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On the tubulin polymerization promoting proteins of zebrafish

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ABSTRACT

Recently, Aoki et al. [15] have been published a paper (Biochem. Biophys. Res. Commun. 445 (2014) 357–362.) in which they identified possible downstream genes required for the extension of peripheral axons in primary sensory neurons of zebrafish. *Tppp* was claimed as one of them but, as I show, it is the *tppp3-like* gene, a paralog of *tppp,* which plays this role. There are three tppp paralogs in fishes: *tppp1* (named also *tppp*), *tppp3* and *tppp3-like*. *Tppp1* and *tppp3* are the orthologs of the corresponding human genes, however, the classification of the third one is ambiguous. It is known that the genomes of the early vertebrate lineage underwent two complete genome duplications, which result in the presence of several paralogs in vertebrates. A teleost fish specific third whole genome duplication also occurred. Thus the *tppp3-like* gene can be either an ortholog of human *TPPP2* or a fourth paralog (*tppp4*) absent in tetrapods but present in fishes; finally a *tppp3a* gene which can be originated from the third, fish specific, whole genome duplication. Comparing the sequences of vertebrate and recently available lamprey tppps I show that the *tppp3-like* gene is a *TPPP2* ortholog. Synteny data are in accordance with this suggestion.

1. Introduction

The family of TPPP-like proteins was described recently [1]. Its first member, tubulin polymerization promoting protein (TPPP or TPPP1) was first isolated from bovine brain [2] and later found to promote tubulin polymerization and stabilization of microtubules [3,4]. There are three TPPP paralogous genes in human, *TPPP1*, *TPPP2* and *TPPP3* (TPPP/p25, TPPP2/p18 and TPPP3/p20 at protein level) [5]. These paralogs can also be found in mammals, birds and reptiles. In fish, three paralogs exist as well; *tppp1* and *tppp3* are the orthologs of the corresponding human genes/proteins, however, the classification of the third one is ambiguous. Sometimes it is named as *tppp3-like* gene in databases. The reason of this name can be the fact that these proteins are more similar, indeed, to tetrapod TPPP3s than to TPPP2s or TPPP1s [6]. It is known that the genomes of the early vertebrate lineage underwent two complete genome duplications, which result in the presence of several paralogs in vertebrates in comparison with the single copy of their invertebrate orthologs [7–10]. A teleost fish specific third whole genome duplication also occurred [11–14]. Earlier, I have shown by synteny analysis that the probable history of the two-rounds duplication of the single invertebrate *tppp* gene was that the diversification of *tppp1* and the precursor of *tppp2*/*tppp3* occurred in the first round of whole-genome duplication which was followed by two further splits, *tppp1*/lost and *tppp3*/*tppp2*, in the second round [6]. However, it remained an open question the position of the fish-specific group of *tppps*. It can be considered either as *TPPP2* ortholog or as the fourth paralog (*tppp4*) that was lost in tetrapods but remained in fish; finally as *tppp3a* gene which is originated from the third, teleost fish specific, whole genome duplication [6].

Recently, Aoki et al. [15] have been published a paper in Biochemical and Biophysical Research Communications, in which they identified possible downstream genes required for the extension of peripheral axons in primary sensory neurons of zebrafish. *Tppp* was claimed as one of the several candidate genes. However, there is confusion in the paper since the three tppp paralogs are mixed up. In the text *tppp* is mentioned and the properties of vertebrate TPPP1 are discussed. It is claimed that its expression was investigated in various tissues. However, the supplementary table showing the genes investigated lists not *tppp* but "*tubulin polymerization-promoting protein family member 3*" i.e. *tppp3*. To reach a complete confusion, the NCBI Accession number XM_682834 is given in a table, which is the mRNA of the *tubulin polymerization-promoting protein family member 3-like* gene according to the NCBI Database.

Thus it seems to be necessary to clarify this question.

Abbreviations: TPPP, tubulin polymerization promoting protein.

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0006-291X/

Table 1
TPPP genes/proteins of *Danio rerio*.

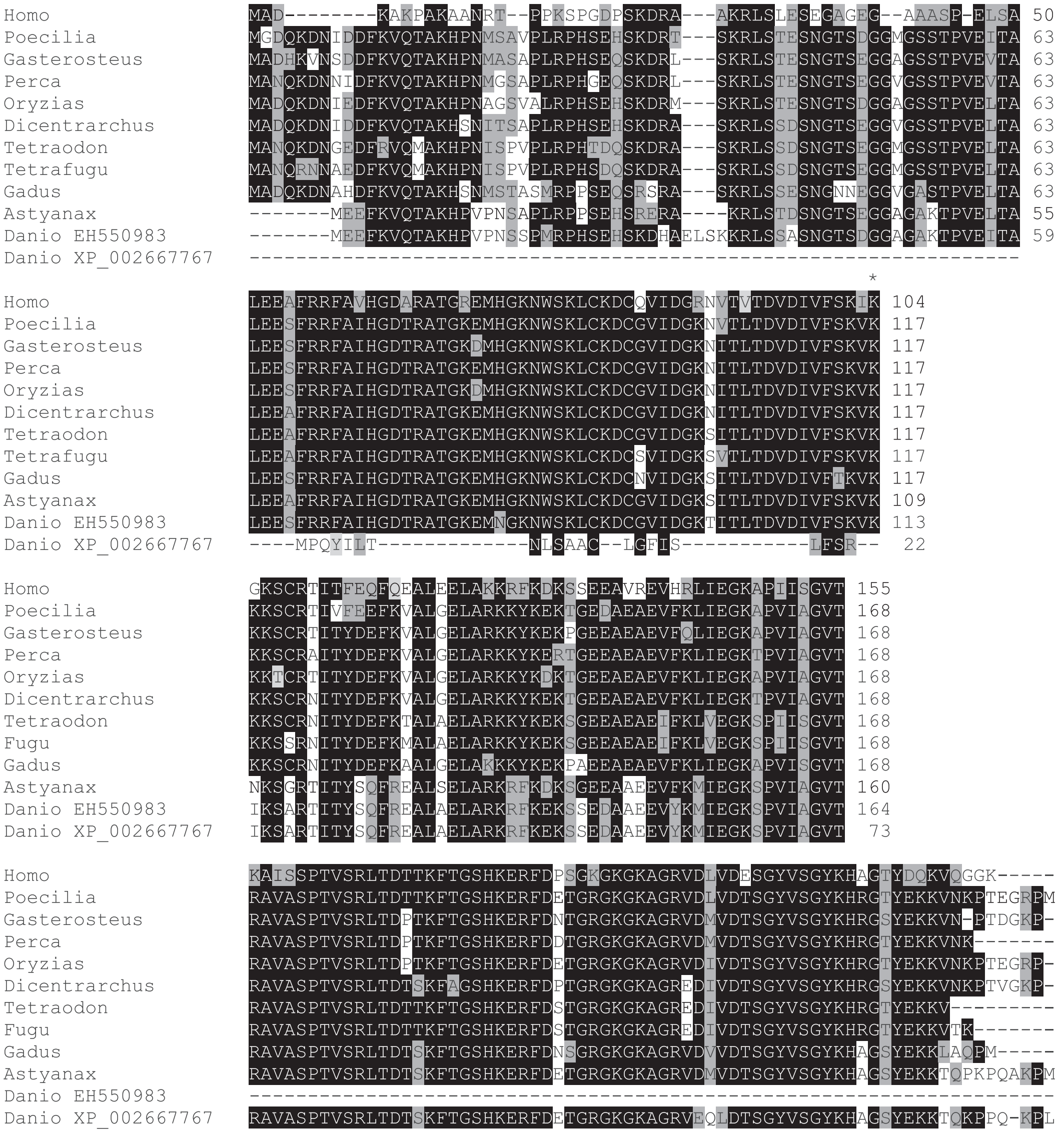
Name	Short name	Gene	GeneID	mRNA	Protein	Chromosome
Tubulin polymerization-promoting protein	*tppp*	*LOC100333482*	100333482	XM_002667721 EH550983[a] EH572114[b]	XP_002667767	Dre16 Unknown
Tubulin polymerization-promoting protein family member 3-like	*tppp3-like*	*LOC559490*	559490	XM_682834	XP_687926	Dre5
Tubulin polymerization-promoting protein family member 3	*tppp3*	*tppp3*	393825	NM_201335	NP_958492	Dre7

[a] 5′ Read.
[b] 3′ Read.

2. Materials and methods

2.1. Database homology search

TPPP homologs were identified with an NCBI blast search using the sequences of human TPPP proteins (NP_008961; NP_776245; NP_057048) as queries. BLASTP or TBLASTN analysis [16] was performed on complete genome sequences and EST collections available at the NCBI website (http://www.ncbi.nlm.nih.gov/BLAST/). Similar search was carried out on various fish databases: http://www.fugu-sg.org/; http://www.sanger.ac.uk/Projects/D_rerio/; http://www.ensembl.org/Tetraodon_nigroviridis/; http://dolphin.



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Homo                MAD--------KAKPAKAANRT--PPKSPGDPSKDRA---AKRLSLESEGAGEG--AAASP-ELSA 50
Poecilia            MGDQKDNIDDFKVQTAKHPNMSAVPLRPHSEHSKDRT---SKRLSTESNGTSDGGMGSSTPVELTA 63
Gasterosteus        MADHKVNSDDFKVQTAKHPNMASAPLRPHSEQSKDRL---SKRLSTESNGTSEGGAGSSTPVEVTA 63
Perca               MANQKDNNIDFKVQTAKHPNMGSAPLRPHGEQSKDRL---SKRLSTESNGTSEGGVGSSTPVEVTA 63
Oryzias             MADQKDNIEDFKVQTAKHPNAGSVALRPHSEHSKDRM---SKRLSTESNGTSDGGAGSSTPVELTA 63
Dicentrarchus       MADQKDNIDDFKVQTAKHSNITSAPLRPHSEHSKDRA---SKRLSSDSNGTSEGGVGSSTPVELTA 63
Tetraodon           MANQKDNGEDFRVQMAKHPNISPVPLRPHTDQSKDRA---SKRLSSDSNGTSEGGMGSSTPVELTA 63
Tetrafugu           MANQRNNAEDFKVQMAKHPNISPVPLRPHSDQSKDRA---SKRLSSDSNGTSEGGMGSSTPVELTA 63
Gadus               MADQKDNAHDFKVQTAKHSNMSTASMRPPSEQSRSRA---SKRLSSESNGNNEGGVGASTPVELTA 63
Astyanax            -------MEEFKVQTAKHPVPNSAPLRPPSEHSRERA----KRLSTDSNGTSEGGAGAKTPVELTA 55
Danio EH550983      -------MEEFKVQTAKHPVPNSSPMRPHSEHSKDHAELSKKRLSSASNGTSDGGAGAKTPVEITA 59
Danio XP_002667767  ------------------------------------------------------------------
                                                                         *
Homo                LEEAFRRFAVHGDARATGREMHGKNWSKLCKDCQVIDGRNVTVTDVDIVFSKIK 104
Poecilia            LEESFRRFAIHGDTRATGKEMHGKNWSKLCKDCGVIDGKNVTLTDVDIVFSKVK 117
Gasterosteus        LEESFRRFAIHGDTRATGKDMHGKNWSKLCKDCGVIDGKNITLTDVDIVFSKVK 117
Perca               LEESFRRFAIHGDTRATGKEMHGKNWSKLCKDCGVIDGKNITLTDVDIVFSKVK 117
Oryzias             LEESFRRFAIHGDTRATGKDMHGKNWSKLCKDCGVIDGKNITLTDVDIVFSKVK 117
Dicentrarchus       LEEAFRRFAIHGDTRATGKEMHGKNWSKLCKDCGVIDGKNITLTDVDIVFSKVK 117
Tetraodon           LEEAFRRFAIHGDTRATGKEMHGKNWSKLCKDCGVIDGKSITLTDVDIVFSKVK 117
Tetrafugu           LEEAFRRFAIHGDTRATGKEMHGKNWSKLCKDCSVIDGKSVTLTDVDIVFSKVK 117
Gadus               LEESFRRFAIHGDTRATGKEMHGKNWSKLCKDCNVIDGKSITLTDVDIVFTKVK 117
Astyanax            LEEAFRRFAIHGDTRATGKEMHGKNWSKLCKDCGVIDGKSITLTDVDIVFSKVK 109
Danio EH550983      LEESFRRFAIHGDTRATGKEMNGKNWSKLCKDCGVIDGKTITLTDVDIVFSKVK 113
Danio XP_002667767  ----MPQYILT-------------NLSAAC--LGFIS-----------LFSR--  22

Homo                GKSCRTITFEQFQEALEELAKKRFKDKSSEEAVREVHRLIEGKAPIISGVT 155
Poecilia            KKSCRTIVFEEFKVALGELARKKYKEKTGEDAEAEVFKLIEGKAPVIAGVT 168
Gasterosteus        KKSCRTITYDEFKVALGELARKKYKEKPGEEAEAEVFQLIEGKAPVIAGVT 168
Perca               KKSCRAITYDEFKVALGELARKKYKERTGEEAEAEVFKLIEGKTPVIAGVT 168
Oryzias             KKTCRTITYDEFKVALGELARKKYKDKTGEEAEAEVFKLIEGKAPVIAGVT 168
Dicentrarchus       KKSCRNITYDEFKVALGELARKKYKEKTGEEAEAEVFKLIEGKTPVIAGVT 168
Tetraodon           KKSCRNITYDEFKTALAELARKKYKEKSGEEAEAEIFKLVEGKSPIISGVT 168
Fugu                KKSSRNITYDEFKMALAELARKKYKEKSGEEAEAEIFKLVEGKSPIISGVT 168
Gadus               KKSCRNITYDEFKAALGELAKKKYKEKPAEEAEAEVFKLIEGKAPVISGVT 168
Astyanax            NKSGRTITYSQFREALSELARKRFKDKSGEEAAEEVFKMIEGKSPVIAGVT 160
Danio EH550983      IKSARTITYSQFREALAELARKRFKEKSSEDAAEEVYKMIEGKSPVIAGVT 164
Danio XP_002667767  IKSARTITYSQFREALAELARKRFKEKSSEDAAEEVYKMIEGKSPVIAGVT  73

Homo                KAISSPTVSRLTDTTKFTGSHKERFDPSGKGKGKAGRVDLVDESGYVSGYKHAGTYDQKVQGGK----- 219
Poecilia            RAVASPTVSRLTDTTKFTGSHKERFDETGRGKGKAGRVDLVDTSGYVSGYKHRGTYEKKVNKPTEGRPM 237
Gasterosteus        RAVASPTVSRLTDPTKFTGSHKERFDNTGRGKGKAGRVDMVDTSGYVSGYKHRGSYEKKVN-PTDGKP- 235
Perca               RAVASPTVSRLTDPTKFTGSHKERFDDTGRGKGKAGRVDMVDTSGYVSGYKHRGTYEKKVNK------- 230
Oryzias             RAVASPTVSRLTDPTKFTGSHKERFDETGRGKGKAGRVDIVDTSGYVSGYKHRGTYEKKVNKPTEGRP- 236
Dicentrarchus       RAVASPTVSRLTDTSKFAGSHKERFDPTGRGKGKAGREDIVDTSGYVSGYKHRGSYEKKVNKPTVGKP- 236
Tetraodon           RAVASPTVSRLTDTTKFTGSHKERFDSTGRGKGKAGREDIVDTSGYVSGYKHRGTYEKKV--------- 228
Fugu                RAVASPTVSRLTDTTKFTGSHKERFDSTGRGKGKAGREDIVDTSGYVSGYKHRGTYEKKVTK------- 230
Gadus               RAVASPTVSRLTDTSKFTGSHKERFDNSGRGKGKAGRVDVVDTSGYVSGYKHAGSYEKKLAQPM----- 232
Astyanax            RAVASPTVSRLTDTSKFTGSHKERFDETGRGKGKAGRVDMVDTSGYVSGYKHAGSYEKKTQPKPQAKPM 229
Danio EH550983      ---------------------------------------------------------------------
Danio XP_002667767  RAVASPTVSRLTDTSKFTGSHKERFDETGRGKGKAGRVEQLDTSGYVSGYKHAGSYEKKTQKPPQ-KPL 141
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Fig. 1. Multiple sequence alignment of several fish TPPP1s by ClustalOmega. The alignment was refined manually. Residues identical and similar in the majority of the species are indicated by black and grey backgrounds, respectively. The first two lines represent the first coding exon; the third and the fourth lines correspond to the second and third exons, respectively. Asterisk notes that these amino acids are coded by the last two nucleotides of the first and the first nucleotide of the second exon. Proteins and ESTs (*) are: *Homo sapiens* NP_008961; *Poecilia reticulate* XP_008430776; *Gasterosteus aculeatus* DN734108*; *Perca flavescens* GO572248*; *Oryzias latipes* XP_004078142; *Dicentrarchus labrax* FM023946*; *Tetraodon nigroviridis* CAG11971; *Takifugu rubripes* XP_003966223; *Gadus morhua* GW848004*; *Astyanax mexicanus* XP_007234837; *Danio rerio* EH550983*, *Danio rerio* XP_002667767.