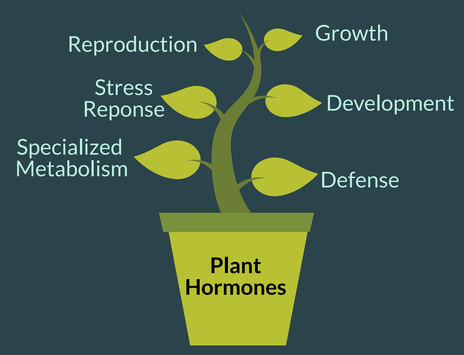
HormonomicsDB: A New Tool for the Analysis of Plant Growth Regulators

Ryland T. Giebelhaus, Lauren A E Erland, and Susan J Murch
Chemistry, University of British Columbia, Syilx Okanagan Nation Territory, Kelowna, BC

ryland.giebelhaus@ubc.ca
hormonomicsdb.com

What is Hormonomics

Hormonomics is the study of the full spectrum of metabolites with hormone function. Hormones are signaling molecules which are found in very low concentrations.



Hormones are transported between cells and tissues to regulate physiological responses.

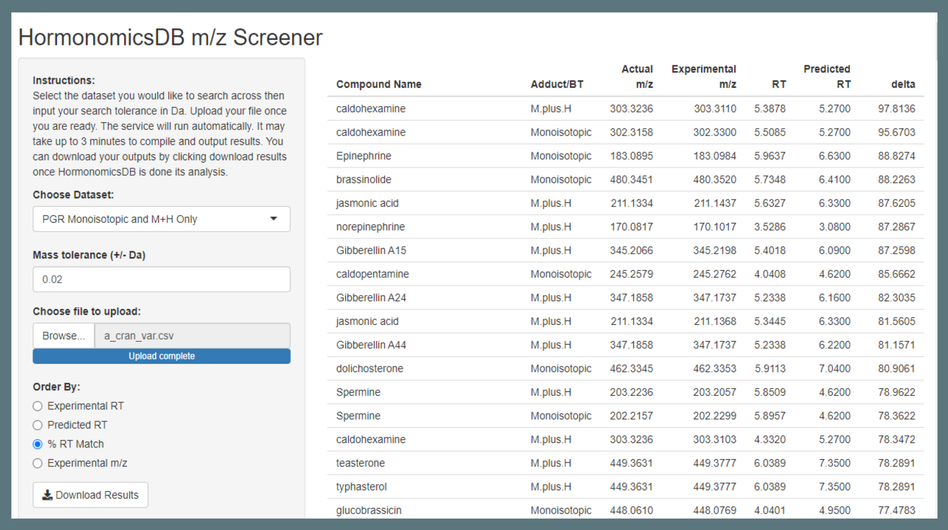
Hormonomics not only looks at hormones in their native state but is also concerned with conjugates, precursors, catabolites, and storage forms.

Initially designed for plants, but it has applications for other species.

HormonomicsDB

Programming and Design:
- Coded in the R computational language (v4.0.3).
- User interface designed with R Shiny (v1.5.0).
- In silico prediction of retention times (RTs) by ReTip.
- Proof of concept using an in house training dataset.
- Output includes 248 real and hypothesized plant hormones.
- Hypothesized metabolites were generated by synthetic biotransformation.

Use:
- **Users can query against the M and M+H, common adducts, and synthetic biotransformations of these hormones in both ESI positive and negative.**
- Upload standard format .csv files with m/z and RTs.
- Select database to query.
- Custom databases can be searched with the new "shell" feature (v1.1).
- User's data is not saved.


HormonomicsDB m/z Screener

Instructions:
Select the dataset you would like to search across then input your search tolerance in Da. Upload your file once you are ready. The service will run automatically. It may take up to 3 minutes to compile and output results. You can download your outputs by clicking download results once HormonomicsDB is done its analysis.

Choose Dataset: PGR Monoisotopic and M+H Only

Mass tolerance (+/- Da): 0.02

Choose file to upload: Browse... a_cran_var.csv — Upload complete

Order By:
- Experimental RT
- Predicted RT
- % RT Match
- Experimental m/z

Download Results

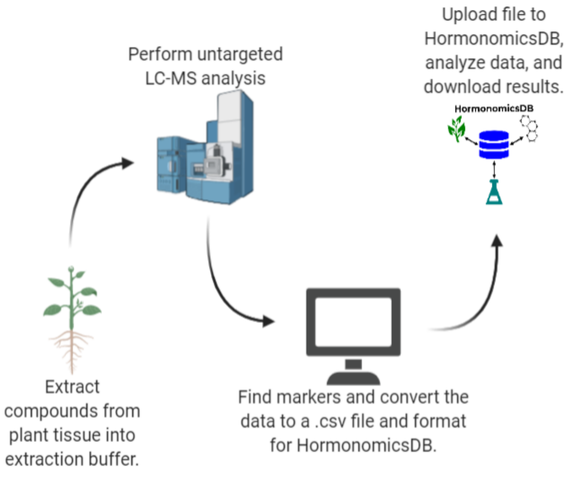
Compound Name	Adduct/BT	Actual m/z	Experimental m/z	RT	Predicted RT	delta
caldohexamine	M.plus.H	303.3236	303.3110	5.3878	5.2700	97.8136
caldohexamine	Monoisotopic	302.3158	302.3300	5.5085	5.2700	95.6703
Epinephrine	Monoisotopic	183.0895	183.0984	5.9637	6.6300	88.8274
brassinolide	Monoisotopic	480.3451	480.3520	5.7348	6.4100	88.2263
jasmonic acid	M.plus.H	211.1334	211.1437	5.6327	6.3300	87.6205
norepinephrine	M.plus.H	170.0817	170.1017	3.5286	3.0800	87.2867
Gibberellin A15	M.plus.H	345.2066	345.2198	5.4018	6.0900	87.2598
caldopentamine	Monoisotopic	245.2579	245.2762	4.0408	4.6200	85.6662
Gibberellin A24	M.plus.H	347.1858	347.1737	5.2338	6.1600	82.3035
jasmonic acid	M.plus.H	211.1334	211.1368	5.3445	6.3300	81.5605
Gibberellin A44	M.plus.H	347.1858	347.1737	5.2338	6.2200	81.1571
dolichosterone	Monoisotopic	462.3345	462.3353	5.9113	7.0400	80.9061
Spermine	M.plus.H	203.2236	203.2057	5.8509	4.6200	78.9622
Spermine	Monoisotopic	202.2157	202.2299	5.8957	4.6200	78.3622
caldohexamine	M.plus.H	303.3236	303.3103	4.3320	5.2700	78.3472
teasterone	M.plus.H	449.3631	449.3777	6.0389	7.3500	78.2891
typhasterol	M.plus.H	449.3631	449.3777	6.0389	7.3500	78.2891
glucobrassicin	Monoisotopic	448.0610	448.0769	4.0401	4.9500	77.4783

Screenshot of the tool showing the input panel and the matches to the monoisotopic and M+H dataset. Data is sorted by match to predicted retention time.

Hormonomics Workflow

The Hormonomics workflow was designed to be simple and reproducible across laboratories. A standard C18 column with a linear ACN and acidified water gradient is used.

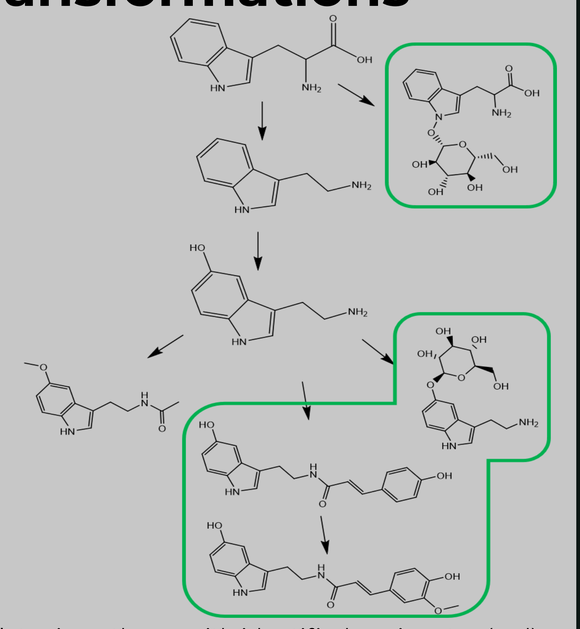
Data is then processed using HormonomicsDB
.



Synthetic Biotransformations

To assist in hypothesis generation, datasets can be searched for synthetic transformations of the compounds in HormonomicsDB. This is performed by searching for the m/z resulting from (de)methylation, (de)amination, (de)hydroxylation, (de)glycosylation reactions.

Limitations: RTs cannot be predicted and some transformations are not feasible



Melatonin pathway with identified conjugates (red). HormonomicsDB could help uncover more conjugates.

Validation and Applications

A dataset from the untargeted metabolomics experiment reported in Brown et al. (2012) was loaded into HormonomicsDB returning a >100% match rate. This could be attributed to redundant compounds, duplicate hits, non feasible biotranformations, and noise.

The biotranformation approach in HormonomicsDB provides insight into potential new plant hormone conjugates, leading to hypothesis generation.

The ability to use the tool as a shell allows for the potential to use HormonomicsDB for a wide range of applications.

1) Paolo Bonini, Tobias Kind, Hiroshi Tsugawa, Dinesh Kumar Barupal, and Oliver Fiehn Analytical Chemistry 2020 92 (11), 7515-7522.
2)Brown PN, Turi CE, Shipley PR, Murch SJ Planta Med. 2012;78(6):630-640.
3) Erland, L.A.E., Turi, C.E., Saxena, P.K., Murch SJ Metabolomics 16, 62 (2020).
4) Šimura J, Antoniadi I, Široká J, Tarkowská D, Strnad M, Ljung K, Novák O. Plant Physiol. 177(2):476-489 (2018).