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My laboratory investigates different aspects of post-transcriptional regulation, with a special focus on RNA binding proteins. We used a variety of approaches that include bioinformatics, genomics and molecular biology to characterize the regulatory networks formed by RNA binding proteins and their target RNAs. The main projects of the lab are listed below:

- We are using SAGE, MPSS and Microarray data to determine the pattern of expression of RNA binding proteins in normal and tumor tissue. The main goal of this project is to identify tissue specific RNA binding proteins and RNA binding proteins that are aberrantly expressed in tumor tissue. The main candidates derived from these lists will be explored as to their participation in tissue/organ development and tumor formation.
- The fate of a given mRNA is determined by elements located on its UTRs. These elements will dictate levels of translation, stability and will be necessary for transport and localization. We are mapping regulatory elements located on UTRs using a combined *in silico/in vivo* method. We initiated our analysis by identifying short nucleotide sequences (*n-mers*) that are over-represented in either 5' or 3' UTRs. A given *n-mer* is considered over-represented if it appears more frequently than its mathematical expected frequency. This strategy has been used successfully to map regulatory sequences in promoters. It is possibe that over-represented sequences in UTRs might function as binding sites for RNA binding proteins and non-coding RNAS, functioning thus as regulatory elements. In order to select the best candidates for *in vivo* validation, we performed cluster and gene ontology analyses of large groups and groups containing 2 or more identical *n-mers*. In several cases, the analysis indicated strong commonalities amongst members of the same group, suggesting that they in fact belong to the same gene network.
- The participation of RNA binding proteins in tumorigenesis is poorly understood. There are just a few examples of RNA binding proteins that appear to work as oncogenes. The characterization of RNA binding proteins that are aberrantly expressed in tumors is necessary as an initial step to establish stronger links between RNA binding proteins and tumor formation. Our lab is currently dissecting the participation of the protein Musashi1 in glioblastoma and medulloblastoma formation. A RIP-Chip analysis was conducted, leading to the identification of ~200 new RNA targets. The Gene Ontology analysis indicated that Musashi1 regulates several genes involved in the cell cycle. We have also established that the knockdown of Musashi1 interferes with the ability of medulloblastoma cells in forming colonies.
- Another important aspect of post-transcriptional regulation is alternative splicing. Due to technical limitations, the study of alternative splicing had been restricted to individual analysis (one alternative splicing event : one regulator). This scenario has changed recently with the advent of alternative slicing microarrays. We are conducting alternative splicing microarray analysis in partnership with Jivan Biologicals. Our two areas of interest are: the identification of splicing events prevalent in glioblastoma cells and the function of WT1 and WTAP (Wilms' Tumor 1 and Wilms' Tumor Associating Protein respectively) in regulated splicing.