Tumor heterogeneity driven by sharing genetic and signaling code between microbiota and breast carcinoma

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There are emerging views to substantiate the inumerable population of microbioata making their choice of residence within human body parts including intestine and mammay glad tissue. In a focussed way, possibly the presence of microbes in mammar gland could be explained by the entry of microbes from the skin. There are possibility of presence of proteobacteria including taxa such as Bacillus, Acinetobacter, Pseudomonas, Staphylococcus and Propionibacterium. It is true that presence of these microbes can impact the normal and tumor mammay glad tissue. In other way, the role of these microbes may be extended to possibility that descernible presence of intra-tumoral heterogeneity in breast tumor could be driven one of potential routes through microbes and cellular communities including cancer cell, immune cells and stromal cells. In view of plethora of microbiot and tumor cellular components interactions, first elucidation may come from the study of molecular signaling crosstalk between microbes and tumor cell. Possibly, molecular signaling crosstalk needs to be focussed at the level of metabolites secretion and sharing between microbes and tumor cells. Therefore, metabolome of tumor tissue needs to be highlighted with reference to microbes and tumor tissue niches. Another possible communication between microbes and tumor cell could be possible through the transfer of genetic materials between in the form of extra-chromosomal circular DNA like plasmid and small non-coding RNAs. In this era of science, theer are evidence of natural transfer of extra-chromosomal circular DNA and small RNAs may be possible through natural genetic mateiral exchange process among prokaryotes and eukaryotes. Hence, one potential question emerges that whether transfer of microbe origin plasmid with a potential of drug resistance gene can be transfered to cancer cells within the tumor niches. These plasmid genetic materials with drug resistance may be able to confer the reinforcing capability to the heterogeneous nature of tumor cellular communities for better growth, suvival and drug resistance. Currently, we are investigating the contribution of microbiota mediated plasmid transfer to push tumor heterogeneity. To achieve this goal, we use next generation sequencing, metabolomic profiling and molecular techniques. Therefore, this paper highlight the need for scienetific attempt to address the interplay of microbes and tumor heterogeneity. Also precisely unravell the contribution of transfer of drug resistance plasmid from microbes to tumor cell by generating drug resistant and robust heterogeneous population with their niches.

Speaker Biography

Nilesh Kumar Sharma has completed his PhD from Indian Institute of Technology Roorkee, India in the year 2009 within Health Science specialization. He completed his Post-doctoral research training for more than three years in DNA repair genetic and cancer biology at NIEHS, NIH, USA and Rutgers University, NJMS, NJ, USA. Since July 2016, he is working as an Associate Professor at Dr. D Y Patil Biotechnology & Bioinformatics, Dr. D Y Patil, Vidyapeeth, Pune, India as a faculty and Principal Investigator in DST and DPU funded research project. He has been credited with more than 25 research publications in indexed international journals and two book chapters.

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