

Parallel Session

Cancer II

**STRUCTURE AND DYNAMICS OF A GENE
REGULATORY NETWORK DRIVING
HEPATOCELLULAR CARCINOMA**

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Hepatocellular carcinomas show distinct gene expression profile and response to therapy in different patients. Therefore, design of efficient therapeutic strategies requires understanding of the function of tumor-promoting genes in individual tumors, and faithful prediction of the therapeutic response of the molecular network in which the tumor promoting genes exert their function. Here, we identify a gene regulatory network (GRN) which drives development of HCC. The activity of the network correlates with vital prognosis of HCC patients, with proliferation and embryonic markers and was found to be specific to gastrointestinal cancers. Based on data from the The Cancer Genome Atlas and transfection experiments, we generated and calibrated a quantitative mathematical model which allows to theoretically predict the impact of one GRN component on the expression of all the others. We then compared the impact on the GRN of pharmacological inhibition of a network component in cultured HCC cell lines with the model's predictions of a pharmacological inhibition. The experimental data faithfully recapitulated the model predictions. We conclude that the mathematical model, which is made available via two user-friendly applications deployed on a web platform, can be used as a tool to predict the impact of therapeutic agents targeting the GRN.