Infection by *Toxoplasma gondii* atypical strain induces higher systemic and airway inflammation and contributes to the impairment of lung homeostasis

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Toxoplasma gondii displays a populational structure with great genetic diversity, mainly in Latin America. Studies suggest that infection by *T. gondii* atypical strains might be related to the severity of human toxoplasmosis. In this sense, our study sought to analyse the effects of chronic infection by *T. gondii* atypical strain in the bronchoalveolar lavage fluid (BALF) and during airway allergic inflammation in mice. In this study, male BALB/c mice were infected by tissue cysts of *T. gondii* atypical strain TgCkBrRN2 (CK2), identified as belonging to the genotype #163; or infected by the clonal Type II strain ME49. All mice were accompanied during sixty days until the establishment of chronic infection; the mortality and weight variations were registered. The airway allergic inflammation was induced by ovalbumin sensitization and intranasal instillation challenge after establishment of chronic infection. During acute (15 dpi) and chronic (60 dpi) infection, blood samples were withdrawn, and the serum was used to quantify systemic anti-*T. gondii* IgG and cytokine levels; BALF samples collected were used to perform multiparametric flow cytometry. During the infection course, all mice survived; however, the atypical strain CK2 induced marked decrease of body weight when compared to mice infected by ME49. Both strains were able to induce chronic infection and displayed similar levels of specific IgG antibodies; however, the atypical strain induced greater number of tissue cysts in the brain and higher levels of systemic IFN-ɣ and IL-12. Analysis of BALF revealed that infection by *T. gondii* induced alveolar macrophages death via apoptosis during the acute stage, in addition to increased inflammatory infiltrate composed by $CD3^+$ T lymphocytes and inflammatory $Ly6C^{hi}$ monocytes. During the chronic infection, the atypical strain CK2 sustained higher infiltrate of T $CD4^+$ and T $CD8^+$ lymphocytes when compared to ME49-infected mice. Furthermore, using dimensionality reduction and machine learning analysis it was possible to conclude that the myeloid cell population found during chronic infection displayed origin and phenotype distinct from the alveolar macrophages present in the BALF of non-infected mice. In addition, *T. gondii* infection was also able to modulate the establishment of allergic-specific inflammatory response induced by ovalbumin. In our work, we demonstrated that, besides the marked infiltration of T lymphocytes and inflammatory monocytes, *T. gondii* infection induced apoptosis of alveolar macrophages as early as the establishment of acute stage of infection. Surprisingly, it was found that the myeloid cells present in the BALF during the chronic infection comprises a distinct population, suggesting the ability of periphery-derived recruited inflammatory monocytes to repopulate the niche, although displaying a distinct phenotype, after alveolar macrophage depletion. Finally, our study highlights the ability of *T. gondii* distinct strains to interfere in the homeostasis and cellular functioning in the lungs, with repercussions in the establishment of effective immune response during experimental model of asthmatic inflammation.