

Short-Term Transcriptomic Points-of-Departure are Consistent with Chronic Points-of-Departure for Three Organophosphate Pesticides in Rodents



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Benchmark dose-response modeling is superior to identifying a point of departure in risk assessment



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Molecular changes from short-term exposures can be modeled to estimate chronic exposure biological effects





Gene expression can provide a transcriptomic point of departure (TPOD)

Liver transcriptome-based POD from short-term exposures can estimate apical PODs from long-term exposures





OPPs cause acetylcholinesterase inhibition, which was used to set the chronic apical POD (APOD) in rodents





Several genes were considered to have a dose-responsive behavior at 7 days



Diseases	P value
Cancer	2.60E-05
Neurological	
diseases	1.40E-04
Immunological	
diseases	2.50E-04
Inflammatory	
Diseases	2.50E-04



BMDT and BMDLT median levels and ranges suggest relative low variability in the modeled genes

BMDT

BMDLT = TPOD





Dose-responsive genes were mapped to a wide range of GO biological processes (GO: BP)

Number of GO: BP categories for BMDT and BMDLT, respectively.





Comparison between transcriptomic PODs and apical PODs

Chemical	GO:BP	Gene Symbols	BMDT (mg/kg-d)	BMDLT or TPOD (mg/kg-d)	APOD (mg/kg-d)	Ratio APOD: TPOD
Fenthion	multicellular organismal water homeostasis	wfs1;scd1;plec;gba ;cela2a	0.02	0.01	0.03	3.4
Methidathion	G2/M transition of mitotic cell cycle	fbxl21;plk1;nes;ccn a2;birc5	0.29	0.17	1.60	9.4
Parathion	phosphatidylinositol phosphate biosynthetic process	socs2;fam126a;pik 3r3;pik3c2g;socs3	1.54	0.19	0.10	2.0

TPODs, derived from 7-day exposure, were generally more sensitive than APOD derived from acetylcholinesterase inhibition after chronic exposure.



Short-term, molecular-based assays help reduce reliance on chronic animal studies



- Molecular changes can be used to set PODs.
- Liver is a potentially useful surrogate for identifying TPODs.
- This approach is applicable to ecological studies.
- Short-term *in vivo* molecular changes can help translate *in vitro* transcriptomics data to chronic adverse effects.



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Mentor

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<u>Reference</u> Rooney J. et al. Tox 2021 (doi: 10.1016/j.tox.2021.153046)



Questions





Several genes overlapped with known genes associated with organophosphate toxicity



Ache was among the overlapped genes across all organophosphate treatments



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