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Published in:
Frontiers in cellular and infection microbiology

DOI:
10.3389/fcimb.2014.00004

2014

Link to publication

Citation for published version (APA):
HMGB1 in severe soft tissue infections caused by *Streptococcus pyogenes*

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**INTRODUCTION**

High mobility group box protein 1 (HMGB1) is a ubiquitously expressed, highly conserved nuclear protein that is released either through active secretion by innate immune cells, enterocytes and hepatocytes or through passive release by injured, autophagic or necrotic cells (Bianchi et al., 1989; Tsung et al., 2007; Livesey et al., 2009; Skinner, 2010; Tang et al., 2010; Thomas and Stott, 2012). Extracellular HMGB1 has been reported to act as an alarmin with the ability to activate the immune system leading to cell proliferation, adhesion, migration, and cytokine release (Harris et al., 2012). Several receptors have been shown to interact with HMGB1 including toll-like receptor 4 (TLR4), the receptor for advanced glycation end products (RAGE) and CD24-Siglec-10 (Lotze and Tracey, 2005; Tian et al., 2007; Chen et al., 2009). Studies have suggested differential responses depending on receptor engagement, with TLR4 being involved in cytokine release (Yang et al., 2010) whereas RAGE is involved in cell migration (Penzo et al., 2010). Importantly post-translational modifications, including acetylation, phosphorylation, methylation and redox state of the cysteine residues, influence receptor interactions, and thereby, elicited responses (Harris et al., 2012; Venereau et al., 2012; Yang et al., 2012).

HMGB1 has been implicated in a variety of clinical conditions including arthritis, sepsis and chronic kidney disease (Harris et al., 2012). In sepsis, murine experimental data demonstrated a critical role of HMGB1 as a late mediator contributing to mortality (Wang et al., 1999). Subsequently, elevated levels of HMGB1 have been readily detectable in circulation of patients with severe sepsis and septic shock (Sunden-Cullberg et al., 2005). However, little is known about local HMGB1 responses in acute necrotizing bacterial soft tissue infections (STIs), such as necrotizing fasciitis. These are life-threatening infections where the vast majority of patients require intensive care and extensive surgical interventions. Despite modern medicine, the mortality associated with necrotizing soft tissue infections (NSTIs) is high, often exceeding 30% (Anaya et al., 2005; Marwick et al., 2011). Although a number of bacteria can cause NSTI, the main causative microbes are *Streptococcus pyogenes* and *Staphylococcus aureus* (McHenry et al., 1995). Here we set out to gain insight into events occurring in the microenvironment at the infected tissue site by delineating...
HMGB1 responses in acute necrotic STIs caused by *Streptococcus pyogenes*. Analyses of tissue biopsies from patients with varying severity of *S. pyogenes* infections revealed a significant correlation between increased HMGB1 and severity of tissue infection.

**MATERIALS AND METHODS**

**PATIENT MATERIAL**

The biopsy material from severe streptococcal infections has been described previously in (Thulin et al., 2006). The material included snap-frozen tissue biopsies (*n* = 25) collected from six patients with necrotizing fasciitis (*n* = 22) or cellulitis (*n* = 3), caused by *S. pyogenes* of varying serotypes (Table 1). Biopsies received a clinical grade at the time of sampling (grade 1: distal tissue not visually inflamed; *n* = 5; grade 2: inflamed tissue including cellulitis, fasciitis, and necrotizing fasciitis; *n* = 20) (Thulin et al., 2006). Snap-frozen punch biopsies collected from patients with erysipelas (*n* = 11) were also included (Linder et al., 2010).

Plasma samples collected at admission from patients with Streptococcal Toxic Shock Syndrome (STSS) were included (*n* = 14) (Darenberg et al., 2003) as well as plasma samples from 14 healthy volunteers (controls).

All samples were obtained from the patients after written informed consent and from healthy volunteers, according to protocols approved by the ethics committee at respective University and in accordance with the Declaration of Helsinki Principles.

**IMMUNOSTAININGS OF TISSUE BIOPSY SPECIMEN**

Biopsies were cryosectioned (8 μm), fixed in 2% formaldehyde and immunostained as previously described (Norrby-Teglund et al., 2001; Thulin et al., 2006; Johansson et al., 2009). The immunohistochemical staining was modified to include an initial blocking step with 10% FCS in Earl's balanced salt solution and 0.1% saponin at room temperature for 30 min. The brown color reaction was developed by diaminobenzidine (DAB-kit from Vector Lab Inc.). The staining pattern of HMGB1 in the biopsies revealed both intracellular and extracellular HMGB1; however, not all cells stained positive despite the fact that this is a nuclear factor. This has also been noted by others (Ulfgren et al., 2004), and is likely due to technical limitations in identification of nuclear HMGB1, potentially through insufficient antibody access to the nuclei. The immunohistochemically stained sections were analyzed by acquired computerized image analysis (ACIA), which has proven to be a robust method for semiquantitative assessment of cell infiltrates and inflammatory markers in single cells and tissue (Norrby-Teglund et al., 2001; Thulin et al., 2006; Johansson et al., 2008). Analyzed cell area (defined by the haematoxylin counterstaining) ranged from 0.2 × 10^5 to 7.9 × 10^5 μm^2 for deep tissue biopsies and 9.6 × 10^5 to 7 × 10^6 μm^2 for erysipelas biopsies. The results are presented as ACIA value, i.e., percent positively stained area × mean intensity of positive staining.

Single and dual immunofluorescence stainings were performed as previously described (Thulin et al., 2006) and visualized using either a Leica confocal scanner TCS2 AOBS with an inverted Leica DMIRE2 microscope (Wetzlar, Germany) or a Nikon A1R confocal microscope (Nikon Instruments, Amstelveen, the Netherlands).

**Table 1 | Characteristics of tissue biopsy material.**

<table>
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<tr>
<th>Patient ID</th>
<th>Diagnosis</th>
<th>GAS serotype</th>
<th>Day of sampling</th>
<th>Type of tissue</th>
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<td>n.a.</td>
<td>2</td>
<td>Skin</td>
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</tbody>
</table>

GAS, Group A Streptococcus; STSS, streptococcal toxic shock syndrome; NF, necrotizing fasciitis; n.a., not available.

*After onset of diagnosis.*

The following antibodies were used: anti-CD68, anti-neutrophil elastase, anti-mast cell tryptase (DAKO, Glostrup, Denmark), biotinylated anti-IL-1β/IL-1F2, anti-CXCL12 (R&D systems, Minneapolis, MN), and anti-CD1a (BD Biosciences Pharmingen, San Diego, CA). HMGB1 was initially identified using a polyclonal anti-HMGB1 from BD Biosciences Pharmingen (55628, BD Diagnostics, San Diego, CA) or anti-human HMGB1 (ab18256, Abcam, Cambridge, UK).
Streptococcus pyogenes were identified with a polyclonal rabbit antisera specific for the Lancefield group A carbohydrate (Difco, BD Diagnostics, Sparks MD). Biotinylated secondary antibodies included goat-anti-mouse IgG and goat-anti-mouse IgG (both from Vector Laboratories, Burlingame, CA).

**BACTERIAL STRAINS**

Two clinical M3 isolates of *S. pyogenes*, obtained during the collection of the Canadian patient described above, were grown over night (16–18 h) in Todd-Hewitt broth complemented with 1.5% yeast extract. A clinical isolate of *Escherichia coli*, obtained from a sepsis patient, was also included in the study and was grown over night in Luria Broth medium. Before infection the bacterial cultures were centrifuged at 2500 rpm for 10 min and resuspended in RPMI 1640 cell culture medium supplemented with 5% heat inactivated FCS, 10 mM L-glutamine, and 25 mmol/L HEPES (all from Thermo Scientific, Hyclone).

**INFECrION OF PRIMARY HUMAN MONOCyTE-DERIVED MACROPHAGES**

Human monocyte-derived macrophages were isolated form healthy blood donors using RosetteSep (Stemcell Technology) and Lymphoprep (Axis-Shield) gradient centrifugation, as previously described (Hertzen et al., 2010). After isolation, the isolated cells were resuspended in RPMI 1640 cell culture medium supplemented with 5% heat inactivated FCS, 10 mM L-glutamine, Penicillin (100 U/ml)/Streptomycin (100 μg/ml) solution, and 25 mmol/L HEPES (all from Thermo Scientific, Hyclone) as well as 50 ng/ml of Macrophage colony stimulating factor (Immunotools). Cells were seeded at a concentration of 1 × 10^6 cells/ml in 6-well low adherence tissue culture plates (Corning) and cultured for 7–8 days to obtain macrophages. At day 8 cells were washed with phosphate buffered saline (PBS; Sigma-Aldrich, St Louis, MO), harvested and resuspended in RPMI 1640 cell culture medium supplemented with 5% heat inactivated FCS, 10 mM L-glutamine and 25 mmol/L HEPES. Cells were seeded in 24-well tissue culture plate, containing a sterile coverslip at the bottom of each well, at a concentration of 1.5 × 10^6 cells/ml in 6-well low adherence tissue culture plates (Corning) and cultured for 7–8 days to obtain macrophages. At day 8 cells were washed with phosphate buffered saline (PBS; Sigma-Aldrich, St Louis, MO), harvested and resuspended in RPMI 1640 cell culture medium supplemented with 5% heat inactivated FCS, 10 mM L-glutamine and 25 mmol/L HEPES. Cells were seeded in 24-well tissue culture plate, containing a sterile coverslip at the bottom of each well, at a concentration of 1.5 × 10^6 cells/ml and incubated overnight at 37°C with 5% CO₂. Cells were then infected with *S. pyogenes* or *E. coli*, at a multiplicity of infection (MOI) of 1–11 bacteria per cell. Four hours post infection cell supernatants were collected and centrifuged at 2500 rpm for 10 min, aliquoted and stored at −20°C. The cells, situated on coverslips were fixed with 2% paraformaldehyde for 15 min at room temperature. After fixation, the coverslips were washed with PBS, dried and stored at −20°C.

**HMGB1 ELISA**

HMGB-1 was measured by ELISA (Shino-Test Corporation, Tokyo, Japan) according to manufacturer’s instructions. The range of detection was 2.5–80 ng/ml. All samples were analyzed in duplicates.

**IL-8 LUMINEX**

Plasma level of IL-8 was determined by Luminex IL8 human singleplex bead kit (Invitrogen, Paisley, UK), and the Luminex (100) instrument (Luminex, Invitrogen, Paisley, UK). All samples were analyzed in duplicate.

**RESULTS**

**LEVEL OF HMGB1 RESPONSE CORRELATES TO SEVERITY OF *S. PYOGENES* TISSUE INFECTIONS**

First we sought to determine the presence of HMGB1 at the local tissue site in *S. pyogenes* infected patients. To this end, a tissue material collected from patients with varying severity of streptococcal tissue infections, i.e., mild erysipelas (*n* = 11), to more severe STIs including severe cellulitis and necrotizing fasciitis (*n* = 6) (Table 1), were immuno-histochemically stained for HMGB1, bacterial load, and inflammatory cells. Stainings were evaluated by microscopy and *in situ* image analysis. HMGB1 was detected in all analyzed biopsies (11 erysipelas and 25 severe STIs) and demonstrated both a diffuse, supposedly secreted HMGB1, as well as distinct intracellular staining (evident in some but not all cells) (Figures 1A,B). In agreement with our previous publication (Thulin et al., 2006), in severe STIs all biopsies displayed high...
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FIGURE 1 | HMGB1 at the local site of infection. Snap-frozen tissue biopsies (n = 25) from patients with severe soft tissue infections caused by S. pyogenes were immunohistochemically stained for S. pyogenes, macrophages identified by CD68-positivity, neutrophils identified by neutrophil elastase positivity, and HMGB1. A control staining where the primary antibody was omitted was also performed (control). (A) Representative immunohistochemically stained biopsies taken from the site of infection at day 1 from two patients (patient 8271, top panel, and patient 8611, bottom panel) (Table 1). Positive stainings for cell markers and for HMGB1 are indicated by a brown color, and all cellular nuclei are stained blue by haematoxylin. Bars indicate 50 μm. (B) Staining’s for HMGB1 revealed both a diffuse (top picture, indicated by white stars) and a distinct intracellular staining (bottom picture, indicated by the black arrow). Bars indicate 50 μm. (C) Image analysis values for S. pyogenes, macrophages (CD68), neutrophils (NE), and HMGB1 in the different biopsies were obtained by ACIA; for details see Materials and Methods. The horizontal lines denote median.

bacterial burden and heavy infiltration of both macrophages and neutrophils (Figures 1A,C). Although HMGB1 was commonly found in the areas with dense bacteria load and inflammatory cell infiltrates (Figure 1A), neither bacterial load, nor phagocytic cellular infiltration correlated significantly with amount of HMGB1 (data not shown). It seems likely that this lack of association might be due to the lack of tissue integrity caused by the high degree of necrosis present in severe STI biopsies. In fact in erysipelas where no necrosis is present, HMGB1 significantly correlated with the neutrophil infiltration (r = 0.78; p = 0.0064) (Figure 2A), but not with macrophage infiltration or bacterial load (data not shown). The latter is not surprising as the bacterial load is substantially lower in erysipelas than in severe STIs (Linder et al., 2010).

Importantly, semiquantitative assessment of HMGB1 at the infected site in patients with erysipelas compared to severe STIs revealed an increase in parallel to disease severity (p = 0.0023) (Figure 2B). The lowest values were noted in erysipelas biopsies, followed by biopsies from severe STIs taken in distal visually not inflamed areas, and the highest were found at the center of infection in biopsies from STI (Figure 2B). Similarly, analyses of biopsies taken from a patient with erysipelas at the center of infection, distal (5 cm outside the lesion) and healthy region (other non-infected leg) demonstrated that both HMGB1 and bacterial load increased with more involved inflamed tissue (Figures 2C,D).

This marked local HMGB1 response led us to explore systemic HMGB1 levels in a cohort of patients with the most severe manifestation of invasive S. pyogenes infections, namely STSS. Plasma levels of HMGB1 were measured at the day of inclusion. Significantly elevated levels of HMGB1 were detected in patients as compared to healthy controls (Figure 3A, p = 0.0001). For comparison, all STSS samples were also analyzed for IL-8, a commonly used marker for systemic inflammation. A significant correlation was found between the two markers (r = 0.82; p < 0.0001) (Figure 3B).

HMGB1 IN RELATION TO INFLAMMATORY CELLS AND INNATE IMMUNE FACTORS IN VIVO AND IN VITRO

To further characterize HMGB1 at the local site of infection in relation to inflammatory cells dual immunofluorescence stainings were performed, using anti-HMGB1 combined with antibodies against various cell markers, including CD68 (macrophages), neutrophil elastase, mast cell tryptase, and CD1a (Langerhans cells). In both erysipelas and severe STI, confocal microscopy analyses revealed that HMGB1 in tissue cells display a characteristic vesicular staining pattern (Figures 4A,D); a pattern consistent with active nuclear translocation of HMGB1 to the cytoplasm.
FIGURE 2 | HMGB1 correlates with severity of infection. Snap-frozen tissue biopsies (n = 11) from patients with erysipelas were immunohistochemically stained for S. pyogenes, neutrophils identified by neutrophil elastase positivity and HMGB1. (A) Correlation between neutrophil infiltration in relation to HMGB1 ACIA value (for details see Materials and Methods) in erysipelas biopsies. Significant correlation, as determined by Pearson's correlation test, is indicated by p- and r-values. (B) Image analysis data of HMGB1 in tissue from patients with erysipelas were compared with biopsies from patients with severe streptococcal soft tissue infection of clinical grade 1 and 2 (for details see Materials and Methods). Statistically significant differences were determined by 1way ANOVA, Kruskal-Wallis; p = 0.0023. (C) Representative immunohistochemical pictures of erysipelas tissue biopsies collected at the inflamed center, 5 cm outside the lesion and from the healthy leg. Bars indicate 50 μm. (D) Acquired computerized image analysis values of the whole tissue biopsy.

FIGURE 3 | Elevated HMGB1 in circulation in patients with STSS. HMGB1 and IL-8 levels in plasma collected on the day of inclusion were measured with ELISA and Luminex respectively, for details see Materials and Methods. Shown in (A) is systemic HMGB1 in STSS patients (n = 19) and healthy controls (n = 14). Statistically significant differences were determined by two-tailed t-test; p = 0.0001. Shown in (B) is systemic HMGB1 and IL-8 in patients with STSS (n = 19 patients). Significant correlation, as determined by Pearson's correlation test, indicated by p- and r-values.

(Gardella et al., 2002). Importantly, the only two cell types in the tissue that demonstrated this intracellular HMGB1 were macrophages (Figure 4A) and mast cells (Figure 4B). The latter of which constituted only a minor part of the HMGB1 positive population, due to the low frequency of mast cells in skin and soft tissue. Thus, the data demonstrates that macrophages are the major source of active released HMGB1 at the infected tissue site. To further support this finding, human monocyte-derived macrophages were infected with two different clinical strains of S. pyogenes for 4h. The levels of HMGB1 in the cell supernatant were measured with an ELISA. HMGB1 was readily detected in the culture medium of infected macrophages compared with non-infected macrophages (Figure 4C).

Co-staining of neutrophils and HMGB1 revealed that the neutrophils were present in areas of HMGB1, but not co-localizing with HMGB1. In fact, in some areas neutrophil infiltrates were found to surround HMGB1 positive cell populations (Figure 4D). As previous studies have attributed the chemotactic activity to the redox state of HMGB1 (Harris et al., 2012), we next sought to determine the form of HMGB1 in the tissue. Therefore, protein extracts of tissue biopsy sections were separated on a SDS-PAGE gel under non-reducing conditions and analyzed by Western blot. Detection of HMGB1 in tissue sections revealed two bands with a similar size and shift that was previously reported corresponding to the reduced chemotactic all-thiol-HMGB1 and the pro-inflammatory disulfide-HMGB1 (Venereau et al., 2012). The effect of HMGB1 on neutrophil motility was tested in a human whole-blood transwell migration assay using different concentrations of HMGB1. Both
surrounding areas with IL-1β, and HMGB1. Our data showed both CXCL12 and IL-1β in the tissue, and these stainings coincided with areas that had high HMGB1 expression (Figure 5A). Furthermore, sections were immunofluorescently stained for HMGB1 in combination with either CXCL12 or IL-1β. Confocal microscopy analyses revealed HMGB1 overlapping with IL-1β (yellow areas, Figure 5B) suggesting co-localization. In contrast, this staining pattern was not noted with HMGB1 and CXCL12. The two proteins appeared in the same area but did not overlap (Figure 5C).

**DISCUSSION**

Despite HMGB1’s direct link to necrosis and pro-inflammatory actions (Harris et al., 2012), there are, to the best of our knowledge, no clinical data to support these mechanistic actions in necrotizing bacterial infections. Here, we utilized biopsies from patients with skin and STIs caused by S. pyogenes to assess the presence of HMGB1 at the local infected site of infections characterized by inflammation and necrosis. Microscopy analyses revealed HMGB1 in all investigated biopsies, and notably, the levels correlated with severity of infection. For example, higher amounts of HMGB1 were found in biopsies from severe STIs as compared to erysipelas, as well as in the center as compared to distal site of infection. Per definition, necrotizing fasciitis is characterized by tissue necrosis. Intuitively, the HMGB1 noted at the tissue site is likely, at least in part, due to passive release from necrotic cells. However, our vesicular staining pattern of HMGB1 in the infiltrating immune cells indicates that there is also an active release of HMGB1 predominantly from macrophages, which likely involves the non-classical vesicle-mediated secretory pathway (Gardella et al., 2002). This was further strengthened by in vivo infection of human monocyte-derived macrophages with S. pyogenes resulted in a release of HMGB1.

In both erysipelas and soft tissue biopsies, infiltrates of neutrophils, and macrophages were present. In agreement with our previous publications (Thulin et al., 2006; Johansson et al., 2009; Linder et al., 2010), the severe STI biopsies showed massive cellular infiltrates, substantially higher than in erysipelas. Co-stainings of cellular markers and HMGB1 revealed a pattern where neutrophils were found close to, and in part, surrounding areas with S. pyogenes infection of human monocyte-derived macrophages with S. pyogenes characterized by tissue necrosis. Microscopy analyses revealed HMGB1 at the local infected site of infections characterized by inflammation and necrosis. Microscopy analyses revealed HMGB1 in all investigated biopsies, and notably, the levels correlated with severity of infection. For example, higher amounts of HMGB1 were found in biopsies from severe STIs as compared to erysipelas, as well as in the center as compared to distal site of infection. Per definition, necrotizing fasciitis is characterized by tissue necrosis. Intuitively, the HMGB1 noted at the tissue site is likely, at least in part, due to passive release from necrotic cells. However, our vesicular staining pattern of HMGB1 in the infiltrating immune cells indicates that there is also an active release of HMGB1 predominantly from macrophages, which likely involves the non-classical vesicle-mediated secretory pathway (Gardella et al., 2002). This was further strengthened by in vivo infection of human monocyte-derived macrophages with S. pyogenes resulted in a release of HMGB1.

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In both erysipelas and soft tissue biopsies, infiltrates of neutrophils, and macrophages were present. In agreement with our previous publications (Thulin et al., 2006; Johansson et al., 2009; Linder et al., 2010), the severe STI biopsies showed massive cellular infiltrates, substantially higher than in erysipelas. Co-stainings of cellular markers and HMGB1 revealed a pattern where neutrophils were found close to, and in part, surrounding areas with S. pyogenes infection of human monocyte-derived macrophages with S. pyogenes characterized by tissue necrosis. Microscopy analyses revealed HMGB1 at the local infected site of infections characterized by inflammation and necrosis. Microscopy analyses revealed HMGB1 in all investigated biopsies, and notably, the levels correlated with severity of infection. For example, higher amounts of HMGB1 were found in biopsies from severe STIs as compared to erysipelas, as well as in the center as compared to distal site of infection. Per definition, necrotizing fasciitis is characterized by tissue necrosis. Intuitively, the HMGB1 noted at the tissue site is likely, at least in part, due to passive release from necrotic cells. However, our vesicular staining pattern of HMGB1 in the infiltrating immune cells indicates that there is also an active release of HMGB1 predominantly from macrophages, which likely involves the non-classical vesicle-mediated secretory pathway (Gardella et al., 2002). This was further strengthened by in vivo infection of human monocyte-derived macrophages with S. pyogenes resulted in a release of HMGB1.
FIGURE 5 | Presence of pro-inflammatory mediators at the local site of tissue infection. The figure shows representative images of a snap-frozen cryo-sectioned biopsy, from a patient with severe streptococcal soft tissue infection. (A) Tissue sections were immunohistochemically stained for HMGB1, CXCL12, and IL-1β. A control staining, omitting the primary antibody was also made (control). Bars indicate 50 μm. Snap frozen tissue biopsies were also immunofluorescently stained for HMGB1 (green) in combination with (B) IL-1β (red) or (C) CXCL12 (red). Cell nuclei were stained blue with DAPI. Bars indicate 20 μm.

Recently, attention has been given to the function of HMGB1 as an alarmin that forms immunostimulatory complexes with cytokines and chemotactic factors (Harris et al., 2012; Schiraldi et al., 2012). These complexes, such as those formed with IL-1β and CXCL12, have in vitro been shown to be superior in their inflammatory or chemotactic properties. In our analysis, staining for IL-1β and CXCL12 showed that both factors are present in the tissue. Moreover, in the case of IL-1β a substantial overlay with HMGB1 was noted, providing proof-of-principle support for formation of these complexes in vivo given the close proximity of the factors in the infected tissue. Such complexes could theoretically contribute to the tissue destruction by augmentation of inflammation and leukocyte migration and thus, to disease pathogenesis.

AUTHOR CONTRIBUTIONS
Experimental design (Linda Johansson, Anna Norrby-Teglund, Carl-Johan Treutiger, Pontus Thulin, Johanna Snäll, Anna Linnér, Parham Sendi, Adam Linder), acquisition of experiments (Linda Johansson, Johanna Snäll, Anna Linnér, Parham Sendi, Pontus Thulin, Adam Linder), data analysis (Linda Johansson, Johanna Snäll, Anna Linnér, Parham Sendi, Pontus Thulin, Anna Norrby-Teglund), and interpretation of data (Linda Johansson, Johanna Snäll, Anna Linnér, Parham Sendi, Pontus Thulin, Anna Norrby-Teglund, Carl-Johan Treutiger, Adam Linder). Manuscript writing (Linda Johansson, Anna Norrby-Teglund, Johanna Snäll, Carl-Johan Treutiger, Parham Sendi) and critical revision (Pontus Thulin, Carl-Johan Treutiger, Adam Linder). Final approval of the version to be published as well as agreement to be accountable for all aspects of the work in ensuring that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved (Linda Johansson, Anna Norrby-Teglund, Johanna Snäll, Anna Linnér, Pontus Thulin, Parham Sendi, Adam Linder, Carl-Johan Treutiger).

ACKNOWLEDGMENTS
We would like to thank Prof. Don E Low for providing us with tissue material as well as critically reviewing our manuscript. Sofia Björnnot is acknowledged for helpful technical support with the flow cytometry analysis. This project was supported by The Swedish Research Council (Anna Norrby-Teglund: 12610; Linda Johansson: 522-2010-2868 and 521-2013-2445), Karolinska Institutet (Anna Norrby-Teglund; Linda Johansson), Karolinska University Hospital (Anna Norrby-Teglund), Torsten and Ragnar Söderberg’s Foundation (Anna Norrby-Teglund), Kurt and Alice Wallenberg Foundation (Anna Norrby-Teglund), The Swedish Society of Medicine (Linda Johansson), Lars Hierta Memorial foundation (Linda Johansson), The Swiss National Science Foundation (Parham Sendi), and the Margareta and Walter Lichtensteinstiftung (Parham Sendi). The research leading to these results has received funding from the European Union...

REFERENCES


Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Received: 19 December 2013; paper pending published: 04 January 2014; accepted: 09 January 2014; published online: 30 January 2014.


This article was submitted to the journal Frontiers in Cellular and Infection Microbiology.

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