

A metabolomic approach to evaluate the attractant and phagostimulant mechanism of different yeast species to Drosophila suzukii

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Introduction



Since 2011 the invasive species Drosophila suzukii has affected the cultivation of soft and stone fruits in South Tyrol causing important harvest losses. Up until today the chemical control available is not enough efficient.



Yeasts have been shown to influence the fitness and be a primary food source in the nutrition of many Drosophila species.

The project Dromytal has the aim of developing an "attract&kill" formulation as a control strategy against Drosophila suzukii based on the association of an attractant yeast and a last generation insecticide. The yeasts should not only attract the insect, but also favor phagostimulant activity in the flies to promote the insecticide ingestion on the targeted treated surfaces enhancing insect mortality.

Materials and methods

1) Yeast sample preparation



Four nutritionally relevant yeast species (H.uvarum, I.terricola, M.pulcherrima, S.cerevisiae) have been chosen based on previous studies. Yeast cultures were inoculated in liquid growth media for 30 hours.

2) Extraction of intracellular metabolites



After quenching with cold methanol, intracellular metabolites were extracted using organic solvent (ACN:MeOH:H2O, 4:4:2)

3) Analysis of yeast metabolites

Hydrophilic interaction liquid chromatography coupled with quadrupole/time-of-flight mass spectrometry (HILIC-QTOFMS) was used to detect diverse chemical compound classes using an "untargeted approach".

Results

Untargeted analysis of intracellular metabolites of four yeast species (H.uvarum 3.4, I.terricola 2.1, M.pulcherrima 3.2, S.cerevisiae 288) using HILIC-QTOFMS



HEAT MAP

131 distinct metabolites have been annotated and/or identified.



PLSDA analysis

Discrimination between the four different species on the first two components.

The most significant features for the discrimination of samples are dipeptides, carnitines and quaternary



veast

ammonium salts.



ChemRICH analysis of H.uvarum versus S.cerevisiae

Significantly impacted metabolite clusters have been found: in H.uvarum dipeptides increase, whereas basic amino acids, glycerophosphocholines and carnitines decrease (color code: red = increased, blue = decreased).



In summary, we found significant global metabolic alterations in the different yeast species and were able to detect significantly altered metabolite classes (dipeptides, carnitines).

Aknowledgements

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