Characterization of RNA networks regulated by transcription factors in malignant B cells

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Transcription factors (TFs) have been identified as key regulators of RNA regulatory networks in aggressive subtypes of chronic lymphocytic leukemia (CLL) and follicular lymphoma (FL). It has been shown that both diseases harbor complex deregulation of interconnected TFs that leads to aberrant mRNA expression profile together with dysregulated expression of post-transcriptional regulators such as RNA-binding proteins and microRNAs. In malignant B cells, we aimed to describe the regulatory landscape of 3 selected transcription factors. We optimized CHIP-PCR and subsequently conducted the first CEBPB CHIPseq to identify the binding of this transcription factor in B cells. The binding of FOXO1 in the genome has been optimized using Cut&Taq approach (including nuclear extraction). Our preliminary data indicated that each of these TFs is involved in the regulation of essential cellular programs such as survival, proliferation or migration. We also prepared knockout MEC1 cell lines for FOXO1 and HMGA1 (and performed siRNA experiments) and investigate gene expression analysis in these cells to understand the impact of TF modulation on gene expression.

During the duration of INTEG-RNA project 2 PhD students and the PI participated in an EMBL conference “The non-coding genome”, one PhD student participated at EMBO practical course “FISHing for RNAs: classical to single molecule approaches”, and also at a research visit to EMBL.