Antimyogenic Effect of SARS-CoV Spike Protein in C2C12 Myoblasts

Chih-Fong Chou[*,1,2], Geetha Mahadevappa[1,3], Wanjin Hong[1] and Yee-Joo Tan[1]

[1]*Institute of Molecular and Cell Biology, 61 Biopolis Drive, Proteos, 138673, Singapore*

[2]*Current Address: Waseda-Olympus Bioscience Research Institute, 11 Biopolis Way, Helios # 05-01/02, 138667, Singapore*

[3]*Current Address: Pharmaceutical Services Corporation, 26 Boonlay Way, #01-92 TradeHub 21, 609970, Singapore*

Abstract: C2C12 myoblasts serve as well-established model system to study myogenesis, as they fuse to form multinucleated myotubes. Severe acute respiratory syndrome coronavirus (SARS–CoV) spike (S) protein plays a crucial role in viral entry. Exogenous expression of S protein in C2C12 myoblasts inhibits the formation of myotubes. Global changes in gene expression were studied in C2C12 cells expressing S protein using oligonucleotide microarray analysis. The expression profile showed that, most of the myogenic marker genes were downregulated. Next, we used RT-PCR analysis to reexamine some downregulated and upregulated genes. To further study the antimyogenic effects induced by the S protein, we introduced antisense *Plf* (proliferin), an upregulated gene, into the antimyogenic cells. Antisense *Ace2* (angiotensin-converting enzyme 2), the cellular receptor of S protein, was also introduced into C2C12 myoblasts. Results indicated that antimyogenic effect induced by S protein was partially rescued in cells expressing antisense *Plf*, while C2C12 cells expressing antisense *Ace2* showed upregulation of *Plf*.

Keywords: Ace2, microarray, myogenesis, proliferin.

INTRODUCTION

Highly contagious SARS–CoV affected around 30 countries with more than 8000 cases of infection resulting in 800 fatalities (http://www.who.int/csr/sars/country/en/). Spike protein (S) of this virus was responsible for virus binding, fusion and entry, hence became a main focus of study as a major inducer of neutralizing antibodies against the disease. Functional studies in S protein were mainly concentrated on the interaction with ACE2 (angiotensin-converting enzyme 2) receptor as a preliminary requirement for cell-viral membrane fusion. It has been demonstrated that S protein decreases surface level expression of human and mouse overexpressed ACE2 in 293 cells and deteriorated acute lung failure upon *in vivo* injections [1].

Myogenesis is an important process during embryonic development and muscle regeneration. Murine skeletal muscle cells (C2C12 myoblasts), are known to have pluripotent mesenchymal character, which allows them to differentiate into adipocyte [2] and osteoblast [3] lineages. C2C12 myoblasts are extensively used to study differentiation of skeletal myogenesis [4]. We have previously established a method for quantifying the cell-cell fusion mediated by S-ACE2 interaction [5], C2C12 cell line stably expressing S (C2C12-SG) was used to confirm the process. The key stage of myogenesis involves the fusion of myoblasts to form myotubes. Hence, we explored the effects of S protein on cell-cell fusion during myogenesis. Muscle weakness and elevated creatine kinase levels were shown to be associated with SARS [6]. Few cases of rhabdomyolysis associated with probable SARS cases were reported as well [7]. However, the nature and cause of myopathy in association with SARS remains unknown. In this paper, we show that the S protein inhibits myogenesis by upregulating *Plf* (proliferin). ACE2 is known to balance the role of angiotensin-converting enzyme (ACE) in renin-angiotensin system (RAS) in conversion of angiotensin II (AngII) to Ang 1-7, a vasodilator and helps in decreasing blood pressure [8]. The existence of RAS constituents in skeletal muscle, including ACE, Ang II receptor, and local de novo Ang II production [9] had been reported, suggesting existence of RAS in myogenesis. Therefore, in this study we were interested in understanding the antimyogenic effect of S protein and additional factors required to facilitate the effect as well. We were also interested in understanding whether the antimyogenic effect of S protein was responsible for downregulation of *Ace2* in C2C12 cells.

MATERIALS AND METHODOLOGY

Cell Culture

C2C12 cells were purchased from ATCC (CRL 1772: Bethesda, MD), and cultured in a humidified incubator at 37 ^{o}C with 5 % CO2 in DMEM (growth medium, GM) containing 1 g L^{-1} glucose, 1X Pen/Strep (0.1 mg ml^{-1} streptomycin, 100 U ml^{-1} penicillin, Sigma) and 10 % FBS (HyClone). C2C12-SG and C2C12-E2G were selected using 1 mg ml^{-1} G418 (Gibco BRL) while C2C12-ACE2R cells were selected using 0.5 mg ml^{-1} of Hygromycin B (Roche). C2C12-SG-MyoD, C2C12-SG-PLFR and C2C12-SG-ZAKI-4R cells were grown in medium containing both the antibiotics. To induce differentiation, nearly confluent C2C12 cells were incubated in DMEM containing 10 % heat-inactivated horse

*Address correspondence to this author at the Waseda-Olympus Bioscience Research Institute, 11 Biopolis Way, Helios #05-01/02, 138667, Singapore; Tel: 65-64789721; E-mail: chouchihfong@yahoo.com

1874-2793/09

serum (Invitrogen) and 1X Pen/Strep (differentiation medium, DM) for 7 days unless addressed specifically.

Analysis of Gene Expression by Oligonucleotide Microarray and RT-PCR

For microarray expression analysis, total RNA was extracted from C2C12 and C2C12-SG cells cultured in GM or DM using the RNeasy Kit (Qiagen). RNA samples (10 μg each) were processed, labeled and hybridized to Affymetrix MOE 430A GeneChips according to standard protocols available from Affymetrix. For RT-PCR analysis, total RNA was extracted from C2C12 myoblasts and derivative cell lines using Trizol reagent (Gibco BRL) following manufacturer's protocol. 1 μg of total RNA from each sample was reverse transcribed using Superscript II RNase H^- reverse transcriptase (Invitrogen). 1 μl of the product was then used as the template for PCR amplification using specific primers listed in Supplementary Data (SD) 1 Table **1**. PCR was performed using HotStar Taq DNA polymerase (Qiagen) under following conditions: 95 ºC for 2 min, followed by 33 cycles of 95 ºC for 30 sec, 55 ºC for 30 sec, 72 ºC for 45 sec, and a final extension at 72 ºC for 5 min. Amplification of *Ace2* was an exception as it required 42 cycles. All RT-PCR were repeated more than three times for consistent results. *Myod*, or anti-sense *Ace2* (*ACE2R*), *Plf* (*PLFR*) and *ZAKI-4* (*ZAKI-4R*) were amplified using Expand High Fidelity PCR System (Roche), and same PCR conditions were used except for *Myod* which required extension of 90 sec at 72°C. Representative RT-PCR products were sequenced to confirm their identity. PCR template for *Myod* was from mouse skeletal muscle cDNA [10], for *PLFR* and *ZAKI-4R* from C2C12-SG cDNA and for *ACE2R* from C2C12 cDNA. Primers used for construction and comparison of *Myod*, *ACE2R*, *PLFR* and *ZAKI-4R* are listed in SD1.

Plasmid Constructs and Establishment of Stable Cell Lines

C2C12-SG and C2C12-E2G cell lines were established as previously reported [5]. Plasmid pAM (SD1) containing *Myod*, *PLFR*, *ZAKI-4R* and *ACE2R* was transfected into C2C12-SG or C2C12 cells using lipofectamine (Invitrogen). Stable transfectants C2C12-ACE2R were selected on Hygromycin B medium while C2C12-SG-MyoD, C2C12-SG-PLFR and C2C12-SG-ZAKI-4R were selected on medium containing both G418 and Hygromycin B. C2C12-SG derivative cell lines were established by pooling maximum of 10 colonies and surface expression of S protein was observed using cell-cell fusion assay [5].

RESULTS AND DISCUSSION

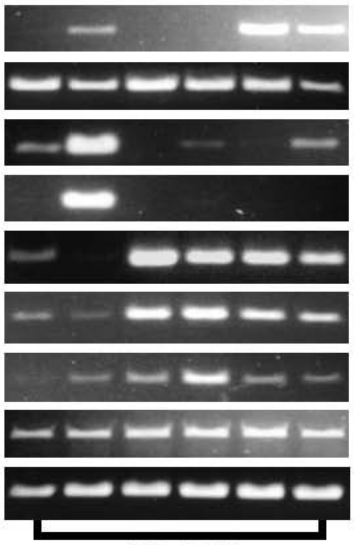
Defective Myogenic Phenotype of C2C12-SG Cells

Myogenesis of C2C12 cells is characterized by growth factor depletion (cultured in DM) and cell cycle exit followed by myoblast cell-cell fusion to form myotubes. C2C12-SG cell line, cultured in DM did not form myotubes where as cell line C2C12-E2G [5] expressing ectodomain of Hepatitis C virus E2 protein showed normal myogenesis (SD1 Fig. **1**). C2C12-SG and C2C12-E2G cells express ectodomains of S [1,173 amino acid (a.a.) residues] and E2 (310 a.a. residues) respectively, apart from that both the fusion proteins were identical. Hence, we conclude that the ectodomain of S protein was solely responsible for myogenic inhibition in C2C12-SG cells.

Differential Myogenic Gene Expression in C2C12 and C2C12-SG Cell Lines

Myogenesis involves dynamic and complex set of processes. Microarray technology was exploited to analyze the

C2C12		C2C12-SG			
GM (A)	DM (B)	GM (C)	DM (D)	Accession no.	
688	**1961**	57	14	NM_010866.1	*Myod*
13	6	445	**1085**	NM_008656.1	*Myf5*
210	**2791**	157	67	NM_007710.1	*Ckm*
65	**4623**	8	2	AJ002522.1	*Myh1*
400	110	**16384**	5925	X75557.1	*Plf*
126	107	**6874**	6124	NM_011581.1	*Thbs2*
218	377	805	**2497**	AB061524.1	*ZAKI-4*
9	7	649	**653**	M20480.1	*Nfl*
1809	**4946**	2131	4184	AA738859	*Des*



Microarray signals

RT-PCR

Fig. (1). Comparative analysis of microarray and RT-PCR results for nine genes. RNA samples for both analyses were prepared from C2C12 (**A** & **B**) and C2C12-SG (**C** & **D**) cells cultured in GM and DM respectively. RNA samples from C2C12-SG-MyoD cells are shown in lane **E** & **F** represent cells grown in GM and DM respectively. Bolded number represent highest microarray signal of the gene.

differential expression of genes in C2C12 and C2C12-SG cells grown in GM or DM (SD2). Microarray analysis between C2C12-SG and C2C12 cells cultured in DM medium showed 1,188 genes (SD2-1) have log2-ratios (LR) below -1 (two fold downregulated) and 944 genes (SD2-2) above 1 (two fold upregulated). Skeletal muscle genes such as *Tncs* (troponin C, fast skeletal; LR-10.4), *Myh1* (myosin heavy chain 2X, LR -10.2), *Tnni1* (troponin I, skeletal, slow 1; LR -10.2) and *Myh2* (myosin, heavy polypeptide 2; LR-10) were the most downregulated genes in DM cultured C2C12-SG cells. *Myod* (LR-7), one of the key players in myogenesis, was strongly downregulated as well. Our data indicated that the expression of myogenic marker genes in C2C12-SG cells were remarkably inhibited, however, the cell line still retained myoblast characters as seen by the expression of *Des* (desmin), the gene for muscle-specific intermediate filament protein. The reliability of the microarray data (SD2) was further confirmed by studying the expression of enzymes involved in TCA cycle to confirm that relevant signals among all 4 samples were uniform.

Rhabdomyolysis refers to disintegration of striated muscle. Pathogenesis of myolysis is often associated with bacterial, fungal and viral infections. This is thought to be the result of direct cell invasion and cellular degeneration by the pathogen. Influenza A and B are most common viruses associated with myolysis, studies estimate that upto 25% of AIDS (Acquired immuno deficiency syndrome) patients suffer from a myopathic disease that may be complicated by rhabdomyolysis [11].

It has been shown that Myod plays a key role in conversion of normal dermal fibroblasts and chondroblasts into elongated post-mitotic mononucleated striated myoblasts [12]. It has also been reported that overexpressed MyoD was able to rescue the myogenic defect [13]. As a first attempt to rescue the myogenesis in C2C12-SG cells, we developed another cell line C2C12-SG-MyoD that expressed *Myod* ectopically, however the myogenic phenotype could not be rescued. Amongst all the up and down regulated transcripts, we further selected upregulated *Plf* (LR 5.6), *Thbs2* (thrombospondin 2, LR 5.4), *ZAKI-4* (calcineurin inhibitory protein, LR 2.3) and *Nfl* (neurofilament-L, LR 5.6) genes and myogenic markers *Myod*, *Myf5* (LR 7.7), *Ckm* (muscle type creatine kinase, LR -4.8), *Myh1* and *Des* genes for confirmation by RT-PCR. However, RT-PCR amplification results of *Myf5* and *Nf1* did not match with the microarray signals (Fig. **1**) as RT-PCR amplifications showed the relatively constant level of both the RNA samples. Both microarray and RT-PCR analyses correlated well with respect to upregulated genes *Plf*, *Thbs2* and *ZAKI-4*, as well as downregulated genes *Myod*, *Ckm* and *Myh1* (Fig. **1**, lanes **A**-**D**). The ectopic *Myod* expression reduced the upregulation of *Plf*, *Thbs2* and *ZAKI-4* when grown in DM. The downregulation of *Ckm* was also similarly reversed, however *Myh1* remained unaffected (Fig. **1**, lanes **E**, **F**).

We also checked expression of other genes that are involved in myogenesis or important in muscle development by RT-PCR, most of the genes tested were very weak or absent in the microarray data such as *Mstn*, *Pax7* and *Agtr2* (primers are listed in SD1 Table **1**). We did not observe any signals relative to these genes either from C2C12 or C2C12-SG cDNA samples, but we detected high expression levels of myostatin (*Mstn*) from mouse skeletal muscle cDNA sample (data not shown). C2C12 cells cultured in DM showed upregulation of P21, cyclin-dependent kinase inhibitor, which facilitates cell cycle withdrawal in differentiating myoblasts. Microarray data (SD2) showed that irrespective of the medium used for culturing C2C12-SG cells expressed same levels of P21 as undifferentiated C2C12 cells, however the results of RT-PCR (SD1 Fig. **2**) showed reverse P21 regulation of C2C12 and C2C12-SG cells.

Partial Myogenic Rescue of C2C12-SG Cells by Antisense *Plf*

Plf is a secreted glycoprotein in the prolactin-growth hormone family. It has been shown to partially inhibit the differentiation of C2C12 cells by reducing the level of *Myod* mRNA [14] and downregulating reporter driven expression by *Ckm* promoter [15]. ZAKI-4, inhibits calcineurin which regulates skeletal muscle differentiation. To determine the myogenesis recovering ability of C2C12-SG cells we used antisense RNA of these two upregulated genes. However, we could not establish C2C12-SG clones expressing antisense *Thbs2*.which was one of the target genes.

To drive the ectopic expression of targeted genes, promoter of *Takifugu rubripes* beta actin1 (GenBank accession no. **U37499**) was used for the expression in C2C12 or C2C12-SG cells. EGFP expression of both undifferentiated C2C12 myoblasts and differentiated C2C12 myotubes is shown in SD1 Fig. (**3**). The expressions of ectopic *Myod*, antisense *Plf* (*PLFR*) and *ZAKI-4* (*ZAKI-4R*) was driven by the promoter. C2C12-SG-PLFR and C2C12-SG-ZAKI-4R are two C2C12-SG derivative cell lines expressing *PLFR* or *ZAKI-4R*. Our RT-PCR results showed that antisense genes were expressed only in modified cell lines but not in their respective controls (Fig. **2A**). Expression of *Myod*, *Ckm*, *Myh1*, *Plf* and *Myf5* in cell lines C2C12-SG, C2C12-SG-PLFR and C2C12-SG-ZAKI-4R cultured in DM (Fig. **2B**) were studied as a next step. Among the three downregulated myogenic genes *Myod*, *Ckm* and *Myh1* studied, only *Ckm* was fully recovered in C2C12-SG-PLFR cells while *Myod* was partially recovered where as *Myh1* changed trivially. The myogenesis inhibition in C2C12-SG cells were partially rescued with *PLFR* and indicating that downregulation of *Ckm* in C2C12-SG cells is certainly linked to the expression of *Plf* which is in concordance with *Ckm* promoter studies [15]. As for the *Plf* expression, C2C12-SG-PLFR had the lowest level of expression when compared to other two cell lines C2C12-SG and C2C12-SG-ZAKI-4R, therefore the expression of *PLFR* and *Plf* were compared (Fig. **2C**) using cDNA samples from C2C12-SG-PLFR cells. C2C12-SG-PLFR cells cultured in DM showed partial recovery of myogenic phenotype (Fig. **2D**). Shorter and lesser myotubes differentiated from C2C12-SG-PLFR culture which, may be due to partially recovered myogenic genes. Our data suggested that the myogenic defect in C2C12-SG culture was partly due to upregulated *Plf* or more efficient *Plf* downregulation is required for complete recovery of myogenesis.

Upregulation of *Plf* in *Ace2* Antisensed C2C12 Cells

Ectodomain of S protein is much bulkier than ectodomain of E2 protein by 863 a.a residues. Because of this major difference between C1C12-SG and C2C12-E2G cell

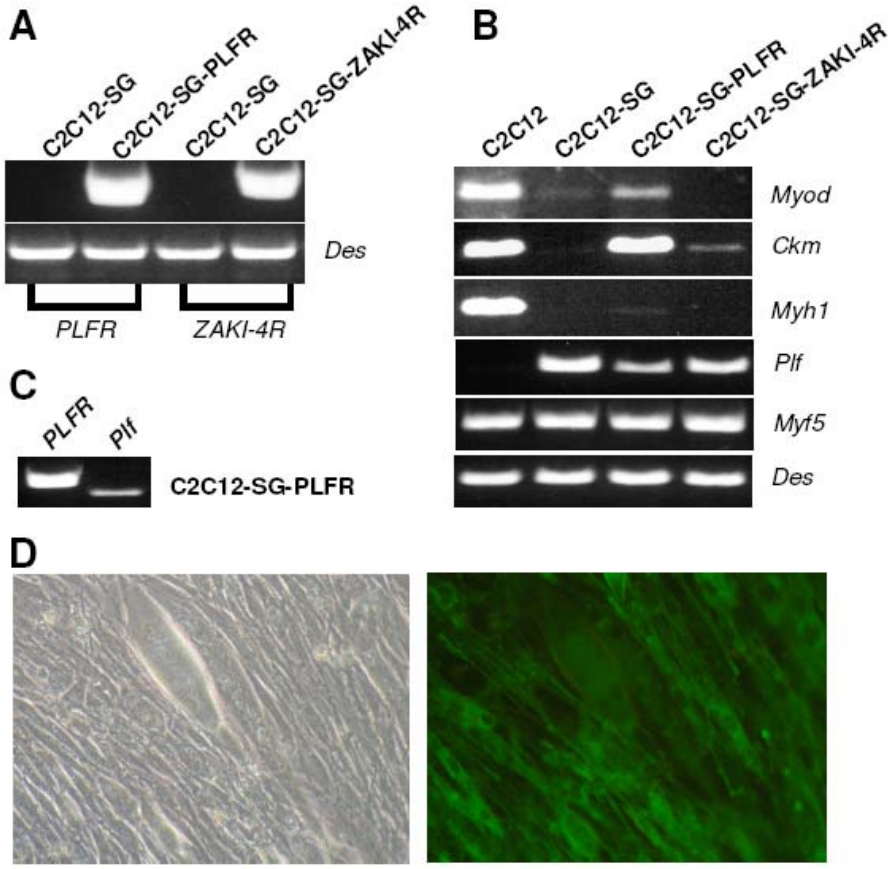


Fig. (2). Expression of (**A**) *PLFR* (antisense *Plf*) and *ZAKI4R* (antisense *ZAKI-4*) in C2C12-SG-PLFR and C2C12-SG-ZAKI-4R cells, (**B**) expressions of *Myod*, *Ckm*, *Myh1*, *Plf*, *Myf5* genes in C2C12, C2C12-SG, C2C12-SG-PLFR and C2C12-SG-ZAKI-4R cells, (**C**) *PLFR* and *Plf* in C2C12-SG-PLFR cells after RT-PCR. *PLFR* and *Plf* (SD1) has 70 nt difference between them. *Des* was used as the internal control for (**A**) and (**B**). (**D**), Shorter myotube formation from C2C12-SG-PLFR cells cultured in DM. The photos were taken under 400 x magnifications. Left panel indicates brightfield and right panel photo indicates fluorescence microscopy fitted with FITC filter. The presence of green fluorescence is due to the S protein tagged with EGFP at C-terminus.

```
hACE2: GIRDRKKKNKA*R*SG*E*NP*Y*ASIDI**S**KG**E**NNPGFQNTDDVQTSF
mAce2: GIKGRKKKNE**T***K***R****E***NP*Y*DSMDIGKGESNAGFQNSDDAQTSF
cAce2: GIRNRRKNNQA*R*SE*E*NP*Y*ASVDL**S**KG**E**NNPGFQHADDVQTSF
bAce2: GIRNRRKKNQA**S**SE**E**NPYGSVDLNKGENNSGFQNIDDVQTSL
gAce2: GQRDKRKKARGRANEAG**S**NC**E**VNPYDEDGR**S**N**K**GFEQSEETQTSF
xAce2: GYKERKTKQK**S**QG**D**KEAVELSQNANNPEPATLEITQENTGQMNKAF
fAce2: GVRERRKKPIAVDNPYIDNDGHMNKAYDD**S**DN**E**QTGF
tAce2: GVRERRKKPKAVHNPYIEDDGQINKAYDD**S**DN**E**QTGF

hACE: **S**Q**R**LF**S**I**R**HRSLHRHSHGPQFG**S**EV**E**LRHS
mAce: AHRLYNIRNHH**S**L**R**RPHRGPQFG**S**EV**E**LRHS
rAce: AHRLYNIHNHH**S**L**R**RPHRGPQFG**S**EV**E**LRHS
oAce: **T**Q**R**LF**S**I**R**YQ**S**L**R**QPHHGPQFG**S**EV**E**LRHS
```

Fig. (3). Cytoplasmic domains of ACE2s and ACEs. The source of ACE2s is prefixed by h (human, GenBank accession no. **BAB40370**), m (mouse, GenBank accession no. **AAH26801**), c (cat, GenBank accession no. **Q56H28**), b (cattle, GenBank accession no. **AAI05341**), g (chicken, GenBank accession no. **XP_416822**), x (*Xenopus tropicalis*), f (*Fugu*) and t (*Tetraodon*). The sequences of *Xenopus tropicalis*, *Fugu*, and *Tetraodon* ACE2 are listed in the Supplementary Data 1 of [22]. ACEs are prefixed by h (human, GenBank accession no. **EAW94312**), m (mouse, GenBank accession no. **AAI10363**), r (rat, GenBank accession no. **AAP80809**) and o (rabbit, GenBank accession no. **AAA31153**; the domain of ACE in sheep, pig, horse and dog etc. are highly similar to oACE). Amino acid residues represent the consensus motif of tyrosine kinase phosphorylation sites are bolded and italiced (***K***/***R***XX***E***/***D***XX***Y***), bolded residues (**S**/**T**XX**E**/**D**) are for casein kinase II and bolded and underlined (**S**/**T**X**K**/**R**) are for protein kinase C.

lines, we suspected that S protein may impinge on the surface membrane remodeling which is very much required for myoblasts cell-cell fusion. However, microarray and RT-PCR analysis clearly showed that myogenic inhibition of C2C12-SG cells were not just morphological but was due to altered global gene expression patterns, thereby leading to the possibility of altered downstream signaling events.

RAS enzymes ACE and ACE2 have been in main focus of study with respect to their ability to regulate blood pressure in cardiovascular, kidney and lung diseases. The role of RAS in myogenesis has been studied in stimulation of hypertrophy by Ang II in C2C12 myoblasts [16]. It was demonstrated that ACE inhibitor and AT2 antagonist significantly upregulated myogenesis in differentiating C2C12 cells resulting in hypertrophic myotubes [17]. The short cytoplasmic tail of ACE at a.a. residue Ser^{1270}, phosphorylated by casein kinase II (CK2), was shown to physically interact with the kinase [18]. The phosphorylation site is involved in the regulation of enzyme shedding (cleavage/secretion). Mitogen-activated protein kinase 7 and c-Jun N-terminal kinase were also found to be associated with the cytoplasmic domain of ACE, hence in ACE signaling cascade [18]. Although ACE2 is relatively new player in RAS system, it is a well known cellular receptor of the S protein. To study the possibility of ACE2 in cell signaling, 8 ACE2 and 4 ACE sequences were compared (Fig. **3**). Protein cytoplasmic domains of these proteins from different vertebrates showed conserved phosphorylation sites of tyrosine kinase, CK2 and protein kinase C. The motifs were predicted based on Motif Scan at http://myhits.isb-sib.ch/cgi-bin/motif_scan [19]. The consensus motifs of CK2 in ACE and ACE2 are highly conserved in most, if not all, vertebrates (Fig. **3**). It has been depicted that ACE2s may also play role in signaling apart from being a peptidase. Our studies clearly indicated that the inhibition of myogenesis by S protein is associated with upregulation of *Plf*, however mechanism remain unclear. In order to determine whether inhibition of myogenesis was associated with downregulation of cell surface expression of Ace2, cell line C2C12-ACE2R, expressing antisense mouse *Ace2* (*ACE2R*), was established. *ACE2R* expression was confirmed by RT-PCR using cDNA samples of both C2C12 and C2C12-ACE2R cells (Fig. **4A**). Expression of *ACE2R* and *Ace2* from C2C12-ACE2R cDNA is shown in Fig. (**4B**). The level of *Ace2* was too low to be identified.

Expression of *Plf* in C2C12-ACE2R, C2C12, C2C12-SG and C2C12-SG-PLFR cells cultured in different differentiation conditions (GM, DM and 10 days in DM) is shown in Fig. (**4C**). Our results indicated that there was consistent low level expression of *Plf* in C2C12 whereas C2C12-SG cells showed high level expression. Whereas, C2C12-ACE2R cells cultured in DM showed time dependent increase in expression of *Plf* and reaching the levels as C2C12-SG cultured in GM while C2C12-SG-PLFR showed time dependent decrease in expression reaching the expression levels similar to C2C12 cells. Results in Fig. (**4D**) of our experiments indicated that *Ace2* mRNA levels were not only downregulated by *ACE2R* (in C2C12-ACE2R cells) but was also down regulated in cell lines expressing S protein (C2C12-SG and C2C12-SG-PLFR cell lines). Mechanism of downregulation of *Ace2* expression at transcription level by S protein is an

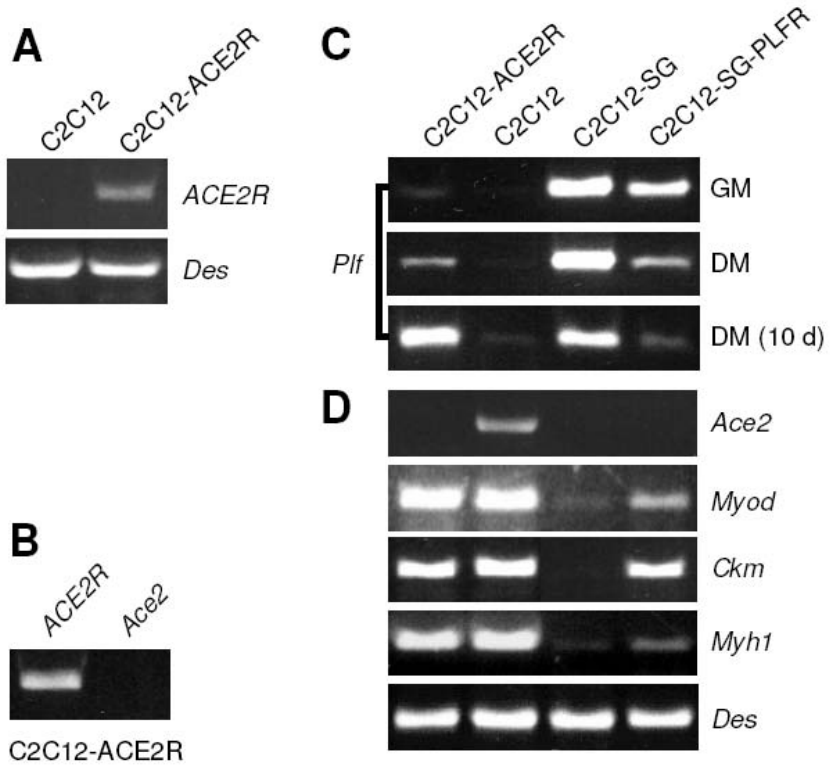


Fig. (4). Expression of (**A**) *ACE2R* (antisense *Ace2*) in C2C12-ACE2R cells, (**B**) *ACE2R* and sensed *Ace2* in C2C12-ACE2R cells, (**C**) *Plf* expressions in C2C12-ACE2R, C2C12, C2C12-SG, C2C12-SG-PLFR cells that were cultured in GM, DM or 10 d in DM, (**D**) *Ace2*, *Myod1*, *Ckm* and *Myh1* in C2C12-ACE2R, C2C12, C2C12-SG, C2C12-SG-PLFR cells cultured in DM for 10 days. *Des* was used as the internal control for (**A**) and (**D**).

interesting issue to be explored. However, C2C12-ACE2R cells, with downregulated *Ace2* and upregulated *Plf*, still differentiated, formed myotubes, and also expressed myogenic marker genes *Myod*, *Ckm* and *Myh1*. In addition, the expression level of *Plf* increased in C2C12-ACE2R cells cultured in DM for 10 d, *Ckm* was not downregulated suggesting the regulation of *ACE2R* was not fully equivalent to the regulation of S protein.

CONCLUSION

In this paper, we show that ectodomain of SARS-CoV S protein inhibits myogenesis of C2C12 myoblasts, and the effect was partially due to upregulated *Plf*. We demonstrate that the downregulation of mouse *Ace2* plays a role in upregulating *Plf*. Expression levels of *Plf*, also known as mitogen-regulated protein, is high during the transition from G1-S phase of cell cycle which prohibit myoblasts withdrawal from cell cycle, however reverse and time dependent upregulation in C2C12-ACE2R cells cultured in DM remains to be unveiled. *Msx1* had been shown to inhibit C2C12 myogenesis, it was identified to dedifferentiate C2C12 myotubes into mononucleated cells with the induced capability to redifferentiate into cells that express chondrogenic, adipogenic, myogenic, or osteogenic markers [20]. To test the hypothesis, we tried to work in same way with Tet-On system, the dedifferentiation effect did not appear suggesting the signaling roles of either *Plf* or *Ace2* are relatively downstream. Finally, severe impairment in myocardial contractility with higher AngII levels has been observed in Ace2 null mice, and this cardiac defect was completely rescued by genetic ablation (double knockouts) of Ace [21]. The antagonist of antimyogenic (Ace2 downregulated by S protein) and hypermyogenic (ACE inhibitor) effects offers an alternative angle to study.

ACKNOWLEDGEMENTS

We thank Ms. Hui Meng Soo and Dr. Jinrong Peng for performing the microarray analysis, Dr Byrappa Venkatesh for providing the promoter of Takifugu rubripes beta actin 1 and the IMCB DNA Sequencing Facility for its help in sequencing. This project was supported by the Agency for Science and Technology (A*STAR). Singapore.

ABBREVIATION

RT-PCR = Reverse transcription-polymerase chain reaction

SUPPLEMENTARY MATERIAL

This article also contain supplementary data and it can be viewed at www.bentham.org/open/toidj

REFERENCES

[1] Kuba K, Imai Y, Rao S, *et al.* A crucial role of angiotensin converting enzyme 2 (ACE2) in SARS coronavirus-induced lung injury. Nat Med 2005; 11: 875-9.

[2] Mancini A, El Bounkari O, Norrenbrock AF, *et al.* FMIP controls the adipocyte lineage commitment of C2C12 cells by downmodulation of C/EBP alpha. Oncogene 2007; 27: 1020-7.

[3] Susperregui AR, Viñals F, Ho PW, Gillespie MT, Martin TJ, Ventura F. BMP-2 regulation of PTHrP and osteoclastogenic factors during osteoblast differentiation of C2C12 cells. J Cell Physiol 2008; 216: 144-52.

[4] Andres V, Walsh K. Myogenin expression, cell cycle withdrawal, and phenotypic differentiation are temporally separable events that precede cell fusion upon myogenesis. J Cell Biol 1996; 132: 657-66.

[5] Chou CF, Shen S, Mahadevappa G, Lim SG, Hong W, Tan YJ. The use of hepatitis C virus NS3/4A and secreted alkaline phosphatase to quantitate cell-cell membrane fusion mediated by severe acute respiratory syndrome coronavirus S protein and the receptor angiotensin-converting enzyme 2. Anal Biochem 2007; 366: 190-6.

[6] Leung TW, Wong KS, Hui AC, *et al.* Myopathic changes associated with severe acute respiratory syndrome: a postmortem case series. Arch Neurol 2005; 62: 1113-7.

[7] Wu VC, Hsueh PR, Lin WC, *et al.* Acute renal failure in SARS patients: more than rhabdomyolysis. Nephrol Dial Transplant 2004; 19: 3180-82.

[8] Donoghue M, Hsieh F, Baronas E, *et al.* A novel angiotensin-converting enzyme–related carboxypeptidase (ACE2) converts angiotensin I to angiotensin 1-9. Circ Res 2000; 87: E1-9.

[9] Jones A, Woods DR. Skeletal muscle RAS and exercise performance. Int J Biochem Cell Biol 2003; 35: 855-66.

[10] Brenner S, Venkatesh B, Yap WH, *et al.* Conserved regulation of the lymphocyte-specific expression of lck in the Fugu and mammals. Proc Natl Acad Sci USA 2002; 99: 2936-41.

[11] Huerta-Aklin AI, Varon J, Marik PE. Bench to bedside review: rhabdomyolysis – an overview for clinicians. Crit Care 2005; 9: 158-69.

[12] Choi J, Costa ML, Mermelstein CS, Chagas C, Holtzer S. MyoD converts primary dermal fibroblasts, chondroblasts, smooth muscle, and retinal pigmented epithelial cells into striated mononucleated myoblasts and multinucleated myotubes. Proc Natl Acad Sci USA 1990; 87: 7988-92.

[13] Morosetti R, Mirabella M, Gliubizzi C, *et al.* MyoD expression restores defective myogenic differentiation of human mesoangioblasts from inclusion-body myositis muscle. Proc Nat Acad Sci USA 2006; 103: 16995-7000.

[14] Muscat GE, Gobius K, Emery J. Proliferin, a prolactin/growth hormone-like peptide represses myogenic- specific transcription by the suppression of an essential serum response factor-like DNA-binding activity. Mol Endocrinol 1991; 5: 802-14.

[15] Wilder EL, Linzer DI. Participation of multiple factors, including proliferin, in the inhibition of myogenic differentiation. Mol Cell Biol 1989; 9: 430-41.

[16] Hlaing M, Spitz P, Padmanabhan K, Cabezas B, Barker CS, Bernstein HS. E2F-1 regulates the expression of a subset of target genes during skeletal myoblast hypertrophy. J Biol Chem 2004; 279: 43625-33.

[17] Mori S, Tokuyama K. Variation in ACE activity affects myogenic differentiation in C2C12 cells. Biochem Biophys Res Commun 2007; 353: 369-75.

[18] Fleming I. Signaling by the angiotensin-converting enzyme. Circ Res 2006; 98: 887-96.

[19] Falquet L, Pagni M, Bucher P, *et al.* The PROSITE database, its status in 2002. Nucleic Acids Res 2002; 30: 235-8.

[20] Odelberg SJ, Kollhoff A, Keating MT. Dedifferentiation of mammalian myotubes induced by msx1. Cell 2000; 103: 1099-109.

[21] Oudit GY, Crackower MA, Backx PH, Penninger JM. The role of ACE2 in cardiovascular physiology. Trends Cardiovasc Med 2003; 12: 93-101.

[22] Chou CF, Loh CB, Foo YK, *et al.* ACE2 orthologues in non-mammalian vertebrates (Danio, Gallus, Fugu, Tetraodon and Xenopus). Gene 2006; 377: 46-55.

Received: November 18, 2008 Revised: December 17, 2008 Accepted: December 23, 2008