenting the genetic interaction between \(Dhc64C\) alleles and the GI\(^{l}\) mutation. (a and a′) An eye from a wild-type OregonR adult fly. (b and b′) The heteroallelic combination of \(Dhc64C\) alleles \(Dhc64C^{32}/Dhc64C^{6I′}\) produces a rough eye phenotype. (c and c′) The phenotype of the dominant mutation GI\(^{l}\), in which the ommatidia appear disorganized, misshapen, and the alignment of bristles is disrupted. (d and d′) The \(Su(GI)102\) mutation suppresses the GI\(^{l}\) rough eye phenotype; the bristles and ommatidia in the eye are normally aligned. (e and e′) The \(Dhc64C^{C6}\) allele suppresses the GI\(^{l}\) rough eye phenotype, except in the most posterior region of the eye, similar to the \(Su(GI)102\) mutation (d and d′). (f and f′) The third chromosome deficiency, \(Df(3L)10H\), in combination with GI\(^{l}\) does not alter the rough eye phenotype. (g and g′) The \(Dhc64C^{C10}\) allele enhances the GI\(^{l}\) rough eye phenotype in that the eye is smaller, has fewer ommatidia of abnormal shape and size, and duplicated or missing bristles. A similar result is obtained with the \(Dhc64C^{C6}\) allele (data not shown). (h and h′) Addition of a wild-type copy of the \(Dhc64C\) transgene can rescue the enhancement of GI\(^{l}\) by the \(Dhc64C^{C10}\) allele. The alignment of ommatidia and bristles is less disrupted than in the \(Dhc64C^{C10}/GI^{l}\) combination (g and g′). The same result is obtained when the \(Dhc64C\) transgene is present in \(Dhc64C^{C6}/GI^{l}\) flies (data not shown). 

The Journal of Cell Biology, Volume 131, 1995

The genotypes of the flies represented in each panel are (a and a′) wild-type OregonR; (b and b′) \(Dhc64C^{C32}/Dhc64C^{C6}\); (c and c′) GI\(^{l}\); (d and d′) \(Su(GI)102 +/+ GI^{l}\); (e and e′) \(Dhc64C^{C6} +/+ GI^{l}\); (f and f′) \(Df(10H)3L +/+ GI^{l}\); (g and g′) \(Dhc64C^{C10} +/+ GI^{l}\); (h and h′) \(P(Dhc^{c})/w,Dhc64C^{C10} +/+ GI^{l}\). Crosses to generate flies of the above genotypes are described in Materials and Methods.
Table I. Summary of Eye Phenotypes in Flies Doubly Heterozygous for Glued and Dhc64C Mutations

| Genotype*                                      | Eye phenotype†                                      |
|-----------------------------------------------|----------------------------------------------------|
| Dhc64C6-6/Gl+                               | Rough eyes, misshapen ommatidia, abnormal bristle distribution |
| Dhc64C6-6/Gl-                               | Gl1 rough eye is suppressed, normal hexagonally shaped ommatidia except in the most posterior of the eye |
| Dhc64C6-6/Gl-                               | Gl1 rough eye is enhanced, eyes are reduced in size, frequently fused ommatidia |
| Dhc64C6-6/Gl+                               | Gl1 rough eye is enhanced, eyes are reduced in size, frequently fused ommatidia |
| Dhc64C6-6/Bf-                               | Rough eyes, similar to the original Gl1 rough eye phenotype |
| Dhc64C6-6/Gl-                               | Gl1 rough eye phenotype is neither suppressed nor enhanced |
| Wild-type eyes                               | indictment Critical Class. The lethal phenotype of the Su(Gl)102 mutation in combination with the Dhc64C2 mutations strongly suggests that Su(Gl)102 is a Dhc64C allele. Interestingly, Su(Gl)102 is viable in combination with the two Dhc64C alleles, Dhc64C5-8 and Dhc64C5-10, which act as enhancers of the Gl1 mutation (Tables I and II). To confirm that Su(Gl)102 is an allele of Dhc64C, we have shown that the lethality of the Su(Gl)102 mutation in combination with other Dhc64C alleles is rescued by a wild-type Dhc64C transgene. As shown in Table III, flies doubly heterozygous for Su(Gl)102 and a Dhc64C allele, and which also carry one copy of a wild-type Dhc64C transgene on the X chromosome (designated P(Dhc+)), are viable (column labeled P(Dhc+); m/Su(Gl)102, where m indicates the appropriate Dhc64C allele). The wild-type dynein transgene also rescues the lethality of Su(Gl)102 in combination with the deficiency, Df(3L)10H (Table III). These results demonstrate that an independently isolated suppressor of the Gl1 mutation, Su(Gl)102, is a Dhc64C allele. The characterization of Dhc64C alleles that act as allele-specific, dominant second-site modifiers of the Gl1 mutation suggests that the functional interaction of the dynein motor complex and Glued complex is mediated by their physical interaction in vivo.

Discussion

Previous work has described the structural similarity between the Drosophila Glued gene and the gene encoding the p150 subunit of the dynactin complex in rat and chick (Swaroop et al., 1987; Gill et al., 1991; Holzbaur et al., 1991). In this report, we have demonstrated that the products of the Drosophila Glued gene are subunits of a 20S complex similar to the homologous components in vertebrates. In addition, we have provided cell biological evidence for the physical association of the Glued and cytoplasmic dynein motor complexes. Specific mutations in the dynein heavy chain gene, Dhc64C, result in the coincident mislocalization of both the dynein heavy chain and Glued polypeptides in late stage oocytes. Finally, our analysis of genetic interactions between a dominant Glued mutation, Gl1, and Dhc64C mutations demonstrates the functional interaction in vivo between the Drosophila Glued and dynein complexes.

Similar to the Glued-related polypeptides in chicken (Gill et al., 1991), the three major species of Drosophila Glued polypeptides have apparent molecular masses of 160, 145, and 135 kD, show tissue-specific variations in abundance (Fig. 3). Although multiple electrophoretic species of Glued polypeptides are present, we and others detect a single copy of the Glued gene (data not shown; see Swaroop et al., 1986), as well as a single predominant transcript throughout development (Fig. 1). While these results suggest that the multiple Glued polypeptides in Drosophila may result from posttranslational modifications, we cannot exclude the possibility that alternate transcripts of low abundance contribute to the heterogeneity of the Glued gene.

Table II. Suppressor of Glued1 Mutation, Su(Gl)102, Is Lethal in Combination with Dhc64C Mutations

| Genotypes of mated flies*                      | Critical class5 | Sibling classes |
|-----------------------------------------------|-----------------|----------------|
|                                      | Su(Gl)102/TM6 | m/TM3 | TM3/TM6 |
| Df(3L)10H/TM6 c/Y × Su(Gl)102/TM3 ✓ | 0               | 107 | 99   | 62   |
| Dhc64C4-6/TM6 c/Y × Su(Gl)102/TM3 ✓ | 0               | 104 | 149  | 24   |
| Dhc64C4-16/TM6 c/Y × Su(Gl)102/TM3 ✓ | 0               | 28  | 37   | 7    |
| Dhc64C4-16/TM6 c/Y × Su(Gl)102/TM3 ✓ | 0               | 183 | 228  | 71   |
| Dhc64C4-16/TM6 c/Y × Su(Gl)102/TM3 ✓ | 7Y              | 75  | 79   | 21   |
| Dhc64C4-16/TM6 c/Y × Su(Gl)102/TM3 ✓ | 148T            | 133 | 154  | 56   |

*Male (c/Y) heterozygous for the deficiency Df(3L)10H or a Dhc64C mutation were mated with virgin females (✓) heterozygous for the Su(Gl)102 mutation. TM6 and TM3 refer to multiply marked balancer chromosomes which are wild type at the Dhc64C locus.

†Critical class (Su(Gl)102) refers to the class of progeny that carries both the Su(Gl)102 mutation and the Dhc64C allele (m). The absence of progeny of this genotype demonstrates that Su(Gl)102 fails to complement, or is lethal in combination with the deficiency Df(3L)10H or the Dhc64C alleles Dhc64C4-6, Dhc64C4-16, and Dhc64C4-16.

‡The presence of the critical class in these two crosses demonstrates that the Su(Gl)102 mutation is viable in combination with the Dhc64C4-6 and Dhc64C4-16 alleles.
of polypeptides. In this regard, multiple transcripts have been described for the Glued homologue in chicken (Gill et al., 1994) and human (Tokita, K. M. K. M. Y. Lee, and E. L. F. Holzbaur 1993. Mol. Biol. Cell. Abstracts 4:162).

In our characterization of the Drosophila Glued polypeptides we show that each of the polypeptides partially copurifies with microtubules and is present in the 20S Glued complex. In addition, we show that the truncated polypeptide encoded by the Gl1 mutation also copurifies with microtubules. In this case, the failure of the truncated polypeptide to incorporate into the 20S complex suggests that the microtubule association observed for the Glued polypeptides is independent of their presence in the 20S complex. Although the multiple Glued polypeptides are not distinguished by their biochemical properties, the functional significance of the variation in expression of each species is suggested by the apparent restriction of the Gl1 dominant phenotype to the eye. In extracts derived from head tissue of wild-type flies, a single 160-kD species is the predominant Glued polypeptide. In Gl1/+ heterozygous flies, the mutant truncated polypeptide is more abundant in head extracts than in the other tissues examined. Whether a dominant effect of the truncated polypeptide is limited to the eye because of the level of its expression, or is the predominant Glued polypeptide. In this case, the failure of the truncated Glued polypeptide to cosediment or to be spread across the gradient fractions.

The dominant Gl1 mutation was previously shown to result from the insertion of a transposable element that causes the premature termination of the Glued transcript (Swaroop et al., 1985). In Gl1/+ heterozygous flies, both the wild-type transcript of 6.0 kb and a shorter transcript of 5.1 kb are detected. The shorter transcript has been proposed to encode a truncated polypeptide that lacks a COOH-terminal domain. Since the Glued gene is required for normal development (Harte and Kankel, 1982), the expression of a dominant phenotype in Gl1/+ adult flies suggests the defective gene product functionally competes with the wild-type product, rather than completely blocking the function of the wild-type Glued polypeptide. Consistent with this hypothesis, gene dosage analysis has shown that the mutation behaves as an antimorphic mutation, most likely as the result of the truncated Glued polypeptide acting to poison the function of the wild-type Glued gene product. This “poison product” or dominant-negative mechanism is distinct from dominant phenotypes that can arise from alterations in the amount of wild-type gene product (Lindsley et al., 1972) or that arise from the misexpression of a mutant gene (Struhl, 1981). As pointed out by Herskowitz (1987), for proteins whose activity depends on multiple functional sites, a variant that retains only a subset of these sites could act to compete with the wild-type counterpart for its substrate or ligands. The relative stoichiometry of the major components in the bovine brain and chicken dynactin complex is 1.5-2:5:10 (p150/160:p50:Arp-1:actin) (Paschal et al., 1993; Schafer et al., 1994). The extended regions of heptad repeat sequences present in the Glued polypeptide may form coiled-coil structural domains that mediate the dimerization of the polypeptide and/or the association of the Glued polypeptides with the 20S complex. In this regard, the dominant effect observed for the truncated Glued polypeptide could result from its dimerization with an intact Glued polypeptide and its incorporation into a defective Glued complex.

In support of a dominant negative mechanism underlying the Gl1 phenotype, we have identified a truncated ~130-kD Glued polypeptide in cytoplasmic extracts of tissues from heterozygous Gl1/+ flies. However, the sedimentation of the truncated polypeptide in the 6-7S fractions on sucrose density gradients demonstrates that the truncated polypeptide cannot assemble into the 20S Glued complex. We conclude that the dominant phenotype is not due to the truncated polypeptide acting as a structural poison to render the Glued complex defective. The separation of the wild-type and truncated Glued polypeptides in two distinct peak fractions of 20S and 7S, respectively, suggests that partial complexes containing less than a full complement of Glued subunits do not form. If this were the case, one would expect both the wild-type and/or truncated polypeptides to cosediment or to spread across the gradient fractions.

How can the dominant and dosage-sensitive effect of the truncated Glued polypeptide be explained? One possibility is that although the truncated polypeptide fails to incorporate into the Glued complex, it does compete with the wild-type Glued polypeptide for some other limiting component that is required for the assembly and/or function of the complete Glued complex. As a consequence of the titration of such a limiting component, the level of wild-type Glued complex might fall below a required threshold. An alternative possibility is that the dominant effect could be mediated by the ability of the truncated

### Table III. Su(Gl)102 Mutation is a Dhc64C Allele

| Genotypes of mated flies* | Genotypes of Progeny Classes (total number of surviving adults)* |
|--------------------------|---------------------------------------------------------------|
|                          | P(Dhc+/+; m/Su(Gl)102) | +/Y; m/Su(Gl)102 | P(Dhc+/+; +/Y; Su(Gl)102/TM6) | +/Y; Su(Gl)102/TM6 | +/Y; P(Dhc+/+; m/TM6) | +/Y; m/TM6 |
| +/+; Dhc64C+/+TM6        | 115                  | 111               | 111                       | 111               | 111               | 111               |
| +/+; Dhc64C+/+TM6        | 89                   | 89                | 92                        | 92                | 67                | 67                |
| +/+; Dhc64C+/+TM6        | 97                   | 97                | 90                        | 90                | 76                | 76                |
| +/+; Dhc64C+/+TM6        | 76                   | 76                | 85                        | 85                | 61                | 61                |

*Virgin females (♀) heterozygous for the Dhc64C mutation or the deficiency Df(3L)10H were mated with males (♂) heterozygous for the Su(Gl)102 mutation. The wild-type Dhc64C transgene, P(Dhc+/+), is on the paternal X chromosome. Y, Y chromosome; +/+, maternal X chromosome pair.

1 At the top of each column the genotype of the class is indicated. Note that female and male progeny are shown in separate columns. Because male progeny inherit their X chromosome from the mother, only female progeny inherit the Dhc+ transgene present on the paternal X chromosome. The presence of female progeny of the class P(Dhc+/+; m/Su(Gl)102) demonstrates that the Dhc+ transgene rescues the lethality of the Su(Gl)102 mutation in heterozygous combination with the dynactin mutations (m). In the absence of the Dhc+ transgene, males doubly heterozygous for Su(Gl)102 and the dynactin mutation (m) do not survive.
polypeptide to compete with the wild-type 20S Glued complex for binding sites on the dynein complex and/or microtubules. In the context of previously proposed models in which the dynactin complex acts as a cargo adaptor (Gill et al., 1991; Paschal et al., 1993; Holzbaur et al., 1994), the truncated Glued polypeptide may interfere with the native Glued complex in the docking of cellular cargoes to cytoplasmic dynein and/or microtubules.

The sedimentation behavior of the mutant Glued product demonstrates that the COOH-terminal ~20-kD domain missing from the truncated protein is required for the association of the wild-type Glued polypeptide with itself and/or the native 20S Glued complex. The transposon insertion in the GluG mutation is located in a region close to or within the conserved COOH-terminal stretch of ~130 residues which exhibit a-helical coiled-coil characteristics (Swaroop et al., 1987). The interruption, or absence, of this potential coiled-coil domain may prevent the mutant polypeptide from dimerizing with the wild-type Glued product, and could account for its distinct sedimentation on the gradient. Alternatively, the inability of the truncated polypeptide to incorporate into a particle with a higher sedimentation value may reflect the absence of the conserved cluster of charged residues LKEK, which lies COOH-terminal to the site of transposon insertion and would be missing in the mutant polypeptide. In vitro studies of the p150 component of dynactin from rat suggest that the homologous sequence, KKEK, mediates the binding of p150 to the centrinactin/ARP-1 subunit of the dynactin complex (Waterman-Storer et al., 1995).

In contrast to the potential role in dimerization of the Glued polypeptide and/or its incorporation into the Glued complex, the COOH-terminal ~20-kD domain is not strictly required for association of the Glued polypeptide with microtubules. We have shown that the truncated Glued product pellets with microtubules and elutes from microtubules with ATP-dependent, microtubule-associated proteins. These observations are consistent with studies by Waterman-Storer et al. (1995) reporting the existence of a microtubule-binding motif within the NH2-terminal 39–150 residues of the p150 subunit of dynactin from rat. However, our study does not distinguish between the direct binding of the truncated polypeptide to microtubules and an indirect association mediated by an unknown component present in the cytoplasmic extract.

Although we have not yet determined the specific molecular lesions in the dynein alleles that enhance or suppress the dominant GluG eye phenotype, the genetic interactions exhibit several characteristics that provide insight into the nature of the mutations. We have shown that certain Dhc64G alleles act to suppress the rough eye phenotype, while other alleles act to enhance the rough eye phenotype of the GluG mutation. The observed dominant interactions are likely not due to mutations that up-regulate Dhc64G expression, as additional copies of a wild-type Dhc64G transgene in heterozygous GluG flies have no effect on the severity of the GluG rough eye phenotype (data not shown). Moreover, since a deficiency that entirely removes the Dhc64G gene does not modify the severity of the GluG rough eye phenotype, the suppressor and enhancer alleles do not represent complete loss-of-function alleles. In other words, the specificity of the genetic interactions between certain dynein alleles and the GluG mutation suggests that the mutant dynein heavy chains retain some wild-type activity. In addition, the suppressor and enhancer Dhc64G alleles fail to produce eye phenotypes when present in combination with a deletion of the Glued gene (GluG+D), or in combination with other recessive lethal Glued alleles. This allele specificity indicates that the dominant interactions require the presence of both the mutant Dhc64G gene product and the truncated Glued polypeptide. The analysis of the lesions in the interacting Dhc64G alleles may help to identify domains in the dynein heavy chain involved in the association of the Glued and dynein motor complexes.

What molecular mechanism can account for the ability of certain dynein alleles to enhance the GluG rough eye phenotype, while other alleles suppress the phenotype? Given the allele-specific characteristics of the genetic interactions and the truncated product encoded by the GluG mutation, we favor a model in which the truncated Glued product retains the ability to associate with the dynein complex, thereby competing with the wild-type Glued complex and its attached cargo for association with dynein. The dynein alleles that suppress the dominant effect of the GluG mutation would do so by acting to eliminate or reduce the defective Glue product from interfering in dynein motor function. One possibility would be that the suppressor alleles encode dynein heavy chains that incorporate into a dynactin complex that can associate with the defective Glued polypeptide as well as the wild-type Glued complex, but fails to associate with cellular cargoes. The remaining wild-type dynein heavy chain and Glued polypeptides in the transheterozygote would provide sufficient levels of functional complexes to ensure proper cargo transport within the cell. In contrast, the enhancer alleles may encode dynein heavy chains that incorporate into the motor complex and retain the ability to attach with cellular cargoes, but cannot support cargo transport. The enhanced rough eye phenotype would result from the combined effects of the truncated Glued product and the defective dynein motor competing with wild-type dynein and Glued complexes for the proper association and transport of cargoes.

Regardless of the detailed mechanism of interaction, the allele specificity of the observed suppression and enhancement implies that the truncated Glued product is capable of associating with the dynein complex. Additional evidence of the physical association between the Glued complex and cytoplasmic dynein is provided by our observation that the pattern of localization of the Glued polypeptides is dependent on dynein function. We show that mutations in the Dhc64G gene that disrupt the localization of dynein result in the coincident mislocalization of the Glued polypeptides. Furthermore, other genes required for dynein localization during oogenesis, including the Bicaudal-D, egalitarian, cappucino, and spire genes, are also required for proper Glued localization. Whether the association of the dynein and Glued complexes in vivo involves the direct binding of the Glued polypeptide to the dynein heavy chain, or to another subunit of the dynein complex, is not known. However, recent in vitro evidence indicates that the 74-kD intermediate chain subunit of cytoplasmic dynein can mediate the association of dynein
with the dynactin complex (Vaughan et al., 1995; Karki, S., K. T. Vaughan, R. B. Vallee, and E. L. F. Holzbaur, 1994. Mol. Biol. Cell. Abstracts, H113.).

Examples of genetic interactions between genes whose products interact in the formation of complex structures or in common cellular processes have been reported in a number of organisms. In Chlamydomonas, extrageneic suppressors of paralyzed flagellar mutations have identified loci that alter the outer and inner dynein arm structures (Huang et al., 1982; Porter et al., 1992; 1994), as well as regulatory components (Huang et al., 1982; Piperno et al., 1992, 1994; Gardner et al., 1994) of the flagellar axoneme. Similarly, in Aspergillus nidulans, extrageneic suppressors of mutations in the β tubulin gene, benA, have identified α tubulin (Morris et al., 1979) and γ tubulin genes (Oakley and Oakley, 1989). In other examples, dominant enhancer, or second-site noncomplementing, mutations have revealed structural interactions between gene products. For example, mutations in the Caenorhabditis elegans collagen gene sqt-1 (Kramer et al., 1988) show unusual dominant interactions with mutations in other loci, causing defects in cuticle structure and body shape (Kusch and Edgar, 1986). Like sqt-1, these loci may encode other collagens or components of the worm cuticle. In addition, mutations in the α tubulin genes of S. cerevisiae (Stearns and Botstein, 1988) and Drosophila (Hays et al., 1989) have been identified by their failure to complement mutant alleles of β tubulin genes. As in the examples cited above, the dominant allele-specific interactions between the Drosophila Dhc64C and Glued mutants reflect a functional interaction between the Glued and dynein complexes.

The eye phenotypes observed for the dominant GlI mutations and certain intragenic combinations of Dhc64C alleles, as well as the enhancement and suppression of the GlI rough-eyed phenotype by specific Dhc64C alleles, make clear the necessity for dynein and Glued function during Drosophila eye development. Previous studies have described the effect of GlI on the projection of axons from the retina to the optic tectum in adult flies (Meyerowitz and Kankel, 1978). This defect could reflect the disruption of dynein function in retrograde axonal transport. Perhaps dynein transport is required for the delivery of a signal from the optic tectum back to the retinal cell body and nucleus that indicates formation of the proper synaptic connection. Alternatively, the defective projection of retinal axons could result from an earlier defect in dynein or Glued function during the development of the retinal epithelium. Differentiation of the eye disc epithelium is accompanied by a highly orchestrated series of events including the synchronization of cell cycles and divisions, cell shape changes, cell-specific patterns of nuclear migration, and the formation of the founder cell clusters that give rise to the ommatidia. Renfranz and Benzer (1989) have described an apparent failure to complete and/or maintain the ommatidial clusters of cells in GlI eye imaginal discs in the third larval instar. Additional analysis will be required to reveal the underlying basis of the rough eye phenotype caused by the dynein and Glued mutants.

In addition to the eye phenotypes described above, certain alleles of both the Glued (Harte and Kankel, 1982) and Dhc64C (Gepner, J., M.-g. Li, S. Ludmann, C. Kortas, K. Boylem, M. McGrai1, and T. S. Hays, manuscript in preparation) genes exhibit female-sterile phenotypes. Together with our observations that dynein and Glued colocalize during oogenesis and share similar genetic requirements for localization, the female-sterile phenotypes indicate a role for dynein and Glued in the development of the egg. There is growing evidence implicating microtubule motors and cytoskeletal components in the specification and differentiation of the oocyte (Cooley and Theurkauf, 1994). We are currently conducting genetic screens for additional second-site modifiers of Dhc64C and Glued mutations to identify other gene products that may provide a link between dynein motor function and the mechanisms that regulate specification and differentiation of cell fate.

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