

Abstract

Polycystic ovary syndrome (PCOS) is a heterogeneous disease of reproductive age. Small noncoding microRNAs (miRNAs) act as biomarker for PCOS patient stratification. An altered miRNA expression profile was observed in few previous studies. The aim of current study was to assess the miRNA expression profile and its risk factors specifically in Pakistani PCOS patients and healthy, regularly cycling matched controls. Experimental case-control study including 50 PCOS women and 50 healthy age and body mass index matched women. Anthropometric and other relevant clinical baseline measurements were obtained from each patient and control. Relative expression of miRNA levels were estimated using quantitative RT-PCR. PCOS women had decreased levels of miR-15, 195 and 457 compared with controls. Furthermore, miR-16 was differentially expressed within the PCOS group with high levels observed in the hyperandrogenic married group compared with the normo-androgenic PCOS patients. Distinction between PCOS and controls was made using miR-16 alone with an area under the curve of 0.91 or a combination of four selected miRNAs (area under the curve, 0.93). Our study provides evidence that the miRNA expression profile altered in PCOS and indicates that specific miRNAs are associated with phenotypical traits of PCOS. An altered miRNA profile holds potentials for new methods of PCOS patient stratification and may contribute to and in part explain the heterogeneous nature found within PCOS women. All women of reproductive ages and most importantly young girls are at higher risk for different metabolic syndrome and Diabetes mellitus type 2; particularly obese young girls having hyperandrogenism are more susceptible to PCOS