each other. Till now, there is no work related to the interaction between lncRNA and ARID3A in cancers. Herein we try to find a probable interactive role between these in cancers.

In this study, 12 different cancer cell lines, 1 osteoblast cell line and 19 different types of normal human tissues RNAs were selected for expression analysis of ERICD and ARID3A. After RNA isolation, cDNA was converted from their RNAs. Expression profile analysis of ERICD and ARID3A in different cancer cell lines and normal tissues was done using ImageJ Program for semiquantitative and $2^{(-\Delta\Delta Ct)}$ method for quantitative RT-PCR.

Among used cancer cell lines, ERICD was highly expressed and ARID3A had lower expression in U-2OS (osteosarcoma), A-172 (glioblastoma) and A549 (lung cancer). At the same time, ERICD expression was lower and ARID3A had high expression in hFOB 1.19 (osteoblast cell line) and normal tissues like brain and lung .

Both ERICD and ARID3A are cell cycle regulated and are commonly regulated by E2F. They have just opposite roles in apoptosis during DNA damage. These two genes have a probability of reciprocal interaction between each other in cancer.

Our results indicate that both ERICD and ARID3A might have opposite roles in lung cancer, glioblastoma and osteosarcoma. ERICD and ARID3A might act as cancer promoting and tumor suppressor genes respectively in these cancers.

P-01.03.3-018
The importance of miRNA expressions in Infertilty

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Implantation process is controlled with endometrium, factors secreted by the embryos and in accordance with these factors embryo and/or endometrium via receptors on. More than 700 human MicroRNA (miRNAs) that are small noncoding RNAs were shown to play an important role in intracelluler cycle regulation in both normal and pathological conditions. In this study we aim to identify miRNAs and controlling molecules expressions in different time period of endometrium in fertile and infertile cases.

The endometrial samples were taken from fertile and infertile patients in proliferation and early secretion periods. The samples are fixed and stained either with hematoxylen-eosin for morphological analysis or with immunohistochemistry for distributions of anti-dicer, anti-drosha, anti-eIf2α and anti-eIF2C. miR-17-5p, miR-23a, miR-23b, miR-542-3p, miR-21, miR-199a*, miR-705, miR-20a, miR-26a, miR-125b, miR-200a/b/c were analyzed with qRT-PCR.

While Dicer immunoreactivity was detected weakly only proliferation phase of fertile group, this immunoreactivity were detected strongly in both proliferation and early secretory phases of infertile group. Drosha immunoreactivitiy was also weakly detected in the proliferation phase of fertile group, it was moderately detected in both proliferation and early secretory phases of infertile group. eIF2α immunoreactivitiy was similar in each groups but there were a few differences between fertile and infertile group. eIF2C immunoreactivitiy was negative in all groups. miR-21, miR-199a* and miR-23a were highly expressed in proliferation phase of fertile group, miR-23a and miR-125b were highly expressed in early secretion phase of infertile group.

In conclusion, Dicer and Drosha immunoreactivities and different expression of miRNA's were detected in all groups. Implantation problems may be reason for different miRNA expression which controlling with Dicer and Drosha in the infertile endometrium in both proliferation and early secretory phases.

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Identification of conserved microRNA molecules in einkorn wheat (*Triticum monococcum* spp. *monococcum*) by deep sequencing analysis

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Wheat is an important agricultural crop with an over 615.8 million metric tons harvesting capacity annually. Drought and salinity are environmental stress factors that affect yield and quality of wheat, dramatically. There are different defense mechanisms against these stress conditions in plants. Altering gene expression profiles by microRNAs at post-transcriptional level is one of the most conserved mechanisms among plants. microRNAs are an extensive class of noncoding RNAs, approximately 22 nucleotide length which regulates the expression of genes by binding to the 3′-untranslated regions of specific mRNAs. microRNAs implicated under salt and drought stress have widely been reported in numerous plant species and wheat genomes in the last years; however, studies on einkorn wheat (*Triticum monococcum* spp. *monococcum*) are not yet available. The goal of this study is identification of conserved microRNAs from einkorn wheat using next generation sequencing technology and bioinformatic analysis. In this study, small RNA molecules were extracted from pooled plant samples grown under normal, drought and salinity conditions. Sequencing analysis revealed 75 164 unique small RNA sequences obtained from 15 139 448 raw reads. After bioinformatic analysis based on comparative genomics approaches, we identified 168 putative mature microRNA sequences belonging to 142 distinct microRNA families. Since chromosomal sequence data is not available for *Triticum monococcum* spp. *monococcum*, we used available sequences from *Triticum urartu,* a close relative, as template to extract precursor microRNA sequences. 111 of precursor sequences showing 100% homology to *Triticum urartu* genome were analyzed for secondary structure prediction using Mfold software. Data provided in this study is critical to investigate transcriptional regulation of genes involved in stress metabolism in einkorn wheat.

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The role of VIM-AS1, a natural antisense transcript, in cancer

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Introduction: A mass of indication suggest that the majority of human genome is transcribed into functional non-coding RNA transcripts called lncRNAs. Of these transcripts, natural antisense transcripts (NATs) are of special interest because they are oriented in the opposite strand complementary to either a protein-