

Chemical and HTS Profiling of 63 Cleft Palate Teratogens from ToxCast

Nancy C. Baker¹, Nisha S. Sipes², Christopher M. Grulke¹, Maxwell C. K. Leung³, Jill A. Franzosa³, Barbara D. Abbott⁴, Richard S. Judson⁵, Thomas B. Knudsen⁵

Lockheed Martin, ²NIH/NIEHS/Division of the National Toxicology Program, ³Oak Ridge Institute for Science and Education, Oak Ridge, Tennessee, 37831, ⁴ National Health and Environmental Effects Research Laboratory,

SNational Center for Computational Toxicology, Office of Research and Development, U.S. Environmental Protection Agency, Research Triangle Park, North Carolina 27711

Nancy Baker I baker.nancy@epa.gov I 919-541-268

Introduction

Cleft palate (CP) is a birth defect that has been linked to both genetic and environmental factors. To characterize the potential molecular targets and biological processes across mechanistically diverse teratogens that cause cleft palate in animal studies, we mined the ToxCast high-throughput screening (HTS) database for chemical-assay-structure relationships.

Objectives:

Step 1) A dataset was created from 63 CP-active (CP(+))

chemicals (chemicals found either in ToxRefDB to cause

CP-inactive (CP(-)) chemicals (chemicals that have been

tested in developmental studies and that showed no CP).

chemical. The arrays consisted of ToxCast gene scores [1]

An array of data elements was constructed for each

Step 2) Weka data-mining software was used to build

models to predict CP activity [3]. The models showed

consistently low performance, even when resampling

techniques were used to address the class imbalance.

clustered the CP(+) set using the same array of data

Ward's method. Several small but clear clusters were

cluster (gene or chemotype) that was common to the

Step 4) We took each of the features identified in Step 3

and found all the chemicals (CP(+) AND CP(-)) that had that

Step 5) We then looked for patterns, either through sorting

Step 6) Starting with the genes found to be common and

informative in each cluster we used the biomedical literature

2. Yang, C., et al. (2015). "New Publicly Available Chemical Query Language, CSRML, To Suppor

3. Hall, M., et al. (2009). "The WEKA Data Mining Software: An Update." SIGKDD Explorations 11(1).

or clustering that would help predict CP activity in this

restricted set of chemicals and features [4].

Step 3) We then focused on the CP(+) chemicals only. We

elements used in the predictive modeling. Clustering was

performed using Partek software and Pearson Dissimilarity,

apparent. For each cluster, we identified the feature of the

and chemotype information [2].

chemicals and informative.

CP or in articles found in the biomedical literature) and 437

- Describe patterns and linkages in the data that identify molecular activity that may be linked to CP.
- Elucidate a plausible AOP based on high-throughput literature mining and analysis.

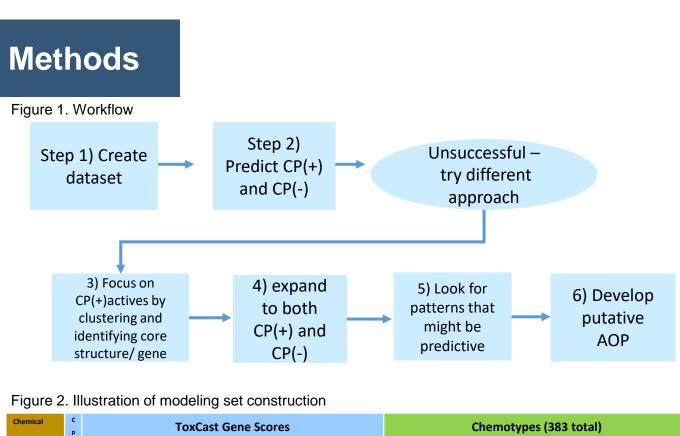


Figure 2. Illustration of modeling set construction

Chemical

C P ToxCast Gene Scores

Chemotypes (383 total)

Abl1 Ache Acp1 Adcy5 Adora1 [...272 Vdr Xbp1 O=P H-S O=C C-N N-C=S [...376 O-S O=S=O types ...]

Chem 1 1 0 2.4 0 0 0 3.4 0.7 1 0 1 0 0 1 0 0

Chem 2 1 0 0 3.1 0.3 0 0.4 1.7 1 0 0 1 0 0 1 0

Chem 3 0 7.2 0 4.4 0 0.3 3.2 5.7 0 1 0 0 0 1 0 0

Results

Chemicals

Gene scores

Chemotypes

Characteristics

Chemotypes

Chemotypes

Characteristics

Chemotypes

Characteristics

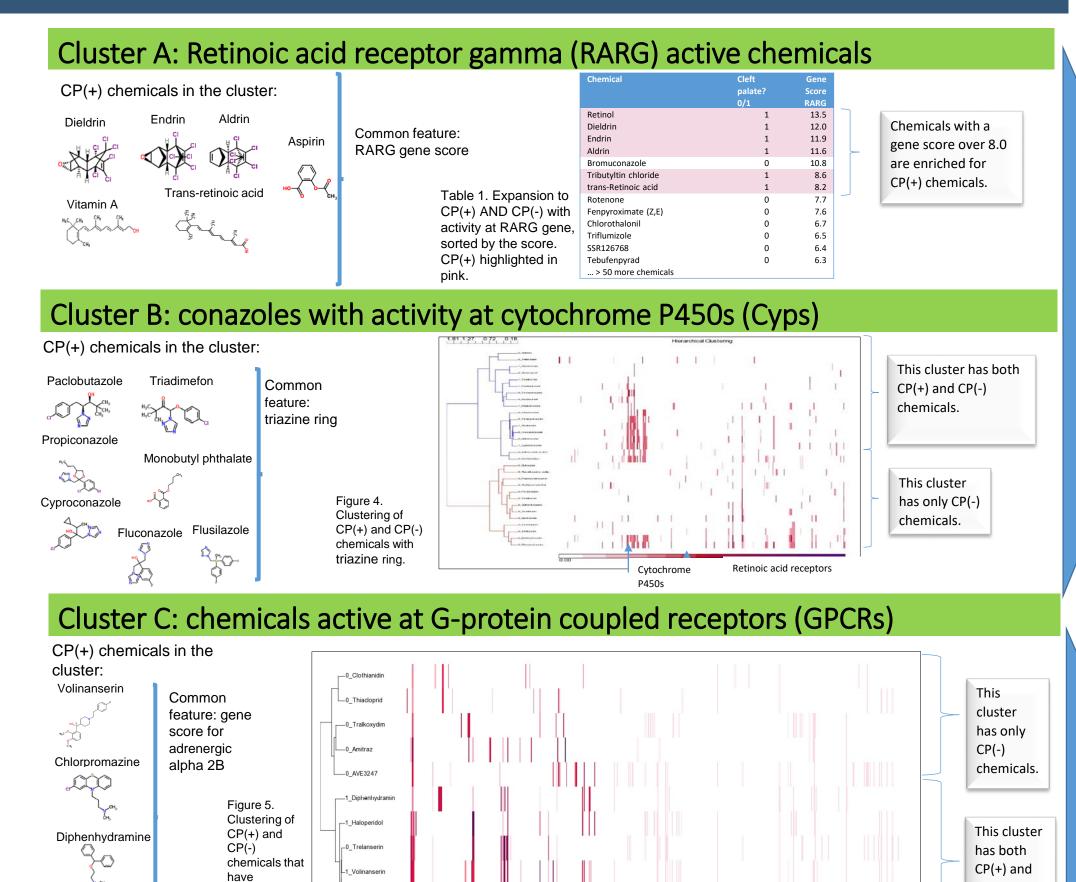
Chemotype

Figure 3. Clustering of CP(+) chemicals by gene scores and structural chemotypes. Scale represents range of gene scores (0-15).

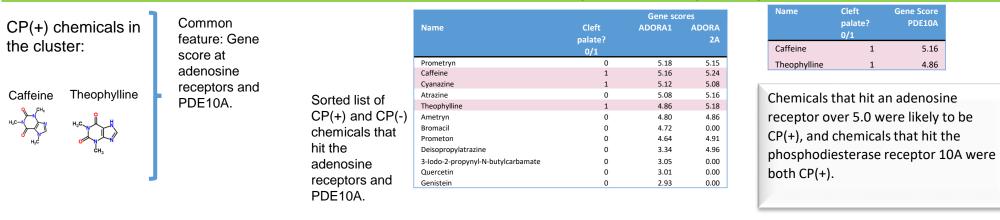
Chemotypes were scaled: 0 (not present) and 3 (present).

DISCLAIMER: does not reflect EPA policy

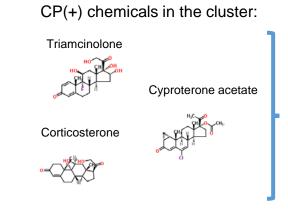
Results



Cluster D: chemicals active at adenosine receptor and phosphodiesterase 10



Cluster E: corticosteroids active at the glucocorticoid receptor



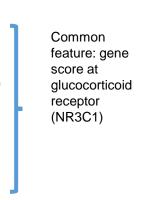
adrenergic

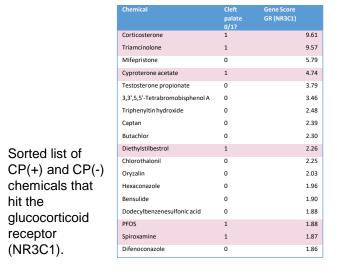
alpha 2B

activity by

gene scores and structural

Haloperido



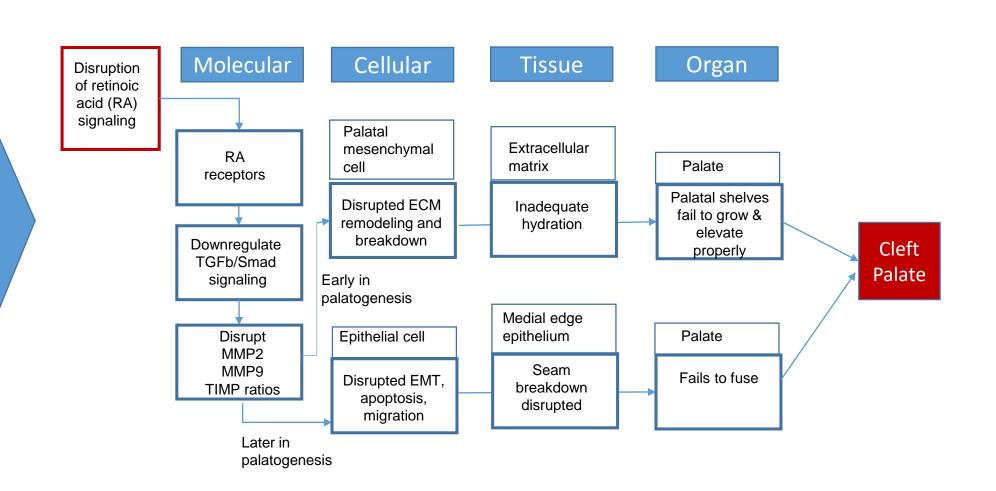


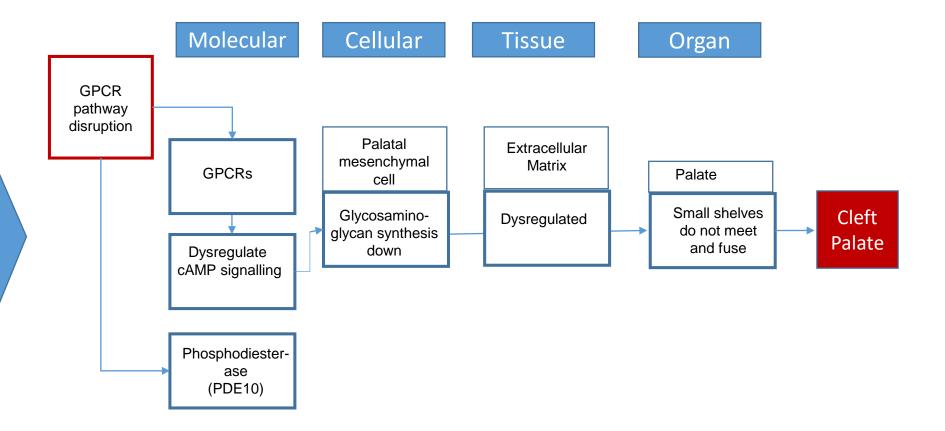
Those chemicals that hit NR3C1 (GR receptor) with a potency over 4.00 have a high likelihood of being CP(+).

CP(-)

chemicals.

Putative Adverse Outcome Pathways (AOPs)





Conclusion

- Through a methodology of zooming in and out around key data points in our dataset constructed from ToxCast gene scores and chemotypes, we were able to find the level where ToxCast gene activity and structure data correlated significantly with CP activity.
- Using this ToxCast gene activity as a possible molecular initiating event and using the biomedical literature to support the relationships, we constructed putative adverse outcome pathways for CP.



