Gene network activity in cultivated primary hepatocytes is highly similar to diseased mammalian liver tissue.

Godoy P, Widera A, Schmidt-Heck W, Campos G, Meyer C, Cadenas C, Reif R, Stöber R, Hammad S, Pütter L, Gianmoena K, Marchan R, Ghallab A, Edlund K, Nüssler A, Thasler WE, Damm G, Seehofer D, Weiss TS, Dirsch O, Dahmen U, Gebhardt R, Chaudhari U, Meganathan K, Sachinidis A, Kelm J, Hofmann U, Zahedi RP, Guthke R, Blüthgen N, Dooley S, Hengstler JG (2016) Gene network activity in cultivated primary hepatocytes is highly similar to diseased mammalian liver tissue. *Arch Toxicol* 90(10), 2513-2529.

Details

PubMed

Abstract

It is well known that isolation and cultivation of primary hepatocytes cause major gene expression alterations. In the present genome-wide, time-resolved study of cultivated human and mouse hepatocytes, we made the observation that expression changes in culture strongly resemble alterations in liver diseases. Hepatocytes of both species were cultivated in collagen sandwich and in monolayer conditions. Genome-wide data were also obtained from human NAFLD, cirrhosis, HCC and hepatitis B virus-infected tissue as well as mouse livers after partial hepatectomy, CCl4 intoxication, obesity, HCC and LPS. A strong similarity between cultivation and disease-induced expression alterations was observed. For example, expression changes in hepatocytes induced by 1-day cultivation and 1-day CCl4 exposure in vivo correlated with R = 0.615 (p

Beteiligte Forschungseinheiten

Microbiome Dynamics Gianni Panagiotou Mehr erfahren

Leibniz-HKI-Autor*innen



Reinhard Guthke

Details



Wolfgang Schmidt-Heck

Details

Themenfelder

Systembiologie der Leber

Awards

Patricio Godoy, Agata Widera and Wolfgang Schmidt-Heck share first authorship.

Identifier

doi: 10.1007/s00204-016-1761-4

PMID: 27339419