Impact of Small Non Coding RNAs Deregulation in Endometrial Carcinogenesis
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Small non-coding RNAs (sncRNAs) belong to a heterogeneous group of transcripts (< 200 nt), whose involvement in regulation of multiple biological and pathological processes, such as tumor transformation and progression, is nowadays of major interest. Next generation sequencing (NGS) provides a high-throughput platform for exploring the sncRNA population and to investigate their involvement in the development and progression of several cancer subtypes, including endometrial carcinoma. Endometrial cancer represents one of most common and fatal gynecologic cancer. Usually hysteroscopy is used for its diagnosis, discriminating between endometrial hyperplasia and carcinoma subtypes. Hysteroscopy and endometrial biopsies from tumoral, adjacent normal and hyperplastic tissue specimens (when available) from 10 patients were selected for this study, following initial characterization according to defined clinico-pathological parameters. RNA samples were isolated from each biopsy and subjected to sncRNA-Seq and gene expression profiling to explore possible relationships between tumoral progression, sncRNAs and their downstream target deregulation. A signature of differentially expressed miRNAs, piRNAs and other sncRNAs, discriminating among different tumor stages was identified. These results suggest that a “sncRNA tumour signature”, associated with hysteroscopy, may serve as early diagnostic and prognostic marker in endometrial carcinogenesis.

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