



LC/HRMS-BASED METABOLIC FINGERPRINTING AND MULTIVARIATE ANALYSIS IN AUTHENTICATION OF MEAT

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INTRODUCTION

Food authentication is a rapidly growing field due to increasing public awareness concerning food quality and safety. In recent years, food frauds and adulterations have increased significantly. This practice is motivated by fast economical gains and has an enormous impact on public health. The mislabeling of meat species can expose consumer to risks associated with meat allergies, and can lead to economic losses. The accidental or intentional blending of meat from different species is becoming a worldwide problem. The development of advanced analytical methods is crucial to enable efficient testing for food authenticity. High-resolution mass spectrometry based metabolic fingerprinting combined with chemometrics represents a valuable tool for detection of food adulterations.

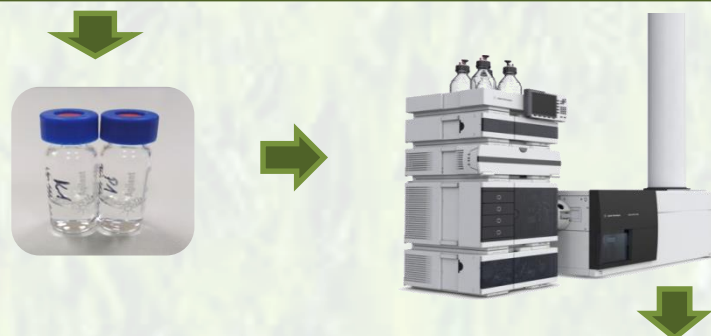
In this work, we studied by means of liquid chromatography - high resolution mass spectrometry the metabolic profiles of meat species, which are the most prone to adulteration. Liquid chromatography coupled to quadrupole time-of-flight mass spectrometry was employed for the analysis of meat extracts and metabolic fingerprints were obtained.

METHODS

Sample preparation

Five raw chicken meat samples and five raw guinea fowl meat samples from different farms were purchased from retailers. All samples were cut into thin pieces and boiled separately in 100 °C water for 30 min. The scheme of the sample preparation, LC-QTOF-MS parameters and chemometric techniques used are presented below.

1. Weight 0,2 g of cooked meat.
2. Homogenize with 1 ml mixture of methanol and ethanol (1:1 v/v).
3. Freeze suspensions in -20 °C for 15 min and centrifuge for 5 min at 13400 rpm.
4. Filter through syringe filters (0.2µm,4mm)



LC-QTOF-MS parameters

Samples were analysed using Agilent HPLC 1290 series coupled to 6550 LC/QTOF mass spectrometer equipped with Jet Stream ESI ion source. Mobile phase consisted of 0.1% FA (A) and 0.1% FA in acetonitrile. Separation was carried out using Agilent Zorbax Eclipse C18 RRHT column (2.1x100mm, 1.8 µm).

Chemometric techniques

Compounds were extracted using Mass Hunter find by molecular feature algorithm. For mass profiling, statistical and chemometric analysis, Mass Profiler Professional and SIMCA were used.

RESULTS

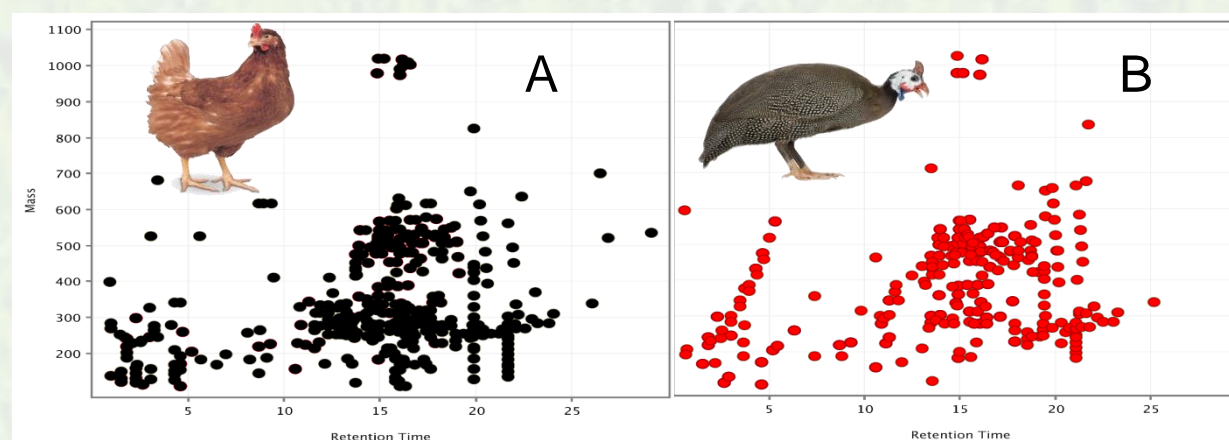


Figure 1. Metabolite mass vs retention time graphs for entities characteristic to chicken meat (A) and guinea fowl meat (B).

PCA and PLS-DA were used to visualise grouping of samples and discriminate meats (Fig.2).

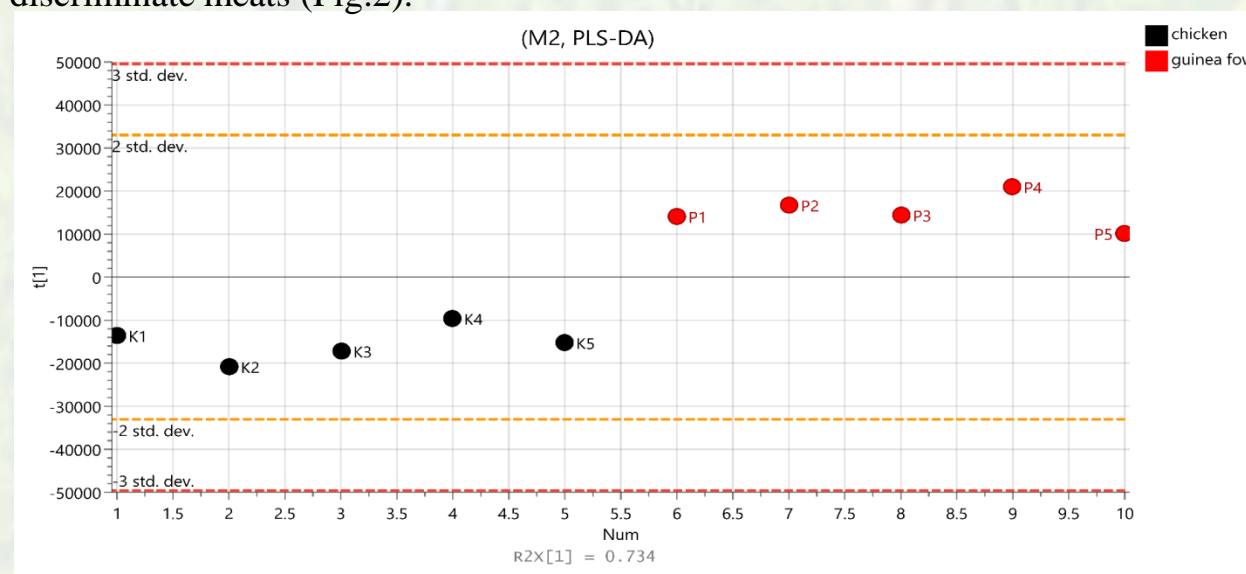


Figure 2. PLS-DA score plot for guinea fowl and chicken meat extracts.

CONCLUSION

The results of mass profiling and multivariate analyses of the acquired high-resolution mass spectrometry (HRMS) data allowed the determination of metabolomic features differentiating guinea fowl meat from chicken meat indicating that LC/MS-based metabolomic fingerprinting can be used for the quality control and authentication of these products as well as for the detection of adulterations.

Mass profiling was used in order to determinate metabolomic features differentiating the guinea fowl meat from chicken meat. The obtained results of MS scan analyzes were processed in order to identify differentiating ions (Fig. 1). As a example, LC-QTOF-MS extracted ion chromatograms of m/z 297.0939 ion present in both types of meat, extracted ion chromatograms of m/z 356.7405 ion specific for chicken meat and extracted ion chromatograms of m/z 355.1369 ion specific for guinea fowl meat are shown in Fig.3.



Figure 3. LC-QTOF-MS/MS extracted ion chromatograms. EIC of m/z 297.0939 confirmed in both types of meat, EIC of m/z 356.7405 confirmed in chicken meat only, and EIC of m/z 355.1369 confirmed in guinea fowl meat only.