

Genomic analyses point to the potential of personalised care for liver cancer patients

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A new study presented today at The International Liver Congress 2015 shows that by using genomic analyses to understand how and when carcinogenic mutations occur in patients with hepatocellular carcinoma (HCC), it is possible to identify specific molecular profiles. It is hoped that these molecular profiles will help identify which patients would benefit from specific anticancer treatments.

Using exome sequencing - a technique for sequencing all the protein-coding genes in a genome - the study identified relationships between environmental exposures, such as tobacco smoke and alcohol use, and mutational patterns in HCC. It also determined the landscape of driver genes and pathways altered in different clinical stages and aetiological backgrounds. Out of eight mutational signatures identified in the study, two new mutational signatures for HCC were found.

Professor Jessica Zucman-Rossi, director of the INSERM/university Paris Descartes "Functional Genomics of Solid Tumors" laboratory explained: "Mutational signatures help with understanding the biological history of a cancer and can enable differentiation between ongoing mutational processes and historical ones. This helps identify potential new targets for [anticancer therapies](#)."

In the study, most [patients](#) had at least one damaging alteration which could potentially be treated with either an FDA-approved drug (28% of patients) or an investigational drug (86% of patients) which has been studied in Phase I to Phase III clinical trials.

"Hepatocarcinogenesis is a multi-step process in which pre-cancerous lesions can ultimately transform into liver cancer. Genomic analyses, such as exome sequencing, allow us to better understand the mutational processes involved in the development of cancers. This detailed knowledge then helps us to unravel the mutagenic processes and to optimise personalised patient care," said Professor Markus Peck, Secretary General, European Association for the Study of the Liver.

The study authors hope that the use of [exome sequencing](#) will lead to the identification of potential new targets for anticancer therapy and create optimised personalised patient care.

Provided by European Association for the Study of the Liver

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