PCOS is arguably the most common endocrinopathy of reproductive-aged women, characterized by
ovulatory dysfunction and hyperandrogenism. It has a highly enigmatic pathophysiology and
manifestation. Transcriptome profiling proffers a valuable approach to identify the candidate genes and
pathways involved in complex diseases. Our aim was to portray the differential gene expression in
peripheral blood of PCOS and normal women. Peripheral blood samples were collected from 4 control
women and 4 PCOS patients (according to Rotterdam criteria). Total RNA was extracted and the array
hybridisation was performed on Illumina Human HT-12 V4 platform. Data were analyzed using
GeneSpring and Ingenuity Pathways Analysis. Microarray results were positively validated using
RT-PCR. To further delineate molecular characteristics of PCOS, we constructed an "integrative
network" combining mRNA and upstream transcription factors. Gene ontology associated with the
network was studied using DAVID 7.0. Gene expression analysis identified 1092 significantly differentially
expressed genes. The integrative TF-mRNA network generated demonstrated that the entries were
extensively interconnected with PCOS hallmarks. To further identify important network clusters we
dissected the integrative network by using a Cytoscape plug-in, clusterMaker. This analysis resulted in 4
nonorphan network clusters including (ATF6, GFI1, HOXA5, STAT3, STAT5B, STAT6, and USF1). The
major biological functions associated with the network profile were cytokine signaling, inflammatory
pathways, IGF-1 signaling, Toll like receptor signaling, oxidative stress, EPO signaling, angiogenesis,
cardiac hypertrophy, insulin signaling and apoptosis. Through this approach we identified important
pathway clusters involved in PCOS etiology and therapeutic interventions based on these clusters can
enable better management of PCOS.