

# ImmunoTools IT-Box-Cy55M-Award 2013



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## **Role of cytokines and growth factors in affecting P. aeruginosa infection in murine cell models**

*Pseudomonas aeruginosa* is a Gram negative bacteria associated with chronic lung infections. *P. aeruginosa* is able to: i) control complement; ii) produce proteases, toxins, and lipases, which inhibit the function of the cells of the immune system (phagocytes, NK cells, T cells), inactivate several cytokines (IL-1, IL-2, IFN-gamma, TNF), cleave immunoglobulins and inactivate complement; iii) resist to phagocytosis by biofilm formation. Interestingly, *P. aeruginosa* establish an immune modulation in the host shifting immune responses away from host protective Th1 responses to pathogen protective Th2 responses<sup>1</sup>. In fact, C3H/HeN and BALB/c, generally known as Th1 and Th2 responders, were challenged with *P. aeruginosa* and C3H/HeN presented a lower mortality in comparison with BALB/c mice. *P. aeruginosa* was cleared more efficiently in C3H/HeN mice and significantly more C3H/HeN mice showed normal lung histopathology<sup>2</sup>.

Interestingly, Qa2 molecules, the murine homolog of human HLA-G<sup>3</sup>, are characterized by an immune inhibitory function and are up-regulated during pathogen infections<sup>4</sup>. Our preliminary results obtained from the analysis of bronchoalveolar lavage fluids (BALs) from *P. aeruginosa* challenged mice showed an increased expression of Qa2 in presence of *P. aeruginosa* infection. Since Qa2 acts as a tolerogenic and anti-inflammatory molecule, we hypothesized that *P. aeruginosa* is able to induce Qa2 expression inducing an immune-inhibited environment that in turn protects bacteria from host immune system through a mechanism of immune-escape.

The purpose of this project is to test the effect of different cytokines and growth factors from the **ImmunoTools** IT-Box-Cy55M on the *P. aeruginosa* virulence. We are mostly interested in analysing the different effect of rm EGF in LL/2 murine lung epithelial cell line and rm IL-10, rm IL-6, rm IL-17A, rm IFN-gamma in IC-21 murine macrophage cell line.

We will evaluate the effect of these molecules on *P. aeruginosa* growth and virulence and on cell activation and Qa2 expression.

The results obtained will represent an important start point to improve our knowledge on the role of environmental cytokines on *P. aeruginosa* infection in lungs and the effect on host immune cells during chronic infection. These data could allow the identification of new therapeutic strategies to reduce and prevent *P. aeruginosa* and biofilm forming bacteria chronic lung infection.

#### References

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2. Moser C, Johansen HK et al. Chronic *Pseudomonas aeruginosa* lung infection is more severe in Th2 responding BALB/c mice compared to Th1 responding C3H/HeN mice. *APMIS*. 1997;105(11):838-42
3. Lau P, Amadou C et al. Characterization of RT1-E2, a multigenic family of highly conserved rat non-classical MHC class I molecules initially identified in cells from immunoprivileged sites. *BMC Immunol* 2003; 4:7.
4. Rizzo R, Bortolotti D, Baricordi OR, Fainardi E. New insight into HLA-G inflammatory diseases. *Inflamm Allergy Drug Targets*. 2012; 11(6):448-63.

### **ImmunoTools** IT-Box-Cy55M for Daria Bortolotti includes 55 recombinant mouse cytokines

rm EGF, rm Eotaxin / CCL11, rm FGF-a / FGF-1, rm FGF-b / FGF-2, rm FGF-8, rm Flt3L / CD135, rm G-CSF, rm GM-CSF, rm GRO-a / CXCL1, rm GRO-b / CXCL2, rm IFN $\gamma$ , rm IL-1 $\alpha$ , rm IL-1 $\beta$ , rm IL-2, rm IL-3, rm IL-4, rm IL-5, rm IL-6, rm IL-7, rm IL-9, rm IL-10, rm IL-11, rm IL-13, rm IL-15, rm IL-16, rm IL-17A, rm IL-17C, rm IL-17F, rm IL-19, rm IL-20, rm IL-21, rm IL-22, rm IL-25 / IL-17E, rm IL-27, rm IL-31, rm IL-33, rm IP-10 / CXCL10, rm LIF, rm MCP1 / CCL2, rm M-CSF, rm MIP-1 $\alpha$  / CCL3, rm MIP-1 $\beta$  / CCL4, rm MIP3 $\alpha$  / CCL20, rm MIP3 $\beta$  / CCL19, rm NGF- $\beta$ , rm PDGF-AA, rm PDGF-BB, rm RANTES / CCL5, rm sCD40L / CD154, rm SCF, rm SDF-1 $\alpha$  / CXCL12a, rm SDF-1 $\beta$  / CXCL12b, rm TNF $\alpha$ , rm TPO, rm VEGF

[DETAILS](#)