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HAL Id: hal-00903042
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Characterisation of the lymph node immune response following *Mycoplasma mycoides* subsp. *Mycoides SC* infection in cattle

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(Received 9 August 2005; accepted 30 January 2006)

Abstract – Contagious bovine pleuropneumonia (CBPP), caused by *Mycoplasma mycoides* subsp. *mycoides* biotype Small Colony (*MmmSC*), is still a major cattle disease in Africa. Development of long-term protective vaccines, the only relevant strategy to achieve CBPP eradication, requires the characterisation of the protective immune mechanism. To this aim, the present study investigated the cellular immune response persisting in the lymph nodes of cattle infected naturally and experimentally by contact, one year post exposure. The lymph node cell composition, *MmmSC* responsiveness and phenotype of the *MmmSC*-responding lymphocytes were compared between animals according to the different outcomes of the infection. To unravel the protective mechanism, the study focussed on the *MmmSC*-specific memory immune response generated in recovered cattle, known to develop long-term immunity and to be resistant to reinfection. An *MmmSC*-specific immune response, mediated by IFNγ-secreting CD4 T-cells, was detected in the lymph nodes of all recovered cattle. Furthermore, the magnitude of this immune response was significantly higher in animals with complete recovery than in recovered animals presenting lung sequestra. The findings suggest that, in recovered cattle, a subset of *MmmSC*-primed IFNγ-secreting CD4 T-cells homed to the regional lymph nodes as *MmmSC*-specific memory T-cells, likely responsible for the protective anamnestic response. Induction and expansion of this subset of *MmmSC*-specific CD4 memory T-cells might be a major goal to develop efficient long term protective vaccines against CBPP.

contagious bovine pleuropneumonia / *Mycoplasma mycoides* subsp. *mycoides* SC / vaccine / cell-mediated immunity / CD4 T-cell response

1. INTRODUCTION

Contagious bovine pleuropneumonia (CBPP) caused by *Mycoplasma mycoides* subsp. *mycoides* biotype Small Colony (*MmmSC*), still remains a major cattle disease in Africa [31]. CBPP is the only bacterial disease included in the list A of the Office International des Epizooties (OIE), leading to the exclusion of infected countries from international trade. The disease is responsible for heavy economic losses due...
to mortality, loss of weight, reduced working ability or fertility. Based on a combination of a stamping out policy, control of cattle movement and quarantine, CBPP has been eradicated from numerous countries such as Australia, the USA and Europe. However, these measures are impracticable in Africa where nomadism and transhumance are a necessity. In Africa, the only realistic prophylaxis has to rely on vaccination. However, the live attenuated vaccines currently in use, based on the T1 strain, are of low efficacy, requiring annual, costly, vaccination campaigns, and still retain some virulence [23, 31]. The development of more efficient vaccines is therefore an important goal to achieve CBPP eradication from Africa. To this aim, understanding the parameters of the MmmSC-specific host immune protection is an important prerequisite.

Several observations point to a critical role of cell-mediated immunity in the pathogenesis and control of MmmSC infections [24, 25, 32]. Furthermore, a recent study of the MmmSC-induced peripheral blood response revealed the predominant contribution of MmmSC-specific IFN-γ-secreting CD4 T-cells to protection against CBPP [5].

The present study focused on the MmmSC-specific immune response persisting in the lymph nodes of cattle recovered from an MmmSC infection transmitted by the natural route, one year post exposure. The objective was to characterise the MmmSC-specific acquired memory. Indeed, after infection, a pool of antigen-experienced lymphocytes homes to the draining lymph nodes as memory cells [10–12, 34]. Memory cells play a critical role in long-term immunity and mediate protective immunity against a new challenge [13, 34]. The characterisation of the MmmSC-specific memory immune cell subsets in recovered animals, known to be refractory to new infection, will help identifying the protective mechanism. The development of vaccines expanding these MmmSC-specific memory immune cells will, therefore, provide an efficient vaccinal strategy against CBPP.

2. MATERIALS AND METHODS

2.1. Experimental infection

The experimental infection protocol was designed according to the French national legislation for animal experimentation and was performed, in accordance with the same guidelines, at the Central Veterinary Laboratory in Bamako (Mali), as already described [20]. The objective was to reproduce a natural in-contact MmmSC infection. Eleven naive Peulh zebus were taken from CBPP-free areas where they had never been vaccinated against CBPP. These animals were 3 to 6 years old and the sex ratio was 3 females for 8 males (Tab. I). These naïve cattle, identified as the “contact” group, were placed in contact with 8 MmmSC-infected N’dama cattle taken from a field outbreak, 3 to 4 weeks after its onset. These 8 cattle, constituting the “infected” group, were 5 to 7 years old with a sex ratio of 5 females for 3 males (Tab. I). All animals were selected for their negative status for foot and mouth disease, tuberculosis and brucellosis and were dewormed before use. The animals were housed in close contact for 12 months, outdoors during the day and indoors at night.

Temperature and clinical signs were recorded daily. A serological follow up of the MmmSC infection was carried out by the complement fixation test (CFT), recommended by the OIE as the standard serological test for CBPP diagnosis [4]. Animals with respiratory distress were directly sacrificed to reduce suffering, and the remaining animals were post-mortem at the end of the experiment. During the post mortem (PM) analysis, two lymph nodes (LN), a mediastinal and a tracheobronchic draining the infected lung region, were taken from each animal of the “contact” group and from the two recovered cattle from the “infected” group. Only one LN was taken from all other cattle of the “infected” group.
2.2. Lymph node cell preparation

LN were collected in Hanks balanced salt solution (Eurobio, Les Ulis, France) supplemented with 100 U/mL penicillin, 100 µg/mL streptomycin and 250 ng/mL amphotericin B (Sigma, St. Quentin, France) and maintained on ice during transport to the laboratory. The cells were released from the LN, in warm RPMI-1640 culture medium (Eurobio), by slicing the tissues in small pieces with a scalpel. Cells were filtered on gauze, centrifuged and washed with Hanks balanced salt solution without calcium and magnesium (Eurobio), supplemented as above. The LN cells were numbered, resuspended in foetal calf serum (Eurobio) supplemented with 10% DMSO (Sigma), and stored frozen at 2 × 10⁷ cells/mL in liquid nitrogen. The cells were maintained frozen in liquid nitrogen during shipment to France.

To assess the non-specific immune response, two LN (mediastinal and tracheobronchic) from four healthy cattle, identified as the “negative control” group, were taken at a slaughterhouse in Montpellier and prepared as described above.

Table 1. Results of the experimental transmission of an MmmSC infection. Eleven naive cattle (“contact” group) were naturally infected by close contact housing with 8 MmmSC-infected cattle (“infected” group) taken from the field as described in Materials and Methods. The animals were assigned to three groups according to the outcome of the MmmSC infection and intensity of the lung lesions. The sex (f: female; m: male) and age (in years) was indicated for each animal.

<table>
<thead>
<tr>
<th>Animals (sex; age)</th>
<th>Clinical form</th>
<th>Outcome</th>
<th>Post mortem analysis</th>
<th>Groups</th>
</tr>
</thead>
<tbody>
<tr>
<td>Contact group</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C3 (m; 4)</td>
<td>Acute</td>
<td>Recovery</td>
<td>Sequestra (5 × 10 cm)</td>
<td>Group 3</td>
</tr>
<tr>
<td>C4 (f; 5)</td>
<td>Subclinical / chronic</td>
<td>Recovery</td>
<td>Resolved lesions</td>
<td>Group 1</td>
</tr>
<tr>
<td>C5 (f; 5)</td>
<td>Subclinical / chronic</td>
<td>Recovery</td>
<td>Small sequestra (0.5 × 1 cm)</td>
<td>Group 3</td>
</tr>
<tr>
<td>C6 (m; 3)</td>
<td>Subclinical / chronic</td>
<td>Recovery</td>
<td>Small sequestra (3 × 5 cm)</td>
<td>Group 3</td>
</tr>
<tr>
<td>C7 (f; 5)</td>
<td>Subclinical / chronic</td>
<td>Recovery</td>
<td>Small sequestra (1 × 2 cm)</td>
<td>Group 3</td>
</tr>
<tr>
<td>C8 (m; 4)</td>
<td>Subclinical / chronic</td>
<td>Recovery</td>
<td>Resolved lesions</td>
<td>Group 1</td>
</tr>
<tr>
<td>C9 (m; 6)</td>
<td>Acute</td>
<td>Recovery</td>
<td>Sequestra (3 × 10 cm)</td>
<td>Group 3</td>
</tr>
<tr>
<td>C11 (m; 6)</td>
<td>Subclinical / chronic</td>
<td>Recovery</td>
<td>Small sequestra (2 × 2 cm)</td>
<td>Group 3</td>
</tr>
<tr>
<td>C12 (m; 3)</td>
<td>Acute</td>
<td>Death (26 wpc)</td>
<td>Lung hepatization and pleural fluid</td>
<td>Not retained</td>
</tr>
<tr>
<td>C13 (m; 4)</td>
<td>Subclinical / chronic</td>
<td>Recovery</td>
<td>Resolved lesions</td>
<td>Group 1</td>
</tr>
<tr>
<td>C14 (m; 3)</td>
<td>Acute</td>
<td>Death (19 wpc)</td>
<td>Lung hepatization and pleural fluid</td>
<td>Not retained</td>
</tr>
<tr>
<td>Infected group</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>I1 (f; 7)</td>
<td>Acute</td>
<td>Death (3 wpc)</td>
<td>Lung hepatization and pleural fluid</td>
<td>Group 2</td>
</tr>
<tr>
<td>I2 (m; 6)</td>
<td>Acute</td>
<td>Death (6 wpc)</td>
<td>Lung hepatization and pleural fluid</td>
<td>Group 2</td>
</tr>
<tr>
<td>I4 (f; 6)</td>
<td>Acute</td>
<td>Death (9 wpc)</td>
<td>Large sequestra (15 × 20 cm)</td>
<td>Group 2</td>
</tr>
<tr>
<td>I5 (f; 7)</td>
<td>Acute</td>
<td>Death (8 wpc)</td>
<td>Large sequestra (15 × 20 cm)</td>
<td>Group 2</td>
</tr>
<tr>
<td>I6 (f; 6)</td>
<td>Acute</td>
<td>Death (6 wpc)</td>
<td>Multiple sequestras</td>
<td>Group 2</td>
</tr>
<tr>
<td>I11 (f; 6)</td>
<td>Acute</td>
<td>Death (7 wpc)</td>
<td>Large sequestra (15 × 20 cm)</td>
<td>Group 2</td>
</tr>
<tr>
<td>I9 (m; 7)</td>
<td>Subclinical / chronic</td>
<td>Recovery</td>
<td>Resolved lesions</td>
<td>Group 1</td>
</tr>
<tr>
<td>I12 (m; 5)</td>
<td>Subclinical / chronic</td>
<td>Recovery</td>
<td>Resolved lesions</td>
<td>Group 1</td>
</tr>
</tbody>
</table>

wpc: weeks post contact.
2.3. *MmmSC* strain and growth conditions and antigen preparation

The *MmmSC* T1 attenuated strain was used for all in vitro stimulation for practical reasons (level 2 confinements). Cultures were as previously described [5]. Heat-inactivated *MmmSC* were obtained after one hour incubation at 60 °C. The *MmmSC* total proteins in the crude cell suspension were titrated by the bicinchoninic acid method [30].

2.4. Lymphoproliferation assays and cell phenotyping

LN cells were prepared as previously described [5]. One millilitre (2.5 x 10⁶ cells/mL) was then distributed into each well of a 24-well microtitre plate and incubated with heat-inactivated *MmmSC* (5 µg/mL), concanavalin A (2.5 µg/mL; Sigma) as a positive control to verify cell viability or in RPMI media (negative control), for 5 days at 37 °C with 5% CO₂.

The cell phenotyping was performed by immunofluorescence staining, as previously described [5], using specific mouse monoclonal antibodies (MAb) to the following bovine leukocyte antigens: WC1 (CC15, SEROTEC, Cergy St. Christophe, France), CD2 (IL-A26), CD4 (IL-A12), CD8 (IL-A105), major histocompatibility complex class II (MHCII) molecules (J11), interleukin-2 receptor CD25 (IL-A111) [1, 14, 16, 18]. Except for the former, all other MAb s were from the International Livestock Research Institute (ILRI, Nairobi, Kenya). MAb DU₂-104, kindly provided by W. Hein, was used to detect the B-cells [17]. Flow cytometry analysis, measurement of blastogenesis, of the various cell subsets and of their state of activation (CD25 expression) have already been described [5].

The *MmmSC*-responsiveness was investigated by measuring the *MmmSC*-induced (1) blastogenesis, (2) percentage of CD25⁺ cells within the total population, (3) percentage of CD25⁺ cells within the CD4 T-cell subset and (4) IFNγ production. The relative activation of the CD4 T-cells was also evaluated by measuring the median of fluorescence intensity (MdFI) of the gated CD25⁺ CD4 T-cells. The *MmmSC*-specific responsiveness was validated if at least 2 of the 4 immune parameters were above cut off values determined from the “negative control” group. These cut off points were defined for each immune parameter as the mean value of *MmmSC*-induced minus unstimulated data plus 2 standard deviations (SD) among negative control cattle.

2.5. IFNγ ELISA

Lymphoproliferation assay supernatants were collected on day 5 to quantify gamma interferon (IFNγ) production using a commercially available enzyme-linked immunosorbent assay (Bovigam γ interferon test, BioCore, Omaha, NE, USA) according to the manufacturer’s instructions. Data were expressed as the mean OD units (± SD) of duplicate assays.

2.6. Statistical analysis

The unpaired Student t-Test was used for comparative analysis between the “negative control” group and the various groups of “*MmmSC*-infected” cattle and to compare these groups between themselves. The Paired Student t-Test was used for comparison between in vitro unstimulated and *MmmSC*-stimulated cells. P-values less than 0.05 were considered significant. P-values less than 0.01 were considered highly significant.

3. RESULTS

3.1. Experimental infection

The results of the experiment are presented in Table I (clinical form, outcome and post mortem (PM) analysis). All animals from either the “contact” or the “infected” group presented clinical signs of an *MmmSC* infection (temperature, cough, nasal discharge, dyspnoea) accompanied...
by a significant MmmSC-specific serological response measured by the CFT (data not shown). As shown in Table I, two “contact” cattle died from acute infection (C12, C14) while nine recovered either from a subclinical/chronic form or after an acute clinical period. Unfortunately, the death of the two acutely-infected zebus occurred at night, thus no viable cell samples could be taken. Therefore, in order to study animals succumbing from the infection, six cattle from the “infected” group with acute infection leading to death were included in the study as well as two recovered animals. Although several parameters were different between both groups of cattle, the comparative analysis, according to the epidemiological data discussed below, was assumed to be relevant. The animals were assigned to three groups according to the outcome of the infection and intensity of the lung lesions: group 1: animals with complete recovery (C4, C8, C13, I9, I12), group 2: animals with acute infection leading to death (I1, I2, I4, I5, I11) or multiple sequestra (I6) involving almost completely one lung lobe. Instead recovered animals presented either fibrotic scars (C4, C8, C13, I9, I12) or small sequestra (C5, C6, C7, C11), although 2 cattle showed a medium size sequestra (C3 and C9).

### 3.2. Ex vivo phenotypic analysis of the lymph node cells

The percentage of each cell subset (CD4 and CD8 T-cells, WC1+ γδ T-cells and B-cells) as well as the percentage of activated (CD25+) cells was monitored for each LN from each animal. Table II presents the results (mean percentage ± SD) obtained for the three groups compared to the “negative control” group.

#### Table II. Ex vivo phenotypic analysis of the lymph node cells. The mean percentage and standard deviation of each cell subset are presented for the different groups of animals: “negative control” cattle (n = 4), animals with complete recovery (group 1; n = 5), animals with acute infection leading to death (n = 6), animals recovered with persisting lung lesions (n = 6).

<table>
<thead>
<tr>
<th>Lymphocyte subsets</th>
<th>CD4 (%)</th>
<th>CD8 (%)</th>
<th>WC1 (%)</th>
<th>B (%)</th>
<th>CD25 (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>“Negative control”</td>
<td>27.06 ± 5.14</td>
<td>8.08 ± 1.11</td>
<td>1.52 ± 0.59</td>
<td>49.39 ± 4.2</td>
<td>9.62 ± 3.75</td>
</tr>
<tr>
<td>Group 1: complete recovery</td>
<td>35.49 ± 1.23</td>
<td>17.74 ± 3.56</td>
<td>0.98 ± 0.46</td>
<td>43.87 ± 3.56</td>
<td>10.2 ± 2.34</td>
</tr>
<tr>
<td>Group 2: death</td>
<td>26.98 ± 6.53</td>
<td>12.42 ± 6.41</td>
<td>0.52 ± 0.24</td>
<td>53.97 ± 11.75</td>
<td>9.08 ± 4.20</td>
</tr>
<tr>
<td>Group 3: recovery + sequestra</td>
<td>26.17 ± 3.37</td>
<td>14.77 ± 3.30</td>
<td>1.3 ± 0.46</td>
<td>53.09 ± 4.53</td>
<td>5.85 ± 1.87</td>
</tr>
</tbody>
</table>

* Significant difference (p < 0.05) and ** highly significant difference (p < 0.01) with the “negative control” group. # Significant (p < 0.05) and ## highly significant difference (p < 0.01) with group 1. ⋄ Significant (p < 0.05) and ⋄⋄ highly significant difference (p < 0.01) with group 2. ⋄⋄⋄ Highly significant difference (p < 0.01) with group 3.

The PM analysis revealed that animals with acute infection were characterised by typical CBPP lesions such as lung hepatisation and large quantities of pleural fluid (C12, C14, I1, I2), large (I4, I5, I11) or multiple sequestra (I6) involving almost completely one lung lobe. Instead recovered animals presented either fibrotic scars (C4, C8, C13, I9, I12) or small sequestra (C5, C6, C7, C11), although 2 cattle showed a medium size sequestra (C3 and C9).
observed in group 1 compared to the “negative control” group (p < 0.05) and to group 2 (p < 0.05) and 3 (p < 0.01). A significant decrease of the γδ T-cells was also noticed in group 1 animals compared to the “negative control” group (p < 0.05). However, group 2 animals were characterised by the lowest percentage of γδ T-cells compared to either the “negative control” group (p < 0.05), group 1 (p < 0.05) or group 3 (p < 0.01). Nevertheless, the very low proportion of the γδ T-cell subset in the cattle lymph nodes has to be noticed. No other difference was measured either between groups 2 or 3 and the “negative control” group or between groups 2 and 3.

The measurement of the CD25-expressing cells revealed a significant decrease in group 3 compared to the “negative control” group (p < 0.01), to group 1 (p < 0.01) and group 2 (p < 0.05).

3.3. MmmSC responsiveness of lymph node cells

The MmmSC responsiveness of the LN cells was then compared between the 3 groups of animals. For accurate discrimination between MmmSC-specific and non specific response, cut off values were first determined (Tab. III) with LN cells from the “negative control” group, as described in Materials and methods.

A preliminary analysis was performed on 10 MmmSC-infected cattle to assess whether variability in the MmmSC-specific immune response occurred between the mediastinal and the tracheobronchic LN. The results, shown in Table IV, revealed no significant difference for any of the immune parameter tested. Accordingly, the data from both LN were treated regardless of their origin.

The first finding of the study was that all the MmmSC-infected cattle presented an MmmSC-specific cellular responsiveness except two animals. Indeed, I1 and I2 were unable to develop an in vitro response to MmmSC stimulation, likely due to the severe lung lesions. Both animals were characterised after 5 days of culture by a very low percentage of CD4 T-cells, 6.10 ± 3.73%, while a mean percentage of 25.20 ± 7.26% of CD4 T-cells was observed in all other animals.

Figure 1 presents the mean value (+ SD) of each parameter obtained after MmmSC stimulation minus unstimulated control for all the MmmSC-responding samples in each group of animals, after excluding I1 and I2 from group 2. One LN (mediastinal) from animal C8 was also excluded in
Table IV. Comparative analysis of the *Mmm*SC-specific immune response between the mediastinal and the tracheobronchic lymph nodes. Lymph node cells from the 10 *Mmm*SC-infected cattle, for which both lymph nodes were available, were stimulated for 5 days in vitro with *Mmm*SC and the percentage of blastic cells, CD25+ cells, CD4+CD25+ cells and IFNγ production were determined by flow cytometry and ELISA, respectively. The percentage of CD4+CD25+ cells was calculated within the CD4 T-cell gate and expressed as a percentage of the CD4 T-cell subset. Data are the mean percentage or OD Units (± SD) obtained after *Mmm*SC stimulation minus the unstimulated control.

<table>
<thead>
<tr>
<th></th>
<th>Mediastinal lymph node (% of cells)</th>
<th>Tracheobronchic lymph node (% of cells)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blasts</td>
<td>11.53 ± 5.40</td>
<td>11.35 ± 8.05</td>
</tr>
<tr>
<td>CD25</td>
<td>12.76 ± 5.01</td>
<td>10.16 ± 6.29</td>
</tr>
<tr>
<td>CD4+ CD25+</td>
<td>26.51 ± 9.35</td>
<td>24.36 ± 9.09</td>
</tr>
<tr>
<td>IFNγ</td>
<td>1.68 ± 1.04</td>
<td>1.53 ± 1.01</td>
</tr>
</tbody>
</table>

3.4. Phenotyping of the *Mmm*SC-responding lymphocytes

A phenotypic study of the *Mmm*SC-responding lymphocytes was then performed on 4 *Mmm*SC-responding lymph nodes within each group. Figure 2 presents the results (mean value ± SD) obtained after *Mmm*SC stimulation compared to unstimulated cultures for the three groups of animals. Before comparing the results between the three groups, a first analysis was performed with the paired Student t-Test to assess the statistical significance of the *Mmm*SC-induced data compared to unstimulated cells. This analysis demonstrated that exposure to *Mmm*SC triggered, in group 1, a significant (*p* < 0.05) increase of MHCII-bearing cells (74.13 ± 3.36% with *Mmm*SC versus 61.8 ± 8.32% without stimulation). As shown in Figure 2, this increase might be due in part to B-cells, since all B-cells were expressing MHC II (data not shown), although the *Mmm*SC-induced B-cell proliferation and increase of CD25+B-cells were not statistically significant compared to unstimulated cells. Instead, the significant CD4 T-cell activation observed after *Mmm*SC exposure indicated that these cells were the main *Mmm*SC-responding lymphocytes. Indeed, the CD4 T-cell subpopulation was the only subset presenting a highly significant (*p* < 0.01) increase in the percentage of CD25+cells in response to
MmmSC stimulation (60.96 ± 12.37% versus 26.74 ± 7.07% in unstimulated cells). Furthermore, not only this percentage increased but also did the relative level of CD25 expression per CD4 T-cell as shown by the significant \((p < 0.05)\) rise of the MdFI after MmmSC stimulation (474.23 ± 190.51 fluorescent units) compared to unstimulated cells (116.53 ± 25.62 fluorescent units). However, MmmSC did not trigger any CD4 T-cell proliferation. The proportion of CD25+γδ T-cells was constantly negligible (below 2% of the total cells) and thus not included in Figure 2. A similar result was observed for the CD25+CD8 T-cells in 3 samples while the 4th sample showed a strong increase in the CD25+CD8 T-cell percentage after exposure to MmmSC.

For group 2, except for the significant CD4 T-cell activation elicited by MmmSC, no other change was noticed compared to unstimulated cultures. Exposure to MmmSC led to a significant \((p < 0.05)\) increase of the percentage (36.61 ± 11.76% versus 16.50 ± 7.72% in unstimulated cells) and MdFI (112.04 ± 31.70 versus 53.28 ± 10.32 fluorescent units in unstimulated cells) of CD25+CD4 T-cells without cell proliferation. The percentage of CD25+CD8 T-cells was always below the cut off. In contrast to group 1, a decrease of the mean percentage of MHCII-bearing cells, although non significant, was observed after MmmSC stimulation. Moreover, a decrease of the fluorescence intensity of the MHC II cell surface expression, after exposure to MmmSC, was also noticed during flow cytometry analysis (data not shown).

In group 3, MmmSC triggered a significant \((p < 0.05)\) increase of the percentage of MHCII-expressing cells (66.19 ± 3.33%) and CD25+ cells within the B-cell subset (4.79 ± 1.83%), CD4 (37.78 ± 8.93%) and CD8 (31.67 ± 3.81%) T-cell subsets, compared to unstimulated cells (57.98 ± 2.68%, 0.4 ± 0.63%, 24.5 ± 6.76%, 14.9 ± 2.35%, respectively). MmmSC stimulation also led to a significant \((p < 0.05)\) increase of the MdFI of the CD25+CD4 subset (211.24 ± 77.54 fluorescent units versus 135 ± 59.66 fluorescent units without stimulation). As noticed above for groups 1 and 2, no T-cell...
SC-specific lymph node immune response was triggered by MmmSC while a significant \((p < 0.05)\) B-cell proliferation occurred \((63.61 \pm 2.11\% \text{ versus } 56.66 \pm 3.48\% \text{ in unstimulated cells})\).

A comparative analysis of the MmmSC-specific CD4 T-cell activation was then performed between the three groups. The results confirmed that the percentage of CD4 T-cells responding to MmmSC stimulation \((\text{CD25-expressing})\) as well as the relative level of activation of these CD4 T-cells \((\text{MdFI})\) was significantly higher in group 1 \((p < 0.05)\) compared to groups 2 and 3. No significant difference was measured between groups 2 and 3.
4. DISCUSSION

The aim of the study was to unravel the protective immune mechanism elicited in cattle recovered from an MmmSC infection and known to develop a long-term immunity [15, 21]. Antigen recognition in the context of infection generates two subsets of immune cells, the effector cells remaining in the infected tissues to enable immediate protection and the memory cells homing to the draining lymph nodes and responsible for the anamnestic response [9, 11, 22]. The MmmSC-specific immune mechanism generated, therefore, during the primary immune response and persisting in the regional lymph nodes should represent the MmmSC-specific memory response, basis of the protective secondary response.

An experimental infection was thus implemented by natural transmission of the MmmSC infection from infected cattle (infected group) to a group of naive animals (contact group). For immunological relevance, a natural infection (respiratory route) of the natural host (cattle) was used, although CBPP is described as difficult to reproduce. The MmmSC-specific immune response of the regional lymph nodes was then analysed. This study demonstrated that an MmmSC-cell-mediated immune response was, indeed, persisting in the mediastinal and tracheobronchic lymph nodes of all recovered animals, several months after the MmmSC infection. A significant proportion of lymph node cells underwent blast transformation, expressed a CD25+ phenotype (a correlate of cell activation) and produced IFNγ, after in vitro re-exposure to MmmSC. Phenotyping indicated that the main MmmSC-responding lymphocytes were CD4 T-cells. Similar results were obtained from the study of MmmSC-specific peripheral immune responses where IFNγ-secreting CD4 T-cells were detected in the blood of all recovered cattle [5]. These findings suggest that the MmmSC-specific IFNγ-secreting CD4 T-cell responses detected in the blood of all recovered cattle and persisting in their regional lymph nodes play a significant role in the protective mechanism against CBPP. Nevertheless, the absence of CD4 T-cell proliferation in response to MmmSC, observed in both studies, is striking and might suggest an immunosuppressive mechanism (regulatory T-cells, IL-10, TGF-β). Further analysis of the cytokine response will determine their involvement; instead, the role of Treg in cattle still requires relevant reagents. However, the significant IFNγ production, confirming T-cell activation, and an ongoing study showing that T-cell proliferation was measurable eight days after MmmSC stimulation¹ do not support an immunosuppressive process. The present study, instead, seems to demonstrate that following the primary immune response, a subset of in vivo MmmSC-primed IFNγ-secreting CD4 T-cells homed to the draining lymph nodes. This suggests that these cells are MmmSC-specific memory T-cells, likely responsible for the protective anamnestic response.

A main role for the CD4 T-cells was predictable since MmmSC, like the majority of mycoplasma, is an extracellular pathogen [27]. The CD4 T-cell response is thus initiated by “antigen presenting cell” engulfing and processing MmmSC and MHC class II presentation of MmmSC epitopes. We assume that protection relies on the role of IFNγ to promote vigorous phagocyte response and thus MmmSC capture. A protective role for the IFNγ-induced IgG2 antibody [3], only able to promote killing by neutrophils in cattle [8, 19], is also expected since neutrophil recruitment has been observed in CBPP lung lesions² [26]. However, confirmation of a typical Th1-like T-cell response requires the assessment of the Th2 cytokines. This study will be implemented since immunological reagents are now commercially available to develop ELISA for bovine Th2 cytokines. In contrast, the role of the CD8 T-cells, generally linked to intracellular pathogens observed

¹ Totte P., personal communication.
² Ferronha M.H., personal communication.
in animals with lung sequestras is not clear. Although *MmmSC* have been immunohistochemically detected in macrophages, data are lacking to confirm its viability in any host cell [27, 29]. A bystander effect of the *MmmSC*-specific CD4 T-cell response was rather suggested [5]. Further studies are required to assess the cytokine environment and determine whether these cells play a role in protection. Significant γδ T-cell activation was observed in the *MmmSC*-specific peripheral immune response [5] while it could not be detected in this study. Indeed, while γδ T-cells are a significant component of the afferent and efferent lymph and, in ruminants, may constitute up to 50% of the PBMC in young animals, they are only a minor population within the lymph nodes, suggesting that they re-circulate preferentially through non lymphoid tissues [33].

Recovery from an *MmmSC* infection and protection requires thus an *MmmSC*-specific IFNγ-secreting CD4 T-cell response. Its onset and magnitude but also other immune parameters such as the local immune response, since CBPP is a mucosal disease, are likely to play a role. A recent study demonstrated, indeed, a significant correlation between the presence of *MmmSC*-specific IgA and an attenuation of the clinical impact of the *MmmSC* infection. The significantly lower magnitude of the *MmmSC*-specific IFNγ-secreting CD4 T-cell response detected in the group of cattle recovered but with sequestras might explain this outcome. While likely involved in the process of recovery, this response was not sufficient to efficiently control the *MmmSC* infection. Nevertheless, sequestras, as granulomas, develop as part of the protective host response to block the deleterious effects of the pathogen [21, 28, 29]. The intensity of the immune response detected in the lymph nodes of some animals succumbing from infection was also significantly lower than in animals with complete recovery. The presence of viable *MmmSC* in the respiratory lymph nodes, described in acute cases of CBPP [2, 29], might also have played a role. Indeed, although not proved in vivo, the in vitro ability of viable *MmmSC* to trigger apoptosis in bovine leucocytes has been demonstrated [6]. The *MmmSC* unresponsiveness, observed in two cattle with strong acute lung lesions, might represent the final step of this immunopathological process. A correlation between progression of CBPP and a decreased ability of the PBMC to produce IFNγ was previously observed [5] while in this study the lymph node CD4 T-cells were able to produce IFNγ. Unfortunately, data on the kinetic of the blood immune response, but also on the Th1/Th2 balance, are lacking for this group of cattle in order to further unravel the immunopathological mechanism leading to a fatal issue.

The comparative analysis of these groups of animals might be limited by the introduction of different parameters (breeds, age, sex ratio...), however several epidemiological data support this comparison: (1) both breeds, N'Dama cattle and Peulh zebus, belong to the genus *Bos* and are thus susceptible to naturally occurring CBPP, (2) a full susceptibility to *MmmSC* infection is described for animals over two years of age and (3) variation in the susceptibility according to the sex of the animals has not been reported [7, 15, 21]. According to these authors, the difference in the ratio of acute versus chronic CBPP formed between both groups might be due to (1) the fact that only cattle with evident clinical signs of CBPP were selected in the former group while in a newly infected herd, nearly a third of the animals developed an acute form, (2) geographical difference in the susceptibility of N'Dama cattle observed between some African countries and (3) a decrease of infection pressure on the “contact” group resulting from the rapid death of cattle from the “infected” group but also from the time-dependent decrease of the *MmmSC* strain virulence already described within a herd, although no molecular tools are available to assess this parameter.

3 Niang M., paper in preparation.
Therefore, animals with total recovery were characterised by the highest magnitude of the *MmmSC*-specific CD4 T-cell response, likely responsible for a more efficient control of the *MmmSC* infection before the development of lung lesions. The long-term protection developed in these animals should thus rely on the ability of these memory T-cells, after a new antigen encounter, to rapidly adopt an effector phenotype, migrate to the site of infection and trigger a faster and stronger response [11, 12]. Indeed, memory cells, in contrast to naive cells, are activated at lower antigen concentration and are less dependent on co-stimulation factors leading to higher response even at the early onset of infection [13]. Future studies will focus on the anamnestic response triggered by a second *MmmSC* challenge to help confirm the protective mechanism. Nevertheless, the induction and expansion of this subset of *MmmSC*-specific CD4 memory T-cells appear to be one of the required goals in order to develop efficient long-term protective vaccines against CBPP.

ACKNOWLEDGEMENTS

This work was part of an INCO project entitled “Development of an improved vaccine against contagious bovine pleuropneumonia” supported by a European Commission research grant (ICA4-CT-2000-30015). The authors would like to dedicate this work to the memory of Mahamadou Diallo for his strong participation in this project.

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