EDITORIAL

miRNA and Cancer; Computational and Experimental Approaches

Human genome sequencing was started to solve four letter algorithm of the genome to understand the complex nature of human metabolism. However, after completion of Human Genome Project many scientists realized that sequence information alone was not sufficient to solve the biochemical mechanism of the organism through classical approaches. Non-coding parts of the genome produce small conserved ribonucleic acids, miRNAs to control cellular and physiological processes [1, 2]. This breakthrough discovery directed researches to examine role of miRNA in cancer since miRNAs are involved in the development, cell differentiation, and regulation of cell cycle [3]. The first paper of the special issue provides general information of miRNA in cancer research.

This thematic issue presents two computational approaches for miRNA identification and their role in cancer. The first one comes from Dr. Wang and his presented work predicts cancer-related miRNAs by using expression profiles in tumor tissues. The work relies on R-squared method to investigate miRNA-mRNA regulatory relationship between miRNAs and mRNAs from different tissues and predicts miRNAs associated with colon, prostate, pancreatic, lung, breast, bladder, and kidney cancer. The second paper by Allmer *et al.* examines miRNA-gene regulatory networks and their implications in cancer. Their work provides complex network of expression regulation and miRNAs' role in personalized medicine.

miRNAs regulate tumor progression and metastasis by interacting with target genes in the cells. Exosomal shuttle small RNAs mediate cell to cell communication and regulate cancer metastasis. The regulation via heterotypic signals in the microenvironment was explained by Dr. Liang and Dr. Yu groups.

The rest of the issue highlights the roles of miRNAs on multiple myeloma, non-small cell lung cancer, urological malignancies, myeloid leukemia, and laryngeal squamous cell carcinoma.

Proliferation of bone marrow of malignant plasma cells leads multiple myeloma and this accounts for ten percent of the hematological tumors. miRNAs biology in multiple myeloma and miRNA study methods was discussed by Dr. Cho's group along with translational therapeutics.

Dr. Papavassiliou highlights recent literature on miRNA-colerectal cancer. miRNA in colorectal cancer regulates tumor specific markers and these markers have oncogenic and tumor suppressive functions as other types of cancer. The paper overviews miRNA biomarkers extracted from plasma and fecal samples and also explain novel therapeutic applications by miRNA delivery and inhibition.

Lung cancer is the leading cause of cancer deaths and non-small cell lung cancer shows poor prognosis and recurrence. Drug resistance limits current treatments and miRNA based gene therapy provides an alternative and attractive method for cancer inhibition since dysregulation of specific miRNAs involved in cancer cell resistance. Therefore, Dr. Giovannetti group explains current efforts in developing miRNA mimickers or antagomiRs for drug resistance mechanism.

Dr. Ellinger and Dr. Müller present a comprehensive review on urological malignancies. The relationship between miRNAs and urological malignancies including prostate, renal cell carcinoma, testicular cancer, and bladder cancer and current literature were provided. The paper stimulates discussion on various bodily fluids and detectable miRNAs in patients' circulation. Thus, specific emphasis was given on circulating miRNAs and diagnostic-prognostic information.

Last two papers of the issue provide roles of specific miRNAs in myeloid leukemia and laryngeal squamous cell carcinoma. Dr. Vasconcelos showed that overexpression of miR-128 decreased acute myeloid leukemia cells and increased the DNA damage. Laryngeal squamous cell carcinoma is the largest subgroup of squamous cell carcinoma in head and neck. And Dr. Guo investigated regulation and expression of three miRNAs; miR-21, miR-106b and miR-375. The paper reported these miRNAs as potential biomarkers for laryngeal squamous cell carcinoma diagnosis.

miRNAs involved in several metabolic pathways and their roles are yet to be elucidated. This thematic issue presents current efforts in determination of miRNAs at different cancer types. Each day determined miRNAs are deposited to the databases and scientists give a lot of effort to understand the biogenesis of these small molecules. These scientific studies and approaches are expected to improve current technologies for therapy and biomarker detection.

REFERENCES

- [1] Alexander, R.P.; Fang, G.; Rozowsky, J.; Snyder, M.; Gerstein, M.B. Annotating non-coding regions of the genome. *Nature Rev. Genetics*, **2010**, *11*, 559-571.
- [2] Tutar, Y. Pseudogenes. Comp. Funct. Genomics, 2012, 424526, 1-4.
- [3] Bartel, D.P. MicroRNAs: Target recognition and regulatory functions. *Cell*, **2009**, *136*, 215-233.

Prof. Dr. Yusuf Tutar

Guest Editor: Current Pharmaceutical Biotechnology
Cumhuriyet University
Faculty of Pharmacy
Division of Biochemistry
58140 Sivas, Turkey
E-mails: ytutar@cumhuriyet.edu.tr; ytutar@yahoo.com