Claims

1. A method of identifying a plurality of lipids in a sample that is profiled using a combined Liquid Chromatography-Mass Spectrometry (LC-MS) technique, comprising the steps of:

a) providing a list of Liquid Chromatography-Mass Spectrometry (LC-MS)-based mass features;

b) deconvoluting said list of LC-MS-based mass features;

c) inferring daughter ions from the deconvoluted list of LC-MS-based mass features;

d) identifying one or more parental exact masses from the inferred daughter ions;

e) scoring each of the one more parental exact masses based on the inferred daughter ions;

f) determining characteristic mass features in response to the scoring of each of the one or more parental exact masses; and

g) determining each of the plurality of lipids based on the characteristic mass features thereof,

wherein step b) comprises deconvoluting intensity mass features comprising high intensity mass features, low intensity mass features or combinations thereof in the list of LC-MS-based mass features to separate the LC-MS-based mass features into groups, each of the groups arising from a same lipid specie.

2. The method according to claim 1, further comprising the step of validating the inferred daughter ions and/ or the plurality of lipids.

3. The method according to claim 1 or 2, wherein step b) deconvoluting the intensity mass features to separate the LC-MS-based mass features into groups reduces false lipid identification of each of the plurality of lipids, and wherein the false lipid identification comprises a false positive, a false negative, or a combination of false positive and false negative.

4. The method according to any one of claims 1-3, wherein step c) comprises inferring common daughter ions, specific daughter ions or combinations thereof.

5. The method according to any one of claims 1-4, wherein step c) further comprises independently classifying common daughter ions and specific daughter ions as dominant and non-dominant daughter ions.

6. The method according to any one of claims 1-5, further comprising the step of preparing the sample comprising the plurality of lipids, prior to step a).

7. The method according to any one of claims 1-6, wherein deconvoluting the list of LC-MS-based mass features of step b) comprises the steps of:

b1) providing quality control (QC) samples at regular intervals, wherein the QC samples are selected to be representative of a type of the sample being profiled using the combined LC-MS technique;

b2) providing a model of intensity drift based on the LC-MS-based mass features in the QC samples; and

b3) correcting the intensity mass features of said list of LC-MS-based mass features using the model of step b2).

8. The method according to claim 7, wherein step b2) comprises performing a regression procedure on the LC-MS-based mass features.

9. The method according to claim 8, wherein step b2) comprises performing the regression procedure on the LC-MS-based intensity mass features of the QC samples.

10. The method according to claim 8 or 9, the regression procedure comprises one or more of a linear regression, a non-linear regression, or a 'LOcal regrESSion' (LOESS).

11. The method according to any one of claims 1-10, wherein deconvoluting the list of LC-MS-based mass features comprises reconstructing individual spectra of each of the plurality of lipids.

12. The method according to claim 11, wherein reconstructing individual spectra of each of the plurality of lipids comprises the step of clustering the LC-MS-based mass features according to locations and intensity profiles along a retention time (RT) dimension to reconstruct the individual spectra.

13. The method according to claim 12, wherein inferring the daughter ions comprises the step of matching mass-to-charge (m/z) values of the reconstructed individual spectra with a database to obtain a list of candidate exact-masses from which the one or more parental exact masses will be extracted.

14. The method of claim 13, wherein the database comprises an in-source fragment database, a specific adduct database or a combination thereof.

15. The method according to claim 14, wherein inferring the daughter ions further comprises a presumptive screening step to derive a list of preferred ions for each lipid class.

16. The method according to claim 15, wherein the presumptive screening step comprises iteratively assigning individual m/z values in each spectrum with a list of product ions to account for the inferred daughter ions absent in the database.

17. The method according to any one of claims 13-16, wherein identifying the one or more parental exact masses further comprises the step of grouping all candidate exact masses in the list of candidate exact-masses into one or more groups of candidate exact-masses, each candidate exact-mass within a group having an exact-mass within an average spacing of less than two-times machine resolution of every candidate exact-mass in the group.

18. The method according to any one of claims 15-17, wherein step e) scoring each of the one or more parental exact masses based on the inferred daughter ions comprises calculating a feature score based on the database m/z matching step and the presumptive screening step.

19. The method according to any one of claims 1-18, wherein determining each of the plurality of lipids based on characteristic mass features comprises the step of matching unique masses with an organism-specific mass database.

20. The method according to claim 2, wherein validating a lipid of the plurality of lipids comprises confirming that an ion annotation of a most intense mass feature corresponds to one of a preferred product-ion for a lipid class to which the lipid belongs.

21. The method according to claim 2, wherein the step of validating each of the plurality of lipids comprises the step of selecting a lipid with a best parental exact mass score.

22. The method according to claim 2, wherein validating each of the plurality of lipids, comprises identifying each lipid separately using a suitable method.

23. The method according to claim 22, wherein the suitable method is a tandem mass spectroscopy (MS^2) technique.

24. The method according to any one of claims 1-23, wherein the inferred daughter ions comprise one or more dominant daughter ions.

25. Use of the method of any one of claims 1-24 to identify a plurality of lipids undergoing in-source fragmentation.