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Increased bone mass, altered trabecular architecture and modified growth plate organization in the growing skeleton of SOCS2 deficient mice

MacRae V. E.¹, Horvat, S.², Pells S.C.¹, Dale, H.³, Collinson, R.S.³, Pitsillides, A.A.³, Ahmed, S.F.⁴ & Farquharson, C.¹

1. Bone Biology Group, The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Roslin Biocentre, Roslin, UK

2. University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Domzale, Slovenia

3. Department of Veterinary Basic Sciences, Royal Veterinary College, London, UK

4. Bone & Endocrine Research Group, Royal Hospital for Sick Children, Glasgow, UK

Corresponding author: Dr Vicky MacRae, Bone Biology Group, The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Roslin Biocentre,

Roslin, UK Tel: 44 131 5274259; Fax 44 131 4400434; e-mail: vicky.macrae@roslin.ed.ac.uk

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- **SOCS2**
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Abstract

Suppressor of Cytokine Signaling-2 (SOCS2) negatively regulates the signal transduction of several cytokines. *Socs2*^{-/-} mice show increased longitudinal skeletal growth associated with deregulated GH/IGF-1 signaling. The present study examined the role of SOCS2 in endochondral ossification and trabecular and cortical bone formation, and investigated whether pro-inflammatory cytokines associated with pediatric chronic inflammatory disorders mediate their effects through SOCS2.

7-week-old *Socs2*^{-/-} mice were heavier (27%; P<0.001) and longer (6%; P<0.001) than wild-type mice. *Socs2*^{-/-} tibiae were longer (8%; P<0.001) and broader (18%; P<0.001) than that of wild-type mice, and the *Socs2*^{-/-} mice had wider growth plates (24%; P<0.001) with wider proliferative and hypertrophic zones (10% (P<0.05) and 14% (P<0.001) respectively).

Socs2^{-/-} mice showed increased total cross-sectional bone area (16%; P<0.001), coupled to increased total tissue area (17%; P<0.05) compared to tibia from wild-type mice. *Socs2*^{-/-} mice showed increased percent bone volume (101%; P<0.001), trabecular number (82%; P<0.001) and trabecular thickness (11%; P<0.001), with associated decreases in trabecular separation (19%; P<0.001). TNF α exposure to growth plate chondrocytes for 48h increased SOCS2 protein expression. Growth of metatarsals from 1-day-old *Socs2*^{-/-} and *Socs2*^{+/+} mice, as well as expression of *Aggrecan*, *Collagen Type II* and *Collagen Type X*, were inhibited by TNF α , with no effect of genotype.

Our data indicate that physiological levels of SOCS2 negatively regulate bone formation and endochondral growth. Our results further suggest that pro-inflammatory cytokines

mediate their inhibitory effects on longitudinal bone growth through a mechanism that is independent of SOCS2.

Introduction

Suppressor of Cytokine Signaling (SOCS) proteins are transcribed in response to cytokine stimulation and utilise various receptor-mediated mechanisms to down-regulate cytokine signal transduction pathways (Leroith and Nissley 2005; Rico-Bautista et al. 2006). The molecular mechanisms of SOCS action involve inhibiting Janus kinase (JAK) activity, blocking signal transducers and activators of transcription (STAT) binding sites on cytokine receptors or promoting the degradation of specific signaling proteins. SOCS proteins thereby form part of a classical negative feedback circuit to avoid the detrimental consequences of excessive stimulation. (Krebs and Hilton 2001).

It has been demonstrated that SOCS2, one of eight SOCS family members (Yoshimura et al. 2007), is also an important regulator of somatic growth through its regulation of GH/IGF-I signaling. SOCS2 is able to bind the GH receptor through tyrosine residues Y595 and Y487 (Greenhalgh et al. 2005), and since Y595 is a known binding site for STAT5, SOCS2 may therefore block access of STAT5 to the activated GH receptor (Smit et al. 1996), although this has recently been questioned (Uyttendaele et al. 2007). SOCS2 can also inhibit JAK2 tyrosine phosphorylation (Ram and Waxman 1999), suggesting that SOCS2 may inhibit GH signaling by directly binding to JAK2. SOCS2 may bind to the IGF-I receptor (Dey et al. 1998) and inhibit IGF-I induced STAT3 activation (Zong et al. 2000).

Socs2 null mice display an increased longitudinal skeletal growth and a proportionate augmentation of most visceral organs (Metcalf et al. 2000). A similar phenotype is also observed in the *high-growth (hg)* mutation, which is caused by the deletion of the *Socs2* locus (Horvat and Medrano 2001). These effects are associated with deregulated GH/IGF-I signaling, supporting the concept that SOCS2 is an important negative regulator of the GH/IGF-I signaling pathway. Indeed, SOCS2 may be a potential target for the development of novel treatment strategies for growth disturbances observed in children with chronic inflammatory disorders such as Juvenile Idiopathic Arthritis and Inflammatory Bowel Disease. Systemic concentrations of pro-inflammatory cytokines such as tumor necrosis factor-alpha ($TNF\alpha$) are often elevated in children with these disorders and may inhibit longitudinal growth (MacRae et al. 2006a,b) by directly inhibiting growth plate chondrocyte dynamics (Martensson et al. 2004; MacRae et al. 2006c).

Interestingly, reduced bone mineral density (BMD) has been reported in *Socs2* null mice by both dual x-ray absorptiometry (DXA) analyses and peripheral quantitative computerized tomography (pQCT) (Lorentzon et al. 2005). These results are not consistent with the expected augmented GH/IGF-I signaling observed in the *Socs2* null mice and therefore warrant re-examination. In addition, it is unknown if cortical and trabecular bone volume are increased in the *Socs2* null mice which would be consistent with increased GH/IGF-I signaling. To address these issues we have, in this study, exploited the capabilities of microCT which offers high resolution analyses of trabecular bone architecture and cortical bone geometry. In contrast, the increased longitudinal

bone growth observed in *Socs2* null mice (Metcalf et al. 2000; Lorentzon et al. 2005) is indeed consistent with increased signaling through the GH/IGF-I axis and indicates that SOCS2 protein has a functional role in growth plate chondrocyte dynamics. Nevertheless, previous histological analyses failed to disclose any obvious abnormalities of the epiphyseal growth plate of the tibia and femur (Metcalf et al. 2000). Subtle changes would only be revealed by a comprehensive histomorphometric analysis, however, and these may have been missed. Therefore, in addition to clarifying the function of SOCS2 in structural bone development, we considered it essential to understand more fully the effects of *Socs2* deficiency on growth plate structure and bone growth. Such an approach will also improve our understanding of inflammatory growth disorders associated with abnormal GH/IGF-I signaling.

In the present study, we have generated *Socs2* null (*Socs2*^{-/-}) mice in order to perform a detailed examination of the role of SOCS2 in endochondral ossification and trabecular and cortical bone formation. We have also investigated whether the pro-inflammatory cytokines that are associated with pediatric chronic inflammatory disorders, such as TNF α , mediate their negative effects on bone growth through SOCS2.

Material and Methods

Generation of the targeting construct and mutant mice

A BAC clone, 520L19, containing the *Socs2* locus has been isolated previously ((Horvat & Medrano, 1998) and used to subclone the plasmid with 7517 bp-long *Xba*I genomic fragment (positions 94841854 to 94849370 bp on chromosome 10; mouse genome

Ensembl release 45 - Jun 2007; http://www.ensembl.org/Mus_musculus/). This fragment contains exons 2 and 3 of the *Socs2* transcript (Ensembl ID ENSMUST00000020215). This construct was partially digested with *KpnI* and the reporter-selection marker cassette from plasmid pGT1.8Ires β geo⁽³²⁾ was inserted into the *KpnI* site within exon 2 (Figure 1A). The targeting construct was therefore bicistronic, combining the picornaviral internal ribosome-entry site (IRES) with the *lacZ-neoR* (β -geo) fusion gene (Mountford et al. 1994). The *KpnI* site was chosen for insertion of 70 nucleotides upstream of the translation start site to ensure that the polyadenylation site within the β -geo cassette would prematurely terminate transcription and cause lack of *Socs2* function. 300 μ g of the *NotI*-linearised construct was electroporated into 10⁷ HM1 embryonic stem (ES) cells from strain 129Sv (Magin et al. 1992) and after 48 h in culture selected in 160 μ g/ml G418 (Geneticin, Life Technologies, MD, USA) to obtain drug resistant ES cell colonies. Positive targeted events were identified in the ES clones by Southern analysis of *BamHI* digested genomic DNA (see Figure 1) using an external hybridisation probe, downstream of the 3' homology arm (*EcoRI* to *XhoI* fragment, Figure 1A), to detect clones with the expected fragment size of the wild type and targeted alleles. Targeted ES clones were identified by the presence of an appropriate doublet, a ~24-kb wild type band and a ~22-kb targeted fragment, which was shorter due to an additional *BamHI* site between the *neo* and *LacZ* genes within the β -geo cassette (Fig. 1A and 1B). Identical Southern blot screening was also used to identify homozygous individuals in the F₂ generation for phenotypic analysis.

From several positively targeted ES clones, two karyotypically normal G418 resistant clones were selected for injection into C57BL/6J blastocysts to generate chimeras (Bradley et al. 1987), which in turn were back-crossed with C57BL/6J mice. Germline transmission was confirmed in agouti coat-coloured offspring and potential founder animals identified using DNA isolated from tail biopsies and Southern blot analysis (as above). Subsequent generations were tested by tail biopsy followed by DNA isolation and analysis using PCR. Primers for *Socs2* wild-type allele (Forward 5'CAA CTT TAG TGT CTT GGA TCT; Reverse 5'TGT TTG ACT GAG CTC GCG C3') and *neo* (5'CGG CCG CTT GGG TGG AGA GGC3'; Reverse 5'TCG GGC ATG CGC GCC TTG AGC3') were used. The *neo* gene was present only in heterozygotes and homozygotes for targeted *Socs2* allele, while the *Socs2* wild type allele was present only in wild type homozygote and heterozygote animals.

Growth analysis

At weekly intervals, from 3 to 7 weeks of age, six female wild-type and six female *Socs2*^{-/-} mice were weighed. Following euthanasia at 7 weeks of age, body length (crown – rump) measurements were recorded.

Micro-computed tomography

Tibiae were dissected from 7 week old female wild-type and *Socs2*^{-/-} mice (n=5), fixed in 10% neutral buffered formalin for 48h, rinsed in tap water for 3h and stored in 70% ethanol. The tibiae were briefly rehydrated in physiological saline (0.09%) prior to being scanned using a micro-computed tomography (μ CT) system (Skyscan 1172 X-Ray

Microtomograph, Aartselaar, Belgium) to evaluate trabecular architecture and cortical bone geometry. High-resolution scans with an isotropic voxel size of 5 μ m were acquired (scan time approximately 1h 30mins for each bone), then reconstructed using NRecon (Skyscan, Belgium) and analyzed using CTAn (Skyscan, Belgium).

In trabecular bone, bone volume (BV/TV), trabecular number (Tb.N; /mm), trabecular thickness (Tb.Th; mm), trabecular separation (Tb.Sp), structure model index (SMI) and trabecular pattern factor (TPF) were evaluated. For each bone, a 5% region (of total bone length) of the metaphysis was analyzed, extending from 10% distal to the proximal head of the tibia. Bone mineral density (BMD g/cm³) of the trabecular bone was also calculated after appropriate calibration of the Skyscan CT analyser with known density calcium hydroxyapatite phantoms.

In cortical bone, tissue area, periosteal perimeter, bone area, endosteal perimeter, cortical thickness, mean moment of inertia (MMI polar) (more difficult to bend) and eccentricity (deviation from a circular shape) were evaluated in a 0.5mm segment of the mid-diaphysis, 0.25mm either side of the mid-diaphysis of the bone. Bone mineral density (BMD g/cm³) of the cortical bone was determined as described above.

Analysis of tibiae

To measure tibia dimensions, tibiae were dissected from 7 week-old female wild-type and *Socs2*^{-/-} mice (n=6). Tibia length and width were measured using DigiMax digital vernier callipers (R. S. Components Ltd, Corby, Northants, UK), after which the bones

were processed through to wax as previously described (Mushtaq et al. 2004). The size of the growth plate, and the proliferating and hypertrophic zones of seven wild-type and nine *Socs2*^{-/-} tibiae were determined using image analysis software (Nikon, Kingston upon Thames, Surrey, UK) on Toluidine blue stained paraffin sections. The width of the growth plate and the two distinct maturational zones was determined at 10 different points along the breadth of the growth plate in two sections from each bone.

Serum analysis

Immediately following euthanasia, blood samples from six 7-week-old female wild-type and five female *Socs2*^{-/-} mice were obtained by cardiac puncture and serum samples were prepared. A solid phase immunofixed enzyme activity assay was used to determine osteoclast-derived tartrate-resistant acid phosphatase form 5b (TRAP 5b) in the serum (Mouse TRAPTM assay; Immunodiagnostic Systems, Boldon, Tyne and Wear, UK). A sandwich ELISA kit was used to measure serum levels of osteocalcin (Mouse Osteocalcin EIA Kit; Immunodiagnostic Systems). An immunoenzymometric assay was used to determine serum IGF-I concentrations (Rat/Mouse IGF-I ELISA; Immunodiagnostic Systems).

ATDC5 chondrocyte cell culture

The ATDC5 chondrocyte cell line was sourced from the RIKEN cell bank (Ibaraki, Japan) and maintained as described by Atsumi and colleagues (Atsumi et al. 1990). Cells were cultured as described previously (MacRae et al. 2006c) and samples collected on day 6 and day 13. At these time points, the cells express established markers of

chondrogenesis (collagen type II and aggrecan) and the differentiated phenotype (collagen type X), respectively (Mushtaq et al. 2002).

Isolation of Primary Murine Chondrocytes

All animal experiments were approved by Roslin Institute's Animal Users Committee and the animals were maintained in accordance with Home Office guidelines for the care and use of laboratory animals. Primary chondrocyte cultures were prepared from male and female fetal (E14-E19) and neonatal (1 and 9-day-old) mouse chondrocostal growth plates using an isolation procedure and culture system previously described (Lefebvre et al. 1994). Briefly, the rib cage and sternum were dissected, rinsed in PBS, incubated at 37°C for 30min in 2mg/ml pronase (Sigma, Poole, Dorset, UK) in PBS, and then in 3mg/ml collagenase type 2 (Worthington Biochemical Corporation, Lakewood, New Jersey, US) in DMEM containing 4.5g/L glucose and L-Glutamine (Invitrogen, Paisley, Strathclyde, UK) for 30min. Soft tissues were detached from the cartilage by repeated gentle pipetting. The denser cartilage was subsequently allowed to sediment, and the soft tissues aspirated; the cartilage was then further digested with collagenase for 3h. Undigested bony parts were discarded and the remaining cell suspension was aspirated repeatedly with a Pasteur pipette, filtered through a 45µM cell sieve, and rinsed in DMEM.

Cell culture

Chondrocytes from 1-day-old female neonatal mice were seeded in 6-well plates at 100,000 cells per well in DMEM containing 4.5g/L glucose and L-Glutamine,

supplemented with 10% FCS (Invitrogen), 50µg/ml gentamycin (Invitrogen) and 50µg/ml L-ascorbic acid phosphate (Wako Pure Chemicals Ltd, Neuss, North Rhine-Westphalia, Germany). To study the effects of pro-inflammatory cytokines, chondrocytes were exposed to TNFα (10ng/ml) (Autogen Bioclear, Calne, Wiltshire, UK) for 48h before RNA or protein extraction.

Organ culture

The middle three metatarsals were aseptically dissected from male and female 19 day-old fetal and 1 day-old neonatal wild-type and *Socs2*^{-/-} mice. Bones were cultured and metatarsal lengths were measured as described previously (MacRae et al. 2006c, 2007). TNFα was added at a final concentration of 10ng/ml for the duration of the experiment (8 days). All results are expressed as a percentage change from harvesting length, which was regarded as baseline.

Western blotting analysis

Cells were lysed in RIPA buffer (20mM Tris-HCl, 135mM NaCl, 10% glycerol, 1% IGEPAL, 0.1% SDS, 0.5% deoxycholic acid, 2mM EDTA) containing “Complete” protease inhibitor cocktail according to manufacturer's instructions (Roche, East Sussex, UK). Immunoblotting was undertaken as described previously (MacRae et al. 2006d). Nitrocellulose membranes were probed overnight at 4°C with anti-SOCS2 primary antibody (1:500 dilution in 5% milk) (Abcam Plc, Cambridge, UK), washed in TBST and incubated with anti-rabbit IgG-peroxidase (Cell Signaling Technology, Beverly, MA, USA) for 1h (1:1000 dilution in 5% milk). Membranes were then washed in ‘stripping

buffer' (Pierce, Rockford, IL, USA) and re-probed for 1h for β -actin expression (1:5000 dilution in 5% milk; anti β -actin clone AC15; Sigma). After washing, membranes were incubated with anti-mouse IgG-peroxidase for 1h (Sigma). Semi-quantitative assessment of band intensity was achieved using Quantity One image analysis software (Bio-Rad Labs Inc., Hercules, CA, USA).

Immunohistochemistry

Tibiae were dissected from 3 week-old female Swiss mice that had been euthanized, fixed in 100% ethanol, decalcified in 10% EDTA (pH 8.0) for 4 days at 4°C, dehydrated and embedded in paraffin wax before sectioning at 5 μ m. For histological analysis, sections were de-waxed and de-masked for 10min in 0.1% trypsin. Endogenous peroxidases and non-specific antibody binding were blocked before overnight incubation at 4°C with 0.5 μ g IgG/ml anti-SOCS2 antibody. The sections were then washed in PBS, incubated with goat anti-rabbit IgG peroxidase (1:100 dilution; DAKO, Glostrup, Denmark) for 60min, and incubated with DAB substrate reagent (0.06% DAB, 0.1% H₂O₂ in PBS) for 5min. The sections were finally dehydrated, counterstained and mounted in DePeX. Control sections were incubated with non-immune rabbit IgG (0.5 μ g IgG/ml) in place of the primary SOCS2 antibody.

Analysis of Socs2 expression using semi-quantitative RT-PCR

RNA was extracted from chondrocytes using RNeasy total RNA (Qiagen Ltd, Crawley, West Sussex, UK), according to the manufacturer's instructions. For each sample, total RNA content was assessed by absorbance at 260nm and purity by A260/A280 ratios.

RNA was reverse transcribed and the PCR reaction undertaken as described previously (Farquharson et al. 1999; Houston et al. 1999). For the PCR reaction, primers for *18S* rRNA gene (20 cycles) (Ambion, Huntingdon, Cambs, UK, sequence unknown) and *Socs2* (35 cycles) (SuperArray Bioscience, Maryland, USA; sequence unknown) were used.

Analysis of chondrogenic gene expression using quantitative RT-PCR

RNA was extracted, quantified and reverse transcribed as described above. RT-qPCR was performed using the Stratagene Mx3000P real-time QPCR system (Stratagene, CA, USA). Primers were designed to span at least one intron. Primers for *collagen type II*, *Col2a1* (Accession number NM031163) (Forward 5'CGG TCC TAC GGT GTC AGG3'; Reverse 5'GCA GAG GAC ATT CCC AGT GT3'), *collagen type X*, *Col10a1* (Accession number NM009925) (Forward 5'CAT AAA GGG CCC ACT TGC TA3', Reverse 5'CAG GAA TGC CTT GTT CTC CT3') and *Gapdh* (Accession number NM008084) (Forward 5'TGAGGCCGGTGCTGAGTATGTCG3', Reverse 5'CCA CAG TCT TCT GGG TGG CAG TG3') were used. Primers for *aggrecan* (Accession number NM007424) were obtained from SuperArray Bioscience (sequence unknown).

Statistical analysis

General Linear Model analysis incorporating ANOVA and the Students t-test were used to assess the data. All data are expressed as the mean +/- S.E.M. Statistical analysis was performed using Minitab 14. $P < 0.05$ was considered to be significant.

Results

Growth of $Socs2^{-/-}$ mice

Initial studies addressed whether the $Socs2^{-/-}$ mice displayed an increased growth phenotype resembling that previously reported for $Socs2$ null mice (Metcalf et al. 2000). We found that the weight of the $Socs2^{-/-}$ mice was indistinguishable from wild-type mice prior to weaning (Fig. 2), but the $Socs2^{-/-}$ mice were significantly heavier (15%; $P < 0.01$) than their wild-type counterparts by 4 weeks of age; a difference that became more pronounced during the 7-week study period. More detailed analysis of 7 week-old female mice indicated that the $Socs2^{-/-}$ mice were significantly heavier (27%; $P < 0.001$) and longer (6%; $P < 0.001$) than wild-type mice (Table 1). In addition, the tibiae of $Socs2^{-/-}$ mice were longer (8%; $P < 0.001$) and broader (18%; $P < 0.001$) than that of wild-type mice (Table 1), and furthermore, the $Socs2^{-/-}$ mice had wider growth plates (24%; $P < 0.001$) with significantly wider proliferative and hypertrophic zones (10% ($P < 0.05$) and 14% ($P < 0.001$) respectively) (Table 1). Our data confirm previous studies that a deletion of the $Socs2$ gene causes increased growth and bone length, but also extends these findings to disclose structural changes to the growth plate which may account for the increased bone growth.

Bone architecture in $Socs2^{-/-}$ mice

The reduced BMD observed in $Socs2$ null mice by Lorentzon and colleagues (Lorentzon et al. 2005), is not consistent with the enhanced GH/IGF-I signaling observed in the $Socs2$ null mice. Therefore, we completed a comprehensive high resolution (5 μ m) μ CT

analysis of the tibia to more fully examine the effects of *Socs2* deficiency on bone phenotype. Examination of the mid-diaphyseal cortical bone of tibiae from *Socs2*^{-/-} mice showed increased total cross-sectional bone area (16%; P<0.001), coupled to increased total tissue area (17%; P<0.05) compared to tibia from wild-type mice (Table 2). Tibiae from *Socs2*^{-/-} mice also showed an increased mean moment of inertia (39%; P<0.001). No difference in periosteal and endosteal perimeter, eccentricity, BMD or cortical cross-sectional thickness was observed between genotypes (Table 2).

Increased bone volume in *Socs2*^{-/-} mice was apparent in the trabecular compartment of the tibia, where *Socs2*^{-/-} mice showed increased percent trabecular bone volume (101%; P<0.001; Fig. 3), trabecular number (82%; P<0.001) and trabecular thickness (11%; P<0.001), with associated decreases in trabecular separation (19%; P<0.001) (Table 2). The structure model index (SMI), which quantifies the characteristic form of a 3D structure in terms of amounts of plates and rods composing the structure (Hildebrand and Ruegsegger 1997), was also significantly lower in tibia from *Socs2*^{-/-} mice (22%; P<0.001). This indicates that the trabeculae in *Socs2*^{-/-} mice appear to be more 'plate-like' and more connected, which is consistent with greater 'strength' (Table 2). Trabecular BMD measured by μ CT was unchanged in the *Socs2*^{-/-} mice. These results indicate that *Socs2*^{-/-} mice have increased bone mass in both the cortical and trabecular compartments of the tibia, and that changes in bone architectural organization in *Socs2*^{-/-} mice are likely to be consistent with a greater resistance to bending.

Biochemical markers of bone formation and resorption

Serum concentrations of TRAP5b, a marker of bone resorption, were significantly increased in the *Socs2*^{-/-} mice compared with wild-type mice (110%; P<0.001) (Table 3). Similarly, a trend for elevated concentration of osteocalcin, a marker of bone formation, was also observed in the *Socs2*^{-/-} mice (35%; NS) (Table 3). Serum IGF-I concentrations were not significantly different between the *Socs2*^{-/-} and wild-type mice (Table 3). These results suggest a tendency for increased bone turnover in *Socs2*^{-/-} mice.

SOCS2 expression in the growth plate

To determine if the increased growth observed in *Socs2*^{-/-} mice was likely to be due to direct effects at the growth plate, it was first necessary to confirm that chondrocytes do indeed express *Socs2* mRNA and protein. Primary chondrocytes derived from both fetal (E14-E18) and neonatal (1 and 9-day-old) cartilage were found to express *Socs2* mRNA (Fig. 4a), whereas terminally-differentiated ATDC5 cells showed decreased SOCS2 protein levels compared to ATDC5 cells in the chondrogenic phase (Fig. 4b). Immunohistochemical analysis of sections of tibia revealed SOCS2 labeling in both proliferating and hypertrophic chondrocytes of the growth plate (Fig. 5). Consistent with changes in the levels of SOCS2 expression levels observed during ATDC5 cell differentiation (Fig. 4b), more intense SOCS2 labeling was observed in cells of the less mature proliferative zone than the hypertrophic zone of the growth plate (Fig. 4a). These studies confirm that growth plate chondrocytes express SOCS2, highlighting the likelihood that the increased bone growth and observed structural differences within the

epiphysis observed in *Socs2*^{-/-} mice is a direct consequence of altered SOCS2 signaling in chondrocytes of the growth plate.

Effect of pro-inflammatory cytokine exposure on chondrocyte gene expression

Increased SOCS2 protein expression in response to cytokine stimulation is known to be involved in the suppression of cytokine signal transduction pathways in various cell types. If increased SOCS2 expression is responsible for mediating the growth inhibitory effects of pro-inflammatory at the growth plate, it is evident that SOCS2 expression in chondrocytes should also be increased following cytokine exposure. This was indeed the case; we found that exposure to TNF α (10ng/ml) for 48h increased SOCS2 protein expression in primary 1 day-old murine chondrocytes (Fig.4c). Having established that TNF α increased chondrocyte SOCS2 expression, we next determined whether cytokine-induced changes in chondrocyte ‘marker’ genes differed in chondrocytes derived from wild-type and *Socs2*^{-/-} mice. RT-qPCR studies revealed that exposure to TNF α significantly reduced, by comparable amounts, the expression of *aggrecan*, *collagen type II* and *collagen type X* mRNA in both wild-type and *Socs2*^{-/-} mice (Fig. 6). This lack of effect of *Socs2* genotype on the cytokine-induced diminution in chondrocyte marker genes indicates that chondrocytes from 1 day-old wild-type and *Socs2*^{-/-} mice are equally susceptible to the adverse effects of pro-inflammatory cytokines and, therefore, that SOCS2 is unlikely to mediate these effects.

Growth of cultured wild-type and $Socs2^{-/-}$ murine metatarsals and their response to pro-inflammatory cytokine exposure.

We next aimed to determine if the growth trajectories of metatarsals from wild-type and $Socs2^{-/-}$ mice differed under basal conditions or in response to pro-inflammatory cytokines. Our findings show that neither the length of freshly dissected metatarsals from 19 day-old fetal and 1 day-old neonatal $Socs2^{-/-}$ mice, nor their growth over the ensuing 8 days in culture, differed significantly from age-matched wild-type control metatarsals (Figs 7a and 7b). Growth of wild-type and $Socs2^{-/-}$ fetal metatarsals was also significantly inhibited, by comparable amounts, following exposure to $TNF\alpha$ (26% and 27% respectively; both $p < 0.001$) (Fig. 7a). Similarly, $TNF\alpha$ reduced growth to a similar extent in metatarsals derived from 1 day-old neonatal $Socs2^{-/-}$ and wild-type mice (33% and 47% respectively; both $p < 0.001$) (Fig. 7b). This indicates that the $Socs2$ genotype does not modify either the *in vitro* growth of fetal and neonatal metatarsals or their reduced growth following cytokine exposure.

Discussion

Our study has confirmed and extended recent reports that SOCS2 is an important regulator of post-natal skeletal growth. It is also the first study to report that the SOCS2 protein is a negative regulator of bone turnover, mass and architecture.

In the present study, wild-type and $Socs2^{-/-}$ mice showed comparable metatarsal lengths at E19 and 1 day of age and their growth curves did not significantly diverge until 4 weeks of age. At this and later ages, the $Socs2^{-/-}$ mice had greater body weights and lengths, and

had longer and broader tibiae compared to the *wild-type* mice. The wider widths of the proliferative and hypertrophic zones within growth plate of the *Socs2*^{-/-} mice are consistent with increased tibia length. This, together with our observation that SOCS2 protein is present at high levels within the proliferative chondrocytes of the growth plate, suggests that the structural differences in the epiphysis of the *Socs2*^{-/-} mice are a direct consequence of altered chondrocyte SOCS2 signaling. Interestingly, elevated levels of SOCS2 expression were also observed during the chondrogenic, as compared to terminal differentiation phase of ATDC5 growth and this supports our immunohistochemical data. From observations in other cell types, it is possible that SOCS2 may be linked to the transition from the proliferative to the differentiated chondrocyte phenotype. SOCS2 induces the differentiation of C2C12 mesenchymal cells into myoblasts or osteoblasts (Ouyang et al. 2006) as well as the differentiation of neuronal progenitor cells into neurons (Goldshmit et al. 2004; Wang et al. 2004).

Socs2 null mice have been shown to exhibit several features of deregulated GH/IGF-I signaling, including collagen accumulation in the dermis, affected production of major urinary protein, and increased local production of IGF-I in several organs including the heart, lungs and spleen (Metcalf et al. 2000). We, and others (Metcalf et al. 2000; Lorentzon et al. 2005), however have observed no increase in serum IGF-I concentrations in the *Socs2*^{-/-} mice. As the liver is recognised as the major source of circulating IGF-I (Yakar et al. 1999; Sjögren et al. 1999) this observation is consistent with normal IGF-I mRNA expression in the liver of *Socs2*^{-/-} mice (Metcalf et al. 2000). Interestingly, mice with the *high-growth* (*hg*) mutation, which is caused by the deletion of the *Socs2* locus

(Horvat and Medrano 2001), show a 30-50% increment in postnatal growth as well as elevated circulating levels of IGF-I (Medrano et al. 1991). The reasons for the discrepancy in serum IGF-I levels between the *Socs2*^{-/-} and *high-growth* mouse strains are unclear but may involve their different genetic backgrounds. Alternatively, as the *high-growth* mutant strain contains a large deletion of 500-kb in chromosome 10, it is possible that a deletion of other genes or DNA segments flanking *Socs2* locus may be responsible for the elevated circulating IGF-I concentrations in the *high-growth* mutant.

Various studies, encompassing independent targeting or spontaneous null mutations have shown that disruption of the IGF-I gene results in severe intrauterine growth retardation (Liu et al. 1993; Powell-Braxton et al. 1993; Lupu et al. 2001) whereas ablation of GH signaling does not inhibit growth until approximately post-natal day 14 (Lupu et al. 2001). It is therefore more likely that relief of GH inhibition and not IGF-I signaling by SOCS2 is central to the increased post-natal body growth observed in the *Socs2*^{-/-} mice. This is consistent with the knowledge that GH is the major regulator of post-natal growth in mice, where peak GH activity occurs between postnatal days 20-40 (Wang et al. 2004). Additionally, the increased growth of *Socs2*^{-/-} mice was not observed when they were crossed with either mice lacking the STAT5b gene or those with a point mutation in the GH-releasing hormone receptor (*Ghrhr*^{lit/lit} mice) (Greenhalgh et al. 2002, 2005). This provides further confirmation that the *Socs2*^{-/-} overgrowth phenotype is dependent on aberrant GH signaling.

In this present study, we found that the tibia of *Socs2*^{-/-} mice was characterized by an increase in both cortical and trabecular bone mass. This was particularly evident in trabecular bone and these changes in architectural organization are likely to engender greater resistance to bending (or strength) in both compartments. Such changes have not previously been reported in *Socs2*^{-/-} mice and are consistent with an inhibitory role for SOCS2 in the growth of osseous tissues and the enhanced GH/IGF-I signaling seen in *Socs2*^{-/-} mice. The increased bone mass of the *Socs2*^{-/-} mice is associated with a commensurate increase in total mineral content, as volumetric BMD measured by μ CT in both cortical and trabecular bone was similar to wild-type levels. This data contrasts with previous reports where a reduction in both cortical thickness and cortical and trabecular volumetric BMD was reported (Lorentzon et al. 2005). These latter results are difficult to reconcile with the known anabolic effects of enhanced GH/IGF-I signaling on the skeleton (Ohlsson et al. 1998; Andreassen and Oxlund, 2002; Kasukawa et al. 2004) but may be due to the different ages of mice examined, as well as differences in the resolution of the analyses employed. DXA-based measures of BMD are derived from the total bone mass within the projected bone area, and may therefore conceal distinct effects in trabecular and cortical bone. In contrast, both pQCT and μ CT estimate volumetric BMD, distinguish between cortical and trabecular bone, and provide accurate estimates of cortical dimensions, but μ CT allows a greater spatial resolution down to 5-10 microns to be achieved. Increased GH/IGF-I signaling is also consistent with increases in serum indices of bone resorption (TRAP5b) and formation (osteocalcin). It is possible that these indices reflect higher basal rates of bone turnover in *Socs2*^{-/-} mice. We propose that the altered tibial bone structure found in the *Socs2*^{-/-} mice are a consistent and a

direct consequence of increased GH/IGF-I signaling. It remains to be determined, however, whether these altered bone parameters are a consequence only of the faster rates of longitudinal growth evident in *Socs2*^{-/-} mice, or represent a tissue autonomous role for SOCS2 in the maintenance of bone mass.

Previous reports indicate that the induction and/or enhancement of SOCS2 expression by a wide number of pro-inflammatory cytokines in several biological systems, including pancreatic cells (Santangelo et al. 2005), leukocytes (Dogusan et al. 2000) and the liver (Shen et al. 2000) is linked to the behavior of these systems in chronic inflammatory states. We have now shown that SOCS2 expression by chondrocytes increases following exposure to TNF α , a pro-inflammatory cytokine associated with pediatric chronic inflammatory disorders (MacRae et al. 2006a,b). This is the first evidence, indicating a likely role for SOCS2 in mediating cytokine effects on the dynamics of the growth plate.

Abnormal growth patterns are commonly observed in children suffering from chronic inflammatory diseases. These disorders are associated with the increased production of pro-inflammatory cytokines, which inhibit growth plate chondrocyte dynamics (MacRae et al. 2006a,b). To examine whether pro-inflammatory cytokines inhibit bone growth by elevating local SOCS2 to impair the GH/IGF-1 axis, we cultured metatarsals and growth plate chondrocytes derived from *Socs2*^{-/-} and wild-type mice and examined their response to pro-inflammatory cytokines. However, our studies revealed no effect of genotype on either bone growth or chondrogenic markers following TNF α exposure. It is possible that due to low levels of GH signaling, the *in vivo* role of SOCS2 is not essential or is

redundant in pre-weaning mice. It therefore remains possible that distinct biological systems exhibit differing time courses in the development of SOCS2-mediated regulation of cytokine-induced events. This would help to explain why TNF α produced similar effects regardless of the *Socs2* gene context. Our data indicate that in pre-weaning mice, pro-inflammatory cytokines exert their inhibitory effects on the growth plate through a SOCS2-independent mechanism. It is possible that the effects of TNF α may only be revealed in metatarsals from older mice of an age experiencing active GH signaling and which show gigantism in *Socs2* null background. Alternatively, TNF α may mediate their inhibitory effects on bone growth through other SOCS proteins.

In conclusion, the increased bone growth and bone mass observed in the *Socs2*^{-/-} mice support the hypothesis that physiological levels of SOCS2 inhibit signaling through the GH/IGF-I axis and therefore negatively regulate bone formation and endochondral growth. Our data further suggest that pro-inflammatory cytokines mediate their inhibitory effects on longitudinal bone growth through mechanisms that are independent of SOCS2.

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Figure Legends

I. Targeting and screening strategy for construction of *Socs2*^{-/-} mice. (A) The wild type (+) allele and targeting construct (TG) are shown. An insert (~ 7.8 kb) containing IRES- β -geo cassette has been inserted into the *KpnI* site within the exon 2 of the *Socs2* transcript Ensembl ID ENSMUST00000020215 (coding region shown in black). Numbers above restrictions sites are positions within the mouse genome from the Ensembl release 45 - Jun 2007 (<http://www.ensembl.org>). (B) Southern analysis showing a screen for targeted ES clones (left panel) and F₂ mice (right panel). Southern probe (3'-*Socs2* probe) outside the homology arms (see Fig. 1a) was used on *BamHI*-digested genomic DNA to detect the wild type band (~ 24 kb, upper arrow) and a smaller targeted allele-band (~22 kb, lower arrow) due to introduction of additional *BamHI* site within the IRES- β -geo cassette. Left panel shows two targeted ES cell clones (+/-) and original wild type ES cell line (HM1, +/+); HG is high-growth mice DNA known to contain a deletion of this *Soc2* locus; M is a DNA size marker (10 kb ladder). The right panel shows a screen of F₂ mice of homozygous wild type (+/+), heterozygous (+/-) and homozygous knockout (-/-) genotype; HG DNA again serves as a negative control.

Figure II: Body weight (g) growth curves for female wild-type and *Socs2*^{-/-} mice (mean \pm SEM, n=6).

Figure III: Three dimensional μ CT imaging of the metaphyseal trabecular compartment of the tibia in 7-week-old female (a) wild-type and (b) *Socs2*^{-/-} mice.

Figure IV: (a) *Socs2* mRNA expression in wild-type fetal (E14-E18) and neonatal (1 and 9-day-old) primary murine chondrocytes. (b) SOCS2 protein expression in ATDC5 cells during chondrogenesis (C) and terminal differentiation (TD). (c) SOCS2 protein expression in primary costochondral chondrocyte cultures following exposure to TNF α (10ng/ml) for 48h.

Figure V: Immunohistochemical localization of SOCS2 protein expression in a 3-week-old mouse tibia (a) Strong staining within proliferating chondrocytes (arrow heads) whereas weaker staining was observed in the hypertrophic cells (arrows). (b) Osteoblasts (arrows) within the metaphysis close to the chondro-osseous junction stained positive for SOCS2, whereas those in control sections (c) were negative. Scale bars = 50 μ m.

Figure VI: Quantitative RT-PCR analysis of chondrogenic marker expression in primary costochondral chondrocytes of neonatal female wild-type and *Socs2*^{-/-} 1-day-old mice, following exposure to TNF α (10ng/ml) for 48h compared to control. Chondrogenic markers are aggrecan (a) wild-type and (b) *Socs2*^{-/-}; collagen II (c) wild-type and (d) *Socs2*^{-/-}; and collagen X (e) wild-type and (f) *Socs2*^{-/-}. Data are presented as mean \pm SEM, (n=3). Significantly different from control, * P<0.05

Figure VII: Percentage (%) change in length of (a) fetal and (b) postnatal wild-type and *Socs2*^{-/-} murine metatarsals treated with control medium or TNF α (10ng/ml) over an 8 day period (all 10ng/ml) Data are presented as mean \pm SEM, (n=6).