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# A Note on Omics Data are Particularly Useful for the Identification of Molecular Modes of Action or Toxic Pathways

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## Editorial

This special issue of Mutation Research may show the reader how 'omics technologies are beginning to replace other commonly used methodologies for chemical hazard/risk assessment. This is due to the possible added value that omics can provide. Data has been shown to contribute to risk assessment. Improvement of mechanistic understanding and identification modes of operation Furthermore, while transcriptomics is promising, although metabolomics looks to be at least as sensitive as traditional toxicology measures, it may be more sensitive. It is now no-observed detrimental effect levels are widely acknowledged (NOAELs) 'omics research can provide information if they are based on certain criteria. Patterns of change for potentially important biological consequences, i.e., patterns indicating disruptions in adverse outcome pathways can be linked to a hazardous outcome causally. Consequently, this special issue of Mutation Research may demonstrate how omics technologies are beginning to supplant other regularly used approaches for assessing chemical hazard/risk assessment. This is due to the potential for 'omics to give additional value. Data has been shown to help with risk evaluation. detection and improvement of mechanistic understanding operational modes Moreover, while transcriptomics holds promise, Metabolomics appears to be at least as sensitive as standard toxicology measurements, if not more so. Itis now Levels of no-observed negative effects are commonly acknowledged (NOAELs) If certain criteria are met, 'omics research can provide useful information [1].

Patterns of change that could have significant biological effects, such as disturbances in adverse outcome pathways can be causally linked to a dangerous consequence Consequently, Specific patterns of change discovered in 'omics investigations are being developed and employed in the screening of new chemicals to identify toxicological mechanisms of action early. Similarly, omics technology may contribute in the discovery of action modalities. Associated to significant toxicological consequences, such as carcinogenicity or mutagenicity alterations in endocrine function Targeted mechanistic investigations can be designed using this information to eventually pinpoint the mode of activity Larger databases, as well as the development of suitable cell technologies In the future, it is possible that 'omics data will be deemed sufficient proof of a mode of operation action without the necessity for further (animal) research ' in terms of refining and reduction. In terms of the third R (replacement), it is doubtful that *in vitro* data from 'omics analysis will be used as a substitute for *in vivo* investigations in the regulatory arena in the near future.

However, 'omics technologies may already be able to assist bridge the gap between *in vitro* and *in vivo* relevance. An intriguing prospective application of 'omics technologies would be in the REACH legislation's information requirements for data-poor substances. Although this regulation allows for the use of alternate methods for collecting the essential data for data-poor commercial chemicals in the EU, there are currently few alternatives to the established endpoints for local effects and genotoxicity. Alternative approaches for systemic toxicity are completely lacking [2]. It's no wonder, then, that grouping compounds and then reading across to data-rich substances (within a class of chemicals with comparable structures) is the most popular method for reducing the cost of animal testing while still delivering meaningful data for risk assessment.

Omics data, as previously stated, are particularly beneficial for identifying molecular mechanisms of action or hazardous pathways. Furthermore, if enough consistent 'omics data becomes available, compounds should be ranked according to their 'omics profile (together with mode of action information). Because there are currently no acknowledged alternative methods for determining systemic (and reproduction) toxicity, animal studies will undoubtedly be required (certainly for phase 1 and phase 2 base packages). Additional biological samples (e.g. OECD Guideline 407, 408 or 422) might thus be gathered from this research and used to generate 'omics data. The joint evaluation of the toxicological effects observed in these studies, Together with information on mode of action gleaned from 'omics analysis, this should provide a more meaningful means of classifying compounds than just establishing (quantitative) structure–activity connections. By including biological aspects in these considerations, we can advance from QSARs to QBARs (quantitative biological activity relationships) and get closer to realising the toxicity testing in the twenty-first century initiative's concept [3-5]

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## Conflict of Interest

The Author declares there is no conflict of interest associated with this manuscript.

## References

1. Zhi, Hu Zhang, Hongzhan Huang, Anatoly Dritschilo, and Anton Wellstein. “omics data are particularly useful for the identification of molecular modes of action or toxic pathways” *Human Genet Embryol* 13 (2022): 547-571.
2. Brockmeier, K. Erica., Geoff HodgesLami, Emma Butler, and Markus Hecker. “The role of omics in the application of adverse outcome pathways for chemical risk assessment.” *Human Genet Embryol* 13 (2022): 252-262.
3. Canzler, Sebastian, Jana Schor, Wibke Busch, and Kristin Schubert. “Prospects and challenges of multi-omics data integration in toxicology.” *Human Genet Embryol* 13 (2022): 371-388.
4. Seeger, Bettina, Almut Mentz, Constanze Knebel, and Flavia Schmidt. “Assessment of mixture toxicity of (tri)azoles and their hepatotoxic effects *in vitro* by means of omics technologies ” *Human Genet Embryol* 13 (2022): 2321-2333.
5. Wilmes, Anja, Chris Bielow, Christina Ranninger and Patricia Bellwon. “Mechanism of cisplatin proximal tubule toxicity revealed by integrating transcriptomics, proteomics, metabolomics and biokinetics.” *Human Genet Embryol* 13 (2022) 117-127.

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