

Microarray Profile of Gene Expression During Osteoclast Differentiation in Modelled Microgravity

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ABSTRACT

Microgravity (μ Xg) leads to a 10–15% loss of bone mass in astronauts during space flight. Osteoclast (OCL) is the multinucleated bone-resorbing cell. In this study, we used the NASA developed ground-based rotating wall vessel bioreactor (RWV), rotary cell culture system (RCCS) to simulate μ Xg conditions and demonstrated a significant increase (2-fold) in osteoclastogenesis compared to normal gravity control (Xg). Gene expression profiling of RAW 264.7 OCL progenitor cells in modelled μ Xg by Agilent microarray analysis revealed significantly increased expression of critical molecules such as cytokines/growth factors, proteases and signalling proteins, which play an important role in enhanced OCL differentiation/function. Transcription factors such as c-Jun, MITF and CREB implicated in OCL differentiation are upregulated; however no significant change in the levels of NFATc1 expression in preosteoclast cells subjected to modelled μ Xg. We also identified high-level expression of calcium-binding protein, S100A8 (calcium-binding protein molecule A8/calgranulin A) in preosteoclast cells under μ Xg. Furthermore, modelled μ Xg stimulated RAW 264.7 cells showed elevated cytosolic calcium (Ca^{2+}) levels/oscillations compared to Xg cells. siRNA knock-down of S100A8 expression in RAW 264.7 cells resulted in a significant decrease in modelled μ Xg stimulated OCL differentiation. We also identified elevated levels of phospho-CREB in preosteoclast cells subjected to modelled μ Xg compared to Xg. Thus, modelled μ Xg regulated gene expression profiling in preosteoclast cells provide new insights into molecular mechanisms and therapeutic targets of enhanced OCL differentiation/activation to prevent bone loss and fracture risk in astronauts during space flight missions. *J. Cell. Biochem.* 111: 1179–1187, 2010. © 2010 Wiley-Liss, Inc.

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Microgravity (μ Xg) or weightlessness conditions during space flight results in biological changes in astronauts, which include atrophy of the muscular system [Katkovsky and Pomyotov, 1976; Miyamoto et al., 1998], immune system dysfunction [Sonnenfeld et al., 2003] and cardiovascular anomalies [Arbeille et al., 1995; White and Blomqvist, 1998]. A primary challenge for The National Aeronautics and Space Association (NASA) is preventing accelerated bone loss and fracture risk in astronauts. In space, astronauts are exposed to μ Xg; 0.08–0.008g rather than Earth's inherent gravity of 1g. Thus, little to no pressure is exerted on the astronaut's skeletal system. This skeleton unloading over time reduces bone mineral density (BMD), particularly in load-bearing regions of the skeleton such as the legs and lower back may leads to fracture risk in astronauts [Lang et al., 2004; Lang et al., 2006; Keyak et al., 2009]. In fact, morphological changes in bones of

astronauts after space flight resemble osteoporotic patients [Garber et al., 2000; Lang et al., 2006; Keyak et al., 2009]. Furthermore, serum and urine calcium levels are elevated in astronauts throughout the space mission. During long-term space missions, astronauts can lose as much bone mass in the proximal femur in 1 month as post-menopausal women on Earth lose in 1 year [Cavanagh et al., 2005]. It has been reported that astronauts can lose 1–2% of entire bone mass per month, while in space, underscoring the hazards of current and future long-term space flight missions [Carmeliet and Bouillon, 1999]. The possibility of irreversible bone loss has serious implications for long-term inhabitants of the International Space Station. Although nutritional supplementation and regimented exercise are mandated for astronauts, bone loss is still an impending issue. Previously, isolated fetal mouse long bones under near weightless conditions showed decreased mineralization

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and increased calcium release [Van Loon et al., 1995]. Similarly, it has been shown that osteopenia in the immobilized rat hind limb model is associated with increased bone resorption and decreased bone formation. Cell culture systems demonstrated decreased osteoblastic activity under μ Xg conditions [Van Loon et al., 1995; Hughes-Fulford and Lewis, 1996].

The osteoclast (OCL) is the bone-resorbing cell derived from monocyte/macrophage lineage. The TNF family member, receptor activator for nuclear factor κ B ligand (RANKL) is expressed in marrow stromal/osteoblast cells in response to several osteotropic factors and is critical for OCL precursor differentiation to form multinucleated OCL, which resorb bone. M-CSF is required for proliferation and survival of OCL precursors. The interaction of RANKL and RANK expressed on preosteoclast cells results in activation of various signalling cascades during OCL differentiation and bone resorption [Reddy, 2004]. Evidence suggests that μ Xg modulates RANKL and osteoprotegerin (OPG) gene expression in bone marrow stromal/preosteoblast cells, which are key regulators of osteoclastogenesis and bone resorption [Kanematsu et al., 2002; Rucci et al., 2007]. It has also been shown that hypergravity has no effect on the number of OCLs, but enhances bone-resorption activity [Nemoto and Uemura, 2000]. Recently, μ Xg has been reported to reduce osteoblast life-span and enhance IL-6 gene expression, thereby decreasing osteoblast activity and increasing OCL activity to contribute to bone loss associated with weightlessness [Rucci et al., 2002]. Furthermore, intact limb bones of newts flown onboard the biosatellite Cosmos-2229 had increased calcium and histological analysis revealed activation of osteoclastic resorption on the endosteal surface of long bones on the 20th day of space flight [Berezovska et al., 1998]. Thus, increased OCL activity has been reported under μ Xg conditions. μ Xg perturbs bone remodelling by uncoupling bone formation and bone resorption which could account for bone loss [Nichols et al., 2006]. However, the mechanism underlying μ Xg-induced OCL formation/bone resorption activity is unclear. In this study, we used the NASA developed ground-based rotating wall vessel bioreactor (RWV), rotary cell culture system (RCCS) to simulate μ Xg conditions and demonstrated a significant increase in osteoclastogenesis in mouse bone marrow cultures. We further determined the gene expression profiling during OCL differentiation of RAW 264.7 cells subjected to modelled μ Xg by Agilent chip microarray analysis.

METHODS

MODELLED μ Xg AND CELL CULTURE

The RWV, RCCS (Synthecon Inc, TX) is a horizontally rotated, bubble-free cell culture vessel with a silicone membrane for gas exchange. The fluid dynamic principles of the RCCS allow oxygenation without turbulence, co-localization of particles with different sedimentation rates and reduction of fluid shear forces [Goodwin et al., 1993; Zayzafoon et al., 2004]. Suspension of cells established a uniform, very low shear, three-dimensional (3D) spatial freedom and fluid suspension orbit within the cell culture vessel. The vessel containing mouse bone marrow-derived non-adherent cells or RAW 264.7 cells suspended in α -MEM containing 10% foetal bovine serum (FBS) was rotated at 16 rpm for 24 h to

simulate a μ Xg (0.008g) environment, termed as modelled μ Xg, in a humidified incubator at 37°C with 5% CO₂. Cells cultured under normal gravity conditions termed as control (Xg).

OSTEOCLAST CULTURE

Bone marrow was flushed from long bones of 6- to 8-week-old mice (C57BL/6) using α -MEM. Cells were pelleted at 1,500 rpm for 7 min at room temperature and plated in α -MEM with 10% FBS supplemented with M-CSF (10 ng/ml) and cultured overnight. Non-adherent mouse bone marrow cells (1.5×10^6 /ml) or RAW 264.7 cells (1×10^4 /ml) subjected to modelled μ Xg in RCCS for 24 h were cultured in a 24-well plate for 7 or 5 days, respectively, in the presence of M-CSF (10 ng/ml) and RANKL (80 ng/ml; R&D Systems Inc., Minneapolis, MN). Cells were fixed with 2% glutaraldehyde in phosphate-buffered saline (PBS) and stained for tartrate-resistant acid phosphatase (TRAP) activity using a histochemical kit (Sigma Chemical Co., St. Louis, MO). TRAP-positive multinucleated cells (MNC) containing three or more nuclei were scored as OCLs under a microscope as described [Shanmugarajan et al., 2007].

siRNA INTERFERENCE

RAW 264.7 cells were seeded (5×10^5 cells/well) in six-well plates and supplemented with DMEM containing 10% FBS. One day after seeding, cells were transfected with double-stranded-specific siRNA (10 μ mol/L) against S100A8 (Santa Cruz Biotechnology, Inc., CA) by oligofectamine as per the manufacturer instructions (Invitrogen Life Technologies, Inc., Carlsbad, CA). Non-specific scrambled siRNA-transfected cells served as control. Cells were cultured in modelled μ Xg for 24 h and both Xg and μ Xg subjected cells were cultured in the presence of M-CSF (10 ng/ml) and RANKL (80 ng/ml) for 5 days to form OCLs.

MICROARRAY ANALYSIS

RAW 264.7 cells (1.5×10^6 /ml) were subjected to RCCS with DMEM containing 10% FBS for 24 h and stimulated with RANKL (80 ng/ml) for 24 h in parallel with Xg cells. Total RNA isolated using RNazol reagent (Biotecx Labs, Houston, TX) was hybridized with Agilent whole genome 4 K \times 44 K array system (~26,000 genes). Slides were washed and scanned by using an Agilent G2565 microarray scanner. Data obtained were analyzed with Agilent feature extraction and GeneSpring GX v7.3.1 software packages (Genus Biosystem, Inc. Northbrook, IL). Gene Ontology Tree Machine (GOTM) is a web-based platform used for interpreting gene sets including microarray data using Gene Ontology hierarchies [Zhang et al., 2004]. The GOTM provides classification and distribution of genes as well as analytical tools for comparison of the significantly enriched gene numbers in the catalogue of gene ontology in a pathway or gene family oriented way for differential gene expression with a reference gene set, which includes all the genes in the mouse genome. The hypergeometric test, which is appropriate for sampling without replacement, was adopted by GOTM to determine whether those enrichments are statistically significant.

QUANTITATIVE REAL-TIME RT-PCR

Total RNA was isolated from mouse bone marrow-derived non-adherent cells subjected to modelled μ Xg or Xg conditions were

treated with or without of M-CSF (10 ng/ml) and RANKL (80 ng/ml) for 24 h using RNazol reagent (Biotech Labs). The reverse transcription reaction was performed using poly-dT primer and Moloney murine leukemia virus reverse transcriptase (Applied Biosystems, Foster City, CA) in a 25 μ l reaction volume containing total RNA (2 μ g), 1 \times PCR buffer and 2 mM MgCl₂, at 42°C for 15 min followed by 95°C for 5 min. The quantitative real-time PCR was performed using IQ™ SYBR Green Supermix in an iCycler (iCycler iQ Single-color Real-Time PCR detection system; Bio-Rad, Hercules, CA). The forward and reverse primer sequences used to amplify the selected genes are listed as follow:

Primer	Forward (5'–3')	Reverse (5'–3')
Cathepsin-L	GCTTGGGAACAGCCTTAG	GTTGCTGTATCCCCGTGT
Cathepsin-B	TGAAGAAGCTGTGTGGCACT	GTTCCGGTCAGAAATGGCTTC
Cathepsin-K	CTCTCGGCGTTAATTTGGG	GCTAAATGCAGAGGGTACAGAG
MMP-8	AGGGCTGAAGTGAACACAGC	ATTCCATTGGGTCCATCAAA
MMP-12	TGAAAGGAGTCTGCACAATGA	CAGAGTTGAGTTGTCCAGTTGC
MMP-13	ATCCTGGCCACCTTCTCT	TTTCTCGGAGCCTGTCAACT
CAR-4	CCTGGAGCCTGTAAGGAGAA	AGCGTCATCTCCACTGTGTG
ATPase	AGCTTGGGAAGTCCAATTT	GGTTTTACCGGTGTCCATA
S100A8	GAGAAGGCCTTGAGCAACC	TGACCATTTCTTGAAGTCAATC
c-Jun	TGACTGCAAAGATGGAAACG	GAGGTGCGGCTTCAGACT
MITF	AGGGAGCAGCAGCAGAAG	AGGACTTGGCTGGCATGTT
GAPDH	CCTACCCCAATGTATC CGTTGTG	GGAGGAATGGGAGTTGCTG TTGAA

Thermal cycling parameters were 94°C for 3 min, followed by 40 cycles of amplifications at 94°C for 30 s, 60°C for 1 min, 72°C for 1 min and 72°C for 5 min as the final elongation step. Relative levels of mRNA expression were normalized in all the samples analyzed with respect to the levels of GAPDH amplification as described [Bustin, 2000].

WESTERN BLOT ANALYSIS

Mouse bone marrow-derived non-adherent cells or RAW 264.7 cells supplemented with α -MEM containing 10% FBS were subjected to modelled μ Xg. Cells were stimulated with or without RANKL (80 ng/ml) in the presence of M-CSF (10 ng/ml) for 24 h and total cell lysates were prepared in a buffer containing 20 mM Tris-HCl at pH 7.4, 1% Triton X-100, 1 mM EDTA, 1.5 mM MgCl₂; 10% glycerol, 150 mM NaCl, 0.1 mM Na₃VO₄ and 1 \times protease inhibitor cocktail. The protein content of the samples was measured using the BCA protein assay reagent (Pierce, Rockford, IL). Protein (100 μ g) samples were then subjected to SDS-PAGE using 4–15% Tris-HCl gradient gels and blot transferred on to a PVDF membrane, immunoblotted with anti-cathepsin K (Ctsk), anti-S100A8, anti-NFATc1 (Santa Cruz Biotechnology Inc., CA) and anti-phospho-CREB (R&D Systems Inc.) antibodies. The bands were detected using the enhanced chemiluminescence detection system (Pierce). The band intensity was quantified by densitometric analysis using the NIH ImageJ Program.

Ca²⁺ MEASUREMENTS

RAW 264.7 cells subjected to modelled μ Xg or Xg were incubated with RANKL (80 ng/ml) for 24 h and then with 4.6 μ M fluo-4 AM and 14 μ M Fura Red AM and 0.05% pluronic F127 for 30 min. Cells were rinsed 3 \times with Ringers solution and then equilibrated in serum-free IMDM medium without Phenol Red and stimulated with

RANKL (80 ng/ml) for 20 min. Calcium (Ca²⁺) levels/oscillations were analyzed by live cell confocal microscopy (Leica Microsystems, Heidelberg, Germany) and fluorescence was continuously recorded at 520 and 600 nm emission. The ratio of fluorescence intensity of Fluo-4 to Fura Red was calculated to estimate relative changes in cytosolic Ca²⁺ levels as described [Takayanagi et al., 2002a].

STATISTICAL ANALYSIS

Results are presented as mean \pm SD for three independent experiments and were compared using the Student's *t*-test. Results were considered significantly different for *P* < 0.05. Pearson's correlation coefficient (*R*²) was calculated using Microsoft Excel 2000 software.

RESULTS

μ Xg MODULATION OF OCLs FORMATION

μ Xg associated with space flight is a challenge for normal bone homeostasis. To determine the effect of simulated μ Xg on OCL differentiation in vitro, mouse bone marrow-derived non-adherent cells were subjected to modelled μ Xg in the RCCS as described in Methods Section. After 24 h both Xg and μ Xg subjected cells were stimulated with M-CSF (10 ng/ml) and RANKL (80 ng/ml) for 7 days to form multinucleated OCLs. As shown in Figure 1A,B, modelled

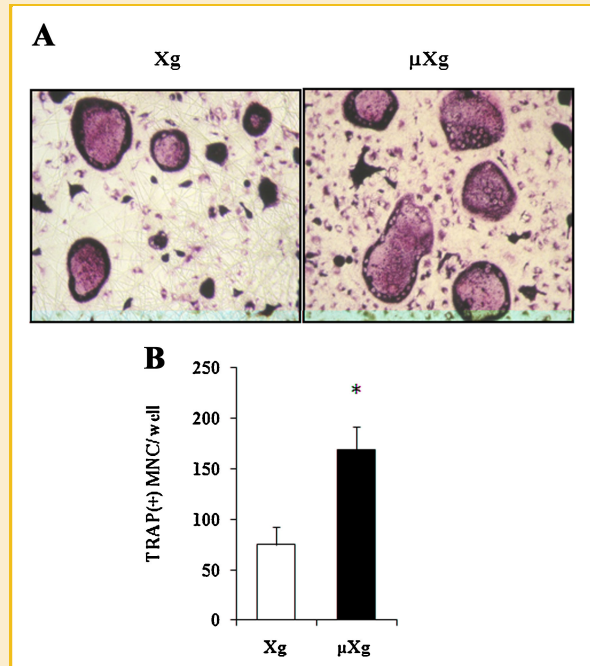


Fig. 1. Microgravity (μ Xg) modulation of osteoclastogenesis. A: Mouse bone marrow-derived non-adherent cells were either subjected to modelled μ Xg for 24 h or control (Xg) and cultured with M-CSF (10 ng/ml) and RANKL (80 ng/ml) for 7 days to form OCLs. Cells were fixed and stained for TRAP activity. Photomicrographs were taken at magnification \times 20. B: TRAP-positive multinucleated cells (MNC) containing three or more nuclei were scored as OCL. The results represent quadruplicate cultures of three independent experiments (**P* < 0.05). [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com]

μ Xg resulted in a significant increase in number and size of TRAP-positive multinucleated OCL formation compared to Xg cultures. These results are consistent with the recent findings in a space flight (FOTON-M3 mission) that μ Xg modulates osteoclastogenesis [Tamma et al., 2009].

GENE EXPRESSION PROFILE OF PREOSTEOCLASTS IN MODELLED μ Xg

To assess the gene expression pattern of preosteoclasts under μ Xg, we performed large-scale gene expression profiling using the Agilent whole genome 4K \times 44K array system which analyzes \sim 26,000 genes. We subjected a homogeneous population of RAW 264.7 OCL progenitor cells to modelled μ Xg in RCCS for 24 h and stimulated with RANKL (80 μ g/ml) for 24 h. Agilent chips were hybridized with total RNA isolated from Xg and μ Xg subjected RAW 264.7 cells. Gene array data were analyzed using stringent criteria that restricted the scored genes for specific hybridization values \geq 2-fold. Thus, 3,404 genes were identified that are differentially expressed in preosteoclast cells under μ Xg conditions. Scatter plot and functional gene cluster analysis revealed differential gene expression in modelled μ Xg compared to static Xg (Fig. 2A,B). Microarray profiling of modelled μ Xg regulated gene expression in RAW 264.7 preosteoclast cells was deposited in Gene Expression

Omnibus (GEO) database repository at NCBI (Accession #GSE21093). Gene expression profiles were analyzed by GOTM, a web-based platform and modelled μ Xg-induced genes were functionally grouped for cytokines/growth factors, chemokines, signalling/interacting proteins, adhesion and trafficking proteins, proteases, calcium signalling and ATPases genes (Supplemental Tables I–VII). Thus, 11.4% of the genes analyzed were differentially regulated by μ Xg; of these 54% were upregulated and 45% were downregulated. Several genes important for osteoclastogenesis and bone resorption function were elevated in modelled μ Xg compared to Xg. Specifically, μ Xg upregulated mRNA expression of colony stimulating factor 3 (granulocyte; csf3, 16-fold), Fc receptor2b (Fcgr2b, 7-fold), integrin α V (Itgav, 3-fold), bone matrix degrading proteases (matrix metalloproteinase) MMP-8 (30-fold), MMP-12 (10-fold), MMP-13 (7-fold), cathepsin B (Ctsb, 3.5-fold), cathepsin L (Ctsl, 2.4-fold), Ctsk (2.3-fold), ATPase, H⁺ transporting lysosomal (Atp6v0a1, 3.5-fold), chloride channel calcium activated 1 (Clca1, 3.8-fold), transcription factors, c-Jun (2-fold) MITF (2.2-fold), c-AMP responsive element-binding proteins (CREBs, 2.2- to 3.4-fold), vesicular secretion factors, carboxypeptidase E (Cpe, 14-fold) and ATP-binding cassette C (Abcc3, 10-fold). Furthermore, μ Xg elevated gene expression of adhesion molecules such as podoplanin (Pdpn, 138-fold), integrin β 7 (Itgb7, 11.8-fold), integrin β 5 (Itgb5, 6.2-fold), integrin α M (Itgam, 4-fold), integrin β 4 (Itgb4,

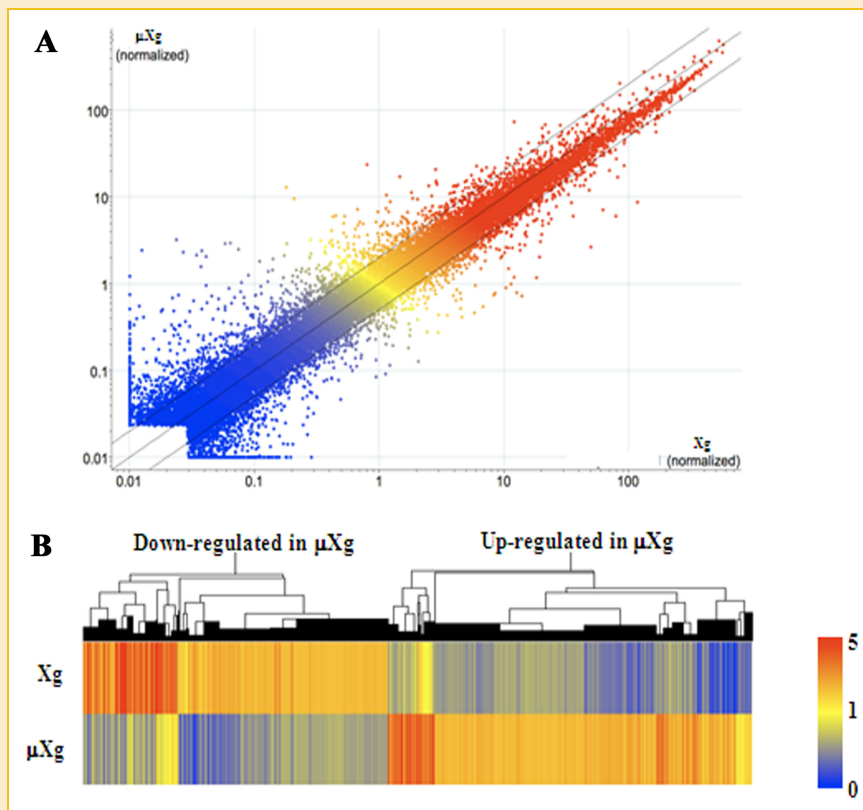


Fig. 2. Microarray profiling of gene expression in RAW 264.7 cells under μ Xg. RAW 264.7 cells were cultured in modelled μ Xg for 24 h and stimulated with RANKL (80 ng/ml) for 24 h. Preosteoclast cultures under normal gravity (Xg) served as control cells. Total RNA isolated from the cells was subjected to Agilent whole genome 4K \times 44K array system for microarray analysis. (A) Scatter plot and (B) Cluster analysis of \sim 26,000 genes revealed differential gene expression in modelled μ Xg. Gene expression profile presented as: Red—high expression; Yellow—medium expression; Blue—low expression. Pearson's correlation coefficient ($R^2 = 0.53$) for Scatter plot was calculated. [Color figure can be viewed in the online issue, which is available at wileyonlinelibrary.com]

3.3-fold), integrin α L (Itgal, 2.6-fold) and caveolin (Cav1, 6-fold). In addition, cytokines/growth factors such as VEGF, TGF- β , FGF-23 and 11, interleukins (1 α , 33 and 10), and PDGF gene expression is significantly increased in modelled μ Xg. Chemokines are chemotactic and modulate cellular functions in bone environment [Galliera et al., 2008]. Modelled μ Xg upregulated gene expression of chemokines such as CXCL4 (30-fold), CXCL14 (9.2-fold), CXCL2 (7.3-fold), CCL7 (16-fold), CCL8 (15-fold), CCL24 (4.7-fold) and CXCR4 (4-fold). Also, we identify that Ca²⁺ binding protein S100A8 was highly upregulated (72-fold) in modelled μ Xg, implicating a potential role of Ca²⁺ signalling in OCL activation under μ Xg conditions. Further, μ Xg significantly downregulated some negative regulators of OCL differentiation such as interleukin (IL)-12 β (-7.7-fold), G-protein-coupled receptor (GPCR) 48 (-3.5-fold), estrogen receptor (ER)- β (-3.3-fold), P58 repressor (-2.2-fold) and interferon regulatory factor (IRF)-9 (-2.1-fold; Supplemental Table VIII). These results indicate that differential gene expression under μ Xg may have direct effect on OCL formation/function.

EVALUATION OF μ Xg-INDUCED GENE EXPRESSION DURING OCL DIFFERENTIATION

We confirmed the modelled μ Xg induced gene expression during OCL differentiation by real-time RT-PCR and Western blot analysis

of mouse bone marrow cultures. As shown in Figure 3A, real-time RT-PCR analysis of total RNA isolated from bone marrow-derived non-adherent cells subjected to modelled μ Xg and stimulated with RANKL demonstrated a significant increase in the levels of MMP-8, MMP-12, MMP-13, CTS-L, CTS-B, CTS-K, CAR4, ATPase, S100A8, c-Jun and MITF mRNA expression compared to Xg cells. Western blot analysis of total cell lysates obtained from mouse bone marrow-derived preosteoclast cells revealed that Ctsk expression is significantly (2-fold) elevated under μ Xg compared to Xg cells (Fig. 3B). These results validate the microarray data and suggest modelled μ Xg stimulates cathepsins and MMPs expression in preosteoclast cells, which play an important role in matrix degradation/bone loss.

μ Xg MODULATION OF Ca²⁺

RANKL signalling evokes Ca²⁺ oscillations during OCL differentiation [Takayanagi et al., 2002a]. Microarray analysis identified high-level expression of S100A8 (calcium-binding protein molecule A8/calgranulin A), a calcium-binding protein involved in the cell signal transduction and differentiation [Riau et al., 2009]. Interestingly, Western blot analysis of total cell lysates obtained from mouse bone marrow-derived non-adherent cells subjected to modelled μ Xg revealed induced expression (12-fold) of S100A8 in the presence or absence of RANKL stimulation (Fig. 3C). We then examined relative

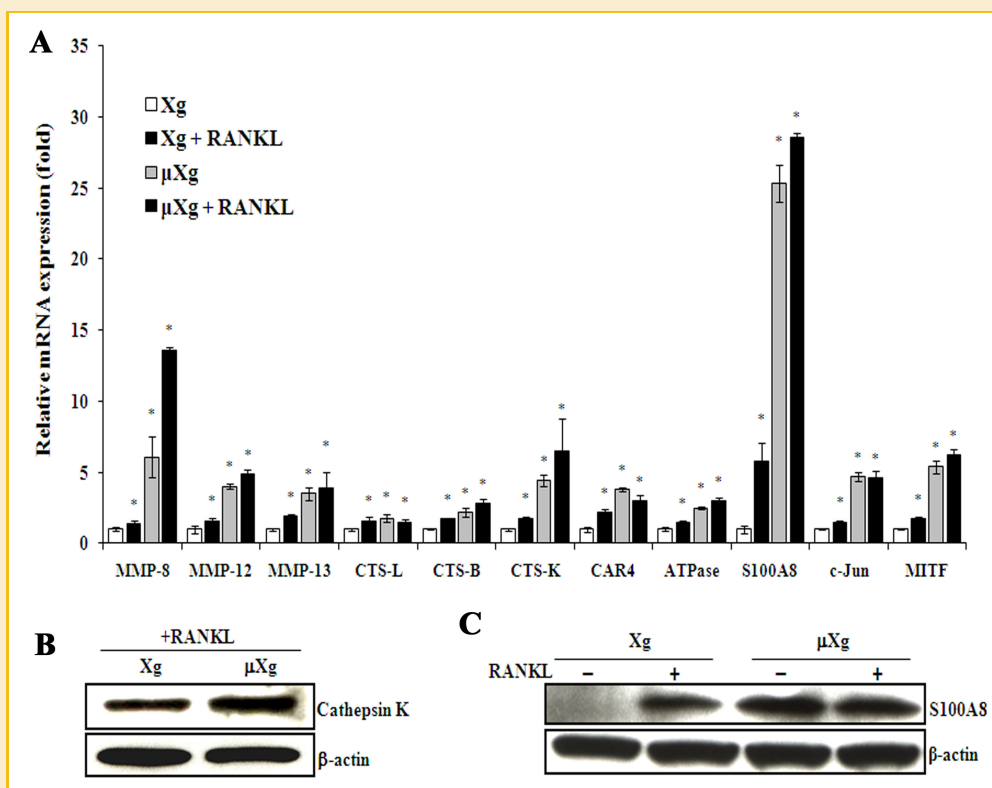


Fig. 3. Evaluation of μ Xg-induced gene expression by real-time RT-PCR and Western blot analysis. Mouse bone marrow-derived non-adherent cells were subjected to modelled μ Xg for 24 h or control (Xg) cells were stimulated with or without RANKL (80 ng/ml) for 24 h. A: Total RNA isolated was subjected to real-time RT-PCR using gene-specific primers as listed in Methods Section. The mRNA expression was normalized with respect to GAPDH amplification. Each bar represents the mean \pm SD of three independent experiments (* P < 0.05). B: Total cell lysates obtained were subjected to Western blot analysis using anti-cathepsin K and (C) anti-S100A8 antibodies. β -actin expression served as loading control.

changes in cytosolic calcium (Ca^{2+}) levels and oscillation patterns in RAW 264.7 cells subjected to modelled μXg . As shown in Figure 4A, modelled μXg elevated Ca^{2+} in these cells. Ca^{2+} changes were estimated as the ratio of fluorescence intensity of the Fluo-4 to Fura Red. Furthermore, Ca^{2+} oscillations were also elevated in RAW 264.7 cells subjected to modelled μXg compared to Xg cells (Fig. 4B). These results suggest that μXg elevated intracellular Ca^{2+} levels/oscillations which play important roles in OCL differentiation/activity. We further examined participation of S100A8 in μXg stimulated OCL differentiation. RAW 264.7 cells were transiently transfected with double-stranded siRNA against S100A8 using oligofectamine were subjected to modelled μXg for 24 h and cultured for 5 days to form multinucleated OCLs as described in Methods Section. As shown in Figure 4C, RAW 264.7 cells knock-down for S100A8 resulted in a significant decrease in OCL formation compared to scrambled non-specific siRNA transfected Xg cells. Ca^{2+} signalling activates calcineurin (CN) and calmodulin kinases (CaMKs) pathways which induce NFATc1 and CREB activation respectively, during OCL differentiation [Sato et al., 2006]. Therefore, we further determined NFATc1 and phospho-CREB (p-CREB) levels in RAW 264.7 cells subjected to modelled μXg . Western blot analysis of total cell lysates obtained from RAW 264.7 cells subjected to modelled μXg and stimulated with RANKL for 24 h period demonstrated no significant change in the levels of NFATc1 expression; however, a 5-fold increase in the levels of p-CREB compared to Xg (Fig. 4D,E). Taken together, these results implicate a functional role for S100A8 and elevated Ca^{2+} levels in μXg stimulated OCL differentiation.

DISCUSSION

Space flight is a challenge for normal bone homeostasis, and astronauts experience significant bone loss. Earlier, studies with the NASA developed RWV, RCCS revealed that modelled μXg stimulates osteoclastogenesis and bone resorption by increasing the RANKL/OPG ratio [Rucci et al., 2007]. Others have also reported that RCCS modelled μXg inhibits osteoblastogenesis and stimulates osteoclastogenesis [Saxena et al., 2007]. However, in studies using a 3D clinostat system to simulate μXg , inhibition of MC3T3-E1 cell differentiation and suppression of RANKL and OPG gene expression was observed. In addition, inhibition of fusion of RAW 264.7 cells to form multinucleated OCLs was reported, implicating long-term mechanical unloading and suppression of bone formation/resorption [Makihira et al., 2008]. More recently, in-flight studies conducted during the FOTON-3 mission revealed OCLs and their precursors as direct targets for μXg and that mechanical forces modulate genes associated with OCL differentiation/activity [Tamma et al., 2009]. Also, studies with mouse osteoblast cultures using the RWV bioreactor identified μXg regulated mechanoresponsive genes in osteoblasts [Patel et al., 2007; Capulli et al., 2009]. The present study confirms stimulation of osteoclastogenesis in modelled μXg using the RCCS. We further analyzed gene expression profile by Agilent microarray analysis during OCL differentiation of a homogeneous population of RAW 264.7 progenitor cells in a modelled μXg environment. Several genes

important for osteoclastogenesis/bone resorption function are elevated under conditions of μXg compared to Xg cells. However, the differential gene expression in preosteoclast cells subjected to μXg and stimulated with RANKL for a short period (24 h) excludes the possibility due to differences in maturation of osteoclasts. Granulocyte colony-stimulating factor (G-CSF) has been shown to be a potent stimulator of OCL activity and inhibit osteoblasts activity [Hirbe et al., 2007; Horiuchi et al., 2009]. Therefore, μXg upregulated G-CSF expression may affect both OCL and osteoblast activity in the bone microenvironment. Furthermore, growth factors such as VEGF, TGF- β , FGF and PDGF play important roles in osteoclastogenesis [Zhang et al., 1998; Chikazu et al., 2000; Nakagawa et al., 2000; Fox et al., 2008]. TGF- β has multiple functions in the bone environment and is required for early OCL progenitor commitment and suppress OCL apoptosis [Janssens et al., 2005; Gingery et al., 2008]. Elevated TGF- β receptors I and II implicates a potential role in μXg -induced osteoclastogenesis.

Matrix metalloproteinases and cathepsins, cysteine protease expression in OCLs plays an important role in bone-resorption activity [Troen, 2004; Sundaram et al., 2007]. Microarray analysis revealed upregulation of cytokines/growth factors and several matrix-degrading proteases to suggest μXg modulation of OCL bone-resorption activity. Furthermore, elevated expression of integrins contributes to the OCL's localization and attachment to the bone surface [Lakkakorpi et al., 1991]. Modelled μXg upregulation of transcription factors, c-Jun, MITF and CREBs indicate μXg modulation of RANKL-RANK signalling critical for OCL differentiation. Likewise, Ctsk mRNA expression has been shown to be upregulated in OCL cultured in bioreactors that were subjected to space flight [Tamma et al., 2009] which support data from our microarray profile using RCCS modelled μXg . Our finding of elevated several growth factors in preosteoclast cells under μXg may alter RANKL and OPG levels in bone environment and facilitate enhanced OCL activity. We show modelled μXg elevated levels of cytosolic Ca^{2+} and calcium-binding protein S100A8 compared to Xg cells. The S100A8 molecule is associated with multiple targets that promote cell growth and differentiation, cell cycle regulation, gene transcription, cell surface receptor activities [Donato, 2001; Heizmann et al., 2002] and anti-apoptotic function [Lee et al., 2008]. Furthermore, our findings with high-level expression of S100A8 calcium-binding protein is associated with Ca^{2+} oscillations implicates an essential role in OCL differentiation under μXg conditions. We confirmed that S100A8 suppression in RAW 264.7 cells significantly decreased modelled μXg stimulated OCL differentiation. Ca^{2+} signalling through CN pathway induces NFATc1 transcription factor critical for OCL-specific gene expression such as cathepsins and MMPs [Takayanagi et al., 2002a; Sundaram et al., 2007; Balkan et al., 2009]. We find no significant change in the levels of NFATc1 expression, however increased levels of c-Jun, MITF and CREBs transcription factors in modelled μXg suggested that elevated Ca^{2+} oscillations modulates CaMK-CREB pathway during OCL differentiation. Accordingly, we identify elevated levels of p-CREB in preosteoclast cells subjected to modelled μXg compared to Xg gravity conditions. The CaMK-CREB pathway also regulates the expression of osteoclast-specific genes in cooperation with NFATc1 [Sato et al., 2006]. Previously,

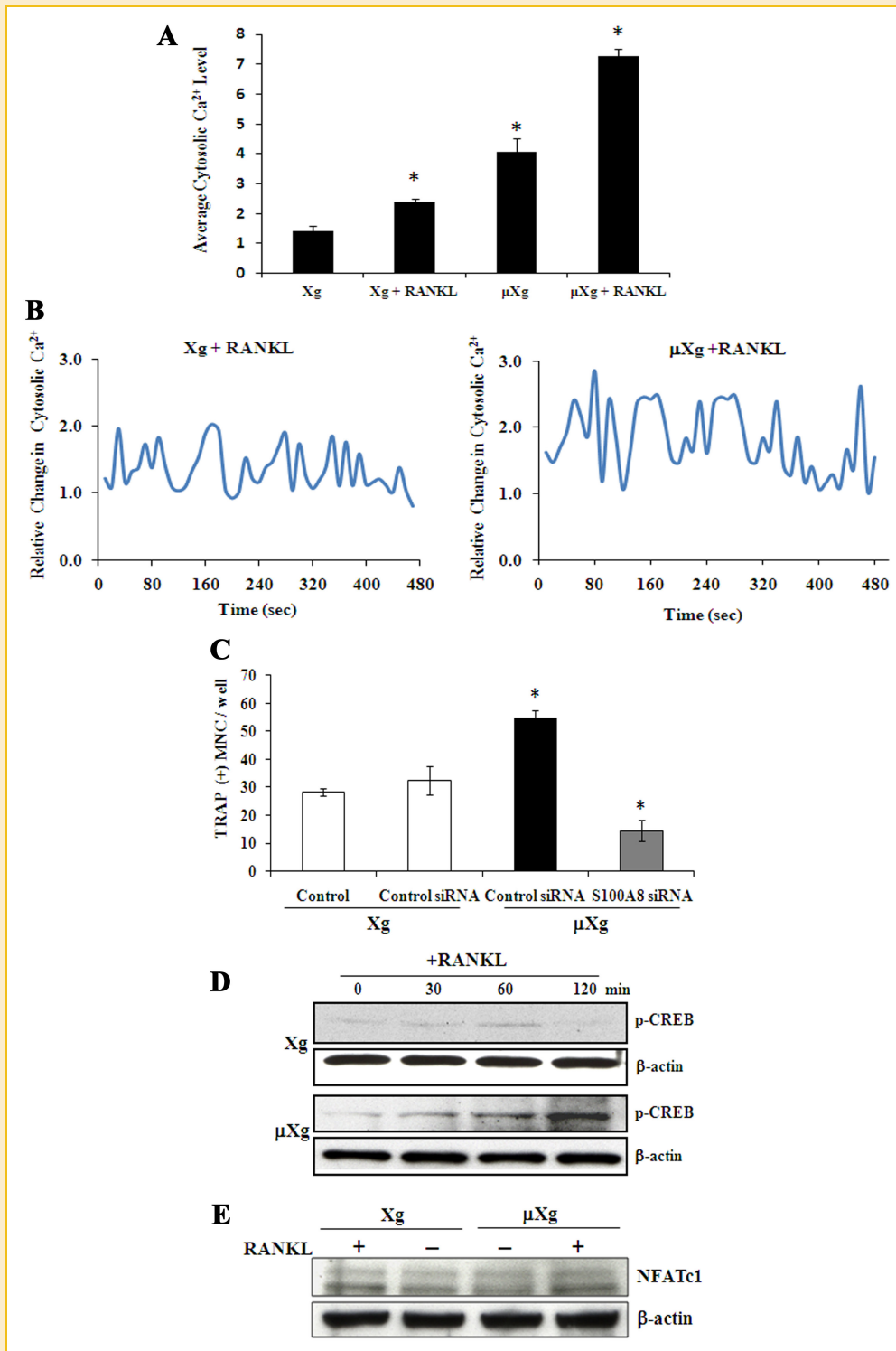


Fig. 4. Modelled μ Xg modulation of Ca^{2+} in RAW 264.7 cells. A: μ Xg modulates cytosolic Ca^{2+} levels in RAW 264.7 cells. Cells were incubated in the presence of fluo-4 AM (4.6 μM), and Fura Red AM (14 μM) and pluronic F127 (0.05%) for 30 min. Cells were post-incubated in IMDM medium without phenol red, 10% FBS, M-CSF (10 ng/ml) and RANKL (80 ng/ml) for 20 min and analyzed by a live-cell confocal microscope. The ratio of fluorescence intensity of Fluo-4 to Fura Red was calculated to estimate the intracellular calcium levels of the cells. Each bar represents the mean \pm SD of three independent experiments ($^*P < 0.05$). B: μ Xg elevates Ca^{2+} oscillations in RAW 264.7 cells. Ca^{2+} oscillations were recorded in control (Xg) and modelled μ Xg subjected RAW 264.7 cells as the ratio of fluorescence intensity of the Fluo-4 to Fura Red plotted at 10 s intervals. The two fluorophores were equally distributed in cytosol and had identical ratios under saturating conditions. The fluorescence ratios were calculated using R_{min} and R_{max} . Results represent an average of 10 individual cells of three independent experiments. Pearson's correlation coefficient of the two groups, Xg ($R^2 = 0.29$) and μ Xg ($R^2 = 0.55$) were calculated. C: S100A8 regulates osteoclastogenesis in modelled μ Xg. RAW 264.7 cells were transiently transfected with double-stranded S100A8 siRNA using oligofectamine. Cells were subjected to either modelled μ Xg for 24 h or Xg and stimulated with RANKL (80 ng/ml) for 5 days. TRAP-positive multinucleated cells (MNC) containing three or more nuclei were scored as OCL. The results represent quadruplicate cultures of three independent experiments ($^*P < 0.05$). D: Modelled μ Xg elevates phospho-CREB (p-CREB) levels in RAW 264.7 cells. Total cell lysates obtained from RAW 264.7 cells subjected to modelled μ Xg or Xg and stimulated with RANKL (80 ng/ml) for indicated period (0–120 min) were analyzed by Western blot using anti-p-CREB specific antibody. E: NFATc1 expression in RAW 264.7 cells. Total cell lysates obtained from RAW 264.7 cells subjected to modelled μ Xg or Xg and stimulated with or without RANKL (80 ng/ml) for 24 h were analyzed for NFATc1 expression using anti-NFATc1 antibody. β -actin expression in all the samples analyzed served as loading control. [Color figure can be viewed in the online issue, which is available at www.interscience.wiley.com]

CaMK-CREB dependent c-Jun activation by calcium signalling has been demonstrated [Cruzalegui et al., 1999]. Furthermore, downregulation of negative regulators of osteoclastogenesis such as IL-12 β , IL-13, GPCR 48, IFN- β downstream signalling molecules such as P58 repressor and IRF-9 implicates a potential role in OCL differentiation/activity under μ Xg conditions [Hayashi et al., 2002; Takayanagi et al., 2002b; Luo et al., 2009]. Collectively, our results suggest that modelled μ Xg modulates OCL development/function. In summary, modelled μ Xg regulated gene expression profiling in preosteoclast cells provide new insights into molecular mechanisms and therapeutic targets of OCL differentiation/activation to prevent bone loss and fracture risk in astronauts during space flight missions.

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