

ABSTRACT

Endometriosis is a gynecological condition that affects the female reproductive system and ultimately caused infertility. This disease is present worldwide in all racial groups. Incapacitating signs and symptoms with global prevalence were the reasons of unrevealed pathogenic mechanism of endometriosis. Various risky health phenomenon in relation to endometriosis may triggered by plasma micro RNA (miRNAs) which possibly, could be changed by therapeutic techniques used for endometriosis. For early diagnosis of endometriosis, the miRNAs role as biomarker is crucial. The blood samples of genetically unrelated endometriosis women and controls, 80 each, were used to isolate RNA. This total RNA was used to synthesize cDNA. This cDNA was used to identify miRNAs either down regulated or up regulated for further confirmation of endometriosis by real time PCR. Twenty microRNAs were differentially expressed in women with endometriosis and their controls. Out of which six microRNAs (miR-15a, miR-15b, miR-16-1, miR-16-2, miR-195 and miR-497) were selected for validation. MiR-15a, miR-15b and miR-195 were significantly down-regulated in women with endometriosis when compared with controls ($p= 0.011, 0.002$ and 0.002 , respectively), yielding an area under the receiver operator characteristics curve of 0.74 (95% CI: 0.58–0.90; 0.79 (95% CI: 0.65–0.93) and 0.85 (95% CI: 0.71–0.98) in endometriosis from controls respectively. miRNAs appear to be potent regulators of gene expression in endometriosis and its associated reproductive disorders, raising the prospect of using miRNAs as biomarkers and therapeutic tools in endometriosis. Identification of miRNAs lessens the health care cost and improves the work productivity of endometriotic females.