

# ImmunoTools IT-Box-139 Award 2013



## Larissa Lhoest

PhD Supervisor: Prof. Dr. Catherine Verfaillie

Stem Cell Institute KU Leuven  
ON4 Herestraat 49 bus 804  
3000 Leuven

Primary myelodysplastic syndromes (MDS) are clonal hematopoietic stem cell (HSC) disorders, characterized by ineffective and dysplastic hematopoiesis with a varying degree of peripheral cytopenias and an increased probability of developing acute leukemia. The etiology of bone marrow failure in MDS is not yet fully understood, but is believed to be multifactorial. Intrinsic defects in the HSCs, like the 5q- syndrome or aberrant expression of *Evi-1*, can contribute to MDS pathogenesis. In addition, defects in the bone marrow HSC niche have been described, such as upregulation of pro-inflammatory cytokines, alterations in T-, B- and NK-cell numbers, etc.

A number of murine MDS models have already been described, e.g. transplantation of *Evi-1* transduced bone marrow cells leads to hypoplastic MDS. Although these mouse models recreate human MDS with some fidelity, they have not been thoroughly evaluated for the dominant role of the immune/inflammatory system in hypoplastic MDS development and evolution. Therefore, we plan to define the immunological/inflammatory fingerprint of 2 MDS mouse models, the *Evi-1* and *Osx-GFP-Cre<sup>+</sup> Dicer<sup>fl/fl</sup>* model. In addition, we plan to define the immunological/inflammatory fingerprint of newly-diagnosed low-grade MDS patients, in a sequential manner, to obtain a global view of the immune/inflammatory aberrations present and the progression with time. This study will represent the first comprehensive immune/inflammatory fingerprint in mouse models of MDS and in patients with MDS, as well as identify similarities and differences between human MDS and murine models. Moreover, the sequential evaluation will allow the identification of biomarkers for disease progression.

For this project we will use an immune phenotyping platform that allows the maximum amount of immunological information to be determined from each individual patient on a small amount of blood. Leukocyte subsets will be quantified by flow cytometric analysis using a panel of antibodies specific for lineage markers from [IT-Box-139](#) to distinguish B cells (CD19, CD27), T cells (CD3, CD4, CD8, CD45RA, CD31, CD25, CD57, CD62L), NK cells (CD56, CD3) and dendritic cells (CD11c, HLA-DR).

**ImmunoTools** *IT-Box-139.2* for **Larissa Lhoest** includes 100 antibodies

**FITC** - conjugated anti-human CD1a, CD3, CD4, CD5, CD6, CD7, CD8, CD14, CD15, CD16, CD19, CD21, CD25, CD29, CD35, CD36, CD41a, CD42b, CD45, CD45RA, CD45RB, CD45RO, CD49d, CD53, CD57, CD61, CD63, CD80, CD86, HLA-DR, IL-6, Control-IgG1, Control-IgG2a, Control-IgG2b, Annexin V

**PE** - conjugated anti-human CD3, CD4, CD8, CD11b, CD15, CD14, CD18, CD19, CD20, CD21, CD22, CD31, CD33, CD38, CD40, CD45, CD45RB, CD50, CD52, CD56, CD58, CD62p, CD72, CD95, CD105, CD147, CD177, CD235a, HLA-ABC, IL-6, Control-IgG1, Control-IgG2a, Control-IgG2b, Annexin V

**PE/Dy647** -tandem conjugated anti-human CD3, CD4, CD8, CD14, CD19, CD20, CD25, CD54

**APC** -conjugated anti-human CD2, CD3, CD4, CD8, CD10, CD11a, CD11c, CD14, CD16, CD27, CD37, CD42b, CD44, CD45, CD59, CD62L, CD69, CD71, IL-6, Control-IgG1, Control-IgG2a, Control-IgG2b, Annexin V

[DETAILS](#)