



# 2763/ P229. Quantifying the DARTable Genome for Prediction of Teratogenic Doses - a case study using retinoic acid pathway-induced developmental toxicity

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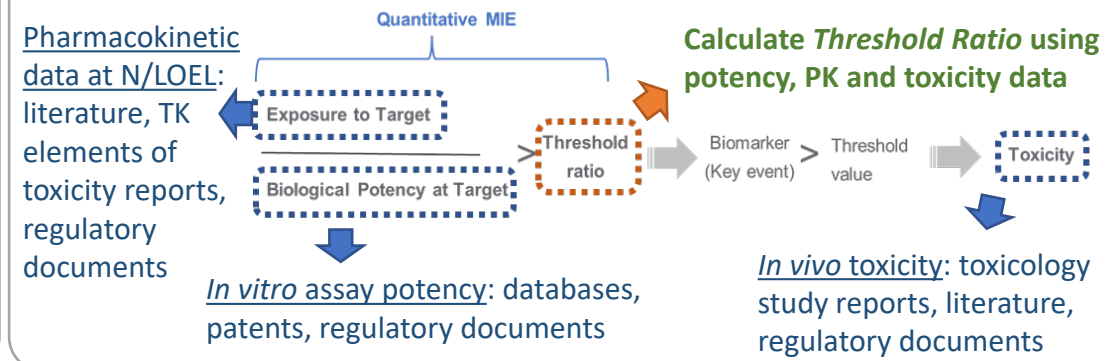
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## 1. Introduction

- The goal of the HESI DARTable Genome Working Group is to build a compendium of quantitative molecular initiating events (MIEs) and key event biomarkers for teratogenicity prediction.
- Our initial case study focused on an AOP framework linking adverse developmental outcome(s) to perturbation of each of the three retinoic acid receptor isotypes: alpha (RARα), beta (RARβ) and gamma (RARγ).
- This investigation focused on the relationship(s) between chemical potency on RAR targets and the quantitative threshold of maternal systemic exposure necessary to produce a teratogenic outcome.

## 2. Building a quantitative model for the DARTable genome: all-trans retinoic acid (ATRA) signaling.

This model can be used to calculate a Threshold Ratio of exposure below (or above) which the likelihood of a chemical causing a toxicity by that AOP is low (or high).



## 3. Reference Compounds.

- For 20 compounds with known retinoid agonist or antagonist activity we compiled RAR potency for each RAR-isotype, including pharmacokinetic and toxicology information for rat and rabbits.
- Here, we present results for 3 retinoids that had complete data in the rat, and 2 of which also had suitable rabbit data.

## 4. Results of Threshold Ratio visualization on 3 retinoid case examples.

- We calculated Threshold Ratios for each RAR isotype utilizing the estimated dam or doe steady-state blood concentration at the NOEL and LOEL.
- Model returns a Threshold Ratio for exposure-biological potency driving developmental toxicity at each RAR isotype.
- An exposure-potency threshold > 2 for RARα or RARγ best characterized LOELs for retinoid developmental toxicity; RARβ did not fit the pattern.

| compound     | receptor | Rat ratio |      | Rabbit ratio |      |
|--------------|----------|-----------|------|--------------|------|
|              |          | NOEL      | LOEL | NOEL         | LOEL |
| alitretinoin | RARα     | 1.3       | 2.9  | nd           | 1.91 |
|              | RARβ     | 0.10      | 0.22 | nd           | 0.14 |
|              | RARγ     | 0.29      | 0.65 | nd           | 0.43 |
| trifarotene  | RARα     | 0.01      | 0.03 | 0.002        | 0.02 |
|              | RARβ     | 0.04      | 0.12 | 0.008        | 0.06 |
|              | RARγ     | 0.69      | 2.1  | 0.126        | 1.04 |
| tazarotene   | RARα     | 0.65      | 13   | nd           | nd   |
|              | RARβ     | 2.8       | 57   | nd           | nd   |
|              | RARγ     | 0.65      | 13   | nd           | nd   |

## 5. Conclusions, lessons learned and next steps

- The model derived DART-predictive exposure-potency Threshold Ratios to predict developmental toxicity; PK data was the largest missing data type.
- Toxic responses considered as thresholds were driven by RARα or RARγ from public data sources; however, RARβ did not fit the pattern.
- Relevant data overall can be unstructured or incomplete and difficult to find, access, or compile into a computable model.
- 'FAIR' data principles are vital to enable sharing of the toxicity, potency and pharmacokinetic data for predictive toxicology.
- It will be informative to determine if patterns for retinoid-based RAR target ratios generalize to chemicals that alter ATRA metabolism.
- The next case study selected for the DARTable genome will focus on Thalidomide-like compounds.