FoxO1 is not a key transcription factor in the regulation of myostatin (mstn-1a and mstn-1b) gene expression in trout myotubes

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Seiliez I, Sabin N, Gabillard JC. FoxO1 is not a key transcription factor in the regulation of myostatin (mstn-1a and mstn-1b) gene expression in trout myotubes. Am J Physiol Regul Integr Comp Physiol 301: R97–R104, 2011. First published April 13, 2011; doi:10.1152/ajpregu.00828.2010.—In mammals, much evidence has demonstrated the important role of myostatin (MSTN) in regulating muscle mass and identified the transcription factor forkhead box O (FoxO) 1 as a key regulator of its gene expression during atrophy. However, in trout, food deprivation leads to muscle atrophy without an increase of the expression of mstn genes in the muscle. We therefore studied the relationship between FoxO1 activity and the expression of both mstn genes (mstn1a and mstn1b) in primary culture of trout myotubes. To this aim, two complementary studies were undertaken. In the former, FoxO1 protein activity was modified with insulin-like growth factor-I (IGF-I) treatment, and the consequences on the expression of both mstn genes were monitored. In the second experiment, the expression of both studied genes was modified with growth hormone (GH) treatment, and the activation of FoxO1 protein was investigated. We found that IGF-I induced the phosphorylation of FoxO1 and FoxO4. Moreover, under IGF-I stimulation, FoxO1 was no longer localized in the nucleus, indicating that this growth factor inhibited FoxO1 activity. However, IGF-I treatment had no effect on mstn1a and mstn1b expression, suggesting that FoxO1 would not regulate the expression of mstn genes in trout myotubes. Furthermore, the treatment of myotubes with GH decreased the expression of both mstn genes but has no effect on the phosphorylation of FoxO1, FoxO3, and FoxO4 nor on the nuclear translocation of FoxO1. Altogether, our results showed that mstn1a and mstn1b expressions were not associated with FoxO activity, indicating that FoxO1 is likely not a key regulator of mstn genes in trout myotubes.

forkhead box O; myostatin; fish; muscle; atrophy; growth hormone; insulin-like growth factor-1

In the last decade, myostatin (MSTN), a member of the transforming growth factor-β superfamily, has emerged as a key factor in muscle growth regulation (43). The importance of the mstn gene in muscle growth comes from the phenotype of MSTN-deficient cattle (natural mutation or deletion) called double-muscled bovines, like the Belgium Blue breed (29, 44). In these bovines, muscle overgrowth is due to both hyperplasia (increased number of muscle fibers) and hypertrophy (increased size of individual muscle fibers). Similarly, inactivation of the mstn gene or MSTN function is reported to cause increased muscle mass in a variety of species, including mice (Mus musculus) (43), dogs (Canis familiaris) (47), sheep (Ovis aries) (8), humans (Homo sapiens) (56), zebrafish (Danio rerio) (35), and trout (36, 45). Reversely, overexpression of MSTN in transgenic mice has been shown to induce muscle atrophy in vivo (50). These data demonstrate the predominant role of MSTN in regulating muscle size in both lower and higher vertebrates.

In agreement with its role as a negative regulator of skeletal muscle mass, expression data from a wide variety of mammalian models show that mstn is upregulated during muscle atrophy induced by hindlimb unloading (9), thermal injury (31), and food deprivation (2). However, other findings show some differences in the response of the mstn gene to environmental changes depending on the species or the conditions studied (20, 25, 26, 63). To make inroads in the understanding of mstn regulation, several groups investigate the regulatory elements controlling mstn expression. Conserved sequences in the mstn promoter from several species have thus been identified that share many binding sites for forkhead box O (FoxO) transcription factors (3, 4, 13). Furthermore, some of these FoxO-binding sites were shown to be critical for FoxO1 binding and mstn gene expression (3, 4). FoxO1, which belongs to a subfamily of transcription factors consisting of FoxO1, FoxO3, FoxO4, and FoxO6 (39), is also known as the main coordinator of the two main proteolytic pathways (the ubiquitin proteasome and the autophagy lysosome) by inducing several autophagy-related genes as well as the two musclespecific ubiquitin ligases atrogin-1 and muprl1 (40, 64). Nuclear localization and transcriptional activity of the FoxO transcription factors are inhibited via phosphorylation by the phosphatidylinositol 3-kinase (PI 3-kinase)/protein kinase B (Akt) signaling pathway, which in turn is activated by insulin-like growth factor-I (IGF-I) binding to its cell surface receptor (55, 61). Thus the regulation of FoxO function may play a central role in mediating effects on gene expression in response to atrophic and/or hypertrophic signaling.

In fish, less is known on the regulation of the expression of mstn genes (52). A recent phylogenetic analysis of the entire mstn subfamily (30) indicates that fish possess multiple mstn genes and that a gene duplication event during early fish radiation (5, 49) produced two distinct mstn clades: mstn-1 and mstn-2. A second duplication event within salmonids, likely resulting from tetraploidization, produced two subsequent divisions, one in each clade. This suggests that most, if not all, salmonids possess four distinct mstn genes: two within the first clade (1a and 1b) and two in the second (2a and 2b). In rainbow trout, from these four mstn genes only two (mstn1a and mstn1b)}

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mstn1b) are expressed in the muscle and are downregulated during starvation (28). In addition, they are differentially regulated under different conditions. Indeed, muscle atrophy during the reproductive stage is associated with a decrease of mstn1b expression, whereas mstn1a expression is unaffected (51). Injection of growth hormone (GH) upregulates mstn1a and downregulates mstn1b gene expression in muscle (7, 16). Overall, these data suggest that, in rainbow trout, regulation of mstn gene expression is complex and likely different from that observed in mammals.

Recent in vitro studies show that the hormonal (insulin and/or IGF-I) regulation of the Akt-FoxO signaling in rainbow trout is well conserved (10, 12, 32, 48, 57, 58). Furthermore, similarly to what is observed in mammalian and birds, this pathway has been shown to be associated with muscle atrophy in this species (59). However, we know little about the molecular mechanisms regulating the expression of the mstn genes in any fish species. The purpose of the present work was therefore to determine the role of FoxO1 in regulating the expression of the muscle antigrowth factors mstn1a and mstn1b in rainbow trout. To establish a causal link between FoxO activity and the expression of both mstn genes, two complementary experiments were performed in primary cultures of trout muscle cells. In the former, FoxO1 protein activity was modified with IGF-I treatment, and the consequences on the expression of both mstn genes were monitored. In the second experiment, the expression of both studied genes was modified with GH treatment, and the activation of FoxO1 protein was investigated.

MATERIALS AND METHODS

Animals. Rainbow trout were maintained at the “Station Commune de Recherches en Ichtyophysiologie, Biodiversité et Environnement” (Rennes, France) in 0.6-m³ tanks in a recirculated system at 18°C. All experiments were carried out in accordance with legislation governing the ethical treatment of animals (Decret No. 2001-464, May 29, 2001), and investigators were certified by the French Government to carry out animal experiments (No. agrément 35– 47). All animal work was approved by the Ministére de l’Enseignement Superieur et de le Recherche (Autorisation A.No. A352386).

Myosatellite cell isolation and culture. Primary cultures of skeletal muscle cells were carried out as follows: for each culture, 30–60 animals, each weighing ~5 g, were killed by a blow to the head and then immersed for 30 s in 70% ethanol to sterilize external surfaces. Cells were isolated, pooled, and cultured following previously described protocols (15, 58). Briefly, after removal of the skin, dorsal white muscle was isolated under sterile conditions and collected in Dulbecco’s modified Eagle’s medium (DMEM) containing 9 mM NaHCO3, 20 mM HEPES, 15% horse serum, and antibiotic-antimycotic cocktail (100 U/ml penicillin, 100 μg/ml streptomycin, and 0.25 g/ml fungizone) at pH 7.4. After mechanical dissociation of the muscle in small pieces, the tissue was enzymatically digested with a 0.1% trypsin solution in DMEM for 20 min at 18°C and the resulting pellet was subjected to two rounds of enzymatic digestion with a 0.1% trypsin solution in DMEM for 20 min at 18°C and gentle agitation. After each round of trypsinization, the suspension was centrifuged, and the supernatant was diluted in two volumes of cold DMEM supplemented with 15% horse serum and the same antibiotic-antimycotic cocktail mentioned above. After two washes with DMEM, the cellular suspension was filtered through 100- and 40-μm nylon filters. All experiments were conducted with cells seeded at a density of 160,000/cm², in 6-well or 24-well plastic plates (Nunc, Roskilde, Denmark), and left for 30 min before medium change. Plates and cover slips were previously treated with poly-L-lysine and laminin to facilitate satellite cell adhesion. Cells were incubated at 18°C, the optimal temperature for culture, with DMEM (no. D7777; Sigma) containing 9 mM NaHCO3, 20 mM HEPES, 10% FBS, and antibiotic-antimycotic cocktail under an air atmosphere. The medium was renewed every 2 days, and observations of morphology were regularly made to control the state of the cells. They were cultured for 7 days to obtain myotubes.

Treatment conditions. The experiments of the present study were performed on myotubes that, compared with myoblasts, are closer to a myofiber and thus more relevant at a physiological point of view. On the day of the experiment, cells were deprived of serum for 24 h and subsequently incubated in the presence or absence of 100 nM salmon/trout IGF-I (WU100 GroPep) or 0.5 and 5 nM of trout GH [homemade recombinant GH (34)] for 15 min, 30 min, 1 h, 2 h, 5 h, or 24 h. Each experiment was performed at least two times.

Gene expression analysis. Treatment medium was removed, and wells were washed twice with PBS. Total RNA was extracted with a Nucleosip RNAs kit (no. N0740–902–50; Macherey-Nagel) according to the manufacturer’s recommendations. The total amount of RNA was determined as a function of absorbance at 260 nm (Nanodrop ND-1000 spectrophotometer). cDNA was generated with 0.5 μg total RNA using a commercial kit (no. 4368813; Applied Biosystems). Briefly, 0.5 μg of total RNA was incubated in a 25-μl mixture (10× RT buffer, 25× dNTPs, 10× random primers, 50 IU/μl MultiScribe Reverse Transcriptase, and nuclease-free water) at 25°C for 10 min and then at 37°C for 120 min. The reaction was set at 200 μl by the addition of nuclease-free water. Target gene expression levels were determined by quantitative RT-PCR using a StepOnePlus system (Applied Biosystems). Analyses were carried out using a real-time PCR kit (fast SyberGreen Master mix, no. 4385612; Applied Biosystems) with 300 nM of each primer. The primer sequences (Table 1) were already published and validated (28). Amplification was then performed using the following cycle: 95°C for 3 s and 60°C for 15 s, 40 times for all primers. Real-time PCR data were normalized according to elongation factor 1α (EF1α) mRNA abundance in each sample. Melting curves were systematically monitored (temperature gradient at 0.5°C/10 s from 55 to 94°C) at the end of the last amplification cycle to confirm the specificity of the amplification reaction. Each PCR run included replicate samples (duplicate of reverse transcription and PCR amplification) and negative controls (reverse transcriptase-free and RNA-free samples).

The relative expression ratio of a target gene was calculated on the basis of real-time PCR efficiency and the cycle threshold (CT) deviation (ΔCT) of the unknown sample vs. a control sample and expressed compared with the EF1α reference gene. PCR efficiency was measured by the slope of a standard curve using serial dilutions of cDNA. PCR efficiency values ranged between 1.9 and 2.

Protein extraction and western blotting. After two washes with cold PBS, proteins were extracted with RIPA buffer (50 mM Tris, pH 8, 1 mM EDTA, 0.5 mM EGTA, 1% Nonidet P-40, 0.5% sodium deoxycholate, 0.1% SDS, and 150 mM NaCl) supplemented with 5 mM NaF, 1 mM NaVO4, and protease inhibitor cocktail (Roche). Laemmli buffer was added to the sample and heated at 90°C for 5 min. Cell lysates were subjected to SDS-PAGE and Western blotting using

| Table 1. Sequences of the primer pairs used for real-time quantitative RT-PCR |
|----------------------------------|----------------------------------|
| Gene  | 5’-3’ Forward Primer  | 5’-3’ Reverse Primer  |
| mstn1a  | CCGCTTCCAATATGCAGCAA  | CGAAGCTTGGTCAAGTACCA |
| mstn1b  | AGTCGCGTTCGCACTGAGAA  | AGGACGCTTGGTCAAGTACCA |
| Atrogen-1  | TGATGATTTTGCACACTGACT  | AGGCCGACAGCAGTACCA |
| EF1α  | TGCTGTTTGGTGGTTTGCGG  | AGGCCGACAGCAGTACCA |

GenBank accession no.: myostatin (mstn) 1a, AF273035; mstn1b, AF273036; atrogen-1, CX026010; elongation factor 1α (EF1α), AF498320.
Table 2. Location and sequences of sites matching the consensus for FoxO binding ([C/G][A/T]AAA[C/T]A) in mstn1a and mstn1b promoters

<table>
<thead>
<tr>
<th>Location</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>mstn1a</td>
<td></td>
</tr>
<tr>
<td>−837 to −843</td>
<td>gtaaata</td>
</tr>
<tr>
<td>−862 to −868</td>
<td>cttaaaat</td>
</tr>
<tr>
<td>−1153 to −1159</td>
<td>gaaata</td>
</tr>
<tr>
<td>mstn1b</td>
<td></td>
</tr>
<tr>
<td>−793 to −799</td>
<td>gtaaata</td>
</tr>
<tr>
<td>−883 to −889</td>
<td>gtaaata</td>
</tr>
<tr>
<td>−1121 to −1127</td>
<td>gtaaata</td>
</tr>
<tr>
<td>−1765 to −1771</td>
<td>cttaaaat</td>
</tr>
<tr>
<td>−2247 to −2253</td>
<td>gtaaata</td>
</tr>
</tbody>
</table>

*The table shows the location of the putative forkhead box O (FoxO)-binding sites within the trout mstn1a and mstn1b promoter sequences previously published by Garikipati et al. (17). Nos. represent the position of these elements relative to the transcription start site.

The appropriate antibody. Anti-phospho Akt (Ser473) (no. 9271), anti-Akt (no. 9272), anti-phospho-FoxO1 (Thr24)/FoxO3 (Thr25) (no. 9464), and anti-phospho-FoxO1 (Ser319)/FoxO4 (Ser262) (no. 2487) were purchased from Cell Signaling Technologies (Ozyme, Saint Quentin Yvelines, France). Anti-FoxO1 (no. 1874–1) was purchased from Epitomics, and anti-β-actin (no. sc-47778) was from Santa Cruz Biotechnology. Anti-Akt, anti-phospho-Akt, anti-phospho-FoxO1 (Thr24)/FoxO3 (Thr25), and anti-phospho-FoxO1 (Ser319)/FoxO4 (Ser262) antibodies have been previously validated in trout (12, 58).

Fig. 1. Effect of insulin-like growth factor-I (IGF-I) on the protein kinase B (Akt)-forkhead box O (FoxO) signaling pathway in primary culture of trout muscle cells. Seven-day-old cells were serum starved for 24 h and then stimulated or not with 100 nM of trout IGF-I for 15 min, 30 min, 1 h, 2 h, or 5 h before harvest. Cell lysates were analyzed by Western blot with the indicated antibodies. β-Actin was used as a loading control. P, phosphorylated. Each treatment was performed in triplicate, and similar results were obtained. This figure shows a representative blot.
expression. Overall, these results indicate that IGF-I inhibits FoxO1 activity without changing mstn1a and mstn1b gene expression.

GH downregulates mstn1a and mstn1b gene expression but has no effect on the Akt-FoxO signaling pathway. Another way to study the involvement of FoxO transcription factors in the regulation of mstn1a and mstn1b gene expression was to analyze the Akt-FoxO signaling pathway in cells over- or underexpressing the studied genes. GH has been previously shown to regulate the expression of both mstn1a and mstn1b in rainbow trout (7, 16). Therefore, we first investigated the effect of GH on mstn1a and mstn1b gene expression in our cell culture model. Trout cultured myotubes (day 7 of culture) were serum-deprived for 24 h and subsequently incubated in the absence or presence of trout GH (0.5 or 5 nM) for 24 h. As shown in Fig. 4, both mstn1a and mstn1b genes were downregulated (~7- and 20-fold, respectively) after 24 h of stimulation with 5 nM of GH. Thus these GH-treated cells may serve as a relevant model to characterize the factors involved in the transcriptional regulation of mstn genes.

We then monitored the activity of the Akt-FoxO signaling pathway in these GH-treated cells. Previous studies had identified signal transducer and activator of transcription 5 (STAT5) as a key transcription factor in GH signaling (62), and we therefore monitored its phosphorylation status as a positive control. As expected, the phosphorylation of STAT5 was highly induced after 1 h of stimulation with GH (Fig. 5). In contrast, the hormonal treatment has no effect on the phosphorylation of Akt at Ser473, FoxO1 at Ser319, FoxO3 at Thr32, and FoxO4 at Ser262.

Finally, we monitored by immunofluorescence the localization of FoxO1 in serum-deprived cells for 24 h and incubated or not with 0.5 nM of GH or 100 nM of IGF-I for 1–5 h. As shown in Fig. 6, immunofluorescence of serum-starved and GH-treated cells revealed that FoxO1 remained colocalized with Hoescht staining, indicating a nuclear localization of the studied protein. In contrast, IGF-I-treated cells showed a loss
of nuclear localization of FoxO1. Taken together, these results show that GH downregulates mstn1a and mstn1b gene expression in a FoxO-independent manner.

**DISCUSSION**

In mammals, there is accumulating evidence on the important role of the MSTN in regulating muscle mass and on the role of transcription factor FoxO1 as a key regulator of its gene expression in response to atrophic signaling (3, 4). In this regard, expression data from several mammalian models show that muscle atrophy is often associated with an increase of mstn expression (2, 9, 31). However, in rainbow trout, food deprivation leads to muscle atrophy without an increase of mstn expression in muscle (11, 28, 46). Therefore, the purpose of the present work was to determine the role of FoxO1 in regulating the expression of the muscle antigrowth factors mstn1a and mstn1b in rainbow trout.

To address this issue, we first conducted an in silico analysis aiming at identifying the presence of putative FoxO-binding sites within trout mstn1a and mstn1b promoter sequences previously published (17). The very well conservation of the DNA-binding domain of FoxO proteins along the evolution (6) lets us hypothesize that the DNA sequence to which FoxO binds is the same between lower and higher vertebrates. Sequence analysis based on the consensus sequence for FoxO-binding sites ((C/G)(A/T)AAA(C/T)A) derived from a previous study (21) identified the presence of several putative FoxO-binding sites in both trout mstn promoters. This suggested the possible involvement of FoxO transcription factors on the control of mstn1a and mstn1b expression.

In mammals, FOXO proteins are known to mediate the transcriptional output of insulin/IGF-I signal transduction (33, 61). When insulin/IGF-I signaling is active, a PI 3-kinase/Akt kinase cascade phosphorylates FOXO, leading to its nuclear exclusion. When insulin/IGF-I signaling is inhibited, unphosphorylated FOXO enters the nucleus where it induces the expression of several genes coding for key mediators of skeletal muscle atrophy, including mstn (reviewed in Ref. 18). We therefore investigated the effect of IGF-I on the Akt-FoxO signaling pathway and the expression of mstn1a and mstn1b genes in our cell culture model. Our results showed that the treatment of cells with IGF-I enhanced the phosphorylation of Akt at Ser473, FoxO1 at Ser319, and Foxo4 at Ser262. Moreover, immunolocalization of FoxO1 clearly showed that IGF-I stimulation led to the loss of nuclear localization of FoxO1. The effect of IGF-I on the phosphorylation of Akt and FoxO1 in primary culture of trout muscle cells has already been reported (10, 12, 58). The results presented here are in good agreement with these data and provide evidence for the first time that the effect of IGF-I is also accompanied by a nuclear exclusion of FoxO1 in this cell culture model, leading to the loss of FoxO1 staining. Indeed, Akt-mediated phosphorylation of FOXO leads to their proteasomal degradation through polyubiquitination by the E3 ubiquitin ligase Skp2 (24, 42). In this study, we did not examine the effects of IGF-I on the nuclear translocation of other FoxO family members. However, according to data on mammals showing that both FoxO1 and FoxO3 are downstream targets of the insulin/IGF-I signaling (55), it is probable that IGF-I may have similar effects on the activation...
of FoxO3 and other FoxO family members. In this regard, we recently showed that the treatment of primary culture of trout muscle cells with IGF-I enhances the phosphorylation of FoxO3 at Thr32 (58). To validate this decrease of FoxO activity, we then measured the expression of atrogin-1, a gene well-known to be dependent on FoxO activity (55, 61). As expected, IGF-I stimulation decreased the expression of atrogin-1 in trout myotubes. This result confirmed that IGF-I stimulation induced a strong decrease of FoxO activity and thus validated our experimental conditions. However, under the same conditions, we were not able to observe any significant changes of mstn1a and mstn1b gene expressions. Therefore, our results showed that, despite a strong decrease of FoxO1 activity, mstn gene expressions remained constant. These results suggest a slight role for the Akt-FoxO signaling pathway in the regulation of the expression of mstn genes in our cell culture model but do not exclude that other factors may mask the requirement of this intracellular pathway in the regulation of the studied genes. For example, new findings have provided direct evidence on the role of the transcription factors SMAD and CCAAT/enhancer-binding factor in mediating the induction of the expression of mstn gene in muscle wasting (1, 4). Whether some of these factors are affected in our cell culture model is worth investigating.

Another way to study the involvement of FoxO transcription factors in the regulation of mstn1a and mstn1b gene expression was to analyze the activation of the Akt-FoxO signaling pathway in cells over- or underexpressing the studied genes. GH has been previously shown to regulate the expression of mstn in the muscle of human (38) and rainbow trout (7, 16) as well as in the murine myoblast cell line C2C12 (38). The mechanism underlying GH-mediated regulation of mstn expression is yet unknown. However, this effect could involve the Akt-FoxO signaling, as suggested by the induction of Akt phosphorylation in many cell systems stimulated by GH (22, 27, 54). Thus GH-stimulated cells may serve as a relevant model to study the involvement of FoxO1 in regulating the expression of the muscle antigrowth factors mstn1a and mstn1b. Our in vitro results clearly showed that GH decreased the expression of both mstn1a and mstn1b in trout myotubes. These results contrast with previous in vivo studies in trout showing that GH injection differentially regulates both mstn genes (7, 16), possibly reflecting inherent differences between cells in vivo and cells in culture. To gain insight on the involvement of Akt-FoxO signaling in the GH-mediated downregulation of both trout mstn genes in our in vitro model, we then monitored the activity of this signaling pathway in cells stimulated with GH. Our Western blot analysis clearly showed that GH stimulation induced a strong phosphorylation of Stat5, known to be the major target of the cytokine signaling pathway (JAK/Stat) (23). However, under the same conditions, we did not observe any phosphorylation of Akt, FoxO1, FoxO3, and FoxO4. Moreover, FoxO1 protein remained in the nucleus after GH stimulation. Altogether, these results showed that GH did not change FoxO1 activity although GH strongly downregulated mstn1a and mstn1b expression in trout myotubes. In others words, the GH-induced decrease of mstn expression cannot be explained by a drop of FoxO1 activity in trout myotubes.

In this study, we clearly show that IGF-I inhibits FoxO1 activity without any changes of mstn1a and mstn1b expressions and that GH stimulation strongly decreases mstn expressions without any changes in FoxO1 activity. Altogether, these results indicate that FoxO1 is not a key transcription factor in the regulation of the expression of both trout mstn genes in trout myotubes. In mammals, FoxO transcription factors are recognized to play a central role in the control of the expression of several genes coding for key mediators of skeletal muscle atrophy in response to atrophic and/or hypertrophic signaling (18). Therefore, the results presented here could be related to previous in vivo studies in trout showing no induction of the expression of either mstn1a or mstn1b gene during muscle atrophy induced by starvation (11, 28, 46). Furthermore, in tilapia (Oreochromis mossambicus), a decrease of mstn expression after food deprivation has even been observed (53), whereas, in zebrafish, mstn expression was shown to be independent of food restriction (41). In addition, during the reproduction period, trout undergoes muscle atrophy that is associated with a decrease of mstn1b expression (51). Altogether, these data show that the regulation of mstn gene in these fish species differs from that described in mammals and that the
involvement of FoxO transcription factors in this process may account for a part in this difference. Furthermore, they indicate that, although the antigrowth properties of MSTN seem to be conserved throughout evolution (19, 37), the regulation of the mstn gene has dramatically evolved and remains to be explored in lower vertebrates.

**Perspectives and Significance**

The highly homologous sequences of MSTN protein’s COOH-terminal active region among species ranging from zebrafish to humans suggested that the functions of MSTN were extremely conserved throughout evolution (17, 19, 37). However, there were higher differences for the promoter region among animals compared with the coding region (14, 17, 19), resulting in some interspecies differences in the response of mstn gene to environmental changes (7, 16, 20, 26, 51, 53, 63). The search for regulatory factors of mstn gene expression in different (model or livestock) species would therefore help the understanding of its function in the regulation of muscle mass. In this regard, rainbow trout is a very interesting model because of its two mstn genes differentially regulated in several environmental conditions. The present data indicate that FoxO1 activity is not a determining factor in the regulation of the expression of both mstn1a and mstn1b genes in primary culture of trout myotubes. Further studies are warranted to follow these specific genes as affected by nutritional and hormonal factors.

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**DISCLOSURES**

No conflicts of interest are declared by the authors.

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