

Abstract

Studies of the immunological environment in the female genital tract (FGT) are critical for the development of vaccines or microbicides to halt the spread of sexually transmitted infections. Challenges arise due to the difficulties of sampling from this site, and the majority of studies have been conducted utilising peripheral blood mononuclear cells. Identifying functional differences between immune cells of the FGT and peripheral blood would aid in our understanding of mucosal immunology. We compared the gene expression profile of mononuclear cells at these two sites. Messenger RNA expression analysis was performed using gene expression arrays on matched cervical mononuclear cells and peripheral blood mononuclear cells. Further cellular phenotyping was done by 10 colour flow cytometry. Of the 22,185 genes expressed by these samples, 5345 genes were significantly differentially expressed between the cell populations. Most differences can be explained by significantly lower levels of T and B cells and higher levels of macrophages and dendritic cells in the FGT compared with peripheral blood. Several immunologically relevant pathways such as apoptosis and innate immune signalling, and a variety of cytokines and cytokine receptors were differentially expressed. This study highlights the importance of the unique immunological environment of the FGT and identifies important differences between systemic and mucosal immune compartments.