

Zebrafish embryos as an alternative model for screening of drug-induced organ toxicity

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Zebrafish have initially emerged as model in developmental biology. The ease of maintenance, high number of offspring, transparency of the eggs and its suitability in mutagenicity screens to unravel developmental pathways contributed to its popularity. Today, it can be considered as one of the best characterised vertebrate models and more than 1,000 labs worldwide use the zebrafish (Strähle et al. 2012). At around 1990 zebrafish were discovered also as a toxicology model (Gorge and Nagel 1990), and the popularity is still increasing (Busch et al. 2011). A major reason for the attractiveness of this small teleost is associated with the suitability of its embryonic life stages. Early life stages are considered to sentinel no or less pain or discomfort when exposed to chemicals. Hence, according to European regulation (EU 2010), they are accepted as alternatives to animal experiments (Embry et al. 2010; Halder et al. 2010). Furthermore, the zebrafish embryo model has the principal capacity of high-throughput analysis and can be used in, for example, screenings for low toxicity of drug candidates.

Zebrafish embryos provide an enormous versatility of applications in both environmental and human hazard assessment ranging from acute systemic toxicity (Ali et al. 2011; Lammer et al. 2009; Padilla et al. 2012), chronic toxicity (Volz et al. 2011), teratogenicity (Gustafson et al. 2012; Selderslaghs et al. 2009), neuractivity/neurotoxicity (Kokel et al. 2010; Selderslaghs et al. 2010), and endocrine disruption (Brion et al. 2012; Thienpont et al. 2011) to specific organ toxicities (Berghmans et al. 2008; Parng et al. 2002).

As outlined by the paper of Driessen et al. in this issue of Archives in toxicology, hepatotoxicity is one of the major concerns of organ toxicity in drug development. Identification of hepatotoxicity as early as possible in the drug development pipeline would reduce the costs associated with development of new medicines. Traditional animal models are time and cost intensive and subject to ethical concerns. Genuine cell-based *in vitro* methods do not provide the complexity of animal models and may provide only limited predictivity. Therefore, the zebrafish embryo has been proposed also as a better model to identify organ toxicity. As shown by Driessen et al., zebrafish embryos can indeed be used to identify hepatotoxicity. However, it is important to translate the observations appropriately, since histopathological effects or individual gene responses may differ among vertebrates.

Identification of key events and conserved mechanisms can be supported by toxicogenomic analysis, and hence, it is not surprising that the number of studies in zebrafish embryos supported or accompanied by toxicogenomic analysis is increasing (e.g. Büttner et al. 2012; Hermsen et al. 2012; Pelayo et al. 2012; Schiller et al. 2012; Yang et al. 2007). Transcriptional profiling of whole embryos is even able to reveal organ-specific profiles—as shown in the Driessen paper in this issue and by various other studies (e.g. Klüver et al. 2011; Yang et al. 2007). With the advent of next generation sequencing (NGS), new perspectives for transcriptome profiling by RNA-sequencing (RNA-seq) are provided also for the zebrafish embryo model (Aanes et al. 2011; Vesterlund et al. 2011). With RNA-seq, novel transcripts from annotated or non-annotated regions not available in predefined probe sets, alternative splicing forms and rare transcripts can be detected. This could be important for the comparative analysis and identification of conserved key toxicity pathways in vertebrates. At present,

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the technology of RNA-seq is still rather expensive but as has been shown by the Driessen paper, pooling of samples is possible and can partially overcome the limitation. In the future, the use of barcode technology may allow to analyse multiple samples in parallel, providing another way to reduce cost. RNA-seq may also be applied for a genuine organ-specific analysis in zebrafish embryos, by using transgenic strains, in which specific organs are labelled by the expression of a reporter gene or protein, respectively. Cell dissociation protocols are available and fluorescence-activated cell sorting would allow restriction of toxicogenomic analysis to specific cell types in early life stages (Cui et al. 2011). A potential drawback of RNA-seq is that important signals detected by microarrays may not be sufficiently read due to coverage limitations. Thus, although RNA-seq holds good promises for routine use, it may at present not fully replace microarrays but provide complementary data.

A major issue of future research particularly for the extrapolations from zebrafish embryos to humans is also how the effect concentrations in embryos can be related to appropriate effect levels in mammalian models. Pharmacokinetics in genuine in vitro as well as in fish embryo models differ fundamentally from mammalian models (Noorlander et al. 2008). In the latter, drugs are often administered by single or repeated (oral) doses leading to specific time courses of plasma concentrations depending on the adsorption, distribution, metabolism and excretion rates of the drug. In fish embryos, exposure is static and internal concentrations are established by partition equilibrium. Physiologically based kinetic models could provide a link between fish embryo and mammalian toxicity, but such models have not been developed for the fish embryo so far (Louisse et al. 2010). Furthermore, support by chemical analytics for the time-course of internal concentration in fish embryos would be needed. An alternative approach that may rely less on pharmacokinetic modelling could be the comparison of concentration–response curves for drug targets (therapeutic targets) with the appropriate curves for adverse effects such as hepatotoxicity. Clearly separated effect concentrations could identify promising compounds in drug screening approaches. This requires, however, also an appropriate concentration–response analysis that is lacking in most of zebrafish embryo studies with molecular endpoints or toxicogenomic analysis (Gündel et al. 2012). With the further development of technologies for transcriptional profiling, this can be expected to be facilitated.

The study of Driessen et al. has provided pioneering data for the use of zebrafish embryos as a hepatotoxic model and is the first study that compares embryonic and adult stages of fish with mouse and in vitro cellular models. The study provides promising evidence that the zebrafish

embryo could be developed as a model to predict hepatotoxicity for humans.

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