During the oestrous cycle, the bovine Endometrium exhibits characteristic morphological and functional changes, which are mainly induced by progesterone (P4), oestrogens and oxytocin. We studied the response of the Endometrium to this changing hormonal environment at the transcriptome level using a custom-made cDNA microarray. Endometrium samples were recovered from Simmental heifers on days 0 (oestrus), 3.5 (metoestrus), 12 (dioestrus) and 18. the latter group was divided into animals with high (late dioestrus) and low P4 levels (preoestrus). Significance analysis of microarrays revealed 269 genes exhibiting significant changes in their transcript levels during the oestrous cycle in distinct temporal patterns. Two major types of expression profiles were observed, which showed the highest mRNA levels during the oestrous phase in the highest levels during the luteal phase respectively.