Evidence for a Stabilizer Element in the Untranslated Regions of Drosophila Glutathione S-Transferase D1 mRNA*

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The neighboring genes gstD1 and gstD21 share 70% sequence identity. gstD1 encodes a 1,1,1-trichloro-2,2-bis-(P-chlorophenyl)ethane dehydrochlorinase; gstD21, a ligandin. Both of their mRNAs are inducible by pentobarbital but otherwise behave very differently. Intact gstD21 mRNA is intrinsically labile, but becomes stabilized when separated from its native untranslated region (UTR). In contrast, whereas gstD1 mRNA is very stable in its entirety, without its native UTRs it becomes even more labile than that of gstD21. Decay patterns from four chimeric D1-D21 mRNAs, designed to reveal the individual importance of each molecular region to stability, strongly indicate the presence of destabilizing elements in the coding region of gstD1 mRNA. Thus, the UTRs of this molecule must contain a dominant stabilizer element that overrides the destabilizing influence of the coding region and confers overall stability to the entire molecule. The suspected presence of such a stabilizer element in gstD1 mRNA extends a concept from mRNA metabolism in yeast and cultured mammalian cells to include a multicellular organism, Drosophila melanogaster. The complementary presence of destabilizing and stabilizer elements on the same mRNA reveals a regulatory mechanism by which an abundant mRNA can be further induced by a chemical stimulus, or otherwise be returned to normal levels during recovery.

An effective way to regulate gene expression involves controlling mRNA stability (1–3). The major measure of mRNA stability is its half-life (1, 4), which determines the time required for a mRNA to reach a new steady state following a change in transcription rate (e.g. by inducers such as pentobarbital).

We have been using mRNAs of the Drosophila glutathione S-transferase (gst)† genes D1 and D21 as reporters to investigate pentobarbital-mediated changes in mRNA stability. The early paradigm for RNA metabolism associates mRNA decay rates largely with the strength of the destabilizing sequences of the molecule (1–3, 5). But the recent discovery of a handful of active stabilizer elements (STE) in certain mammalian and yeast mRNAs (6–9) has called for a revision to this model. Although gstD21 mRNA is labile, the coding region of the gene gains stability when separated from its native UTRs. Just the opposite is true for mRNA of the D21 homologue, gstD1. This mRNA is very stable, but the coding region of the molecule alone, without native UTRs, is even more labile than intrinsically unstable gstD21 mRNA. To further investigate the nature and the cause of this instability, we assembled chimeric D1-D21 mRNAs containing various segments of the D1 coding sequence. We observed that these chimeras were also unstable in the same context of heterologous UTRs as the D1 coding sequence. We repeatedly detected putative decay intermediates from the D21 portion, but seldom the D1 segment of these chimeric mRNAs. Such patterns are strong evidence for the presence of cryptic destabilizing cis-acting elements in the coding region of gstD1 mRNA. Our observations also suggest that the stability of already abundant gstD1 mRNA is maintained by a stabilizer element in its UTRs, which overrides any destabilizing elements in the coding region. We speculate that this combination of stabilizer and destabilizing elements helps to regulate gstD1 mRNA levels in response to pentobarbital induction and to generally maintain mRNA stability. As we compare the characteristics of labile gstD21 mRNA with those of gstD1 mRNA, in which a completely different arrangement of cis-acting elements govern RNA metabolism, we note the potential for significant diversity in the regulation of different members of a single multigene family.

EXPERIMENTAL PROCEDURES

Materials—Bacteriological media were purchased from Invitrogen, and chemicals from ICN, Invitrogen, or Sigma. Oligonucleotides were products of either Integrated DNA Technologies, Inc. (Corailville, IA) or Invitrogen. Radioactive nucleotides ([α-32P]UTP) were purchased from ICN (Irvine, CA). RPA III kits were purchased from Amobin (Austin, TX). Restriction enzymes were products of New England Biolabs, and chemicals from Promega. Tobacco acid pyrophosphatase was a product of Epicentre Technologies (Madison, WI). T7 RNA polymerase was a generous gift from Bi-Cheng Wang (University of Georgia, Athens, GA). Escherichia coli DH5α competent cells and Pfx DNA polymerase were products of Invitrogen. The plasmid vector pCaSpeR-hs-act for Drosophila transformation was obtained from C. S. Thummel of the University of Utah (10). The 22–3 line [Pf cyt 22–3(99B)] (11) expressing transposase and the yw line were obtained from Susan Abmayr and David Gilmore, respectively, both of the Department of Biochemistry and Molecular Biology, the Pennsylvania State University. The E. coli expression plasmids for GST D1 (pGTDm1-KK) and GST D21 (pGTDm21-KK) were previously reported (12). The plasmids for C-
Transgenic Constructs and Nomenclature—Site-directed mutagenesis was carried out according to the QuikChange™ mutagenesis procedure (Stratagene). All clones were sequenced at the Penn State Nucleic Acid Facility prior to microinjection into embryos.

The primers D1-F-5′/H11032 (GGAATTCCCCAACATGGTTGACTTCTACT-ACC) and D1-F-3′/H11032 (CGGGATCCGTGAATATCAGGCTTACT) were used to PCR amplify the gstD1.F coding region. PCR amplification (12) of the D1-D21 and D21-D1 chimeras was set up using the appropriate pair permutations of primers from the set D1-F-5′/H11032, D1-F-3′/H11032, D21-F-5′/H11032 (GG-AATTCCCCAACATGGACTTTTACTACGCC), and D21-F-3′ (CGG-GATCCTCGTATCGCCATAC). The coding region ofgstD1, with a FLAG octapeptide at its C terminus (gstD1-F), was PCR-amplified from pGTDm1-FLAG-KK using primers D1-F-5′/H11032 and D1-F-3′/H11032 (KK refers to the pKK223-3 expression vector (Amersham Biosciences)). The BamHI-EcoRI-digested fragment was cloned into pCaSpeR-hs-act (10) to obtain pBA1-CaSpeR. The pmRNA is called D1F-UTR (D1-FLAG/H11002 UTR). Primers D21-F-5′/H11032 and D21-F-3′/H11032 were used to introduce by PCR BamHI and EcoRI sites at the ends of the D21-F-G8S,G9S coding region. The PCR products were then digested with BamHI and EcoRI and ligated into BamHI-EcoRI-digested pCaSpeR-hs-act to generate pBA3-CaSpeR.

To switch segments of GST D1 and GST D21 at the 66th and 65th residues (Fig. 1), primers D1-F-R66-SmaI-S (GTGGGAGTCCCGCGCATCCAGGTG) and D1-F-R66-SmaI-AS (CACCTGGATGGCCTCTCCCAG) were used to introduce a SmaI site into pGTDm1-KK by site-directed mutagenesis without changing the amino acid sequence encoded by the template. The SmaI fragment of the resulting plasmid (pGTDm1-Sma1-KK) was cloned into calf intestinal alkaline phosphatase-treated, SmaI-digested pGTDm1-FLAG-G8S,G9S-KK to obtain pBA12-KK. The transgene, which contains the N-terminal 65 amino acids of D21 and C-terminal 150 amino acids of D1F, is called D21-65-
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D1. The opposite swap, resulting in pBA10-KK, was made by inserting the Smal fragment of pGTDm21-FLAG-KK into calf intestinal alkaline phosphatase-treated, Smal-digested pGTDm1-FLAG-KK. The transgene, which contains the N-terminal 66 amino acids of D1 and C-terminal 157 amino acids of D21, is called D1–D21. The exchange at the 171st and 217th amino acid positions was initiated by the introduction of an XhoI site into both pGTDm1-FLAG-KK (D1F-F171L-XhoI-S (GCAGTGTTGGCAACTCGGATGACGACAACTCG-G)) and pGTDm1-FLAG-GS8,GS9-KK (D21F-F171L-XhoI-S (GTCGAGTTAGTATGTCGGATCAGAGCTACGCTC)) and D21-F171L-XhoI-AS (GAGACTTTTCTCGACTACGTAA-CCTTGCAA), which yield pBA1-XhoI-KK and pBA2-XhoI-KK, respectively. The XhoI-Smal fragment of pBA1-XhoI-KK was cloned into XhoI-digested pBA1-XhoI-KK to generate pBA13-KK. This led to the transgene D1–171-D21, which contains 171 amino acids of D1 followed by 52 amino acids of D21–F at the C terminus. Because the gstD1 coding region has a second Smal site that interferes with cloning, the XhoI-PstI fragment of pBA1-XhoI-KK was cloned into pBA2-XhoI-KK, resulting in pBA15-KK. The corresponding transgene is called D21–170-D1, which contains 170 amino acids of D1 followed by 45 amino acids from the C-terminal of D1–F. Prior to cloning into pCaSpeR-hs-act DNA, BamHI and EcoRI restriction sites were introduced by PCR at the desired ends of the constructs described thus far, using a pair of appropriate primers from the set D1-F-S, D1-F-3′, D21-F-5′, and D21-F-3′. A FLAG-less version of pBA1-CaSpeR (i.e. pBA22-CaSpeR) was constructed using the same strategy, but changing the 3′-end primer pair to D1-3′ (GGGATTAGTATGTCGGATCAGAGCTACGCTC) from D1-F-3′. This transgene is called D1-UTR. Construction of transgene D21L-UTR will be described elsewhere.

All clones in pKK23-3 and pCaSpeR-hs-act vectors were sequenced at the Penn State Nucleic Acid Facility. Results also showed that the four chimeric proteins (D1–66-D21, D21–65-D1, D1–171-D21, and D21–170-D1) were successfully expressed from pKK23-3-based constructs described (13, 14). The newly enclosed G0 flies were crossed singly to w1118 females to remove any transposase background. Yellow-to red-eyed G1 progeny were distributed into clean milk bottles in approximately equal numbers using a Concert™ rapid plasmid DNA isolation kit (Invitrogen).

RESULTS

DNA Isolation and RPA Analysis—RPA was isolated from pulverized flies according to a protocol from Ulrich et al. (16). The templates used to prepare our radiolabeled riboprobes, pSP64(A)/D21AS, pSP64(A)/D1AS, and pSP64(A)/RP-49AS, were constructed by RT-PCR amplification. Each plasmid DNA was linearized with an appropriate restriction enzyme then transcribed in vitro using [α-32P]UTP. RPA analyses of 40 μg of total RNA samples were conducted according to procedures specified by Ambion, manufacturer of the RPAIII kits. In our figures, we call the protection product of endogenous gstD1 mRNA “endo-D1.” For transgenes, protection products of expected sizes were labeled as “transgene”; those smaller than the expected sizes are called “decoy intermediates” (15). Identification of Cryptic Destabilizing Element(s) in the gstD1 mRNA—The 5′-end sequence of the gstD1 mRNA was determined by primer extension using the primer 5′-AGCAGGAGGGAGGAGGGCGGCA-3′ and by circular RT-PCR (17, 18). Decapping, DNase I treatment, and circularization of RNA were carried out according to a procedure by Couttet et al. (18). 5 μg of circularized RNAs was used for reverse transcription using a GSTD1-specific primer 5′-GGCGGATCCTGGGCGCTCGTACGACGACGACG-3′. The resulting cDNA reaction mixture was boiled for 5 min and then digested with a mixture of RNase A and RNase T1. The treated cDNA was recovered by phenol extraction and ethanol precipitation. One percent of the recovered cDNA was taken for PCR amplification, using 1 unit of Phusion DNA polymerase and the primer pair 5′-GGCGGATCCTGGGCGCTCGTACGACGACGACG-3′ and 5′-GGCGGATCCTGGGCGCTCGTACGACGACGACG-3′, as described by Invitrogen. The PCR product was digested, gel-purified, and then cloned into BamHI-SacI-digested pSP64(A). Two clones were randomly selected for sequencing to determine the 5′ and 3′ end sequences of the gstD1 mRNA. Finally, Southern blot analysis was carried out with 5′- and 3′-end-labeled oligo(DT)18 to determine the length of the poly(A) of each mRNA (19).

Complete Sequence of the gstD1 mRNA—Based on sequencing results obtained for the cRT-PCR clones, the 5′-UTR of gstD1 mRNA spans 64 nucleotides, and primer extension yielded multiple bands, marking D1 mRNAs with 5′-UTR sequences of 67, 66, 64, 63, 61, and 60 nucleotides in length (data not shown). Two cRT-PCR clones were sequenced. One had a 5′-UTR of 63 nucleotides, the other, one of 64 nucleotides. The 3′-UTR of gstD1 mRNA is 132–135 nucleotides long, with variation because of uncertain cleavage over a stretch of As in the genomic sequence (20, 22). Total RNAs from control or PB-treated flies yielded cRT-PCR products of gstD1 mRNA. Moreover, they did so regardless of decapitation by tobacco acid pyrophosphatase, indicating the presence of uncapped D1 mRNA (Fig. 2). The presence of multiple primer extension products of varying size supports the notion that some gstD1 mRNAs are uncapped and missing a few nucleotides at the 5′-end.

In contrast, the same preparations of RNAs yielded no cRT-PCR products for gstD21 in the absence of tobacco acid pyrophosphatase when a D21 primer pair was used under the same set of experimental conditions (data not shown). This affirms that a small contingent of stable, uncapped gstD1 mRNA exists among a capped majority population whose molecules have an average of ~10 As at the 3′ ends under both control and PB-treated conditions. The uncapped and shorter than full-length gstD1 mRNA molecules with short poly(A) tails are probably decay intermediates stabilized by a stabilizer element (Ref. 9 and see “Discussion”).
D21L sequence minus the native UTRs. Whereas chimeric the same sequence minus the FLAG TM; and D21L-UTR, the structs: D1F-UTR (D1F-UTR region to yield transgenic line D1F-UTR. We used RPA to compare the mRNA expression levels of three chimeric constructs: D1F-UTR (D1F-UTR lanes 5 and hatched rectangle) and D1-F (rectangle D1 mRNA (1–gst 829).

The sizes of the protected fragments are 829 nucleotides for endogenous gstD21(L) product of chimeric D1 mRNAs; –3 and 5). We were surprised to observe, then, that contrary to the current paradigm of mRNA stability, we did not anticipate the relative instability of the transgenic D1 mRNAs. These unexpected results strongly suggest that the coding region of gstD1 mRNA contains one or more cryptic destabilizing element in the UTRs. This association reflects the standing model, chimeric D1 mRNA, which contains only the D1 coding sequence, was actually very labile (Fig. 3 C) showed that this chimeric D1F-UTR mRNA expression was induced to a great extent by 1 h of heat shock at 35 °C (Fig. 3B). Results of shortened heat shock treatments (of incubation lasting 5–40 min at 35 °C) showed that this chimeric D1F-UTR mRNA was inducible by heat shock but yielded very labile product (Fig. 3D). Chimeric D1F-UTR mRNA levels increased with the duration of heat shock for up to 40 min, but always remained much lower than those of endogenous gstD1 mRNA (Fig. 3, C and D). Thus, this particular nonspecific 3′ end extension to the D1 coding sequence did not sufficiently replace the function of the native 3′-UTR sequence.

The critical difference between the endogenous gstD1 mRNA and the transgenic D1 mRNAs, from D1-UTR and D1F-UTR, is in the presence or absence of native gstD1 UTRs. We had previously observed that endogenous gstD1 mRNA is stable under both control and PB treatment conditions (15). Given the current paradigm of mRNA stability, we did not anticipate the relative instability of the transgenic D1 mRNAs. These unexpected results strongly suggest that the coding region of gstD1 mRNA contains one or more cryptic destabilizing element in the UTRs. This association reflects the standing model, chimeric D1 mRNA, which contains only the D1 coding sequence, was actually very labile (Fig. 3 C) showed that this chimeric D1F-UTR mRNA expression was induced to a great extent by 1 h of heat shock at 35 °C (Fig. 3B). Results of shortened heat shock treatments (of incubation lasting 5–40 min at 35 °C) showed that this chimeric D1F-UTR mRNA was inducible by heat shock but yielded very labile product (Fig. 3D). Chimeric D1F-UTR mRNA levels increased with the duration of heat shock for up to 40 min, but always remained much lower than those of endogenous gstD1 mRNA (Fig. 3, C and D). Thus, this particular nonspecific 3′ end extension to the D1 coding sequence did not sufficiently replace the function of the native 3′-UTR sequence.

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was unstable, particularly in the 201-nucleotide region of D1 (codons numbers 1–67). A time course analysis of heat shock induction (Fig. 4B, D1–66-D21) revealed that the chimeric mRNA was induced as soon as the inside of the experiment bottle reached 32 °C, between 5 and 10 min inside the 35 °C oven. This protected band from the D21 segment appeared exclusively for the transgene D1–66-D21 and was not observed in other transgenic or nontransgenic lines. The D1 portion, on the other hand, for which no band showed, probably degraded rapidly (Fig. 5B, D1–66–D21). Because the stable D21 component lies downstream from the D1 region in the chimeric mRNA (D1–66–D21), we know that degradation of the D1 sequence cannot be caused by 3’ → 5’ exonucleases from the poly(A) end (23–25).

In analyses of other chimeric mRNAs, the full-length D21 probe protected multiple fragments of the chimeric D21-170-D1 RNA (Figs. 4E and 5E). But this same probe protected only one fragment, and which was smaller than expected, in chimeric D21-65-D1 mRNA (Figs. 4C and 5C), and three very small fragments in D1-171-D21 mRNA (Figs. 4D and 5D). Recalling that endogenous gstD21 mRNAs are not induced by heat shock, the protected D21 subfragments must trace to the induced chimeric mRNAs.

The D1 riboprobe clearly protected endogenous gstD1 mRNA but as for the D1 portions of chimeric mRNAs yielded protection products at low to undetectable levels. No bands appeared for the D1-66-D21 and D21-170-D1 constructs (Fig. 5, B and E), and the D1 portions of chimeric mRNAs from D21-65-D1 and D1-171-D21 were detectable but only at very low levels (Fig. 5, C and D). Our results show these four D1-D21 (D21-D1) chimeric RNAs to be very labile, conceivably because of the presence of destabilizing D1 sequences. The instability of these chimeras was manifest very early into heat shock induction, with some decay intermediates appearing before induced chimeric mRNAs could be detected (Fig. 4, D and E). These decay intermediates were not generated during RNA isolation but, rather, increased along with the duration of heat shock. Meanwhile the reference RP-49 mRNAs remained intact throughout our time course analysis.

Results in Figs. 4 and 5 along with the demonstrated stability of the chimeric D21L-UTR mRNA (Fig. 3B), support the notion that the gstD1 coding sequence contains cryptic destabilizing elements. These cis-acting elements apparently exert their degradative influence in the absence of the native UTRs from the mRNA. A conceivable explanation, then, for how full-length gstD1 mRNA maintains its stability is that the UTRs contain a dominant STE(D1) that overrides any destabilizing influence from the coding region. This hypothesis, substantially supported by our findings, expands the current paradigm of mRNA stability regulation with this new detail of an additional stabilizer element.

Mapping Putative Decay Intermediates—We set out to identify a decay pattern for the D21 portion of the chimeric D21-D1 mRNAs by mapping the decay intermediates of each molecule from D21-65-D1, D1-171-D21, and D21-170-D1 flies with a nested set of D21 riboprobes. (We passed over the D1 portion because its intermediates were barely detectable.) RPA results are shown in Fig. 6. The decay intermediate from D21-65-D1 (Fig. 6A, Int-Sa) spanned ~100 nucleotides of the D21 sequence (numbers 81–181 of the 198 nucleotides from codons 1 to 66). The D1 portion of chimeric D21-65-D1 mRNA was barely detectable and only so very early into heat shock treatment (Fig. 5C). Three pieces of decay intermediates spanning ~50, 55, and 60 nucleotides were detected from D1-171-D21 by the D21 probe (Fig. 6A, Int-1, Int-2, and Int-3). As the sum of these lengths exceeds the entire D21 stretch (129 nt, numbers 567–627).
696 of the complete \textit{gstD21(L)} mRNA of the chimeric mRNA; they must partially overlap. Decay of the D21 part of the chimeric D21-170-D1 mRNA probably involves an endonucleolytic cleavage near the \textit{Sma}I site (number 228 of the \textit{gstD21(L)} sequence).\(^2\) One major decay intermediate (\textit{Int-1} in Fig. 4E and fragments marked by arrows in Fig. 6B) was mapped to the region of 81–547 of the D21 mRNA sequence, another intermediate (\textit{Int-2}) to the region of 245–460, and a third (\textit{Int-3} in Fig. 4E and \textit{Int-3-Sa} in Fig. 6B) to the region of 81–245 (Fig. 6B and C). The early appearance of stable decay intermediates from the induced transgene(s) indicates that the half-lives of the intact chimeric D21-D1 mRNAs are shorter than 20 min (Figs. 4 and 5). Given that the half-life of chimeric D21L-UTR mRNA in the same context of UTRs is much longer (Fig. 3B),\(^2\) dramatically shorter half-lives for the D21-D1 chimeras strongly suggests, then, that the D1 coding sequence contains active destabilizing elements. The summary of mapping results (Fig. 6C) suggests that these destabilizing elements most likely are located in the first 67, and the last 37, codons of the D1 coding sequence. Chimeric RNAs containing these sequences are either undetectable (transgenes D1-66-D21 and D21-170-D1) or detectable only at very low levels (transgenes D21-65-D1 and D1-171-D21). These destabilizing elements are suppressed in endogenous \textit{gstD1} mRNA, which must contain the proposed dominant stabilizer element \textit{STE(D1)} in its native UTRs.

\section*{DISCUSSION}

mRNA stability is an important regulatory factor in gene expression. The relative stability of mRNA determines its lifespan and, thus, its translatability, in the cytoplasm (1–5). Endogenous \textit{gstD1} mRNA is quite stable under both control and PB treatment conditions. A \(~2\)-fold PB-induced increase in the transcription rate of \textit{gstD1} accordingly resulted in a \(~2\)-fold increase in the steady-state level of \textit{gstD1} mRNA (15). How, then, does stable \textit{gstD1} mRNA return to normal levels after the PB inducer is removed from the flies? The presence of cryptic, \textit{cis}-acting, destabilizing elements in the coding region of \textit{gstD1} provides a possible avenue. Just how they exert their influence, however, remains to be elucidated.

In the absence of their native UTRs, D1 portions of the D1-D21 chimeric RNAs were shown not only to be degraded themselves, but also to destabilize segments of the D21 coding sequence that we know is stable in the cytoplasm (1–6).\(^2\) Mapped decay intermediates from the chimeric D1-D21 mRNAs display patterns that are consistent with the hypothesis that the destabilizing elements are, most likely, located in the N-terminal (codons 1–67) and C-terminal (codons 172–209) regions of the GST D1 coding sequence. It also indicates that endonucleolytic cleavage(s) are probably involved in the decay pathway(s).

The stability of endogenous \textit{gstD1} mRNA, therefore, must
rely on a dominant STE that overrides these destabilizing elements. The fact that both chimeric D1 mRNAs from transgenes D1-UTR and D1F-UTR, which lack native UTRs, are both very labile is strong evidence that this putative STE(D1) resides in the UTRs of gstD1 mRNA. The presence of STE(D1) may also explain the occurrence of a small fraction of stable, decapped, and shorter than full-length gstD1 mRNAs in control and PB-treated RNA populations (see Fig. 2).

Studies in the yeast Saccharomyces cerevisiae have revealed that decapping triggered poly(A)-shortening leads to 5' exoribonuclease degradation. This pathway of mRNA decay has also been detected in mammalian cells. If this same pathway also persists in D. melanogaster, then the presence of stable decapped gstD1 mRNA would indeed be impossible without the function of a stabilizer element. The P-STE stabilizer, found in the coding region of the yeast PGK1 mRNA, has been shown to block deadenylation-dependent mRNA decay (9). The short poly(A) (~40 As) of the intact molecules and presence of decapped gstD1 mRNA in the natural population suggest that the putative STE(D1) functions similarly to the

FIG. 6. A summary of mapping the decay intermediates (Int) in transgenic lines. A diagram of the transgene(s) is shown above each RPA pattern in both panels A and B. The restriction sites are indicated for D21.AS DNA used in riboprobe synthesis. Nucleotides of the complete gstD21(L) cDNA are numbered from 1 to 780, so are the D21 portions of each chimeric transgene. The same strategy was used to determine the sizes and the locations of the intermediates from total RNAs of D21-65-D1, D1-171-D21 (Panel A), and D21-170-D1 (Panel B). Total RNAs for the RPA assays were isolated from combined heat shock and PB-treated flies. Riboprobes were obtained from Sac1 (S), Nco1 (N), Sma1 (Sm), HindIII (H), or TfiI-digested D21.AS (T). The RP-49.Sac1 riboprobe was included in the RPA analyses of D21-65-D1 and D1-171-D21 to demonstrate that the intermediates are not the result of poor RNA quality. Fragments protected in RPA are regions overlapping with the D21 portion (open rectangles) beginning from the G8S,G9S mutation. The expected sizes are 170 nucleotides for D21-65-D1, 130 nucleotides for D1-171-D21, and 490 nucleotides for D21-170-D1. The protected RP49 bands are 400 and 300 nucleotides. The sizes of the bands from Int-1 of D21-170-D1 mRNA (marked by arrows) are: 480 (lane Sa), 405 (lane N), 300 (lane Sm), 180 (lane H), and 110 (lane T) nucleotides. Panel C, a summary of RPA analyses of the four D1-D21 chimeric mRNAs by both the D1 and D21 riboprobes in Figs. 4 and 5. Hatched rectangles represent the D1 coding sequence and open rectangles represent the D21 coding sequence. Solid squares represent the FLAG epitope. Decay intermediates are indicated by thick lines. The G8S,G9S mutations in GST D21, Arg66 junction, and 170/171 junctions are indicated by ‡, *, and $, respectively. Numbers indicate nucleotide positions of the full-length gstD21(L) sequence. ND, not detectable.
STEs are a known feature of yeast and mammalian mRNAs (6–9). Several yeast mRNAs that contain upstream open reading frames in the 5′-UTR are degraded through nonsense-mediated decay (3, 8, 28). But for certain genes, such as GCN4 and YAP1, mRNAs are known to harbor a stabilizer element in the 5′-UTR just upstream of the main open reading frame. In GCN4 mRNA this STE protects the molecule from rapid decay by interacting with the RNA-binding protein Pub1p, which is required in the nonsense-mediated decay pathway (8). Our findings provide solid evidence that such a STE(D1) works similarly on the mRNA of a multicellular eukaryotic organism. Moreover, this STE would be similarly located to the stabilizer element of the α-globin mRNA if it should fall in the 3′-UTR of \( \text{gst} \text{D1} \) mRNA (6, 7). There is, however, no pyrimidine-rich segment in \( \text{gst} \text{D1} \) UTRs as there is in the 3′-UTR of α-globin mRNA (7).

The Drosophila \( \text{gst} \text{D1} \) and \( \text{gst} \text{D21} \) genes are adjacentl located but divergently transcribed (20). Although their coding sequences share 70% identity, their products perform very different enzymatic functions. GST D1 is a 1,1,1-trichloro-2,2-bis-(P-chlorophenyl)ethane dehydrochlorinase as well as a glutathione S-transferase. GST D21, on the other hand, does not exhibit normal GST activity (12) but may be an important ligand-binding protein (i.e. ligandin). The UTRs of both the \( \text{gst} \text{D1} \) and \( \text{gst} \text{D21} \) mRNAs appear to contain cis-acting regulatory element(s), but ones which function quite differently. The native UTRs of the \( \text{gst} \text{D1} \) mRNA are essential to the stability of the molecule, whereas those of \( \text{gst} \text{D21} \) mRNA contain one or more element(s) that render the molecule very unstable in the absence of PB. The coding regions of \( \text{gst} \text{D1} \) and \( \text{gst} \text{D21} \) also exhibit contrasting behaviors with respect to mRNA stability. In the same context of the \( \text{hsp}70 \) 5′-UTR and the \( \text{actin}5C \) 3′-UTR, we observe that, on the one hand, the D21 coding sequence remains very stable (Fig. 3B), but that, on the other, the D1 coding sequence becomes very labile. The stark differences in behavior between \( \text{gst} \text{D1} \) mRNA and \( \text{gst} \text{D21} \) mRNA with regard to stability show the potential for diversity in yet another aspect of expression regulation within a multigene family.

Acknowledgments—We thank Yen-Sheng L. Tu for technical assistance, Leslie Tu for manuscript editing, and Eileen McConnell for secretarial assistance.

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*J. Biol. Chem.* 2002, 277:34700-34707.
doi: 10.1074/jbc.M200985200 originally published online July 12, 2002

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