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# Electrical Stimulation Induces Calcium-dependent Up-regulation of Neuregulin-1 $\beta$ in Dystrophic Skeletal Muscle Cell Lines

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# **Key Words**

Muscle gene expression • Excitation-transcription coupling • Inositol-1,4,5-trisphophate receptors • Dystrophin

#### **Abstract**

Duchenne muscular dystrophy (DMD) is a neuromuscular disease originated by reduced or no expression of dystrophin, a cytoskeletal protein that provides structural integrity to muscle fibres. A promising pharmacological treatment for DMD aims to increase the level of a structural dystrophin homolog called utrophin. Neuregulin-1 (NRG-1), a growth factor that potentiates myogenesis, induces utrophin expression in skeletal muscle cells. Microarray analysis of total gene expression allowed us to determine that neuregulin-1β (NRG-1β) is one of 150 differentially expressed genes in electrically stimulated (400 pulses, 1 ms, 45 Hz) dystrophic human skeletal muscle cells (RCDMD). We investigated the effect of depolarization, and the involvement of intracellular Ca2+ and PKC isoforms on NRG-1β expression in dystrophic myotubes. Electrical stimulation of RCDMD increased NRG-1β

mRNA and protein levels, and mRNA enhancement was abolished by actinomycin D. NRG-1ß transcription was inhibited by BAPTA-AM, an intracellular Ca2+ chelator, and by inhibitors of IP2-dependent slow Ca2+ transients, like 2-APB, Ly 294002 and Xestospongin B. Ryanodine, a fast Ca2+ signal inhibitor, had no effect on electrical stimulation-induced expression. BIM VI (general inhibitor of PKC isoforms) and Gö 6976 (specific inhibitor of Ca2+-dependent PKC isoforms) abolished NRG-1ß mRNA induction. Our results suggest that depolarization induced slow Ca<sup>2+</sup> signals stimulate NRG-1B transcription in RCDMD cells, and that Ca2+-dependent PKC isoforms are involved in this process. Based on utrophin's ability to partially compensate dystrophin disfunction, knowledge on the mechanism involved on NRG-1 up-regulation could be important for new therapeutic strategies design.

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### Introduction

Duchenne muscular dystrophy (DMD) is a devastating neuromuscular disease affecting 1/3,500 male births [1]. It is caused by several mutations in the dystrophin gene, that results in little or no production of a functional

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cytoskeletal protein, normally expressed at the inner surface of the sarcolemma of muscle fibers [2].

Dystrophin associates with a large complex of proteins known as the dystrophin-associated proteins (DAPs). Dystrophin-DAPs complex (DAPC) serves as a link between the extracellular matrix and the intracellular actin cytoskeleton, providing structural integrity to muscle fibers [3, 4]. Failure in dystrophin expression results in loss of DAPs and impairment of plasma membrane stability [5] leading to degeneration and progressive weakness of heart and skeletal muscle, and causing disability and death in adolescence or young adulthood [6].

Although no therapy has been described to effectively slow or halt muscle degeneration in dystrophic patients, different strategies have been designed to correct the deleterious consequences of dystrophin absence and to alleviate the secondary effects of the disease [7]. One of them consists in expressing a protein that could functionally compensate for the lack of dystrophin. Utrophin, a protein that shares structural and functional motifs with dystrophin and also associates with members of the DAPC, is a good candidate for such a role.

It has been established that increased utrophin levels in muscle fibers of dystrophin-deficient *mdx* mice restores sarcolemmal expression of DAPs members and improves dystrophic phenotype. This observation has raised the possibility that up-regulation of utrophin expression might be able to counteract dystrophin deficiency in DMD patients. This promising pharmacological treatment requires the identification of signals and regulatory pathways that modulate utrophin expression in the muscle [reviewed in 8].

Neuregulin growth factor [NRG; also known as heregulin, neu differentiation factor, acetylcholine receptor (AchR)-inducing activity, glial growth factor II and sensory motor neuron-derived factor] is one of many factors that increase utrophin expression [reviewed in 8].

NRG-1 treatment leads to increased utrophin mRNA levels and transcriptional activity in mouse and human myotubes [9, 10]. Furthermore, Krag et al. (2004) described that intraperitoneal injection of a small peptide region of NRG-1 ectodomain increases utrophin expression in *mdx* mice. Observed increase was accompanied by a reduction in muscle degeneration and inflammation, and by decreased susceptibility to the damage induced by lengthening contractions. Improvement in muscle function was deemed to result specifically from the utrophin up-regulation because NRG-1 administration has no beneficial effect in dystrophin/utrophin double-knockout ani-

mals [11].

NRG-1 belongs to a family of proteins structurally related to the epidermal growth factor (EGF) that are synthesized in and secreted from motoneurons and muscle [12]. Four members of NRG proteins, NRG-1 to NRG-4, have been identified. The best studied and most characterized products are those encoded by NRG-1 gene. At least 15 different isoforms are generated by alternative splicing and differential promotor usage of NRG-1 gene. All identified NRGs feature an EGF-like motif, necessary and sufficient for biological activity, that binds to NRG receptors and activates downstream signals [13, reviewed in 14]. Variations in the EGF-like domain, give rise to  $\alpha$ ,  $\beta$ , and  $\gamma$  isoforms, with different affinities for NRG receptors [reviewed in 14].

NRG-1 has relevant effects on several other processes in the muscle [12, 15] such as myogenesis [16], muscle fiber survival [17], muscle spindle development [18], and in the differentiation of satellite cells during muscle regeneration [19]. In addition, NRG-1 contributes to the regulation of skeletal muscle mass by increasing protein synthesis [20], mitochondrial oxidative capacity and insulin sensitivity [21].

Regardless the evidences supporting such important roles for NRG-1 in skeletal muscle, the molecular mechanisms involved in its expression are still unclear.

The role of Ca<sup>2+</sup> in the induction of specific transcriptional response in skeletal muscle has been a current subject of study in our laboratory. We have shown that depolarization of cultured muscle cells, either by high K<sup>+</sup> treatment or electrical stimulation, produces a biphasic increase in intracellular Ca<sup>2+</sup> concentration [22-25]. The first increase or fast Ca2+ transient, localized in the cytoplasm, is related to the ryanodine receptor (RyR) and is associated to excitation-contraction (EC) coupling. The second one or slow Ca<sup>2+</sup> transient, generated by Ca<sup>2+</sup> release through inositol-1,4,5-trisphosphate (IP<sub>3</sub>) regulated channels and associated to nuclei [22], has been involved in early steps leading to gene expression. We have already described that IP<sub>3</sub>-mediated Ca<sup>2+</sup> signals induce an increase in mRNA levels of early and late genes in normal skeletal muscle cells after depolarization [26-29].

Several works suggest that alterations in IP<sub>3</sub> pathways are involved in DMD physiopathology [30, 31]. Both IP<sub>3</sub> total mass and the amount of IP<sub>3</sub> receptors (IP<sub>3</sub>Rs) are largely increased in dystrophic lines compared to normal cells [30]. Furthermore, expression and localization of IP<sub>3</sub>Rs are different in both cell lines, and IP<sub>3</sub>-dependent slow Ca<sup>2+</sup> transients evoked by electrical stimulation are larger and faster in dystrophic (RCDMD) than in

normal (RCMH) myotubes [32].

The aim of this study was to investigate the effect of electrical stimulation on NRG-1 expression in normal and dystrophic cells, and to explore whether  $Ca^{2+}$  dependent mechanisms are involved in the process. Using microarrays technology, we showed that electrical stimulation up-regulates the expression of NRG-1 isoforms  $\beta$  and  $\gamma$  in RCDMD cells. By real time PCR, we confirmed that depolarization induces NRG-1 $\beta$  gene expression in this cell line, whereas it has not a significative effect in RCMH cells in the same time period. Our results suggest that  $IP_3$ -dependent slow  $Ca^{2+}$  signals evoked by electrical stimulation stimulate NRG-1 $\beta$  transcription in dystrophic RCDMD cells.

#### **Materials and Methods**

Materials

Dulbecco's modified Eagle's medium-F12 (DMEM-F12) and horse serum were from Sigma (Sigma Chemical, St. Louis, MO). Fetal bovine serum from GIBCO BRL (Carlsbad, CA). Antibiotics and antimycotics from Life Technologies (Burlington, Ontario). 2-aminoethoxydiphenil borate (2-APB) was purchased from Aldrich. Ly 294002 and actinomycin D (Act D) were from Calbiochem (La Jolla, CA, USA). BAPTA-AM from Molecular Probes (Eugene, OR). Ryanodine (Rya) was purchased from BIOMOL Research Laboratories (Plympouth Meeting, PA). Bisindolymaleimide VI (BIM VI) was from Sigma Aldrich and Gö 6976 from Alexis Biochemicals. Xestospongin B was kindly provided by Dr. Jordi Molgó (Institut de Neurobiologie Alfred Fessard, Centre National de la Recherche Scientifique, France).

Illumina 22K human oligonucleotide microarrays were prepared by National Cancer Institute, NCI (Frederick, Maryland, USA). Alexa 555-AHA-dUTP, Alexa 647-AHA-dUTP, human Cot-1 DNA, SuperScript II, Taq DNA polymerase, SYBR(R) Green Nucleic A and Platinum Taq DNA polymerase were from Invitrogen (Carlsbad, CA). Recombinant RNAsin from Promega. All other reagents were from Sigma or Life Technologies.

Antibody directed against Neuregulin-1β/GGF2 goat polyclonal IgG (C-18; sc-1793), secondary antibody chicken anti-goat IgG- Horseradish peroxidase (HRP) (sc-2953) and antibody anti-actin rabbit polyclonal IgG (H-300, sc-10731) were obtained from Santa Cruz Biotechnology, Inc (Palo Alto, CA, EEUU). Secondary HRP-conjugated anti-mouse antibody and Coomassie Plus Protein Assay were from Pierce Biotechnology (Rockford, ILL, USA). Enhanced chemiluminescence (ECL) reagents were from Pierce Biotechnology or Amersham Biosciences (Piscataway, NJ. USA).

Cell culture

Dystrophic human myoblasts of the RCDMD cell line [33] and normal human myoblasts RCMH [34] were cultured in

DMEM-F12 (1:1) supplemented with 10% fetal bovine serum and 10% horse serum at 37°C and 5% CO<sub>2</sub>. Myogenic differentiation was accomplished by mere horse serum reduction to 1%

Both cell lines have been well characterized previously [30, 33, 34]. In addition, immunofluorescence studies to detect dystrophin expression in RCMH and RCDMD cells have been performed to test possible reversions in either the phenotype or the genotype that could have occurred during several culture passages. RCMH cells retained full expression of dystrophin on the cell membrane region, whereas RCDMD cells did not show any staining [32].

Microarray analysis

Microarray analysis was used to identify up- or down-regulated genes in RCDMD cell lines after 4 h post-electrical stimulation.

Total RNA from RCDMD cells was obtained employing Trizol reagent (Invitrogen, Corp., Carlsbad, CA, USA) according to manufacturer's protocol. cDNA from control and stimulated samples was labeled with Alexa 555 or 647 dyes, respectively. Briefly, cDNA was obtained by priming 20 µg of total RNA with 2 µM of oligodT in the presence of either 0.02 mM Alexa 555 or Alexa 647-AHA-dUTP (Invitrogen), 0.5 mM of each dATP, dGTP, dCTP, 0.08 mM dTTP, 2 U RNAsin, 1X buffer RT in a total volume of 50 µl. Reaction was started by addition of 1.5 µl of SuperScript II Reverse Transcriptase. To suppress gene specific dye effects, reciprocal labeling was performed. After 3 h incubation at 37°C, reaction was stopped with 5 µl 0.5 M EDTA. Template RNA was hydrolyzed with 1 µl 10 M NaOH during 15 min at 70°C, and then 10 µl 2 M Tris-HCl pH 7.5 was added. Cleanup of labeled cDNA was performed using MinBiospin columns (Biorad, Laboratories, Hercules, CA, USA). Illumina 22K human oligonucleotide microarray was kindly provided by Dr. David J. Munroe [National Cancer Institute (NCI), Frederick, Maryland, USA]. Hybridization and scanning was performed as previously described [28].

#### Microarrays data processing

Images were analyzed with GenePix Pro III software (Axon instruments, Foster City, CA, USA). GenePix Pro files (gpr) and JEPG images were deposited at the NCI's Microarray Database ("mAdb"; http://nciarray.nci.nih.gov). Annotated files were retrieved from mAdb and print-tip loess normalized, scale was corrected by means of DNMAD (http://dnmad.bioinfo.cnio.es/). Data set size was 3,226 clones after the elimination of genes found in less than 70% of arrays. Missing values were estimated by KNN-impute at the Preprocessor of GEPAS (http://gepas.bioinfo.cipf.es/). Mean and standard deviations were calculated for total data size (3,226 clones). Mean expression ± 2 standard deviation was considered as the statistical criteria to state differential expression. Then, filtered data were averaged and expressed as mean log, ratios.

Electrical stimulation

Myotubes were depolarized using electrical stimulation as previously described [25]. The electrical pulse train

stimulation consisted in 400 pulses of 1 ms-duration at 45 Hz. Then, cells were maintained in resting conditions for different times. When pharmacological inhibitors were used, myotubes were preincubated for 30 min and afterwards depolarized in the same medium. Inhibitors were not present during the subsequent incubation period.

All experiments were matched with vehicle-treated controls to discard pharmacological agent's non-specific effects. Both control and experimental cells were submitted to the same procedures.

#### Semiquantitative RT-PCR

Total RNA was prepared by TRIzol Reagent (Invitrogen, Carlsbad, CA) extraction and reverse transcribed by using SuperScrip II, RNase H - Reverse Transcriptase (Invitrogen, Carlsbad, CA). cDNA was amplified using human specific NRG-1β primers [35]. DNA concentration was normalized to glyceraldehyde-3-phosphate dehydrogenase (GAPDH) expression.

The primers used were:

Neuregulin-18:

5'-GGT GAT CGC TGC CAA AAC TA-3' (sense)

5'-GAG TGA TGG GCT GTG GAA GT-3' (antisense)

5'-TCC CAT CAC CAT CTT CCA-3' (sense)

5'-CAT CAC GCC ACA GTT TCC-3' (antisense)

PCR amplification was maintained in the exponential phase for each product. PCR conditions were: one cycle of 95°C for 2 min followed by 26 cycles at 95°C for 1 min, 55°C for 2 min, 72°C for 1 min and a final cycle of 10 min at 72°C. PCR products (NRG-1β: 370 bp and GAPDH: 379 bp) were resolved by electrophoresis on 2% agarose gel and stained with ethidium bromide. Bands were quantified by densitometric analysis with the Scion Image program from NIH.

#### Real time PCR

cDNA was prepared by reverse transcription of 1 µg of total RNA, using SuperScript II according to manufacturer's protocol. Real time PCR was performed using a Stratagene Mx3000P (Stratagene, La Jolla, CA) as follows: the reaction mixture consisted of 2 µl buffer PCR 10X, 0.2 µl Platinum Taq DNA polymerase 5U/µl, 1.4 µl MgCl, 50 mM, 1 µl sense primer 10 pmol/μl, 1 μl antisense primer 10 pmol/μl, 0.4 μl dNTPs 10X, 2 μl SYBR(R) Green Nucleic A (1/2000) and 1 μl cDNA. The final volume of the mixture was adjusted to 20 µl with the addition of DNase- and RNase-free H<sub>2</sub>O. Thermocycling conditions were as follow: 95°C for 2 min and 45 cycles of 95°C for 20 sec, 55°C for 20 sec, 72°C for 20 sec and 90°C for 7 sec, and a final cycle of 7 sec at 72°C. PCR amplification of the housekeeping gene GAPDH, was performed as a control. mRNAs were quantified and expressed in nanograms. Results are showed as mean log, NRG-1β/ GAPDH ratio (of porcentage of control).

## Western blot analysis

Stimulated cells were lysed in 60 µl of ice-cold lysis buffer containing 50 mM Tris-HCl pH 7.4, 150 mM NaCl, 1 mM EDTA, 1% Nonidet P-40, 5 mM Na, VO<sub>4</sub>, 20 mM NaF, 10 mM sodium

pyrophosphate, and a protease inhibitor mixture (Calbiochem). Cell lysates were sonicated for 1 min, incubated on ice for 20 min, and centrifuged to remove debris. Protein concentration of the supernatants was determined using bovine serum albumin as standard. 50 ug of lysate were suspended in Laemmli buffer, separated in 10% SDS-polyacrylamide gels, and transferred to polyvinylidene difluoride membranes (Millipore). The membranes were blocked at room temperature for 1 h in Trisbuffered saline containing 3% fat-free milk and 0.2% Tween 20, and then incubated overnight with the appropriate primary antibody anti-NRG-18 (dilution 1:1000). After washing with Trisbuffered saline, the membranes were incubated with the secondary antibody HRP-conjugated anti-goat dilution (1:2000) at room temperature for 2 h. Immunoreactive proteins were detected using ECL reagents according to the manufacturer's instructions. Films were scanned, and Image J program was employed for densitometric analysis of the bands. To correct for loading, the membranes were stripped in buffer containing 30% trichloroacetic acid, 30% sulfosalicilic acid and 2% ponceau solution, at room temperature for 60 min and reprobed with the corresponding control antibodies: primary antibody anti-actin (dilution 1:1000) and secondary antibody HRPcongujated anti-mouse (dilution 1:1500) [36].

#### Statistics

Results are expressed as a mean  $\pm$  S.E., and the significance of differences was evaluated using Student's t test for paired data, ANOVA followed by Dunnett's multiple comparison test or Bonferroni's test for comparison between groups.

#### Results

Differential gene expression in dystrophic human skeletal muscle cell lines induced by membrane depolarization

To identify differentially expressed genes in dystrophic human skeletal muscle cells (RCDMD) after electrical stimulation, we used an oligonucleotide microarray representing 21,920 different human genes (Illumina 22K). Total RNA from RCDMD samples was obtained 4 h after stimulation (400 pulses, 1 ms, 45 Hz). Assessment of differential gene expression was achieved by simultaneous hybridization of Alexa 555-labeled cDNA from control non-depolarized RCDMD cells and Alexa 647-labeled cDNA from stimulated RCDMD samples. Images obtained were analyzed with GenePix Pro III software. Ratio of Alexa 647 to Alexa 555 signals, calculated for each spot on the array, indicates relative gene expression. Mean and standard deviations were calculated for total data size (3,226 clones). Mean expression  $\pm 2$  standard deviation was considered as the statistical criteria to state differential expression. This analysis resulted in total 150 differentially expressed

**Table 1.** Highest differentially expressed genes in RCDMD myotubes after electrical stimulation. Microarray analysis was used to identify up- or down- regulated genes in RCDMD cell lines after 4 h postelectrical stimulation. Results from 4 arrays (stimulated RCDMD cells vs control nondepolarized RCDMD cells). Mean expression  $\pm 2$  standard deviation was considered as the statistical criteria to state differential expression. Mean log, ratios was ranked from the highest positive (up-regulated genes) and highest negative (down-regulated genes). Analysis was performed on 150 differentially expressed genes. Further details in Materials and Methods.

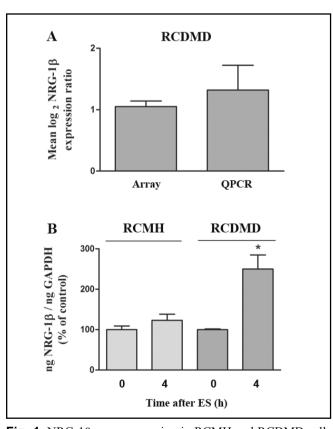
Gene	Description	Mean log <sub>2</sub> ratios
	Up-regulated genes	
C17orf64	chromosome 17 open reading frame 64	2.187
RAD54B	RAD54 homolog B S. cerevisiae	1.230
PARP10	poly ADP-ribose polymerase family member 10	1.194
C6orf115	PREDICTED chromosome 6 open reading frame 115	1.082
NRG1-beta	neuregulin 1 transcript variant HRG-beta2	1.051
MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5	1.020
NRG1-gamma	neuregulin 1 transcript variant HRG-gamma	0.991
FHL1	four and a half LIM domains 1	0.973
WBP4	WW domain binding protein 4 formin binding protein 21	0.970
TNFRSF10C	Tumor necrosis factor receptor superfamily member 10c decoy without an intracellular doma	in 0.943
	Down-regulated genes	
LOC285141	PREDICTED similar to CG14853-PB LOC285141 mRNA	-1.358
SMAD6	SMAD family member 6	-1.357
SEPTIN5	septin 5	-1.078
TSC22D3	TSC22 domain family member 3	-0.955
MCFD2	multiple coagulation factor deficiency 2	-0.955
EFS	embryonal Fyn-associated substrate	-0.942
CD79A	CD79a molecule immunoglobulin-associated alpha	-0.931
NDST1	N-deacetylase/N-sulfotransferase heparan glucosaminyl 1	-0.927
GGTLA4	gamma-glutamyltransferase-like activity 4	-0.907
MAPK11	mitogen-activated protein kinase 11	-0.897

genes, in depolarized samples related to controls (data not shown).

Highest differentially expressed genes at 4 h postelectrical stimulation are shown in Table 1. Results were expressed as  $\log_2$  of the average of relative expression intensity values of depolarized samples related to control. Differences were ranked separately from highest to lowest positive (up-regulated genes) or negative (downregulated genes) values ( $\log_2$ =1 corresponds to two fold induction).

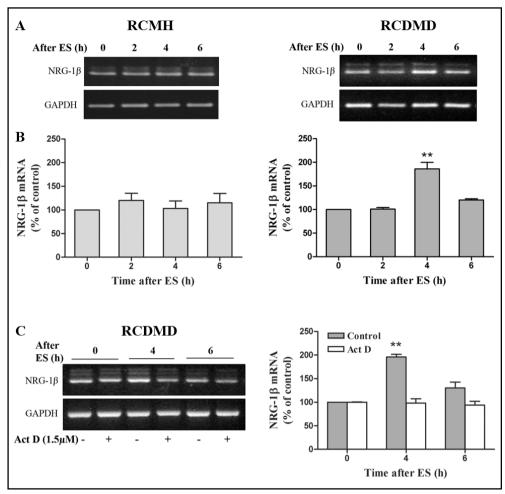
An interesting finding was the induction of neuregulin-1 transcript variant HRG-beta2 (NRG-1 $\beta$ ) and transcript variant HRG-gamma (NRG-1 $\gamma$ ), isoforms of NRG-1, a growth factor that stimulates utrophin expression [9, 10].

Increased NRG-1 gene expression from stimulated vs control RCDMD cells, were 2.07 fold ( $\log_2$  scale 1.051) for NRG-1 $\beta$ , and 1.99 fold ( $\log_2$  scale 0.991) for NRG-1 $\gamma$ . We validated NRG-1 up-regulation by real time PCR (QPCR) and focused our interest on NRG-1 $\beta$  isoform that displays a higher affinity for NRG receptors (Fig. 1A).



**Fig. 1.** NRG-1β gene expression in RCMH and RCDMD cells after electrical stimulation. (A) Microarray (n=4) and QPCR (n=3) analysis of NRG-1β gene expression in RCDMD cells. Results are expressed as mean  $\log_2$  ratios. (B) NRG-1β gene expression in RCMH and RCDMD cells submitted to electrical stimulation. Results, normalized to GAPDH, are expressed as percentage of non-depolarized control (100%, n=3). ES: electrical stimulation.

Fig. 2. Electrical stimulation increases NRG-1B gene expression in RCDMD cell line. Total RNA was isolated from electrically stimulated RCMH and RCDMD myotubes and maintained in resting medium for the times indicated. NRG-1B mRNA levels were analyzed by semiquantitative RT-PCR. (A) Representative agarose gel of products from NRG-1B and GAPDH mRNA amplification. (B) Results were normalized to GAPDH expression and expressed as a percentage of corresponding non-depolarized control (100%). Bars represent mean  $\pm$  S.E (n=3). \*\*P<0.01 ANOVA followed by Dunnett's multiple comparison test. (C) Characteristic agarose gel of RT-PCR products from RCDMD cells depolarized in the presence of either 1.5 µM actimomycin D (Act D) or vehicle (DMSO). Bars represent mean  $\pm$  S.E (n=3). \*\*P<0.01 vs corresponding control, evaluated by Bonferroni's test. ES: electrical stimulation.

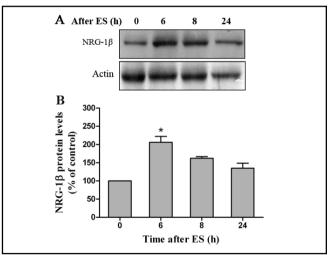


Effect of electrical stimulation in NRG-1 $\beta$  gene expression in normal and dystrophic human skeletal muscle cell lines

Given the NRG-1 $\beta$  gene up-regulation in depolarized dystrophic cell line and the important role of NRG-1 protein in muscle function, we decided to contrast its expression in normal and dystrophic cells after electrical stimulation. We used normal RCMH and dystrophic RCDMD human skeletal muscle cell lines as experimental models, and QPCR for quantitative analysis.

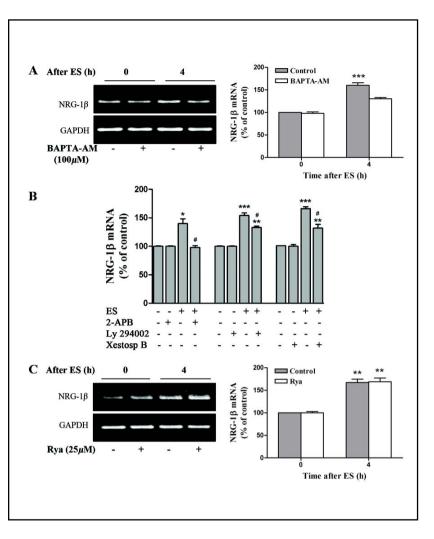
Total RNA from RCMH and RCDMD myotubes was obtained 4 h post-electrical stimulation. Our results, normalized to GAPDH expression, indicate that electrical stimulation induces a significant increase in NRG-1 $\beta$  mRNA level in RCDMD cells ( $100 \pm 3\%$  to  $250 \pm 60\%$ , n=3), but has no effect on RCMH cells at this time, in which basal expression remains unchanged ( $100 \pm 16\%$  to  $123 \pm 26\%$ , n=3) [Fig. 1B].

In order to establish the time course of NRG-1 $\beta$  gene expression evoked by depolarization, RCMH and RCDMD cells were electrically stimulated, changed to



**Fig. 3.** Electrical stimulation increases NRG-1 $\beta$  protein level in RCDMD cell lines. RCDMD myotubes were electrically stimulated and maintained in resting medium for the times indicated. Proteins were isolated and analyzed by Western blot. (A) Representative gel of NRG-1 $\beta$  and actin inmunoblot. (B) Results were normalized to actin protein level and are presented as a percentage of untreated control cells (100%) (mean  $\pm$ S.E; n=3). \*P<0.05 ANOVA followed by Dunnett's multiple comparison test.

Fig. 4. Slow calcium transient involvement in NRG-1ß mRNA increased levels, in RCDMD cell line. Dystrophic cells were depolarized in the presence of different pharmacological agents. After a 30 min preincubation period with or without these agents, myotubes were depolarized and then maintained in resting medium for 4 h. Inhibitors were present during the whole depolarization period. NRG-1\beta mRNA levels were analyzed by semiquantitative RT-PCR after electrical stimulation (ES). (A) BAPTA-AM effect. Characteristic agarose gel of RT-PCR products from cells depolarized in the presence of either 100 µM BAPTA-AM or vehicle (20% pluoronic acid in DMSO). Results were normalized to GAPDH expression and expressed as a percentage of control (100%; mean  $\pm$  S.E, n=3). \*\*\*P<0.001 vs corresponding control, evaluated by Bonferroni's test. (B) IP, pathway inhibitors effects. Dystrophic cells were depolarized in the presence of either 50 µM 2-APB, 40 µM Ly 294002, 5 µM Xestospongin B (Xestosp B), or vehicle (ethanol for 2-APB, DMSO for Ly 294002 and Xestospongin B). Bars represent mean ± S.E, n=3. \*P<0.05; \*\*P<0.01; \*\*\*P<0.001 vs corresponding non-depolarized control; #P<0.05 vs depolarized conditions, evaluated Bonferroni's test. (C) Ryanodine effect. Characteristic agarose gel of RT-PCR products from cells depolarized in the presence of either 25 µM ryanodine or vehicle (ethanol). Bars represent mean ± S.E, n=3. \*\*P<0.01 vs corresponding control, evaluated by Bonferroni's test.



resting conditions and collected for semiquantitative RT-PCR analysis at different times. Results were normalized to GAPDH expression.

We observed that depolarization of RCDMD cells produces a transient increase on NRG-1 $\beta$  mRNA levels, compared with non-depolarized controls, reaching a 1.8 fold maximal stimulation 4 h after treatment (186 ± 24%, n=3). Electrical stimulation of RCMH cells has not effect on NRG-1 $\beta$  mRNA levels at all times studied (Fig. 2A and B).

In addition, we observed that the effect on RCDMD cells was abolished by actinomycin D (Fig. 2C), suggesting that up-regulation occurs by stimulation of NRG-1 $\beta$  transcriptional activity.

Electrical stimulation increases NRG-1  $\beta$  protein level in RCDMD cells

Based on preceding results, we analyzed whether observed increase in NRG-1β mRNA level in dystrophic

cell line goes together with a raise in protein quantity. RCDMD cells were electrically stimulated, changed to resting conditions and then collected at different times. Whole cells lysates were analyzed by Western blot using selective antibodies against NRG-1 $\beta$  (40 kDa). Results were normalized to actin expression.

Our results revealed a significant increase in NRG-1 $\beta$  protein level in depolarized cells, reaching a 2-fold maximal level (206  $\pm$  28%, n=3), at 6 h after stimulation (Fig. 3).

Calcium requirement for NRG-1 $\beta$  induction: role of intracellular  $Ca^{2+}$ 

To investigate intracellular  $Ca^{2+}$  involvement in NRG-1 $\beta$  gene expression, we made use of the cell-permeable  $Ca^{+2}$  chelator BAPTA-AM. Preloading of RCDMD cells with 100  $\mu$ M BAPTA-AM for 30 min under resting conditions, followed by electrical stimulation in the presence of BAPTA-AM, resulted in an inhibition

on NRG-1β mRNA increased levels evoked by depolarization (Fig. 4A), suggesting intracellular Ca<sup>2+</sup> participation in NRG-1β gene expression.

Depolarization-induced slow Ca<sup>2+</sup> transients

increase NRG-1β mRNA levels in RCDMD cells Ca<sup>2+</sup> increase induced by high K<sup>+</sup> depolarization or electrical stimulation of skeletal muscle cells involves at least two components with different kinetics, the fast one is associated to RyR, and the slower transient is mediated by an intracellular IP<sub>3</sub> increase. Slow component of Ca<sup>2+</sup> increase evoked by depolarization is blocked by compounds that interfere with the IP<sub>3</sub> system, such as 2-APB, inhibitor of IP<sub>3</sub>-mediated Ca<sup>2+</sup> release, Ly 294002, a phosphatidylinositol 3-kinase (PI3K) inhibitor, and

Xestospongin B, an IP<sub>3</sub>R blocker [23, 37], whereas high concentrations of Ryanodine (Rya) eliminate just the initial

fast Ca+2 increase, while the slow Ca2+ transient is

preserved [38].

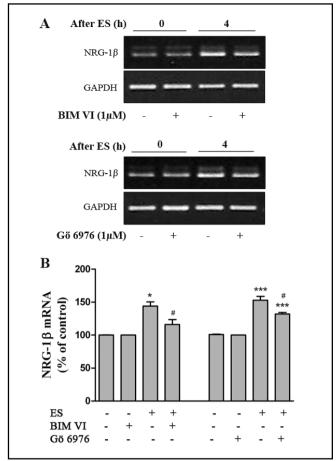
In order to define which component participates on NRG-1 $\beta$  induction in dystrophic muscle cells, we used specific inhibitors that selectively abolish one of them. Dystrophic myotubes were incubated separately with either 50  $\mu$ M 2-APB, 40  $\mu$ M Ly 294002, 5  $\mu$ M Xestospongin B or vehicle (Fig. 4B). Treatment of RCDMD myotubes with 2-APB resulted in complete inhibition of maximal induced NRG-1 $\beta$  expression at 4 h (140  $\pm$  14% to 98  $\pm$  5%, n=3), whereas partial inhibition was observed after exposure to Ly 294002 (154  $\pm$  8% to 133  $\pm$  4%, n=3) or Xestospongin B (166  $\pm$  6% to 132  $\pm$  11%, n=3) [Fig. 4B].

Treatment of myotubes with 25  $\mu M$  Rya, did not prevent NRG-1 $\beta$  mRNA induction observed in depolarized cultures (Fig. 4C).

These experiments, as a whole, suggest that  $IP_3$ -mediated  $Ca^{2+}$  release associated with the slow  $Ca^{2+}$  wave is needed for triggering the cascade leading to NRG-1 $\beta$  expression, but other signalling pathways might also be involved in the process.

 $Ca^{2+}$ -dependent PKC isoforms are involved in NRG-1 $\beta$ -induced expression in depolarized RCDMD cells

We have previously reported that  $IP_3$ -dependent  $Ca^{2+}$  signals are involved in the activation and translocation of a  $Ca^{2+}$ -dependent PKC isoform (PKC $\alpha$ ) to the nucleus [36]. Although it has been demonstrated that PKC activation promotes NRG-1 cleavage and release of the extracellular EGF-like domain [39], their involvement in NRG-1 expression has not been described.



**Fig. 5.** Ca<sup>2+</sup>-dependent PKC isoforms are involved in NRG-1β-induced expression in depolarized RCDMD cells. Cells were depolarized in the presence of PKC inhibitors. NRG-1β mRNA levels were analyzed by semiquantitative RT-PCR at 4 h after electrical stimulation (ES). (A) Characteristic agarose gel of RT-PCR products from cells depolarized in the presence of either BIM VI, Go¨6976 or vehicle (DMSO) (n=3). (B) Results were normalized to GAPDH expression and expressed as a percentage of corresponding non-depolarized control (100%; mean ± S.E, n=3). \*P<0.05; \*\*\*P<0.001 vs correspondent non-depolarized control; #P<0.05 vs depolarized conditions, evaluated by Bonferroni´s test.

To study the participation of PKC in NRG-1 $\beta$  gene expression, dystrophic cells were depolarized in the presence of either 1  $\mu$ M BIM VI, a general inhibitor of PKC isoforms or 1  $\mu$ M Gö 6976, a specific inhibitor of Ca<sup>2+</sup>-dependent PKCs. Our results show a significant decrease in up-regulated NRG-1 $\beta$  mRNA levels at 4 h post-stimulation with both inhibitors (144  $\pm$  11% to 116  $\pm$  13% for BIM VI, n=3; 153  $\pm$  10% to 132  $\pm$  4% for Gö 6976, n=3), suggesting that Ca<sup>2+</sup>-dependent PKC isoforms could be needed for activation of NRG-1 $\beta$  expression evoked by depolarization [Fig. 5].

#### Discussion

Here we provide evidence that membrane potential changes, induced by electrical stimulation, result in significant up-regulation of genes encoding NRG-1 isoforms  $\beta$  and  $\gamma$  in dystrophic RCDMD cells. We demonstrated that depolarization increases NRG-1 $\beta$  mRNA and protein levels in this cell line. We ascertain the role of depolarization induced slow Ca²+ transients as an early signal leading to NRG-1 $\beta$  expression in dystrophic cells. Our results suggest that Ca²+ released from IP₃-sensitive intracellular stores participates in NRG-1 $\beta$  mRNA induction and that Ca²+-dependent PKC isoforms are involved in the process.

Neuregulin-1 (NRG-1) growth factor was initially described as a neurotrophic factor involved in neuromuscular junction formation in skeletal muscle, but recently it has emerged as a myokine, with relevant effects on myogenesis, muscle metabolism and regeneration, and as a strong candidate to transduce muscle adaptation to chronic exercise [40, reviewed in 14]. Furthermore, NRG-1 is been presently explored as a therapy for DMD [41] due to its ability to activate utrophin promoter, increasing utrophin mRNA levels in cultured myotubes [9]. It has been reported that intraperitoneal injections of a small peptide region of the NRG-1 ectodomain up-regulates utrophin expression and improves dystrophic phenotype in *mdx* mice [11].

Initially we focused our study on the effect of membrane depolarization on global gene expression in dystrophic RCDMD cells. Electrical stimulation resulted in 150 differentially expressed genes compared to non-stimulated cells at 4 h. Among these it was particularly interesting to find that two NRG-1 isoforms ( $\beta$  and  $\gamma$ ) appear within the ten highest up-regulated genes.

Taking into account the important biological effects of NRG-1 in the muscle and its potential clinical implication in DMD, we focused our study on the regulation of NRG-1 expression, specifically on NRG-1 $\beta$  isoform, that displays a higher affinity for NRG receptor.

Time course experiments revealed that electrical stimulation induces a transient increase of NRG-1 $\beta$  mRNA levels in RCDMD cells, with a maximum at 4 h post-stimuli. We observed that depolarization had not effect on NRG-1 $\beta$  expression in RCMH cells treated with the same procedure. Western blot analysis of stimulated RCDMD cells demonstrates that observed increase in NRG-1 $\beta$  mRNA levels was followed by actual enhancement of the corresponding protein.

Differential NRG-1β expression in dystrophic vs nor-

mal cells could be explained by dissimilarities in IP<sub>3</sub>Rs and slow Ca<sup>2+</sup> signals kinetic between both cell lines. We have previously demonstrated that IP<sub>3</sub>-induced Ca<sup>2+</sup> signals, which appear most prominently in the nuclei, are involved in the regulation of several transcription-related events following membrane depolarization in normal muscle cells [23, 24, 26-28].

We have recently reported an abnormal expression and distribution of IP<sub>3</sub>Rs in human biopsies of DMD patients compared to normal human samples; these differences are also apparent when comparing RCDMD *vs* RCMH muscle cells. In addition, we described that IP<sub>3</sub>-dependent slow Ca<sup>2+</sup> signals induced by tetanic stimulus are significantly larger and faster in RCDMD than in RCMH cells [32].

To further investigate the involvement of  $Ca^{2+}$  transients in NRG-1 $\beta$  gene expression in dystrophic cells, RCDMD were electrically stimulated in the presence of specific inhibitors. We demonstrated that NRG-1 $\beta$  gene expression was inhibited in the presence of BAPTA-AM, an intracellular  $Ca^{2+}$  chelator, whereas depolarization of myotubes performed in the presence of high concentrations of Rya, that eliminates just the initial fast  $Ca^{2+}$  increase, did not prevent NRG-1 $\beta$  mRNA induction observed in depolarized cultures.

Concerning the effect of IP<sub>3</sub>-dependent slow Ca<sup>2+</sup> transients inhibitors, we found that 2-APB treatment resulted in complete inhibition of maximal induced NRG-1β expression at 4 h, whereas partial inhibition was observed after exposure of myotubes to either Ly 294002 or Xestospongin B. 2-APB inhibits IP<sub>3</sub>-mediated Ca<sup>2+</sup> signals in various cell systems [42, 43], including depolarized myotubes [22, 38], but its specificity has been a matter of discussion [44, 45]. However, results obtained after Ly 294002 or Xestospongin B treatment, operating by a different mechanism, support 2-APB effect and give evidence for the involvement of Ca2+ released from IP3sensitive intracellular stores in the regulation of NRG-1B transcriptional activity. Taken together, our results suggest that IP<sub>3</sub>-dependent slow Ca<sup>2+</sup> signals induced by depolarization stimulate NRG-18 transcription in RCDMD cells, although other signalling pathways might be involved in the process.

Accumulating evidence suggests that integral DAPC components are implicated in signalling in DMD [46]. Thus, it is likely that loss of DAPC proteins in cell membrane affect in some way the regulation of  $Ca^{2+}$  transients and subsequently NRG-1 $\beta$  gene expression in electrically stimulated dystrophic cells. In fact, experiments performed using SolC1(-) dystrophin deficient myotubes,

and SolD(+) transfected myotubes for mini-dystrophin expression, both originated from the same cell line, have demonstrated that Ca<sup>2+</sup> rise evoked by depolarization is higher in SolC1(-) than in SolD(+) myotubes [31]. Analysis of the kinetics of Ca<sup>2+</sup> rise, reveals that IP<sub>3</sub>-dependent slow Ca<sup>2+</sup> release is increased in SolC1(-) compared to SolD(+), suggesting an inhibitory effect of mini-dystrophin on slow Ca<sup>2+</sup> transients. Moreover, it has been demonstrated that IP<sub>3</sub> production after depolarization is significantly elevated in SolC1(-) and that the presence of mini-dystrophin under the membrane leads to reduced IP<sub>3</sub> production [31].

Our laboratory has reported that  $IP_3$ -dependent  $Ca^{2+}$  signals regulate the activation and translocation of a  $Ca^{2+}$ -dependent PKC isoform (PKC $\alpha$ ) to the nucleus, in depolarized myotubes [36]. PKCs are a family of serine/threonine kinases, classified into three main subgroups based on their amino acid sequence and lipid dependent activation requirements. Conventional PKC isoforms require  $Ca^{2+}$  and diacylglycerol (DAG) for activation, the novel PKC isoforms are  $Ca^{2+}$ -independent but DAG-dependent, and atypical PKC isoforms are unresponsive to DAG and/or  $Ca^{2+}$  [47].

To investigate a possible involvement of PKC on NRG-1β transcriptional activity in our experimental model, we treated RCDMD cells with a general inhibitor of PKC and with a specific inhibitor for Ca<sup>2+</sup>-dependent isoforms. Our results suggest that Ca<sup>2+</sup>-dependent PKC isoforms are needed for activation of NRG-1β expression.

NRG-1 promoter region has been characterized in breast cancer cells, and a NF- $\kappa$ B consensus sequence described as Ca<sup>2+</sup> responsive regulatory element in other promoters has been identified [48]. It has been reported that membrane depolarization of skeletal muscle cells induces the activation of nuclear transcription factor NF- $\kappa$ B by a mechanism that involves sequential changes in intracellular Ca<sup>2+</sup> level, mediated by both RyR and IP<sub>3</sub>Rs [49]. Based on these antecedents, it is possible that NRG-1 $\beta$  gene expression induced by electrical stimulation could be mediated by NF- $\kappa$ B activation in the dystrophic cell line. Further studies are needed in order to assess a possible role of NF- $\kappa$ B in NRG-1 $\beta$  gene expression.

Our findings can be inserted in a mechanistic model, previously reported by our group, depicting the pathways that link membrane depolarization and intracellular Ca<sup>2+</sup> increase to gene expression in skeletal muscle cells. This model has been described in normal skeletal muscle cells and includes receptors and pathways known to be

involved in IP<sub>3</sub>-generated Ca<sup>2+</sup> signals. The signalling pathway begins in the dihydropyridine receptor, which by a mechanism that involves ATP release and purinergic receptors [50], via a G protein [51], activates PI3 kinase and PLC to produce IP<sub>3</sub>. It diffuses into the cytosol and reaches IP<sub>3</sub>Rs located both at the sarcoplasmic reticulum membrane and at the nuclear envelope, inducing Ca<sup>2+</sup> release [24]. As a consequence several Ca<sup>2+</sup>-dependent mechanisms, including different kinases and transcription factors [24, 26], are activated and lead to regulation of gene expression [26-28].

It has been postulated that the absence of dystrophin under the membrane increases  $IP_3$  production in depolarized dystrophic cells [31], generating larger and faster slow  $Ca^{2+}$  transients [31, 32]. We propose that these signals stimulate  $Ca^{2+}$ -dependent PKC isoforms and its translocation to the nucleus [36], increasing NRG-1 $\beta$  expression in dystrophic cells.

In summary, our results point out to an important role of slow Ca<sup>2+</sup> transients evoked by electrical stimulation in the activation of pathways that couple excitation to NRG-1β expression in dystrophin-deficient RCDMD cell lines. To our knowledge, this is the first report describing the involvement of IP<sub>3</sub>-mediated slow Ca<sup>2+</sup> signals on NRG-1 transcriptional activity in dystrophic skeletal muscle cells. Further studies using IP<sub>3</sub>R over-expression, knockout or knockdown with interference RNA could provide additional proofs on the subject.

The strong similarities between dystrophin and utrophin encouraged the hypothesis that utrophin up-regulation could lead to the functional replacement of dystrophin in the sarcolemma. Since NRG-1 pathway induces utrophin expression, the understanding of the molecular events that regulate its expression will give new insights to the design of a therapeutic strategy in order to potentiate muscle survival and regeneration in DMD.

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