Abstract

Microchimerism arises from the exchange of cells between genetically distinct individuals. The coexistence of genetically distinct cell populations within a single organism has possible effects on health and functioning of individuals immune systems, but the exact mechanisms of action are often not yet known. With the development of microscopic technologies and software for data analysis, the possibilities of detection and phenotyping of these rare cell populations are expanding. My intention in this work is to find maternal microchimerism in embryonic tissues (E13) and intestines of breastfed pups using MHCII/EGFP *knock-in* mouse model.

Several different technologies potentially suitable for the detection of maternal microchimeric cells in offspring tissues (light sheet fluorescent microscopy – LSFM, virtual slide microscopy and flow cytometry) were selected. Advanced analysis of the obtained samples from the light sheet microscopy using the creation of a neural network was used here.

The presence of maternal microchimerism was not demonstrated by flow cytometry. Using LSFM, image data were obtained from intestinal samples of suckling pups, which were processed by the neural network method. Data analysis of embryos (E13) obtained by the same method did not allow data analysis due to high autofluorescence. The method of virtual slide microscopy was used for comparison, but these data will need further investigation. This work is the first step to a deeper understanding of the phenomenon. The introduction of a new model and methodology presented in this work, including quantitative histological analysis, can significantly help us in further research on this issue.