

P039 Analysis of poly(A) tail changes by poly(A) fractionation
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The poly(A) tail of an mRNA plays an important role during mRNA metabolism. In general, a long poly(A) tail is thought to be linked to mRNA stability and active translation while a short poly(A) tail is concomitant with RNA degradation and translational repression. We decided to investigate if oligoadenylate mRNAs are present in somatic cells. To this end, we developed a fast and highly reproducible technique for separating mRNAs depending on the length of their poly(A) tail (Poly(A) fractionation). This enabled us to determine the length of poly(A) tail of endogenous mRNAs. The poly(A) fractionation method was used to divide RNA from NIH3T3 (mouse embryonic fibroblast) cells dependent on the length of their poly(A) tail into fractions. Subsequently, the fractions with short and long poly(A) tails were subjected to microarray analysis and validated by Northern blotting, RT-PCR and LM-PAT (ligase mediated polyadenylation test). Our data indicate that oligoadenylated and deadenylated (<15 As) mRNAs do exist in somatic cells. We also used the poly(A) fractionation method to study the role of poly(A) tail changes.