

Response to a Letter to the Editor from Rodgers regarding “Overexpression of Myostatin2 in zebrafish reduces the expression of dystrophin associated protein complex (DAPC) which leads to muscle dystrophy”

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We appreciate being made aware of earlier published work on the cloning of zebrafish myostatin 2 (MSTN-2), nomenclature of MSTN family. In the published version of this article, we reported one zebrafish MSTN-2 cDNA (GenBank accession number: AY614000), which is different from two published zebrafish MSTN-2 according to comparison of nucleotide and deduced amino acid sequences (Fig. 1b). However, two previous published articles which identified zebrafish MSTN-2 cDNA (GenBank accession number: AY687474) [1] and gene (GenBank accession number: AY693972) [2] was not referenced in this article. We apologize for neglecting pertinent references. According to new nomenclature of myostatin family [3], we construct new phylogenetic tree including three zebrafish MSTN-2 to replace old Fig. 3.

References

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Fig. 1b Alignment of deduced amino acids of three zebrafish MSTN-2, including MSTN-2c (AY614000), MSTN-2b (AY693972) and MSTN-2a (AY687474). Variant amino acid residues in N-terminal of MSTN-2c and in unique domain within matured peptide of zebrafish MSTN-2c and MSTN-2b are indicated with asterisks and underlined, respectively

B

*	20	*	40	*	60	*	80	*	
zFMSTN-2c :	<u>M</u> FLLFYLSFWGVLGQSQNQNLS <u>TTTTT</u> QAFVT <u>P</u> GDDNGQ <u>C</u> T <u>C</u> QFRQQSKLLRLHSI <u>S</u> QILSILRLE <u>Q</u> APNI <u>S</u> R <u>D</u> TVK <u>L</u> LLPK <u>A</u> PL <u>R</u>								: 90
zFMSTN-2b :	<u>M</u> FLLFYLSFWGVLGQSQNQNLS <u>TTTTT</u> QAFVT <u>P</u> GDDNGQ <u>C</u> T <u>C</u> QFRQQSKLLRLHSI <u>S</u> QILSILRLE <u>Q</u> APNI <u>S</u> R <u>D</u> TVK <u>L</u> LLPK <u>A</u> PL <u>R</u>								: 90
zFMSTN-2a :	<u>M</u> FLLFYLSFWGVLGQSQNQNLS <u>TTTTT</u> QAFVT <u>P</u> GDDNGQ <u>C</u> T <u>C</u> QFRQQSKLLRLHSI <u>S</u> QILSILRLE <u>Q</u> APNI <u>S</u> R <u>D</u> TVK <u>L</u> LLPK <u>A</u> PL <u>R</u>								: 90
*									
100	*	120	*	140	*	160	*	180	*
zFMSTN-2c :	<u>E</u> LLDQYDQN <u>G</u> GI <u>S</u> DEE <u>Q</u> AS <u>S</u> ET <u>I</u> IT <u>M</u> ATE <u>P</u> QAI <u>T</u> QLVGMP <u>K</u> CC <u>M</u> F <u>A</u> LSP <u>K</u> IL <u>P</u> D <u>S</u> IL <u>K</u> ALL <u>W</u> YL <u>R</u> PA <u>E</u> PT <u>V</u> Y <u>I</u> Q <u>I</u> SH <u>L</u> ESS <u>S</u> E <u>G</u> NN								: 180
zFMSTN-2b :	<u>E</u> LLDQYDQN <u>G</u> GI <u>S</u> DEE <u>Q</u> AS <u>S</u> ET <u>I</u> IT <u>M</u> ATE <u>P</u> QAI <u>T</u> QLVGMP <u>K</u> CC <u>M</u> F <u>A</u> LSP <u>K</u> IL <u>P</u> D <u>S</u> IL <u>K</u> ALL <u>W</u> YL <u>R</u> PA <u>E</u> PT <u>V</u> Y <u>I</u> Q <u>I</u> SH <u>L</u> ESS <u>S</u> E <u>G</u> NN								: 180
zFMSTN-2a :	<u>E</u> LLDQYDQN <u>G</u> GI <u>S</u> DEE <u>Q</u> AS <u>S</u> ET <u>I</u> IT <u>M</u> ATE <u>P</u> QAI <u>T</u> QLVGMP <u>K</u> CC <u>M</u> F <u>A</u> LSP <u>K</u> IL <u>P</u> D <u>S</u> IL <u>K</u> ALL <u>W</u> YL <u>R</u> PA <u>E</u> PT <u>V</u> Y <u>I</u> Q <u>I</u> SH <u>L</u> ESS <u>S</u> E <u>G</u> NN								: 180
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200	*	220	*	240	*	260	*	280	*
zFMSTN-2c :	<u>H</u> SRIRAQ <u>K</u> IDVNART <u>D</u> SW <u>H</u> IM <u>D</u> K <u>Q</u> LL <u>K</u> WL <u>K</u> Q <u>P</u> SN <u>F</u> GI <u>E</u> I <u>K</u> A <u>D</u> ANG <u>N</u> DL <u>A</u> VT <u>S</u> ES <u>G</u> EE <u>E</u> GL <u>Q</u> PF <u>L</u> EV <u>R</u> IS <u>D</u> T <u>G</u> K <u>R</u> S <u>R</u> RT <u>G</u> <u>E</u> <u>D</u> CD <u>E</u> H								: 270
zFMSTN-2b :	<u>H</u> SRIRAQ <u>K</u> IDVNART <u>N</u> SW <u>H</u> IM <u>D</u> K <u>Q</u> LL <u>K</u> WL <u>K</u> Q <u>P</u> SN <u>F</u> GI <u>E</u> I <u>K</u> A <u>D</u> ANG <u>N</u> DL <u>A</u> VT <u>S</u> ES <u>G</u> EE <u>E</u> GL <u>Q</u> PF <u>L</u> EV <u>R</u> IS <u>D</u> T <u>G</u> K <u>R</u> S <u>R</u> RT <u>G</u> <u>E</u> <u>D</u> CD <u>E</u> H								: 270
zFMSTN-2a :	<u>H</u> SRIRAQ <u>K</u> IDVNART <u>N</u> SW <u>H</u> IM <u>D</u> K <u>Q</u> LL <u>K</u> WL <u>K</u> Q <u>P</u> SN <u>F</u> GI <u>E</u> I <u>K</u> A <u>D</u> ANG <u>N</u> DL <u>A</u> VT <u>S</u> ES <u>G</u> EE <u>E</u> GL <u>Q</u> PF <u>L</u> EV <u>R</u> IS <u>D</u> T <u>G</u> K <u>R</u> S <u>R</u> RT <u>G</u> <u>E</u> <u>D</u> CD <u>E</u> H								: 270
*									*
280	*	300	*	320	*	340	*	360	*
zFMSTN-2c :	<u>S</u> TE <u>S</u> R <u>C</u> CR <u>P</u> LT <u>V</u> D <u>F</u> E <u>D</u> F <u>G</u> W <u>D</u> W <u>I</u> AP <u>K</u> RY <u>K</u> AN <u>C</u> SG <u>E</u> CV <u>K</u> Y <u>P</u> SH <u>H</u> IV <u>N</u> K <u>A</u> NP <u>I</u> FF <u>A</u> G <u>P</u> CC <u>I</u> LT <u>K</u> M <u>S</u> PI <u>N</u> ML <u>Y</u> F <u>N</u> D <u>R</u> EQ <u>I</u> IY <u>G</u> K <u>I</u> PS <u>M</u> V <u>V</u>								: 360
zFMSTN-2b :	<u>S</u> TE <u>S</u> R <u>C</u> CR <u>P</u> LT <u>V</u> D <u>F</u> E <u>D</u> F <u>G</u> W <u>D</u> W <u>I</u> AP <u>K</u> RY <u>K</u> AN <u>C</u> SG <u>E</u> CV <u>K</u> Y <u>P</u> SH <u>H</u> IV <u>N</u> K <u>A</u> NP <u>I</u> FF <u>A</u> G <u>P</u> CC <u>I</u> LT <u>K</u> M <u>S</u> PI <u>N</u> ML <u>Y</u> F <u>N</u> D <u>R</u> EQ <u>I</u> IY <u>G</u> K <u>I</u> PS <u>M</u> V <u>V</u>								: 360
zFMSTN-2a :	<u>S</u> TE <u>S</u> R <u>C</u> CR <u>P</u> LT <u>V</u> D <u>F</u> E <u>D</u> F <u>G</u> W <u>D</u> W <u>I</u> AP <u>K</u> RY <u>K</u> AN <u>C</u> SG <u>E</u> CV <u>K</u> Y <u>P</u> SH <u>H</u> IV <u>N</u> K <u>A</u> NP <u>I</u> FF <u>A</u> G <u>P</u> CC <u>I</u> LT <u>K</u> M <u>S</u> PI <u>N</u> ML <u>Y</u> F <u>N</u> D <u>R</u> EQ <u>I</u> IY <u>G</u> K <u>I</u> PS <u>M</u> V <u>V</u>								: 360
*									
zFMSTN-2c :	<u>D</u> LC <u>G</u> C <u>S</u> * : 366								
zFMSTN-2b :	<u>D</u> LC <u>G</u> C <u>S</u> * : 366								
zFMSTN-2a :	<u>D</u> LC <u>G</u> C <u>S</u> * : 366								

Fig. 3 Phylogenetic tree of MSTNs. Phylogenetic and molecular evolutionary analyses were conducted using Molecular Evolutionary Genetics Analysis MEGA 4 software (<http://www.megasoftware.net/index.html>). Tree construction and distance correction were followed by neighbor-joining and Poisson correction methods, respectively. Four GDF11 from mammalian and zebrafish were used as an out group. Sequences, in addition to those in Fig. 2, used in construction of this phylogenetic tree are baboon MSTN (AF019619), goose MSTN (AY448009), turkey MSTN (AF019625), chicken MSTN (AY448007), dog MSTN (AY367768), pig MSTN (AY448008), horse MSTN (AB033541), goat MSTN (AY436347), sheep MSTN (AF019622), blue catfish MSTN-1 (AY540992), channel catfish MSTN-1 (AF396747), gilthead seabream MSTN-1 (AF258448), gilthead seabream MSTN-2 (AY046314), striped bass MSTN-1 (AF290910), white perch MSTN-1 (AF290911), white bass MSTN-1 (AF197194), shidrum MSTN-1 (AF316881), shidrum MSTN-2 (AY059386), human GDF-11 (NM_005811), mouse GDF-11 (NM_010272), rat GDF-11 (XM_343148) and zebrafish GDF-11 (AF411599)

