

BITS :: Call for Abstracts 2021 - Oral communication

Type	Oral communication
Session	Gene regulation, transcriptomics and epigenomics
Title	Variation in the co-expression profile highlights the loss of miRNA-mRNA regulation in several cancers
All Authors	Gerardo Pepe (1), Luca Parca (2), Lorenzo Viviani, Gabriele Ausiello (1), Manuela Helmer-Citterich (1)

Affiliation

(1) Department of Biology, University of Tor Vergata, Rome
(2) IRCCS Casa Sollievo della Sofferenza, Rome

Motivation

Recent research provides insight into the ability of miRNA to regulate various biological processes, such as development, cell differentiation, diseases and many pathways in several cancer types. Despite the great importance given to the miRNA regulation, there are relatively few studies that compare the mRNA-miRNA landscape in tumor vs healthy tissue.

Here we present a thorough analysis of the miRNA-mRNA interaction landscape in different cancer types thus highlighting the differences that exist in the miRNA-mRNA regulatory networks between healthy and tumor tissue.

Methods

We collected samples from TCGA, where both miRNA and mRNA expression had been evaluated. Using Pearson correlation coefficient (PCC), we performed a thorough correlation analysis on 7494 experimentally validated human miRNA-mRNA target-gene pairs in both healthy and tumoral samples.

Results

On average we found 385 miRNA-mRNA pairs negatively correlated across the healthy samples analyzed (PCC < -0.4, adjusted p-value < 0.05) (Fig 1, blue bars). A marked decrease in the number of correlated pairs was found in the tumoral samples, where, on average, only 62 miRNA-mRNA showed a negative correlation across all tumor samples within the defined thresholds (Fig 1, green bars). Moreover, the comparison between healthy and tumoral samples highlighted that only a small number of miRNA-mRNA pairs preserved their correlation in both conditions (Fig 1, green bars).

miR-200 family, miR-155 and miR-1 were identified as the miRNAs that lose the greatest number of interactions with their targets across the analyzed tumoral samples.

Most of the identified miRNA-mRNA dysregulated interactions are shared among different cancer types. 2865 unique miRNA-mRNA pairs were identified across 13 cancer types, \approx 40% of these pairs showed a loss of correlation in the tumoral samples in at least 2 out of the 13 analyzed cancers.

The miR-34a / ALDH2 and miR-9 / MTHFD2 pairs show a switch in their correlation between healthy and tumor kidney samples suggesting a possible change in the regulation exerted by the miRNAs. This analysis shows that the correlation between miRNAs and their targets strongly differs between healthy and tumor and that the critical pairs identified are involved in cellular adhesion, proliferation, and migration.

Info

Fig 1 For each tumor, we report the number of miRNA-mRNA correlating pairs identified in healthy and tumoral samples on the left (blue bars) and on the right (yellow bars), respectively. In green we report the number of miRNA-mRNA correlating pairs that preserved their correlation in tumoral samples.

Figure



Availability <https://docs.google.com/document/d/1B5-JE0RzmHpt2avIWvkCGI0CmpArswZgbYZJIn9I0sE/edit?usp=sharing>

Corresponding Author

Name, Surname Gerardo, Pepe
Email geradopepe0@gmail.com
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Società Italiana di Bioinformatica

C.F. / P.IVA 97319460586

E-mail bits@bioinformatics.it

Sede legale Viale G. Mazzini, 114/B - 00195 Roma

Website bioinformatics.it

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