

## Molecular changes in detrained & retrained adult jaw muscle

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**SUMMARY** A hypofunctional masticatory system was developed in 21-day-old male rats by feeding them a soft diet for 27 weeks. Retraining of a parallel group for 6 weeks was achieved by switching back to a hard diet after 21 weeks. A control group was fed a hard diet for 27 weeks. At the end of the experimental period, the expression levels of the myosin heavy chain isoform genes *MYH 1* and *2* (fast), *3* (embryonic) and *7* (slow) in the deep masseter were compared using qRT-PCR analysis.

The gene expressions of *MYH 3* and *MYH 7* were significantly higher in the rehabilitation group compared with the normal and hypofunctional group, but no significant differences were found in regards to the gene expression of *MYH 1* and *2*.

Retraining made it possible for the slow (*MYH 7*) isoform levels to adapt to the increased mechanical load. The increased level of embryonic (*MYH 3*) isoform could be due to the need of creation of new MYH isoforms.

### Introduction

Adults with an improved masticatory muscle function following orthognathic surgery or after receiving implant-retained bridges may have different functional conditions that could induce significant changes in the myosin heavy chain (MyHC) composition of their jaw closing muscles. This is of particular interest for future therapies and procedures whether functional changes can be reversed or rehabilitated. For example, in finding ways to reduce the risk or to prevent relapse after orthodontic surgery.

Skeletal jaw muscles have an inherent adaptability (Goldspink, 2003), and when muscles adapt to new functional demands, fibre-type changes occur (Adams *et al.*, 1993; Oishi *et al.*, 1998). These changes allow the muscle to optimize its contractile function (Korfage *et al.*, 2005). Changes in muscle structure and properties can be brought about by switching on one subset and repressing another subset of genes. (Goldspink *et al.*, 1992).

Fibre-type changes normally follow a strict order: from slow fibre-type towards fast and then towards faster (I → IIA → IIX → IIB) and *vice versa* (Schiaffino and Reggiani, 1994). It has been shown that the switch from fast to slow is activity dependant (Barton-Davis *et al.*, 1996). In humans, for example, exercise against load increases slow fibres in favour of fast fibres (Hather *et al.*, 1991; Staron *et al.*, 1994).

Histologically, muscle fibres are classified in relation to which MyHCs they contain: this scheme is no longer

particularly simple due to the wide number of MyHCs that are expressed in the same muscle fibre. A MyHC ‘profile’ (protein and/or gene expression) of muscle fibres/groups is more usually reported.

Although regimes of detraining followed by rehabilitation/retraining have been reported for non-masticatory muscle (e.g., immobilization of limbs), similar studies of adult jaw muscle have not been conducted.

Studies in human subjects with varying growth patterns have shown that different craniofacial morphologies are associated with variations in masticatory muscle physiology; individuals with a long face have a weaker bite force than individuals with normal vertical dimensions. (Proffit *et al.*, 1983; Hunt and Cunningham, 1997). Individuals with a short face have a thicker masseter muscle than long-face individuals (Kiliaridis and Kälebo, 1991; Bakke *et al.*, 1992; Benington *et al.*, 1999). The masticatory muscles of an individual with short-face characteristics contain more type II fibres than an individual with normal facial dimensions, while a long-face individual has a reduction in both the size and number of type II fibres (Hunt *et al.*, 2006).

However, these observations have been made in a non-experimental setting where the degree of ‘detraining’ and ‘retraining’ has not been controlled. Animal studies lend themselves to such controlled experiments where adaptive changes have been induced experimentally, e.g., by changing diets. Changing masticatory muscle function, for example, by feeding rats with a soft diet leads to a reduced

masticatory muscle strength (Kiliaridis and Shyu, 1988) and a change of the fibre composition in their deep masseter muscles (Kiliaridis *et al.*, 1988). This in turn causes changes in bone modelling in growing rats. (Mavropoulos *et al.*, 2004; Abed *et al.*, 2007) and alterations in craniofacial growth. It has been shown that rehabilitation of masticatory function in adult rats led to a significant improvement of alveolar bone architecture and change the alveolar process (Mavropoulos *et al.*, 2010).

In order to investigate the effect of masticatory functional changes on deep masseter muscle contractile protein gene expression, an experimental study in non-growing, adult rats was performed.

## Material and methods

### Material

Forty male rats of the Sprague–Dawley strain (average age 21 days) from Charles River, Uppsala, Sweden were used. The experimental protocol obtained approval by the Ethics Committee of University of Gothenburg.

### Experimental design (Fig. 1)

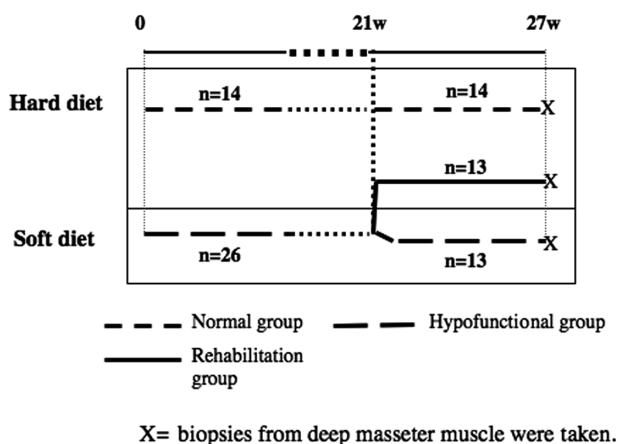
The 40 rats were randomly divided into two groups. Fourteen received ordinary (hard) food during the whole experimental period (normal group). The remaining 26 received a soft diet to develop a hypofunctional masticatory system (Kiliaridis *et al.*, 1988). The soft diet was made of ordinary (hard) food (R34, Lactamin, Södertälje, Sweden) mixed with water in standardized proportions (2:5, R34:water). After a period of 21 weeks on a soft diet these animals, now adults, were divided into two equal groups (matched for weight): one continued on the soft diet (hypofunctional group), and the other changed to an ordinary (hard) diet with the aim of functionally rehabilitating

**Table 1** Amount of rats in the different groups included in the results.

Variables	Amount of rats		
	Normal	Rehabilitation	Hypofunctional
<i>MYH 1</i> and <i>2</i>	12	9	12
<i>MYH 3</i>	13	12	12
<i>MYH 7</i>	12	9	12

their masticatory system (rehabilitation group). Due to losses during the experiment (e.g., loss during qRT-PCR and during preparation for qRT-PCR), the total number of samples reported is lower than the total number of animals that completed the experimental protocol (Table 1). The total experimental period was 27 weeks. Throughout the experimental period, the rats were weighed every second week and were fed and watered *ad libitum*. At the end of the experimental period, the animals were sacrificed in a CO<sub>2</sub> chamber. The deep masseter muscle was excised. The muscle biopsies were immediately frozen in thawing isopentane (−150°C) and stored at −80°C (Kiliaridis *et al.*, 1988; Suchak *et al.*, 2009).

**Quantitative reverse transcriptase polymerase chain reaction (qRT-PCR).** In order to successfully extract ribonucleic acid (RNA) from the rat deep masseter muscle samples, the tissue was initially disrupted using the FastPrep FP120A bench-top reciprocating device (MP Biomedicals Europe, Illkirch, France). Muscle tissue (weighing more than 30 mg) was ‘pulverised’ in 800 µl buffer RLT mixed with 10 µl b-mercaptoethanol per 1 ml buffer (RNeasy Mini Kit, Qiagen Ltd, W Sussex, UK) against silica ceramic beads (Lysing Matrix D, MP Biomedicals Europe) using the FastPrep device. The resulting solution was processed with the RNeasy Mini Kit (Qiagen). The RNA’s quality (A260/A280) and quantity (concentration) was controlled/measured with a Spectrophotometer (Ultrospec 2000 machine, Amersham Pharmacia Biotech, GE Healthcare Ltd, Buckinghamshire, UK). RNA was then converted into complementary deoxyribonucleic acid (cDNA) using a high capacity cDNA archive kit (Applied Biosystems, Cheshire, UK). Quantitative PCR was performed with these cDNA templates using the TaqMan® System (Applied Biosystems). This system uses specific gene probes conjugated to a FAM (6-Carboxyfluorescein) reporter dye that bind to the sequence of interest (e.g., MyHC specific transcripts). During the PCR reaction, the probe is cleaved by the action of DNA polymerase that results in increased fluorescence. Accumulation of PCR products is detected directly by monitoring the increase in fluorescence of the reporter dye using the ABI PRISM® 7300 Sequence Detection System (All from applied Biosystems). Relative quantification studies were conducted using an endogenous control, GAPDH (Genebank NM\_017008.3) (Suchak *et al.*,



**Figure 1** Experimental design.

**Table 2** Myosin heavy chain isoforms investigated in this study.

Gene of interest	Myosin heavy chain protein	Muscle contraction	Genebank messenger RNA
<i>MYH 1</i>	Myosin heavy chain II x	Fast	AF111785.1 BC114545.1
<i>MYH 2</i>	Myosin heavy chain II a	Faster	AF111784.1 BX510904.2 BC126409.1
<i>MYH 3</i>	Embryonic myosin heavy chain	Fairly fast	X13988.1 BP232245.1 BQ956249.1
<i>MYH 7</i>	Beta-cardiac myosin heavy chain, Myosin heavy chain I	Slow	M58018.1 X51591.1 AY518538.1 AB209708.1 DQ248310.1 BC112173.1 BC112171.1 EF560725.1

2009). Masseter muscle derived cDNA was targeted for sequences of MyHC genes (Table 2).

#### Statistical analysis

All data are represented as means and standard deviations (mean  $\pm$  SD). To investigate the morphological differences between the three experimental groups, analysis of variance (ANOVA) was performed. All statistical analyses were performed using the SPSS statistical package (SPSS 16; SPSS, Chicago, IL, USA). A result was considered statistically significant at  $P < 0.05$ .

## Results

#### Body weight

No statistically significant differences in body weight were found at week 27 between the three groups at the end of the experimental period (week 27): the mean body weight ( $\pm$ SD) for the hypofunctional group was 595 g ( $\pm$ 48 g), for the rehabilitation group was 595 g ( $\pm$  43 g), and for normal group was 631 g ( $\pm$ 81 g).

#### Contractile protein gene expression in adult rats

The results showed that the gene expression of *MYH 3* was significantly higher in the rehabilitation group compared with the normal group ( $P = 0.001$ ) and with the hypofunctional group ( $P = 0.025$ ). When comparing between the normal and the hypofunctional group, there were no significant differences.

There were no significant differences in the comparison of the three groups regarding the gene expression of *MYH 1* and *2*.

The analysis showed that there were distinct differences in gene expression of *MYH 7* between the rehabilitation and normal group ( $P = 0.000$ ) and between the rehabilitation

**Table 3** Mean values and standard deviation (in parentheses) of the variables under study for each of the reference and experimental groups.

Variables	ANOVA			Significance
	Normal	Rehabilitation	Hypofunctional	
<b>Gene expression (2<sup>^-</sup>-DDCt)</b>				
<i>MYH 1</i> and <i>2</i>	0.80 (0.71)	3.65 (5.05)	2.81 (4.48)	$P = 0.214$
<i>MYH 3</i>	2.18* (0.80)	8.95** (7.14)	4.47** (3.92)	$P = 0.003$
<i>MYH 7</i>	1.29* (1.24)	142.05** (137.43)	27.6** (34.92)	$P = 0.000$

Analysis of variance (ANOVA) was applied in order to investigate the difference between the three experimental groups (Normal group; Rehabilitation group; Hypofunctional group).

\*, \*\*, superscript characters denote statistical significant pairwise differences (*post hoc* comparisons).

and hypofunctional groups ( $P = 0.001$ ), where the levels were highest in the rehabilitation group and lowest in the normal group. However, again there were no significant differences between the normal and the hypofunctional group. The mean values and standard deviation of the variables under study for each of the groups are found in Table 3.

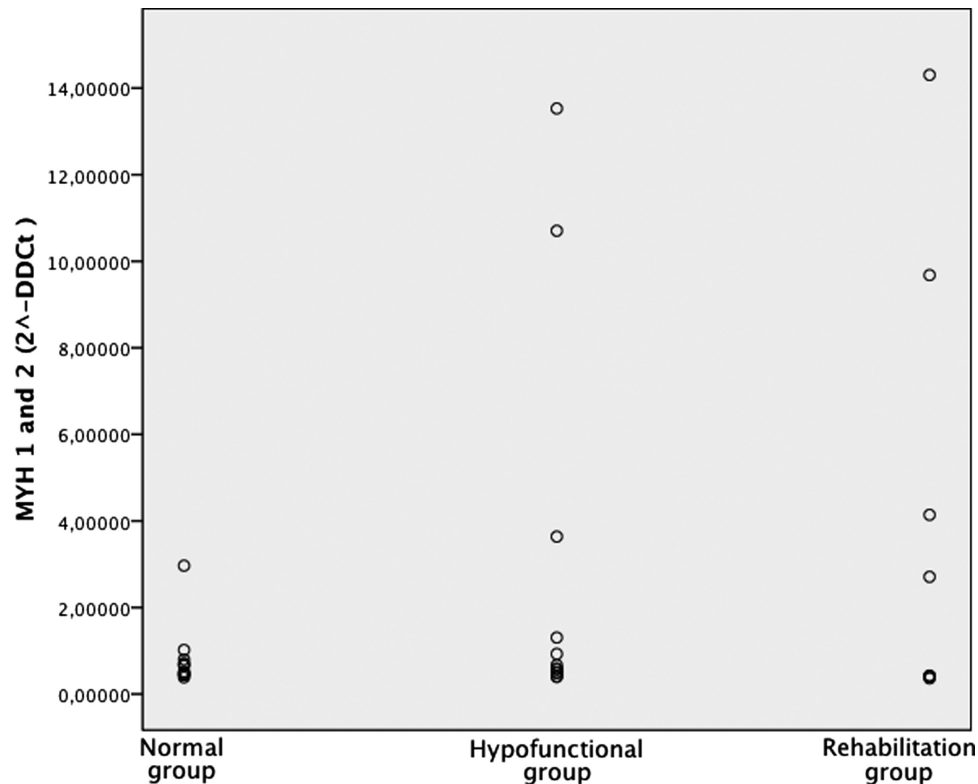
## Discussion

In the present study, we found that a functional rehabilitation of the masticatory system for 6 weeks during adolescence and early adulthood after a prolonged period with low masticatory demands (the rehabilitation group) had a significant effect on the gene expression of *MYH 3* and *MYH 7*, but not on *MYH 1* and *2*.

The significant effect on the *MYH 7* (slow) is in line with earlier muscle studies (Caiozzo *et al.*, 1996), in that activation of the masseter muscle increased the amount of slow MyHC. The increase of slow MyHC is due to the muscle fibres' capacity to adapt to new functional demands (Korfage *et al.*, 2005, Part I).

The level of the *MYH 7* was lowest in the normal group and highest in the rehabilitation group. The low level of *MYH 7* in the normal group is in line with Sano and co-workers' description of the fibre-type composition in a normal rat deep masseter muscle (Sano *et al.*, 2007)

The change of diet from soft to hard in order to rehabilitate their masticatory system had a significant effect on *MYH 3* (coding for embryonic MyHC) gene expression in the rehabilitation group compared with both the normal group and the hypofunctional group. That *MYH 3* was detected in all three groups, with the lowest amount in the normal group and the highest in the rehabilitation group, is not in line with, for example, Jung *et al.* (1998). Using competitive PCR, they could not detect any *MYH 3* at all in the masseter muscle of adult rats. However, it is known that in the limb muscles,



**Figure 2** Scatterplot of the gene expression of MYH 1 and 2 in the different groups.

developmental isoforms can be re-expressed in the case of regeneration and injury (Jung *et al.*, 1998). It seems that this is the case even with the deep masseter muscle of adult rats.

The analysis showed no significant differences in the comparison of the three groups regarding the gene expression of *MYH 1* and *2*, but when studying the rehabilitation group in the *MYH 1* and *2* scatterplot (Fig. 2), it shows that five out of nine are clustered together. In four of the animals, *MYH 1* and *2* were not affected, whereas five of them showed a reduced expression of *MYH 1* and *2*. These data indicate that there is a large degree of individual variation in how jaw muscle reacts to rehabilitation. The decrease in gene expression of *MYH 1* and *2* that can be seen in the scatterplot with the five clustered rats in the rehabilitation group is in line with earlier studies where it has been shown that the fast fibres decrease in favour of the slow fibres (Hather *et al.*, 1991, Staron *et al.*, 1994).

It is known from a description of the fibre-type composition in a normal rat deep masseter muscle (Sano *et al.*, 2007) that two of the fast fibre types exist in all parts of the muscle and that is type IIa and IIx. (*MYH 2* and *MYH1*).

The findings from our rat model experiment cannot be directly extrapolated to humans, but it can give an insight into a better understanding of the mechanisms that influence the interaction between muscle function and craniofacial morphology. For example, it may help in finding ways to reduce the risk or to prevent relapse after orthodontic surgery.

## Conclusion

A 6-week period of masticatory functional rehabilitation in deep masseter muscle of adult rats made it possible for the slow contractile gene expression isoform (*MYH 7*) levels to increase, an adaptation to the increased mechanical load. The increased level of embryonic gene expression isoform (*MYH 3*), which is novel, can be due to the need for the creation of new MyHC isoforms.

## Funding

The European Orthodontic Society; the Swedish Dental Society.

## Acknowledgments

We are grateful to Mrs Stina Olsson and Dr Andrea Bresin for their technical assistance.

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