Poster A-3

Correlation between the expression of splicing factors and the presence of specific patterns of alternative splicing in human and mouse.

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Short Abstract: We observed a significant coefficient correlation between the expression of splicing factors in brain, breast and prostate from human and mouse samples. We intend to analyze different types of expression data of splicing factors in an attempt to gain some insights on the expression of tumor-associated splicing variants.

Long Abstract:
Alternative splicing allows individual genes to express multiple mRNAs that may encode proteins with diverse and antagonistic functions. It is estimated that 40-60% of all human genes undergo alternative splicing and about 80% of alternative splicing results in changes in the respective encoded protein revealing what is likely to be the primary source of human proteomic diversity. Splicing variants have been shown to be associated with features like spreading and progression in several human tumors. The interactions between splicing factors and auxiliary cis-elements that modulate the association of the spliceosome with the pre-mRNA is thought to control alternative splicing. In this study we intend to analyze SAGE and MPSS data in humans and mouse to investigate the expression pattern of splicing factors that might cause the appearance of such tumor associated splicing variants. We analyzed the expression pattern of splicing factors in both normal and tumor tissues. Virtual tags were assigned to 145 genes, encoding proteins involved in splicing as shown by proteomics analysis. The expression pattern of the genes was assessed by analyzing their tag counts in normal and tumor, human and mouse MPSS libraries. Our final group of candidates includes 135 clusters with 157 representative virtual tags in human, and 103 clusters with 162 representative virtual tags in mouse. We observed a significant coefficient correlation between the expression of splicing factors in brain, breast and prostate from human and mouse samples ($R > 0.95$). Both initials approaches showed that, tissue specificity over-expression of splicing factors may support the notion of a broader association between factors splicing and cell transformation. We will continue to study the correlation between the expression of splicing factors and the presence of specific patterns of alternative splicing in human and mouse Furthermore we will continue to analyze the impact of the over-expression of splicing factors in oncogenic pathways.