Bacterial sepsis increases survival in metastatic melanoma: Clamydophila pneumoniae induces macrophage polarization and tumor regression.

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Bacterial sepsis increases survival in metastatic melanoma:

*Chlamyphila pneumoniae* induces macrophage polarization and tumor regression

Short title: *C. pneumoniae* increases survival in melanoma

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Introduction

The initiative of the current study was the unexpected complete tumor regression of a patient with stage IV cutaneous metastatic melanoma, who suffered multifactorial sepsis syndrome during BOLD chemotherapy (Suppl. Fig. 1.). After targeted antibiotic treatment and combined complication-free chemotherapy, the patient's physical condition improved and unexpectedly the metastases disappeared. The patient has been asymptomatic and metastasis-free ever since the end of BOLD therapy. A significant decrease in the volume of the previously palpable axillary and abdominal metastases was observed already when BOLD was interrupted due to sepsis. For a timeline of events, see Table 1.

Molecular genetics research in the last decade helped the development of BRAF inhibitors and immunooncological agents, which brought about a significant improvement of the life expectancy of melanoma patients. Once the gold standard (Avril et al., 2004), Dacarbazine-based chemotherapies are still approved and widely applied in melanoma therapy, but their efficacy is known to be relatively low (Garbe et al., 2011). In the light of this, the fact that clinical improvement was observed quite early during the chemotherapy suggested other factors behind the outcome, and the concurrent sepsis seemed to offer a potential explanation.

It has long been recognized that cancer patients might recover following bacterial infections (Wiemann and Starnes, 1994; Hobohm, 2001). The hypothesis was that fever and TNF-α induced by the infectious agents caused the tumor regression, but this could not be reproduced by TNF-α administration or hyperthermia (Nauts et al., 1946; Tsung and Norton, 2006). It has been observed that an attenuated form of Listeria monocytogenes can infect cancer cells, but not normal cells, and this phenomenon resulted in a potentially effective experimental cancer therapy. (Quispe-Tintaya W et al. 2013)
Vaccination with intracellular pathogens like Bacillus Calmette-Guerin or Vaccinia virus significantly decreased the incidence of melanoma (Krone et al., 2005). However, a convincing explanation is still missing.

While it is generally accepted that anti-tumor immune mechanisms overlap with antibacterial immune responses (Chen et al., 2007; Adams, 2009;), the exact mechanism induced by microbes is not understood.

As immune responses appear to be decisive factors also in the outcome of melanoma (Ridnour et al., 2013; Shimanovsky et al., 2013), we hypothesized that sepsis, by triggering polarized, “joint” anti-bacterial and anti-tumor immune responses, could induce tumor regression. This hypothesis was tested in our experimental model.

To clarify the role of the adaptive immune system in the anti-tumor immune mechanisms induced by C. pneumoniae (CP, successfully identified in the primary melanoma after our patient recovered from sepsis-Suppl. Fig. 1f), lung metastases (LM) were induced in immunocompetent C57BL/6 mice or immunodeficient NSG mice. Animals were then CP- or mock-treated (Suppl. Materials and methods). To assess the effects of treatment, histological, immunological and molecular analyses were done.

Results

In immunocompetent, CP- treated animals, the number of LMs significantly decreased (P=0.003) (Fig. 1a), while the survival (Fig. 1t) significantly increased (P=0.04) compared to mock treatment. This was not observed in immunodeficient mice, and the treated animals did not develop fever (33.2 °C±1.0 mock vs. 34.8 °C±0.5 CP) or high plasma levels of TNF-α either, which is against the “fever hypothesis” (Wiemann and Starnes, 1994; Hobohm, 2001).

Histological analysis of slices from the lungs of mock-treated melanoma-bearing immunocompetent mice showed a high number of LMs, with frequent intra-tumor necrosis.
In contrast, fewer and smaller foci of regressive LMs were observed in the CP-treated immunocompetent animals (Fig. 1f). Moreover, in this group, a high number of tumor-infiltrating mononuclear histiocytes and lymphoid cells were identified in the LMs. The LMs did not exhibit significant intratumor immune reactions in the immunodeficient mice, regardless of treatment type (Fig. 1g, h). Markedly increased immune reaction in the lungs of the CP-treated mice was also verified by immunolabeling of the cell surface activation markers CD11b and CD80 (Fig. 1i-l). Immune cell invasion was not detected after mock treatment - the immune cells were concentrated in the marginal zones of the tumors (Fig. 1i, k). In contrast, after CP treatment, marked infiltration by activated lymphocytes was seen in the internal tumor stroma (Fig. 1j, l); differences were significant (Fig. 1m, n) (P=0.0001).

To assess macrophage polarization, M1 (anti-tumor) or M2 (pro-tumor) macrophage-specific cytokine and chemokine transcriptome profiling was done (Mantovani et al., 2004). Macrophage markers were detected with Q-PCR from pooled lung samples 2, 4 and 12 hours after mock or CP treatment. Four hours after CP application, markedly increased levels of M1-specific mRNA transcripts for CCL2, CCL3, IL6, CXCL10, CCL7, CD80, CXCL11, CXCL9, IL23, and TNFα were detected. In line with this, the mRNA expression of most M2-specific markers decreased. Interestingly, the levels of some important M2 markers (CXCL13, IL1Ra) were actually increased (Suppl. Fig. 2a, b). Upon CP administration, the quantity of M1-specific cytokine and chemokine mRNA was significantly increased (P=0.014) after 4 hours, in comparison to M2-markers.

Alteration in the expression pattern of COX-1 and COX-2 is one of the key markers of macrophage polarization (Martinez et al., 2006; Mantovani et al., 2013). Western blot analysis revealed that 12 hours after CP treatment, protein expression of the M2-specific COX-1 decreased by half, whereas the protein expression of the M1-specific COX-2 increased more than two fold (Suppl. Fig. 2c, d).
Two hours after CP treatment - but not after mock treatment - CXCL1 melanoma growth factor immunoreactivity become undetectable (Suppl. Fig. 3a, b). To assess whether this in vivo phenomenon was due to a direct CP:CXCL1 interaction, equal amounts of recombinant CXCL1 were incubated in vitro (in the presence of protease inhibitors) with increasing quantities of CP. CXCL1 levels were determined by Western blotting. CP depleted CXCL1 in a dose-dependent manner, suggesting a strong and direct binding by CP (Suppl. Fig. 3c, d).

Discussion

Our results seem to indicate that CP treatment does indeed induce a complex anti-tumor response. We showed that CP treatment can suppress LM formation in immunocompetent (but not in immunodeficient) mice. M1-type macrophage polarization was demonstrated, which is associated with anti-tumor effects (Sica et al., 2008). The anti-tumor immune polarization/activation was further supported by the profound enrichment of CD80 and CD11b expressing immune cells in the lungs CP-treated animals (Prebeck et al., 2001). Of special importance, the melanoma growth factor CXCL1 was completely depleted by CP, both in vivo and in vitro.

As (i) CXCL1-induced NF-κB activity was shown to facilitate melanoma transformation by allowing melanocytes to escape apoptosis; and (ii) IκB-α ΔN (super-repressor of NF-κB) reduced tumor growth and metastatic potential of melanoma cells (Dhawan et al., 2002), we consider it a possible scenario that not only the CP induced M1 type macrophage polarization but the induced CXCL1 depletion could significantly contribute to the tumor regression. Evidently, results of the animal study strongly support our assumption about the role of sepsis in the observed outcome; however, these data cannot exclude the role of the BOLD therapy.

The conclusion one can safely draw at this point is that sepsis, in the context of BOLD,
resulted in a dramatic improvement, otherwise not seen in uncomplicated therapy, which suggests that the occurrence of sepsis was an event of key importance.

Competing financial interests

The authors declare no competing financial interests.

Acknowledgements

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References


Table 1: Timeline of Clinical Case Report

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<tr>
<td>-360</td>
<td>The patient herself detected a bleeding nevus-like lesion on the back and an enlarged axillary lymph node; no steps were taken.</td>
</tr>
<tr>
<td>120</td>
<td>Hospital visit. X-ray, mammography and abdominal doppler seems to be negative, axillary lymph node biopsy was proposed. The patient was temporarily lost from follow up.</td>
</tr>
<tr>
<td>0</td>
<td>Hospital visit for abdominal pain, gastritis was diagnosed and a gastric polyp was removed. Tumor masses were discovered in the retroperitoneal lymph nodes (15-20 mm), spleen (67 mm) and bladder (40X68 mm). Another tumor was detected in the brain by CT (40 mm).</td>
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<tr>
<td>4</td>
<td>The intracranial tumor mass was removed surgically and diagnosed as amelanotic melanoma metastasis.</td>
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<td>24</td>
<td>Cranial radiotherapy was initiated.</td>
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<tr>
<td>32</td>
<td>Radiotherapy completed.</td>
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<tr>
<td>35</td>
<td>BOLD (bleomycin, oncovine, lomustine and dacarbazine) chemotherapy initiated.</td>
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<tr>
<td>37</td>
<td>On the 3rd day of chemotherapy, it was suspended because of vomiting and fever. The gastric fluid contained Escherichia coli and Candida albicans. Clostridium difficile toxin was also detected. Fluconazole and ceftriaxone (later metronidazol) treatment was initiated.</td>
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<td>52</td>
<td>CVC was removed because of putative Pseudomonas aeruginosa infection. This was later confirmed by blood test.</td>
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<tr>
<td>59</td>
<td>The primary tumor was excised and analyzed (Melanoma malignum, Br 1.52 mm, C1. III., pT2b).</td>
</tr>
<tr>
<td>77</td>
<td>BOLD, 2nd treatment cycle. Decrease of axillary and abdominal metastases was detected.</td>
</tr>
<tr>
<td>120</td>
<td>BOLD, 3rd cycle. Further improvement of the axillary and intra-abdominal metastases was recorded. No intra-abdominal lymphadenomegalia, a single liver metastasis and shrinking splenic metastasis was detected.</td>
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<tr>
<td>162</td>
<td>BOLD, 4th cycle. Complete remission of the axillary and abdominal metastases was observed.</td>
</tr>
<tr>
<td>210</td>
<td>BOLD, 5th cycle. Complete remission of the axillary and abdominal metastases was observed.</td>
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<tr>
<td>255</td>
<td>BOLD, 6th cycle. The patient is asymptomatic and PET/CT-verified metastases free.</td>
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<td>&gt;1500</td>
<td>The patient is asymptomatic and PET/CT-verified metastases free.</td>
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**Figure 1:**

*C. pneumoniae* treatment results in melanoma metastasis regression and increases survival of animals as well as of CD11b+ and CD80+ immune cell infiltration of tumor tissues.

Number of lung metastases (a, c), melanoma antigen-MART (b, d) and survival rate (t) of mock or *C. pneumoniae* (C. pn.) treated immunocompetent C57BL/6 and immunodeficient NSG mice. Representative images and HE-stained histological sections of dissected lungs of mock (e) and *C. pneumoniae* (f) treated immunocompetent mice, as well as of mock (g) and *C. pneumoniae* (h) treated immunodeficient (NSG) animals. Note that the subpleural metastasis formation is extensive in diameter but not in thickness in NSG mice (arrowheads).

Scale bars, 100 µm. (e) Trophical necroses indicating high tumor burden. Insert: atypical tumor cells and regions of necrosis. (f) Circles and right insert, foci of regressive metastases, left insert: areas of residual pneumonitis after *C. pneumoniae* treatment. (g, h) In both mock and *C. pneumoniae* treated NSG mice, miliary metastases were developed subpleurally (arrowheads) and intraparenchymally (circles) without significant inflammatory reactions (inserts: higher magnification of intraparenchymal metastases). Immunohistochemistry of CD11b (i, j, DAB, brown) and CD80 (k, l, Fast red, red) on lungs of mock (i, k) or *C. pneumoniae* (j, l) treated C57BL/6 mice. Dashed lines indicate tumor border. (i-r) Arrows indicate infiltrating immune cells. Intratumoral number of CD11b+ (m) and CD80+ (n) cells determined as a ratio of 100 tumor cells in C57BL/6 mice. CD80+ cells in NSG lungs counted by square millimeter (s). Data are given as mean ± SD.
Number of lung metastases (a, c), melanoma antigen-MART (b, d) and survival rate (t) of mock or C. pneumoniae (C. pn.) treated immunocompetent C57BL/6 and immunodeficient NSG mice. Representative images and HE-stained histological sections of dissected lungs of mock (e) and C. pneumoniae (f) treated immunocompetent mice, as well as of mock (g) and C. pneumoniae (h) treated immunodeficient (NSG) animals. Note that the subpleural metastases formation is extensive in diameter but not in thickness in NSG mice (arrowheads). Scale bars, 100 µm. (e) Trophical necroses indicating high tumor burden. Insert: atypical tumor cells and regions of necrosis. (f) Circles and right insert, foci of regressive metastases, left insert: areas of residual pneumonitis after C. pneumoniae treatment. (g, h) In both mock and C. pneumoniae treated NSG mice, miliary metastases were developed subpleurally (arrowheads) and intraparenchymally (circles) without significant inflammatory reactions (inserts: higher magnification of intraparenchymal metastases). Immunohistochemistry of CD11b (i, j, DAB, brown) and CD80 (k, l, Fast red, red) on lungs of mock (i, k) or C. pneumoniae (j, l) treated C57BL/6 mice. Dashed lines indicate tumor border. (i-r) Arrows indicate infiltrating immune cells. Intratumoral number of CD11b+ (m) and CD80+ (n)
cells determined as a ratio of 100 tumor cells in C57BL/6 mice. CD80+ cells in NSG lungs counted by square millimeter (s). Data are given as mean ± SD.
Supplementary Discussion:

The blots of the Proteome Profiler (Suppl. Fig. 3a, b) in the upper left lower left and lower right positions are the so-called assay controls, they merely indicate that the test was technically successful. The rest of the proteins –which could be relevant in the anti-tumoral immune response—are as follows (from left to right and from top to bottom): C5a, CD54, CXCL1, MCP-1, IL-16, IL-1Ra, CCL5.

- **C5a** is a complement protein that has been implicated in tumorigenesis. C5a accelerates tumor progression, can directly activate myeloid-derived suppressor cells, stimulate angiogenesis and cell migration. C5a increases VEGF level, prevents the activation of apoptotic caspase 3 and DNA fragmentation, and may function as an anti-apoptotic molecule (Kim et al., 2005; Gunn et al., 2012). We found decreased levels of this protein after treatment.

- **CD54** (ICAM-1) decreased in our in vivo model and expresses with a dose- and time-dependent increase in human malignant melanoma cells on stimulation of TNF-alpha. Inhibition of ICAM-1 expression on melanoma cells reduces the metastatic ability of the melanoma cells, indicating an important role of ICAM-1 in metastasis (Miele et al., 1994). B. Cava et al. described that metastasis reduction of B16 cells is correlated to the reduction of plasma gelatinolitic activity and to the decrease of cells expressing CD44, CD54, and integrin-β₃ adhesion molecules.

- **CXCL1** is a melanoma growth factor and known as M2 marker. Our results suggest that the depletion of CXCL1 could play a role in the reduction of metastasis formation.

- **MCP-1** (decreased in our model) is produced by a variety of tumors, including B16F1 and plays an important role in tumor progression, especially in angiogenesis (Kim et al., 2005; Koga et al., 2008). Tumor cell-activated macrophages release TNFα, which facilitates the
MCP-1 production of tumor cells. Thus, disruption of tumor-stromal cell interaction may inhibit tumor progression by reducing the production of tumor-promoting proinflammatory mediators, such as MCP-1 (Yoshimura et al., 2015).

- **IL-16**: it is a pleiotropic cytokine that functions as a chemoattractant, hence a modulator of T cell activation. The cytokine function is exclusively attributed to the secreted C-terminal peptide, while the N-terminal product may play a role in cell cycle control. Caspase 3 is reported to be involved in the proteolytic processing of this protein (http://www.cancerindex.org/geneweb/IL16.htm). IL-16 appears in the literature remarkably scarcely in connection with cancer, and we could not detect alteration in its level either; therefore, we do not know the relevance of this protein to the discussed observation.

- **IL-1Ra** (moderately decreased or unchanged in our model) is the receptor antagonist of IL-1 and it has been described as pleiotropic (Aubie et al., 2015; Di Mitri et al., 2014). Although IL-1Ra has been described to inhibit subcutaneous B16 melanoma growth *in vivo* (McKenzie et al., 1996) we did not observe significant changes in its level upon treatment; therefore, similar to IL-16, the relevance of this finding is still unknown.

- **CCL5** (decreased in our model) is a chemokine with tumor supportive properties (Adler et al., 2003; Sugawara et al., 2008). In rectal cancer, significant decrease of CCL5 was associated with a favorable response to chemoradiation therapy (Tada et al., 2014). Moreover, Mdr2 and CCR5 (CCL5 receptor) double knock-out mice exhibited significant decrease in tumor incidence and size of hepatocellular carcinoma (Barashi et al., 2013). Finally, CCL5 was found to enhance cytotoxicity of regulatory T cells against CD8+ cells (Chang et al., 2012).
Supplementary Materials and methods

The mouse model

B16F1 melanoma cells (ECACC, Salisbury, UK) were administered intravenously (1x10^5 cell/100 µl) to 6-8 week old female immunocompetent C57BL/6 or immuno-deficient NOD/Scid IL2rg null (NSG) mice (Charles River Laboratories, Budapest, Hungary). One week after the tumor cell administration, mice were treated with *C. pneumoniae* strain CWL-029 (VR-029, ATCC, Wesel, Germany) propagated in Hep2 cells (CCL-23, ATCC, Wesel, Germany) (Mantovani *et al.*, 2004). *C. pneumoniae* and the mock control (processed Hep2 cells) were heat-inactivated at 90°C for 30 minutes. Mice were mildly sedated with sodium pentobarbital (7.5 mg/ml) and treated intranasally with 1×10^6 IFU *C. pneumoniae* 7, 9, 11, 14, and 16 days after tumor implantation. In the case of immune-deficient mice, since physical conditions of NSG mice deteriorated extremely rapidly, animals were euthanized at day 14 after the third *C. pneumoniae* treatment. The special advantages of this model are: (i) with intravenous injection of melanoma cells, visible lung tumor metastases develop within 7 days after injection without significant spreading into other organs; and (ii) *C. pneumoniae* is a lung-specific intracellular pathogen with a significant invasion rate even to the lung metastases. Two hours after the 1st inhalation (day 7), 4 hours after 2nd, 12 hours after 3rd and 24 hours after 5th inhalation, 3 animals/group were anaesthetized and their lungs were harvested for protein, mRNA and histological analysis. The remaining mice received the 4th (day 14) and the 5th (day 16) treatments and were followed for survival. At the end-point, the animals were euthanized, their lungs were removed and 3 independent persons counted the number of surface metastases in a blind fashion.

All animal experiments were performed in accordance with national (1998. XXVIII; 40/2013) and European (2010/63/EU) animal ethics guidelines. The experimental protocols were approved by the Animal Experimentation and Ethics Committee of the Biological
Research Centre of the Hungarian Academy of Sciences and the Hungarian National Animal Experimentation and Ethics Board (clearance number: XVI./03521/2011.). Informed consent was obtained from all subjects.

Survival

For the survival experiments, groups of mice (n=15) were treated as described 5 times after melanoma implantation. Kaplan-Meier survival curves were analyzed by a log-rank statistical test and p ≤ 0.05 was regarded as statistically significant. The body temperatures of 3 animals/group were measured using an AMA Digital AD 15 TH thermometer 2 hours after the 1st treatment and 4 hours after the 2nd inhalation (day 7 and 9). All animal experiments were authorized by the institutional and national animal welfare committees.

Cytokine and Chemokine Expression Analysis by Quantitative Real-time PCR

Total RNA was purified using a NucleoSpin RNA II RNA isolation kit (Macherey-Nagel, Düren, Germany); first-strand cDNA was synthesized and Q-PCR reactions were performed of M1 type (CCL2, CCL3, CD86, IL12, IL6, IL10, CXCL16, CCL7, CD80, CXCL11, CXCL9, IL23, TNFα) and M2 type (CD163, CXCL13, TGFβ, IL1Ra, CD23, CCL1, CCL22, IL4, CCL17, CCL24, CD150, IL10, CXCL1) markers on pooled samples (n=3) on a RotorGene 3000 instrument (Corbett Research) with gene-specific primers and SYBR Green protocol to monitor gene expression. Each individual Ct value was normalized to the average Ct values of four internal control genes (ΔCt values). The final relative gene expression ratios (fold change) were calculated as comparisons of ΔCt values (ΔΔCt values). Non-template control sample was used for each PCR run to check the primer-dimer formation. Primer sequences are available upon request.
C. pneumoniae detection from the primary tumor of patient by PCR

DNA was extracted from the formalin fixed paraffin-embedded (FFPE) samples using Nucleospin® FFPE DNA kit (Macherey-Nagel, Düren, Germany) according to the manufacturer’s instruction. For experiments involving a human subject were performed in accordance with National and Regional Ethics Comittee VI-R-039/01840-2/2012; 25363/2012/EKU; 448/PI/2012. The experimental protocols were approved by the National and Regional Ethics Comittee (clearance number: MCC-INTER-001.)

Histology, immunohistochemistry

Lung specimens were fixed in 4% buffered formaldehyde; then routine HE histology as well as standardized immunohistochemistry tissue microarray were performed using anti-CD11b (clone M1/70; R&D Systems, Minneapolis, MN) and CD80 (B7-1; R&D Systems, Minneapolis, MN) antibodies.

Cytokine and chemokine detection by proteome profiling

Expression levels of different cytokines in pooled lung specimens were determined using Mouse Cytokine Array Panel A (R&D Systems, Minneapolis, MN), according to the manufacturer’s instructions.

Western blot analysis of COX-1 and COX-2

To determine COX-1/COX-2 balance, Western blot analysis was performed using the lung lysates. Samples of total proteins were resolved on NuPAGE 4-12% Bis-Tris Gel, and then transferred to a nitrocellulose membrane. The membrane was incubated with anti-COX-1 (1:250, R&D, Minneapolis, MN) mouse monoclonal antibody and anti-COX-2 (1:200, R&D, Minneapolis, MN) goat polyclonal antibody. After overnight incubation, the membranes were
washed with 1 x TRIS Buffer supplemented with 0.05% Tween20 (Sigma, St. Louis, MO) and incubated for one hour with peroxidase conjugated anti-mouse (1:1000, R&D, Minneapolis, MN) and anti-goat IgG (1:10000, Sigma, St. Louis, MO) and developed using Odyssey Fc chemiluminescence detection system (LiCor Bioscience, Lincoln, NE).

**Western blot analysis of CXCL1**

Recombinant mouse CXCL1 protein (0.5 µg, R&D Systems, Minneapolis, MN) was mixed and incubated (37°C, 30 min) with different 10-fold (10^1-10^0) dilutions of *C. pneumoniae* solutions (3.6 µg-0.00036 µg). CXCL1 protein amounts were then detected by Western blot analysis using an anti-CXCL1 antibody (1:1000, R&D Systems, Minneapolis, MN).

**Statistical analysis**

Kaplan-Meier survival curves were analyzed by a log-rank statistical test and p ≤ 0.05 was regarded as statistically significant. Analyses of other data were performed using two-tailed Student’s *t* test.
Supplementary Figure 1:

Data obtained with the patient: Complete melanoma metastasis regression verified by PET-CT and retrospective PCR analysis-based detection of *C. pneumoniae*

(a, b) Ultrasonography; high tumor burden in the abdominal cavity. (c, d) CT and MRI scans; preoperational brain metastasis in the temporooccipital lobe and postoperational tumor-free brain status, respectively. (e) PET-CT scans; complete tumor regression in the body shortly after the septic event and BOLD treatment. (f) Retrospective detection of *C. pneumoniae* (C. pn.):specific genes by RT-PCR. 16S rRNA: a housekeeping gene of C. pn. GroEL: Heat shock protein 60 of C. pn., a group I chaperonin expressed on the surface of elementary bodies. MOMP: Major Outer Membrane Protein gene of C. pn. A-D: FFPE samples from different sections of primary melanoma; -C: PCR negative control (uninfected Hep2 cells); +C: PCR positive control (Hep2 cells infected by C. pn. strain TW183).

Supplementary Figure 2:

*C. pneumoniae* treatment induces M1 type macrophage polarization

(a) Relative alterations in the levels of individual M1 type and M2 type cytokine/chemokine specific mRNA transcripts in lung samples of *C. pneumoniae* (C. pn.) vs. mock-treated tumor-bearing C57BL/6 mice, as determined by real-time PCR. (b) Mean values of relative M1 and M2 cytokine mRNA expressions; at 4 hours after treatment, M1 and M2 levels are significantly different (two-tailed t-test). (c) Representative Western blot. Expressions of COX-1 and COX-2 were determined in lung samples 12 hours after *C. pneumoniae* or mock treatment of melanoma-bearing C57BL/6 mice (d) Densitometry analysis. Intensity of immunoreactive bands of COX-1 and COX-2 were determined and then normalized to that of
vinculin. Data are presented as fold increase compared to values of the mock-treated group (regarded as 1). A minimum of three experiments yielded similar results.

**Supplementary Figure 3:**

**CXCL1 is depleted by *C. pneumoniae* both *in vivo* and *in vitro***

Assessment of cytokine/chemokine protein levels (Proteome profiler) in lungs of melanoma-bearing C57BL/6 mice 2 hours after mock (a) or *C. pneumoniae* (b) treatment. Squares indicate CXCL1 which disappeared 2 hours after *C. pneumoniae* treatment (c) Representative Western blot. Recombinant mouse CXCL1 protein (0.5 µg) was *in vitro* incubated with 500 IU/ml (1x) *C. pneumoniae*, (C. pn.) or its 10x, 100x, 1,000x, and 10,000x dilutions and then Western blotting was performed. (d) Densitometry analysis of immunoreactive bands shown in panel c. Values of the control (ctrl, vehicle treated) group were regarded as 1. Two experiments yielded similar results.

**Supplementary References**


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(a, b) Ultrasonography; high tumor burden in the abdominal cavity. (c, d) CT and MRI scans; preoperational brain metastasis in the temporooccipital lobe and postoperational tumor-free brain status, respectively. (e) PET-CT scans; complete tumor regression in the body shortly after the septic event and BOLD treatment. (f) Retrospective detection of C. pneumoniae (C. pn.)-specific genes by RT-PCR. 16S rRNA: a housekeeping gene of C. pn. GroEL: Heat shock protein 60 of C. pn., a group I chaperonin expressed on the surface of elementary bodies. MOMP: Major Outer Membrane Protein gene of C. pn. A-D: FFPE samples from different sections of primary melanoma; -C: PCR negative control (uninfected Hep2 cells); +C: PCR positive control (Hep2 cells infected by C. pn. strain TW183).

170x111mm (300 x 300 DPI)
C. pneumoniae treatment induces M1 type macrophage polarization

(a) Relative alterations in the levels of individual M1 type and M2 type cytokine/chemokine specific mRNA transcripts in lung samples of C. pneumoniae (C. pn.) vs. mock-treated tumor-bearing C57BL/6 mice, as determined by real-time PCR. (b) Mean values of relative M1 and M2 cytokine mRNA expressions; at 4 hours after treatment, M1 and M2 levels are significantly different (two-tailed t-test). (c) Representative Western blot. Expressions of COX-1 and COX-2 were determined in lung samples 12 hours after C. pneumoniae or mock treatment of melanoma-bearing C57BL/6 mice (d) Densitometry analysis. Intensity of immunoreactive bands of COX-1 and COX-2 were determined and then normalized to that of vinculin. Data are presented as fold increase compared to values of the mock-treated group (regarded as 1). A minimum of three experiments yielded similar results.

170x123mm (300 x 300 DPI)
CXCL1 is depleted by C. pneumoniae both in vivo and in vitro

Assessment of cytokine/chemokine protein levels (Proteome profiler) in lungs of melanoma-bearing C57BL/6 mice 2 hours after mock (a) or C. pneumoniae (b) treatment. Squares indicate CXCL1 which disappeared 2 hours after C. pneumoniae treatment (c) Representative Western blot. Recombinant mouse CXCL1 protein (0.5 µg) was in vitro incubated with 500 IUFU/µl (1x) C. pneumoniae, (C. pn.) or its 10x, 100x, 1,000x, and 10,000x dilutions and then Western blotting was performed. (d) Densitometry analysis of immunoreactive bands shown in panel c. Values of the control (ctrl, vehicle treated) group were regarded as 1. Two experiments yielded similar results.
Patient's consent for publication of material relating to them in Scientific Reports

To be completed by the corresponding author. Illegible text will not be accepted.

Article title: Bacterial sepsis increases survival in metastatic melanoma: 
Chlamyphila pneumoniae induces macrophage polarization and tumor regression

Article identifier (if known): SREP-14-15021-T

Type of material to be published: 1. case study
2. paraffin-embedded tissue

Patient's name and contact: Tasi Jánosné, Szent Gellért 6., H-5561, Békésszentandrás, Hungary

Corresponding author's name: Krisztina Buzas, Ph. D.
address: Temesvári krt. 62., H-6726 Szeged, Hungary
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To be completed by the patient:

I give my consent for the above material to appear in Scientific Reports and associated publications without limit on the duration of publication. I have seen any pictures/movies and read the material submitted for publication, and/or the Corresponding author named above has explained the purpose of the material and its intended audience.

I understand that:

- The material will be published on the Scientific Reports website and will be included in any reprints of the published article.
- The material will not be used out of context.
- My name will not be published. I understand, however, that complete anonymity and control of all uses cannot be guaranteed after publication.
- I have the right to preview the material in the format it will eventually appear.
- If I decide at any time before publication to withdraw consent, the clinical information and relevant identifying materials will be destroyed.

Signed: Tasi Jánosné Date 01/26/2015


If you are not the patient, what is your relationship to them?
10/29/2015

Prof. Barbara A. Gilchrest
editor-in-chief
Journal of Investigative Dermatology

Dear Prof. Gilchrest,

We apologize for the inconvenience we caused. Indeed, it was our mistake that we mixed up the figure legends in the submission process, and we also agree that the arrows in the mentioned figure might be misleading.

We have corrected these mistakes, but no other changes (either in formatting or content-wise) have been made as compared to the version that had previously been accepted by the Reviewers.

The following corrections have been made:

1. The Figure legends that belongs to Supplementary Figure 3. has been corrected to reflect which is actually in the figure.
2. The arrows in panel b. have been removed from CD54 and CCL5, as requested.

We would also like to express our gratitude for Your kind patience and for having provided us this extra resubmission opportunity.

Sincerely,

Krisztina Buzas
corresponding author
Tumorimmunology and Pharmacology Research Group,
Institute of Biochemistry. Biological Research Centre, Szeged, Hungary
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216x297mm (300 x 300 DPI)