

Does dopamine block the spawning of the acroporid coral *Acropora tenuis*?

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1  cccaacaaccaatcaaatccagtggtactgatccagacattggagacatcttggcagcc
   P N N Q S N P V A T D P D I G D I L A A
61  ctttagtgccttgcttataatgtgacattaatcactaattgttttagtttgcgtaaca
   L L V A L L I I C T L I T N C L V C V T
121 ttttacctatttaaggacctaaggacagtttgtcattattttgtcatcagtttgagcgcg
   F Y L F K D L R T V C H Y F V I S L S A
181 gccgacattcttgttgctgtagtagctatgccggttgggtgtgctgcaactaacttcc
   A D I L V A V V A M P V W C A L Q L T S
241 atgcattggtcgtttagtgactcactgaggacattttggaactgcatggacatactctgt
   M H W S F S D S L R T F W N C M D I L C
301 ggaacagcttcaatcatgaatctcacagcagtgcaattgatcgccatgctgccattact
   G T A S I M N L T A V S I D R H A A I T
361 aagcctttcaactaccgctctgtcatgacttcttttcgcgctatttccatgataatcttt
   K P F N Y P S V M T S F R A I S M I I F
421 gtgtggttttattccatagtggtttcgggattacgcttagcaacctggcacacacaaaaca
   V W F Y S I V V S G L R L A T W H T K T
481 agttatatgcattttgtttctgcaaccagcttttttattcctctcttcattatgataatc
   S Y M H F V S A T S F F I P L F I M I I
541 atgtacacaagaatattttggttgctaggaacaagctcaccgaatgcgtaatggccgt
   M Y T R I Y L V A R K Q A H R M R N G R
601 aactacgcaagtgatgtcaaagccgctaaaacgatcgctatattaatcggcttgttcgta
   N Y A S D V K A A K T I A I L I G L F V
661 ttttgcctggggtccatttttcgccattgtcctatctattgcgcatgatcagacggttgta
   F C W G P F F A I V L S I A H D Q T V V
721 gttccttactcgctgttcaatgtcatcaaattggatgggtgtactgcagttcttgtctgaac
   V P Y S L F N V I K W M V Y C S S C L N
781 cccataatctactcttgtcttaatcgcaactacagacgtgcattgcgtaaaactttgccaa
   P I I Y S C L N R N Y R R A L R K L C Q
841 cgtgtcctcaaaaagcgagaaatgggtcactgagacttctgtcg 882
   R V L K K R E M V T E T S S

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Figure S1. Nucleotide and deduced amino acid sequences of a partial ORF fragment of *Acropora tenuis* dopamine receptor-like cDNA (*At06753*). Oligonucleotide primers used to amplify the cDNA fragment by PCR were designed based on *Acropora digitifera* transcript sequence of aug_v2a.06753.t1. The cDNA was composed of 882 bases encoding a protein of 294 amino acids. The nucleotide numbers are shown to the left of each line. The putative transmembrane domains analyzed by a Kyte and Doolittle hydropathy plot are underlined with solid lines.

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1  gtggtgatgattctgagcgcgtgtgacaactgtgactggagaatggatatttggagcatgg
  V V M I L S A V T T V T G E W I F G A W
61  tgctgtcaggctgtagctgcagcgggtctgactttgtctttcatatcaattcttcacatg
  C C Q A V A A A G L T L S F I S I L H M
121 agctgcctcagtatcgatcgatatattgcaattcagaaacccttagctatgaatccatc
  S C L S I D R Y I A I Q K P F S Y E S I
181 gtcactagaagaagagtgggtgacggttttaatcctgatctgggtgtctggagttgttgtg
  V T R R R V V T V L I L I W V S G V V V
241 cctaataattccgtagcagatgttgaattcagggccgtgacatacggatgttcaagtgtg
  P N I P L A D F E F R A V T Y G C S S V
301 gagtttgaaaacaccggcggtctttttctccttatatttttcttctgctggaatattt
  E F E N T R R S F S P Y I I F L V G I F
361 gttgtcatacctttcgctgttatttggcttttgaacgcagtggttttcaagacagctttt
  V V I P F A V I C F S N A V V F K T A F
421 aatcacgcaagacagctgagcagagttgagaagagtttagagcggcttccagcagatatt
  N H A R Q L S R V E K S L E R S S A D I
481 tgcgaaagggaggagcaacagcaagcgaaccacgcgtagaaaaccactcgttgaaaaga
  C E R E E Q Q Q A K P R V E N H S L K R
541 gagatcaaatacagcgcacacctttgcgctttagtgcggattatttttgctatgttacatt
  E I K S A H T F A L V V G L F L L C Y I
601 ccattttactcagtcggcacctacaggaagctagctcgatccgctaacgtacattctagt
  P F Y S V G T Y R K L A R S A N V H S S
661 gatgtgcgcatcaccatgtgggttgcctttgcgcaattcttttatcaaccggattgtttat
  D V R I T M W V A F A N S F I N P I V Y
721 ggcttgaggatattcaccgtttcggaaagcttttaattattatgtctagcccgcgtgtagt
  G L R Y S P F R K A F K L L C L A R C S
781 gagcgcgccattctcacaactgcaagagaatcagttcttggagacgtgaaagggacgg
  E R R H S H N C K R I S S W R R E R D G
841 accacgttatcaagtacttccgctctctag 870
  T T L S S T S A L *

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Figure S2. Nucleotide and deduced amino acid sequences of a partial ORF fragment of *Acropora tenuis* dopamine receptor-like cDNA (*At07635*). Oligonucleotide primers used to amplify the cDNA fragment by PCR were designed based on *Acropora digitifera* transcript sequence of *aug_v2a.07635.t1*. The cDNA was composed of 870 bases encoding a protein of 289 amino acids. The translation stopcodon is indicated by the asterisk (*). The nucleotide numbers are shown to the left of each line. The putative transmembrane domains analyzed by a Kyte and Doolittle hydrophathy plot are underlined with solid lines.

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1 tatttatcgctcttggctcgttaattgctttgggaggtaatggtttgcttataacggttata
  Y L S L L V V I A L G G N G L L I T V I
61 ctcaagagaaaactccttcaaaaagttcattacttcttcatacttagtctggcgcgctct
  L K R K L L Q K V H Y F F I L S L A A S
121 aatttcttaaacgccttttttaagatacctaccacgattttaggacgctttgatcgaaac
  N F L N A F F K I P T T I L G R F D R N
181 tggtagcctaatcacacaatgatgctacttcaccacccccctgggtgtgctgtttggcgcg
  W Y P N H T I C Y F T T P L G V L F G A
241 gcatctgtgttcagcctatcagcggtagctatcaacagataccttgtgatttcctcgccg
  A S V F S L S A V A I N R Y L V I S S P
301 cctaactattctgatcgaatgccaccgatgttggccaaaagcattttggctggaatttgg
  L N Y S D R M P P M L A K S I L A G I W
361 ttcgcaagtttttctttggccgtccctcctgtcatgtggagagagaaggaagccatttgc
  F A S F S L A V P P V M W R E K E A I C
421 cgaagcggtagaatttccaaagaacattacacctcgaaatgctttactttttcttggcc
  R S G R I S K E H Y T S E M L Y F F L A
481 ttgtggctgtttgtcatcattgttcccttccattgttatgagcatttcttacgtgaagatc
  L W L F V I I V P S I V M S I S Y V K I
541 tttcttattgcgcgctaccacgcgttgcaaatacagacgcgaaatcaagcattcgcagat
  F L I A R Y H A L Q I D T R N Q A F A D
601 tgccaacaaacaaagcgaaggaggaaagacttgaaagctgctgtagttctagcagtgatc
  C Q Q T K R R R K D L K A A V V L A V I
661 ggaggaatcttcattatttggctggattcctttcttctgtgtacagactattcacaagttt
  G G I F I I C W I P F F V V Q T I H K F
721 ggaaagggaacaaattagttctatttacttcaacatatttctctgctcatgtac 776
  G K G K I S S I Y F N I F L C V M Y

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Figure S3. Nucleotide and deduced amino acid sequences of a partial ORF fragment of *Acropora tenuis* dopamine receptor-like cDNA (*At08250*). Oligonucleotide primers used to amplify the cDNA fragment by PCR were designed based on *Acropora digitifera* transcript sequence of *aug_v2a.08250.t1*. The cDNA was composed of 776 bases encoding a protein of 258 amino acids. The nucleotide numbers are shown to the left of each line. The putative transmembrane domains analyzed by a Kyte and Doolittle hydropathy plot are underlined with solid lines.

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1 atggccgtcagcaattctaccgcaatgcccccaacagatatagacggagtttgccaacaa
M A V S N S T A M P P T D I D G V C Q Q
61 gcaacgaagcccagagtttattgtttacagcggttttttgggtgctaatacatgttagccaca
A T K P E F I V Y S V F L V L I M L A T
121 ttgtttggaaatgtgttagttataaccgcggtttatcattttcatcgcttgcgacgaatg
L F G N V L V I T A V Y H F H R L R R M
181 actaattttcttcatcatctctctggccggtttccgatcttctcgttgactaggtcatctg
T N F F I I S L A V S D L L V A L G H L
241 cctctccgtattgatcaaagcgttcacaacaataactgggtgtttcgacaagacgccaat
P L R I D Q S V H N N N W C F D K T P N
301 gatgtaacaacctgcgcgattggatagcaatggacactgtgttcagctgtgctccatt
D V T T C A Y W I A M D T V F S C A S I
361 tgcaatctgggtgtcatatcaattgatcgttttctagccatcaccaaacctttcgaatac
C N L V V I S I D R F L A I T K P F E Y
421 caaacaggatgaccaagcgtgttggcttttcgctcatcgcttttgggtctacgct
Q N R M T K R V G F S L I A F V W V Y A
481 ttactatgggggtgtccttagcctgggttgattggacaagggcagatcctaacgccactcac
L L W G V L S L V D W T R A D P N A T H
541 aggcatactttcgtcatcgtaaaaaatcaacaaatgagcgcgagcgtgaggcaagaagac
R H I F V I V K N Q T N E R A C G K K D
601 aagggtgattacactactgcaatggcgtgttgcgctatttttaccgcttctcatagtcac
K V Y Y T T A M A V A L F L P L L I V I
661 gccacgtatgcctgcggtttccgcttagcgtttacgcaggcgaaagcggtagccctactt
A T Y A C V F R V A F T Q A K A V A L L
721 gatccaaccaaaggaaagagacacattttgcgcaattgaaagcgacaaaactatcgct
D P T K G K R H I L R E L K A T K T I A
781 gttgttatcgggggtattcatgggtgttggctaccgagttttattatcattgtattgagt
V V I G V F M V C W L P S F I I I V L S
841 ctatgggtgcaggactgtttcaagccggttttggacaacaaaaatctttctctctata
L W C Q D C F K P F L D N K N L S L S I
901 aggatcatttttgtgaccattttgccggtcataaacagttctctaaatccgggtgatttat
R I I F V T I L P V I N S S L N P V I Y
961 acagttttcaaccaagagttccgaatggccttcagtcgaatgctctgcagaggtcgaact
T V F N Q E F R M A F S R M L C R G R T
1021 ccacggagcgcagctgacgttgaattctcggttaccgaacaaacaaattctgcaacgcca
P R S A A D V E F S V T E Q T N S A T R
1081 gtgaaagtgcacaaactacaggaaaaagcagacaaaagcctgggttcaatatgaacgggtgga
V K V Q T T G K S R P K A W F N M N G G
1141 ggcgatgcgagcaggtag 1158
G D A S R *

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Figure S4. Nucleotide and deduced amino acid sequences of a complete ORF fragment of *Acropora tenuis* dopamine receptor-like cDNA (*At14160*). Oligonucleotide primers used to amplify the cDNA fragment by PCR were designed based on *Acropora digitifera* transcript sequence of aug_v2a.14160.t1. The cDNA was composed of 1158 bases encoding a protein of 385 amino acids. The translation stopcodon is indicated by the asterisk (*). The nucleotide numbers are shown to the left of each line. The putative transmembrane domains analyzed by a Kyte and Doolittle hydropathy plot are underlined with solid lines.

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1  gtcactgcatctgtggaacttactcgtatgcctggccatttcaactgaacaggcgctta
   V T A I C G N L L V C L A I S L N R R L
61  cgaaagaccaccaactacttcatattctccctggcgatttctgatcttttgacagcatca
   R K T T N Y F I F S L A I S D L L T A S
121 tgctcaatgtcttttgatgttcaagttcttttgcaaccattgggctggaatcacggagag
    C S M S F D V Q V L L Q P L G W N H G E
181 ttgtctgcaatttctggaccttctgtttatctgatcgctgcgccgacctccataacttaat
    F V C N F W T F V Y L I A A P T S I L N
241 cttatggcggtcagcattgacaggtaccaagcaatcagtaatcctctccgatactacgac
    L M A V S I D R Y Q A I S N P L R Y Y D
301 aaaatgagaccgagacgtgctatggctatcatagcagcaatttggctctactccttcgcg
    K M R P R R A M A I I A A I W L Y S F A
361 tttacagttgctgggatggctggttggccctattatgaacaaagtgttcgggatggaatg
    F T V A G M A G W P Y Y E Q S V R D G M
421 tgctatnttaatatcagtccttactattctgtagtgagctcggcgatgaatttcattttc
    C Y F N I S P Y Y S V V S S A M N F I F
481 cccacaatggtgatgtgtgtgatctatttcaaaatctatctgatcgctcgcgcatgca
    P T M V M C V I Y F K I Y L I A R A H A
541 caacggcttgtgcagcatgaggtcccggtcaccaccgcagcaacatcttgctccaacgag
    Q R L V Q H E V P V T T A A T S C S N E
601 gattctggcactataacctctgaaaagaaacgcctgaaaagaaatattaaggcggcaaag
    D S G T I T S E K K R L K R N I K A A K
661 acaatcgccattattgtgtcaacttttctcctatggttgggtccctttcaactttggtttca
    T I A I I V S T F L L C W V P F T L V S
721 accattacttccctctgtcaatactgcatcgccaatttgcggtagttattaactcacta
    T I T S L C Q Y C I A N F A V V I N S L
781 cttgtggtggcgtacatgaactccgcaactcaac 813
    L V V A Y M N S A L N

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Figure S5. Nucleotide and deduced amino acid sequences of a partial ORF fragment of *Acropora tenuis* dopamine receptor-like cDNA (*At17552*). Oligonucleotide primers used to amplify the cDNA fragment by PCR were designed based on *Acropora digitifera* transcript sequence of *aug_v2a.17552.t1*. The cDNA was composed of 813 bases encoding a protein of 271 amino acids. The nucleotide numbers are shown to the left of each line. The putative transmembrane domains analyzed by a Kyte and Doolittle hydropathy plot are underlined with solid lines.

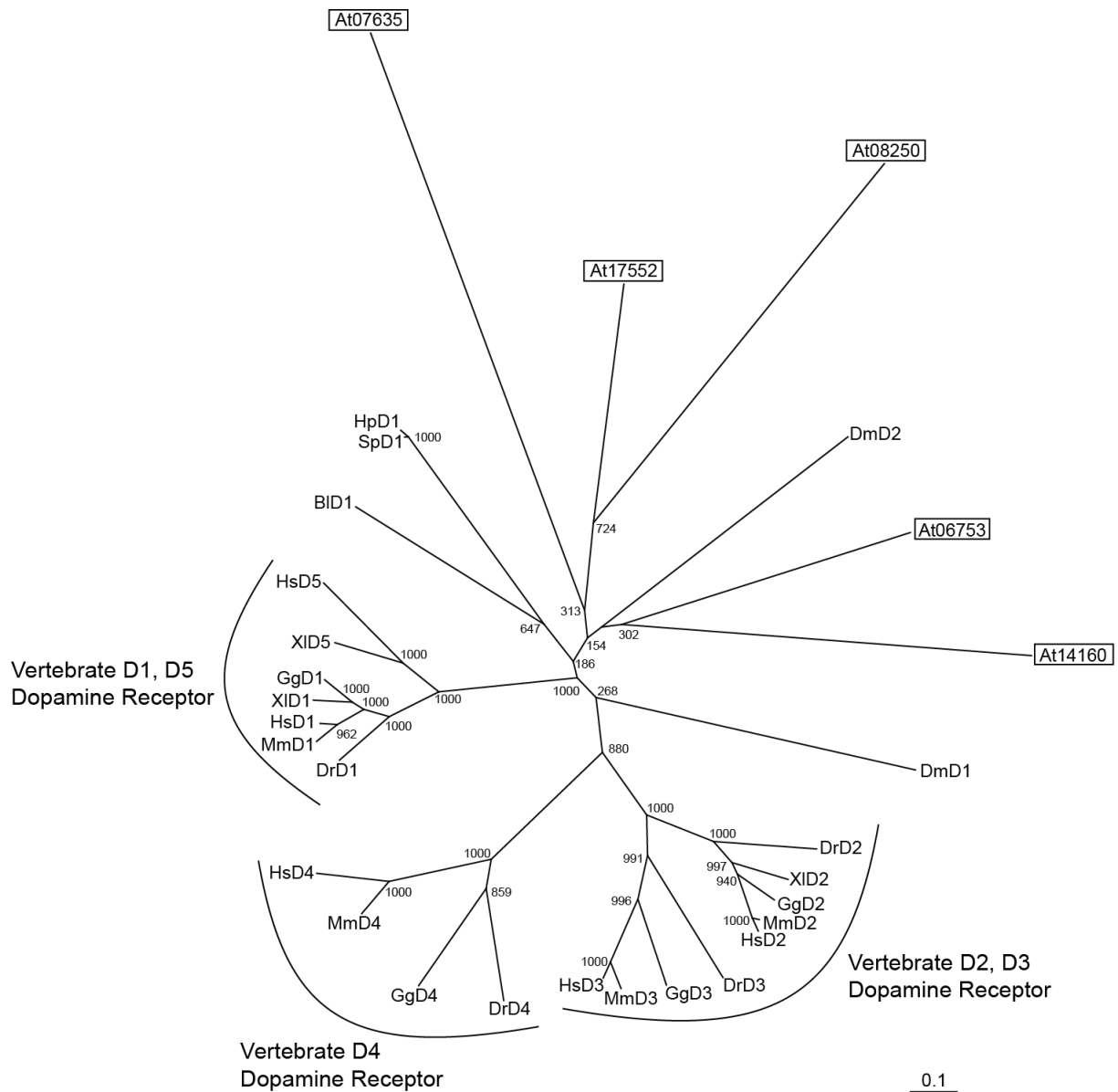


Figure S6. Unrooted phylogenetic tree of dopamine receptor proteins. The neighbor-Joining method and CLUSTAL W (<http://clustalw.ddbj.nig.ac.jp/top-e.html>) were used to construct the phylogenetic tree. One thousand bootstrap repetitions were performed, and bootstrap values are shown at the nodes. The scale bar refers to a phylogenetic distance of 0.1 amino acid substitution per site. The position of the *Acropora tenuis* dopamine receptor-like proteins were indicated by box. The accession numbers for dopamine receptor proteins used in the phylogenetic trees analysis are as follows: BID1 (*Branchiostoma lanceolatum* D1, CAA06536); DmD1 (*Drosophila melanogaster* D1, P41596); DmD2 (*Drosophila melanogaster* D2, Q24563); DrD1 (*Danio rerio* D1, NP_001129448); DrD2 (*Danio rerio* D2, NP_898891); DrD3 (*Danio rerio* D3, NP_898890); DrD4 (*Danio rerio* D4, NP_001012634); GgD1 (*Gallus gallus* D1, NP_001138320); GgD2 (*Gallus gallus* D2, NP_001106761); GgD3 (*Gallus gallus* D3, ACR48171); GgD4 (*Gallus gallus* D4, NP_001136321); HpD1 (*Hemicentrotus pulcherrimus* D1, BAJ14803); HsD1 (*Homo sapiens* D1, NP_000785); HsD2 (*Homo sapiens* D2, AAB26819); HsD3 (*Homo sapiens* D3, P35462); HsD4 (*Homo sapiens* D4, NP_000788); HsD5 (*Homo sapiens* D5, AAA52329); MmD1 (*Mus musculus* D1,

NP_034206); MmD2 (*Mus musculus* D2, NP_034207); MmD3 (*Mus musculus* D3, NP_031903); MmD4 (*Mus musculus* D4, NP_031904); SpD1 (*Strongylocentrotus purpuratus* D1, XP_003726379); XID1 (*Xenopus laevis* D1, P42289); XID2 (*Xenopus laevis* D2, CAA42088); XID5 (*Xenopus laevis* D5, P42290).