

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.

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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

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Awards

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

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