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Breast cancer transcriptome: From triple negative breast cancer to HER2-overexpressing isogenic TNBC Cells

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In recent years, Kumar's lab used high-throughput whole genome sequencing to gain a deeper genomic insight of the triple-negative breast cancer (TNBC), estrogen receptor positive and HER2 positive breast cancers, and revealed new regulatory intricacies and pathways in breast cancer. These results re-validated an expected inter- and intra-tumor genomic heterogeneity due to differential expression of transcripts and splicing and promoter switching. To address the issue of clonal origin of breast cancer, the laboratory also generated isogenic TNBC breast cancer clones stably expressing HER2 as a part of a master dissertation project, and identified HER2-modulated genes through microarray analysis. The laboratory continued with this theme as a part of a doctoral dissertation project and subjected these isogenic clones to RNA-sequencing analysis in the context of HER2-transcriptome. This phase of the work was centered on identifying differential expressed genes and alternative spliced transcripts, transcription and splicing factors modulated by HER2 as an attempt to explain the basis of the noted differential expression in isogenic clones.

Biography

Rakesh Kumar is an internationally recognized Cancer Biologist with a particular focus on breast cancer. His research interests are focused on the mechanisms of cancer progression with special emphasis on chromatin and cytoskeleton remodeling, and targeted cancer therapeutics. He has received several awards and honors for his research work since 1995. He has authored over 220 original research papers, 67 reviews, 10 book chapters and edited 6 books/volumes in the area of cancer research. He has trained over 65 fellows and students, and shared his knowledge by delivering over 220 invited, keynote or plenary lectures at academic institutions, universities and scientific meetings.

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