METWARE BIO

Quantitative Lipidomics

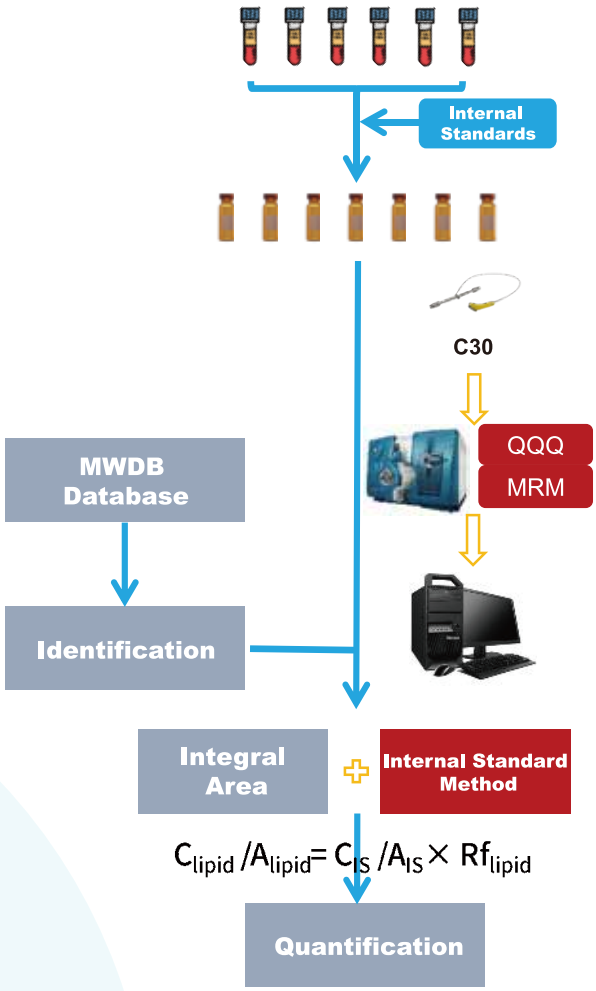
Technology introduction

Quantitative Lipidomics is a high-throughput quantitative lipidomics approach to enable the simultaneous identification and absolute quantification of thousands of lipids in a single experiment. At Metware, our Quantitative Lipidomics approach stands out from many others with features such as:

Using high-resolution mass spectrometers to allow unbiased collection of MS/MS spectrum data;

Highly curated in-house metabolomics database (MWDB) that provides accurate identification of over 3000 lipids;

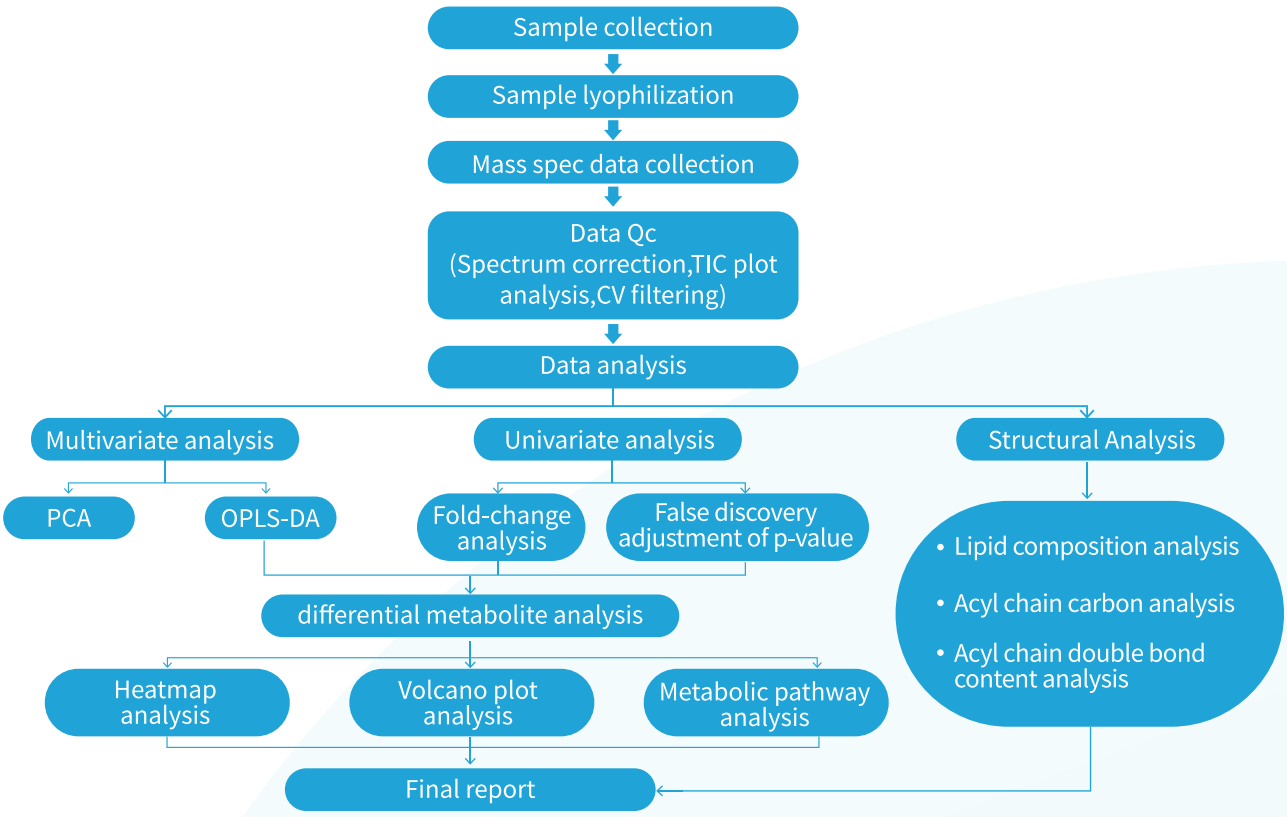
Using MRM analysis from QQQ to accurately quantify metabolites in each sample.



List of Lipids

Number of Lipids		
Class I	Class II	Number
Fatty acyls (FA)	CAR FFA Eicosanoid FAHFA	281
Glycerolipids(GL)	DG、DG-O MG TG、TG-O MGDG DGD	1056
Glycerophospholipids(GP)	LPC、LPC-O LPE、LPE-P LPG LPS PC、PC-O PE、PE-P、PE-O PG PS LPI PI LPA PA PMeOH BMP HMBP LNAPE	1234
Sphingolipids(SL)	SPH CerP HexCer SM Cer、Cert	298
Sterol lipids(ST)	Cho CE BA CASE	128
Prenol lipids(PR)	CoQ	3
Total		3000+

Project workflow



Analysis content display

Sample Correlation Analysis

Intuitively see the correlation of metabolite contents between samples and sample groups.

In this plot, the labels along the left and the diagonal represent sample names. The color boxes represent Pearson correlation coefficients. The darker the red, the stronger the correlation and the darker the blue, the weaker the correlation.

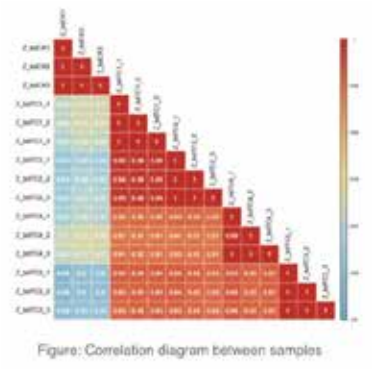
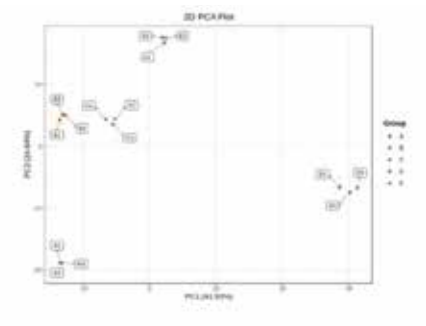


Figure: Correlation diagram between samples

Principal Component Analysis (PCA)

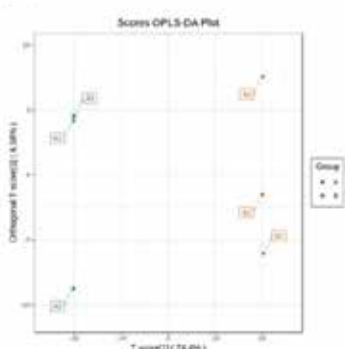
Quickly determine the variance between samples and sample groups.

In PCA plot, each dot represents a sample and samples in the same group are shown with the same color. PC1 and PC2 represent the first and second principal component, respectively. Percentage value describe how well a principal component can explain the sample variance.



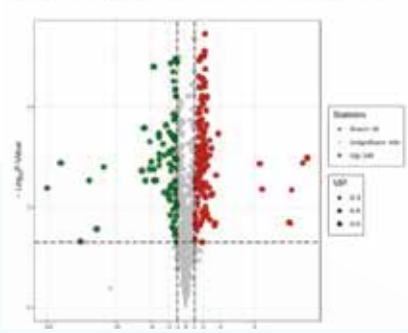
Orthogonal Projections to Latent Structures Discriminant Analysis (OPLS-DA)

OPLS-DA is a statistical model to find which variables are driving the difference between two groups. In this plot, the X-axis represents the predicted principal component and measures the difference between groups. The Y-axis represents the orthogonal principal component and measures the difference within a group. Percentage value indicates the degree to which the component explains the data set. Each dot in the figure represents a sample, samples in the same group are shown with the same color.



Volcano plot

A visual representation of relative differences and the statistical significance of metabolites between two samples or groups. Each point in the volcano plot represents a metabolite with green points represent significantly down-regulated metabolites, red points represent significantly up-regulated metabolites, and gray points represent detected metabolites with no significant differences. The X-axis represents the log2(fold-change) value of metabolites between two groups. The Y-axis represents the level of significance (-log10(p-value)). The size of each dot represents the Variable Importance in Projection (VIP) value.



Chord Plot

This plot captures the correlation of a metabolite with other metabolites. In this figure, the outermost layer shows the differential metabolites. The second layer shows log2FC value as circles and the circle size proportional to FC values. The color for the first and second layer represent different metabolite classification. The chords in the inner most layer reflect the Pearson correlation between the connected metabolites. Red chords represent positive correlation and the blue chords represent neg.

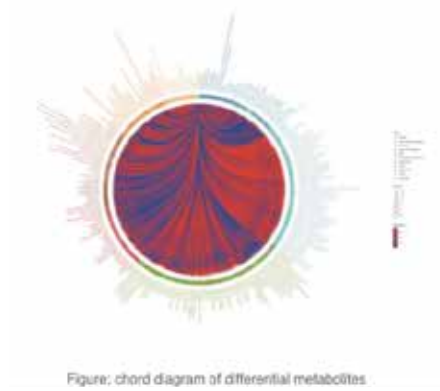


Figure: chord diagram of differential metabolites

Venn diagram

It is a powerful way to depict differential metabolites that are unique or shared between comparisons. Each enclosure represents a comparison group. The number in overlapped parts represent the number of common differential metabolites between comparison groups, and the number in non-overlapped parts represents the number of unique differential metabolites.

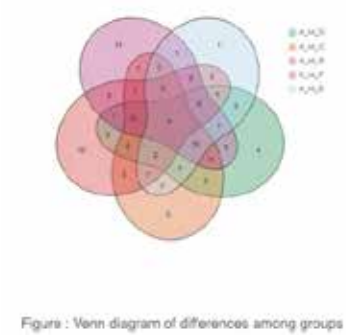


Figure : Venn diagram of differences among groups

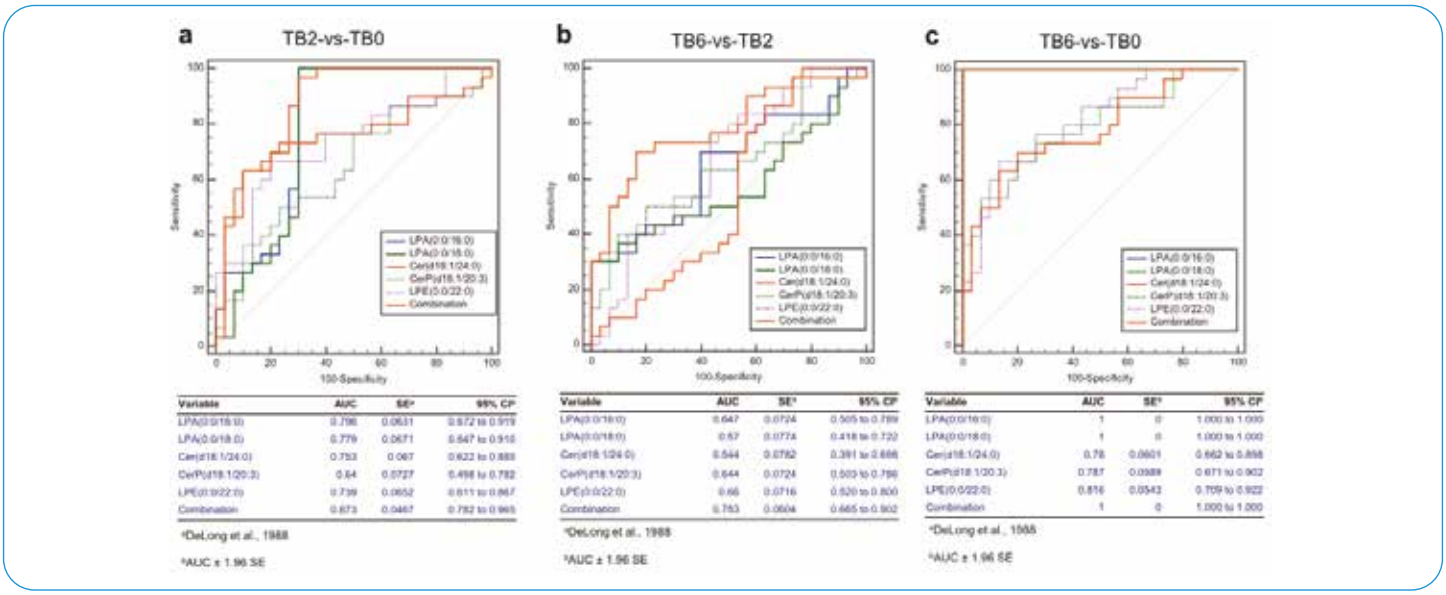
APPLICATIONS

1.Research in Biomarker Screening

Article Spotlight: Novel therapeutic evaluation biomarkers of lipid metabolism targets in uncomplicated pulmonary tuberculosis patients

Currently, the management of pulmonary tuberculosis (TB) lacks potent medications and accurate efficacy evaluation biomarkers.In view of the fact that the host lipids are the important energy source of Mycobacterium tuberculosis(Mtb), UPLC-MS/MS based on lipid metabolism was used to monitor the plasma lipid spectrum of TB patients from the initial diagnosis to cured. The analysis showed that TB patients presented aberrant metabolism of phospholipids, glycerides, and sphingolipids. Upon the treatment, the abnormal expression of Cer (d18:1/24:0), CerP (d18:1/20:3), LPE (0:0/22:0), LPA (0:0/16:0), and LPA (0:0/18:0) in TB patients were gradually normalized, indicating that the intervention of lipid metabolism could block energy metabolism and inhibit the cell wall synthesis ofMtb. Furthermore, the increase in ceramide (Cer) levels could promote autophagosome–lysosome fusion. LPA (0:0/16:0) and LPA (0:0/18:0) had a great potential in the early diagnosis (both sensitivity and specificity were 100%) and efficacy evaluation (both sensitivity and specificity were 100%) of TB, indicating that the above lipid metabolites could be used as potential biomarkers for TB.

Jia-Xi Chen *et al.* Novel therapeutic evaluation biomarkers of lipid metabolism targets in uncomplicated pulmonary tuberculosis patients. Signal Transduction and Targeted Therapy (2021) 6:22.

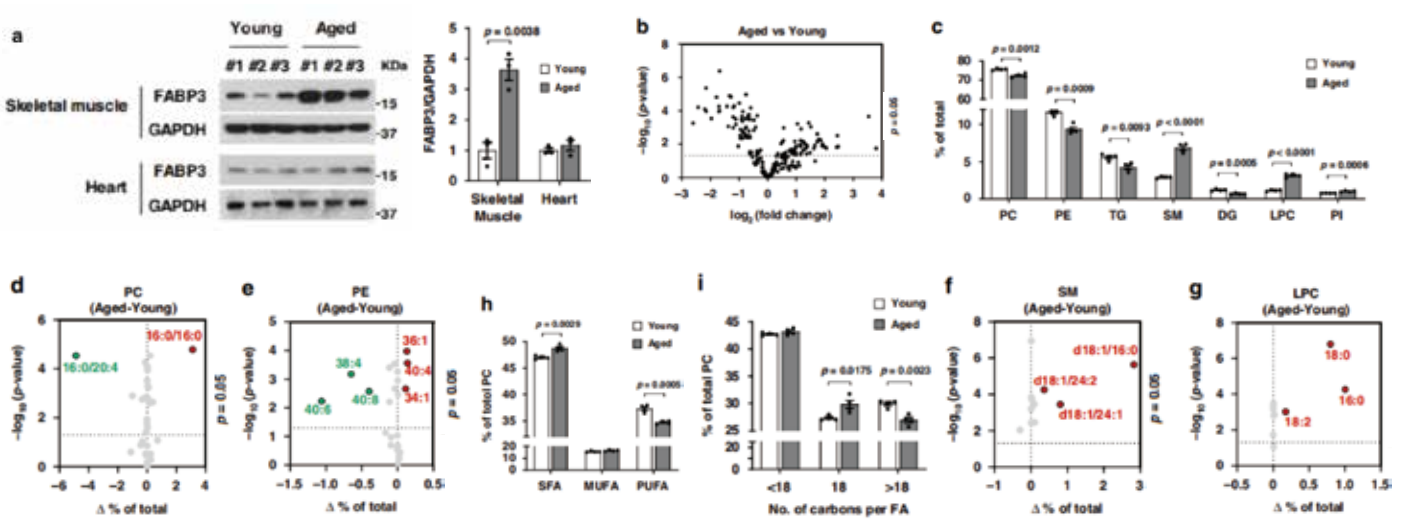


2.Explaining the mechanism of disease development

Article Spotlight: FABP3-mediated membrane lipid saturation alters fluidity and induces ER stress in skeletal muscle with aging

Sarcopenia is characterized by decreased skeletal muscle mass and function with age. Aged muscles have altered lipid compositions; however, the role and regulation of lipids are unknown. Here we report that FABP3 is upregulated in aged skeletal muscles, disrupting homeostasis via lipid remodeling. Lipidomic analyses reveal that FABP3 overexpression in young muscles alters the membrane lipid composition to that of aged muscle by decreasing polyunsaturated phospholipid acyl chains, while increasing sphingomyelin and lysophosphatidylcholine. FABP3-dependent membrane lipid remodeling causes ER stress via the PERK-eIF2α pathway and inhibits protein synthesis, limiting muscle recovery after immobilization. FABP3 knockdown induces a young-like lipid composition in aged muscles, reduces ER stress, and improves protein synthesis and muscle recovery. Further, FABP3 reduces membrane fluidity and knockdown increases fluidity in vitro, potentially causing ER stress. Therefore, FABP3 drives membrane lipid composition-mediated ER stress to regulate muscle homeostasis during aging and is a valuable target for sarcopenia.

Seung-Min Lee,et al. FABP3-mediated membrane lipid saturation alters fluidity and induces ER stress in skeletal muscle with aging. NATURE COMMUNICATIONS (2020) 11:5661.



Sample requirements

Sample type	sample	Recommended sample	Minimum sample	Biological duplication
liquid	Plasma, serum, hemolymph, milk, egg white	100 μL	20μL	human>30 animal>8
	Cerebrospinal fluid, tear fluid, interstitial fluid, uterine fluid, pancreatic fluid and bile, pleural effusion, follicular fluid, corpse fluid, saliva, sputum	100 μL	20μL	human>30 animal>8
	Seminal plasma, amniotic fluid, prostate fluid, rumen fluid, respiratory condensate, gastric lavage fluid, alveolar lavage fluid, urine, sweat	500 μL	100 μL	human>30 animal>8
tissue	Animal tissue, placenta, thrombus, fish skin, mycelium, nematode, slime mold protoplasm, cyanobacteria	100 mg	20 mg	human>30 animal>8
	Whole body, aircraft (wings), pupae	500 mg	20 mg	animal>8
	Zebrafish organs, insect organs	20	10	animal>8
cell	Adherent cells	1*10^6	5*10^5	human>30 animal>8
	Escherichia coli and other microorganisms	1*10^10	5*10^8	samples>8
feces	Feces, iIntestinal contents	200 mg (Wet weight)	50 mg (Wet weight)	human>30 animal>8

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