Application of DART-9.4T FT ICR MS to discovery of geo-location origin markers in small brown planthopper (*Laodelphax striatellus*)

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Overview

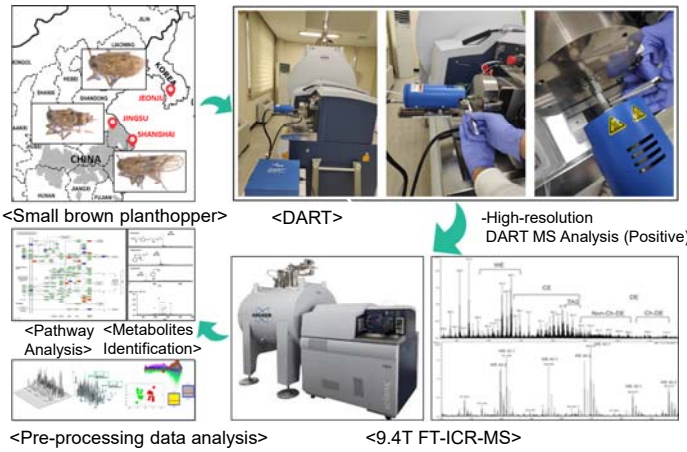
The small brown planthopper (SBP) (*Laodelphax striatellus*) is one of the most destructive pests of rice. It is widespread in countries such as Korea and China. We conducted metabolic studies to investigate the metabolic mechanisms involved in regional differences between planthoppers. Direct Analysis in Real-Time Mass Spectrometry (DART-MS) promises to be a powerful analytical technique for the high-throughput metabolome analysis of insects. In this study, we used DART MS/MS to find tracers related to the origin of SBP in Chinese and domestic collections. We analyzed 80 SBP samples from various regions (n=5). The use of helium gas at 200℃ was observed to allow deprotonation and detected m/z ~1,500 in the previously in positive ion mode. Our results suggest that 4 candidates were selected and identified using principal component analysis (PCA) and partial least squares-discriminate analysis (PLS-DA). This research demonstrates that DART MS/MS can be a useful technology for distinguishing SBP from various regions.

Key words: Small brown planthopper, DART-MS/MS, Metabolomic fingerprinting

Introduction

1. Small brown planthopper, *Laodelphax striatellus* (fallen) occur in Last Asia, causing severe losses in rice, wheat, and other economically important crops. This species is known as a vector insect of rice stripe virus.
2. To investigate the geographic variation, we compared the mechanism of small brown planthopper under various constant regimes among three populations collected from Jeonju, Jingsu, and Shanghai.
3. Direct analysis in real time mass spectrometry (DART-MS/MS), allows the analysis of ordinary objects without complicated sample preparation and time-consuming chromatographic separation.
4. In this experiment, the ultrafast metabolome profiling analysis using FT-ICR MS was applied. Metabolomics can quantify the phenotype.

Materials and Methods



Conclusions

1. PCA and PLS-DA analysis showed a difference between small brown planthopper from Korea(Jeonju) and China (Jingsu and Shanghai) and a quantitative and qualitative analysis results were obtained from the high resolution & high accurate mass spectrometry analysis.

2. In this experiment, we analyzed the different intensity peaks that show a quantitative difference the small brown, and identified with $C_{32}H_{47}N_3$, $C_{13}H_{22}O_2$, $C_{12}H_{30}N_{14}$ and $C_{30}H_{43}O_3$.

3. In future studies,
   - More metabolites needs to be identified
   - A comparative metabolome analysis
   - Needs to pathway analysis for biological interpretation.

REFERENCE

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Results

1. PCA analysis

● Jeonju vs Jingsu

● Jeonju vs Shanghai

● Jeonju vs Shanghai

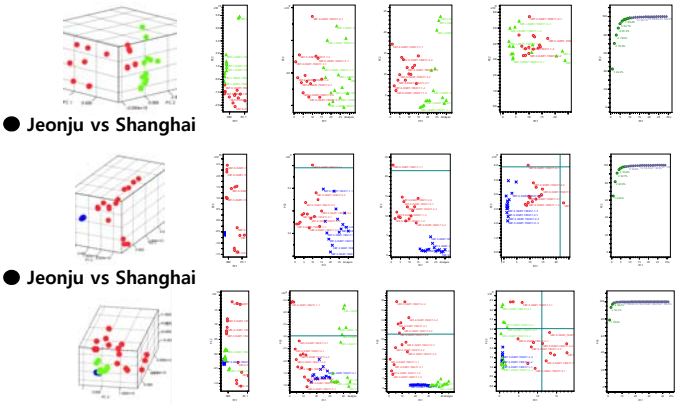

Fig. 2. PCA analysis. Jeonju (Red) vs Jingsu (Green) vs. Shanghai (Blue) A: 3D model, B: Scores and loadings, C: Distance to model, D: hoteling T2, E: Influence, F: Explained variance.

2. PLS-DA analysis

● Jeonju vs Jingsu

● Jeonju vs Shanghai

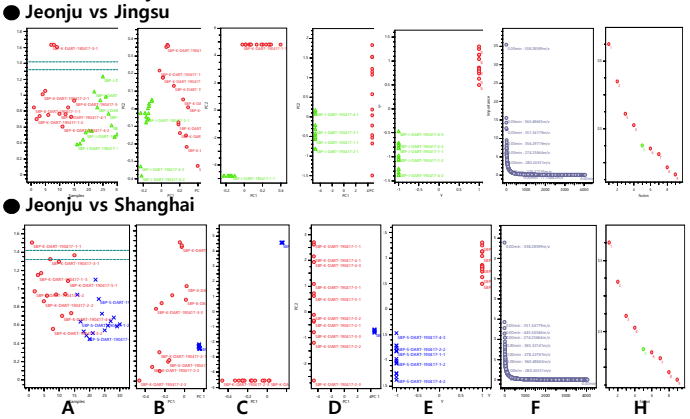

Fig. 3. PLS-DA analysis. Jeonju (Red) vs Jingsu (Green) vs. Shanghai (Blue). A: Distance to model, B: T scores, C: T/U scores, D: U scores, E: Y/Y², F: X loadings, G: variable importance, H: Factor.

3. Volcano plot

● Jeonju vs Jingsu

● Jeonju vs Shanghai

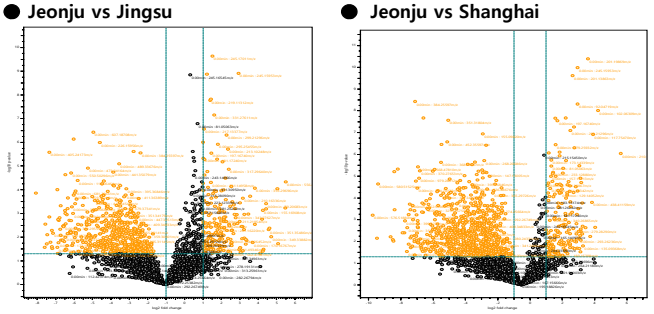

Fig.4. Volcano plot representation of t-test (P<0.05, orange dots ; 4,050) results comparing small brown planthopper from Jeonju vs Jingsu vs Shanghai group.

4. DART-MS/MS

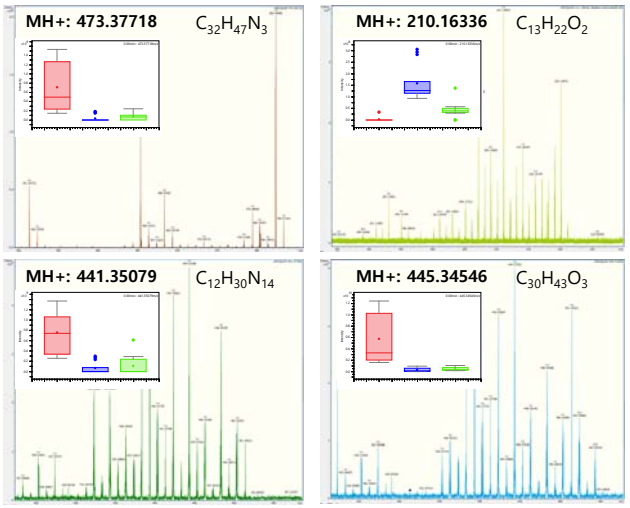

Fig.5. Identification of small brown planthopper by DART-MS/MS.

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