Investigating sex- and age-related differences in murine immunometabolism

Alba Svanosio, Francesco Lapi, Stefania Del Prete, Chiara Damiani
E-mail: a.svanosio@campus.unimib.it
University of Milan-Bicocca, Milan, Italy
German Cancer Research Center (DKFZ), Division of Regulatory Genomics and Cancer Evolution, Heidelberg, Germany

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Abstract
Understanding metabolic regulation in immune cells is crucial for elucidating mechanisms of aging and sex-related differences in immune responses. Here, metabolic differences in immune system cells from young and old mice, both males and females, are investigated using cell-type–level pseudobulk transcriptomic profiles derived from single-cell data. These transcriptomic data are integrated with constraint-based metabolic models to estimate metabolic fluxes and explore how age and sex shape immune metabolism.

The first phase of the work involved the construction of a mouse metabolic core model, based on the human ENGRO2 model, serving as the foundation for flux estimation using pseudobulk data. Subsequently, we will investigate the correlation between metabolic activity and the expression of genes that escape X-chromosome inactivation, with particular attention to the cell types in which the influence of these genes is most pronounced.

This study aims to provide a systematic view of the interactions between metabolism, age, sex, and genes that escape X inactivation in immune cells, ultimately contributing to a deeper understanding of the mechanisms underlying age- and sex-related differences in immune function.