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Andrology & Gynecology 2018, Volume 6
DOI: 10.4172/2327-4360-C1-012

2nd International Conference on
Obstetrics and Gynecology
June 21-22, 2018 | London, UK

RNAi-based tailored therapeutic strategies: Are we there yet?

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A classical technique to determine the function of a gene is to experimentally inhibit its gene expression to examine the resulting phenotype or effect on molecular endpoints and signalling pathways. RNA interference (RNAi) is one of the recent discoveries of a naturally occurring mechanism of gene regulation facilitated by the induction of double stranded RNA into a cell. This event can be utilized to silence the expression of specific genes by transfecting mammalian cells with synthetic short interfering RNAs (siRNAs). siRNAs can be designed to silence the expression of specific genes bearing a target sequence and may potentially be presented as a therapeutic strategy for inhibiting transcriptional regulation of genes, which in such instances constitute a more attractive strategy than small molecule drugs. Low dose drug and siRNA combination studies are promising strategies for identifying synergistic targets that facilitate reduction of undesired gene expression and/or cell growth depending on the research of interest. Commercially available RNAi libraries have made high-throughput genome-scale screening a feasible methodology for studying complex mammalian cell systems. However, it is crucial that any observed phenotypic change be confirmed at either the mRNA and/or protein level to determine the validity of the targeted genes. Currently, qPCR is widely utilized for accurate evaluation and validation of gene expression profiling. In this study, we describe a high-throughput screening of RNAi based gene knock-down approach and qPCR validation of specific transcript levels. Considering such advantageous applications, siRNA technology has become an ideal research tool for studying gene function in research fields including Pharmaceutical Biotechnology and holds the promise that the utilization of siRNA-based therapeutic agents will accelerate drug discovery in clinical trials.

Speaker Biography

Şükrü Tüzmen is a Molecular Biologist and Geneticist. He has more than twenty-eight years of multi-disciplinary research experience integrating studies of the molecular basis of human diseases, including cancer genetics. Tüzmen has a passion for advancing the molecular genetics of diseases by studying the associations between drugs, genes, pathways, and diseases. His mission is to discover and validate links between gene states and disease phenotypes, and further use these links to identify druggable targets to be utilized as biomarkers in the early diagnostic stages of genetic diseases. He has focused his career on developing and applying cutting edge methods and technologies to ensure excellence in translation of his basic scientific research including cancer genetics, from bench to bedside. Tüzmen has been invited to deliver talks in many National and International settings, and he has served on many expert panels including The Research Grant Council, Hong Kong, China.

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