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Commercial Interest:

Granulocyte-macrophage colony stimulating factor as an indirect mediator of nociceptor activation and pain

Nociceptive effects of GM-CSF

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Abstract

The interaction between the immune system and the nervous system has been at the centre of multiple research studies in recent years. While the role played by cytokines as neuronal mediators is no longer contested, the mechanisms by which cytokines modulate pain processing remain to be elucidated. In this study, we have analysed the involvement of Granulocyte-Macrophage Colony Stimulating Factor (GM-CSF) in nociceptor activation in male and female mice. Previous studies have suggested GM-CSF might directly activate neurons. However, here we established the absence of a functional GM-CSF receptor in murine nociceptors, and suggest an indirect mechanism of action, via immune cells. We report that GM-CSF applied directly to magnetically purified nociceptors does not induce any transcriptional changes in nociceptive genes. In contrast, conditioned medium from GM-CSF-treated murine macrophages was able to drive nociceptor transcription. We also found that conditioned medium from nociceptors treated with the well-established pain mediator, Nerve Growth Factor (NGF), could also modify macrophage gene transcription, providing further evidence for a bidirectional crosstalk.

Significance Statement

The interaction of the immune system and the nervous system is known to play an important role in the development and maintenance of chronic pain disorders. Elucidating the mechanisms of these interactions is an important step towards understanding, and therefore treating, chronic pain disorders. This study provides evidence for a two-way cross talk between macrophages and nociceptors in the peripheral nervous system which may contribute to the sensitization of nociceptors by cytokines in pain development.

1. INTRODUCTION

Chronic pain is a debilitating condition affecting large numbers of people (Phillips, 2009), with the prevalence in Europe estimated to be around 20% (Breivik et al., 2006). More surprising perhaps is that more than 50% of those suffering do not respond or get effective relief with current treatments (Nicol et al., 2018). Over the last decade, considerable advances have been made towards understanding the neuro-biological mechanisms underlying chronic pain, with several promising trials of new classes of drug (Ford, 2012; Brown et al., 2012; Schwertner et al., 2013).

Substantial evidence has been presented to suggest that the interaction between neurons and immune cells can result in pain-related conditions stemming from the activation of nociceptors by immune system mediators (Marchand et al., 2005; Hore and Denk, 2019; Cook et al., 2018). Cytokines are also potent neuromodulators that are capable of activation and sensitization of nociceptors (Scholz and Woolf, 2007; Moalem and Tracey, 2006). One such mediator that we have chosen to investigate in this study is granulocyte-macrophage colony stimulating factor (GM-CSF).

GM-CSF has been shown to act as a pro-inflammatory cytokine (Hamilton, 2008). GM-CSF can enhance antigen presentation and drive macrophages into a proinflammatory phenotype that produces inflammatory cytokines such as TNF, IL-6, IL-1β and CCL17 (Cook et al., 2004; Fleetwood et al., 2007; Metcalf, 2008; Achuthan et al., 2016; Hamilton, 2008; Wicks and Roberts, 2016). GM-CSF signalling requires the presence of the GM-CSF receptor (CSF2R), a heterodimer made up of a low-affinity ligand binding α chain (CSF2Rα) and the signal transducing β chain (CSF2Rβ) in a ternary complex (Hamilton, 2008; Hansen et al., 2008; Broughton et al., 2016). Down-stream signalling of GM-CSF involves the Ras/MAPK pathway as well as the JAK/STAT pathway (Hansen et al, 2008; Broughton et al., 2016).

Within the central nervous system, GM-CSF has been shown to play a neuro-inflammatory role by activating microglia (Parajuli et al., 2012; Nicol et al., 2018). The expression of GM-CSFR has also been shown to be increased in infiltrating macrophages and in microglia-like cells in human spinal cord of Multiple Sclerosis patients (Donatien et al., 2018). Inhibition of GM-CSF signalling was found to attenuate arthritic pain (Cook et al., 2012). Additionally, silencing GM-CSF and the gene for its receptor resulted in analgesic effects in models of bone cancer and inflammatory pain (Schweizerhof et al., 2009; Cook et al., 2013). Functional studies have shown that injection of GM-CSF into the paw of laboratory animals produces pain-related behaviour (Acthuthan et al., 2016; Schweizerhof et al., 2009).

However, the pathways and mechanisms behind GM-CSF mediated pain remain elusive (Wicks and Roberts, 2016). There have been claims that the receptor for GM-CSF is expressed in the peripheral nervous system, suggesting that GM-CSF could directly activate nociceptors and thereby drive pain and hyperalgesia (Schweizerhof et al., 2009; Bali et al., 2013). However, multiple recent high throughput RNA sequencing studies suggest that neurons in the dorsal root ganglion (DRG) express the *CSF2Rα* transcript at very low levels but do not express any *CSF2Rβ* (Thakur et al, 2014; Lopes et al., 2017; Flegel et al., 2015; Zeisel et al., 2018). Since both receptor subunits are needed for GM-CSF signalling, these data sets suggest that any effect of GM-CSF on neurons would have to be indirect i.e. via another cell type. Many immune cells found in neuronal tissues do express appropriate receptors. Many studies of GM-CSF have to date studied systems containing multiple cell types, making it difficult to identify direct versus indirect effects.

This study addresses this discrepancy and seeks to elucidate the mechanism behind the activation of nociceptors by GM-CSF. It demonstrates that GM-CSF can exert an indirect effect on nociceptors via macrophages. We show that pain-related genes are transcriptionally upregulated by conditioned media from bone marrow-derived macrophages (BMDMs)

treated *in vitro* with GM-CSF. Hence, while GM-CSF may be incapable of directly activating nociceptors, it can do so indirectly, and contribute to the algesic effects of GM-CSF.

2. METHODS

Animals

For most experiments, adult female C57Bl/6J mice 6-8 weeks of age, weighing around 20-25g were ordered from Envigo, UK. The animals were housed with a 12-hour light/dark cycle with lights on between 7.00 a.m. and 7.00p.m. and unrestricted access to food and water. Animals were housed in groups of 4-8 and cared for in accordance to the United Kingdom Animals Scientific Procedures Act (1986).

In some experiments, adult male and female C57Bl/6J mice from the Walter and Eliza Hall Institute, Parkville, Australia) were used. *Nav1.8*-cre *Csf2rb*$^{fl/fl}$ mice were generated by crossing the *Csf2rb*$^{fl/fl}$ mouse (Croxford et al., 2015) with the *Nav1.8*-cre mouse (gift from JN Wood, London) (described in Stirling et al., 2005), i.e. mice with any GM-CSFR expression deleted in Nav1.8^{+} neurons. Where appropriate, experiments were approved by The University of Melbourne Animal Ethics Committee.

Isolation of DRGs and their dissociation by magnetic separation

Adult female C57Bl/6J mice were terminally euthanized with an overdose of pentobarbital and death confirmed by decapitation. The DRG were taken from all vertebral levels as previously described (Malin et al., 2007). DRG were washed in F12 medium and then dissociated by enzymatic digestion, followed by gentle mechanical dissociation (Thakur et al., 2014). The single cell suspension was exposed to a biotinylated nonneuronal antibody cocktail (Miltenyi MACS Neuron Isolation Kit), followed by antibiotin microbeads (Miltenyi MACS Neuron Isolation Kit). Cells were then run through a LD exclusion column and placed

in a QuadroMACS separator (Miltenyi Biotech) so that only neuronal cells were eluted (>95% pure neuronal cells generated). Neurons were then plated on Matrigel-coated coverslips and cultured for 48 hours (5% CO_2, 95% O_2, at 37°C) in medium with different stimuli as discussed below. For the initial set of experiments, MACS-sorted nociceptor cultures were prepared in parallel to traditional whole DRG cultures. These were treated for 48 hours with either mouse GM-CSF (2µg/ml, Peprotech) or, as a positive control, mouse 2.5S NGF (10ng/ml, Alomone labs).

Bone marrow-derived macrophage isolation and cell culture.

Adult female C57Bl/6J mice were terminally euthanized with pentobarbital and death confirmed by decapitation. The lower body was sterilized with 70% ethanol. The skin, muscles and fat surrounding femur, tibia and fibula were removed, and the bones collected in cold DMEM. The bones were flushed with 5–10 ml of cold PBS and the cells collected, resuspended and plated in DMEM containing 10% FBS, 1% penicillin–streptomycin (Sigma) and macrophage-colony stimulating factor (M-CSF, CSF-1) (Peprotech). Cultures were maintained for 1 week at 37°C (5% CO_2/95% O_2). Once confluent, cells were incubated with non-enzymatic cell dissociation buffer (Millipore) at 37°C for 10 min, scraped carefully and replated at a density of 30,000-50,000 cells per well in DMEM containing M-CSF. Twenty-four hours later, the medium was replaced with M-CSF-free medium and cells were treated with either GM-CSF (2µg/ml) or LPS (100ng/ml) for 48 hours.

Cross stimulation of nociceptor and BMDM cultures

To look for indirect effects of mediators on pure nociceptors and BMDMs, MACS-sorted neurons and BMDMs were cultured for 48 hours with either media alone, GM-CSF or, as a positive control, NGF (for neurons) or LPS (for BMDMs). 48 hours later, fresh cultures of MACS-sorted neurons and BMDMs were plated, as described above. Supernatants from the neurons treated for 48 hours were added to the fresh BMDM cultures, and similarly

supernatants from the BMDMs treated for 48 hours were added to the fresh neuron cultures. Supernatants were centrifuged to remove any cells and then 1ml was added to the respective wells. These were further cultured for 24 hours, following which cells were taken for RNA extraction and gene expression analysis.

RNA extraction and Taqman qPCR array cards

In each of the experiments, cells were lysed and RNA was extracted from cultured whole DRG and MACS-sorted DRG samples using the RNeasy microkit (Qiagen) following the manufacturer's protocol with some minor modifications. RNA integrity was assessed on the Agilent 2100 Bioanalyzer Pico Chip (Agilent, Santa Clara, CA). The RNA integrity number (RIN) for each of the samples used was >8. Samples with a RIN of <8 were not used for qPCR analysis. Following RNA extraction, the samples were amplified and reverse transcribed using the Repli-g WTA single cell amplification kit (Qiagen). The cDNA was used for gene expression analysis by using the Taqman custom-made microfluidic array cards (Thermofisher). These custom-made cards were designed in-house and contained primers and probes to detect 45 test genes as well as three housekeeping genes for reference (18S, GAPDH and Ywhaz (B2M in macrophage card)). Three types of cards were used in this study. The first card, used to look for differences between whole DRG and MACS-sorted samples, contained probe sets for a mixture of neuronal and non-neuronal genes known to be present in the DRG that can be activated by NGF and other mediators. These include genes such as TRPVI and TRPA1, ion-channels widely expressed on neuronal cells known to be involved in nociception (Caterina and Julius, 2001; Bevan, Quallo and Andersson, 2014; Huang et al., 2017). In addition, the array card contained probe sets for some cytokine and chemokine genes. The second card contained probe sets for genes that are known to be specifically involved in axotomy and pain-related behaviour. These included neuropeptides, such as Galanin and Neuropeptide Y, known for their role in nociception (Kerr et al., 2000; Brothers and Wahlestedt, 2010), proteins such as Annexin 1 and ADAM8 known for their

role in modulating inflammatory pain (Chen, Lv and Pei, 2014; Schlomann et al., 2000) in addition to other markers associated with pain such as CSF-1, BDNF and NGF. Finally, the third card contained probe sets for genes that are present in macrophages. They include canonical inflammatory mediators such as IL6, TNF and CCL17 (Laskin, 2009). The transcripts measured by each card are given in **Table 1.**

Each cDNA sample was quantified using a Qubit BR ssDNA assay kit and diluted in PCR grade water to a final concentration of 6ng/µl. This was added to Taqman Universal 2x Master mix (Thermofisher) to achieve a final volume of 100 µl. TaqMan array cards were run on a 7900HT Fast Real-Time PCR system (Applied Biosystems) and gene expression calculated using the ddCT method (normalizing each sample to the average of the three housekeeping genes and then to their respective internal controls, usually the unstimulated/untreated samples). Samples with cycling thresholds of 40 in the unstimulated conditions were not included in the analysis.

Measurement of $[Ca^{2+}]_i$ in DRG neuron

Mouse DRG neurons were dissociated from whole DRGs as previously described (Rajasekhar et al., 2015) and plated onto coverslips coated with poly-L-lysine and 100 µg/ml laminin. The DRG neurons were maintained in DMEM containing antibiotic-antimitotic, 10% FBS, and N-1 supplement at 37°C (5% CO_2/95% O_2) for 24 hours. The DRG neurons were loaded with Fura-2/AM ester (5µM, 45 min, 37 C) in calcium assay buffer (10 mM HEPES, 0.5% BSA, 10 mM D-glucose, 2.2 mM $CaCl_2 \cdot 6H_2O$, 2.6 mM KCl, 150 mM NaCl) containing 4 mM probenecid and 0.05% pluronic F127. Cells were washed and incubated in calcium assay buffer for 30 min before imaging. Cells were observed using a Leica DMI-6000B microscope with an HC PLAN APO 0.4 numerical aperture X 10 objective and maintained at 37° C. Images were collected at 1 second intervals (excitation: 340 nm/380 nm; emission: 530 nm). Cells were challenged sequentially with vehicle, GM-CSF (200 ng/ml),

capsaicin (0.5 μM; TRPV1 agonist). 50mM KCl, in calcium assay buffer containing probenecid, was applied at the end of the experiment to obtain maximal $[Ca^{2+}]i$.

Results are expressed as the 340/380 nm fluorescence emission ratio, which is proportional to changes in $[Ca^{2+}]i$. Data are presented as F/F0, where F is the measured fluorescence intensity and F0 is the basal fluorescence. All F/F0 values have been subtracted by 1. In each experiment two technical replicates were included with 68 – 559 neurons recorded in each repeat. The experiment was repeated three times (n=3) with equivalent results. A response was deemed positive if it was ≥10% above baseline. Results were excluded from the analysis if they showed a fluctuating calcium response prior to addition of GM-CSF or did not show pronounced reversibility (>50%) from the peak response to GM-CSF application and did not respond to KCL addition. This constituted <1% of DRG neurons studied.

Detection of ERK1/2 and STAT5 activation in neurons stimulated with GM-CSF

The dissociated DRG neurons plated onto coverslips, as described above for measurement of $[Ca^{2+}]$ (Rajasekhar et al., 2015), were also used for the detection of ERK1/2 and STAT5 activation following GM-CSF stimulation. Following a 24 hour culture in DMEM containing antibiotic-antimitotic, 10% FBS, and N-1 supplement at 37°C (5% CO_2/95% O_2), the neurons were serum-starved overnight (17-18h) by incubating them in DMEM supplemented with 0.1% (w/v) BSA, 100 U/ml penicillin, 100 mg/ml streptomycin, and 1% (v/v) N1 in a humified incubator at 37° C (95% O_2, 5% for CO_2). Subsequently, neurons were stimulated for 15 min with PBS, GM-CSF (200 ng/ml) or PMA (2 μM, Sigma). Cells were then washed in ice-cold PBS and fixed in 4% paraformaldehyde in PBS for 20 min at room temperature. After 3 washes with PBS, cells were blocked and permeabilized by incubating with PBS supplemented with 0.01% Triton-X, 5% heat-inactivated FBS, and 5% goat serum for 60 min. Neurons were washed (3 x PBS), then stained overnight with mouse anti-mouse NeuN mAb (clone A60) (Millipore) in combination with either rabbit anti-mouse phospho-p44/42 MAPK (Erk1/2) (Thr202/Tyr204) (197G2) mAb (Cell Signaling Technology) or rabbit anti-

mouse phospho-STAT5 (Y694) (D47E7) XP® mAb (Cell Signaling Technology); all primary antibodies were diluted in PBS with 5% FBS and 0.01% Triton-X. Following washing (3 x PBS), neurons were incubated with goat anti-rabbit IgG (H+L) antibody, Alexa Fluor®568 conjugate (ThermoFisher) and goat anti-mouse IgG (H+L) antibody, Alexa Fluor®488 conjugate (ThermoFisher). Neurons were washed (3 x PBS), then stained with DAPI (1 μg/ml, 5 min; EMD Millipore). In all experiments, secondary antibody only and single primary antibody controls were included in order to check for nonspecific secondary binding and bleed-through of fluorochromes, respectively.

Images were obtained with a Zeiss Axioskop 2 at 10X magnification and captured by a Zeiss AxioCam MRm. Each condition included two technical replicates and 5 images were taken from each replicate. Quantification of positive cells was performed with ImageJ software. For neurons, only NeuN positive cells were included in the analysis. To determine when cells were positive a lower threshold for staining intensity in the green channel (Alexa Fluor 488) was set based on the PBS-treated control cells. Cells with fluorescence intensities above this threshold were regarded as positive. A mean of positive cells across the 10 images from each condition was calculated. Three separate experiments were performed.

GM-CSF-induced inflammatory pain

Inflammatory pain was induced by a single intraplantar (i.pl.) injection (10 μl) of GM-CSF (50 ng/paw, R&D Systems) into the left hind footpad (Achuthan et al., 2016; Cook et al., 2018).

mBSA/GM-CSF-induced arthritis

Monoarticular arthritis was induced by an intraarticular injection of methylated BSA (mBSA) (100 μg in 10 μl) into the right knee on day 0, and saline into the left knee, followed by a s.c. injection of GM-CSF (600 ng) into the scruff of the neck on days 0-2, as before (Achuthan et al., 2016; Cook et al., 2018). Mice were sacrificed (day 7) and knee joints were removed, fixed, decalcified and paraffin embedded (Achuthan et al., 2016; Cook et al., 2018). Frontal

sections (7 μm) were stained with H&E and cellular infiltration, synovitis, pannus formation, cartilage damage and bone erosions were each scored separately from 0 (normal) to 5 (severe) as described previously (Achuthan et al., 2016; Cook et al., 2018); these scores were then added to give the total histologic score for each mouse.

Assessment of pain-related behaviours

As an indicator of pain, the differential weight distribution over a 3 second period between the inflamed paw or limb relative to the non-inflamed paw or limb was measured using the incapacitance meter (IITC Life Science Inc). This technique has been validated for measurement of both paw and arthritic knee pain (Achuthan et al., 2016; Cook et al., 2018). Mice were acclimatised to the incapacitance meter on at least 3 separate days prior to the commencement of the experiment. Three measurements were taken for each time point and averaged.

Experimental Design and Statistical Analysis

All data are expressed as mean ± SEM, except where stated as median. Statistical analyses were performed using SPSS (IBM version 23). Kruskal-Wallis non-parametric independent samples tests were used for analysis of Figures 1, 3 and 4. The samples were corrected for multiple testing using the Bonferroni correction. For calcium imaging in Figure 2, GM-CSF activation of neurons and histology, a one-way ANOVA was used, and for pain readings, a two-way ANOVA was used, with either a Bonferroni or Tukey post-hoc test. A p-value less than 0.05 was considered significantly different to the null hypothesis of no difference at the 95% confidence level.

3. RESULTS

The literature around the involvement of GM-CSF in chronic and neuropathic pain remains sparse. However, even within this limited literature there is little consensus on the possible mechanisms behind the actions of GM-CSF in pain. To clarify, we have undertaken a number of experiments, as follows:

3.1 GM-CSF does not modulate gene expression in purified neurons from mouse DRG

Previous studies have reported that GM-CSF can act directly on nociceptive neurons, and as a result, cause hyperalgesia (Schweizerhof et al., 2009; Parajuli et al., 2012). Here, we began by addressing the discrepancy in the literature on the mode of action of GM-CSF by using Magnetically-Activated Cell Sorting (MACS) to enrich for small and medium diameter neurons (which are nearly all nociceptors) from mouse DRG. Thakur et al. (2014) showed that dissociated DRG preparations that are commonly used for analysis actually contain predominantly non-neuronal cells. In contrast, they showed, that following MACS isolation, a culture of 95% pure nociceptors can be produced from adult mouse DRG. Large diameter neurons (>30µm), which are lost during MACS, are largely non-nociceptive (Dubin and Patapoutian, 2010) and hence their absence is an asset rather than a disadvantage when studying the role of GM-CSF is nociception and peripheral sensitization.

Parallel cultures of cells from adult mouse DRG were set up using either the traditional dissociation technique to prepare the mixed (i.e. unsorted) cultures and purified cultures (i.e. sorted) from adult mouse DRG obtained after MACS. For these sets of experiments, 48 genes that are known to be expressed in the DRG, including some internal housekeeping controls (GAPDH, 18S and YWhAZ), were developed into a Taqman qPCR array card (Thermofisher). This card was used as a screening tool to help provide an indication towards

specific pathways or areas of interest to be investigated further. The list of genes present on the card is provided in **Table 1A**.

Figure 1(A) is a heatmap that shows the gene expression changes in mixed DRG cultures and pure neurons following GM-CSF and NGF treatment in the panel tested. It is evident that GM-CSF had an overall greater impact in mixed cultures as compared to pure neuronal cultures. Only 6% of the genes (n=2/34, namely CSF2RA and IL6) showing a greater than 2-fold average increase in expression level following GM-CSF treatment in the purified neuronal cultures and none of the differences reached statistical significance.

However, when GM-CSF was applied to the mixed DRG cultures, 44% of the genes (n=15/34) showed a 2-fold or more average increase in gene expression, and four of these were found to reach statistical significance with an average increase in expression of 2.3-fold. **Figure 1B** shows the significantly altered genes (black dots) along with those showing a greater than 2-fold increase in expression. The overall average increase in gene expression in the mixed cultures with GM-CSF stimulation was 3.9-fold, whereas purified cultures following GM-CSF stimulation showed an average of 1.6-fold increase.

As a positive control, we applied NGF instead of GM-CSF to the mixed and purified cultures and found, as expected, a significantly increased expression of 12 and 5 genes, respectively. 50% of the genes showed a 2-fold or greater average increase in expression in the mixed DRG cultures, whereas around 32% of the genes in purified cultures showed a 2-fold or more average increase in expression. The average fold increase of the significant genes was 5.8 and 2.5 fold in the mixed and purified cell cultures, respectively *(data not shown)*.

These results suggest that GM-CSF is incapable of driving *direct* transcriptional changes in neuronal genes in nociceptors. However, changes in neuronal genes in the mixed cultures following GM-CSF treatment indicate that it might be having an indirect effect on nociceptors via satellite cells or other non-neuronal cell types that make up the majority of

the cells in the DRG, and indeed in the mixed DRG cultures. In order to obtain supporting evidence for the proposal that GM-CSF is incapable of directly stimulating nociceptor transcription, we reviewed recent publications that have made use of RNA sequencing to examine gene expression in mouse and human DRG (**Table 2,** Thakur et al., 2014; Lopes et al., 2017; Zeisel et al., 2018; Flegel et al., 2015; Ray et al., 2018; Ray et al., 2019). The Table compares the expression of the two GM-CSF receptor chains to several control transcripts: *Calca*, one of the most highly expressed genes in DRG; *TrpV1* and *Nav1.8*, which are well expressed in nociceptive neurons; and Dnmt3a, which is very lowly expressed (Saunders et al, 2018). It is evident the two transcripts coding for the receptor chains of the GM-CSF receptor, namely *CSF2Rα* and *CSF2Rβ*, are expressed at levels below our negative control transcript in the DRG - the *CSF2Rβ* gene, in particular, appears to be undetectable, even by a technique as sensitive as RNA-seq. In whole human tibial nerve, mRNA for both receptors can be detected at higher levels, presumably due to a contribution from non-neuronal cells (Ray et al., 2019).

3.2 GM-CSF does not directly activate neurons in vitro and in vivo

To support the above gene expression data, suggesting an indirect effect of GM-CSF on neurons, we monitored some signalling pathways in cultured DRG neurons. We were unable to observe any GM-CSF-stimulated elevation in intracellular Ca^{2+} levels (**Figure 2A and B**) or ERK1/2 phosphorylation (**Figure 2C**) when compared to our positive controls, namely capsaicin and PMA, respectively. We were also unable to detect STAT5 phosphorylation following GM-CSF stimulation in these neurons, unlike in murine macrophages grown from bone marrow cells in GM-CSF (Fleetwood et al, 2007) (*data not shown*).

Table 2B indicates that $Nav1.8^{+}$ neurons do not express the *Csf2rb* gene and therefore cannot express a functional GM-CSFR. In order to demonstrate in vivo that GM-CSF-induced pain development is not due to GM-CSF receptor signalling via $Nav1.8^{+}$ neuronal cells (that is, the

majority of nociceptors), *Nav1.8*-cre *Csf2rb*$^{fl/fl}$ mice were generated by crossing the *Csf2rb*$^{fl/fl}$ mouse (Croxford et al., 2015) with the *Nav1.8*-cre mouse (Stirling et al., 2005) - these mice will lack any functional GM-CSF receptors that may possibility be expressed in Nav1.8^{+} neurons. GM-CSF-induced inflammatory pain and GM-CSF-induced arthritic pain were then initiated, and pain development measured by a change in weight distribution (using the well-validated incapacitance meter method (Achuthan et al., 2016; Cook et al, 2018)). Following intraplantar injection of GM-CSF, pain was evident in *Csf2rb*$^{fl/fl}$ control and also in *Nav1.8*-cre *Csf2rb*$^{fl/fl}$ mice (**Figure 2D**). Similarly, following induction of mBSA/GM-CSF arthritis, similar pain development was evident in WT, *Csf2rb*$^{fl/fl}$ control and *Nav1.8*-cre *Csf2rb*$^{fl/fl}$ mice from day 3 onwards (**Figure 2E**); all three strains developed a similar degree of arthritis (at day 7, as judged by histology) (**Figure 2E**). Taken together, these *in vitro* and *in vivo* data do not support a direct action of GM-CSF on neurons consistent with a lack of GM-CSF receptor gene expression in neurons.

3.3 Nociceptor gene expression can be indirectly modulated by GM-CSF stimulated BMDMs

As mentioned, based on the above data, we hypothesised that GM-CSF might be having an indirect effect on nociceptors via non-neuronal cells that are present within the DRG and in the periphery at a site of injury. Macrophages are one cell type present in the DRG and known to be responsive to GM-CSF as well as being a potential source of pain mediators (Cook et al., 2018, Hore and Denk, 2019). To look for potential indirect effects of GM-CSF, supernatants from GM-CSF-stimulated BMDM cultures were added to sorted neuronal cultures to test whether these BMDMs are capable of producing mediators which can elicit transcriptional changes in neurons. Since our overall aim was to look at the mechanism of GM-CSF action in pain, a second Taqman card containing probe sets for genes that are known to be involved in axotomy and pain-related behaviour was used (**Table 1B**).

Once again, direct treatment of purified nociceptors with GM-CSF did not cause any significant dysregulation in the genes present on this array card (**Figure 3**). Conditioning medium from unstimulated BMDMs had no significant impact on neuronal gene transcription (data not shown). Following treatment with conditioning medium from GM-CSF treated BMDMs, 31% of the genes tested showed 2-fold or more average increase in gene expression, calculated by normalizing the transcriptional changes to neuronal cultures that received supernatants from unstimulated BMDMs. Six genes were found to be significantly dysregulated following indirect stimulation with GM-CSF. These were *ADAM8* (3-fold increase), *ANXA1* (5-fold increase), *IL6* (3.5-fold increase), *PRDM12* (0.5-fold decrease), *CSF-1* (2.4-fold increase) and *JAK2* (2.6-fold increase). In addition to the genes that reached statistical significance, there were several other changes in known pain-related genes, such as *TNFSF12* (3.6-fold increase), *USP18* (5-fold), *GAL* (2.9 fold), *NGF* (2.4 fold) and *NPY* (2.4 fold), which showed increased expression following indirect activation using GM-CSF treated conditioning medium, but which did not reach statistical significance **(Figure 3).**

3.4 Macrophage gene expression can be indirectly modulated by NGF stimulated nociceptors

We investigated next the possibility of cross-talk between stimulated nociceptors and macrophages. While there is growing evidence to support the view that stimulated immune cells can communicate with neurons (Marchand et al., 2005; Scholz and Woolf, 2007; Watkins and Maier, 2002; Sorge et al, 2015, Hore and Denk, 2019), which is supported by the data in Figure 3, the literature on the ability of stimulated neurons to communicate with immune cells is more limited (McMahon, LaRussa and Bennett, 2015). To examine this possibility, we used a similar strategy to that used in Figure 3 to explore whether nociceptors that had been treated with NGF were capable of producing mediators that could modulate macrophage gene expression. A third Taqman card containing 48 genes, of which 29 genes

423 are known to be expressed in macrophages at levels which depend on their functional state
424 (Murray et al., 2014), was used. (**Table 1C**).

425 As positive controls, we found that GM-CSF (Figure 4A) and LPS (Figure 4B) stimulation of
426 BMDMs, as expected, had large impacts on gene transcription. GM-CSF treatment led to
427 55% of the genes having a 2-fold or more increase in expression; out of these, 9 were found
428 to be statistically significant after correcting for multiple testing. They were Ccl17, Ccl22,
429 Ccr2, Il4ra, Irf4, Nfil3, Socs1, Socs2 and Socs3 (**Figure 4A**). Additionally, cytokine genes
430 such as Il6, Il1b and Il27 were also found to be upregulated, although without reaching
431 statistical significance. Stimulation of BMDMs with LPS led to 72% of the genes having a 2-
432 fold or more increase in expression and, out of these, six reached statistical significance,
433 namely, Ccl17, Fcgr1, Il1b, Il6, Socs1 and Socs3 (**Figure 4B**).

434 Conditioning medium from unstimulated neurons had no impact on BMDM gene
435 transcription (*data not shown*). Conditioning medium from NGF treated nociceptors caused a
436 2-fold or more increase in 69% of the genes. Although only four genes reached statistical
437 significance, namely CCR2, IL4Ra, IRF4 and SOCS2 (**Figure 4C**). There were several other
438 genes, namely CCL22, IL1b, IL6, SOCS1 and SOCS3, that showed a trend towards increased
439 expression following treatment with NGF-stimulated conditioning medium (**Figure 4C**). It
440 should be noted that BMDMs do not express the receptors for NGF (TRKA and p75) (e.g. see
441 RNA-seq data in Ostuni et al, 2013; Piccolo et al., 2017; Hill et al., 2018), demonstrating that
442 NGF stimulated neurons can produce mediators capable of activating macrophages.

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4. DISCUSSION AND CONCLUSION

In this present study we provide evidence that GM-CSF does not directly activate nociceptors but suggest that GM-CSF acts through macrophages to produce mediators which interact with nociceptors. We provide evidence for a bi-directional cross-talk between neurons and macrophages.

Previous studies have suggested that GM-CSF can act on and stimulate sensory neurons. Bali et al. (2013) suggested that GM-CSF brought about transcriptional regulation of several pain genes in sensory neurons in a model of cancer pain, an observation replicated by Schweizerhof et al. (2009) and Zhang et al. (2019). Donatien et al., 2018 report that GM-CSF can enhance capsaicin-induced calcium influx in DRG neurons, although not directly induce calcium influx. However, these studies did not separate neuronal cells from non-neuronal cells within the DRG and hence it is difficult to attribute these changes specifically to sensory neurons. In contrast, other recent publications (Lopes et al., 2017; Zeisel et al., 2018) making use of RNA-sequencing to look for transcriptional changes in a cell-specific manner have indicated the absence of the GM-CSFRβ chain on nociceptors, indicating alternate mechanisms of action. In this context, a TrkA inhibitor was able to reduce the GM-CSF enhanced capsaicin-induced calcium influx response, suggesting GM-CSF may be acting indirectly via NGF (Donatien et al., 2018).

Therefore, we looked for changes caused by stimulating purified nociceptors with GM-CSF and found no significant transcriptional changes. Also, even if there was some expression of the GM-CSF receptor on neurons, deleting the Csf2rβ subunit in Nav1.8^{+} neurons (i.e. most nociceptors) *in vivo* showed no effect on the generation of GM-CSF-driven inflammatory and

arthritic pain, suggesting that GM-CSF does not act directly via nociceptors. It has been reported that low and high threshold Aβ fibres respond to GM-CSF (Schweizerhof, 2009). **B**ased on our findings, we consider that these responses are **possibly indirect although further studies are needed to address this issue**. Overall, our results lead us to hypothesise that the reported effects of GM-CSF on DRGs (Bali et al., 2013; Schweizerhof 2009) were predominantly due to the ability of GM-CSF to activate non-neuronal cells associated with nociceptors, likely in the peripheral nerve itself or during myeloid cell infiltration into the DRG. These non-neuronal cells might then indirectly bring about transcriptional changes in nociceptors associated with pain/hyperalgesia.

Macrophages are one of the most commonly studied cell type in the pain field due to their involvement in the pathogenesis of various neuropathies (Lu and Richardson, 1993). Zhang et al. (2016) showed that recruitment of macrophages to the DRG was important for inducing and maintaining chemotherapy-induced peripheral neuropathy, an observation in accordance with several other studies showing increased myeloid cells in the DRG following peripheral injury (Hu and McLachlan, 2002; Fenzi et al., 2001). Furthermore, Shepherd et al. (2018) showed that the angiotensin II receptor (AT2R) antagonist reduces neuropathic pain by blocking the downstream signalling of AT2R in infiltrating peripheral macrophages, as sensory neurons lack expression of this receptor. Blocking of macrophage activation using TLR antagonists (Jurga et al., 2018) and inhibitors of p38 MAPK/MMP9 (Hutchinson et al., 2008; Mika et al., 2007), PI3K and NF-kB (Popiolek-Barczyk et al., 2015) has analgesic effects in various models of neuropathic pain, consistent with our proposed mechanism of action.

We therefore analysed whether factors from stimulated macrophages can bring about transcriptional changes in nociceptors that mimic injured or activated nociceptors. We found that supernatants from GM-CSF stimulated macrophages upregulated several neuronal genes,

namely ADAM8, ANXA1, IL6, CSF-1 and JAK2, which are also significantly upregulated following injury (Chen et al., 2014; Pei et al., 2011; Tang et al., 2018; Guan et al., 2016; Ding et al., 2018; Diaz-DelCastillo et al., 2018). Supernatants from GM-CSF stimulated macrophages were found to significantly down-regulate expression of PRDM12, an important nociceptor gene (Desiderio et al., 2019). There is evidence to suggest that, following injury, activated monocytes from the spleen and lymph nodes infiltrate into the site of injury as well as the associated DRG (Hu and McLachlan, 2002; Schmid et al., 2013). It is expected that inflammatory cytokines from these immune cells can then impact the neurons by affecting their firing rates and causing changes in gene expression (Ozaktay et al., 2006; Ohtori et al., 2004).

Of the mediators that were upregulated in our experimental set up, CSF1 was of particular interest from the perspective of nerve injury. The role of microglia in chronic pain is well established, with various proposed mechanisms to drive microglial activation and central sensitisation in a variety of pains states (Calvo and Bennett, 2012; Denk et al., 2016; Fernandez-Zafra et al., 2018). It has been demonstrated that peripheral nerve injury induces the production of CSF-1 in neurons, which then recruit spinal cord microglia to proliferate (Guan et al., 2016). The presence of large numbers of activated microglia is responsible for further activation of spinal neurons and maintenance of neuropathic pain through the release of inflammatory and neuropathic mediators (Kawasaki et al., 2008, Zhao et al., 2017). The release of CSF-1 from nociceptors raises the possibility of bi-directional cross-talk with nociceptors further recruiting and stimulating macrophages in a positive feedback loop. Therefore, we looked for transcriptional changes in macrophages following treatment with conditioning media from stimulated neurons.

Analysis of macrophages at a site of nerve injury has shown them to be predominantly anti-inflammatory in nature and involved in regeneration and recovery of the nerve (Ydens et al.,

2012; Gaudet, Popovich and Ramer, 2011). Interestingly, macrophages stimulated with supernatants from NGF treated neurons led to an upregulation of cytokine and chemokine receptors (IL4Ra and CCR2) and transcription factors (SOCS2 and IRF4). Since NGF by itself is incapable of directly activating macrophages (Ostuni et al., 2013; Piccolo et al., 2017; Hill et al., 2018), it can be assumed that the transcriptional changes in macrophages were due to mediators being released by these stimulated nociceptors (Vega et al., 2003). Furthermore, these transcriptional changes were distinct from those following direct stimulation with LPS or GM-CSF, suggesting a distinct mechanism of action. We found that NGF stimulated nociceptors upregulate the expression of inflammatory mediators and chemokines, such as IL-1β, IL6 and CCL22, which have the potential to activate and recruit macrophages.

Here we, like many others, have used *in-vitro* dissociated DRG cultures to study nociceptive processes. However, unlike nearly all previous studies, we use highly purified neurons in the culture. This allows us to disambiguate direct versus indirect effects of applied agents – a key advantage and main point of this study. The disadvantage being that the cellular properties inevitably change somewhat over time in culture as seen by transcriptional profiling of such cultures (Thakur et al., 2014; Lopes et al., 2107; Wangzhou et al., 2019). Some of the emergent changes suggest that cultured nociceptors take on a ‘neuropathic’ phenotype (Wangzhou et al., 2019) and so one caveat of the current work is that, inevitably, the neurons we studied are not in their native state.

One of the problems we faced during these experiments was the intra-group variability observed in the transcriptional analysis. Variability in transcriptional analysis is a common phenomenon (Volfson et al, 2006; Raser and O’Shea, 2005) since transcription is not a continuous process, but rather a discontinuous one that takes place in ‘bursts’ and ‘pulses’. Hence differences in the expression levels of lowly and highly expressed genes can be observed even in the absence of any stimulus leading to the observed variability (Chubb and

Liverpool, 2010). In this study, we have made use of stringent statistical tests in order to cover the inherent intra-group variability and hence identify transcripts that are genuinely dysregulated because of the treatments.

It is important to note in this context, that whilst nociceptor transcriptional change is very common in persistent pain states, nociceptors can be activated and sensitised without transcriptional change (eg Wu et al., 2001; Zhang and Strong, 2008). But transcriptional change in nociceptors, when it does occur, can lead to changes in the sensitivity and activity of these neurons and is thereby an important regulator of nociceptor function. In the current experiment we looked for acute effects of GM-CSF on calcium signalling in purified nociceptors but did not observe any of these non-transcriptional actions. Others who have seen non-transcriptional effects of GM-CSF on cultured neurons have used mixed cultures containing a variety of cell types which may allow for indirect activation of nociceptors via non-neuronal cells **(Schweizerhof et al., 2009; Bali et al., 2013; Donatien et al., 2018).** Indeed, in those experiments, the non-transcriptional effects of GM-CSF were blocked by trkA inhibitors, suggesting the release of secondary mediators.

In conclusion, the findings in this study highlight the need to dissect the mechanisms of action of cytokines at a cell-type specific level, with a view to developing more targeted therapies and interventions to treat pain. Our findings support the concept that immune cells and neurons at the site of nerve injury are engaged in a loop that involves cross-talk between them. More specifically, pro-inflammatory mediators and cytokines released from GM-CSF stimulated monocytes or macrophages act on neurons which in turn release neurotransmitters that can further activate these immune cells. The net effect is likely to be peripheral sensitization and consequent chronic pain.

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927

Legends

Table 1: (A) Genes represented on a DRG card. (B) Genes represented on an axotomy card. (C) Genes represented on a macrophage card.

Figure 1: GM-CSF causes dysregulation of genes in mixed DRG cultures but not in purified neuronal cultures. (A) Heatmap representing the transcriptional changes in a panel of genes (see Table 2A) was assessed in mixed DRG cultures and pure MACS sorted neuronal cultures from C57Bl/6J mice following treatment with GM-CSF (2µg/ml) for 48hrs and NGF (10ng/ml). Each column represents average data of n=8 independent experiments. Each individual experiment contained pooled cells from two mice. (B) Genes showing a 2-fold or greater change in expression changes following GM-CSF treatment in unsorted DRG cell cultures as compared to purified neurons. Each dot represents a separate gene which is an average of n=8 experiments. Dotted line represents untreated control. Solid line represents mean of each group. Kruskal-Wallis test was conducted to identify genes that were significantly modulated after treatment with GM-CSF in mixed DRG cultures (highlighted black dots). The results were corrected for multiple comparisons using the Bonferroni correction. None of the genes from purified neuronal cultures reached statistical significance after GM-CSF treatment. *, adj $p<0.05$; * = Genes significantly different from untreated control. +, adj $p<0.05$ and ++, adj $p<0.01$; + = Genes significantly different between whole DRG and purified neurons.

Table 2: Expression values derived from publicly available (A) bulk and (B) single cell RNA-sequencing datasets. Data for Csf2ra and Csf2rb are provided along with the following control/comparison genes: *Calca*, which is one of the most highly expressed genes in DRG; *TrpV1*, which is well expressed in nociceptive neurons; *Dnmt3*a which is very lowly expressed if at all in neurons (Saunders et al., 2018); *Nav1.8*; CD40, a myeloid cell marker;

and *Uchl1*, the gene coding for a protein which is highly expressed in nerve fibres,. FPKM = fragments per kilobase per million mapped reads; TPM = transcripts per million.

Figure 2. GM-CSF does not directly activate neurons in vitro and in vivo. (A-B) Time course and peak Ca^{2+} responses in mixed DRG cultures in response to vehicle, GM-CSF (200 ng/ml), capsaicin (0.5 µM) and KCl (50 mM) (only A), respectively. **(A)** *grey lines*, individual traces from 50 random cells; *black lines*, mean response; **(B)** n=1767 neurons (pooled data from two independent experiments). **(C)** Percentage of DRG neurons positive for phospho-ERK1/2 following stimulation with PBS, PMA or GM-CSF (200 ng/ml) for 15 mins. Three independent experiments were performed. **(D-E)** Pain development (incapacitance meter – ratio of weight bearing on injected relative to noninjected knee/hindpaw – a value of < 100 indicates pain) was measured following **(D)** intraplanatar (i.pl.) injection of GM-CSF (20 ng) in *Csf2rb*$^{fl/fl}$ and *Nav1.8*-cre *Csf2rb*$^{fl/fl}$ mice (n=5-8 mice/group) and **(E)** mBSA/GM-CSF arthritis (mBSA i.a. [day 0]; GM-CSF or saline s.c. [days 0-2]) induction in WT, *Csf2rb*$^{fl/fl}$ and *Nav1.8*-cre *Csf2rb*$^{fl/fl}$ mice (n=4-7 mice/group). For **(E)** arthritis (histology, day 7) was also assessed. (C-E) Data is expressed as mean ± SEM. For (B) and (C), a one-way ANOVA was used. *** $p<0.001$, **** $p<0.0001$.

Figure 3: Nociceptor gene expression can be indirectly modulated by conditioning media from GMCSF stimulated BMDMs. Genes dysregulated by 2-fold or more from nociceptors that received conditioning medium from GM-CSF (2µg/ml) treated BMDMs. Each dot represents a separate gene which is an average of n=10 individual experiments. Kruskal-Wallis test was conducted to identify genes that were significantly modulated after treatment with the conditioning medium (highlighted black dots). The results were corrected for multiple comparisons using the Bonferroni correction. None of the genes from purified neuronal cultures that were treated directly with GM-CSF (2µg/ml) reached statistical significance. Samples with cycling thresholds of 40 in the unstimulated conditions were not

included in the analysis. Dotted line represents untreated control. Solid line represents mean of each group. No significant changes were seen with untreated conditioning media control from BMDMs on neuronal cultures. *, adj $p<0.05$; * = Genes significantly different from untreated control. ++, adj $p<0.01$; + = Genes significantly different between direct GM-CSF stimulation and conditioning media with GM-CSF.

Figure 4: Macrophage gene expression can be indirectly modulated by NGF stimulated nociceptors. BMDMs were treated with (A) GM-CSF, (B) LPS and (C) conditioning medium from NGF-stimulated nociceptors for 48hrs (Materials and Methods). The fold change in the expression of dysregulated genes on a macrophage card (Table 1C) is depicted on a $\log_{10}$ scale. Only significantly dysregulated genes are depicted in (A) and (B). Each dot represents a separate experiment (n=10). Kruskal-Wallis test was conducted to identify genes that were significantly modulated after treatment. The results were corrected for multiple comparisons using the Bonferroni correction. Dotted line represents untreated controls where conditioning media from untreated nociceptors was applied to BMDMs. No significant changes were seen in BMDM cultures treated with conditioning medium from untreated nociceptors as a control. Box and Whisker plots showing maximum to minimum range. Samples with cycling thresholds of 40 in the unstimulated conditions were not included in the analysis. *, adj $p<0.05$; **, adj $p<0.01$ and ***, adj $p<0.001$.

Table 1: Genes probe sets present on qPCR array cards.

(A)

Adcyap1	Tac1
Atf3	Trpa1
Bdnf	Trpv1
Cacna2d1	Gapdh
Calca	Ywhaz
Ccl2	Il6st
Nos1	Ccl4
Vgf	Il6
Gal	Il11
Gch1	Stat3
18S	Tnf
Ngf	Tlr4
Ngfr	Il1b
Npy	Ccl3
Ntrk1	Ccl5
Ntrk2	Cxcl12
Ntrk3	Il18
Oprm1	Areg
P2rx3	Csf1
P2rx4	Csf3
Il6ra	Csf2ra
Scn10a	Ccl20
Scn11a	Il17a
Scn9a	Ereg

(B)

Gapdh	Sfpq
Ywhaz	Scn10a
Hbb	Calca
Fabp7	Hoxb5
Sox10	Kcnt1
CCL21b	Scn4a
Csf1	Prdm12
Il34	Gamt
Gap43	Prmt8
Gal	Ngf
18S	Areg
Bdnf	Il6
Sema6a	Vgf
Npy	Dpysl5
Nts	Jak2
Npy2r	Srrm4
Star	Camk1
Adam8	Usp18
Casp3	Ntrk1
Atf3	Ucn
Cacna2d1	Jun
P2rx3	Anxa1
Kcnmb1	Ngfr
Dnm3	Tnfsf12

(C)

Arg1	Il4ra
B2m	Il6
Gapdh	Irf4
Ccl17	Irf5
Ccl22	Mertk
Ccl24	Mmp9
Ccr2	Nfkbiz
Ccr6	Nos2
Cd19	Ppard
Fcgr1	Pparg
18S	Ptgs2
Chil3	Retnlb
Cybb	Sbno2
Foxp3	Socs1
Gata3	Socs2
Gata6	Socs3
Ido1	Sox10
Ifng	Stat1
Il10	Stat6
Il12a	Tbx21
Il1b	Dpysl5
Il22	Tgfb2
Il27	Tnf
Il4	Nfil3

Table 1: (A) Genes represented on a DRG card. (B) Genes represented on an axotomy card. (C) Genes represented on a macrophage card.

Table 2: GM-CSF receptor subunit expression in neurons by RNA sequencing.

(A)

Bulk-sequencing							
	Mouse Tissue			*Human Tissue*			
	Thakur et al.	Lopes et al.	Lopes et al.	Flegel et al.	Ray et al. a	Ray et al. b	
	MACS-sorted nociceptors	MACS-sorted nociceptors after nerve injury	FACS-sorted nociceptors	whole DRG	whole DRG	human tibial nerve	
Expression Units:	FPKM	FPKM	FPKM	FPKM	TPM		TPM
Csf2ra	4	3	2	0	0	CSF2RA	15
Csf2rb	1	0	0	1	1	CSF2RB	6
Calca	912	3987	10287	313	1701	CD40	49
TrpV1	58	154	112	48	73	TRPV1	7
Dnmt3a	4	2	2	5	4	UCHL1	92

(B)

Single-cell Sequencing of mouse DRG (Zeisel et al; mousebrain.org) - Trinarization Scores						
	Csf2ra	Csf2rb	Calca	TrpV1	Dnmt3a	Nav1.8
Peptidergic (TrpM8), DRG	0.18	0	0.39	2.21	0.36	0
Peptidergic (TrpM8), DRG	0.27	0	0.32	0.67	0.11	0.08
Peptidergic (TrpM8), DRG	0.11	0	4.04	0.31	0.22	0
Peptidergic (PEP1.2), DRG	0.2	0	11.3	3.07	0.1	0.19
Peptidergic (PEP1.3), DRG	0.13	0	43.4	2.68	0.15	1.56
Peptidergic (PEP1.1), DRG	0.19	0	37.3	1.02	0.13	1.16
Peptidergic (PEP1.4), DRG	0.19	0	52.3	3.26	0.32	2.51
Peptidergic (PEP2), DRG	0.12	0	61.6	0.56	0.24	3.38
Neurofilament (NF2/3), DRG	0	0	0.64	0	0.19	0.61
Neurofilament (NF4/5), DRG	0.11	0	0.07	0.05	0.35	0.04
Neurofilament (NF1), DRG	0.08	0	0.07	0	0.13	0.03
Non-peptidergic (TH), DRG	0.18	0	0.17	0.01	0.35	1.08
Non-peptidergic (NP1.1), DRG	0.15	0	6.38	0.06	0.33	3.71
Non-peptidergic (NP1.2), DRG	0.22	0	3.23	0.05	0.27	5.28
Non-peptidergic (NP2.1), DRG	0.24	0	11.1	0.04	0.38	5.47
Non-peptidergic (NP2.2), DRG	0.18	0	34.5	0.73	0.27	4.99
Non-peptidergic (NP3), DRG	0.26	0	0.74	1.95	0.26	4

Table 2: Expression values derived from publicly available (A) bulk and (B) single cell RNA-sequencing datasets. Data for Csf2ra and Csf2rb are provided along with the following control/comparison genes: *Calca*, which is one of the most highly expressed genes in DRG; *TrpV1*, which is well expressed in nociceptive neurons; *Dnmt3*a which is very lowly expressed if at all in neurons (Saunders et al., 2018); *Nav1.8*; CD40, a myeloid cell marker; and *Uchl1*, the gene coding for a protein which is highly expressed in nerve fibres,. FPKM = fragments per kilobase per million mapped reads; TPM = transcripts per million.

Figure1

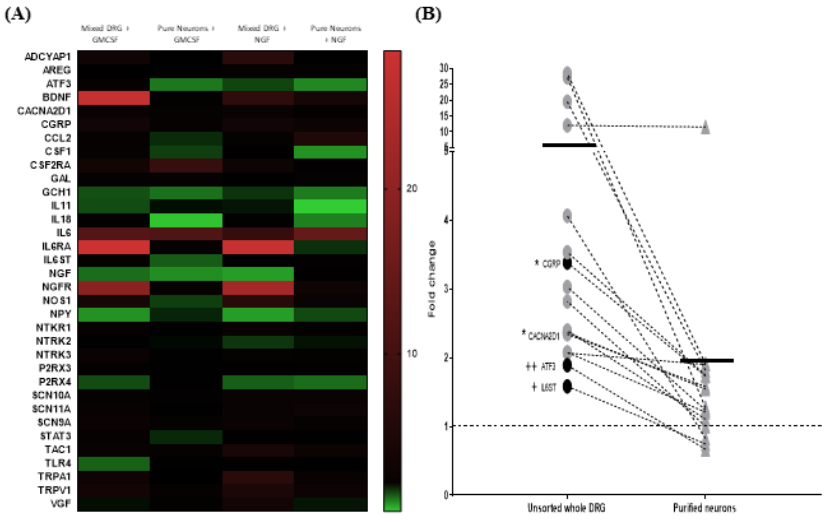

(A)
Mixed DRG + GM/CSF
Pure Neurons + GM/CSF
Mixed DRG + NGF
Pure Neurons + NGF
ADCYAP1
AREG
ATF3
BDNF
CACNA2D1
CGRP
CCL2
CSF1
CSF2RA
GAL
GCH1
IL11
IL18
IL6
IL6RA
IL6ST
NGF
NGFR
NOS1
NPY
NTKR1
NTRK2
NTRK3
P2RX3
P2RX4
SCN10A
SCN11A
SCN9A
STAT3
TAC1
TLR4
TRPA1
TRPV1
VGF
20
10
(B)
Fold change
* CGRP
* CACNA2D1
++ ATF3
+ IL6ST
Unsorted whole DRG
Purified neurons

Figure 2

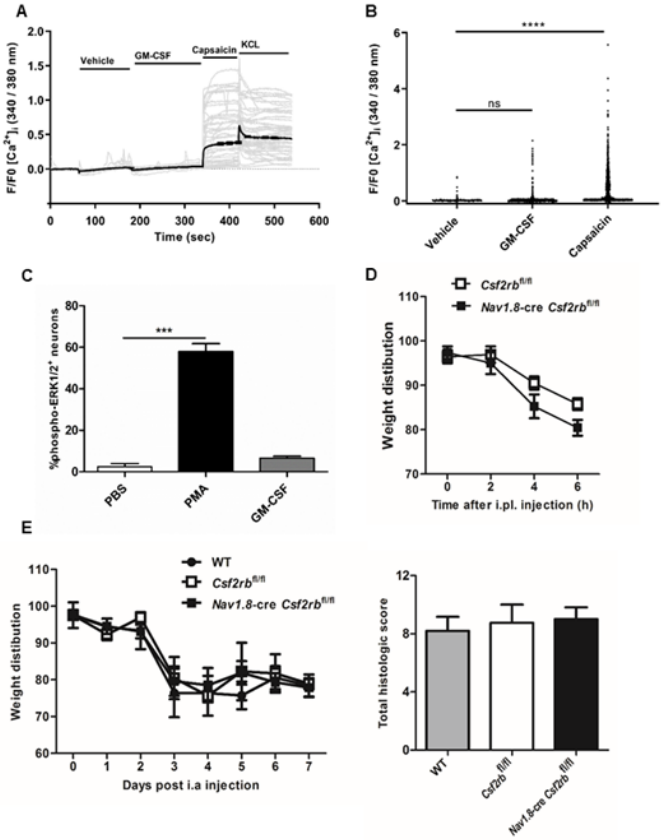

A
Vehicle
GM-CSF
Capsaicin
KCL
F/F0 [Ca2+]i (340 / 380 nm)
Time (sec)
B
****
ns
Vehicle
GM-CSF
Capsaicin
C
***
%phospho-ERK1/2+ neurons
PBS
PMA
GM-CSF
D
Csf2rbfl/fl
Nav1.8-cre Csf2rbfl/fl
Weight distibution
Time after i.pl. injection (h)
E
WT
Csf2rbfl/fl
Nav1.8-cre Csf2rbfl/fl
Weight distibution
Days post i.a injection
Total histologic score
WT
Csf2rbfl/fl
Nav1.8-cre Csf2rbfl/fl

Figure 3

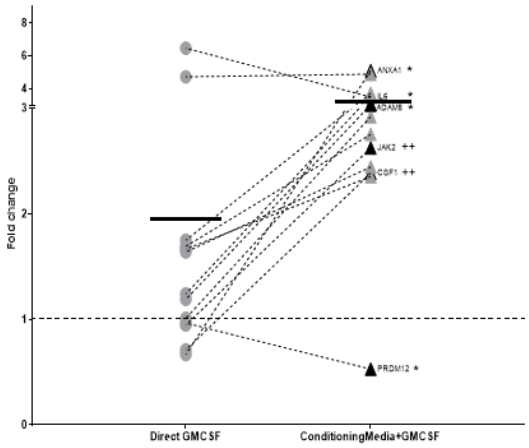
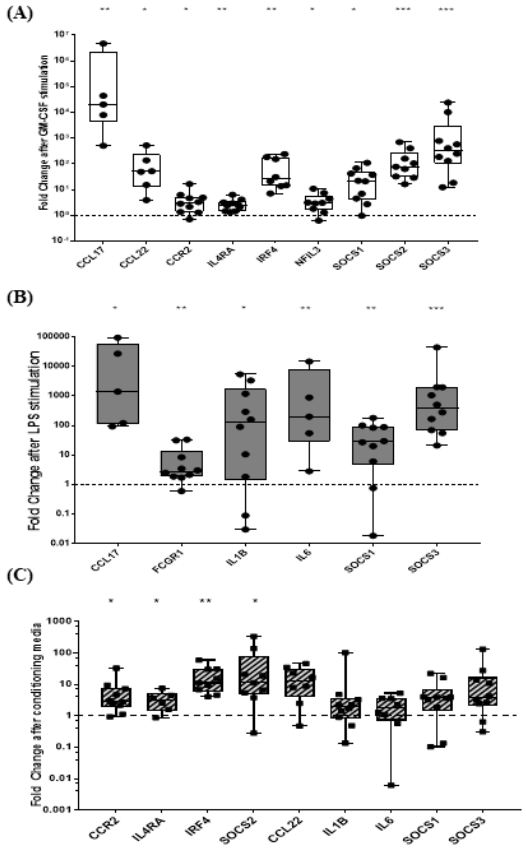

Fold change
8
6
4
3
2
1
0
ANXA1 *
IL6 *
ADAM8 *
JAK2 ++
CSF1 ++
PRDM12 *
Direct GMCSF
ConditioningMedia+GMCSF

Figure 4


(A)
Fold Change after GM-CSF stimulation
CCL17
CCL22
CCR2
IL4RA
IRF4
NFIL3
SOCS1
SOCS2
SOCS3
(B)
Fold Change after LPS stimulation
CCL17
FCGR1
IL1B
IL6
SOCS1
SOCS3
(C)
Fold Change after conditioning media
CCR2
IL4RA
IRF4
SOCS2
CCL22
IL1B
IL6
SOCS1
SOCS3