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Editorial

Stem cells as models in FASD research

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Fetal Alcohol Spectrum Disorder (FASD) is a fairly new concept (earlier called fetal alcohol syndrome, FAS), cf. ICD-9 and ICD-10. From the first papers devoted to it from 1981 and two decades onward only a few papers appeared, but in the past 5 years or so the literature has exploded with more than 250 papers recorded in PubMed to date.

The focus was initially (1981 to 2005) on characterizing clinically the complex birth defect phenotypes that are induced by alcohol consumption during pregnancy. During the past 10 years there were also many neuropsychological studies describing the various psychopathological traits associated with the syndrome. This type of research still dominates the most recent literature. A major problem is therefore that the pathogenesis of FASD is not sufficiently understood. It is necessary to address this by changing the focus towards explaining at the cellular level what happens when cells are exposed to alcohol.

In the present issue of Journal of Pediatric Biochemistry, Krishnamoorthy and coworkers [1] propose to use human embryonal stem cell lines for this purpose, and expect in that way to find clues to the complex birth defects that are induced by alcohol consumption during pregnancy [1]. It has been reported that ethanol has adverse effects on regulators of cell cycle regulation and increases DNA damage. They now show that ethanol, at concentrations encountered in humans consuming alcohol, alters the transcription of some cell cycle genes as well as protein expression levels, which as a result increased the rate of DNA replication, proliferation and differentiation in the studied stem cell lines. While they underline that any deductions about correlation of their findings with the clinical pictures occuring in the syndrome are premature, upon seeing the list of genes they found to be affected, one wonders whether there might not be links between these effects and, for instance, cancer initiation and promotion later in life, which are known to be linked to adult alcohol intake, but it seems to be still unsettled whether cancer could also be among the corollaries to FASD [2]. On a mechanistic level, it is interesting that the gene regulation changes induced by ethanol in stem cells may be accompanied by DNA methylation changes [3], which could possibly result in lasting epigenetic regulation.

This paper exemplifies an additional avenue towards understanding at the molecular level the processes that underly the FASD, and as more data emerge researchers will be rewarded by identifying key regulatory elements of these processes.

References

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