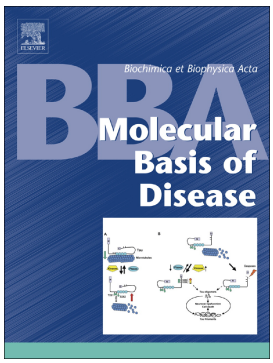

Transgenic expression of the RNA binding protein IMP2 stabilizes miRNA targets in murine microsteatosis

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Transgenic expression of the RNA binding protein IMP2 stabilizes miRNA targets in murine microsteatosis

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Abstract Adult expression of IMP2 is often associated with several types of disease and cancer. The RNA binding protein IMP2 binds and stabilizes the *IGF2* mRNA as well as hundreds of other transcripts during development. To gain insight into the molecular action of IMP2 and its contribution to disease in context of adult cellular metabolism, we analyze transgenic overexpression of *IMP2* in mouse livers, which has been shown to induce a steatosis-like phenotype and enhanced risk to develop hepatocellular carcinoma (HCC). Our data show up-regulation of several HCC marker genes and miRNAs (miR438-3p and miR151-5p). To characterize the impact of miRNAs to their targets, integrative analysis of transcriptome-and miRNAome-dynamics in combination with IMP2 target prediction was carried out. Our analyses show that targets of expressed miRNAs become accumulated in the case that these transcripts have positive IMP2 binding prediction. Therefore, our data indicates that overexpression of IMP2 alters the regulatory capacity of many miRNAs and we conclude that IMP2 competes with miRNAs for binding sites on thousands of transcripts. As a result, our data implicates that overexpression of IMP2 has distinct effects to the regulatory capacity of miRNAs with yet unknown consequences for translational efficiency.

Keywords:

IGF2, IMP2, p62, murine steatosis, miRNA, transcriptome, DLK1/DIO3