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1. Abstract

In contrast to mice or zebrafish, trout exhibits post-larval muscle growth through hypertrophy and formation of new myofibers (hyperplasia). The muscle fibers are formed by the fusion of mononucleated cells (myoblasts) regulated by several muscle-specific proteins such as Myomaker or Myomixer. In this work, we identified a unique gene encoding a Myomixer protein of 77 amino acids (aa) in the trout genome. Sequence analysis and phylogenetic tree showed moderate conservation of the overall protein sequence across teleost fish (61% of aa identity between trout and zebrafish Myomixer sequences). Nevertheless, the functionally essential motif, AxLyCxL is perfectly conserved in all studied sequences of vertebrates. Using *in situ* hybridization, we observed that *myomixer* was highly expressed in the embryonic myotome, particularly in the hyperplasic area. Moreover, *myomixer* remained readily expressed in white muscle of juvenile (1 and 20 g) although its expression decreased in mature fish. We also showed that *myomixer* is up-regulated during muscle regeneration and *in vitro* myoblasts differentiation. Together, these data indicate that *myomixer* expression is consistently associated with the formation of new myofibers during somitogenesis, post-larval growth and muscle regeneration in trout.

2. Introduction

Skeletal muscle consists of myofibers derived from the fusion of progenitor cells called myoblasts. In mammals, myofibers formation occurs throughout embryogenesis and during muscle regeneration in adult. Myoblasts proliferate, differentiate into myocytes that fuse to form multinucleated myotubes, and mature into functional myofibers (Dumont et al., 2015). The fusion process is highly regulated by numerous key proteins involved in distinct steps, including cell-cell recognition and adhesion, cytoskeletal reorganization and finally membrane fusion. Among those proteins, the transmembrane Myomaker protein is expressed only in skeletal muscle and is absolutely required for myoblast fusion (Millay et al., 2013). Indeed, in *myomaker* knockout mice, muscle is formed only by mononucleated myoblasts. Similarly, the muscle of *myomaker* knockout mice fails to regenerate after injury, which shows that *myomaker* is also essential for formation of new myofibers during muscle regeneration (Millay et al., 2014). Consequently, *myomaker* expression is upregulated during periods of myofiber formation (embryogenesis and muscle regeneration), and downregulated thereafter (Millay et al., 2014, 2013). In addition, ectopic expression of *myomaker* in fibroblasts promotes fusion with C2C12 myoblasts, showing its direct involvement in the fusion process (Millay et al., 2016, 2014). The mechanism of action of Myomaker remains poorly understood even though it has been shown that the C-terminal end of the protein is essential to its function (Millay et al., 2016).

Recently, another muscle-specific peptide called Myomixer with fusogenic activity was identified in mice (Bi et al., 2017; Quinn et al., 2017). The *myomixer* knockout in mice leads to muscle formation with mononucleated cells, and *in vitro,* the peptide allows the fusion of a fibroblast with a myoblast. Interestingly, the ectopic expression of *myomixer* and *myomaker* in fibroblasts promotes fibroblast-fibroblast fusion, suggesting that they should act together (Quinn et al., 2017). Nevertheless, Leikina et al. (2018) showed that Myomaker and Myomixer are involved in distinct step of the myoblast fusion process. Whereas Myomaker is essential for hemifusion of the plasma

membrane, Myomixer promotes the formation of fusion pores, and the fusogenic activities of these proteins do not require direct interaction (Leikina et al., 2018).

In zebrafish, Myomaker and Myomixer have been characterized and there are also essential for myoblast fusion (Landemaine et al., 2014; Millay et al., 2016; Shi et al., 2017; Zhang and Roy, 2017). Both proteins are expressed in embryonic myotome and their expression declines before hatching. Recently, we identified the unique *myomaker* ortholog in rainbow trout and revealed its unusual sequence. Indeed, the trout Myomaker protein contains 14 minisatellites and two sequence extensions leading to a protein of 434 aa instead of 221 in zebrafish (Landemaine et al., 2019). *In vitro*, ectopic expression of trout *myomaker* in mouse fibroblasts promotes fusion with C2C12 myoblasts. Given the original structure of trout Myomaker, we wondered whether the sequence and expression pattern of trout *myomixer* were conserved.

In this work, we showed that Myomixer protein sequence was moderately conserved across evolution and that the unique trout *myomixer* gene was highly expressed in skeletal muscle even after hatching and was upregulated during muscle regeneration and myotube formation.

3. Materials and methods

3.1. Animals

All the experiments presented in this article were developed under the current legislation that regulates the ethical handling and care procedures of experimentation animals (décret no. 2001-464, May 29, 2001) and the muscle regeneration study was approved by the INRAE PEIMA (Pisciculture Expérimentale INRAE des Monts d'Arrée) Institutional Animal Care and Use Committee (B29X777-02). The LPGP fish facility was approved by the Ministère de l'Enseignement Supérieur et de la Recherche (authorization no. C35-238-6).

3.2. Muscle regeneration experiment

As described in Landemaine et al., (2019), this experiment was carried out at the INRAE facility PEIMA (Sizun, Britany, France). Briefly, 1530 ± 279 g rainbow trout (*O. mykiss*) were anesthetized with MS-222 (50 mg/l) and using a sterile 1.2-mm needle, the left side of each fish was injured by a puncture behind to the dorsal fin and above the lateral line. The right side was used as a control for each fish. White muscle samples from both sides (within the injured region and opposite) were taken at 0, 1, 2, 4, 8, 16, and 30 days post-injury using a sterile scalpel after proper sacrifice by an MS-222 overdose. The obtained samples were properly stored in liquid nitrogen until further processing for gene expression analyses. Along the experiment, no infection was detected and the survival rate was 100%.

3.3. Trout satellite cell culture

Satellite cells from trout white muscle (15-20g body weight) were cultured as previously described (Froehlich et al., 2013; Gabillard et al., 2010). Briefly, 40 g of tissue were mechanically and enzymatically (collagenase C9891 and trypsin T4799) digested prior to filtration (100 µm and 40 µm). The cells were seeded in poly-L-lysine and laminin precoated 6-well treated polystyrene plates at a density of 80,000 cells/cm^2 and incubated at 18ºC. The cells were cultured for 3 days in F10 medium (medium F10, Sigma, N6635) supplemented with 10% fetal bovine serum to stimulate cell proliferation. Then, the medium was changed to Dulbecco's modified Eagle's medium (Sigma, D7777) containing 2% fetal bovine serum to stimulate cell differentiation and cultured in this medium for an additional 3 days. Cells were washed twice with PBS and collected with TRI reagent solution (Sigma–Aldrich, catalog no. T9424) at 3rd (PM) and 4th (DM1), 5th (DM2) and 6th (DM3) day of culture. Samples were immediately stored at -80ºC until further processing for gene expression analysis.

3.4. Amplification and sequencing of myomixer sequence

The *O. mykiss myomixer* nucleotide sequence containing the full coding region was obtained from the Trout Genome browser of the French National Sequencing Center (Genoscope). We designed PCR (Polymerase Chain Reaction) primers in two different exons (forward, 5'-TTGGCTTTCCTTCCTCTTCAG-3'; and reverse, 5'-TGCGATCTGACTGGTGTCTCC -3'). PCR reaction was carried out from a rainbow trout muscle cDNA (complementary DNA) and the PCR product was run in agarose gel, purified and sequenced (Eurofins) and the obtained sequence was used to design primers for quantitative PCR (qPCR). The validated sequence of *myomixer* cDNA was deposited in GenBank with the accession number MN230110.

3.5. Phylogenetic analysis

Several Myomixer amino acid sequences obtained from different databases were aligned with the Mafft server software, version 7 (https://mafft.cbrc.jp/alignment/server/) using the default parameters and the G-INS-i iterative refinement method. The subsequent phylogenetic analysis was performed using the neighbour-joining method with MEGA X software in a bootstrapped method (500) to assess the robustness of the tree.

3.6. RNA extraction, cDNA synthesis, and quantitative PCR analyses

For three individual fish (~150g), sample of white muscle, red muscle, skin, heart, brain, adipose tissue, liver, spleen, pituitary, kidney, ovary, gill, testis and intestine were collected and immediately stored in liquid nitrogen. Total RNA was extracted from cell cultures or from 100 mg of tissue (or less in the case of some small organs and tissues for the screening) using TRI reagent (Sigma–Aldrich, catalog no. T9424) and its concentration was determined using the NanoDrop ND-1000 spectrophotometer. One µg of total RNA was used for reverse transcription (Applied Biosystems kit, catalog no. 4368813). Trout *myomixer* primers for quantitative PCR (qPCR) (forward, 5'-AGACTTCCGTGACTCCTACCAG-3'; and reverse, 5'-TGCGATCTGACTGGTGTCTCC-3') were designed in two exons to avoid genomic DNA amplification. The secondary structure

formation in the predicted PCR product were determined with the mFOLD software. Quantitative PCR analyses were performed with 5 µl of cDNA using SYBR© Green fluorophore (Applied Biosystems), following the manufacturer's instructions, with a final concentration of 300 nM of each primer. The PCR program used was as follows: 40 cycles of 95 °C for 3 s and 60 °C for 30 s. The relative expression of target cDNAs within the sample set was calculated from a serial dilution (1:4–1:256) (standard curve) of a cDNA pool using StepOneTM software V2.0.2 (Applied Biosystems). Subsequently, qPCR data were normalized using *elongation factor-1 alpha* (*eF1a*) gene expression as previously detailed.

3.7. In situ hybridization

Trout embryos at days 10, 14 and 18 were fixed with 4% paraformaldehyde (PFA 4%) overnight at 4°C and stored in methanol at -20 °C until use. Whole-mount *in situ* hybridization was performed using RNAscope®, an hybridization amplification-based signal system (Wang et al., 2012) according to the manufacturer's protocol (Advanced Cell Diagnostics #322360). Embryos were rehydrated in a decreasing methanol/PBS+0.1% Tween-20 series (75% MetOH/25% PBST; 50% MetOH/50% PBST; 30% MetOH/70% PBST; 100% PBST) for 10 min each. Once rehydrated, embryos were transferred to a 2 ml Eppendorf tube. After 15 min treatment of 1x Target Retrieval (ACD #322000) at 100°C, embryos were treated with Protease Plus solution (ACD #322331), at 40°C for 5-45 min according to the stage. Embryos were incubated with the custom set of probes designed by ACD Biotechne (20 pairs of 18-25 nt) overnight at 40°C in sealed Eppendorf tubes. Detection of specific probe binding sites was performed using RNAscope® 2.5 HD Detection Reagents-RED kit (ACD #322360), according to the manufacturer. Images of the embryos were obtained using a Zeiss Stemi 2000-C stereo microscope. For the histological examination of sections, the samples were embedded in 5% agarose in distilled water. Blocks were sectioned at 35 µm on a Leica vibratome (VT1000S). Images of the sections were obtained using a Nikon 90i microscope.

148 For the detection of *myomixer* and *myomaker* expression in 1 g and 20 g trout muscle, samples of
149 white muscle were fixed with 4% paraformaldehyde overnight at 4°C and embedded in paraffin.
150 Then, cross-sections (7µm) of muscle were cut using a microtome (HM355; Microm Microtech,
151 Francheville, France) and *in situ* hybridization was performed using RNAscope® 2.5HD detection
152 reagent RED kit (ACD #322360). Briefly, sections were baked at 60°C for 1 hour, dewaxed and air-
153 dried. After 10 min in hydrogen peroxyde solution (ACD #322335), sections were treated with 1x
154 Target Retrieval (ACD #322000) for 15 min at 100°C, following 25 min with Protease Plus solution
155 (ACD #322331) at 40°C. All steps at 40°C were performed in a ACD HybEZ II Hybridization
156 System (#321720). Images of the sections were obtained using a Nikon 90i microscope.
157 For multiplex RNAscope *in situ* hybridization, trout embryos of 17 dpf (day post fertilisation) were
158 fixed as previously described in PF4% and embedded in paraffin. Cross-sections (7µm) were then
159 hybridized using the RNAscope Multiplex Fluorescent Assay v2 (ACDBio #323100) according to
160 the manufacturer's protocols. This assay allows simultaneous visualization of up to three RNA
161 targets, with each probe assigned a different channel (C1, C2 or C3). Each channel requires its own
162 amplification steps. *Pax7* and *myomixer* transcripts were targeted with fluorescent dyes Opal 520
163 (Akoya Biosciences #FP1487001KT) and Opal 620 (Akoya Biosciences #FP1495001KT)
164 respectively. Nuclei are counter-stained with DAPI.

165 ### *3.8. Statistical analyses*

166 The data were analyzed using the nonparametric Kruskal–Wallis rank test followed by the
167 Wilcoxon-Mann-Whitney test. All analyses were performed using the R statistical package (3.6.3
168 version).

4. Results

4.1. Identification of the trout myomixer gene

We performed a BLAST search in the trout genome (Berthelot et al., 2014) using the sequence of zebrafish Myomixer protein (Swiss-Prot: P0DP88.1) and we found only one locus with *myomixer* sequence similarity in the scaffold_4105 of the trout genome. We also identified two ESTs (Expressed Sequence Tag; GDKP01024145.1; GDKP01044688.1) corresponding to the *myomixer* transcript that encoded a protein of 77 aa (deposited in GenBank™ with accession number MN230110). Because both ESTs had little overlap, we performed RT-PCR with a primer on each ESTs to confirm that both ESTs belonged to the same transcript. The sequence of the PCR product obtained (599nt), validated that both ESTs belonged to a unique *myomixer* transcript. Sequence alignment between the genomic sequence and the EST sequences revealed the presence of two exons, the first containing the full coding sequence. As shown in the figure 1, the trout Myomixer protein was moderately conserved and shared 61% identity with zebrafish Myomixer and only 25% with the mouse one. In addition, trout Myomixer sequence shared 95% of identity with other salmonid Myomixer but only 60-65% of identity with other teleost fish. Despite this overall moderate sequence conservation, the functionally essential motif, AxLyCxL (x corresponds to leucine, isoleucine, valine and y corresponds to serine, threonine, alanine or glycine) (Shi et al., 2017) was conserved in trout Myomixer as well as several charged amino acids in the middle of the protein (arginine at position 40 and 45; lysine at position 39). The phylogenetic analysis of Myomixer proteins from several vertebrate species showed a phylogenetic tree consistent with the vertebrate evolution (figure 2). It was noteworthy that all the Myomixer protein sequences studied in salmonid were more divergent than the Myomixer sequences in other teleost.

4.2. Myomixer is expressed in embryonic and postlarval trout muscle

We performed whole-mount *in situ* hybridization to examine *myomixer* expression during embryonic myogenesis. *Myomixer* expression was detected as soon as the early stage of

194 somitogenesis (10 dpf) in the deep myotome (figure 3A and D). Then, *myomixer* transcript was
195 readily detected at 14 (figure 3B and E) and 18 (figure 3C and F) dpf in all somites when
196 multinucleated fibers begin to form. *Myomixer* expression was also detected in the head muscles
197 (18dpf) and a transient signal was observed in the otic vesicule (14dpf). In addition, cross-sections
198 (figure 3F) of 18 dpf embryos have shown that *myomixer* expression was highest in the lateral part
199 of the myotome. Double in situ hybridization for *pax7* and *myomixer* indicated that *myomixer* was
200 not expressed in the undifferentiated myogenic dermomyotome-like epithelium surrounding the
201 primary myotome (figure 3G-I) that was positive for *pax7*. In contrast, the myotome strongly
202 expressed *myomixer* but contained rare *pax7* positive cells. After hatching, *myomixer* expression
203 was still readily detected by *in situ* hybridization in the muscle of 1 g and 20 g trout (figure 3J and
204 K). The signal, consisting of small red dots (1-2/fiber cross-section) adhering to myofibers was
205 scattered throughout the muscle and was less frequent in muscle of 20 g trout than in 1 g trout. The
206 patterns of *myomixer* and *myomaker* expression in white muscle of 20 g trout were similar (figure
207 3K and L).

208 The qPCR quantification of *myomixer* expression in white muscle of 15g, 150g and 1500g trout
209 (figure 4A) showed that *myomixer* remained clearly expressed after hatching, although its
210 expression declined as fish weight increased. We also analyzed trout *myomixer* expression in
211 several tissues by qRT-PCR to determine whether its expression was restricted to skeletal muscle.
212 As shown in figure 4B, *myomixer* was strongly expressed in white and red skeletal muscle but not
213 in heart. *Myomixer* expression was also detected at low level in non-muscle tissues such as skin and
214 brain.

215 *4.3. Myomixer is up-regulated during muscle regeneration and myotube formation in* 216 *vitro*

217 To determine whether *myomixer* is up-regulated during the muscle regeneration, we measured its
218 expression in muscle following mechanical injury. In our previous study, we observed that the

219 formation of new fibers and the increase of *myogenin* expression occurred 30 days following injury
220 (Landemaine et al., 2019). Consistently, *myomixer* expression remained stable up to 16 days and
221 was sharply up-regulated on day 30 with 6-fold higher expression in injured muscle than in the
222 control one (figure 5).

223 We extracted satellite cells from white muscle of trout, and induced their differentiation and fusion
224 *in vitro* (Gabillard et al., 2010). Quantitative PCR analysis showed that *myomixer* expression was
225 significantly up-regulated 3 days after differentiation induction and paralleled *myomaker* expression
226 (figure 6A and 6B).

227

228

5. Discussion

The fusion of myocytes is highly regulated by numerous key membrane-anchored proteins such as Myomaker and Myomixer (Petrany and Millay, 2019). In the particular context of the persistence of muscle hyperplasia during post-larval growth of trout and the original structure of trout Myomaker protein, our work aimed at characterizing the sequence of *myomixer* and its expression during *in vivo* and *in vitro* myogenesis in this species.

The *in silico* analysis of the trout genome and the EST databases allowed us to identify a unique *myomixer* gene. The alignments of Myomixer protein sequences evidenced a moderate conservation of the overall amino acid sequence across vertebrate lineage. In addition, phylogenetic analysis showed a greater divergence in salmonid Myomixer sequences. This higher rate of protein sequence evolution could result from a relaxation of selection pressure or changes of the functional constraints on Myomixer protein (Zhang and Yang, 2015) although some amino acid residues are still conserved. For instance, the motif AxLyCxL, essential for Myomixer activity (Shi et al., 2017) is present in trout Myomixer protein and in all vertebrate species studied. Thus, despite overall divergence in Myomixer sequences, the key amino acids are conserved in salmonids.

Our expression analyses showed that *myomixer* is strongly expressed in the embryonic myotome during somitogenesis (10 dpf to 18 dpf), when myoblasts fused to form mature myofibers (Barresi et al., 2001; Steinbacher et al., 2007). Sections of trout embryos of 10 dpf revealed that *myomixer* was expressed in the fibers of the deep myotome formed during the primary wave of myogenesis. Then, the highest expression of *myomixer* was observed in the dorsal, ventral and lateral domains of the myotome, where the secondary wave of myogenesis (stratified hyperplasia) takes place (Steinbacher et al., 2007). In addition, double *in situ* hybridization for *pax7* and *myomixer* showed mutually exclusive expression patterns. Indeed, *pax7* is expressed in undifferentiated myogenic cells present in the dermomyotome-like epithelium surrounding the primary myotome (Dumont et al., 2008). The *pax7*-positive cells spread into the myotome should correspond to the muscle stem

cells (also called satellite cells) that persist in adult muscle. In contrast, *myomixer* is strongly expressed in differentiated myogenic cells in the area of muscle hyperplasia (Steinbacher et al., 2007). This expression pattern is in agreement with those obtained in zebrafish that shows a strong expression of *myomixer* from 14 hpf to 24 hpf (Shi et al., 2017). However, at the end of somitogenesis (18 dpf) of the trout embryos, *myomixer* expression is maintained in all somites, whereas in zebrafish its expression is no longer detected in the anterior somites at a comparable stage (24 dpf). Effectively, in mouse and zebrafish the expression of *myomixer* declines soon after somitogenesis (Bi et al., 2017; Shi et al., 2017), whereas in trout its expression is maintained throughout post-larval growth, *i.e.* in fry, juvenile and to a lesser extend in mature fish. Our results clearly indicate that the expression pattern of *myomixer* is similar to that of the *myomaker* in trout (Landemaine et al., 2019) during embryonic and post-larval stages. In addition, we did not observe *myomixer* and *myomaker* expression in myofibers, but only in small cells that should be fusing muscle precursors. These results are in agreement with those obtained in mouse which show that muscle overload induces *myomaker* expression in muscle precursors (myocytes) but not in myofibers, reinforcing the essential role of this protein in muscle hypertrophy and hyperplasia (Goh and Millay, 2017). Accordingly, in zebrafish, *myomixer* and *myomaker* expression is no longer detected in white muscle after hatching (Landemaine et al., 2014; Shi et al., 2017) after which post-larval muscle growth proceeds only by hypertrophy (Johnston et al., 2009). In contrast, in trout, muscle hyperplasia persists during post-larval growth (Steinbacher et al., 2007) and is accompanied by a maintenance of *myomixer* and *myomaker* expression indicating that they are markers of muscle hyperplasia rather than fiber hypertrophy.

Our qPCR analyses showed that *myomixer* expression was strongly stimulated in white muscle 30 days after injury, in parallel with the appearance of newly formed myofibers (Landemaine et al., 2019; Montfort et al., 2016). This kinetic of *myomixer* expression during muscle regeneration, is comparable to that one of *myomaker* and *myogenin* (Landemaine et al., 2019). Moreover, our results

are in agreement with our previous transcriptomic analysis showing that numerous genes essential for hyperplastic muscle growth (*myod, myogenin, M-cadherin*, etc.) were up regulated 30 days post injury (Montfort et al., 2016). Furthermore, we showed that *myomixer* and *myomaker* were up regulated 3 days after induction of satellite cells differentiation. This latter result is reminiscent to previous data showing that *myogenin* and *myomaker* expression increase during fusion of trout myocytes (Landemaine et al., 2019). Thus, these results strongly suggest that *myomixer* is up regulated during the fusion of myocytes. It is noteworthy that recent studies using loss-of-function approaches (Zhang et al., 2020) demonstrated in human myoblasts that Myomaker and Myomixer function is very well conserved among mammals, although the regulation of these genes by other MRFs could present slight differences. The technical difficulties in performing this kind of experiments in longer-lived fish species same as the rainbow trout caused that this approach was not contemplated in the objectives of the present work, although it would be a logical continuation of the current work to study the interrelationship of Myomaker and Myomixer with other proteins that regulate the muscle growth in salmonids. Taken together, these results strongly suggest that Myomixer, like Myomaker, plays a crucial role in myoblast fusion, muscle development and muscle regeneration.

6. Conclusions

In conclusion, our work shows that despite moderate sequence conservation, *myomixer* expression is consistently associated with the formation of new myofibers during somitogenesis, post-larval growth and muscle regeneration in trout and can be considered as a good marker of hyperplasia.

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Figure 1. The sequence alignment of vertebrate Myomixer proteins.
The alignment was performed from the complete protein sequences using ClustalW multiple alignment tool. The amino acid residues present in all sequences are uppercase and lowercase when present in at least 6 sequences. The AxLyCxL motif was indicated: x corresponds to leucine, isoleucine, valine and y denotes serine, threonine, alanine or glycine. Accession numbers are as follows: *O. mykiss*, QII57370; *D. rerio*, P0DP88 ; *S. salar*, XM-014180492; *S. aurata*, ERR12611_isotig14560 (http://sea.ccmar.ualg.pt:4567/); *G. gallus*, CD218366.1; *C. porosus*, XP_019405207; *M. musculus*, Q2Q5T5 and *H. sapiens*, A0A1B0GTQ4.

Figure 2. Phylogenetic analysis of Myomixer in tetrapods and teleosts.
The phylogenetic tree was constructed from a multiple alignment of the complete sequences of the proteins using the neighbour-joining method. The numbers at the tree nodes represent percentage of bootstrap values after 500 replicates.

Figure 3. Patterns of *myomixer* expression during embryonic development.
(A-F) Embryos were analyzed by whole mounted *in situ* hybridization at day 10, 14 and 18 post fertilization. The corresponding vibratome section (35µm) was presented for each stage. Asterisks indicate the dorsal and ventral domains of the myotome and arrowhead indicates the dermomyotome-like epithelium. (G-I) Double *in situ* hybridization for *pax7* and *myomixer* of 17 dpf embryo sections. The nuclei are counter-stained with DAPI and arrowhead indicates the dermomyotome-like epithelium. (J-L) The expression of *myomixer* and *myomaker* in muscle of 1 g and 20 g trout was also studied using *in situ* hybridization on cross sections (7µm).

Figure 4. Expression of *myomixer* in tissues and white muscle of different-weight trout.
The quantification of *myomixer* expression was performed by qPCR analysis in muscle of different weight trout (A) and in several tissues (150 g; B). The qPCR results are presented as a ratio of *myomixer* and *eF1a* expression, and the bars represent the standard error. The letters (a-d) in A indicate the significant differences between means ($p<0.05$; Kruskal–Wallis rank test followed by the Wilcoxon-Mann-Whitney test).

Figure 5. Expression of *myomixer* during muscle regeneration in trout.
Gene expression profile of *myomixer* during muscle regeneration in rainbow trout normalized with *eF1a* expression. Bars represent the standard error and the letters indicate the significant differences between means within the same treatment (control or injured). The asterisk indicates significant differences between treatments at a given time. Statistical significance ($p < 0.05$) was determined using the Kruskal–Wallis rank test followed by the Wilcoxon-Mann-Whitney test.

Figure 6. Expression of *myomixer* and *myomaker* during trout satellite cell differentiation.
The cells were cultivated in proliferative medium (PM) and then in differentiation medium for 1, 2, and 3 days (DM1, DM2, and DM3). The qPCR results are normalized with *eF1a* expression and bars represent the standard error. Different letters indicate significant differences between means. Statistical significance ($p < 0.05$) was determined using the Kruskal–Wallis rank test followed by the Wilcoxon-Mann-Whitney test.

Figure 1

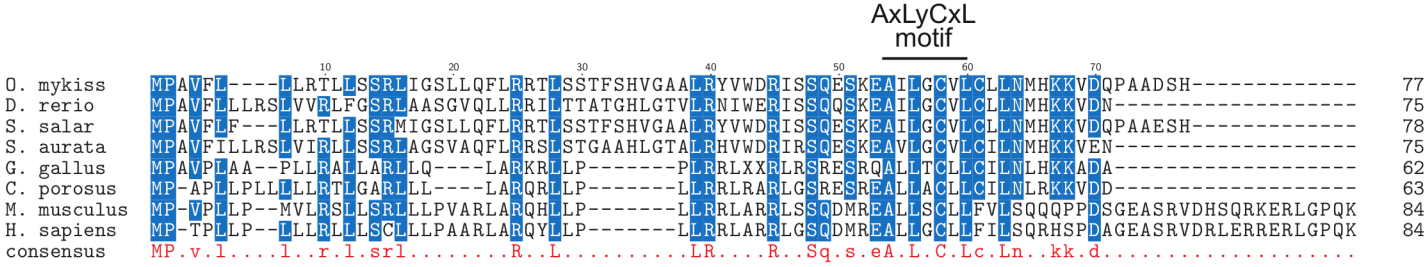

AxLyCxL
motif
10
20
30
40
50
60
70
O. mykiss MPAVFL----LLRTLLSSRLIGSLLQFLRRTLSSTFSHVGAALRYVWDRISSQESKEAILGCVLCLLNMHKKVDQPAADSH---------- 77
D. rerio MPAVFLLLRSLVVRLFGSRLAASGVQLLRRILTTATGHLGTVLRNIWERISSQQSKEAILGCVLCLLNMHKKVDN---------- 75
S. salar MPAVFLF---LLRTLLSSRMIGSLLQFLRRTLSSTFSHVGAALRYVWDRISSQESKEAILGCVLCLLNMHKKVDQPAAESH---------- 78
S. aurata MPAVFILLRSLVIRLLSSRLAGSVAQFLRRSLSTGAAHLGTALRHVWDRIRSQESKEAVLGCVLCILNMHKKVEN---------- 75
G. gallus MPAVPLAA--PLLRALLARLLQ----LARKRLLP-------PLRRLXXRLRSRESRQALLTCLLCILNLHKKADA---------- 62
C. porosus MP-APLLPLLLLLRTLGARLLL----LARQRLLP-------LLRRLRARLGSRESREALLACLLCILNLRKKVDD---------- 63
M. musculus MP-VPLLP--MVLRSLLSRLLLPVARLARQHLLP-------LLRRLARRLSSQDMREALLSCLLFVLSQQQPPDSGEASRVDHSQRKERLGPQK 84
H. sapiens MP-TPLLP--LLLRLLLSCLLLPAARLARQYLLP-------LLRRLARRLGSQDMREALLGCLLFILSQRHSPDAGEASRVDRLERRERLGPQK 84
consensus MP.v.l....l..r.l.srl........R..L..........LR....R..Sq.s.eA.L.C.Lc.Ln..kk.d.....................

Figure 2

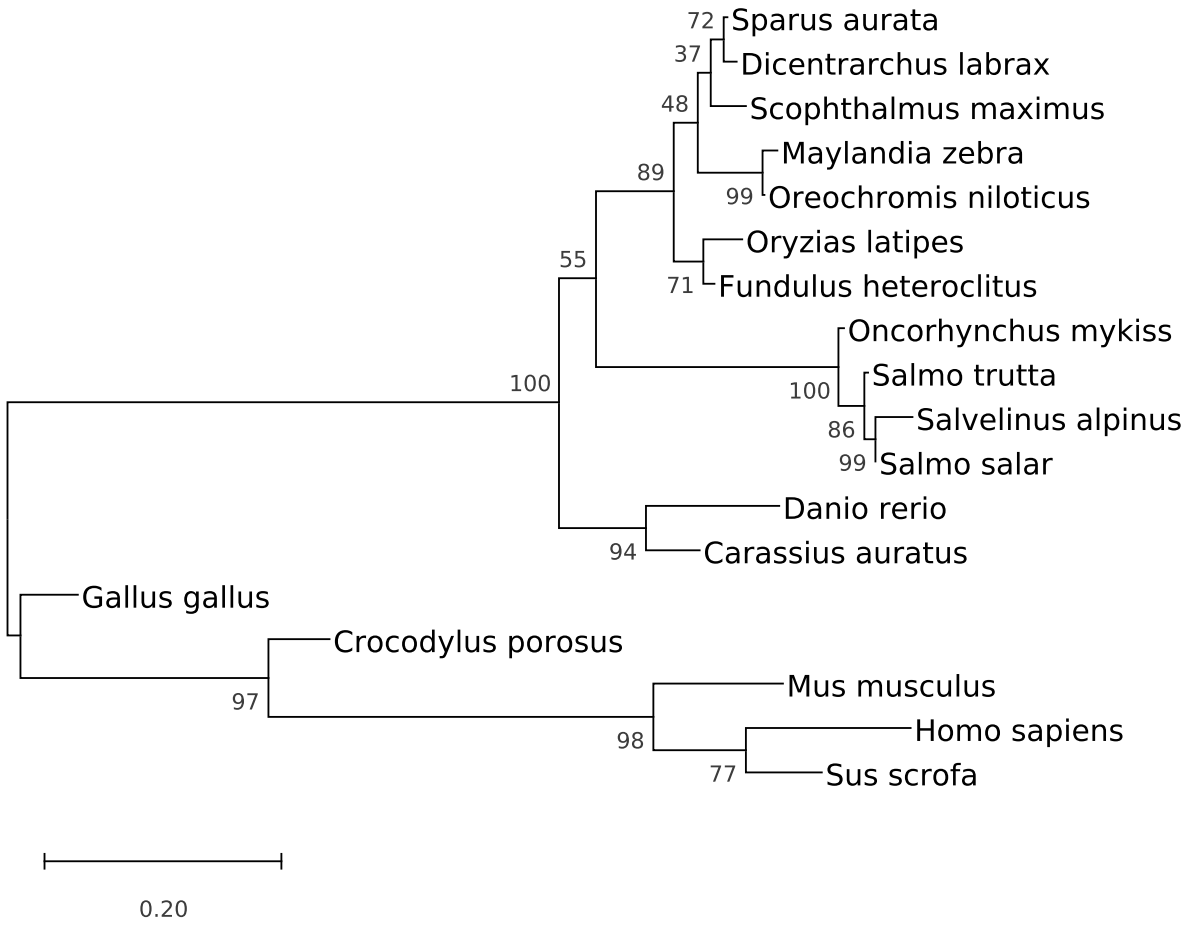

Sparus aurata
Dicentrarchus labrax
Scophthalmus maximus
Maylandia zebra
Oreochromis niloticus
Oryzias latipes
Fundulus heteroclitus
Oncorhynchus mykiss
Salmo trutta
Salvelinus alpinus
Salmo salar
Danio rerio
Carassius auratus
Gallus gallus
Crocodylus porosus
Mus musculus
Homo sapiens
Sus scrofa
72
37
48
89
99
55
71
100
100
86
99
94
97
98
77
0.20

Figure 3

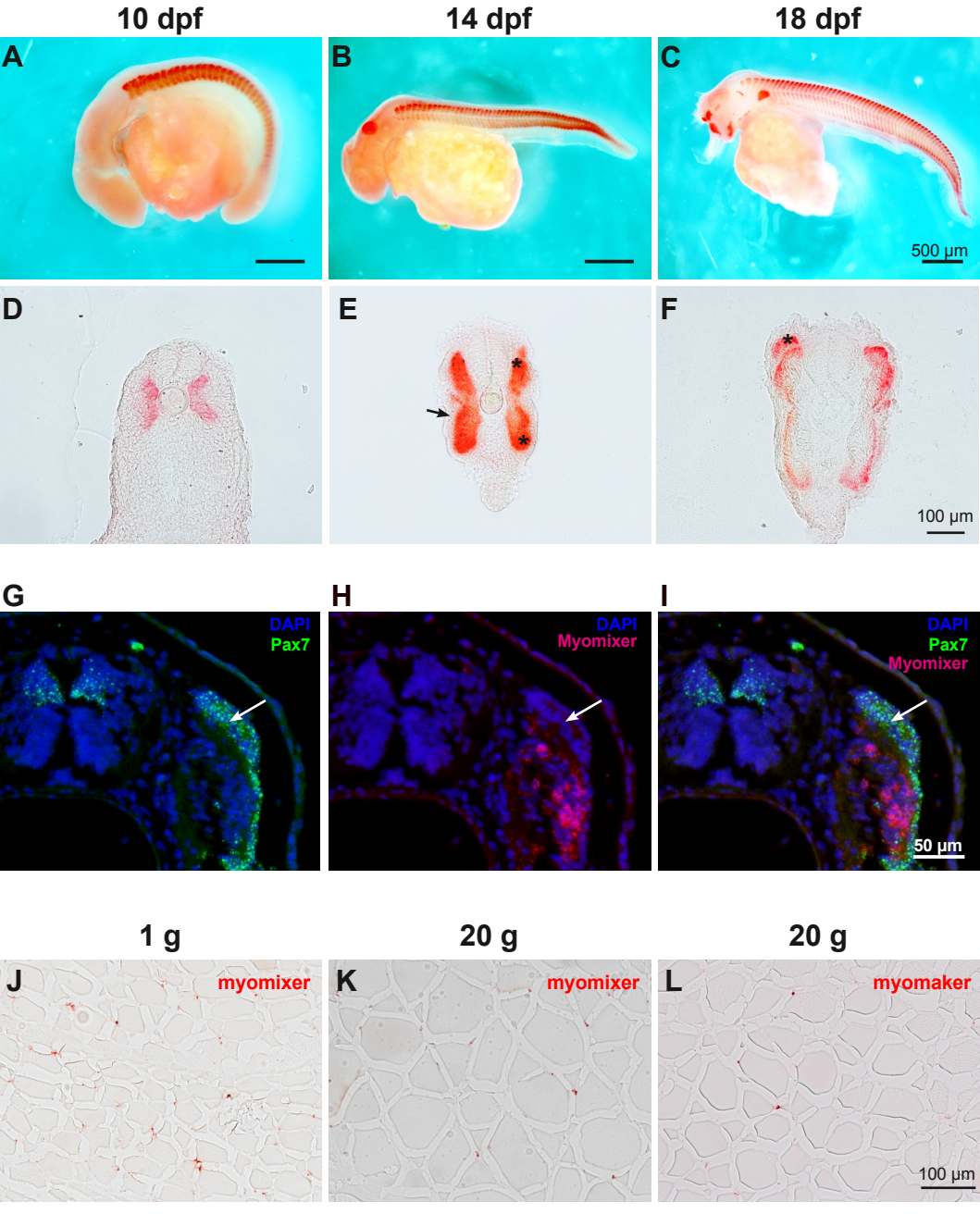

10 dpf
14 dpf
18 dpf
A
B
C
500 µm
D
E
F
100 µm
G
H
I
DAPI
Pax7
DAPI
Myomixer
DAPI
Pax7
Myomixer
50 µm
1 g
20 g
20 g
J
myomixer
K
myomixer
L
myomaker
100 µm

Figure 4

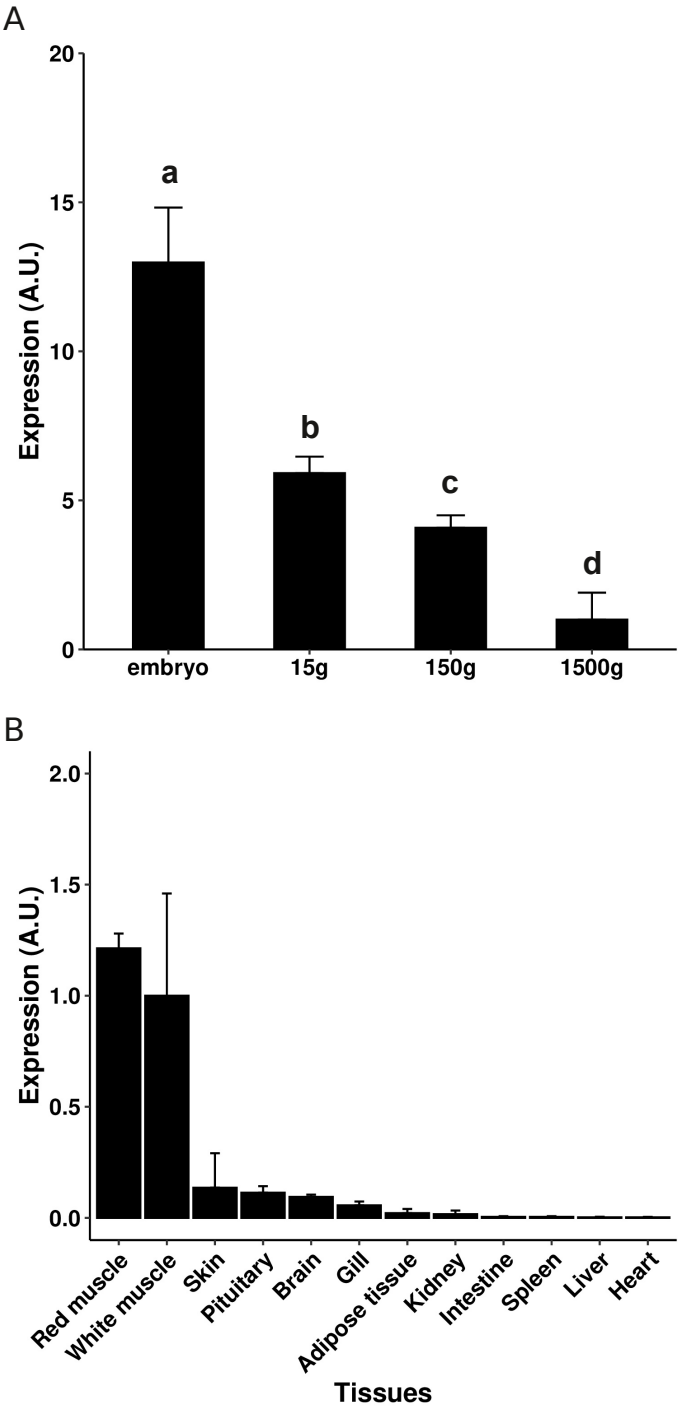

A
20
15
10
5
0
Expression (A.U.)
a
b
c
d
embryo
15g
150g
1500g
B
2.0
1.5
1.0
0.5
0.0
Expression (A.U.)
Red muscle
White muscle
Skin
Pituitary
Brain
Gill
Adipose tissue
Kidney
Intestine
Spleen
Liver
Heart
Tissues

Figure 5

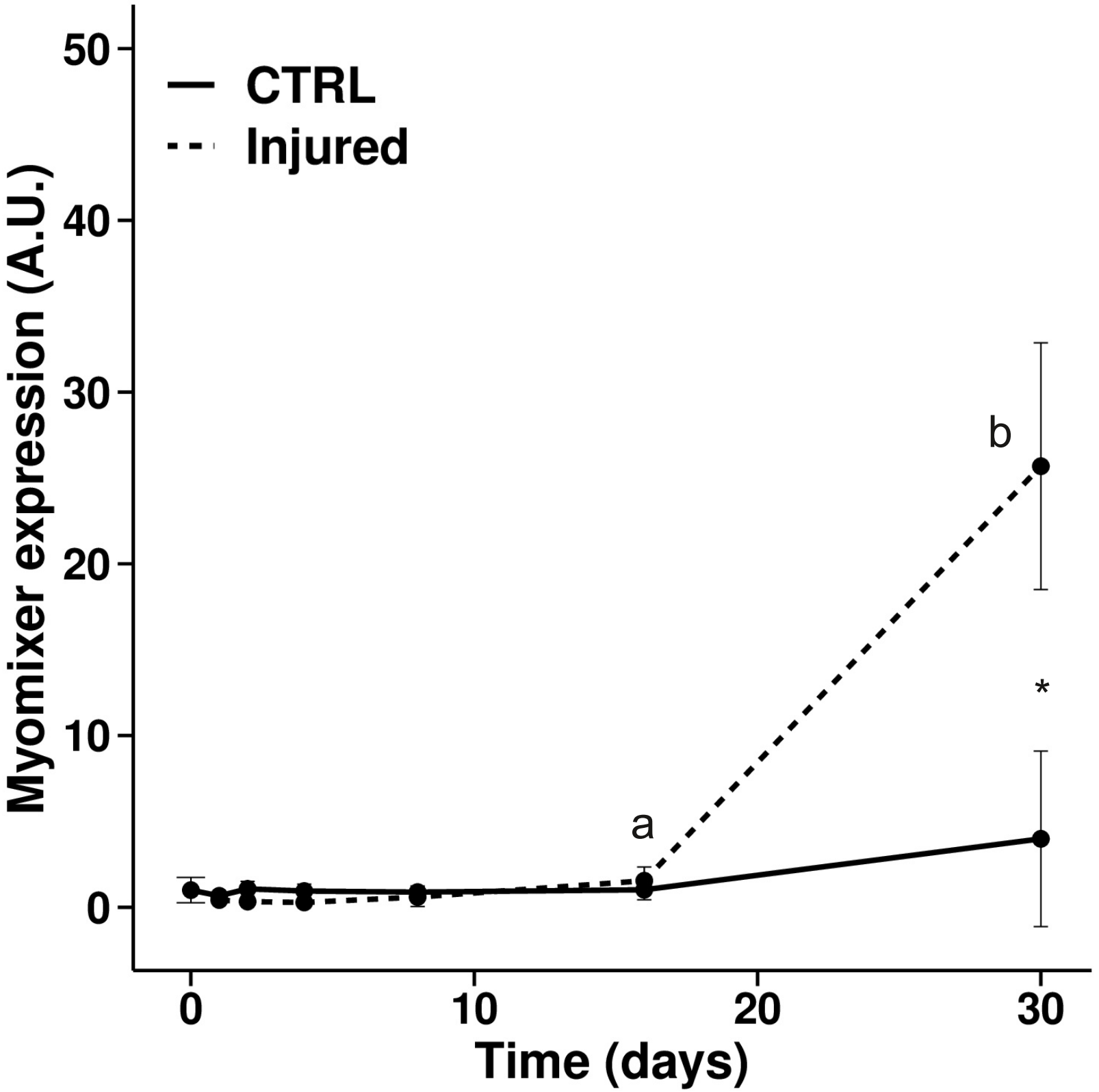
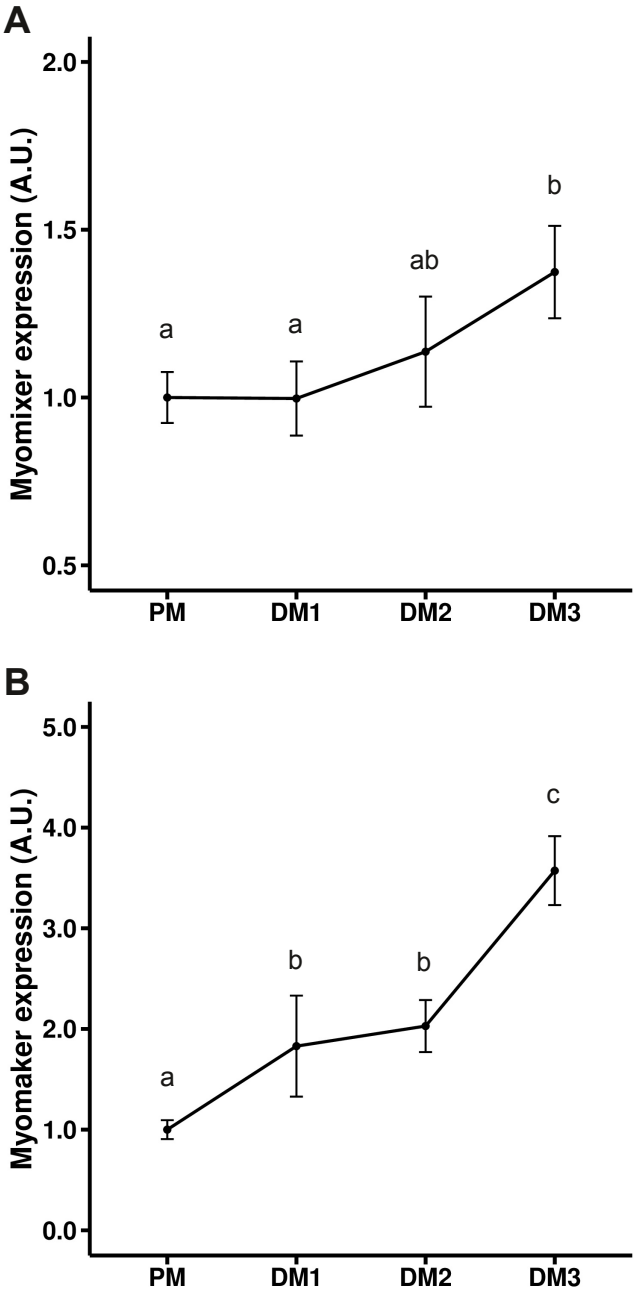

CTRL
Injured
Myomixer expression (A.U.)
50
40
30
20
10
0
0
10
20
30
Time (days)
a
b
*

Figure 6


A
Myomixer expression (A.U.)
2.0
1.5
1.0
0.5
a
a
ab
b
PM
DM1
DM2
DM3
B
Myomaker expression (A.U.)
5.0
4.0
3.0
2.0
1.0
0.0
a
b
b
c
PM
DM1
DM2
DM3