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# Soluble CD14 acts as a DAMP in human macrophages: origin and involvement in inflammatory cytokine/chemokine production

4	Manuella Lévêque <sup>*, ‡</sup> , Karin Simonin-Le Jeune <sup>*, ‡</sup> , Stéphane Jouneau <sup>†, ‡, §</sup> , Solenn Moulis <sup>*, ‡</sup> ,					
5	Benoit Desrues <sup>§, ‡, \$</sup> , Chantal Belleguic <sup>§</sup> , Graziella Brinchault <sup>§</sup> , Sophie Le Trionnaire <sup>*, ‡</sup> , Jean-					
6	Pierre Gangneux <sup>‡, §</sup> Marie-Thérèse Dimanche-Boitrel <sup>*, ‡</sup> and Corinne Martin-Chouly <sup>*, ‡,1</sup>					
7	*Research Institute for Environnemental and Occupationnal Health (IRSET) INSERM U1085,					
8	team 'Stress Membrane and Signaling,' F-35043 Rennes, France.					
9	<sup>†</sup> Research Institute for Environnemental and Occupationnal Health (IRSET) INSERM U1085,					
10	team 'Chemical contaminant immunity and inflammation,' F-35043 Rennes, France.					
11	<sup>‡</sup> University of Rennes 1, UMS Biosit, F-35000 Rennes, France.					
12	<sup>§</sup> Centre Hospitalier Universitaire de Rennes, Centre de Ressource et de Compétences de la					
13	Mucoviscidose, F-35064 Rennes, France					
14	<sup>¢</sup> URL440-COSS, Centre Eugène Marquis, F-35064 Rennes, France					
15						
16	<sup>1</sup> Corresponding author:					
16 17	<sup>1</sup> Corresponding author: Dr. Corinne Martin-Chouly					
17	Dr. Corinne Martin-Chouly					
17 18	Dr. Corinne Martin-Chouly 2, avenue du Pr Léon Bernard					
17 18 19	Dr. Corinne Martin-Chouly 2, avenue du Pr Léon Bernard 35043 RENNES Cedex FRANCE					
17 18 19 20	Dr. Corinne Martin-Chouly 2, avenue du Pr Léon Bernard 35043 RENNES Cedex FRANCE E-mail: corinne.chouly@univ-rennes1.fr					
17 18 19 20 21	Dr. Corinne Martin-Chouly 2, avenue du Pr Léon Bernard 35043 RENNES Cedex FRANCE E-mail: corinne.chouly@univ-rennes1.fr Tel: (+33) 223234904					
17 18 19 20 21 22	Dr. Corinne Martin-Chouly 2, avenue du Pr Léon Bernard 35043 RENNES Cedex FRANCE E-mail: corinne.chouly@univ-rennes1.fr Tel: (+33) 223234904					
17 18 19 20 21 22 23	Dr. Corinne Martin-Chouly 2, avenue du Pr Léon Bernard 35043 RENNES Cedex FRANCE E-mail: corinne.chouly@univ-rennes1.fr Tel: (+33) 223234904 Fax: (+33) 223235055					
17 18 19 20 21 22 23 24	Dr. Corinne Martin-Chouly 2, avenue du Pr Léon Bernard 35043 RENNES Cedex FRANCE E-mail: corinne.chouly@univ-rennes1.fr Tel: (+33) 223234904 Fax: (+33) 223235055					
17 18 19 20 21 22 23 24 25	Dr. Corinne Martin-Chouly 2, avenue du Pr Léon Bernard 35043 RENNES Cedex FRANCE E-mail: corinne.chouly@univ-rennes1.fr Tel: (+33) 223234904 Fax: (+33) 223235055					

#### 29 ABBREVIATIONS

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31 Abbreviations used in this article: sCD14, soluble form of CD14; CF, cystic fibrosis; DAMPs,

32 danger-associated molecular patterns; ER, Endoplasmic Reticulum; FEV1, Force Expiratory

33 Volume in one second; NLRs, NOD-like receptors; PAMPs, pathogen-associated molecular

34 patterns; PI-PLC, phosphatidylinositol-phospholipase C.

- 36 ABSTRACT
- 37

The innate immune system is able to detect bacterial lipopolysaccaride (LPS) through the pattern 38 recognition receptor CD14, which delivers LPS to various TLR signaling complexes that 39 subsequently induce intracellular pro-inflammatory signaling cascades. In a previous study, we 40 showed the overproduction of the soluble form of CD14 (sCD14) by macrophages from patients 41 with cystic fibrosis (CF). CF is an autosomal recessive disorder that is caused by mutations in the 42 gene that encodes the CFTR protein and characterized by persistent inflammation. Macrophages 43 play a significant role in the initial stages of this disease due to their inability to act as suppressor 44 cells leading to chronic inflammation in CF. In this work, we investigated the origin of sCD14 by 45 46 human macrophages and studied the effect of sCD14 on the production of inflammatory cytokine/chemokine. Our data indicate sCD14 stimulate pro-inflammatory 47 that cytokine/chemokine production in a manner that is independent of LPS but dependent on the 48 TLR-4/CD14 membrane complex, NF-kB and the inflammasome. Therefore sCD14, 49 50 overproduced by CF macrophage, originates primarily from the endocytosis/exocytosis process and should be considered to be a DAMP. In fact, this elucidation of the origin and inflammation-51 52 induced mechanisms associated with sCD14 contributes to our understanding of maintained tissue inflammation. 53

- 54
- 55 Key words: inflammation, cystic fibrosis, NF-κB, inflammasome
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#### 60 INTRODUCTION

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62 CD14 was first characterized as a membrane-associated GPI-anchored protein and a cell surface differentiation marker that is present on the surface of monocytes, macrophages, dendritic cells 63 and neutrophils (1-5). CD14 acts as a receptor for bacterial LPS in cooperation with TLR-4 and -64 2 (5, 6) and can bind various bacterial ligands and receptors on phagocytes, thereby mediating the 65 phagocytosis of bacteria and the clearance of apoptotic cells (4, 7-9). CD14 also exists as two 66 soluble forms: a form with a low molecular mass of 48-50 kDa and a form with a high molecular 67 mass of 53-56 kDa. The mechanisms of CD14 production have been reported to be linked to 68 neosynthesis, proteolytic or GPI-tail cleavage by phospholipases or endocytosis/exocytosis (2, 3, 69 10-18). In cells that express membrane CD14, including mononuclear cells, high concentrations 70 of sCD14 are able to inhibit LPS-mediated functional responses (19, 20). In cells that lack 71 72 membrane CD14, including most epithelial and endothelial cells, sCD14 enables these cells to respond to LPS (8, 21). At the local site of infection, pro-inflammatory signals that result from 73 74 sCD14 can be protective, leading to local clearance of invading bacteria. However, widespread infection and activation of this pro-inflammatory signaling pathway can cause fatality through 75 76 sepsis (22, 23). Furthermore, significant levels of sCD14 were detected in both serum and bronchoalveolar lavage fluid from patients with acute respiratory distress syndrome (24). In 77 78 addition, it was demonstrated in a murine model that Streptococcus pneumoniae uses sCD14 in the bronchoalveolar space to cause invasive respiratory tract infections (25). Overall, sCD14 79 appears to act as a key component during pulmonary inflammation/infection. 80

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Chronic bacterial airway infection and subsequent intense neutrophilic inflammation with the 82 release of intracellular proteases are considered to be the main contributors to bronchiectasis and 83 end-stage lung disease CF patients. Recent research highlighted the worsening role of 84 inflammation and immune responses in CF airway disease (26). Macrophages are antigen-85 presenting phagocytes that secrete pro-inflammatory mediators and antimicrobial factors in 86 87 response to challenge by extracellular pathogens. Recently, several studies showed that specific features of macrophage activation in CF patients play an important role during the CF disease 88 process (27–29). In our previous work, we observed an increase in sCD14 secretion by peripheral 89 monocyte-derived macrophages from stable adult CF patients (29). However, the origin and 90

- 91 involvement of sCD14 has not been studied. In this work, we examined the mechanisms involved
- 92 in the release of sCD14 by peripheral monocyte-derived macrophages from adult with CF and the
- 93 inflammatory signaling pathways that are induced by sCD14 in non CF cells.

#### 95 MATERIALS AND METHODS

96

#### 97 CF patients

The experiments were conducted according to the Good Clinical Practice guidelines (Kong, 98 1997) and approved by the Ethics Committee for human subjects of Rennes University Hospital 99 (France, Ethics No. 11/38-827). All patients included in this study gave written informed consent. 100 Sixty stable adult patients with CF were recruited at the 'Centre de Ressources et de 101 Compétences pour la Mucoviscidose' of Rennes University Hospital (France). The CF patients 102 103 considered for inclusion were Caucasian and included 27 males and 33 females, who were aged between 18 and 52 years (mean age:  $30 \pm 9$ ). The CF diagnosis was based on typical clinical 104 manifestations of the disease and confirmed by positive sweat tests and by CFTR gene mutation 105 detection. Stable patients were defined by the absence of changes in symptoms in the 3 months 106 prior to the study. All patients with CF received medication at the time of blood collection, 107 including azithromycin (27%), aerosol DNAse (48%), inhaled corticosteroids (72%) and azole 108 therapy (47%). Oral corticosteroid therapy at the time of blood collection was an exclusion 109 110 criterion, as this therapy may influence inflammatory phenotypes. Patients with the G551D mutation were not treated with ivacafor at the time of their participation in the study (except for 111 112 patient 19, supplemental Table 1). The clinical features of the patients are reported in supplemental Table 1. According to the FEV1 values (% predicted), the majority of our patients 113 (41/60) had mild to moderate lung disease (FEV1 values  $\geq$  55%). In their sputum samples, 32 114 patients had microbiological evidence of Pseudomonas aeruginosa, and Staphylococcus aureus 115 and Aspergillus fumigatus were detected in 45 and 29 patients, respectively. The CF genotypes 116 were representative of the French CF population, with 57% of participants having 117 F508del/F508del mutations, 36% of patients having F508del/other mutations and 7% of patients 118 having no F508del mutations (30). Blood monocyte counts were within the normal range, with a 119 median number of  $0.679 \times 10^9$ /L (range  $0.23 - 1.12 \times 10^9$ /L). 120

121

#### 122 Cell cultures and treatments

Leukocytes were isolated by Ficoll gradient centrifugation, as described previously (31).
Peripheral blood mononuclear cells from healthy non-CF subjects (written consent for the use of

125 blood samples for the research protocol was obtained, according to the regulation for blood transfusion of the French blood organization EFS, Rennes) were seeded according to the specific 126 blood count of each subject. Monocytes, which were selected via a 1-hour adhesion step, were 127 differentiated for 6 days using GM-CSF (400 UI/ml, Genzyme, Lyon, France) in RPMI 1640 128 medium supplemented with 2 mM glutamine, antibiotics and 10% FBS (Lonza, Levallois Perret, 129 France). Before treatment, the macrophages were placed in medium without serum for 24 hours. 130 131 To study proteolytic origin of sCD14, non-CF macrophages were treated by e64d (1 µM, Sigma-Aldrich, Saint-Quentin Fallavier, France), pepstatin A (1 µM, Sigma-Aldrich, Saint-Quentin 132 133 Fallavier, France), EDTA (0.1 mM, Sigma-Aldrich, Saint-Quentin Fallavier, France) or aprotinin (0.3 µg/ml, Sigma-Aldrich, Saint-Quentin Fallavier, France) for 24 hours. To study GPI-tail 134 135 cleavage by phospholipase, PI-PLC (1 U/ml, Life Technologies, ThermoFisher Scientific, Saint Aubin, France) was added to non-CF macrophages for 2 hours in the absence or presence of the 136 137 PI-PLC inhibitor U-73122 (12.5 µM, 1-hour pretreatment, Bertin Pharma, Montigny le Bretonneux, France). In parallel, macrophages from CF patients were treated with U-73122 for 138 139 24 hours. To study membrane trafficking pathways, the cells were supplemented with watersoluble cholesterol (15 to 30 µg/ml, 1-hour pretreatment, followed by 24 hours, Sigma-Aldrich, 140 141 Saint-Quentin Fallavier, France) or with brefeldin A (100 ng/ml, 1-hour pretreatment, followed by 2 h, Cell Signaling Technology, Ozyme, Saint Quentin en Yvelines, France). To study 142 143 inflammatory signaling pathways, human recombinant sCD14 protein (500 ng/ml, <0.1 EU/µg endotoxin, Sigma-Aldrich, Saint-Quentin Fallavier, France) was added to non-CF macrophages 144 145 for 24 hours in the absence or presence of Bay 11-7082 (1 and 10 µM, 1-hour pretreatment, Calbiochem, Merck Millipore, Molsheim, France) or the caspase inhibitor Z-WEHD-FMK (1 to 146 30 µM, 30-min pretreatment, Calbiochem, Merck Millipore, Molsheim, France). To study TLR 147 involvement in the inflammatory effect of sCD14, sCD14 was added to non-CF macrophages in 148 the presence of the TLR-4 antagonist LPS-RS (LPS from the photosynthetic bacterium 149 Rhodobacter sphaeroides, 2 µg/ml, InvivoGen, Toulouse, France), a CD14-neutralizing antibody 150 (anti-hCD14 IgA, 10 µg/ml, 1-hour pretreatment, InvivoGen, Toulouse, France), a TLR4-151 152 neutralizing antibody (anti-hTLR4 IgA, 10 µg/ml, 1-hour pretreatment, Invitrogen, ThermoFisher Scientific, Saint Aubin, France) or control IgG2a (10 µg/ml, 1-hour pretreatment, InvivoGen, 153 Toulouse, France). At the doses used, the treatments did not affect the viability of the 154 macrophages (data not shown). Viability was measured using the CellTiter 96® AQueous One 155

Solution Cell Proliferation Assay (Promega, charbonnières les bains, France) according to theinstructions provided by the manufacturer.

158

#### 159 Gene expression

RNA expression was analyzed using RT-qPCR assays. Briefly, total RNA was isolated from CF 160 macrophages using NucleoSpin® RNA XS (Macherey Nagel, Hoerdt, France) and from non-CF 161 162 macrophages using the PureLink RNA Mini Kit (Ambion®, ThermoFisher Scientific, Saint Aubin, France). The total RNA (1 µg) was reverse transcribed into cDNA using the High 163 Capacity cDNA Reverse Transcription Kit (Applied Biosystems ThermoFisher Scientific, Saint 164 Aubin, France). Real-time PCR was performed using the Power SYBR Green PCR Master kit 165 166 (Applied Biosystems ThermoFisher Scientific, Saint Aubin, France) according to the manufacturer's instructions and an ABI Prism 7300 detector (Applied Biosystem ThermoFisher 167 Scientific, Saint Aubin, France). The gene-specific primers for 18S, CD14, IL-1β, IL-8 were 168 Quantitect®Primer Assay primers obtained from Qiagen (Hilden, Germany). The gene-specific 169 primers for 18S, TNF, MMP-9, MMP-12, Cathepsin B, Cathepsin D, Cathepsin F, Cathepsin K, 170 Cathepsin S, ADAM-9, ADAM-10, ADAM-12, ADAM-17, and PLCy were purchased from 171 Eurogentec (Liège, Belgium). A list of the primer sequences used for the RT-qPCR analysis is 172 reported in supplemental Table 2. The amplification curves of the PCR products were analyzed 173 with the ABI Prism SDS software using the comparative cycle threshold (CT) method. Relative 174 gene expression was calculated by comparing the number of thermal cycles that were necessary 175 to generate threshold amounts of product (CT). The CT was calculated for the each gene and for 176 the housekeeping gene 18S. For each cDNA sample, the 18 S CT was subtracted from the CT for 177 each gene to yield the  $\Delta CT$ , thus normalizing the initial amount of RNA used. The amount of 178 mRNA was calculated as  $2^{-\Delta\Delta CT}$ , where the  $\Delta\Delta CT$  is the difference between the  $\Delta CT$  of the two 179 cDNA samples to be compared. The data from CF samples are expressed relative to the mRNA 180 level found in non-CF samples. The data from the treatment samples are expressed relative to the 181 182 mRNA level found in the controls.

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#### 184 Cytokine/chemokine, sCD14 and NFκB p65 level quantification

185 IL-1 $\beta$ , IL-8, TNF- $\alpha$  and sCD14 levels were measured in the supernatants of the cell cultures and 186 in plasma from CF patients using a Duoset<sup>®</sup> ELISA kit (R&D system, Abingdon, United 187 Kingdom), according to the instructions provided by the manufacturer. The NF $\kappa$ B p65 level was 188 measured in the nuclear fraction of cell cultures using TransAM<sup>®</sup> NF $\kappa$ B p65 (Active Motif, La 189 Hulpe, Belgium), according to the instructions provided by the manufacturer.

190

#### 191 Neosynthesis measurement

Soluble CD14 neosynthesis was measured using Click-IT ® technology (Thermo-fischer 192 scientific). Macrophages were placed in RPMI 1640 medium without methionine (Gibco, 193 ThermoFisher Scientific, Saint Aubin, France). After 30 min incubation (37°C, 5% CO<sub>2</sub>), 194 macrophages were pulse-chase labeled in the presence of Click-IT® L- Azidohomoalanin 195 (50µM; Molecular Probes, ThermoFisher Scientific, Saint Aubin, France) in RPMI 1640 medium 196 without methionine for 3 hours. Afterwards, medium was changed by RPMI 1640 with 197 methionine and macrophages were incubated for 21 hours (37°C, 5% CO<sub>2</sub>). Then supernatants 198 were recovered and analyzed for sCD14 level quantification using Duoset® ELISA kit (R&D 199 system, Abingdon, United Kingdom). . To measure neosynthesis, biotin-coupled detection 200 antibody was substituted by Click-IT® Biotin DIBO Alkyne (Molecular Probes, ThermoFisher 201 Scientific, Saint Aubin, France), for copper-free click chemistry. 202

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#### 204 Cholesterol level quantification

Total lipids were extracted with 200 µl CHCl<sub>3</sub>/MeOH/NP-40 (7:11:0.1; v/v). The sample was 205 206 centrifuged for 10 min at 14,000 rpm. The chloroformic layer was evaporated to dryness under a nitrogen stream. Then, the free cholesterol levels was determined using Cholesterol/Cholesteryl 207 208 Ester Quantitation Kit (Merck Millipore, Molsheim, France), according to the instructions provided by the manufacturer. Cholesterol is oxidized by cholesterol oxidase to yield H<sub>2</sub>O<sub>2</sub>. The 209 resulting H<sub>2</sub>O<sub>2</sub> interacts with a sensitive cholesterol probe to produce resorufin, which can be 210 detected by spectrophotometrically 570 nm. Total protein concentrations were determined using a 211 BCA protein assay kit (Thermoscientific, Saint Aubin, France) to express cholesterol based on 212 the protein concentration for each sample. 213

#### 215 **Zymography assay**

The gelatinolytic activity of secreted MMP-9 was analyzed using gelatin zymography, as 216 described previously (32). The samples were subjected to electrophoresis via 10% SDS-PAGE 217 containing 1 mg/ml of gelatin (Sigma Aldrich, Saint-Quentin Fallavier, France) under non-218 reducing conditions. After electrophoresis, the gels were washed twice with 2.5% Triton X-100, 219 rinsed with water, and incubated at 37°C overnight in reaction buffer (50 mM Tris, 5 mM CaCl<sub>2</sub>, 220 221 and 2.1 mM ZnCl<sub>2</sub>, pH 8.0). The gels were stained with Coomassie brilliant blue (Sigma Aldrich, Saint-Quentin Fallavier, France) and de-stained in a solution of 25% ethanol and 10% acetic acid. 222 223 Gelatinase activity appeared as clear bands against a blue background. The molecular weights of the gelatinolytic bands were estimated using a prestained protein ladder (10 - 250 kDa, 224 225 Euromedex, Souffelweyersheim, France). Images of the zymograms were acquired using the Gel Doc 1000 Gel Documentation System (Bio-Rad laboratories, Marnes-La -Coquette, France), and 226 227 both the surface and intensity of the lysis bands were quantified by densitometry using the MultiGauge software (Fujifilm, Tokyo, Japan). 228

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#### 230 Gene silencing by siRNA

ON-TARGETplus siRNAs against NLRC4 or NLRP3 were synthesized and annealed by Dharmacon RNAi Technologies (ThermoFisher Scientific, Saint Aubin, France). siRNA duplexes were transfected using the Lipofectamine RNAiMAX Reagent (Life Technologies, ThermoFisher Scientific, Saint Aubin, France). The transfection reagent and siRNAs were mixed, and complex formation was allowed to proceed for 5 min at room temperature before the complex was added to the macrophages. After 72 hours, the cells were treated or not treated with sCD14 (500 ng/ml, 24 hours) before being harvested for analysis.

238

#### 239 Immunoblotting

Membrane-bound proteins were extracted from the macrophages by lysing the cells with RIPA
lysis buffer (50 mM Tris-HCl pH 7.5, 150 mM NaCl, 1 mM EDTA, 0.1% SDS, 1% Triton-X100,
12 mM deoxycholate, 2 mM NaF, 1 mM Na<sub>3</sub>VO<sub>4</sub>, 2 mM PMSF, cOmplete<sup>TM</sup> EDTA-free
Protease Inhibitor Cocktail (Roche, Bâle, Switzerland) and PhosSTOP Phosphatase Inhibitor
Cocktail (Roche, Bâle, Switzerland). The macrophages were incubated at 4°C for 30 minutes in
lysis buffer with vortexing for 30 seconds every 10 minutes. The supernatant containing proteins

was obtained by subsequent centrifugation at 10,000 g for 10 minutes at 4°C, and the protein 246 concentration was determined using a BCA protein assay kit (ThermoFisher Scientific, Saint 247 Aubin, France). Proteins were separated via SDS-PAGE and transferred to a nitrocellulose 248 membrane. Then, the membrane was subjected to western blotting using a rabbit anti-I $\kappa$ Ba, rabbit 249 anti-P-I $\kappa$ B $\alpha$ , rabbit polyclonal anti-Caspase 1, mouse anti-IL-1 $\beta$ , rabbit anti-NLRP3, rabbit anti-250 NLRC4 (Cell Signaling Technology, Ozyme, Saint Quentin en Yvelines, France), rabbit anti-251 CD14 (Epitomics, Burlingame, CA, US) or mouse anti-HSC70 (Santa Cruz, Heidelberg, 252 Germany) antibodies. Horseradish peroxidase-conjugated goat anti-rabbit (Cell Signaling 253 Technology, Ozyme, Saint Quentin en Yvelines, France) or goat anti-mouse (Dako, Les Ulis, 254 France) antibodies were used as secondary antibodies, and proteins were detected using enhanced 255 256 chemiluminescence. The images were scanned with the Fujifilm LAS-3000 imager (Fujifilm, Tokyo, Japan) and analyzed with the MultiGauge software (Fujifilm, Tokyo, Japan) for 257 258 densitometry. The intensity of the bands was normalized based on HSC-70.

259

#### 260 Statistical analysis

The number of subjects and experiments used in each group is stated in the respective figures. Statistical significance was evaluated by using the GraphPad Prism software v.6.0 (GraphPad Software Inc., San Diego, CA, US). A non-parametric Mann-Whitney test was used to assess the statistical significance of differences between non-CF and CF groups. A parametric ratio Student's t-test was used to assess statistical significance between treatments. For each analysis, a p-value <0.05 was considered to be significant.

- 268 **RESULTS**
- 269

#### 270 Origin of sCD14 in human CF macrophages

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We previously observed the overproduction of sCD14 in the supernatant of macrophages from stable adult patients with CF (29). However, plasma levels of sCD14 do not differ between stable adult CF patients and healthy subjects (Fig. 1*A*).

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To elucidate the molecular mechanisms that underlie the production of the soluble form of CD14 in human CF macrophages, we studied several hypotheses based on the literature. It was reported that sCD14 could be generated by different mechanisms, including the endocytosis of mCD14, the cleavage of the GPI anchor by PI-PLC, direct proteolytic cleavage from the cell surface and neosynthesis.

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To explore the neosynthesis hypothesis, we examined the regulation of CD14 production at the mRNA level in CF and non-CF macrophages. We found that CD14 mRNA levels were similar between CF and non-CF macrophages (Fig. 1*B*). Furthermore, pulse chase experiments with Click-IT® L- Azidohomoalanin showed no differences in neosynthesis of sCD14 between non-CF and CF macrophages whereas we demonstrated an increase of total sCD14 production in supernatant of CF macrophages (Fig. 1*C*). Thus, neosynthesis can be ruled out as a mechanism.

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sCD14 may be formed by direct proteolytic cleavage from the cell surface. However, the 289 290 inhibitors of metalloproteases (EDTA, Fig. 2A), cysteine proteases (e64d, Fig. 2D), aspartic proteases (pepstatin A, Fig. 2E) or serine proteases (aprotinin, Fig. 2F) did not influenced sCD14 291 production. Furthermore, the gene expression of the metalloproteases MMP-9 (Fig. 2B), MMP-12 292 (Supplemental Fig. 1A), ADAM-9, -10, -12, 17 (Supplemental Fig. 1B to 1E) and cathepsins B, 293 D, F, K and S (Supplemental Fig. 1F to 1J) in CF macrophages is decreased. Moreover, the 294 latent form of the MMP-9 protein and supernatant MMP-9 activity, as measured by zymography, 295 are decreased in CF vs. non-CF macrophages (Fig. 2C). The protease cleavage hypothesis is 296 excluded by these results. 297

The main hypothesis concerning sCD14 generation is the cleavage of the GPI tail by PI-PLC. We 299 investigated this hypothesis by exposing non-CF macrophages to PI-PLC (1 U/ml) with or 300 without its inhibitor, U-73122 (12.5 µM). We observed that PI-PLC significantly increased the 301 production of sCD14 by non-CF macrophages and that this effect was inhibited by U-73122 (Fig. 302 3A). However, the treatment of CF macrophages with U-73122 did not inhibit the increased 303 secretion of sCD14 into their supernatant (Fig. 3B). Furthermore, the expression of the PLC gene 304 does not differ between non-CF and CF macrophages (Supplemental Fig. 1G). Indeed, PI-PLC 305 participates in the production of sCD14 in non-CF macrophages but has no role in sCD14 306 overproduction from CF macrophages. 307

308

Cholesterol has been reported to increase sCD14 secretion through the endocytosis and subsequent cleavage of mCD14. Furthermore cholesterol is increased in CF macrophages (Fig. 4*A*). Thus, we investigated the effect of water-soluble cholesterol supplementation in non-CF macrophages. The results presented in Fig. 4*B* show that sCD14 production by non-CF macrophages is increased by supplementation with water-soluble cholesterol (15  $\mu$ g/ml). By modulating membrane lipid composition, cholesterol could be involved in the production of sCD14 in CF macrophages.

The fungal metabolite brefeldin A blocks forward protein transport between the ER and the Golgi complex but not retrograde transport (33). Incubation with brefeldin A decreased sCD14 secretion in non-CF and CF macrophages, implicating the secretory ER/Golgi pathway in sCD14 secretion in CF (Fig. 4*C*).

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#### 321 Function of human recombinant sCD14 in human macrophages

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To evaluate the inflammatory role of sCD14 in human non-CF macrophages, we used human recombinant sCD14 (hr-sCD14), which did not affect the viability of the cells (data not shown).

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We had to check the effect of human recombinant sCD14 on the NF $\kappa$ B activation, which is required for cytokine/chemokine production. In fact, the mean concentration of sCD14 in CF macrophage supernatants was 14.68 ng/ml per 2x10<sup>6</sup> cells/well (Fig. 3*B*), which corresponds to 220 ng/ml per 30x10<sup>6</sup> cells, in comparison to the mean level of sCD14 observed in non-CF macrophage supernatants, which was 2.35 ng/ml per  $30 \times 10^6$  cells/well (Fig. 4*B*). Indeed, we used increasing concentrations of human recombinant sCD14 (1, 10, 100 and 500 ng/ml on  $30 \times 10^6$ non-CF cells/well) to evaluate its inflammatory role in macrophages.

333

To determine whether sCD14 has an inflammatory effect, we investigated the production of pro-334 inflammatory cytokine/chemokine by non-CF macrophages exposed to sCD14. Treatment with 335 sCD14 significantly increased IL-1 $\beta$ , IL-8 and TNF- $\alpha$  gene expressions at 6 hours and secreted 336 levels at 24 hours in a dose-dependent manner (Fig. 5A and 5B). The effects on gene expression 337 were maintained at 24 hours (Fig. 5A). These results show that sCD14 could participate in 338 chronic inflammation by promoting pro-inflammatory cytokine/chemokine secretion. 339 340 Furthermore, sCD14 potentiates LPS-induced cytokine/chemokine production by non-CF macrophages (Supplemental Fig. 2). 341

342

The NF-κB pathway is one of the pathways involved in cytokine expression. We studied NF-κB 343 activation after sCD14 treatment in non-CF macrophages. The results showed the 344 phosphorylation of IkBa at 10 min, concomitant with a decrease in the IkBa protein and a time-345 346 dependent translocation of the NFkB p65 subunit to the nucleus (Fig. 6A and 6B). Indeed, the NF-kB pathway is activated by sCD14 in non-CF macrophages. To determine whether this 347 activation is related to the expression and secretion of inflammatory cytokines, we pretreated 348 non-CF macrophages with an inhibitor of NF-KB, Bay 11-7082. Bay 11-7082, which is a 349 350 potential anti-inflammatory agent, is an irreversible inhibitor of IKK $\alpha$  and cytokine-inducible IκBα phosphorylation that does not affect constitutive phosphorylation (34). A significant 351 decrease in IL-1 $\beta$ , TNF- $\alpha$  and IL-8 gene expressions and secreted levels was observed with Bay 352 353 11-7082 (Fig. 6C and 6D). These results show that the NF-κB pathway participates in the proinflammatory cytokine/chemokine production induced by non-CF macrophages sCD14 treatment. 354 355

Unlike other pro-inflammatory cytokines, IL-1β production is tightly regulated by a unique twosignal mechanism. The primary signal induces the expression of pro-IL-1β and is mediated in part by NF- $\kappa$ B activation. The secondary signal activates the NLR-subset inflammasome intracellular signaling complexes, which are composed of NLRs, pro-caspase 1, and the adaptor

protein ASC. The formation of the inflammasome complex results in the proteolytic cleavage of 360 pro-caspase 1 to yield active caspase 1, which in turn cleaves pro-IL-1β, producing mature and 361 362 active IL-1<sup>β</sup>. To determine if caspase 1 could be involved in IL-1<sup>β</sup> processing in response to sCD14, we investigated caspase 1 expression and activation. Macrophage exposure to sCD14 363 induced early caspase 1 cleavage starting after 5 min through the early production of pro-caspase 364 1 and the appearance of cleaved caspase 1 (Fig. 7A). This cleavage is followed by the subsequent 365 secretion of IL-1 $\beta$  by macrophages starting after 120 min (Fig. 7B). To investigate the 366 involvement of caspase 1 in IL-1 $\beta$  secretion after sCD14 treatment, we pre-incubated non-CF 367 macrophages with the caspase 1 specific inhibitor Z-WEHD-FMK. The caspase 1 inhibitor 368 369 abolished IL-1 $\beta$  secretion by non-CF macrophages (Fig. 7C). All of these results showed that IL-370  $1\beta$  production in response to sCD14 involves the caspase 1 pathway.

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Caspase 1 pathway activation requires a specific platform called the inflammasome complex. 372 373 However, various inflammasome complexes are formed depending on the stimulus. Concerning the inflammasome complex in macrophages, the most frequently involved stimuli are flagellin or 374 375 LPS. We investigated the NLRC4 and NRLP3 inflammasome complexes by using RNA 376 interference. The efficiency of transfection of NLRC4 siRNA and NLRP3 siRNA was assessed via western blotting of the total protein fraction from non-CF macrophages. Specific siRNAs 377 directed against NLRC4 and NLRP3 turned off NRLC4 and NLRP3 protein expression in 378 macrophages, respectively (Fig. 8A and 8B). Furthermore, while transfection with NLRP3 siRNA 379 or NLRC4 siRNA had no significant effect on IL-1ß secretion, in macrophages treated with 380 381 sCD14, transfection with each siRNA significantly decreases IL-1 $\beta$  secretion (Fig. 8C). These results suggested that both inflammasome platforms (NLRC4 and NLRP3) participate in the 382 induction of IL-1 $\beta$  secretion in response to sCD14 exposure. 383

384

In view of the mechanisms described above, the TLR-4 receptor and its signaling pathways should be involved in the effects induced by sCD14 in macrophages. To efficiently neutralize the biological activity of sCD14, non-CF macrophages were pre-incubated with a CD14-neutralizing antibody, resulting in decreased IL-8, TNF- $\alpha$  and IL-1 $\beta$  levels in the cell supernatants (Fig. 9). Moreover, the pretreatment of non-CF macrophages with an antagonist of TLR-4 (LPS-RS)

- 390 strongly inhibited the TNF- $\alpha$ , IL-8 and IL-1 $\beta$  production induced by sCD14 (Fig. 9). Finally to
- 391 neutralize TLR4, non-CF macrophages were pre-incubated with a TLR4-neutralizing antibody,
- resulting in decreased IL-8 and TNF- $\alpha$  levels in the cell supernatants. Treatment with sCD14 did
- not modify the membrane expression of TLR-4, as measured by flow cytometry, showing that
- 394 TLR-4 is not endocytosed after activation (data not shown). In this context, TLR-4 should be
- involved in the inflammatory effect of sCD14.

396 **DISCUSSION** 

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Macrophages coordinate inflammatory responses by secreting cytokines and chemokines that are responsible for diverse physiological effects that are important in the pathogenesis of CF and result in chronic infection/inflammation (35–37).

401

In a previous study, we observed an increase in cytokine/chemokine production in CF macrophage supernatants and particularly strong secretion of sCD14 (29). Elevated concentrations of sCD14 were also found in serum from patients with bacterial infections (38, 39) or pneumonia (40), as well as in other chronic inflammatory diseases, such as lupus erythematosus (41). However, we did not observe elevated sCD14 levels in plasma from stable adult CF patients, showing that sCD14 is not a systemic marker in CF, as previously observed in the plasma of children with CF (40).

409

410 It has been previously shown that sCD14 could be generated by several mechanisms, which include neosynthesis, direct proteolytic cleavage from the cell surface, cleavage of the GPI 411 412 anchor by phospholipases and endocytosis/exocytosis (2, 3, 10-18). In our study, CD14 gene expression was the same in CF and non-CF macrophages. Moreover, no neosynthesis of sCD14 413 414 was observed in CF macrophage. Indeed, the elevated sCD14 levels observed in CF macrophage supernatants cannot be explained by an increase in gene expression and synthesis. Proteases, 415 416 metalloproteases and/or cathepsins have been demonstrated to be present in large amounts in CF airways (42). However, the gene expression of MMPs, ADAMs as well as cathepsins is lower in 417 CF macrophages than in non-CF macrophages. Furthermore, MMP-9 and its activity are also 418 decreased in CF macrophage supernatants. Regarding these data, the origin of sCD14 in human 419 CF macrophages was not direct proteolytic cleavage from the cell surface, as reported previously, 420 explaining the increase in plasma sCD14 that occurs during sepsis (43). Cleavage of the GPI 421 anchor by phospholipases is also suggested to explain sCD14 release. In our study, PI-PLC 422 induced increased production of sCD14 in non-CF macrophage supernatants. The PI-PLC 423 inhibitor reversed this effect but not the sCD14 overproduction observed in CF macrophages. 424 Thus, PI-PLC participates in the production of sCD14 in non-CF macrophages but has no role in 425 sCD14 overproduction in CF macrophages. Finally, the hypothesis that involves the 426 17 427 endocytosis/exocytosis of CD14 was considered. The depletion of cholesterol from the plasma membrane has been shown to affect endocytosis and protein sorting (44). As an example, 428 cholesterol perturbation by filipin led to the redistribution of GPI-GFP from the cell surface to the 429 Golgi complex (45), and the supplementation of the medium with cholesterol allowed the 430 transport of secretory membrane proteins from the ER to the Golgi (46). In our study, cholesterol 431 level is higher in CF than in non-CF macrophages and cholesterol supplementation in non-CF 432 macrophages increased sCD14 secretion by macrophages. Furthermore, other work has shown 433 that the inhibition of cholesterol synthesis by lovastatin decreased sCD14 production in RAW 434 435 264.7 macrophages (47). Endocytosis/exocytosis appears to be a suitable hypothesis because the use of brefeldin A to block forward transport between the ER and the Golgi complex decreases 436 437 sCD14 secretion in CF macrophages.

438

It is well established that sCD14 alone is not sufficient to promote inflammation, except in cells that do not express mCD14, but the presence of sCD14 can enhance the sensitivity of monocytes and macrophages to LPS or lipopeptide by several orders of magnitude (48). In our study, we show that treatment with sCD14 alone enhances the induced inflammatory response and the effects of LPS by stimulating the secretion of IL-8, TNF- $\alpha$  and IL-1 $\beta$  in non-CF macrophages. However, one question remains to be answered: how can sCD14 induce the production of these inflammatory cytokines and chemokines?

446

447 Therefore, CD14 is assumed to function as a multi-ligand pattern recognition receptor by recognizing and binding to different PAMPs and DAMPs (49). In combination with the TLRs 448 proteins, CD14 is an important mediator of innate immune responses to infection (5, 8). 449 Membrane CD14 is a co-receptor for endotoxin through TLR-4 trans-membrane signaling, both 450 at the cell surface and within the endosomal compartment. TLR-4 has been shown to contribute 451 to the PAMP response of human cells, and its activation results in a pathway based on the 452 453 activation of TIR-containing adaptor molecules: the rapid TIRAP/MyD88 pathway, which 454 activates NF- $\kappa$ B and MAPK, resulting in the expression of pro-inflammatory cytokines and chemokines (50). In human monocyte-derived macrophages, sCD14 promoted the 455 phosphorylation of IkBa, allowing the activation of NF-kB. Bay 11-7082, which is a potential 456 anti- inflammatory agent and an irreversible inhibitor of IKKa and IkBa phosphorylation, 457

diminished sCD14-elicited IL-8, TNF- $\alpha$  and IL-1 $\beta$  expression and secretion, suggesting a role for 458 NFκB signaling in sCD14-dependent macrophage inflammation. Furthermore, macrophage 459 activation with sCD14 induces the activation of pro-caspase 1, leading to the cleaved and active 460 form of caspase 1. Next, pro-IL-1 $\beta$  is cleaved by caspase 1, and IL-1 $\beta$  mature is secreted in 461 macrophage supernatants; this effect is inhibited by Z-WEHD-FMK, which is a specific caspase 462 1 inhibitor. The activation of caspase 1 involves inflammasome complex formation, which 463 requires NLRs. NLRs are pattern recognition receptors and play key roles in the regulation of the 464 innate immune response in cooperation with TLRs. Among the NLRs, NLRC4 and NLRP3 465 466 appear to be the most involved in this response. The infection of macrophages with several Gram-negative bacteria, including Pseudomonas aeruginosa, which currently infects CF patients, 467 468 activates caspase 1 through NLRC4 (51). The activation of caspase 1 through NLRP3 is induced by DAMPs, such as K<sup>+</sup> efflux, ATP via P2XR7, ROS, and cathepsin D from lysosome damage 469 470 (52). We turned off NRLC4 and NLRP3 protein expression using specific siRNAs directed against NLRC4 or NLRP3. The treatment of macrophages with NLRP3 siRNA or NLRC4 471 siRNA abolished IL-1ß secretion, suggesting that both inflammasome platforms (NLRC4 and 472 473 NLRP3) induce IL-1ß secretion in response to sCD14 exposure. Altogether, our data suggest that 474 sCD14 acts as a DAMP in macrophages. In fact, extracellular sCD14 can bind membrane proteins or phospholipids (53) that could be responsible for inflammatory cytokine production. 475 An anti-CD14 neutralizing antibody is able to inhibit the sCD14-induced synthesis of TNF-α, IL-476 8 and IL-1β. To explore the action of sCD14 via the TLR-4 receptor, we used a potent antagonist 477 478 of this receptor LPS-RS and an anti-TLR4 antibody, which decreases partly sCD14-induced cytokine production in macrophages. Thus, part of the effect of sCD14 appears to be mediated by 479 the CD14/TLR-4 complex. However, further investigations are needed to completely understand 480 the molecular mechanisms involved in sCD14 signaling pathway in macrophages. 481

482

In conclusion, numerous mechanisms concerning the origin of sCD14 were considered in this work, but in CF macrophages, the endocytosis/exocytosis process appears to be the main mechanism involved in sCD14 production. We propose that the overproduction of sCD14 previously observed in macrophages from CF patients (29) should be considered to be a DAMP that can induce pro-inflammatory cytokine/chemokine production independent of LPS. Moreover, sCD14 can also enhance the LPS response. Both of these effects are dependent on the
TLR-4/CD14 membrane complex, NF-κB and the inflammasome. The characterization of the
origin and inflammatory function of sCD14 presented in this paper is an important step in
understanding chronic infection/inflammation. Furthermore, this study provides a novel approach
to the development of anti-inflammatory therapeutics in CF.

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#### 650 AUTHOR CONTRIBUTIONS

- 651
- 652 M. Lévêque, K. Simonin-Le Jeune and C. Martin-Chouly designed research; M. Lévêque, K.
- 653 Simonin-Le Jeune and C. Martin-Chouly performed the experiments; S; Moulis, C. Belleguic, G.
- 654 Brinchault, B. Desrues, S. Le Trionnaire, J-P. Gangneux and S. Jouneau contributed new reagents
- 655 or analytic tools; M. Lévêque and C. Martin-Chouly analyzed data; M. Lévêque, M-T.
- Dimanche-Boitrel and C. Martin-Chouly wrote the paper.
- 657

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659

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#### 665 FIGURE LEGENDS

666

Figure 1. Soluble CD14 level in plasma and CD14 gene expression in macrophages. (A) 667 sCD14 levels in plasma from healthy subjects (non-CF, n=8) and CF patients (n=12, patients 1-668 12, supplemental Table 1), as measured using an ELISA assay. Each symbol represents a single 669 individual, and the line is the mean. (B) CD14 gene expression in non-CF macrophages (n=14) 670 and CF macrophages (n=15, patients 6, 13-26; supplemental Table I). mRNA levels were 671 determined by RT-qPCR (supplemental Table 2). Each symbol represents a single individual, and 672 the line is the mean. (C) Neosynthesis (O.D.) and total (pg/ml) sCD14 in macrophage supernatant 673 from healthy subjects (non-CF, n=5) and CF patients (n=5, patients 6, 13-16, supplemental Table 674 1). The data are shown as the mean  $\pm$  SEM. Mann-Whitney test: \* p<0.05 vs. non-CF 675 macrophages. 676

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Figure 2. Altered CF macrophage phenotype is associated with markedly decreased 678 679 expression and activity of proteases. (A) The inhibition of metalloproteases by EDTA (0.1 mM, 24 hours) did not influenced sCD14 secretion in non-CF macrophages (n=8) (B) MMP-9 680 681 expression is reduced in CF macrophages (*n*=6, patients 6, 13-16 and 32, supplemental Table 1) vs. non-CF macrophages (n=9). Gene expression was determined by RT-qPCR (supplemental 682 683 Table 2). (C) In a representative gelatin zymogram, latent MMP-9 (92 kDa) is observed based on proteolysis areas, which appeared as clear bands against a dark background. After scanning the 684 gels, both the surface and intensity of the lysis bands were analyzed by densitometry (bar graph) 685 and showed decreased expression of latent MMP-9 in CF macrophages (n=12, patients 33-44, 686 supplemental Table 1) vs. non-CF macrophages (n=11). The results were expressed vs. the 687 relative latent MMP-9 intensity observed in the supernatant of non-CF macrophages. (D, E, F)688 The inhibition of cysteine proteases by e64d (D, 1  $\mu$ M, 24 hours, n=10), aspartic proteases by 689 pepstatin A (E, 1  $\mu$ M, 24 hours, n=4) and serine proteases by aprotinin (0.3  $\mu$ g/ml, 24 hours, n=9) 690 691 did not influenced sCD14 secretion in non-CF macrophages. The data are shown as the mean  $\pm$ SEM. Mann-Whitney test: \* p<0.05 and \*\* p<0.01 vs. non-CF macrophages. 692

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Figure 3. PI-PLC increases sCD14 production in non-CF macrophages. sCD14 levels were
 measured in supernatants from macrophages using an ELISA assay. (A) PI-PLC (1 U/ml, 2

hours) significantly increases sCD14 production by non-CF macrophages (n=11). The inhibition of PI-PLC by U-73122 (12.5  $\mu$ M, 1 hour pretreatment) inhibited PI-PLC-induced sCD14 secretion in non-CF macrophages (n=7). (*B*) U-73122 (12.5  $\mu$ M, 24 hours) did not prevent spontaneous sCD14 production by CF macrophages (n=6, patients 43, 45-49; supplemental Table 1). The data are shown as the mean  $\pm$  SEM. Ratio Student's t-test: ## p<0.01 *vs.* untreated non-CF macrophages; \*\* p<0.01 *vs.* PI-PLC-treated non-CF macrophages.

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Figure 4. Impact of intracellular protein transport on sCD14 production by non-CF and CF 703 macrophages. (A) Free cholesterol level is increased in CF (n=8, patients 43, 47, 50-55; 704 supplemental Table 1) vs non-CF (n=4) macrophages (B) Water-soluble cholesterol (15 µg/ml; 24 705 706 hours) significantly increases sCD14 production by non-CF macrophages (n=5). (C) Brefeldin A (Bref A; 100 ng/ml; 3 h) significantly decreased sCD14 production by non-CF (n=5) and CF 707 708 (n=5, patients 56-60; supplemental Table 1) macrophages. Levels in the supernatants were measured using an ELISA assay. The data are shown as the mean ± SEM. Mann-Whitney test: \*\* 709 710 p<0.01 vs. non-CF macrophages. Ratio Student's t-test: # p<0.05 vs. untreated non-CF macrophages and  $\S p < 0.05 vs.$  untreated CF macrophages. 711

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714 Figure 5. Human recombinant sCD14 induces the expression and secretion of proinflammatory cytokines in non-CF macrophages. (A) IL-1 $\beta$ , IL-8 and TNF- $\alpha$  mRNA 715 716 expression was quantified by RT-qPCR in non-CF macrophages treated with hr-sCD14 (100 and 500 ng/ml, 6 hours and 24 hours). The data are shown as the mean  $\pm$  SEM of four and five 717 718 independent experiments for 6 hours and 24 hours, respectively. (B) IL-1 $\beta$ , IL-8 and TNF- $\alpha$ release were measured by using an ELISA assay in supernatants from non-CF macrophages 719 treated with hr-sCD14 (1 to 500 ng/ml, 24 hours). The data are shown as the mean  $\pm$  SEM (*n*=6-720 11, n=4 and n=3-6 for IL-1 $\beta$ , IL-8 and TNF- $\alpha$ , respectively). Ratio Student's t-test: \* p<0.05; \*\* 721 p<0.01; \*\*\* p<0.001 and \*\*\*\* p<0.0001 vs. untreated macrophages. 722

723

**Figure 6. NF-κB pathway is involved in the sCD14-induced production of pro-inflammatory** 

**cytokines in non-CF macrophages.** (A) Cytosol P-IκBα and IκBα expression were determined

by Western blotting of the total protein fraction from non-CF macrophages treated with hr-sCD14 726 (500 ng/ml, 0 to 60 min, representative blot of three independent experiments). Equal protein 727 728 loading was controlled via HSC-70 detection. (B) NFkB p65 activation was measured using an assay in non-CF macrophages that were treated or not treated with hr-sCD14 (n=5; 500 ng/ml, 24 729 hours). A positive control was used to establish the result. (C) IL-1 $\beta$ , IL-8 and TNF- $\alpha$  gene 730 731 expression was analyzed by RT-qPCR in non-CF macrophages treated or not treated with hrsCD14 (500 ng/ml, 6 hours) in the absence and presence of an NF-kB inhibitor (Bay 11-7082, 10 732 733  $\mu$ M, 1 hour pretreatment, n=5) (D) IL-1 $\beta$ , IL-8 and TNF- $\alpha$  protein expression were quantified using an ELISA assay in non-CF macrophages that were treated or not treated with hr-sCD14 734 (500 ng/ml, 24 hours) in the absence or presence of Bay 11-7082 (1 and 10  $\mu$ M, 1 hour 735 pretreatment; n=4, n=4 and n=5 for IL-1 $\beta$ , IL-8 and TNF- $\alpha$ , respectively). The data are shown as 736 the mean  $\pm$  SEM. Ratio Student's t-test: \* p<0.05 and \*\*\* p<0.001 vs. untreated macrophages; # 737 738 p<0.05 and ## p<0.01 vs. hr-sCD14-treated macrophages.

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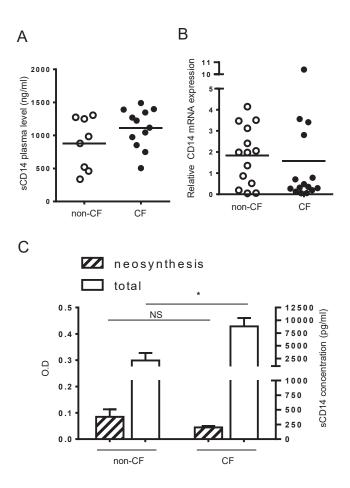
Figure 7. Caspase-1 is involved in the sCD14-induced production of IL-1 $\beta$  in non-CF 740 macrophages. (A) Pro-caspase 1 and caspase 1 expression were determined by Western blotting 741 742 analysis of the total protein fraction from non-CF macrophages treated with hr-sCD14 (500 743 ng/ml, 0 to 60 min, a representative blot of three independent experiments). (B) IL-1β secretion was measured using an ELISA assay in supernatants from non-CF macrophages treated with hr-744 sCD14 (500 ng/ml, 0 to 1440 min). The data are shown as the mean  $\pm$  SEM (n=7). (C) IL-1 $\beta$ 745 secretion was measured using an ELISA assay in supernatants from non-CF macrophages treated 746 747 or not treated with hr-sCD14 (500 ng/ml, 24 hours) in the absence or presence of the caspase 1 inhibitor Z-WEHD-FMK (1 to 30  $\mu$ M, 1-hour pretreatment). The data are shown as the mean  $\pm$ 748 SEM (n=4). Ratio Student's t-test: \* p<0.05 and \*\* p<0.01 vs. untreated macrophages; # p<0.05 749 750 vs. hr-sCD14-treated macrophages.

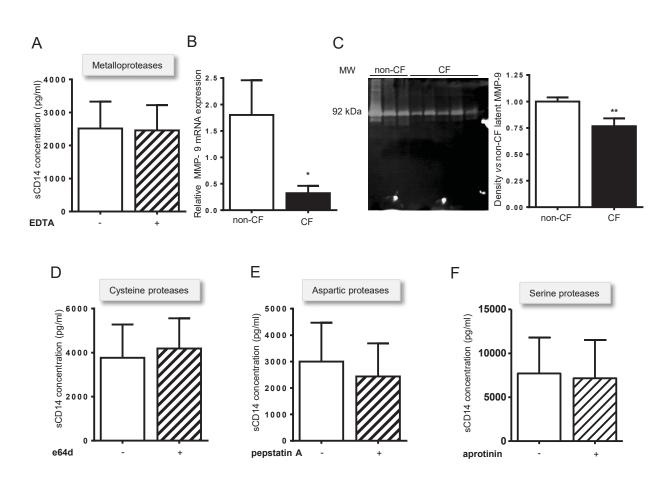
Figure 8. NLRC4 and NLRP3 inflammasome pathways are involved in IL-1 $\beta$  secretion in non-CF macrophages treated with hr-sCD14. (*A and B*) The efficiency of transfection with NLRC4 siRNA or NLRP3 siRNA was assessed by Western blotting of the total protein fraction from non-CF macrophages. The bar graph shows the results of densitometric analysis (*n*=6). The

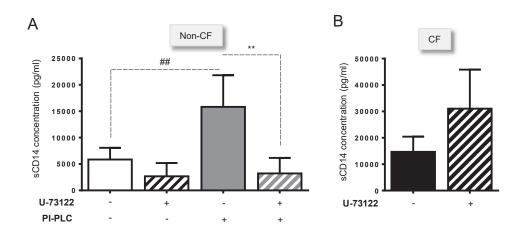
results were expressed *vs.* the relative intensity observed in Control siRNA-treated non-CF macrophages. (*C*) IL-1 $\beta$  release was measured by ELISA in supernatants from non-CF transfected macrophages that were treated or not treated with hr-sCD14 (500 ng/ml, 24 hours; *n=*6). The data are shown as the mean ± SEM. Ratio Student's t-test: \*\* p<0.01 *vs.* siControltreated macrophages; ## p<0.01 *vs.* untreated macrophages; § p<0.05 and §§ p<0.01 *vs.* hrsCD14-treated macrophages.

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Figure 9. sCD14-induced cytokine release by non-CF macrophages is reversed by 763 antagonists that target CD14 or TLR-4. IL-1 $\beta$ , IL-8 and TNF- $\alpha$  secretion was measured by 764 ELISA in supernatants from non-CF macrophages that were treated or not treated with hr-sCD14 765 766 (500 ng/ml, 24 hours) in the absence or presence of an anti-CD14 neutralizing antibody (CD14ab, 10 µg/ml, 1-hour pretreatment), a TLR-4 antagonist (LPS-RS, 2 µg/ml, 1-hour pretreatment), 767 768 an anti-TLR4 neutralizing antibody (TLR4-ab, 10 µg/ml, 1-hour pretreatment) or the IgG2a control (10  $\mu$ g/ml, 1 hour pretreatment). The data are shown as the mean  $\pm$  SEM (n=3-6, n=3-6) 769 and n=3-6 for IL-1 $\beta$ , IL-8 and TNF- $\alpha$ , respectively). Ratio Student's t-test: \* p<0.05 and \*\* 770 p<0.01 vs. hr-sCD14-treated macrophages. 771







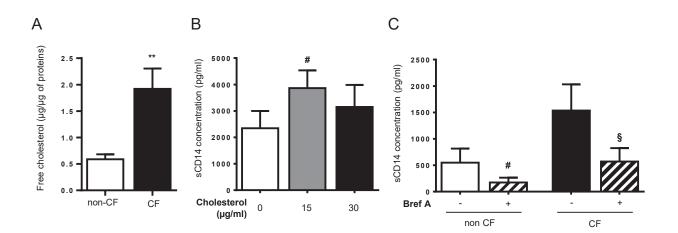
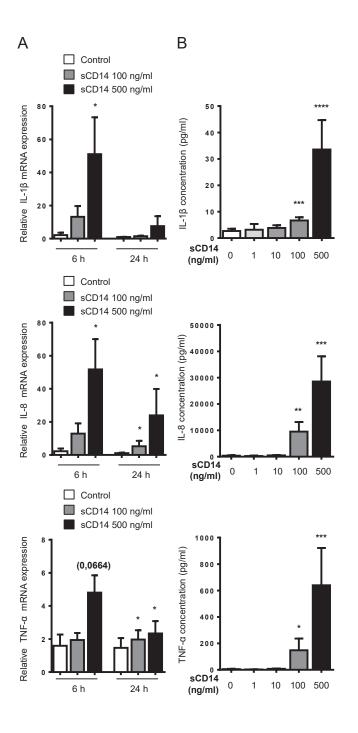
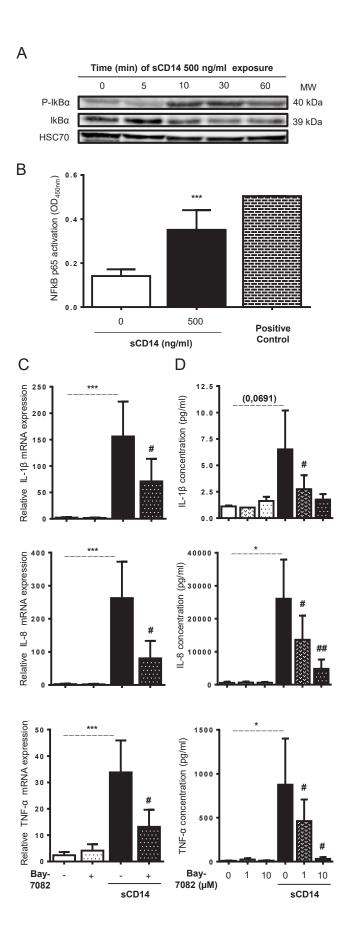
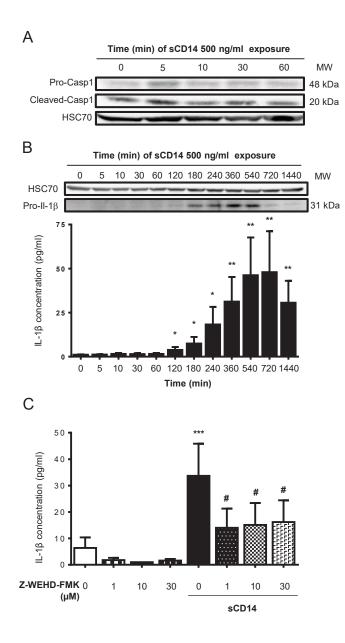


Fig 4







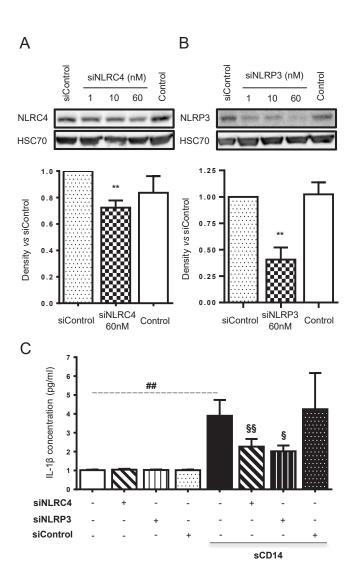
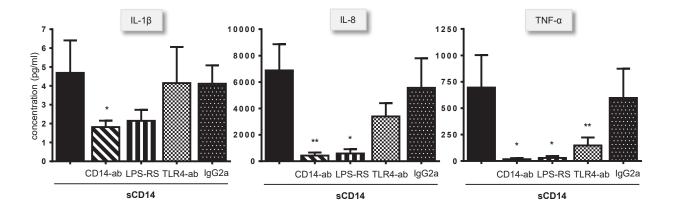


Fig 8



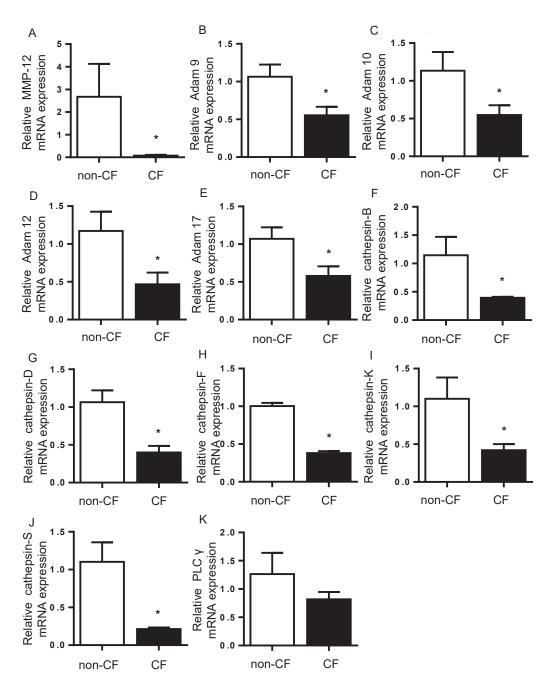
Patient	Age	Sex	Genotype	Microbiology	BMI	FEV1 % predicte
1	32	F	F508del / F508del	P.a / A.f / S.a	15	45
2	33	М	F508del / F508del	P.a / A.f / S.a	22,9	66
3	34	F	F508del / W486X	P.a / S.a	19,6	37
4	22	F	F508del / F508del	P.a / A.f / S.a	16,8	32
5	39	Μ	F508del / G551D	Af	22,1	40
6	32	М	F508del / F508del	P.a / S.a	20,1	82
7	20	М	F508del / F508del	P.a / A.f / S.a	19,9	66
8	20	М	F508del / F508del	S.a	23,2	98
9	39	F	F508del / 2789+5G→A	P.a / S.a	19,3	66
10	22	М	F508del / F508del	A.f / S.a	19,5	78
11	22	F	1248+1G→A	S.a	22,7	104
12	20	F	F508del / I507del	P.a / A.f	18,4	61
13	30	F	F508del / 1248+1G→A	P.a / S.a	18,3	33
14	31	F	F508del / N1303K	P.a / A.f / S.a	15,4	28
15	22	F	F508del / F508del	P.a / A.f / S.a	19,6	79
16	34	М	F508del / F508del	P.a / A.f / S.a	20,5	51
17	27	F	F508del / F508del	A.f / S.a	20,5	97,2
18	35	F	F508del / F508del	P.a / S.a	19,1	30,2
19	43	М	F508del / G551D	P.a	20,9	79,1
20	28	F	1248+1G→A	A.f / S.a	20,7	90,5
21	40	M	F508del / F508del	P.a / A.f	21,9	48,7
22	18	F	F508del / F508del	None	24,1	100,4
23	37	F	R600S / CFTRdup4-10	S.a	18,6	95
24	20	F	F508del / S945L	A.f/S.a	21,3	68,4
25	25	M	F508del / F508del	A.f / S.a	24,4	58,5
26	24	F	F508del / F508del	P.a / A.f / S.a	16,5	28,4
27	19	M	F508del / 2789+5G→A	S.a	22,23	94,7
28	40	F	F508del / S492F	P.a / S.a	27,82	55,3
29	53	F	F508del / 2789+5G→A	P.a / A.f	17,61	36
30	28	M	F508del / F508del	A.f	23,74	103
31	53	M	F508del / 2789+5G→A	S.a	22,14	96,2
32	20	M	F508del / F508del	A.f/S.a	22,14	62
33	20 19	M	F508del / F508del	P.a / A.f	22,3	91
33 34	26	M	F508del / F508del	S.a	20,4 20,2	58,7
				S.a S.a		
35	37	M	F508del / F508del	S.a S.a	21,1	77,4
36	23	F	F508del / F508del		17,1	54,5
37	49	F	F508del / 3272-26A→G	P.a / S.a	22,8	62,2
38	31	F	F508del / G91R	P.a / S.a	24,3	61,5
39	19	F	F508del / F508del	S.a	18,8	96
40	27	M	F508del / F508del	S.a	20,2	73,1
41	26	F	F508del / F508del	P.a / A.f / S.a	19,1	67
42	33	M	F508del / F508del	P.a	22,2	64,4
43	18	F	F508del / F508del	None	25,8	102,1
44	37	F	F508del / F508del	S.a	19,1	77,5
45	21	F	F508del / G551D	S.a	22,5	103,7
46	46	M	F508del / 2789+5G→A	A.f / S.a	22,2	96,6
47	35	F	F508del / F508del	P.a / S.a	19,3	35,2
48	25	М	F508del / F508del	A.f / S.a	23,5	55,3
49	39	M	F508del / F508del	P.a	21	49
50	18	F	F508del / F508del	P.a / A.f / S.a	19,1	62,3
51	23	M	F311L / N1303K	S.a	18,5	93,8
52	21	F	F508del / F508del	P.a / A.f / S.a	18,4	86,7
53	26	M	F508del / S1251N	P.a / S.a	18,81	41,1
54	23	F	F508del / F508del	P.a / S.a	16,86	33,7
55	38	F	F508del / F508del	None	18,2	41
56	30	M	F508del / 1749insTA	P.a / A.f / S.a	18,3	21,1
57	32	F	F508del / 4382delA	P.a / A.f / S.a	18	29,5
58	23	F	F508del / 1677delTA	P.a / A.f	18	49
59	52	M	F508del / 2789+5G→A	Af	22,5	107,9
60	38	М	F508del / 1078delT	P.a / A.f / S.a	21,7	63

Table S1: Characteristics of CF patients

**Abbreviations :** A.f.: Aspergillus fumigatus; P.a.: Pseudomonas aeruginosa; S.a.: Staphylococcus aureus FEV1: Force Expiratory Volume in one second

Target genes	Primer	Sequence (5' to 3')		
18S	Hs_RRN18S_1_SG	QT00199367		
18S	Forward	CGCCGCTAGAGGTGAAATTC		
	Reverse	TTGGCAAATGCTTTCGCTC		
CD14	Hs_CD14_1_SG	QT00208817		
IL-1β	Hs_IL1B_1_SG	QT00021385		
IL-8	Hs_CXCL8_1_SG	QT00000322		
TNFα	Forward	AACCTCCTCTCTGCCATC		
	Reverse	ATGTTCGTCCTCCTCACA		
MMP-9	Forward	TCTTCCCTGGAGACCTGAGA		
	Reverse	ATTTCGACTCTCCACGCATC		
MMP-12	Forward	ACACATTTCGCCTCTCTGCT		
	Reverse	ATTGTCAGGATTTGGCAAGC		
Cathepsin B	Forward	AGAATGGCACACCCTACTGG		
	Reverse	GCCACCACTTCTGATTCGAT		
Cathepsin D	Forward	GTACATGATCCCCTGTGAGAAGGT		
	Reverse	GGGACAGCTTGTAGCCTTTGC		
Cathepsin F	Forward	GCCTGTCCGTCTTTGTCAAT		
	Reverse	TGGCTTGCTTCATCTTGTTG		
Cathepsin K	Forward	CCGCAGTAATGACACCCTTT		
	Reverse	GCACCCACAGAGCTAAAAGC		
Cathepsin S	Forward	TGGGAGACATGACCAGTGAA		
	Reverse	AGCAAGCACCACAAGAACCT		
Adam 9	Forward	TGCAAATGTCTTCAGGGAAC		
	Reverse	TGCATTAACCTCACCGATGAC		
Adam 10	Forward	CATTGCTGAATGGATTGTGG		
	Reverse	GAGCCTGGAAGTGGTTTACG		
Adam 12	Forward	AACCTCGCTGCAAAGAATGTG		
	Reverse	CTCTGAAACTCTCGGTTGTCTG		
Adam 17	Forward	ACCTGAAGAGCTTGTTCATCGAG		
	Reverse	CCATGAAGTGTTCCGATAGATGTC		
PLCγ	Forward	AACCAGAAGTCCTTTGTCTTCATC		
	Reverse	CTGGTTCTTCTCCCAGTACTTCAT		

Table S2: List of primer sequences used for RT-qPCR analysis in this study



**FIGURE S1. Proteases and phospholipase C-** $\gamma$  gene expressions in non-CF and CF macrophages. (*A*) MMP-12 (*n*=4, patients 6, 13, 15-16; supplemental Table 1), (B to E) Adam 9, Adam 10, Adam 12 (n= 6, patients 17-18, 20-22, 24; supplemental Table 1) and Adam 17 (n= 6, patients 17, 21-22, 24, 26, 41; supplemental Table 1), (*F* to *J*) cathepsin-B, cathepsin-D, cathepsin-F, cathepsin-K and cathepsin-S (*n*= 3-6, patients 15-16, 32; supplemental Table 1) and (*K*) phospholipase C- $\gamma$  (PLC $\gamma$ , *n*=5-6, patients 17, 18, 20, 22, 24; supplemental Table 1). Gene (mRNA) expression was quantified in CF and non-CF macrophages by RT-qPCR. The data are shown as the mean ± SEM. Mann-Whitney test: \* p<0.05 *vs.* non-CF macrophages.

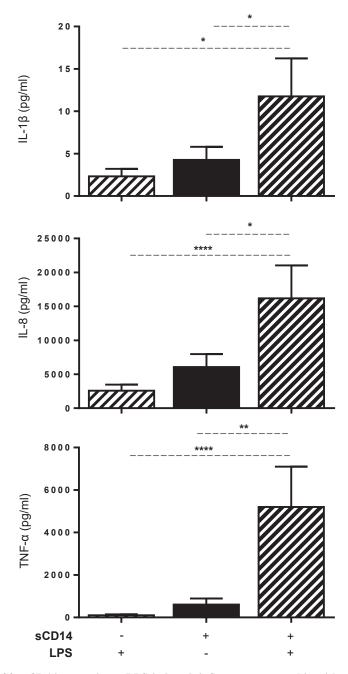


FIGURE S2. sCD14 potentiates LPS-induced inflammatory cytokines/chemokines production in non-CF macrophages. IL-1 $\beta$ , IL-8 and TNF- $\alpha$  levels were measured using an ELISA assay in non-CF macrophages incubated with LPS (from *P. aeruginosa*, 100 ng/ml) in the absence and presence of sCD14 (500 ng/ml) (*n*=8). Ratio Student's t-test: \* p< 0.05; \*\* p< 0.01 and \*\*\*\* p<0.0001 vs LPS-treated macrophages.