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EVIDENCE FOR EVOLUTIONARY DUPLICATION OF GENES IN THE DOPA DECARBOXYLASE REGION OF DROSOPHILA

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ABSTRACT

The region surrounding the dopa decarboxylase gene (*Ddc*) of Drosophila contains a cluster of genes, many of which appear to be functionally related by virtue of their effects on cuticle development and/or catecholamine metabolism. In this report we describe evidence that the *Ddc* gene and the closely linked *alpha-methyldopa hypersensitive* (*amd*) gene share extensive sequence homology and are the products of a gene duplication event. The two genes are transcribed convergently and are separated by 2.4 kb. A gene located between *Ddc* and *amd* expresses a 2.0-kb mRNA and appears to partially overlap the *Ddc* gene. The organization of these transcripts implies a complex series of events giving rise to the present pattern. The patterns of expression of these genes do not support a model of coordinate regulation, but are more consistent with a pattern of duplication and divergence to various related metabolic subspecialties. These data provide the first evidence for structural relationships among genes in the 37C cluster.

THE dopa decarboxylase (*Ddc*) region of Drosophila (*i.e., Df(2L)TW130,* WRIGHT, HODGETTS and SHERALD 1976) contains a cluster of 18 genes, of which at least 14 are thought to be functionally related by virtue of their effects on cuticle development and catecholamine metabolism (*e.g.,* WRIGHT *et al.* 1981; PENTZ and WRIGHT 1986); yet, GILBERT, HIRSH and WRIGHT (1984) were unable to detect any DNA sequence homology within this region, and they concluded that the genes were not structurally related.

We have focused our attention on the *Ddc* and closely linked (0.002 cM) *alpha-methyldopa hypersensitive* gene (*l(2)amd,* abbreviated *amd*). Several observations suggest that the gene product of the *amd* locus is related to the DDC enzyme and involved in catecholamine metabolism (WRIGHT, BEWLEY and SHERALD 1976; MARSH and WRIGHT 1986). First, the recessive lethal phase of both *Ddc* and *amd* is embryonic hatching, with both *amd* and *Ddc* embryos showing abnormal cuticles (SPARROW and WRIGHT 1974; WRIGHT 1977). Second, the amd^+ gene product confers resistance to dietary administration of dopa analogues, specifically alpha-methyldopa (MARSH and WRIGHT 1986),

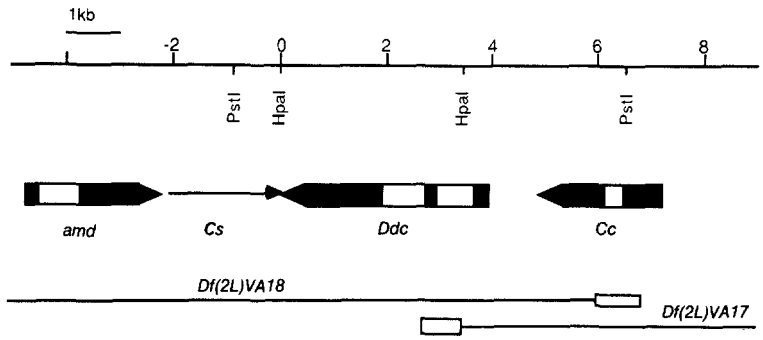

FIGURE 1.—Organization of transcripts in the *Ddc* region. Transcripts discussed in this communication are placed on the genomic map. We have used the *Hpa*I site near the terminus of *Ddc* as a fixed reference point at 0 kb. This is different than the arbitrary zero point used by other authors (*e.g.*, GILBERT, HIRSH and WRIGHT 1984), which would lie at a point slightly greater than 860 bp on our map. The *amd* transcript is described by MARSH, ERFLE and LEEDS (1986). The arrow represents the 2-kb transcript described by SPENCER, GEITZ and HODGETTS (1986). The *Ddc* transcript is positioned according to EVELETH *et al.* (1986). The *Cc* transcript is described in EVELETH and MARSH (1986). Solid bars indicate exon material included in the mature mRNA or cDNA. Arrows indicate direction of transcription from 5′ to 3′. In this figure, the centromere is to the right.

whereas DDC activity is inhibited in cell-free extracts by the same dopa analogues (SPARROW and WRIGHT 1974). Third, temperature-sensitive mutants of *Ddc* shifted to restrictive temperature during the larval stages and larvae fed dopa analogues die at the larval molts or at pupariation and exhibit abnormal pupal cuticles (WRIGHT 1977; WRIGHT *et al.* 1982). Fourth, lethal mutations of the *amd* gene can be rescued by dietary supplements of dopa, tyramine and octopamine and pyridoxal-5′-phosphate (PLP) (P. D. L. GIBBS and J. L. MARSH, unpublished results). Taken together, these observations strongly suggest that the *Ddc* and *amd* genes both encode enzymes involved in the catecholamine biosynthetic pathway and that these gene products both recognize substrates of similar structure.

In addition to the *Ddc* and *amd* genes, several other genes affecting cuticle formation or catecholamine metabolism are located in the *Df(2L)TW130* region including the diphenol oxidase gene (*Dox-A2*) (PENTZ and WRIGHT 1986). These and other observations have led to the hypothesis that *Ddc, amd* and possibly other genes in this cluster may be structurally and evolutionarily related (MARSH and WRIGHT 1979, 1986). We have investigated the origin and physical organization of the transcription units surrounding the *Ddc* gene by direct sequence analysis. This has revealed that the 12-kb interval including the *Ddc* gene also includes three other transcripts (Figure 1). These transcripts are extremely closely spaced, and the *Ddc* and *Cs* transcripts (SPENCER, GEITZ and HODGETTS 1986) actually overlap. In this report, we show that the *Ddc* and *amd* genes are structurally and evolutionarily related. Based on these observations, we propose that the *Ddc* and *amd* genes represent a structurally related gene pair (a paralogous set) that arose by duplication and divergence. These data provide the first evidence for genes structurally related to the *Ddc*

gene in any organism and document that genes in the *Ddc* region of Drosophila are structurally related by gene duplication. These observations support the interpretation of genetic studies that this region contains a cluster of functionally (and now structurally) related genes.

MATERIALS AND METHODS

The sequences used in this analysis are derived from clones originating from the MANIATIS library (MANIATIS *et al.* 1978). The restriction pattern of the cloned DNA resembles the Canton-S haplotype (MARSH and WRIGHT 1986). The sequence of the *amd* gene is described in the accompanying paper (MARSH, ERFLE and LEEDS 1986). The sequence of the *l(2)37Cc* gene is described by EVELETH and MARSH (1986), and the *Ddc* gene structure and sequence by EVELETH *et al.* (1986). The sequence of the region between *Ddc* and *amd* that includes the *Cs* transcript (SPENCER, GEITZ and HODGETTS 1986) was determined by D. D. EVELETH and J. L. MARSH (unpublished observations). Computer analyses of DNA sequences were performed on an IBM-PC employing a series of programs modified from SCHWINDINGER and WARNER (1984) by A. GOLDIN (California Institute of Technology). Dot matrix homology searches employed a set of programs written by B. WARD and G. GUTMAN (Microbiology and Molecular Genetics Department, University of California, Irvine).

RESULTS

Four genes have been mapped within the 12-kb area surrounding the *Ddc* gene. These include the *amd* gene (MARSH, ERFLE and LEEDS, 1986), the *Ddc* gene (HIRSH and DAVIDSON 1981; EVELETH *et al.* 1986), the *l(2)37Cc* (*Cc*) gene (EVELETH and MARSH 1986) and an additional transcript (designated *Cs*) mapping to the region between *amd* and *Ddc* (SPENCER, GEITZ and HODGETTS 1986). The structure and genomic organization of these transcripts is shown in Figure 1.

***Ddc* and *amd* show sequence homology:** We sought to determine whether any of the genes in the region were structurally related by direct sequence comparison. Using computerized dot matrix analysis, we compared the sequences of each gene to the other three in both orientations. A striking homology was found when the *Ddc* and *amd* gene regions were compared in their respective directions of transcription. Figure 2 presents a dot matrix analysis comparing the *amd* gene to a portion of the *Ddc* gene that includes exons II and III and the second intron of *Ddc*. The sequences were scanned for 67% homology with a window size of 15 bases and required match of ten. Regions of sequence similarity that meet this criteria are seen as diagonal rows of dots on the matrix (each dot represents a block of 15 bases, ten of which match). Clear regions of sequence homology (seen as diagonal lines in Figure 2) are seen in the major exons of both genes, showing that the *Ddc* and *amd* genes are structurally related and form a gene pair. Substantial sequence similarity is seen even when the search criteria are raised to 90% (matrix not shown).

Intron sequences and positions are not conserved: Interestingly, sharp discontinuities in the alignment are seen at the intron exon borders of both genes. We have detected no homology between the intron sequences of either *amd* or *Ddc* and any portion of the sequenced region. If one examines the homology between *Ddc* and the sequences flanking the *amd* intron borders, there is clear

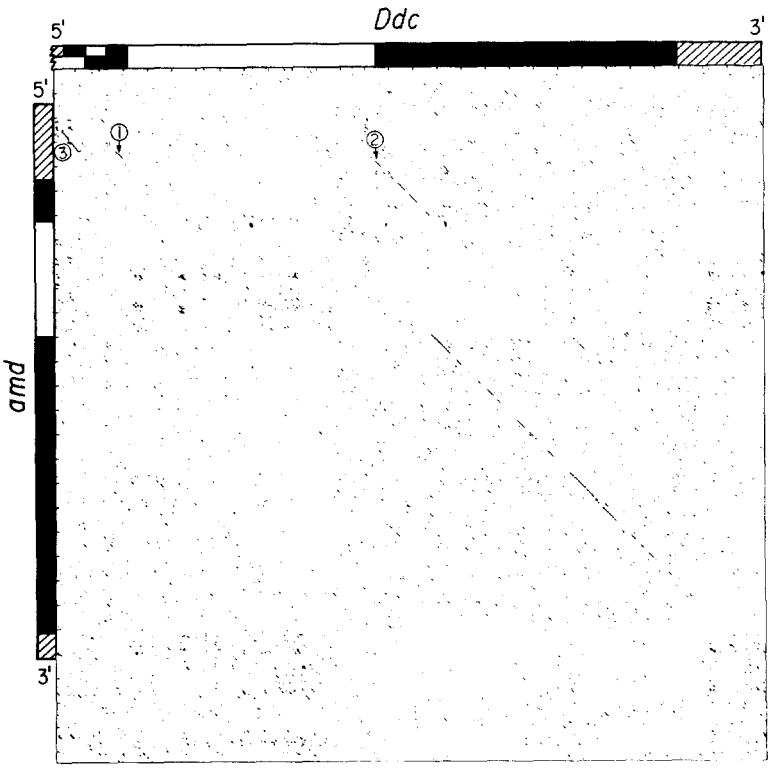

FIGURE 2.—Dot matrix comparison of *amd* and *Ddc* gene sequences. The DNA sequence of the *amd* gene and a portion of the *Ddc* gene were compared at 67% homology (10 of 15 matched). The *Ddc* sequence (EVELETH *et al.* 1986) includes the second and third exons of *Ddc* and the 1031-bp *Ddc* intron. A schematic representation of each gene is depicted on the axes. Units are given in 100 bp. ■, coding regions; ▨, untranslated portions of the mRNA; □, intervening sequences. The *Ddc* axis shows the two proposed splicing modes of *Ddc* in the region of the second exon (EVELETH *et al.* 1986). The boundaries of the *amd* gene are described in MARSH, ERFLE and LEEDS (1986). Regions of homology are seen as diagonal rows of dots. Each dot represents a string of 15 bases, of which ten bases match; homology thus extends up to 15 bases beyond the last dot in a string. Arrows refer to regions discussed in Figure 3.

homology with an uninterrupted portion of the *Ddc* coding region even when examined at higher stringencies, such as at the 73% homology level (11 of 15 match) (matrix not shown). The major regions of homology with the *Ddc* coding region define the borders of the *amd* intron exactly.

The *Ddc* gene produces several transcripts that share a major 1031-base pair (bp) intron (GEITZ and HODGETTS 1985; EVELETH *et al.* 1986). A comparison of the sequences flanking this intron reveals that the 5′ untranslated region of the early embryonic *amd* transcript shows extensive homology to the sequences that border this major *Ddc* intron. This is illustrated by an expanded dot matrix comparison at the 73% homology level (11 of 15 match) between the *amd* cDNA sequence and the spliced *Ddc* sequence (Figure 3) that shows a line of homology extending straight through the splice junction of the *Ddc* intron

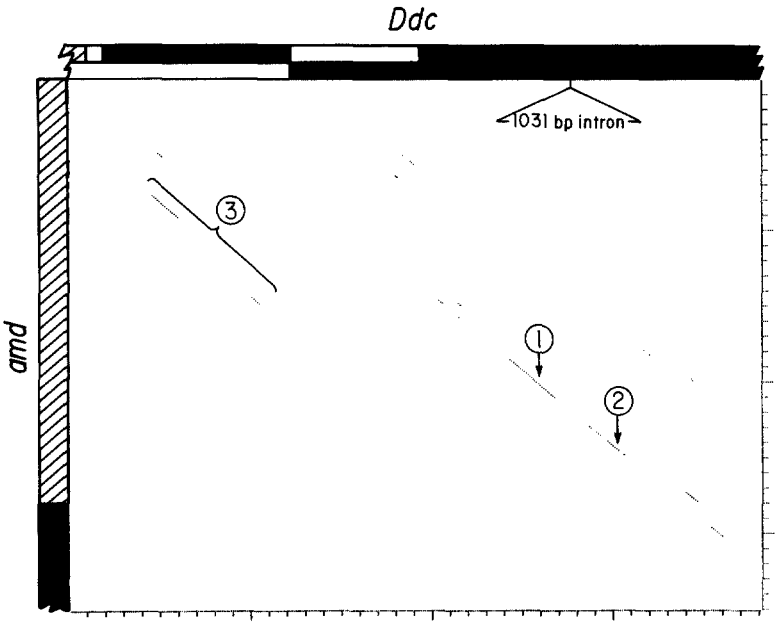

FIGURE 3.—Alignment around the *Ddc* introns. The alignment between the *amd* sequence and the sequences around the borders of the *Ddc* introns is shown. The matrix is as described in legend of Figure 2, except that the scan was performed at a higher stringency requiring that 11 of 15 bases (73%) match. The *amd* sequence includes the 5′ untranslated leader and the beginning of the coding region of the early embryonic *amd* transcript. The *Ddc* sequence represents a partially processed transcript with the 1031-bp intron removed (indicated by a wedge), but the region of the alternative exons is shown unprocessed. This permits comparison of both forms of the *Ddc* mRNA (EVELETH *et al.* 1986). The regions of homology that were seen in the lower stringency scan of Figure 2 are designated. Regions ① and ②, which were split by the intron in Figure 2, are now juxtaposed. While much of the background has been filtered out in this higher stringency scan, the region of homology with the 2.0-kb *Ddc* transcript, which is difficult to resolve in Figure 2, is expanded and indicated by the bracket labeled ③ in both figures.

(*i.e.*, the broken diagonal line indicated by arrows in Figure 2 is continuous in Figure 3).

Recent analysis of the *Ddc* gene (EVELETH *et al.* 1986) has revealed two possible splicing modes near the second exon that may lead to two isoforms of the DDC enzyme. These splicing alternatives are shown graphically on the axes of Figures 2 and 3. One of the splicing modes involves the excision of a 77-base intron. Close inspection of the *Ddc* and *amd* sequences at high stringency (*i.e.*, 73% in Figure 3) reveals only limited homology to the 77-base intron of *Ddc* (Figure 3), even though this is thought to encode one of the DDC isoforms. Regions of limited but significant homology between the coding regions on either side of this intron and the 5′ untranslated leader of *amd* are apparent.

Sequence homology is greatest in two regions: In Table 1 the *amd* cDNA sequence is aligned with portions of the *Ddc* genomic sequence. For purposes of illustration, we have used a partially processed *Ddc* sequence that has the

TABLE 1

Alignment of *amd* cDNA sequence with genomic *Ddc* sequence

```
CTGCTGCACTAATTAGCACTATCTTCAAAAACGCACTTCTATTAATAACACTTTCAATAATCGCACATTC     70

TTTCATATTAGCTCTAACCATTCGAGTTCATATCATTGCAAAAGTCAAACGAAAAGTAAATCTCTGAAAT    140

GAGCCACATACCCATTAGTAACACAATTCCAACAAAACAAACTGATGGTAATGGTAAAGCTAACATTTCG    210
                                    C-GGC-ACTTG-AGG-GCA-C--CGG-T-GGGAAC     35
                                {   small Ddc intron
CCGGATAAGCTGGATCCCAAGGTTTCGGTATGTCTATTGGGTTTAGGTATAGAGCCAACAATTATGCACG    280
TGAA--CGAG-T-GG-AA-CAAA-CAAAA-C-AAA-CG---AAATAAA-CCA-AA---AC-GA-C-T-AA    105
                                    ]
TCTGATAACTAAATACTTTTGCATCCACATCAAGATCGACATGGAGGCGCCGGAGTTCAAGGATTTTGCC    350
AAGTGC--A--G-A-ACGA-ATCG-A----TGTC-G--GT-----T--CAA------TCG---A-- C-G    175
                                                Ddc intron
AAGACAATGGTCGACTTTATAGCCGAATATCTGGAGAATATACGCGAAAGGCGCGTTCTGCCGGAAGTGA    420
---G-CGCCA-T----AC---------C--------------T--G--TGACGA---A-----CA-T---G    245

AGCCTGGCTACCTGAAGCCATTGATTCCGGATGCTGCGCCCGAGAAGCCGGAGAAGTGGCAGGATGTGAT    490
----A-----T---TT-GACC--C-G--CACA-AGAT---G--AG----C--AGC----A-------CC-    315

GCAGGACATCGAGCGAGTCATCATGCCGGGCGTGACACACTGGCACAGTCCCAAGTTTCATGCCTACTTC    560
CGGC-----TAGT--C--------A------AC----C----C-G-GTCG--TC-CA-G----------A-    385

CCCACGGCCAACTCGTATCCAGCGTACGTTGCGGACATGCTGAGTGGAGCGATTGCCTGCATCGGATTCA    630
-----CAG--C---------CT-CATT--G-GC--G------GCCA-C-G-T-C-G-GT-----------    455

CGTGGATCGCCAGTCCCGCGTGCACGGAACTCGAGGTGGTCATGATGGATTGGCTGGGCAAGATGCTGGA    700
GC-------TG---------C-----A-----G--------GG-C-----C-------C----T-C---A-    525
 amd intron
GCTGCCGGCAGAGTTCCTGGCCTGTTCGGGCGGCAAGGGTGGCGGTGTCATCCAGGGCACGGCCAGTGAG    770
------C---C-C----A-CA-GCCAGC-AT--ACCA--A-----G--G--------AT-A--T--C---    595

TCCACACTGGTGGCCTCTGCTGGGAGCCAAGGCCAAGAAGTTGAAGGAGGTGAAGGAGCTCCATCCGGAG    840
G-TGTGT-------TGTCCTA-CTGC-AGG-AA----CT--G-CCAACTACAGG-A-T-G- --------    665

TGGGACTGGAGCACACCATCTTGGGCAAGTTGGTGGGCTACTGCTCGGACCAGGCTCACTCATCCGTGGA    910
CT-AG-GAA--TGAGGTGCG-G-CCGC  -------C-----C----------AG-A--AGC-G-A-T--    735

GCGGGCTGGTCTTCTGGGCGGAGTAAAGCTCCGTTCCGTGCAGTCCGAGAATCACAGAATGCGTGGTGCT    980
-AA------AG-C----CT-CCA-GCC-A-T--A-TGC---C-G-T-GAG-GG-TTTCG-A-T-A-A-GC    805

GCCCTGGAAA AG  GCCATCGAACAGGATGTGGCCGAGGGTTTGATTCCCTTCTAC GCGGTGGTCACC  1,050
-ATACACTG-G--GA--------GG----C-----A-C---CAG------GG-GAT-T---T--C ---T    875

CTGGGCACCACCAACTCCTGCGCCTTCGACTACTTGG ATGAGTGTGGACCGGTGGGAAACAAGCACAAT  1,120
----------GGG-A-T--T----AT---G-TA-T-A--CCC---CCG-T-TCT-CG-GG--TT ---G    945

TTGTGGATCCATGTGGACGCTGCCTATGCCGGATCCGCTTTCATTTGCCCCGAGTATCGCCACCTGATGA  1,190
- ----C--------T--T--C--G-----G-TGGAGC----GC-C--GAGGA-TGT---GATTTGCGAA-  1,015

AGGGCATCGAATCAGCAGACTCTTTCAATTTCAATCCACACAAATGGATGCTGGTGAACTTTGACTGCTC  1,260
G--ATTGGATCG-GTG -----GC-A--C-----C-TG-----G-TC--------C-----C--T-----  1,085

GGCCATGTGGCTGAAGGATCCCAGTTGGGTGGTCAACGCGTTCAATGTGGACCCTCTTTACCTGAAGCAC  1,330
-----------A-G----G---ACAA-------G--AGC----------T-GCA-C--T---------  1,155

GACATGCAGGGATCAGCTCCGGACTATCGTCACTGGCAAATCCCACTTGGACGGCGATTCAGGGCACTGA  1,400
A-GCACG---- ----TCG-AA-T-CCA-A-TTCC-TC-T-GG--AA-CCC-T-G-TCG-C-CTTC-GAG  1,225

AGCTCTGGTTCGTCCTCCGGCTGTACGGTGTCGAGAATCTCCAGGCCCACATCCG      CAGACACTG  1,470
CT--AAAAG--TGGA--ACAT-CCG-AC-C-G--AGCCGAGGGATTG-GA-A--ATGTCGCG-AG---AT  1,295

CAACTTTGCCAAGCAGTTCGGGGATCTCTGCGTGGCGGACTCCAGATTTGAACTGGCCGCCGAGATCAAT  1,540
-G-G--G-----A-----T-A-C-G--TGTGC-CAA---T--GC----C--G----TG--TCCTCGTGCC  1,365
```

The nucleotide sequence of the *amd* cDNA is aligned with that of the partially processed *Ddc* sequence (see legend to Figure 3). The upper line shows the *Ddc* sequence. In the lower lines, nucleotides of the *amd* sequence that match are indicated by a dash (–). Where bases fail to match, the corresponding base is printed. Some gaps have been inserted for sequence alignment. The locations of the 480-bp *amd* intron and the 103-bp *Ddc* intron are indicated by wedges. The boundaries of the optional 77-bp *Ddc* intron are delimited by flags pointing into the intron. There is another 5′ untranslated exon of *Ddc* (not shown) that lies 770 bp upstream.

TABLE 1—*Continued*

```
ATGGGATTGGTCTCGTTCCGGCTGAAGGGCAGCAACGAGCGGAACGAAGCTCTTCTCAAGCGAATCAATG  1,610
C-----C----T-GT-------CC--A--TGA---T---ATT-C-ACCCAGT-G--GC-A--GC-T ---  1,435

GA CGCGGCCACATCCACTTGGTTCCCGCCAAGATCAAGGATGTCTACGGCCTGCGCATGGCCATTTGCT  1,680
--T--AAAGA-G---T--A-----AAG---G--CATGC--G-CGTC-GTTT-----AT-C-T-G-A---G  1,505

CGCGATTCACCCAGTCCGAGGACATGGAGTACTCGTGGAAGGAGGTCAGCGCCGCTGCCGACG AGATGG  1,750
GCATGGA----A-AG--TCC--T--T--T-T-G-C---C-----A--GAGT-TCAA -T----G-CC--C  1,575

AACAGGAGCAGTAAAGTGGTTGTGCAGGTCTGTTCCGTGTTTAGTATATAAATTAATATAGTAAACTTAA  1,820
-GGC---CG-A-CCTTG-TGGCCCGCAAATC-GGAAAC--CGGCG--C-TGCGC-CG-CTTCC-GA-CC-  1,645

ATTGGACCAGTATGATATATAATGCATTGTGACTTGGAACCCGGAACAGACCATACACTTTCCACTTGCG  1,890
TC--AG-ACCG-AA--GC-ACGCA-GAGAAAT--CA-TGAGAAA---G--TA-ACT-T--ATGTT-A-G-  1,715

ACATGTTTAGGGAATTTACATCGCAACAAAAGATGGTTCGTCCATCGCTACATTATATTTATAGTATCCT  1,960
---ACC-AGTTAGT--GCG--GTAGTTTTT-AC-TTCCACATGT-TATA-ATAA-GTGAA--TAA--GTA  1,785

ATCATTGTATCATTGATGTTGTTCATGATTTTTATTGTTAACGTTATGCGCCTAATTAAAAC          2,030
```

1031-bp intron removed but the region containing the alternative splicing events intact, thus permitting comparison of both forms of *Ddc* mRNA. This alignment illustrates the degree of local variation in the homology between these two genes. Overall, approximately 55% of the bases match between the two sequences (excluding intron regions); however, two areas of more extensive homology are apparent. One area beginning near the second exon of *amd* is over 80% homologous over 100 bp, and a second run of 124 bp (700 bp from the 3′ end) is approximately 90% homologous. Although more liberal use of gaps would permit additional alignments, we have attempted to minimize the use of gapping. The locations of introns are indicated in the alignment, thus permitting visualization of the exact nucleotide alignment in the intron regions.

Protein sequence and structure are conserved: In light of the DNA sequence homology, we compared the deduced amino acid sequence of the *amd* and *Ddc* proteins. The alignment shown in Table 2 shows two blocks of considerable amino acid sequence conservation. To ascertain whether these proteins might have retained regions of secondary structure that were not apparent from the amino acid alignment, we compared the proteins for common structural features. We have used the method of GARNIER, OSGUTHORPE and ROBSON (1978) to predict the distribution of potential alpha helices and beta sheets. Regions of structural similarity are observed corresponding primarily to the regions of conserved amino acid sequence. However, a high density of potential alpha helical structures was noted near the carboxy terminus of both proteins in a region of only limited amino acid conservation. Thus, the *amd* and *Ddc* proteins appear to have retained considerable structural, as well as sequence, similarity.

Homology among other genes: Extensive dot matrix analysis of the region surrounding *Ddc* does not reveal any similarity between the *Ddc* or *amd* genes and the *Cc* or *Cs* transcripts, nor is any relationship between the *Cc* and *Cs* transcripts seen. While structural relationships that are not detected by our methods may exist between these genes, these relationships must be limited in length or be much lower in homology than are the relationships between *Ddc* and *amd*.

Homology with other published sequences: We have scanned the National

TABLE 2

Alignment of *Ddc* and *amd* proteins

```
MSHIPISNTIPTKQTDGNGKANISPDKLDPKVSIDMEAPEFKDFAKTMVDFIAEYLENIRERRVLPEVKP    70

GYLKPLIPDAAPEKPEKWQDVMQDIERVIMPGVTHWHSPKFHAYFPTANSYPAYVADMLSGAIACIGFTW   140
          M--E--A-K--LG--S---K--L--SE--HM---Y--ST---SI-GE--ASGFGV---S-    60

IASPACTELEVVMMDWLGKMLELPAEFLACSGGKGGGVIQGTASESTLVASAGSQGQEVEGGEGAPSGVG   210
-C----------V----A-F-K---H-QHA-D-P-------S---AV---VLAARE-A- ANYRESHPEL   130

LEHTILGKLVGYCSDQAHSSVERAGLLGGVKLRSVQS ENHRMRGAALEKAIEQDVAEGLIPFYAVVTLG   280
S-SEVR-R--A-S---SN-CI-K--V-AAMPI-LLPAG-DFVL--DT-RG---E---A-R--VIC-A---   200

TTNSCAFDYLDECGPVGNKHNLWIHVDAAYAGSAFICPEYRHLMKGIESADSFNFNPHKWMLVNFDCSAM   350
--GT--Y-DIESLSA-CEEFKCGSMLMPRMRW-LCSGGMFGFA ---G-RGLAKLQ-AQVHAGQLRLLGH   270

WLKDPSWVVNAFNVDPLYLKHDMQGSAPDYRHWQI  PLGRRFRALKLWFVLRLYGVENLQAHIRRHCNF   420
VA-GCQQGGRQLQCGSHLSEAQAR--VANS-LPSLAN----------V-ITF-TLEA-G-RN-VAK-IEL   340

AKQFGDLCVADSRFELAAEINMGLVSFRLKGSNERNEALLKRINGRGHIHLVPAKIKDVYGLRMAICSRF   490
----EQ-VLK------V-PRAL---C--P--D--ITTQ--Q-LMD-KK-YM-K-EHAGRQF--FVV-GMD   410

TQSEDMEYSWKEVSAAADEMEQEQ                                                  560
-KAS-IDFA-Q-IESQLTDLQADESLVARKSGNVGDLAHDFQIHLSTENATHEKSQ                   480
```

The deduced amino acid sequence of the *amd* protein is compared to that of the DDC protein. The upper line shows the DDC sequence. In the lower line, amino acids of the *amd* protein that match are indicated by a dash (-). Where residues fail to match, the amino acid is printed below. Some gaps have been inserted for sequence alignment. We have used the sequence of DDC isoform I protein (EVELETH *et al.* 1986), although the differences between these two potential isoforms are restricted to the region that does not overlap the *amd* protein; thus, choice of isoform does not affect the alignment.

Institutes of Health DNA sequence data base for genes related to *Ddc* and *amd*. We have scanned both with the entire protein coding sequence, as well as with two strings of approximately 200 bp from the two major regions of sequence homology between these two genes. Using the default parameters of the Bionet IFIND program based on the algorithm of WILBUR and LIPMAN (1983), we identified no significant homologies among the vertebrate or Drosophila sequences. The similarity score for the *amd* and *Ddc* genes compared with each other is 150, whereas the next highest score on any scan was 20 (a score of 8–14 is expected between random sequences). This, perhaps, is not unexpected since this is the first *Ddc* gene sequence available.

The amino acid sequence of the PLP binding domain of pig DDC has been determined (BOSSA *et al.* 1977). The Drosophila DDC protein contains a precisely homologous domain (amino acids 335–342). The corresponding region of the *amd* gene is highly diverged (Table 2). Analysis of PLP binding domains in a series of PLP enzymes that act on different substrates reveals little conservation (each has a PLP binding lysine) (TANASE, KOJIMA and MORINO 1979). However, the observation that dietary PLP can rescue lethal alleles of *amd* (P. D. L. GIBBS and J. L. MARSH, unpublished observations) suggests that the *amd*

gene product may bind PLP. Thus, if the *amd* product fulfills a diverged biosynthetic function, such as an amino transferase activity, the PLP binding domain might be quite different.

DISCUSSION

Relationship of *Ddc* and *amd*: The *Ddc* and *amd* genes are thought to be functionally related by virtue of their interaction with structural analogues of dopa, thus leading to the speculation that the *amd* gene may encode a catalytically active product that recognizes substrates similar to DDC (MARSH and WRIGHT 1979, 1986). Enzymes that recognize similar substrates might be expected to have similar active sites. Evolution of enzymes within a metabolic pathway could occur by gene duplication, followed by divergence to metabolic subspecialties [*e.g.*, paralogous gene families as in bacteria (YEH and ORNSTON 1980) or globins (EFSTRATIADIS *et al.* 1980)]. The comparison of the *Ddc* and *amd* sequences presented here clearly documents extensive homology between these genes.

Detailed alignment of the DNA sequence (Table 1) shows two areas of extensive homology between *Ddc* and *amd*. One area beginning near the second exon of *amd* is over 80% homologous over 100 bp, and a second run of 124 bp (700 bp from the 3′ end) is approximately 90% homologous. These regions of strong homology reflect regions of conserved amino acid sequence and structure and may reflect functionally conserved portions of the peptides. The DDC and *amd* proteins do share at least two features. The DDC enzyme functions as a homodimer (CLARK *et al.* 1978), and genetic evidence suggests that the *amd* protein may also function as a dimer (MARSH and WRIGHT 1986). Thus, one of the conserved protein domains may mediate dimerization, whereas the other may form part of the active site.

An amino acid comparison of the regions of the *Ddc* and *amd* genes that are homologous shows that only 170 of 428 (38%) amino acids are identical. At this level of divergence, the application of molecular clocks is dubious, particularly as the *Ddc* and *amd* genes are a paralogous (fulfilling different enzymatic functions), rather than an orthologous (fulfilling identical functions), set.

The intron of the *amd* gene exhibits no evidence of sequence similarity with any part of the *Ddc* gene; yet, the regions of homology with *Ddc* extend to the precise borders of this intron on both the donor and acceptor side. The almost perfect alignment of the *Ddc* coding sequence across the *amd* intron suggests that this intron was added to the *amd* gene (or removed from *Ddc*) after the duplication event. Similarly, no portion of the major 1031-base *Ddc* intron shows any sequence similarity with any portion of the *amd* gene; yet, the 5′ untranslated sequence of *amd* shows strong homology to the protein coding regions on either side of this *Ddc* intron. This finding suggests that this intron was also added after the duplication event that gave rise to these two genes. Although the homology is limited, the lack of substantial homology to the 77-base intron of the 2.3-kb transcript of *Ddc* (EVELETH *et al.* 1986), while

regions flanking this intron show greater similarity, suggests that this intron may also have been added to *Ddc* (or removed from *amd*) after the duplication.

One can propose two models for the genesis of this pattern: (1) Different introns were added to the ancestral duplicates of these genes, but in different locations; (2) the original duplicated gene had all the introns of both genes (and maybe more), and the *amd* intron was lost giving rise to the present *Ddc* gene, whereas the 1031-base intron of *Ddc* (and possibly the 77-base intron) were lost in giving rise to the *amd* gene. Although intron positions in homologous genes are usually conserved [*e.g.*, globins (MANIATIS *et al.* 1980), vitellogenin genes (WAHLI *et al.* 1980), ovalbumin X-Y (ROYAL *et al.* 1979)], some examples have been noted in which introns occur at new positions [*e.g.*, actin (FYRBERG *et al.* 1981)] or are deleted (GILBERT 1985). The complete lack of homology between the intron borders of either the *amd* or *Ddc* introns and any portion of the corresponding gene argues strongly against intron migration. Although precise deletion of introns has been documented (PERLER *et al.* 1980) and is a formal possibility for the origin of different intron patterns (CRABTREE *et al.* 1985), an intron deletion model implies that the primordial genes must have had a very large number of introns (at least all those found in contemporary genes) (SHARP 1985). Thus, we favor the view that the introns of *Ddc* and *amd* have been added to these genes after the duplication event. It has been proposed (*e.g.*, GILBERT 1978; DUESTER, JORNVALL and HATFIELD 1986) that introns separate functional domains of proteins, thus enhancing the shuffling of exons to produce novel gene products. In the case of the *Ddc* and *amd* genes, no evidence of exon shuffling in the body of either gene is present. Although information regarding the boundaries of functional domains in the *Ddc* and *amd* proteins is slight, there is no evidence that the existing introns delineate such domains.

Time of expression: The genes in this cluster exhibit different patterns of expression. The *amd* transcript begins accumulating on polysomes after gastrulation and reaches a maximum in the later stages of embryogenesis, from approximately 12 to 16 hr (MARSH, ERFLE and LEEDS 1986). Very low levels of the 2.0-kb *amd* mRNA are observed in adults, and little or none of the 2.0-kb mRNA can be detected in third instar larvae. The *Cs* transcript (SPENCER, GEITZ and HODGETTS 1986) is transcribed in the same orientation as *amd*; it is most abundant in adult males and very early embryos and decreases in amount during the first 8 hr of embryogenesis, thus exhibiting almost the opposite pattern of expression as the *amd* transcript. The *Ddc* transcripts begin accumulating only after 12 hr of embryogenesis and reach a maximum at about 18 hr (GEITZ and HODGETTS 1985). Transcription is reinitiated at pupariation and just before adult eclosion (it is also assumed to peak at each of the molts). The *Cc* transcript upstream of *Ddc* is present in both early and late stages of embryogenesis, as well as at pupariation and in adults (EVELETH and MARSH 1986). Thus, the transcripts in this region do not represent a cluster of coordinately expressed genes, as might have been expected from a chromosomal domain hypothesis of expression (WEINTRAUB 1985). Rather, the *Ddc* and *amd*

genes appear to serve different metabolic subspecialties of catecholamine metabolism and to have evolved separate control features.

The four transcripts discussed here lie within 12 kb of genomic DNA, and the primary transcripts from these genes account for over 10.5 kb after processing for addition of the poly-A tail. If transcription termination in Drosophila occurs as much as 1 kb downstream of the poly-A addition processing site (*e.g.*, CITRON *et al.* 1984), the gene arrangement seen here implies that the primary transcripts from these genes actually overlap one another, and in fact, the poly-A addition signals for the *Ddc* and *Cs* transcripts overlap by about 80 bp (D. D. EVELETH and J. L. MARSH, unpublished observations). If the *Ddc* gene is located within the large 37C1 salivary gland chromosome band (WRIGHT *et al.* 1981; GILBERT, HIRSH and WRIGHT 1984), our data imply that at least four genes are contained within this band. We would find it surprising, in the absence of selection, for each of these genes to remain functionally intact through the chromosomal rearrangements that gave rise to the present arrangement. Thus, we think it likely that all four of these genes are subject to some positive selection. This is clearly the case for *Ddc*, *amd* and *Cc*, and this argument suggests that the *Cs* transcript may also represent a vital gene locus.

Origin of the gene arrangement: A simple duplication event does not readily account for the arrangement and orientation of the *amd*, *Ddc* and *Cs* genes (Figure 1). Several models can be envisioned for the generation of this arrangement. One could assume that the "ancestral state" was two closely linked genes (*Cs* and a *Ddc/amd* precursor) and that a transposition event created an inverted copy of the *Ddc/amd* ancestor. This model does not readily account for the overlap of the *Ddc* and *Cs* genes. A single-step scheme (two breaks) giving rise to the *Ddc/amd* duplication could be imagined, but this might be expected to result in sequence homology (symmetry around the duplication breakpoint). No internal homology within the *Cs* gene can be detected that would support this model. Unfortunately, the domains outside of the coding regions of the two genes are quite diverged, raising the possibility that such symmetry might have diverged to undetectability in the *Cs* gene. A more complex postulate is that *Ddc* and *amd* were duplicated in a transposition event (minimum of three breaks) and that the *Cs* gene then evolved by other means, either a second transposition event or evolution from sequences already *in situ*. Either of these models predicts that the present form of the *Cs* gene postdates the *Ddc/amd* duplication event. Since the region between *Ddc* and *amd* is almost completely occupied by the *Cs* gene, which, in fact, overlaps the *Ddc* transcript, any preexisting proto-*Cs* gene would be severely disrupted by the event giving rise to the *Ddc/amd* gene pair. Thus, we favor the interpretation that the *Cs* gene has arisen either by insertion or by more gradual mechanisms after the *Ddc/amd* duplication event. It has been noted (SNYDER *et al.* 1982) that inverted orientation of closely spaced homologous genes will suppress gene duplication by unequal crossing over and will prevent gene correction mechanisms; thus leaving the gene sequences free to diverge.

An alternative explanation for these data is that the structural similarity between *Ddc* and *amd* is the result of convergent evolution. We feel that this

is unlikely because the degree of similarity between *Ddc* and *amd* is greater than that required to generate similar functions from independent precursors. For example, the ADH protein of humans shares only 25% amino acid homology with yeast ADH (DUESTER, JORNVALL and HATFIELD 1986). Since *Ddc* and *amd* do not share the same enzymatic function, somewhat less homology may be required to satisfy a convergence hypothesis.

Although many examples of structural gene duplication exist, precedent for duplication of catalytic genes within a pathway is less common. One example is the β-ketoadipate pathway of bacteria, in which several genes that share a common evolutionary history now catalyze a variety of reactions in this catabolic process (YEH and ORNSTON 1980). A second example is found among the genes of catecholamine metabolism in vertebrates, in which recent studies suggest that tyrosine hydroxylase (TH), dopamine-beta-hydroxylase (DBH) and phenylethanolamine-*N*-methyltransferase (PNMT) are antigenically related. In addition, cDNA clones for DBH and PNMT appear to cross-hybridize, and DNA blotting experiments suggest that DBH and PNMT may be tightly linked within approximately 4 kb. JOH *et al.* (1983) conclude that TH, DBH and PNMT share a common evolutionary history. They have not yet detected any gene products related to DDC.

Our analysis provides the first demonstration of structural homology between *Ddc* and any other gene in any organism. Our data also provide the first evidence for structural relationships among the genes of the 37C cluster in Drosophila and suggest that the genetic observations indicating functional relationships among the genes in the *Ddc* region may be a consequence of the fact that at least some of the genes in this region share common evolutionary histories. This conclusion is in disagreement with those of GILBERT, HIRSH and WRIGHT (1984), who concluded that this region contains no extensive DNA sequence homology and that the genes in this region are not evolutionarily related. We would speculate that additional analysis may reveal a region of active gene duplication and divergence leading to a cluster of structurally related genes functionally related to catecholamine metabolism.

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