## Regulatory mechanisms involved in muscle and bone remodeling during refeeding in gilthead sea bream

Lavajoo, F.<sup>§1</sup>, Perelló-Amorós, M.<sup>§</sup>, Vélez, E.J.<sup>2</sup>, Sánchez-Moya, A., Balbuena-Pecino, S., Riera-Heredia, N., Fernández-Borràs, J., Blasco, J., Navarro, I., Capilla, E.<sup>¥</sup> and Gutiérrez J.<sup>¥</sup>\*

Department of Cell Biology, Physiology and Immunology, Faculty of Biology, University of Barcelona, Barcelona, Spain

<sup>§</sup> Equal contribution; <sup>¥</sup> Equal contribution

<sup>1</sup>Present address: Department of Marine Biology, Faculty of Marine Science and Technology, University of Hormozgan, I. R. Iran

<sup>2</sup>Present address: Department of Veterinary Biomedical Sciences, Western College of Veterinary Medicine, University of Saskatchewan, Saskatoon, Saskatchewan S7N 5B4, Canada

\*Corresponding author: Joaquim Gutiérrez

Department of Cell Biology, Physiology and Immunology, Faculty of Biology, University of Barcelona, Av. Diagonal 643, 08028, Barcelona, Spain. Tel: (+34) 934021532, E-mail: jgutierrez@ub.edu

	Gene	Sequences	Ta (°C)	Accession Number
GH/IGF family	igfla	F: AGGACAGCACAGCAGCCAGACAAGAC R: TTCGGACCATTGTTAGCCTCCTCTCTG	60	AY996779
	igflab	F: AGTCATTCATCCTTCAAGGAAGTGCATCC	60	EF688015
	igflabc	F: ACAGAATGTAGGGACGGAGCGAATGGAC	60	EF688016
	iof2	F: TGGGATCGTAGAGGAGTGTTGT	60	AY996778
	ioflug	R: CTGTAGAGAGGTGGCCGACA F: AGCATCAAAGACGAACTGG	60	VT156946
	igjira	R: CTCCTCGCTGTAGAAGAAGC F: GCTAATGCGAATGTGTTGG	00	K1150840
	igf1rb	R: CGTCCTTTATGCTGCTGATG	55	KT156847
	igfbp1	R: TCTCTTTAAGGGCACTCGGC	60	KM522771
	igfbp4	F: TCCACAAACCAGAGAAGCAA R: GGGTATGGGGGATTGTGAAGA	60	F5T95CD02JMZ9K
	igfbp5b	F: TTTCTCTCTCGGTGTGC R: TCAAGTATCGGCTCCAG	60	AM963285
	ghr1	F: ACCTGTCAGCCACCACATGA R: TCGTGCAGATCTGGGTCGTA	60	AF438176
	ghr2	F: GAGTGAACCCGGCCTGACAG	60	AY573601
	akt	F: GCTCACCCCACTCTTCAGAC	60	AY996779
81	tor	F: CAGACTGACGAGGATGCTGA	60	EF688015
Signalir	70c6k	R: AGTTGAGCAGCGGGTCATAG F: GCACCAGAAAGGCATCATCT	60	EE699016
	70s0k	R: AAGGTGTGGGGTCACTGTTCC F: CCAACCTGCGACTCATCTCT	00	EF088010
	4ebp1	R: GTTCCTCTCATCCTCCCACA	60	KM522771
	foxo3	R: CCAGCTCTGAGAGGTCTGCT	60	
	pax7	F: ATGAACACTGTCGGCAACG R: AGGCTGTCCACACTCTTGATG	64	JN034418
	pcna	F: TGTTTGAGGCACGTCTGGTT R: TGGCTAGGTTTCTGTCGC	60	AY550963.1
	myf5	F: CTACGAGAGCAGGTGGAGAACT R: TGTCTTATCGCCCAAAGTGTC	64	JN034420
ited	myod1	F: TTTGAGGACCTGGACCC R: CTTCTGCGTGGTGATGGA	60	AF478568.1
th-reld	myod2	F: CACTACAGCGGGGGATTCAGAC R: CGTTTGCTTCTCCTGGACTC	60	AF478569
e grow	myog	F: CAGAGGCTGCCCAAGGTGGAG	68	EF462191
Muscle	mrf4	F: CATCCCACAGCTTTAAAGGCA	60	JN034421
	mstn 1	K: GAGGACGCCGAAGATTCACT F: GTACGACGTGCTGGGAGACG	60	AF258448 1
		R: CGTACGATTCGATTCGCTTG F: ACCTGGTGAACAAAGCCAAC		AV046214
	mstn2	R: TGCGGTTGAAGTAGAGCATG F: GCCCCATCAACTTCACCGTCTTT	60	AYU46314
	mlc2a	R: GGTTGGTCATCTCCTCAGCGG	60	AF150904

**Supplementary Table 1:** Sequences, annealing temperatures (Ta) and GenBank accession numbers of the primers used for *Sparus aurata* real-time quantitative PCR.

	mlath	F: TCCCTTTGCTATTCTGCCTTC	60	EC618631	
	mic2D	R: AAATCAGCCCTATTCCCCATA	00	10010031	
us tems	ognu l	F: CCTACGAGATGAGGATGGCT	56	VE444900	
	capn1	R: AGTTGTCAAAGTCGGCGGT	50	КГ444099	
	agen 2	F: ACCCACGCTCAGACGGCAAA	61	KF444900	
	cupnz	R: CGTTCCCGCTGTCATCCATCA	01		
	capn3	F: AGAGGGTTTCAGCCTTGAGA	56	FP P000874	
		R: CGCTTTGATCTTTCTCCACA	50	LICI 000074	
	capnsla	F: CGCAGATACAGCGATGAAAA	56	KF444901	
		R: GTTTTGAAGGAACGGCACAT	50		
	capns1b	F: ATGGACAGCGACAGCACA	56	ERP000874	
		R: AGAGGTATTTGAACTCGTGGAAG	50		
ic s.	ctsda	F: CCTCCATTCACTGCTCCTTC	56	AF036319	
olyt	cisuu	R: ACCGGATGGAAAACTCTGTG	50		
otec	etsl	F: ACTCCTTGGGCAAACACA	54	DO875320	
$Pr_{r}$	Cisi	R: CCTTGAACTTCCTCTCCGT	54	DQ07552)	
	ub	F: ACTGGCAAGACCATTACCTT	54	KJ524459	
	ио	R: TGGATGTTGTAGTCGGAAAG	54		
	murf1	F: GTGACGGCGAGGATGTGC	60	FM145056	
	marjı	R: CTTCGGCTCCTTGGTGTCTT	00		
	mafbx	F: GGTCACCTGGAGTGGAAGAA	60	ERA047531	
	таубл	R: GGTGCAACTTTCTGGGTTGT	00		
	n3	F: AGACACACACTGAACCCGA	54	KJ524458	
		R: TTCCTGAAGCGAACCAGA			
	runx2	F: ACCCGTCCTACCTGAGTCC	60	JX232063	
		R: AGAAGAACCTGGCAATCGTC			
	fib1a	F: CGGTAATAACTACAGAATCGGTGAG	60	FG262933	
	<i>j</i> ··· - ··	R: CGCATTTGAACTCGCCCTTG			
1	col1a1	F: GAGATGGCGGTGATGTGGCGGAGTC	68	DQ324363	
atec		R: GCCTGGTTTGGCTGGATGAAGAGGG			
-rel	ocn	F: TCCGCAGTGGTGAGACAGAAG	56	AF048703	
-əuc		R: CGGTCCGTAGTAGGCCGTGTAG			
Bc	on		68	AY239014	
	ctsk		60	DQ875329	
	mmp9		60	AM905938	
tce					
	efla		60	AF184170	
	rps18			AM490061.1	
			60		
ereı					
Refi	b-actin	F. ICCIOCOUAAICCAIOAOA R. GACGTCGCACTTCATGATGCT	60	X89920	
	rpl27		68	AY188520	
		K. CITCIOCCIUITUAUUAAUUA			

**Supplementary Table 2:** Body weight (BW), body length (BL), condition factor (CF), hepatosomatic index (HSI), viscerosomatic index (VSI) and ratio of Gh and Igf1 plasma levels along the fasting and refeeding experiment. Data are shown as means  $\pm$  SEM (n=6). Letters indicate significant differences (p < 0.05) by one-way ANOVA, LSD and Tukey HSD test.

	-21 Days	0h	2h	5h	24h	7 Days
BW (g)	$53{,}9\pm3{,}0$	$47,2 \pm 3,2$	$49,\!4\pm1,\!9$	$50{,}8\pm2{,}3$	$46{,}8\pm1{,}7$	$54,\!4\pm3,\!5$
BL (cm)	$12,\!9\pm0,\!27$	$13,1\pm0,34$	$13,1\pm0,\!21$	$13,\!2\pm0,\!24$	$13,\!0\pm0,\!18$	$13,\!4\pm0,\!29$
CF	$2,49 \pm 0,05$ (A)	2,11 ± 0,06 (B)	$\begin{array}{c} 2,22\pm0,05\\ (B)\end{array}$	2,23 ± 0,03 (B)	$\begin{array}{c} 2,14\pm0,04\\ (B)\end{array}$	$2,27 \pm 0,03$ (B)
HSI	$1,27 \pm 0,11$ (B)	$0,58 \pm 0,06$ (C)	$\begin{array}{c} 0,58\pm0,06\\ (C)\end{array}$	$\begin{array}{c} 0,\!68\pm0,\!06\\ (C)\end{array}$	$0,81 \pm 0,08$ (C)	1,66 ± 0,1 (A)
VSI	$\begin{array}{c} 0,\!66\pm0,\!13\\ (AB) \end{array}$	0,36 ± 0,11 (C)	0,64 ± 0,13 (A)	$\begin{array}{c} 0,37\pm0,13\\ (AB) \end{array}$	0,3 ± 0,09 (AB)	$0,55 \pm 0,06$ (AB)
[Gh]/[Igf1]	$0,06 \pm 0,08$ (B)	$2,97 \pm 0,80$ (A)	3,4 ± 0,23 (A)	2,85 ±1,13 (A)	$3,24 \pm 1,04$ (A)	$0,89 \pm 0,48$ (AB)

**Supplementary information 3 - Western blot full length gels:** the six samples of each time group were evenly distributed in three gels resulting in 2 samples/gel/group. Due to that in each western blot, different proteins were analyzed, it was necessary to crop the membranes in order to incubate them with different primary antibodies. Tor (289 kDa MW) and Akt (60 kDa MW) phosphorylated and total forms, were analyzed in the same western blot by cutting the membranes in two. The top part was used to blot Tor antibodies and the bottom part for Akt. Phosphorylated forms were analyzed first and after stripping, the corresponding total forms were determined in the same membranes. Moreover, Ctsd (33 kDa MW) and Ctsl (23 kDa MW) were analyzed in cropped membranes of different western blots each along with other proteins that were unsuccessful (data not shown).

Western blot membranes 1, 2 and 3 top: Total Tor

Western blot membranes 1, 2 and 3 top: pTor



Western blot membranes 1, 2 and 3 bottom: pAkt

Western blot membranes 1, 2 and 3 bottom: Total Akt



Western blot membranes 4, 5 and 6: Ctsd



Western blot membranes 7, 8 and 9: Ctsl