Isolation and characterization of the glucose-6-phosphate dehydrogenase gene of *Drosophila melanogaster*

(IMmunoselection of mRNA; library screening; in situ hybridization; gene copy number; dosage compensation; \( \lambda \) vector, recombinant DNA; cloning)

Ranjan Ganguly, Nivedita Ganguly and Jerry E. Manning *

*Department of Molecular Biology and Biochemistry, School of Biological Science, University of California at Irvine, Irvine, CA 92717, (U.S.A.) Tel. (714)856-7102*

(Received October 9th, 1984)
(Revision received December 27th, 1984)
(Accepted January 8th, 1985)

**SUMMARY**

To investigate the molecular basis of dosage compensation in *Drosophila*, a recombinant \( \lambda \) phage containing the *Drosophila melanogaster* glucose-6-phosphatase dehydrogenase (G6PD) gene was isolated by differential screening of a *Drosophila* genomic \( \lambda \) library with poly(A) + RNA obtained from polyribosomes enriched for or depleted of G6PD mRNA sequences. Of 44,000 plaques screened, a single phage, \( \lambda \) DmG21, showed hybridization with the enriched poly(A) + RNA but not the depleted one. Confirmation that the *Drosophila* DNA fragment cloned in \( \lambda \) DmG21 contains the G6PD gene sequence is based on the following observations. \( \lambda \) DmG21 DNA shows hybridization only to the 18D region of the salivary gland X-chromosome, which is the known cytological locus for the G6PD gene. In vitro translation of the poly(A) + mRNA selected by hybridization to \( \lambda \) DmG21 DNA sequences shows a polypeptide product of apparent \( M_r \) 55,000, identical to that of the monomeric unit of G6PD. When the putative coding sequence of G6PD is cloned into the expression vector \( \lambda \) gt11, recombinant plaques are recognized by anti-G6PD immunoglobulin. A transcriptional map of the G6PD gene shows that it is divided into two exons, 0.9 kb (exon I) and 1.8 kb (exon II) long, which are separated by a 2.4-kb intron. The G6PD mRNA is 2.0 kb in length and the steady-state level of the mRNA is similar in both sexes. Measurement of the copy number of the G6PD gene in males and females shows the gene to be present once per X-chromosome in both sexes. No amplification of the gene sequence was observed in males. These results are, therefore, in agreement with the previous suggestion that dosage compensation is the result of enhanced transcription of X-linked genes in males.

*To whom correspondence and reprint requests should be addressed.

**Abbreviations:** Adh, alcohol dehydrogenase; bp, base pairs; DBM, diazobenzyloxymethyl; G6PD, glucose-6-phosphate dehydrogenase; IgG, immunoglobulin; kb, kilobases or 1000 bp; PAGE, polyacrylamide gel electrophoresis; PBS, phosphate-buffered saline; Rd, mol of ribonucleotides per liter \( \times \) time (s); SDS, sodium dodecyl sulfate; 6PGD, 6-phosphogluconate dehydrogenase; TCA, trichloroacetic acid; TEMG, see MATERIALS AND METHODS, section a; u, units.

0378-1119/85/$03.00 © 1985 Elsevier Science Publishers
INTRODUCTION

Glucose-6-phosphate dehydrogenase (G6PD; EC 1.1.1.49) is widely distributed in the animal kingdom and catalyzes the first reaction in the pentose phosphate pathway. In *D. melanogaster*, the gene encoding G6PD has been genetically mapped to the X-chromosome at position l-63.6 and is designated Zw (Young et al., 1963). Cytogenetic analysis has further localized Zw within the cytological interval proximal to 18D1-2 but distal to 18F (Stewart and Merriam, 1974).

G6PD is one of a small number of X-linked enzymes that have been extensively utilized for investigation of dosage compensation at the level of enzyme synthesis (for review, see Lucchesi, 1977; Stewart and Merriam, 1980) Dosage compensation is the equalization of X-linked gene products in males and females (Muller et al., 1931). Unlike mammals, where equalization of X-linked gene products occurs by X-chromosomal inactivation (Lyon, 1961) both X-chromosomes remain active in female *Drosophila* (Kazazian et al., 1965). The equalization of X-linked gene products in male *Drosophila*, which have one dose of X-linked genes and female *Drosophila*, which have two doses of such genes, is believed to be mediated by enhancing the level of transcription of X-linked genes in males (Mukherjee and Beerman, 1965; Korge 1970; Holmquist, 1972). Although these studies suggest that the steady-state level of mRNA transcripts from dosage compensated X-linked genes would be equivalent in males and females, no direct evidence has been published.

Recent studies have shown that the autosomal-linked xanthine dehydrogenase gene (Spradling and Rubin, 1983) and dopadecarboxylase gene (Scholnick et al., 1983) show partial dosage compensation when inserted into the X-chromosome via P-element-mediated transformation (Spradling and Rubin, 1982; Rubin and Spradling, 1982). Conversely, seven cases have been observed in which the X-linked white gene was inserted into autosomal sites, and in each case the white gene was partially dosage-compensated (Hazeldigg et al., 1984). These observations have led to the suggestion that cis-acting 'receptor' sequences may mediate dosage compensation and that such sequences are numerous on the X-chromosome (Hazeldigg et al., 1984).

This hypothesis suggests that other X-linked genes may have closely adjacent receptor sequences and thus retain the ability to exhibit dosage compensation when translocated to autosomal sites. To determine if this is the case, and to investigate other possible mechanisms that might mediate dosage compensation in *Drosophila*, we have chosen the gene encoding G6PD as a model. In this paper we report the isolation and structural organization of the G6PD gene sequence in *D. melanogaster*. We also present evidence that dosage compensation of the G6PD gene in males is manifested at the level of transcription.

MATERIALS AND METHODS

(a) Purification of glucose-6-phosphate dehydrogenase and preparation of anti-G6PD immunoglobulin

Adult *D. melanogaster* (Oregon R+; 10 g) was homogenized at 4°C in 80 ml of 50 mM Tris, pH 8.0, 1 mM EDTA, 7 mM 2-mercaptoethanol, 10% glycerol (TEMG; Steele et al., 1969). The homogenate was centrifuged at 16000 x g for 30 min, and the supernatant was applied to a 2', 5'-ADP agarose (PL Biochemicals) affinity column (110 x 10 mm) equilibrated with TEMG. After washing with 45 ml of TEMG, G6PD was eluted with 9.0 ml of TEMG containing 0.1 mM NADP+ (Brodelius et al., 1974). The enzyme was placed on a DE-52 cellulose column (50 x 5 mm) equilibrated with TEMG and the column was washed with 10 ml of TEMG, containing 50 mM NaCl. The enzyme was eluted with 5 ml TEMG containing 150 mM NaCl. In a typical experiment, the yield of G6PD was determined to be 24%, and the specific activity was approx. 70 u/mg protein. The purification factor was 1296, in excellent agreement with previously reported values (Hori and Tanda, 1980). Enzyme activity at each step of purification was assayed according to Steele et al. (1969).

SDS-PAGE of the purified enzyme showed a major Coomassie blue-stained band of apparent Mr, 55000, which is the apparent Mr of the monomeric unit of G6PD (Lee et al., 1978). A minor band, representing less than 10% of the intensity of the 55-kDa band was observed at apparent Mr, 65000. The
enzyme preparation was free of contamination by 6PGD activity, as assayed by staining the gel with 6PGD specific stain (Hori and Tanda, 1980).

Rabbit antibody against G6PD was prepared as described by DeFlora et al. (1977). Anti-G6PD IgG was purified from rabbit serum by (NH₄)₂SO₄ precipitation, DE-52 cellulose column chromatography (Weir, 1967), and affinity chromatography on a protein A-Sepharose CL-4B column (Goudswaard et al., 1978). Heparin (20 μl/ml) was added to the antibody preparation to inhibit RNase activity.

(b) Enrichment of G6PD mRNA

Polyribosomes were isolated from adult Droso- phila by the method of Benyajati et al. (1980), and suspended in polyribosome buffer (0.3 M NaCl, 50 mM Tris, pH 7.5, 5 mM MgCl₂, 1 μg/ml of cycloheximide, 20 μl/ml of heparin) at a concentration of 1000 A₂₆₀ μ/ml. One ml of anti-G6PD IgG, at 1 mg/ml in PBS was added to 1.0 ml of polyribosomes, and the mixture was incubated for 2 h at 4°C. The mixture was applied to a 1.5-ml protein A-Sepharose CL-4B (Pharmacia) column at 4°C and washed with 80 ml of polyribosome buffer; mRNA in bound polyribosomes was eluted with 3.0 ml of 25 mM Tris, pH 7.6, 20 mM EDTA, 20 μl/ml of heparin (Shapiro and Young, 1981). RNA in the unbound polyribosome fraction (i.e., depleted polyribosomes) and in the specifically bound polyribosomes (i.e., enriched polyribosomes) was further purified by phenol-chloroform extraction, and polyadenylated RNA was isolated by oligo(dT)-cellulose chromatography (Levy and Manning, 1981). This procedure was repeated until approx. 10,000 A₂₆₀ μ of polyribosomes had been processed. Total poly(A)⁺ RNA obtained from the depleted and enriched polyribosomes were 2.0 mg and 14 μg, respectively.

(c) Determination of transcription orientation

(1) S1 protection assay

The 1.2-kb BgIII-AvaI fragment (see Fig. 2) within exonII was ³²P-labeled at the 5' terminus and digested with endonuclease PstI to generate a 0.4-kb BgIII-PstI fragment and 0.8-kb PstI-AvaI fragment. These DNA fragments (approx. 1 x 10⁻⁸ μg of coding sequence) were hybridized to adult polyribo- somal poly(A)⁺ RNA (30 μg) under conditions that allow RNA-DNA hybridization, but do not allow DNA-DNA reannealing (Casey and Davidson, 1977; Levy et al., 1982). The R₀ₐₚ value achieved was 460, which is approx. ten times that required for saturation hybridization under these conditions (Levy et al., 1982). After hybridization the sample was treated with S1 nuclease and the RNA-protected DNA was electrophoresed on an alkaline agarose gel (Maniatis et al., 1982). After electrophoresis the gel was neutralized in 3 M NaCl, 0.5 M Tris, pH 7.0, blotted to nitrocellulose, and exposed for autoradiography.

(2) Southern hybridization

G6PD-enriched poly(A)⁺ RNA was partially hydrolyzed at alkaline pH and 5'-end labeled as described (Levy et al., 1982). End-labeled RNA was purified by Sephadex G-50 chromatography and fractionated by oligo(dT) chromatography into a 5'-enriched probe (unbound) and a 3'-enriched probe (bound). Restriction fragments spanning different parts of the G6PD gene (see RESULTS, section c) were electrophoresed on agarose gels, Southern transferred, and hybridized with 5'- or 3'-end enriched RNA probes (Levy et al., 1982). The blots were subjected to autoradiography.

(d) Radiolabeling of DNA and RNA

DNA was nick-translated with [α-³²P]dCTP (Amersham) to a specific activity of 2-4 x 10⁸ cpm/μg using a nick-translation kit from Bethesda Research Laboratory (BRL). The radiolabeled DNA was then purified as described by Levy et al. (1982). RNA was 5'-end-labeled to a specific activity of 3-5 x 10⁷ cpm/μg using T4 polynucleotide kinase (Boehringer-Mannheim) and [γ-³²P]ATP (Levy et al., 1982).

(e) Restriction enzymes, preparation of RNA and DNA, electrophoresis, Southern transfer, Northern transfer, library screening and subcloning

All restriction enzymes were purchased from BRL and used as recommended. Isolation and electrophoresis of nucleic acids and Southern and Northern transfers are described elsewhere (Levy and Manning, 1981; Levy et al., 1982). Hybridization of
5’-end-labeled RNA to Southern blots and filters for library screening was according to Fouts et al. (1981). Northern blots were prehybridized and hybridized as described by Thomas (1980).

The DNA clone described here was selected by in situ plaque hybridization technique (Benton and Davis, 1977) from a library of *D. melanogaster* genomic DNA cloned in phage λ Charon 4 (Maniatis et al., 1978).

The DNA fragments, 3.0-kb *SalI* and 3.9-kb *EcoRI*, containing exon I and exon II, respectively, were subcloned in the polylinker of the vector pUC9 (Vieira and Messing, 1982), and the subclones were named pDMG20/3.0SalI and pDMG20/3.9RI, respectively. A subclone, sAC-1 (Goldberg, 1980), containing the *Adh* gene of *D. melanogaster* was obtained from Dr. J.C. Lucchesi, University of North Carolina.

(f) Hybrid selection of G6PD mRNA

For hybrid selection of G6PD mRNA, recombinant plasmid DNA pDMG20/3.9RI containing exon II was linearized with *HindIII* and covalently coupled to DBM-cellulose (Anderson et al., 1979). Enriched polyribosomal poly(A)+RNA (1 μg) was hybridized to 1.3 μg of cellulose-bound DNA in 10 μl of 70% formamide containing 0.1 M Tris, pH 7.8, 0.3 M NaCl, 10 mM EDTA at 46°C for 24 h. The DNA-DBM-cellulose was washed three times with 200 μl of 0.3 M Na-acetate, pH 7.5, three times with 200 μl of 55% formamide containing 0.7 M NaCl, 0.2 M Tris, pH 7.5, at 25°C and twice with 200 μl of the 55% formamide solution at 42°C. Hybridized RNA was recovered by incubating the DNA-DBM-cellulose in 300 μl of 99% formamide for 2 min at 60°C followed by ethanol precipitation (Anderson et al., 1979). The hybrid-selected poly(A)+RNA was translated in a rabbit reticulocyte cell-free translation system (Bethesda Research Laboratory) using *3H*leucine as label. To analyze G6PD synthesis 20 μl of post-ribosomal supernatant of the reaction mixture (approx. 25 000 TCA-precipitable cpm) 30 μl of PBS, 2.5 μg anti-G6PD-IgG and 30 μg goat anti-rabbit-IgG (Sigma), were mixed and immunoprecipitated (Rosen, 1976). The precipitate was dissolved in 20 μl sample buffer (Laemmli, 1970), heated at 100°C for 2 min and adjusted to 5 M urea. For total product analysis 10 μl of the post-ribosomal supernatant was digested with 100 μg/ml RNAse for 30 min at 37°C and adjusted with sample buffer and urea. The total (lanes a, c) and anti-G6PD-IgG-precipitable products (lanes b, d) synthesized in the cell-free system were analyzed by SDS-urea PAGE (Storti et al., 1976) and fluorography. Lanes a, b: enriched poly(A)+RNA; lanes c, d: depleted poly(A)+RNA: lane e shows polypeptide synthesized by globin mRNA which is not precipitated by anti-G6PD-IgG (lane f). The arrow shows a 55-kDa polypeptide synthesized by the enriched poly(A)+RNA. Mr markers (left margin): BSA (66 kDal), ovalbumin (45 kDal), pepsin (34.7 kDal), trypsinogen (24 kDal).

shown in Fig. 1. Although the major translation products of enriched and depleted poly(A)+RNA of the two RNAs are essentially identical, a minor polypeptide of apparent Mr, 55 000, the size of the G6PD monomer (Lee et al., 1978), is visible only in the translation products directed by the enriched poly(A)+RNA.

RESULTS

(a) Isolation of the G6PD gene

An electrophoretic profile of the translation products of enriched and depleted poly(A)+RNA is shown in Fig. 1. Although the major translation products of enriched and depleted poly(A)+RNA of the two RNAs are essentially identical, a minor polypeptide of apparent Mr, 55 000, the size of the G6PD monomer (Lee et al., 1978), is visible only in the translation products directed by the enriched poly(A)+RNA. Immunoprecipitation of these pro-
ducts with anti-G6PD IgG shows a polypeptide band of Mr 55,000 and a few smaller polypeptide bands (Fig. 1, lanes b and d), which may represent premature termination of synthesis of G6PD or proteolytic degradation of the G6PD monomer in the cell-free translation system. The intensity of the 55-kDa polypeptide band in the enriched poly(A)* RNA translation products was consistently higher (three experiments) than that observed for the depleted poly(A)* RNA, indicating a detectable difference in the abundance of G6PD mRNA between the two poly(A)* RNAs. As discussed below, the abundance of G6PD mRNA in the enriched poly(A)* RNA is approx. 67-fold higher than that in the depleted poly(A)* RNA.

To isolate the G6PD gene sequence pairs of duplicate plaque filters of the Drosophila genomic library were hybridized with [32P]RNA probes from the enriched and depleted poly(A)* RNAs, respectively. From an initial screening of approx. 44,000 plaques a single clone, λDmG21, was observed upon successive plaque purifications to hybridize only with the enriched poly(A)+ RNA (not shown).

Fig. 2 shows the restriction map of the cloned 13.0-kb EcoRI Drosophila genomic DNA fragment in λDmG21. Hybridization of enriched [32P]poly(A)* RNA to Southern (1975) blots of restricted λDmG21 DNA was confined to two separate regions of the DNA, the 0.9-kb PvuII-BamHI fragment and the 1.8-kb BglII-PvuI fragment. Depleted [32P]poly(A)* RNA was also observed to hybridize with these two DNA fragments, although the intensity of the hybridization signal was notably less than that observed with the enriched poly(A)* RNA. These results suggest that the coding region of the putative G6PD gene is contained within the 13.0-kb EcoRI fragment and is interrupted by at least one intron 2.4 kb in length.

That λDmG21 contains the coding sequence for G6PD was confirmed by three methods. [3H]λDmG21 DNA and the 3.9-kb EcoRI fragment containing exonI1 were separately hybridized in situ to larval salivary gland polytene chromosomes. Hybridization of either [3H]-labeled probe was observed only at the 18D region of the X-chromosome (Fig. 3), consistent with the chromosomal position of the Zw+ locus (Stewart and Merriam, 1974). In the second method, poly(A)* RNA complimentary to exonI1 was hybrid-selected and translated in a rabbit reticulocyte lysate system. SDS-urea PAGE of the translational products (Fig. 4b) showed three polypeptides of apparent Mr 92,500, 55,000 and 50,000. The bands at Mr 92,500 and Mr 50,000 are likely due to the presence of endogenous RNA in the reticulocyte lysate (Robson et al., 1982), since these bands are also observed in the absence of exogenous RNA (Fig. 4a). The 55-kDa polypeptide, identical in apparent Mr to the monomeric unit of G6PD, is observed only upon addition of the hybrid selected poly(A)* RNA. In the third method, the 3.9-kb EcoRI fragment containing exonI1 was partially digested with exonuclease BAL31, repaired with the Klenow fragment of DNA polymerase I and blunt-end-ligated with EcoRI linkers. Following digestion with EcoRI, the fragments were inserted into the EcoRI restriction site of the expression vector λgtl1 (Young and Davis, 1983), and recombinant λ phages were screened with anti-G6PD IgG. Approx. 20% of the recombinant phages showed a positive signal, which is in reasonable agreement with the expected number of 1 in 6, assuming random orientation of the EcoRI fragments in coding phase. Based upon these results we conclude that λDmG21 contains sequences coding for G6PD.

Fig. 2. Restriction map of the Drosophila DNA insert (box) in λDmG21. The location of the transcribed regions is denoted (exonI and exonI1) and was determined by hybridization of enriched [32P]poly(A)* mRNA to Southern blots containing DNA fragments generated by digestion with various restriction endonucleases. The direction of transcription (5' → 3') is from left to right.
Fig. 3. Chromosomal localization of the G6PD gene. DmG21 was labeled with [3H]dCTP and [3H]dTTP by nick-translation and hybridized to the salivary gland polytene chromosomes (Levy et al., 1982). The results show that the DNA hybridizes to the 18D region of the X-chromosome. Similar results were obtained when a 3.9-kb EcoRI fragment was used as a probe. The cytological map described by Lefevre (1976) was used for chromosomal localization.

(b) Measurement of G6PD mRNA size and relative abundance in males and females

[3H]Uridine incorporation into the single polytenic X chromosome of male larval salivary glands and the paired X chromosomes of females is equivalent (Mukherjee and Beermann, 1965), suggesting that dosage compensation is a transcriptional phenomenon. Since this observation suggests that the steady-state level of mRNA encoded by X-linked dosage compensated gene sequences is equivalent in males and females, we determined the relative level of G6PD mRNA in the two sexes.

Initially, the size and relative abundance of G6PD mRNA in the enriched and depleted poly(A)+ RNA preparations was measured by Northern blot hybridization. As shown in Fig. 5, the length of the G6PD mRNA transcript is 2.0 kb and the abundance of G6PD mRNA in the enriched poly(A)+ RNA is greater than in the depleted poly(A)+ RNA. Overexposure of the autoradiogram of Fig. 5 showed the presence of a minor band of length 2.3 kb. Possible implications of this RNA species are discussed below (see DISCUSSION, section b). To quantitate the relative abundance of the two RNA fractions, the area of each blot containing only the intensely hybridizing band was removed and counted by liquid scintillation. When the 3.9-kb EcoRI fragment was used as the probe, G6PD mRNA transcripts were seen to be 67 times more...
Fig. 5. Blot hybridization of poly(A)* RNAs enriched for and depleted of G6PD mRNA sequences. Northern blots of poly(A)* RNA enriched for or depleted of G6PD mRNA sequences were hybridized either with [32P] DNA of subclone pDmG20/3.9RI (lanes a–c) or pDmG20/3.0 SalI (lanes d–f). Lanes a, b: 0.5 µg of enriched poly(A)* RNA from polyribosome preparations 1 and 2, respectively; lane c: 10.0 µg of depleted poly(A)* RNA from preparation 1; lane d: 0.2 µg of enriched poly(A)* RNA from preparation 2; lanes e, f: 0.2 and 5.0 µg, respectively, of depleted poly(A)* RNA from preparation 1. Numbers in kb on the margin refer to the migration of 32P-labeled HindIII fragments of phage λ DNA.

abundant in the enriched poly(A)* RNA than in the depleted poly(A)* RNA (Fig. 5, lanes a–c). A similar difference (i.e., 58-fold) in the abundance of G6PD mRNA transcripts between the two RNAs was observed when the 3.0-kb SalI fragment was used as the hybridization probe (Fig. 5, lanes d and f).

To determine the steady-state level of G6PD mRNA transcripts in male and female Drosophila equivalent amounts of polyribosomal poly(A)* RNA from adult male and female flies were analyzed by Northern blot hybridization (Fig. 6). Quantitation of radioactivity in the hybridizing bands showed the level of G6PD mRNA transcripts in adult male RNA to be slightly greater than that of the female RNA. Essentially identical results were obtained when the 3.0-kb SalI fragment was used as the DNA probe (not shown). To determine whether the observed difference in the steady-state level of G6PD mRNA in males and females is a result of inaccuracy in RNA quantitation, the steady-state level of Adh mRNA in these two RNA samples was measured. As shown in Fig. 6 and Table I, male RNA has a slightly higher level of Adh mRNA than female RNA. The ratio of the steady-state levels of G6PD...
TABLE I
Levels of G6PD and Adh mRNAs in male and female polyribosomal poly(A)⁺ RNA

<table>
<thead>
<tr>
<th>Probes*</th>
<th>µg RNA</th>
<th>cpm hybridized</th>
<th>G6PD/Adh ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Male</td>
<td>Female</td>
<td>Male</td>
</tr>
<tr>
<td>G6PD DNA</td>
<td>1.0</td>
<td>581</td>
<td>454</td>
</tr>
<tr>
<td>G6PD DNA</td>
<td>2.0</td>
<td>1225</td>
<td>1146</td>
</tr>
<tr>
<td>Adh DNA</td>
<td>0.5</td>
<td>4555</td>
<td>3976</td>
</tr>
</tbody>
</table>

* Respective areas of the Northern blot showing hybridization in Fig. 6 were excised out and radioactivity determined. Nitrocellulose of an equivalent area was excised where no hybridization was observed and counted to determine background radioactivity.

b Probes used were [²³P]-labeled pDmG20/3.9RI (G6PD DNA) and sac-1 (Adh DNA).

mRNA and Adh mRNA in the two sexes is found to be essentially identical, thus indicating that the steady-state level of G6PD mRNA in male and female Drosophila is equivalent.

(c) Transcription orientation

Two methods were used to determine the transcriptional orientation of the G6PD gene on the restriction map shown in Fig. 2. First, a 0.4-kb BglII-PstI fragment and a 0.8-kb PstI-AvaI fragment were 5' end-labeled at the BglII and AvaI sites, respectively, and hybridized with a large sequence excess of adult polyribosomal poly(A)⁺ RNA. Following S1 nuclease digestion (Fig. 7) only the 0.8-kb PstI-AvaI fragment is protected, thus providing the 5'-3' orientation shown in Fig. 2.

In the second method enriched poly(A)⁺ RNA was partially hydrolyzed, 5'-end-labeled with [γ²³P]ATP (Levy et al., 1982), and chromatographed on an oligo(dT) cellulose column. The 5' end-enriched (unbound) and 3' end-enriched (bound) sequences were hybridized to Southern blots containing the following DNA fragments in equimolar amounts (Fig. 2): (a) 1.5-kb SalI-BamHI containing exon I; (b) 1.8-kb EcoRI-AvaI containing exon II and (c) 0.45-kb AvaI located at the 3' end of exon II. The 5'-end-enriched RNA sequences hybridized with the 1.5-kb SalI-BamHI and 1.8-kb EcoRI-AvaI fragments but not with the 0.45-kb AvaI fragment (results not shown). When 3'-end-enriched RNA sequences were used as a probe, hybridization was seen only with the 1.8-kb EcoRI-AvaI and 0.45-kb AvaI fragments, but not with the 1.5-kb SalI-BamHI fragment. These results suggest that the 1.5-kb SalI-BamHI fragment is located at the 5' end of the G6PD mRNA and the 0.45-kb AvaI fragment is located near the 3' end of the G6PD mRNA. This leads to the 5'-3' orientation shown in Fig. 2 and is consistent with the results of the S1 nuclease mapping experiment.
(d) Copy number of the G6PD gene in male and female *Drosophila* genomes

As shown above, the steady-state amount of G6PD mRNA is approximately equivalent in both male and female *Drosophila*. One explanation for this would be a single duplication of the G6PD gene in males, thus providing G6PD mRNA equivalence between the sexes.

We therefore examined the average copy number of the G6PD gene sequence in the genomes of male and female *Drosophila*. Genomic DNA from adults was digested with *PstI* and blotted to nitrocellulose after gel electrophoresis. Included on the Southern blot was DNA from subclone pDmG20/3.9RI, containing exonII equivalent to 1, 2, 4 and 6 copies per haploid female genome (i.e., one set of autosomes and one X-chromosome). When the Southern blot was probed with a 32P-labeled 1.35-kb *PstI* fragment containing the 3'-distal half of exonII, the only genomic DNA band that hybridized was of length 1.35 kb (Fig. 8). When the intensities of the hybridization in the genomic DNAs are compared with those of the various equivalents in the cloned DNA, it is apparent that both males and females have one copy of the G6PD gene sequence per X chromosome and that the G6PD gene in the male X-chromosome is not duplicated.

**DISCUSSION**

(a) Isolation of the G6PD gene sequence

We have been able to select from a *Drosophila* genomic λ library a recombinant phage, λDmG21, containing the DNA sequence encoding G6PD. Three separate approaches were employed to confirm the presence of G6PD coding sequences in the recombinant λ phage. First, the genomic location of the inserted *Drosophila* DNA fragment was shown by in situ hybridization to correspond to the chromosomal site of G6PD. Second, the in vitro translation product of hybrid-selected mRNA was identical in *M* (i.e., 55000) to the monomeric unit of G6PD. Due to the low abundance of G6PD mRNA in the total RNA population, amounts of hybrid-selected RNA could not be obtained in sufficient quantities to determine whether the 55-kDal translation product is recognized by antisera directed against G6PD. However, digestion of the 3.9-kb *EcoRI* fragment containing exon II with BAL 31 nuclease, followed by insertion of the resected DNA fragments into the expression vector λ gt11 (Young and Davis, 1983), did yield recombinant phages, 20% of which reacted positively with anti G6PD IgG. Collectively, these results indicate that λ DmG21 contains sequences that encode G6PD.

![Fig. 8. Determination of the G6PD gene copy number in adult male and female *Drosophila* DNA. Nuclear DNAs (10 μg each) from adult male (lane a) and female (lane b) flies digested with *PstI* and electrophoresed on a 1.0% agarose gel. Included in the gel was DNA from subclone pDmG20/3.9RI, 1.0, 2.0, 4.0 and 6.0 female haploid genome equivalents (lanes c-f, respectively). A Southern blot of the gel was hybridized to a radiolabeled 1.35-kb *PstI* fragment contained in exon II.](image)
(b) G6PD mRNA

As shown in Fig. 6, the size of the G6PD mRNA in adult male and female flies is 2.0 kb, and the steady-state levels of the mRNAs in the somatic cells of the two sexes are similar. This observation indicates that similar levels of G6PD enzyme activity in the two sexes (Seecof et al., 1969) is due to the steady-state level of G6PD mRNA. Also, it supports the previous conclusions, based on studies using salivary gland chromosomes (Mukherjee and Beermann, 1965), that dosage compensation is the result of increased transcriptional activity of the male X chromosome. Our results do not, however, eliminate differential RNA processing and/or RNA turnover rates as possible mechanisms for generating equivalent levels of G6PD mRNA in the two sexes.

Overexposure of the autoradiogram (Fig. 6) shows the presence of a minor RNA species of length 2.3 kb in both male and female poly(A)+ RNA. Since the 2.3-kb RNA hybridizes with exon I and exon II gene probes, it is possible that this RNA represents a minor species of G6PD mRNA. Whether this RNA results from either differential processing of the G6PD primary transcript or a different transcriptional start or stop site from that of the major 2.0-kb mRNA has not been determined. We have observed, however, the 2.3-kb RNA to be present in the poly(A)+ RNA from several embryonic stages of development as well as the three larval stages and the pupal stage (R.G. and J.E.M., unpublished observation). In all cases the ratio of the 2.3- and 2.0-kb mRNAs remains unaltered. Thus it is unlikely that this RNA species represents a minor component in one stage of development and a major component in another.

(c) Gene copy number

It is formally possible that the equivalent steady-state levels of G6PD mRNA in the two sexes result from duplication of the G6PD gene sequence in males. To examine this possibility, the copy number of the G6PD gene was determined in total genomic DNA from both male and female flies (Fig. 8). The results of this experiment show that the number of G6PD gene sequences in male and female genomes is directly proportional to the number of X-chromosomes in the two sexes, and that the G6PD gene is present as a single copy sequence on the X-chromosome. Dosage compensation of G6PD is not, therefore, due to amplification of the G6PD gene in males.

ACKNOWLEDGEMENTS

We thank R. Yamamoto for his help with the immunization of rabbits and D. Peterson for help in cloning in λ gt11 and immunological screening. We also thank Dr. John Lucchesi for helpful suggestions and J. Massey for technical assistance. This investigation was supported by Grant GM 22207 awarded by the National Institute of Health.

REFERENCES


Communicated by A.D. Riggs.