Genome-wide expression analysis of estrogen action on macrophages *in vivo*

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Several clinical and experimental studies show that estrogens are able to positively influence inflammatory pathological conditions, such as wound healing, atherosclerosis and ischemia, by decreasing disease susceptibility, severity and damage. Macrophages are innate immune cells that are primarily involved in the response against pathogen invasion and tissue injuries and drive the initiation, maintenance and resolution of inflammation through several mechanisms, including immune activation, phagocytosis and tissue repair.
Several lines of evidence showed that estrogen action in inflammatory conditions occurs by a direct modification of macrophage reactivity; however, the underlying molecular mechanisms are still poorly understood. In order to fill this gap of knowledge we performed a genome-wide gene expression study through RNA-sequencing analysis of peritoneal macrophages isolated from female mice under different endogenous estrogen levels or following 17β-estradiol (E_2) administration. Bioinformatic analyses using Gene Ontology databases allowed to cluster differentially expressed genes based on their biological activity; our data show that E_2 is mainly involved in the expression of genes associated with immune and polarization processes. Confirmation of the biological role of estrogen-macrophage interplay was achieved using zymosan-induced peritonitis in mice; this experiment showed the relevance of E_2 action in macrophage alternative activation. Additional studies will be discussed.