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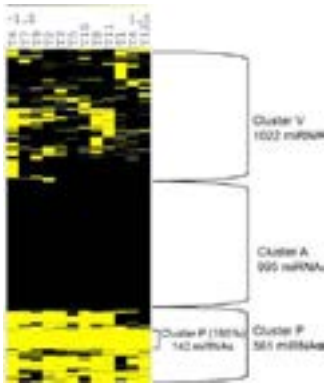
Veronica Ponce Castaneda

Medical Research Unit in Infectious Disease, Mexico

Whole miRNOME perspective identify a critical 30 miRNA Core in retinoblastoma

miRNAs have a prominent position in the negative control of gene expression and are involved in many cellular processes including carcinogenesis. Analysis and published results of high throughput miRNA profiles lack a robust approach to describe their findings with a real integrative approach. We examined the whole miRNome using a high throughput microarray platform including 2578 mature miRNAs in 12 samples of primary human retinoblastoma, an intraocular malignant tumor of early childhood and probably the most robust clinical model of genetic predisposition to develop cancer. This work delineates the miRNA landscape in human retinoblastoma samples with a non-biased approach using detection call scores as an approximation to expressed/not-expressed state for each miRNA. With this approach we discovered a central cluster of 30 miRNAs highly expressed in all the cases, a cluster of 993 not expressed in all cases and 1022 variably detected in the samples accounting for inter tumor heterogeneity. We further explored mRNA targets, pathways and biological processes affected by some of these miRNAs. The 30 miRs core represent shared miRNA machinery in retinoblastoma affecting most pathways considered hallmarks of cancer. We identified miR-3613 as a potential down regulator hub, because is highly expressed by all the samples and has at least 36 tumor suppressor genes as potential mRNA targets including the RB1 gene itself. Our results indicate that human retinoblastoma share a common and fundamental miRNA expression profile regardless of heterogeneity.



Biography

Professor in Department of Cell Biology at National Autonomous University of Mexico. Dr. Martha is a Medical Surgeon and Doctorate in Biomedical Sciences MD, Ph.D.

vponce@ifc.unam.mx