2/+ were analyzed. The gene minus has a cytological location at the region 59 D9-C1 of the chromosome 2. The analysis by light microscope did not reveal any chromosomal rearrangements in this and close to this region. However, we can not exclude the microdeletion which is detectable only by molecular genetics methods. Mutations *abb*, *mi*, *mr* and slite (*slt*; 2-106,7) constitute a group of genes with the similar phenotypical expression, which are located within the limits of a small chromosomal region. Possibly, the genes responsible for the normal development of imaginal disks are located in this chromosomal fragment. The abnormalities of these genes may cause the arising of phenotypically similar mutations. On the other hand, the *mi*-#89381 allele described above is related by phenotypical expression to the gene morula. The minus and morula genes are probably the duplications of one and the same gene, which diverged in evolution. The analysis of functioning of such genes, the knowledge of their pleiotropic effect, peculiarities of expression of different genetic variants are necessary for solving the problems of genome evolution, chromosome structure and regulation of gene expression.

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Ryerse, J., J. Swarthout, and B. Nagel. Department of Pathology, St. Louis University Health Sciences Center, 1402 South Grand Avenue, St. Louis, M0 63104. tel 314-577-8480; fax 314-577-8489; e-mail ryersejs@sluvca.slu.edu Cloning and molecular characterization of a partial ATP citrate lyase cDNA from *Drosophila melanogaster*.

ATP citrate lyase (ATPCL) catalyzes the conversion of citrate and CoA to oxaloacetate and acetyl-CoA. Acetyl CoA is an essential intermediary metabolite in the biosynthesis of cellular fatty acids and cholesterol (Kornacker and Lowenstein, 1965; Sullivan *et al.*, 1973; Singh *et al.*, 1976). ATPCLs have been cloned from the rat (Elshourbagy, *et al.*, 1990; Kim *et al.*, 1994) and the human (Elshourbagy *et al.*, 1992). We report here a partial ATP citrate lyase cDNA from *Drosophila melanogaster*, denoted DmATPCL.

While screening a *D. melanogaster* Canton S 2-14 hour embryonic cDNA library (Stratagene) with antibodies to candidate gap junction proteins (Ryerse, 1993, 1995), a clone was isolated with sequence homology to ATPCLs from the human and rat. The nucleotide sequence of the *D. melanogaster* ATPCL cDNA is 1623 bps in length (including the polyA tail) and contains an open reading frame which codes for a protein of 391 amino acids (Figure 1).

GCG PileUp alignment of the human, rat and fly ATPCL amino acid sequences is shown in Figure 2. The fly sequence is proximally incomplete, beginning at amino acid 710 of the human sequence. In the region of overlap, DmATPCL has 75.5% and 75.7% identity with human and rat ATPCLs, respectively (GCG BESTFIT analysis).

Human and rat ATPCLs contain domains which are considered essential for enzyme function (Elshourbagy *et al.*, 1992), including a catalytic phosphorylation site at His759, two ATP binding domains (aa 700-720 and 751-777) and a potential acetyl-CoA binding site (aa 778-788). His759 is phosphorylated by nucleoside diphosphate kinase and ATP (Wagner and Vu, 1995). His759 is conserved in the DmATPCL sequence. DmATPCL has 64% identity with the first ATP binding domain, 74% identity with the second ATP binding domain and 50% identity with the putative acetyl-CoA binding region in the human sequence (Figure 2). ATPCL is thought to associate with the ATP conducting voltage dependent anion channel (VDAC) in the outer mitochondrial membrane (Brdiczka, 1990), presumably for ready access to newly synthesized ATP. DmATPCL has been assigned Genebank accession number U87317.

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Figures 1 and 2 on following two pages.

Figure 1. Nucleotide and amino acid sequence of DmATPCL. * = stop codon.

```
5' 1  aaaccaagctgattgtccttttaggagaggttggtggaaccgaggagtac
   1      T  K  L  I  V  L  L  G  E  V  G  G  T  E  E  Y
  51 gacgtttgtgccgctctgaaggacggacgtattaccaagcctctggtggcc
  17    D  V  C  A  A  L  K  D  G  R  I  T  K  P  L  V  A
 102 tggtgcattggtacctgcgccagcatgtttacttcggaagtccagtttggc
  34    W  C  I  G  T  C  A  S  M  F  T  S  E  V  Q  F  G
 153 catgccggatcctgcgcgaactccgaccgagagacggctacggccaagaac
  51    H  A  G  S  C  A  N  S  D  R  E  T  A  T  A  K  N
 204 aagggtctgcgagatgccggcgcctacgttcctgattcgttcgacacgctg
  68    K  G  L  R  D  A  G  A  Y  V  P  D  S  F  D  T  L
 255 ggtgaactcatccaccacgtgtacggcgagctggttaagactggtcgagta
  85    G  E  L  I  H  H  V  Y  G  E  L  V  K  T  G  R  V
 306 gtgccgaaGgaggaggtgccaccaccaactgtgcccatggattattcgtgg
 102    V  P  K  E  E  V  P  P  P  T  V  P  M  D  Y  S  W
 357 gcccgcgagctgggtcttattcgcaagcccgcgtcattcatgacgtcgatc
 119    A  R  E  L  G  L  I  R  K  P  A  S  F  M  T  S  I
 408 tgcgacgagcgtggccaggagcttatctacgcaggaatgccgatcagcgag
 136    C  D  E  R  G  Q  E  L  I  Y  A  G  M  P  I  S  E
 459 gtccttagcaaggacgtcggcattggcggtgtcatctcactgctatggttc
 153    V  L  S  K  D  V  G  I  G  G  V  I  S  L  L  W  F
 510 cagcgctgcctgccttcatacgtgtgcaagttcttcgagatgtgcctgatg
 170    Q  R  C  L  P  S  Y  V  C  K  F  F  E  M  C  L  M
 561 gttactgcggatcacggtcccgcagtttctggggctcacaacaccattgtg
 187    V  T  A  D  H  G  P  A  V  S  G  A  H  N  T  I  V
 612 tgcgcccgtgctggcaaggacctggtgtcctcagtcgtgagcggtcttctg
 204    C  A  R  A  G  K  D  L  V  S  S  V  V  S  G  L  L
 663 actatcggggatcgatttggaggcgccctggacggatcggctcgacagttc
 221    T  I  G  D  R  F  G  G  A  L  D  G  S  A  R  Q  F
 714 tctgaggcatacgacaccaacctgcacccaatggagttcgtaaacaagatg
 238    S  E  A  Y  D  T  N  L  H  P  M  E  F  V  N  K  M
 765 cgcaaagagggcaagcttatcctgggtattggccaccgtgtaaagtccatt
 255    R  K  E  G  K  L  I  L  G  I  G  H  R  V  K  S  I
 816 aataaccccgatgtgcgcgtgaagatcattaaggaattcgtactggagaac
 272    N  N  P  D  V  R  V  K  I  I  K  E  F  V  L  E  N
 867 ttccctgcgtgtccacttctcaaatacgccttggaggttgagaagattacc
 289    F  P  A  C  P  L  L  K  Y  A  L  E  V  E  K  I  T
 918 accaacaagaaaccgaatcttatcctcaatgtggacggtgtgatagccacc
 306    T  N  K  K  P  N  L  I  L  N  V  D  G  V  I  A  T
 969 gcatttgtagacatgctgcgtaacagcggctcatttaccagtgaggaagca
 323    A  F  V  D  M  L  R  N  S  G  S  F  T  S  E  E  A
1020 caggagtacattaatgtcggcgcgatcaactcgttgttcgttctgggccgc
 340    Q  E  Y  I  N  V  G  A  I  N  S  L  F  V  L  G  R
1071 agcataggatttattggccattacatggatcagaaacgtctcaaacagggc
 357    S  I  G  F  I  G  H  Y  M  D  Q  K  R  L  K  Q  G
1122 ctgtaccgtcatccgtgggacgacatctcatacgtcattcccgagcagtac
 374    L  Y  R  H  P  W  D  D  I  S  Y  V  I  P  E  Q  Y
1173 aactaaggcgtgctgatgaagccgcgacgatgttatatatatatttagcta
 391    N  *
1224 tatacaagcatatatattattcggaagttgttgtagttaagcacagatgta
1275 tgatgttaggcaaagaggtcacccgctccactggatggaaggatccattga
1326 ggtctatccgcgcatgtgactctccccagatccctttccctctcacttatc
1377 ctgcatttaaagttcttaagttaccatcattaccctcgttgtttttgtaag
1428 cgctgcgtgtccccggagcccttaggggttttggaatctagacctagttaa
1479 atctagtgctccgagcggcacaacacaccagtacccggcataacattattt
1530 tgatacttttatactttagtttggatgctcacaattgtctagacaacaaga
1581 gaataaattgttgcaaaagcttaaaaaaaaaaaaaaaaaaaaa
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Figure 2. Comparison of human, rat, and fly ATP citrate lyase amino acid sequences.
* = identity, - = no amino acid.

```
Hum MSAKAISEQT GKELLYKFIC TTSAIQNRFK YARVTPDTDW ARLLQDHPWL   50
Rat ********** *******Y** ********** ********** *H********
Hum LSQNLVVKPD QLIKRRGKLG LVGVNLTLDG VKSWLKPRLG QEATVGKATG  100
Rat ***S****** ********** ******S*** ********** H*******K*
Hum FLKNFLIEPF VPHSQAEEFY VCIYATREGD YVLFHHEGGV DVGDVDAKAQ  150
Rat ********** ********** ********** ********** ******T***
Hum KLLVGVDEKL NPEDIKKHLL VHAPDDKKEI LASFISGLFN FYEDLYFTYL  200
Rat ********** *A****R*** ****E***** ********** **********
Hum EINPLVVTKD GVYVLDLAAK VDATADYICK VKWGDIEFPP PFGREAYPEE  250
Rat ********** ***I****** ********** ********** **********
Hum AYIADLDAKS GASLKLTLLN PKGRIWTMVA GGGASVVYSD TICDLGGVNE  300
Rat ********** ********** ********** ********** **********
Hum LANYGEYSGA PSEQQTYDYA KTILSLMTRE KHPDGKILII GGSIANFTNV  350
Rat ********** ********** ********** ********** **********
Hum AATFKGIVRA IRDYQGPLKE HEVTIFVRRG GPNYQEGLRV MGEVGKTTGI  400
Rat ********** ******S*** ********** ********** **********
Hum PIHVFGTETH MTAIVGMALG HRPIPNQPPT AAHTANFLLN ASGSTSTPAP  450
Rat ********** *******WA -PA******* ********** **********
Hum SRTASFSESR ADEVAPAKKA KPAMPQDSVP SPRSLQGKST TLFSRHTKAI  500
Rat ********** ********** ********** *********A **********
Hum VWGMQTRAVQ GMLDFDYVCS RDEPSVAAMV YPFTGDHKQK FYWGHKEILI  550
Rat ********** ********** ********** ********** **********
Hum PVFKNMADAM RKHPEVDVLI NFASLRSAYD STMETMNYAQ IRTIAIIAEG  600
Rat ********** K********* ********** ********** **********
Hum IPEALTRKLI KKADQKGVTI IGPATVGGIK PGCFKIGNTG GMLDNILASK  650
Rat ********** *****----- ---------- ---------- ----------
Hum LYRPGSVAYV SRSGGMSNEL NNIISRTTDG VYEGVAIGGD RYPGSTFMDH  700
Rat -******--** ********** ********** ********** **********
Hum VLRYQDTPGV KMIVVLGEIG GTEEYKICRG IKEGRLTKPI VCWCIGTCAT  750
Rat VLRYQDTPGV ********** ********** *********V **********
Dm             T KL**L***V* *****DV*AA L*D**I***L *A*******S
Hum MFSSEVQFGH AGACANQASE TAVAKNQALK EAGVFVPRSF DELGEIIQSV  800
Rat ********** ********** ********** ********** **********
Dm  **T******* **S***SDR* **T***KG*R D**AY**D** *T***L*HH*
Hum YEDLVANGVI VPAQEVPPPT VPMDYSWARE LGLIRKPASF MTSICDERGQ  850
Rat ******K*A* ********** ********** ********** **********
Dm  *GE**KT*RV **KE****** ********** ********** **********
Hum ELIYAGMPIT EVFKEEMGIG GVLGLLWFQK RLPKYSCQFI EMCLMVTADH  900
Rat ********** ********** ********** ********** **********
Dm  *********S **LSKDV*** **IS*****R C**S*V*K*F **********
Hum GPAVSGAHNT IICARAGKDL VSSLTSGLLT IGDRFGGALD AAAKMFSKAF  950
Rat ********** ********** ********** ********** **********
Dm  ********** *V******** ***VV***** ********** GS*RQ**E*Y
Hum DSGIIPMEFV NKMKKEGKLI MGIGHRVKSI NNPDMRVQIL KDYVRQHFPA 1000
Rat ********** ********** ********** ********** **F*K*****
Dm  *TNLH***** ***R****** L********* ****V**K*I *EF*LEN***
Hum TPLLDYALEV EKITTSKKPN LILNVDGLIG VAFVDMLRNC GSFTREEADE 1050
Rat ********** ********** *******F** ********** **********
Dm  C***K***** *****N**** *******V*A T********S ****S***Q*
Hum YIDIGALNGI FVLGRSMGFI GHYLDQKRLK QGLYRHPWDD ISYVLPEHMS 1100
Rat *V********V ********** ********** ********** **********
Dm  **NV**I*SL ******I*** ***M****** ********** ****I**QYN
Hum M 1101
Rat M     97.5% identity with human (aa 1-1101)
Dm  -     75.5% identity with human (aa 710-1100)
```