

Aplicação de técnica de metabolômica ao estudo de alimentos

Edy Sousa de Brito




FORMAÇÃO ACADÊMICA

- **1998: Bacharel em Química Industrial pela UFPB**
- **1993: Mestrado em Ciência e Tecnologia de Alimentos (UFPB)**
- **2000: Doutorado em Tecnologia de Alimentos (Unicamp)**

- **2001: Pesquisador Embrapa Agroindústria Tropical (Fortaleza-CE)**

**de Brito, Edy
Sousa**

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ResearcherID:

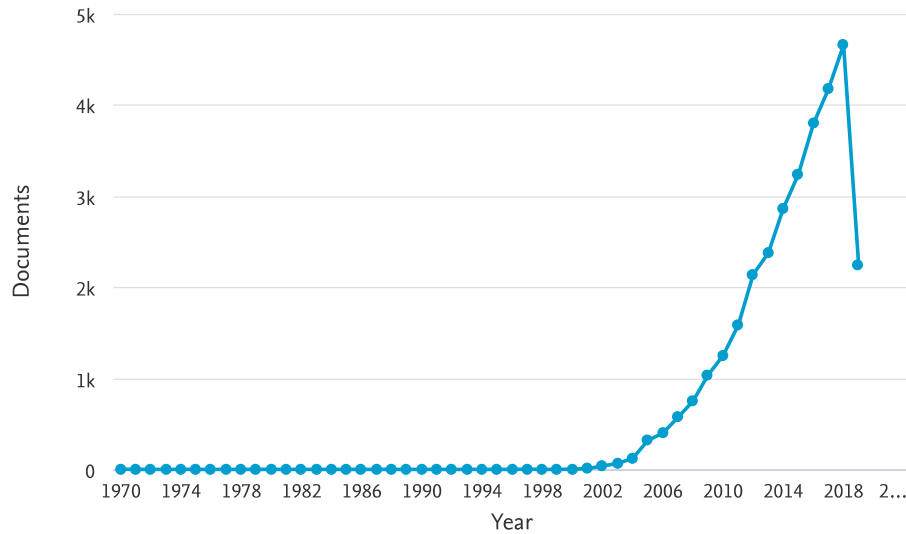
I-3587-2012

metabolomic

Scopus junho 2019

31,643 document results

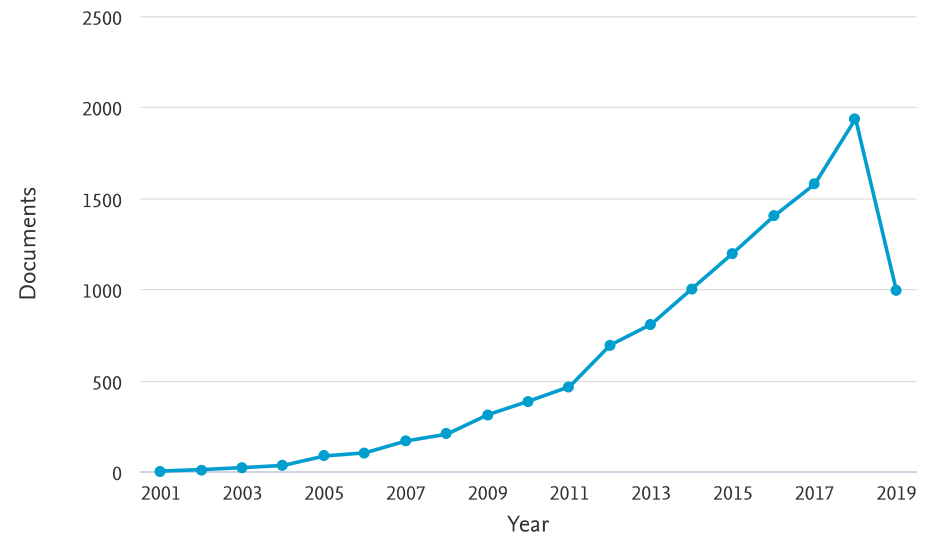
Documents by year



metabolomic AND food

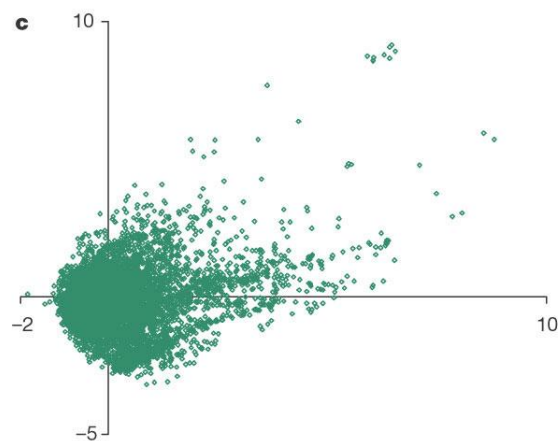
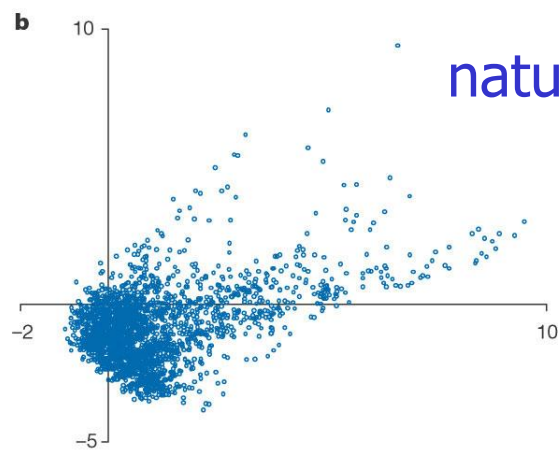
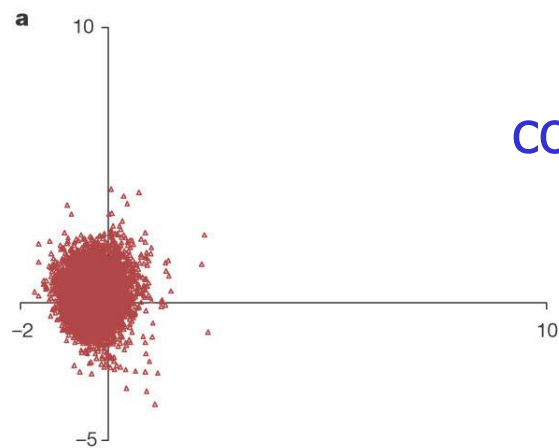
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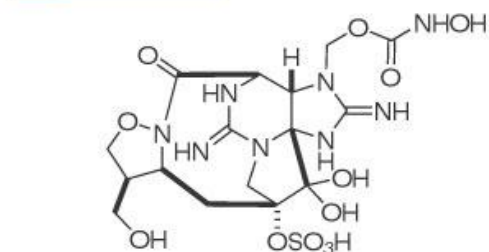
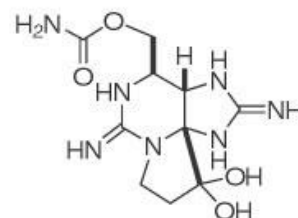
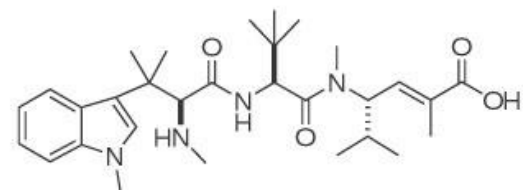
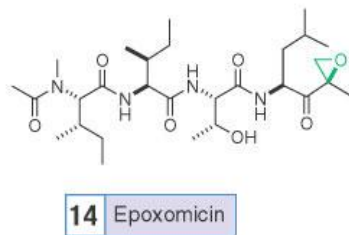
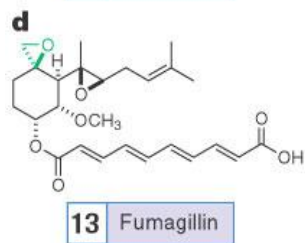
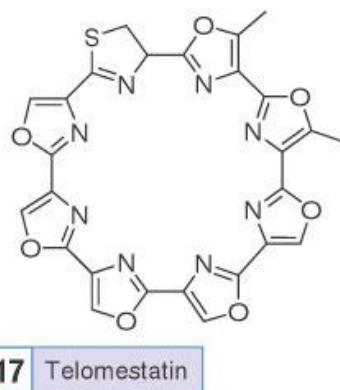
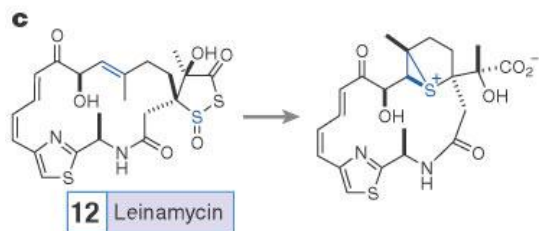
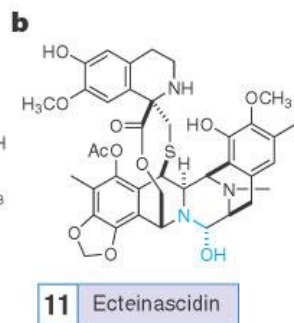
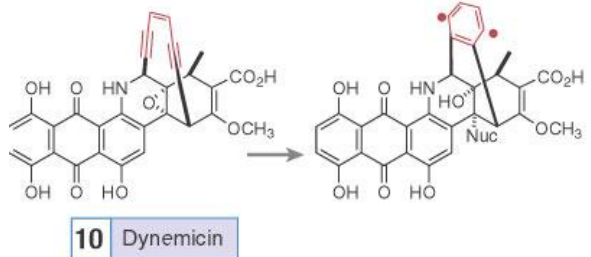
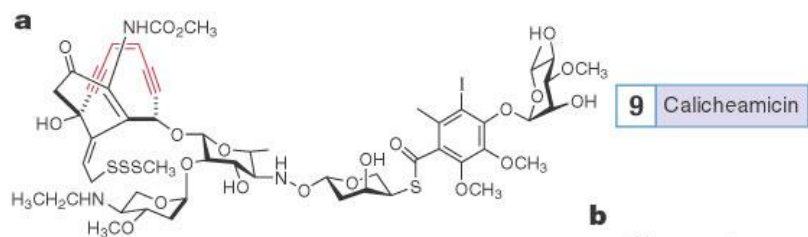
Documents by year



Espaço Químico

basis of a variety of molecular properties





File



DATA SOURCES

Abbott kinase dataset

PLOTS

FLT1 vs FLT3

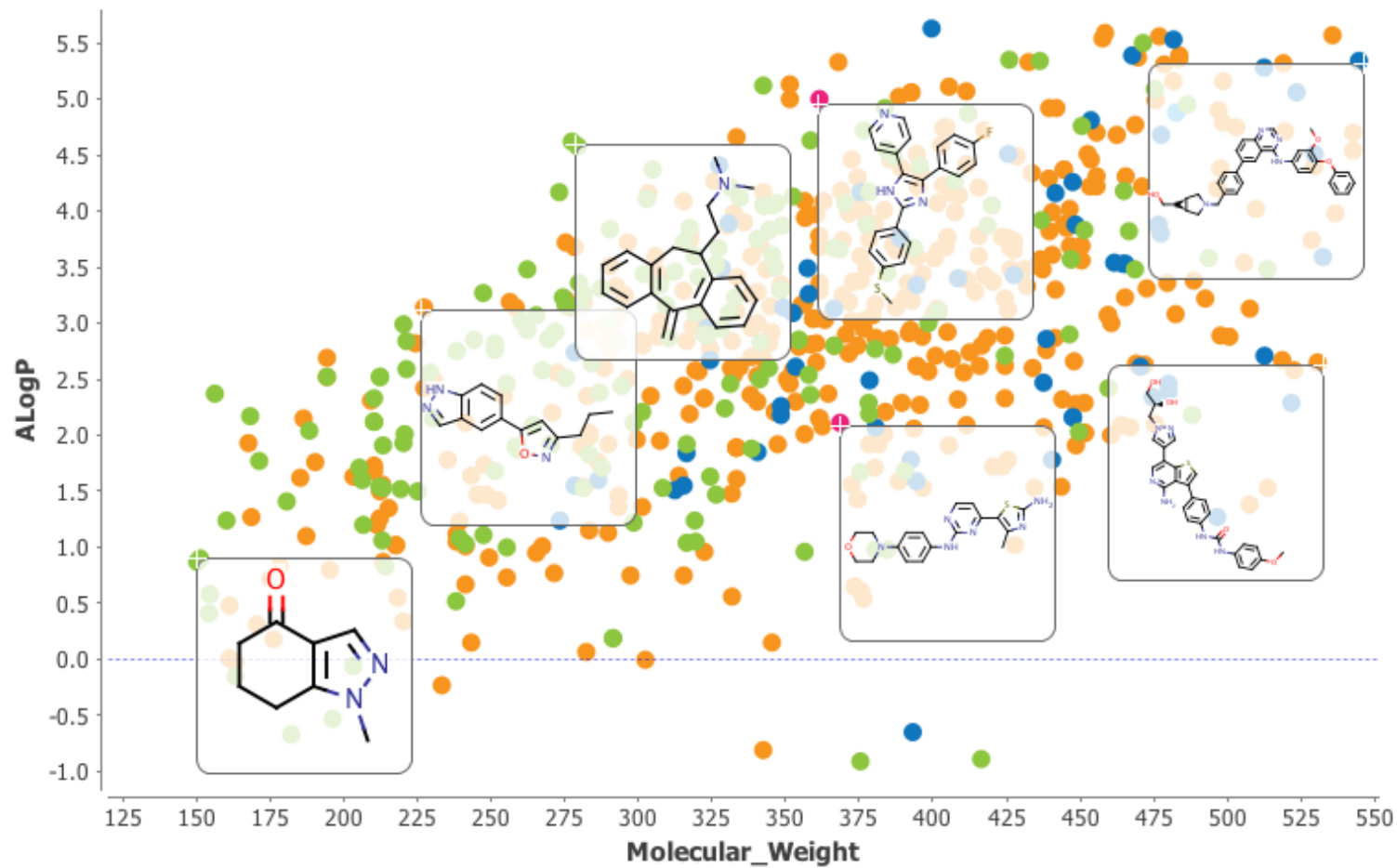
Alogp vs MWT

AKT1 vs AKT2

JAK2 vs JAK3

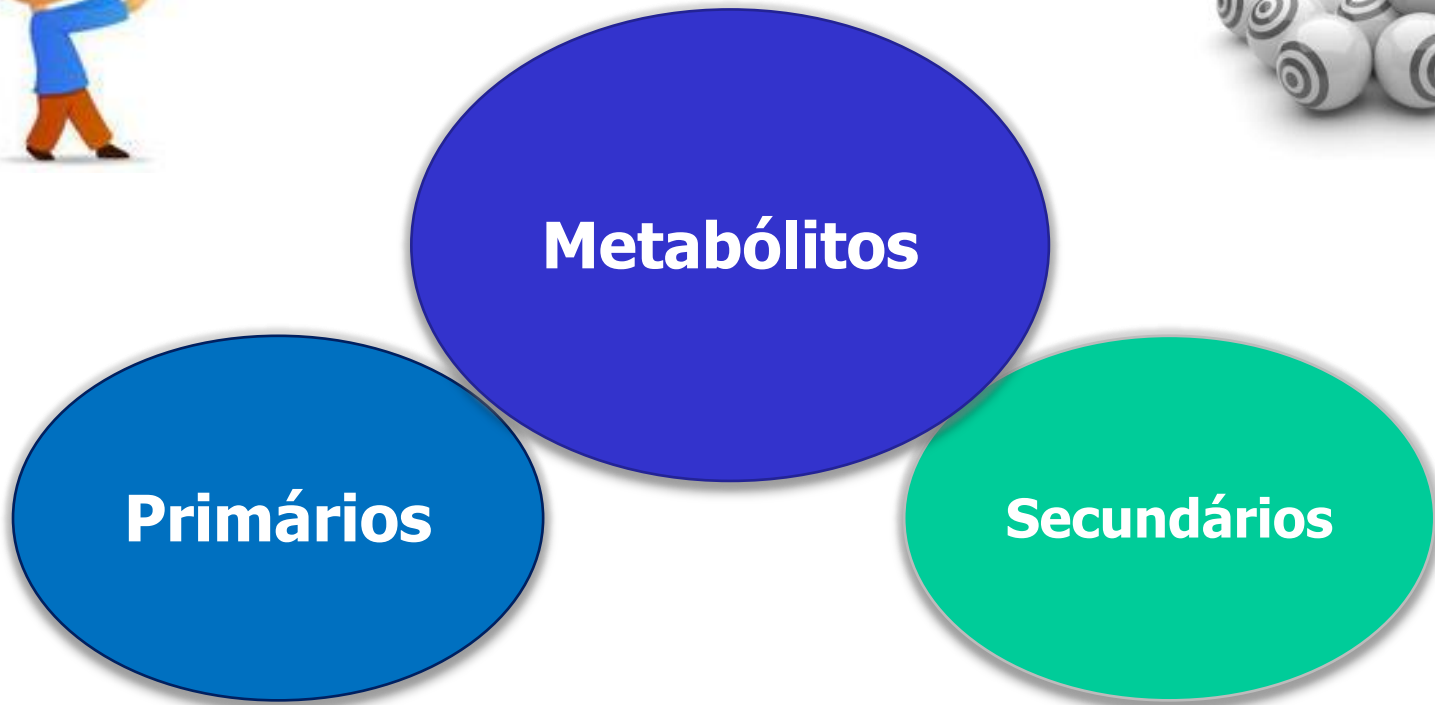
DYRK1A vs DYRK1B

Alogp vs MWT



Legend: ACD (green), MDDR (blue), PubChem (orange), WOMBAT (cyan), ZINC (pink)

Metabolômica: Desafios



**Lipídeos, açucares,
ácidos graxos**

**Policetídeos, alcaloides,
NRP, terpenos**

Metabolomica



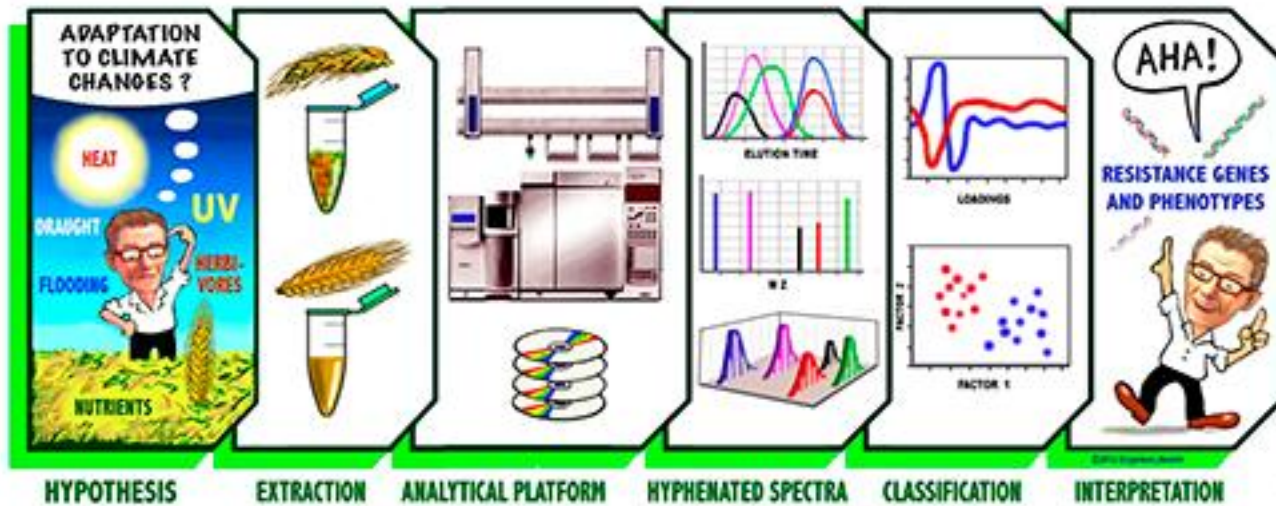
Foodomics é uma disciplina que examina todo o conjunto de substâncias presentes em nossos alimentos (foodome). A disciplina utiliza plataformas analíticas avançadas para investigar a composição do alimento e, assim, suas propriedades nutricionais e impacto na saúde. As novas técnicas também fornecem uma imagem detalhada da qualidade dos alimentos e podem ser usadas para detectar fraudes em alimentos e encontrar soluções para outros desafios na produção de alimentos. Os resultados de pesquisas de foodomics têm um impacto direto sobre os consumidores, a indústria de alimentos e a sociedade.

Engelsen

(https://food.ku.dk/english/research_at_food/research_fields/foodomics/)

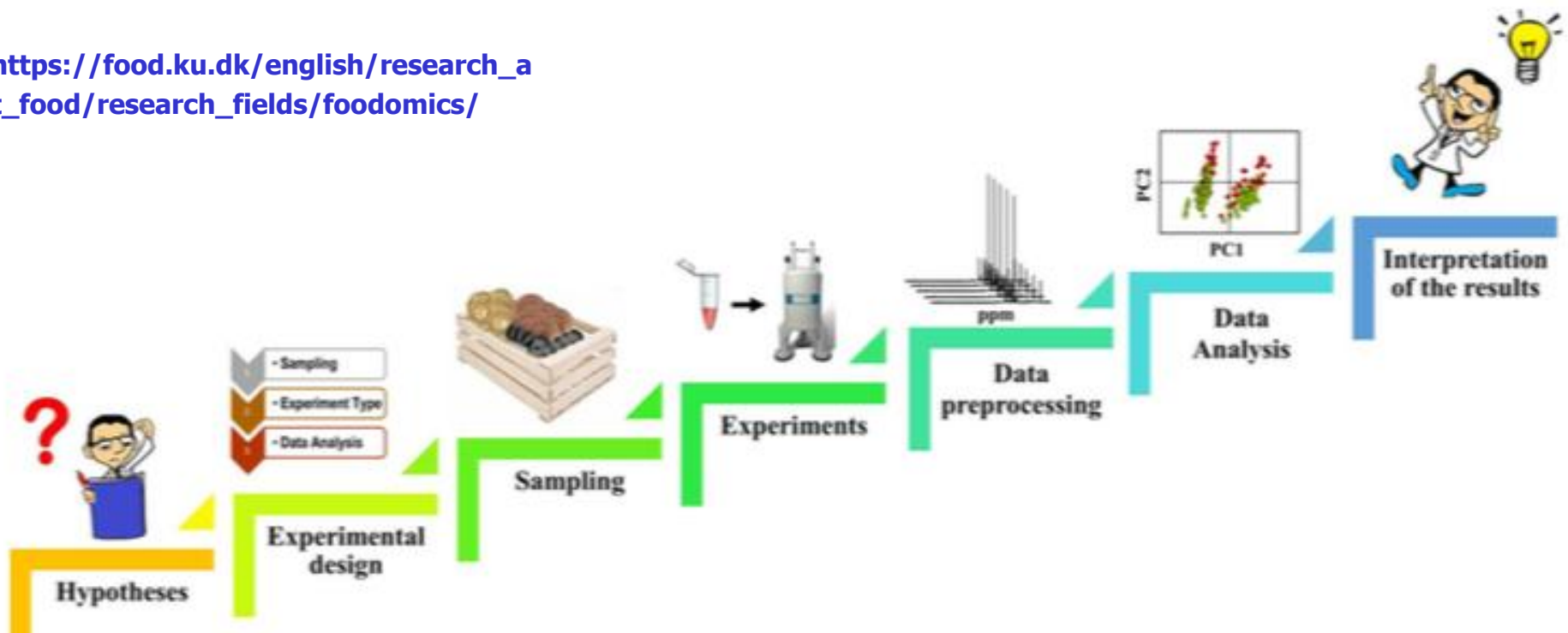
***Foodomics*—a discipline that studies the food and nutrition domains through the application of advanced omics technologies to improve the consumer's well-being, health, and knowledge.**

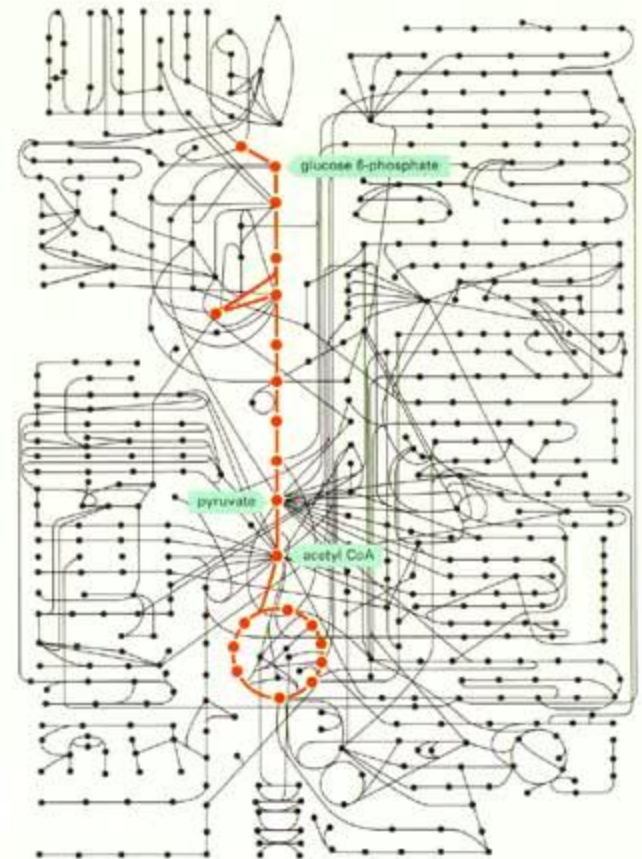
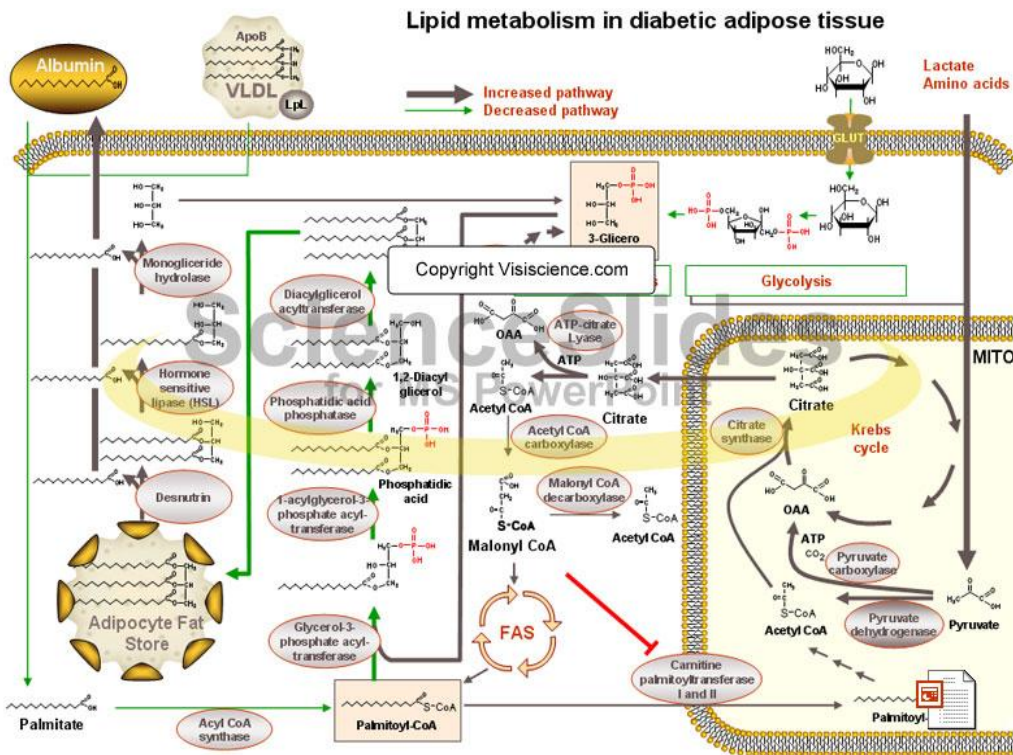
Khakimov & Engelsen, 2017



Foodomics. Illustration by Søren B. Engelsen and Tim Newlin ©

https://food.ku.dk/english/research_at_food/research_fields/foodomics/





Metabolite Profile





fingerprint

Table 1. Main Features of Most The Popular Techniques for Metabolomics

technique	CE-MS	GC-MS	LC-MS	NMR 1D	NMR 2D
universality	++	+	+ / ++	+++	+++
accuracy	- / ++ ^a	- / ++ ^a	- / ++ ^a	+++	+++
reproducibility	++ / - ^a	++ / - ^a	++ / - ^a	+++	+++
sensitivity	+	++ / +++ ^a	+++	-	-
resolution	++	+++	+++	+	++
efficiency	++	-	+	++	++

^aAccuracy, repeatability, and sensitivity mainly depend on the analyzer. GC-MS and LC-MS are usually performed either with a quadrupole or time-of-flight analyzer. “+” or “-” in front of and behind “/” represent quadrupole and time-of-flight analyzer, respectively.

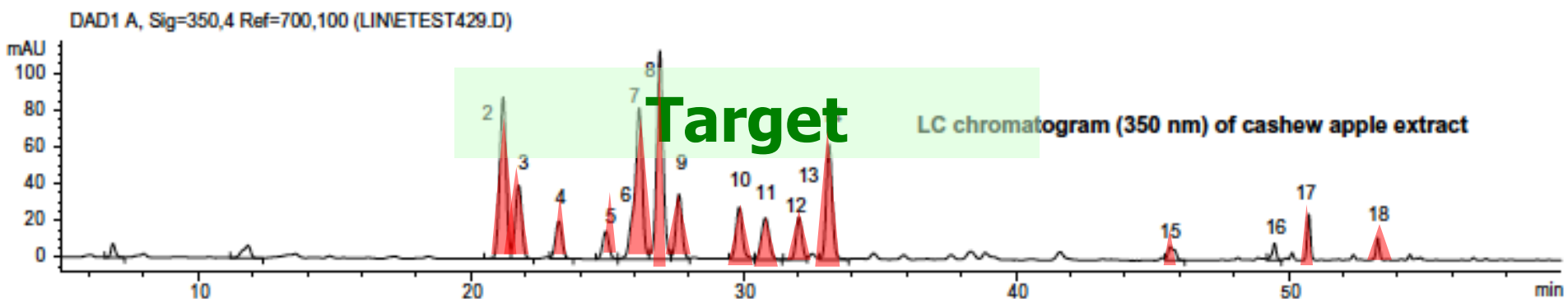
ABORDAGEM?

COMPOSTOS

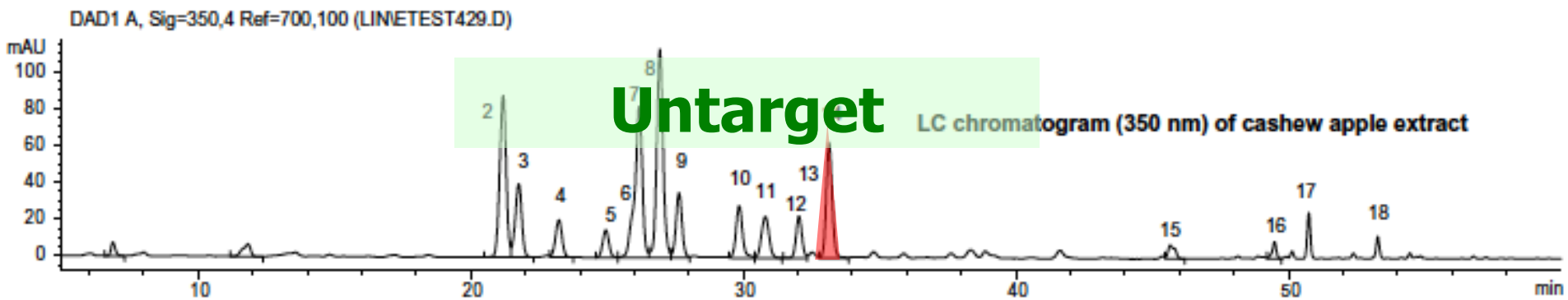
ALVO

NÃO ALVO

Caracterização completa e quantificação



Definição de marcadores e sua posterior quantificação



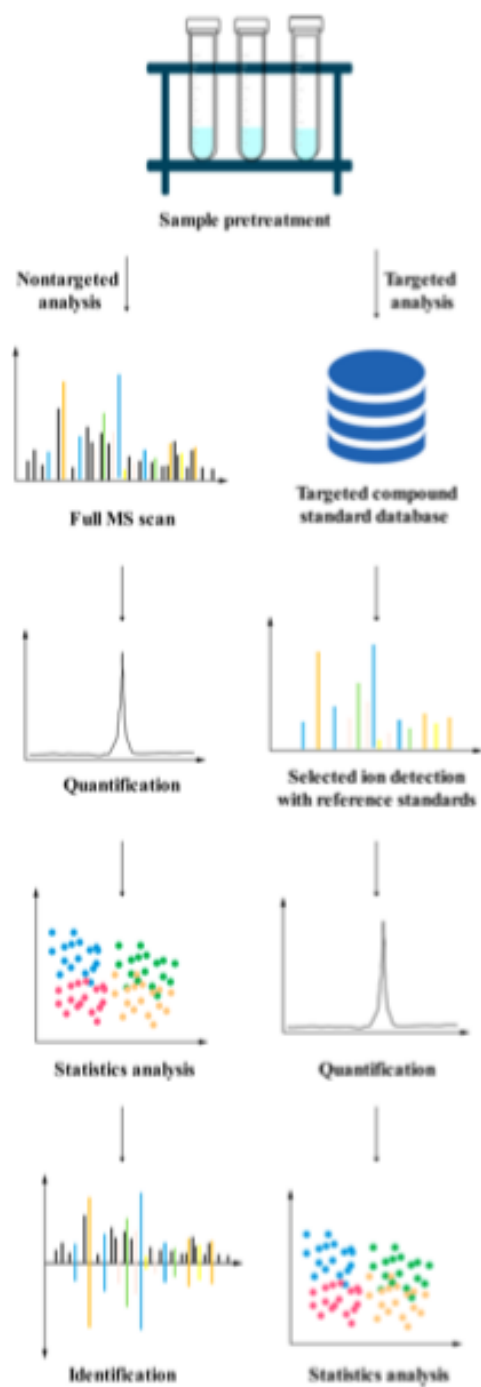


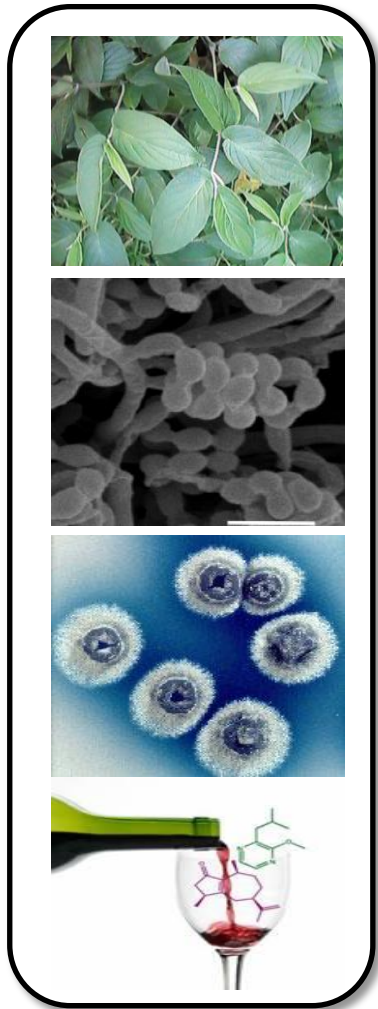
Figure 1. Workflow of metabolomics.

Table 1

Reported applications of metabolomics in life sciences research and practice

Basic research	References
Functional genomics	[2,5,6]
Interaction between metabolome, transcriptome and proteome	[7,8]
Discovery of new biochemical pathways	[9]
Interaction between species	[10]
Analysis of metabolic regulation	[11]
Applied research	References
Medical applications	
Understanding of disease pathophysiology	[12,13]
Disease biomarker identification	[14,15]
Early diagnosis	[16]
Personalized medicine	[17–19]
Clinical trial monitoring	[32,33]
Drug discovery	[34,35]
Toxicology–Drug safety	[36]
Agricultural/Nutrition Applications	
Identification of metabolic engineering targets	[20,21]
Understanding of stress response	[22,23]
Classification of special varieties of produce (e.g. tea, ginseng, fish)	[24–26]
Genetically modified (GM) food certification	[27–29]
Human nutrition	[30,31]
Industrial Applications	
Identification of metabolic engineering targets in <i>Escherichia coli</i> , yeast, algae	[37]
Fermentation process improvement	[38]
Biologics production and fermentation process optimization	[39]

Instrumentação: UPLC – QTOF – MS/MS

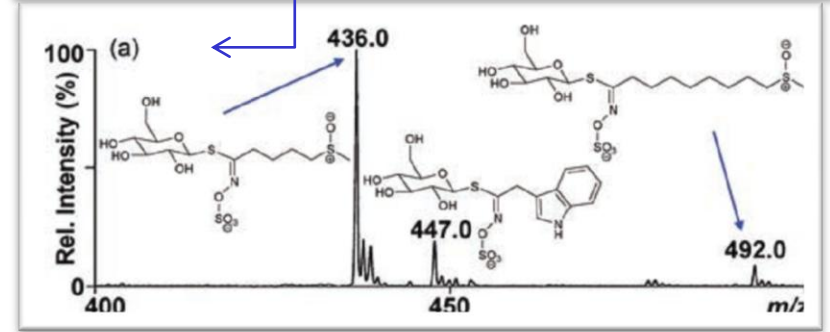
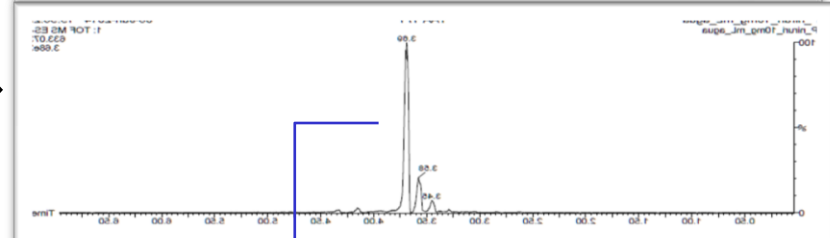
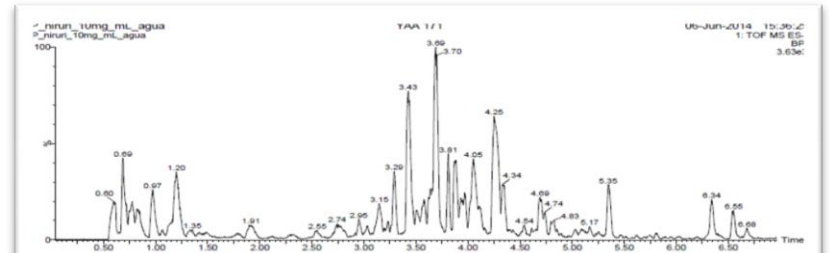


Agumas aplicações:

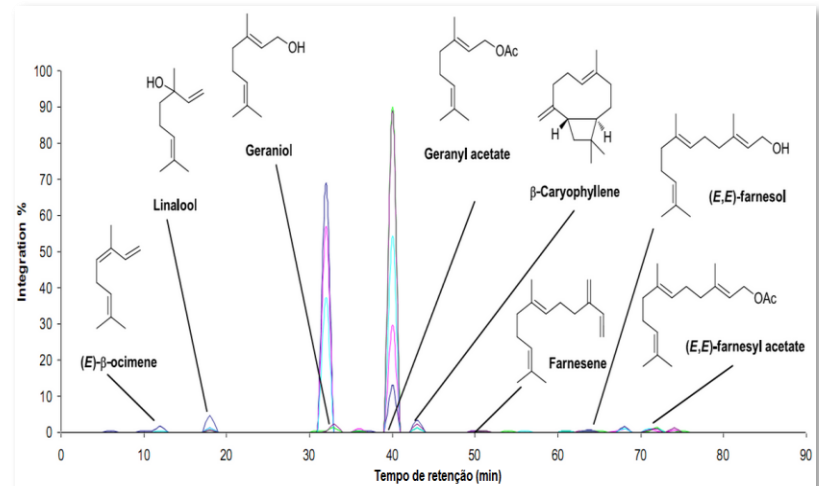
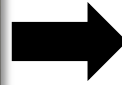
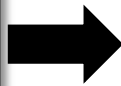
Produtos naturais -

Insumos agroindustriais

Determinação estrutural de substâncias de origem vegetal, animal e de microorganismos



Instrumentação: GC-MS/MS



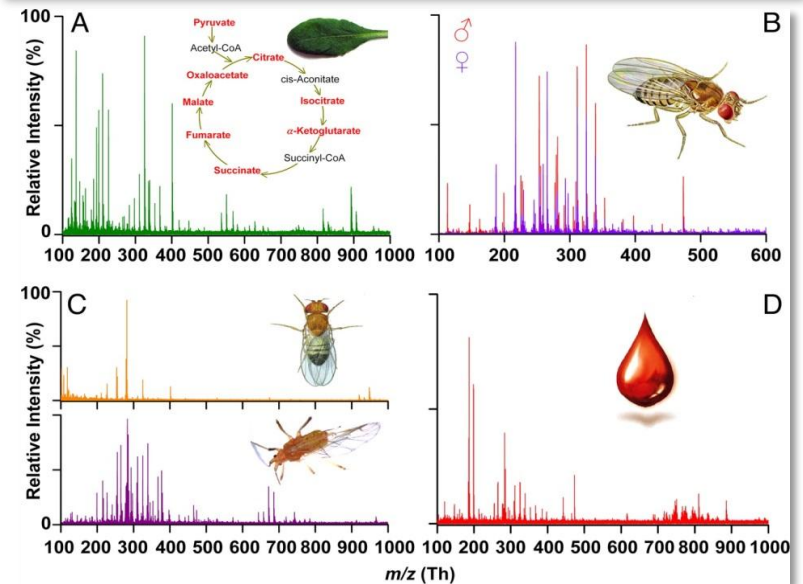
Algumas aplicações:

Análises de aromas de vinhos

Óleos essenciais

Feromônios

Estudos de ecologia química



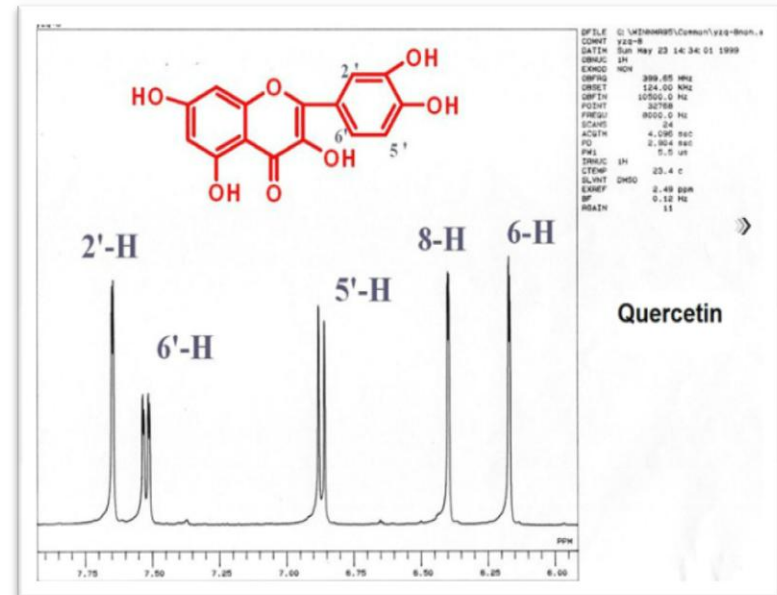
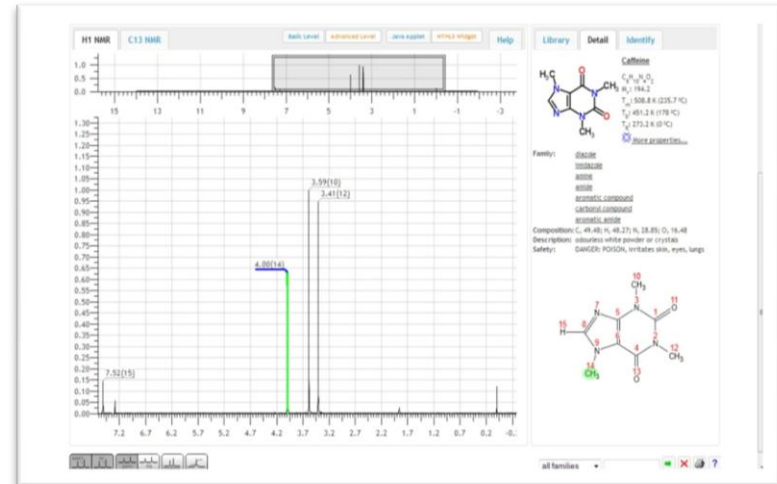
Instrumentação: Ressonância Magnética Nuclear (RMN)

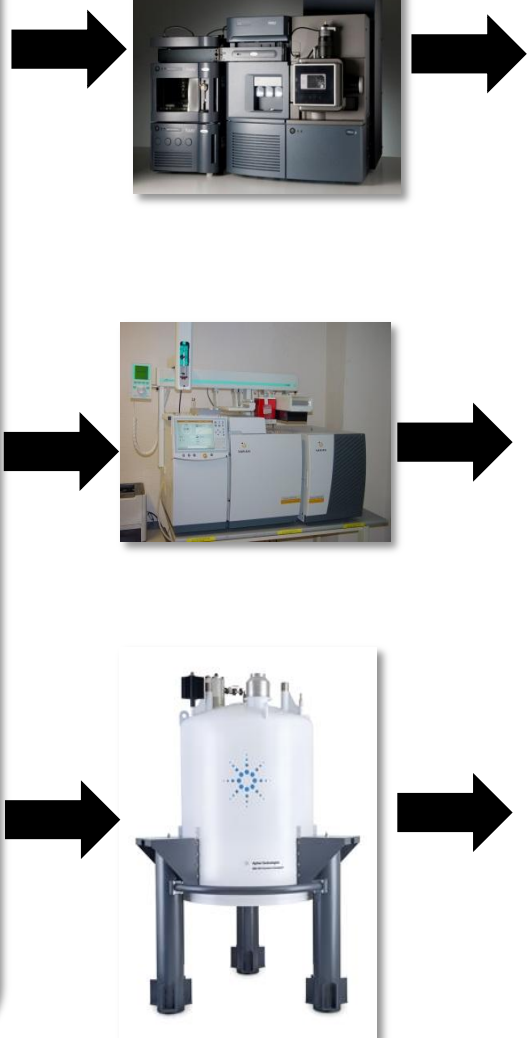


Sistema de detecção universal

Estudos de Metabolômica e Elucidação estrutural

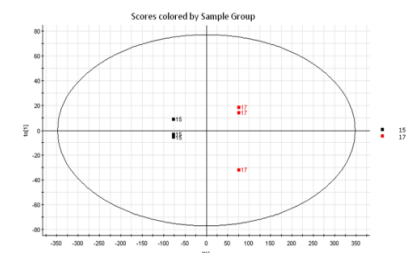
Quantificação sem necessidade de padrões analíticos





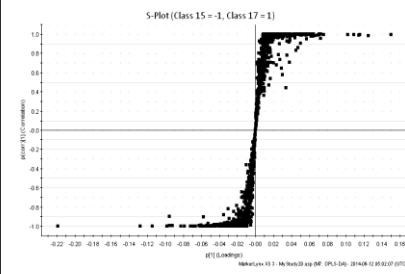
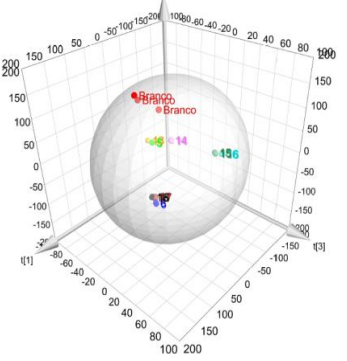
Métodos Quimiométricos

Análise de Componentes Principais (PCA)

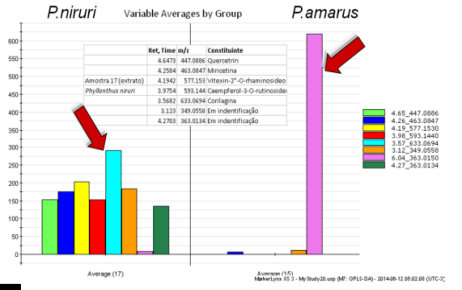


Amostra 17 - P.niruri, Exp. II 1 colheita (8 Hrs)
 Amostra 15 - P.pamarus, Exp. II 1 colheita (8 Hrs)

Scores Comp[1] vs. Comp[3] vs. Comp[2]. colored by Sample Group



OPLS-DA



Determinação de Biomarcadores

Interpretação de grande volume de dados

Metabolite profiling by GC-EI-TOF covers ~ 50-550 Da

R-OH (a) methoxymation

R-COOH →

R-NH₂ (b) silylation

R₂-NH (manually or automated)

R-SH

R-OTMS

R-COOTMS

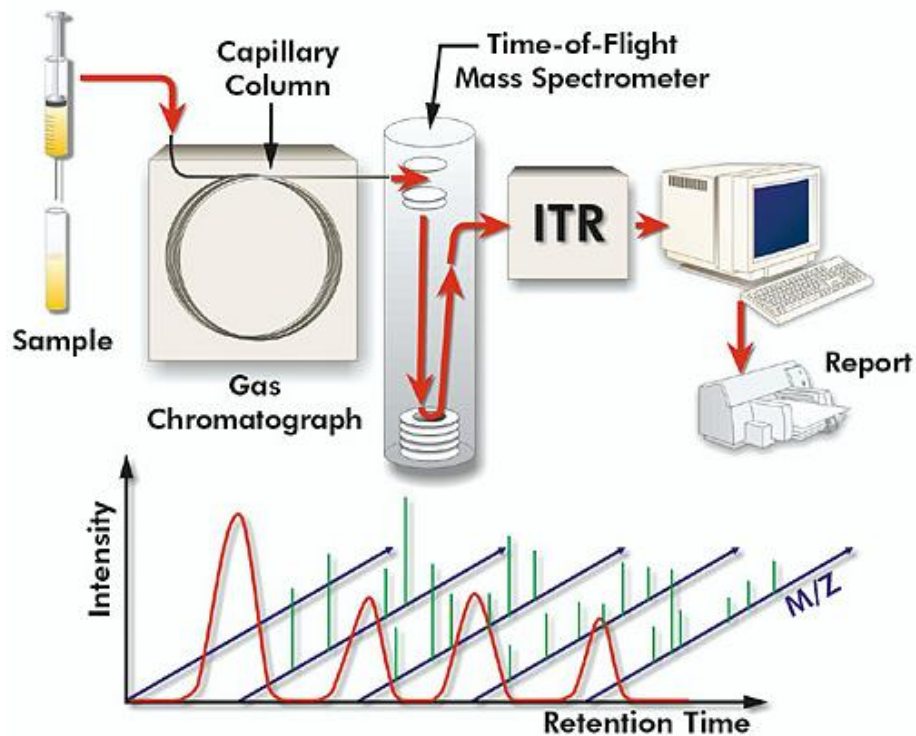
R-NTMS₂

R₂-NTMS

R-STMS

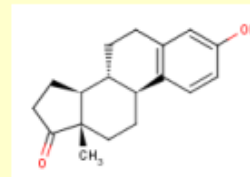
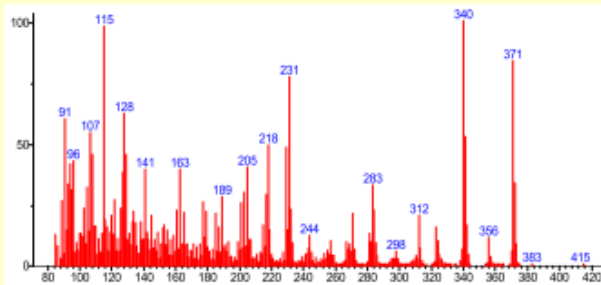
R₂-CNOCH₃

Exchange of H
against TMS
removes H-
bridges to
increase volatility



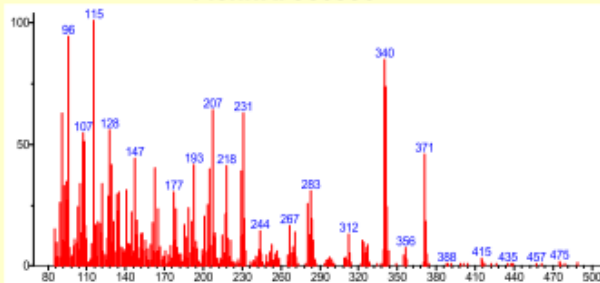
Library – Naming convention must be consistent but is not trivial

Estrone major
FiehnRI 948753



Estrone

Estrone minor
FiehnRI 950990

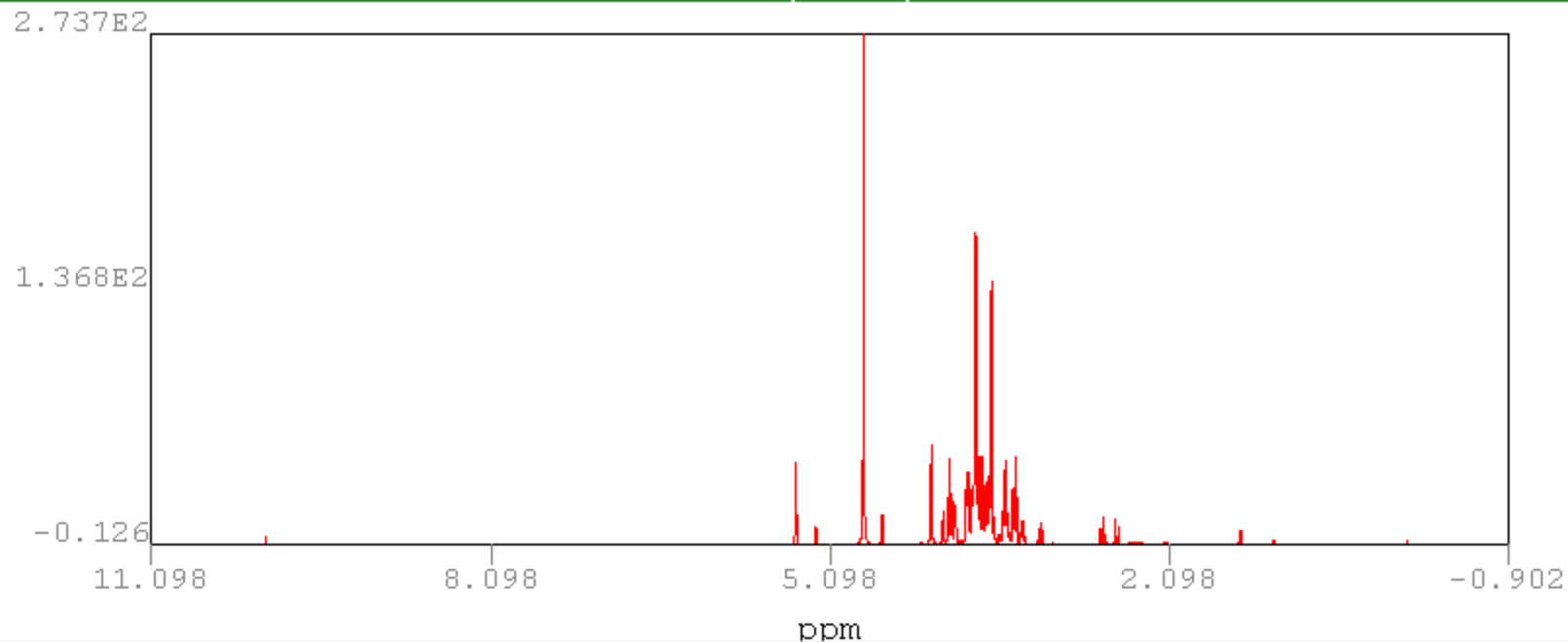


Solution:

mass spectra + retention time
point to the biological name estrone
with PubChem [CID: 5870](#) and KEGG ID and
InChIKey=DNXHEGUUPJUMQT-UHFFFAOYAI

Information Viewer Compounds Edit Log

C.1304.2 (1H NMR)

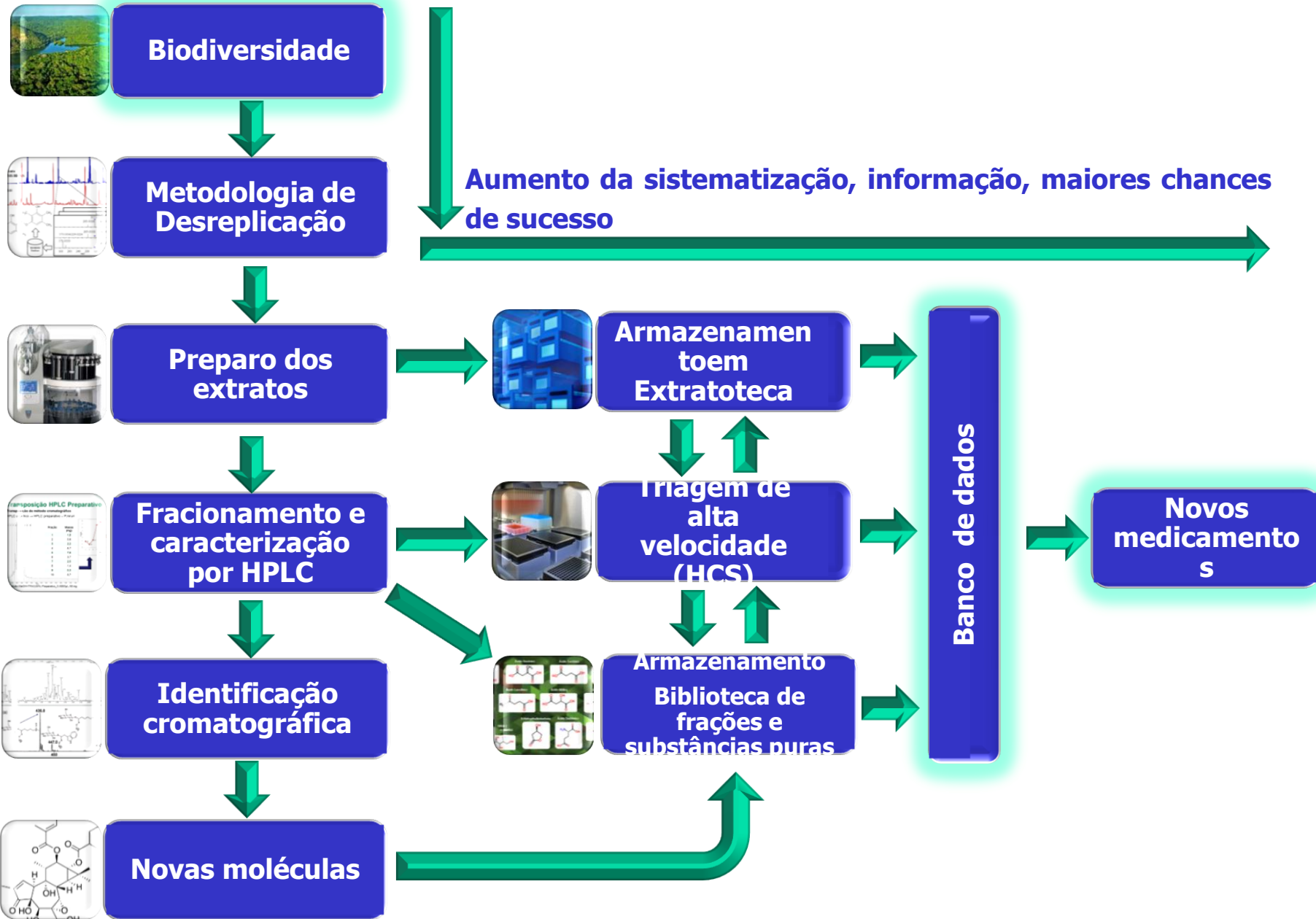


ppm=8.4643, I=-0.1259

Xindow: Imax: Zoom:

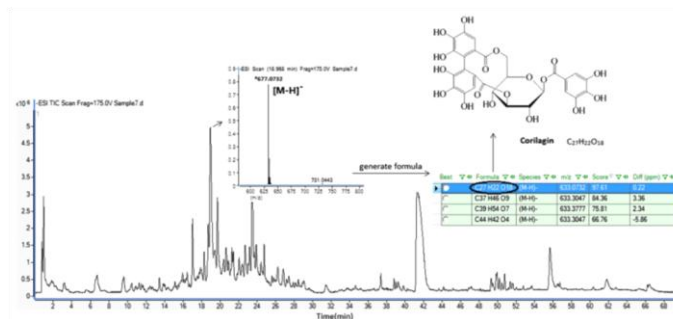
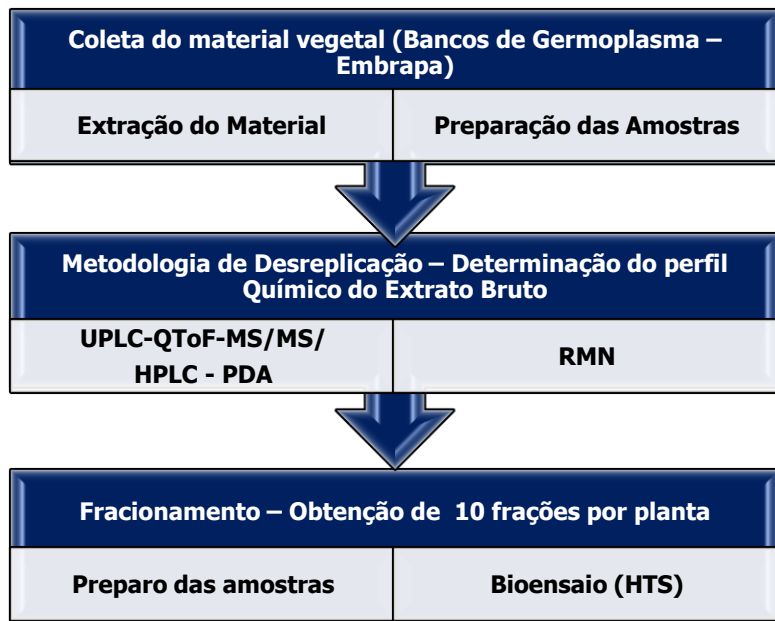
RMN

Bioprospecção de Moléculas com Potencial Terapêutico



Estratégia de Desreplicação

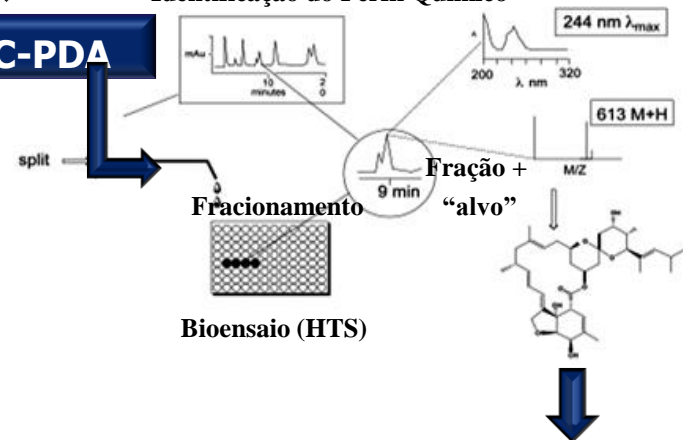
Dinâmica de Pesquisa



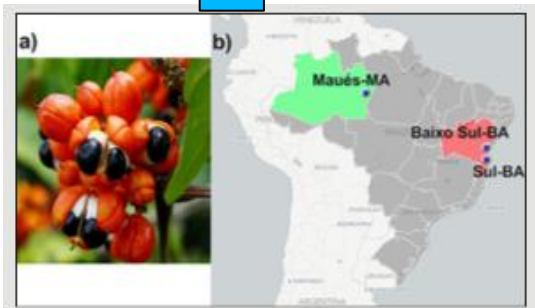
UPLC-HRMS

HPLC-PDA

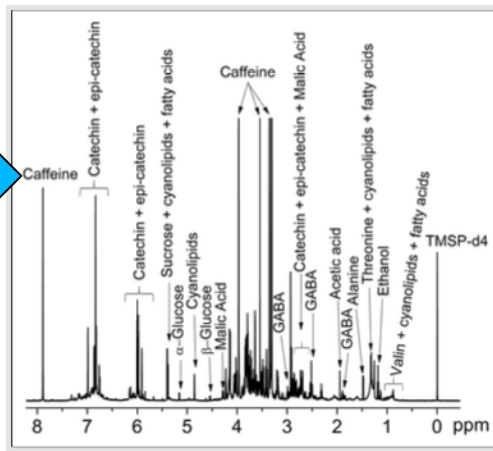
Identificação do Perfil Químico



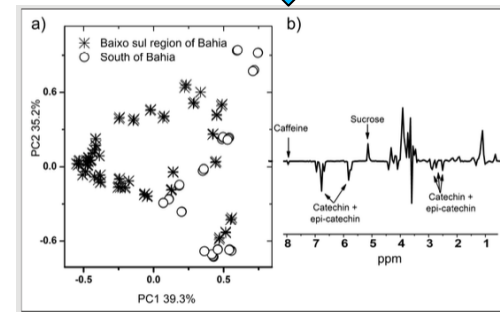
Confirmação estrutural via RMN



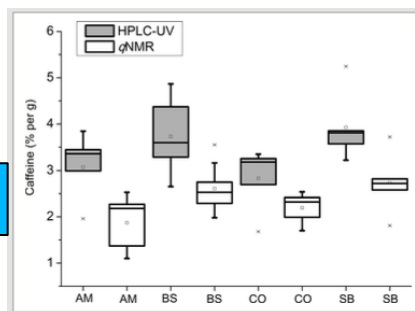
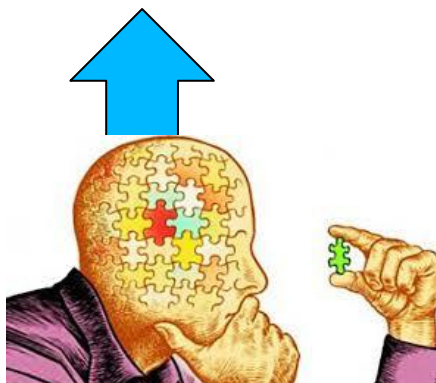
Sample set



fingerprint



chemometrics



quantitation

Qual a minha hipótese?

Metabolômica e Nutrição: condições experimentais

Molecular Nutrition
Food Research

Review | [Free Access](#)

Nutrimetabolomics: An Integrative Action for Metabolomic Analyses in Human Nutritional Studies

Marynka M. Ulaszewska, Christoph H. Weinert, Alessia Trimigno, Reto Portmann ... [See all authors](#)



[Volume 63, Issue 1](#)
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January 2019
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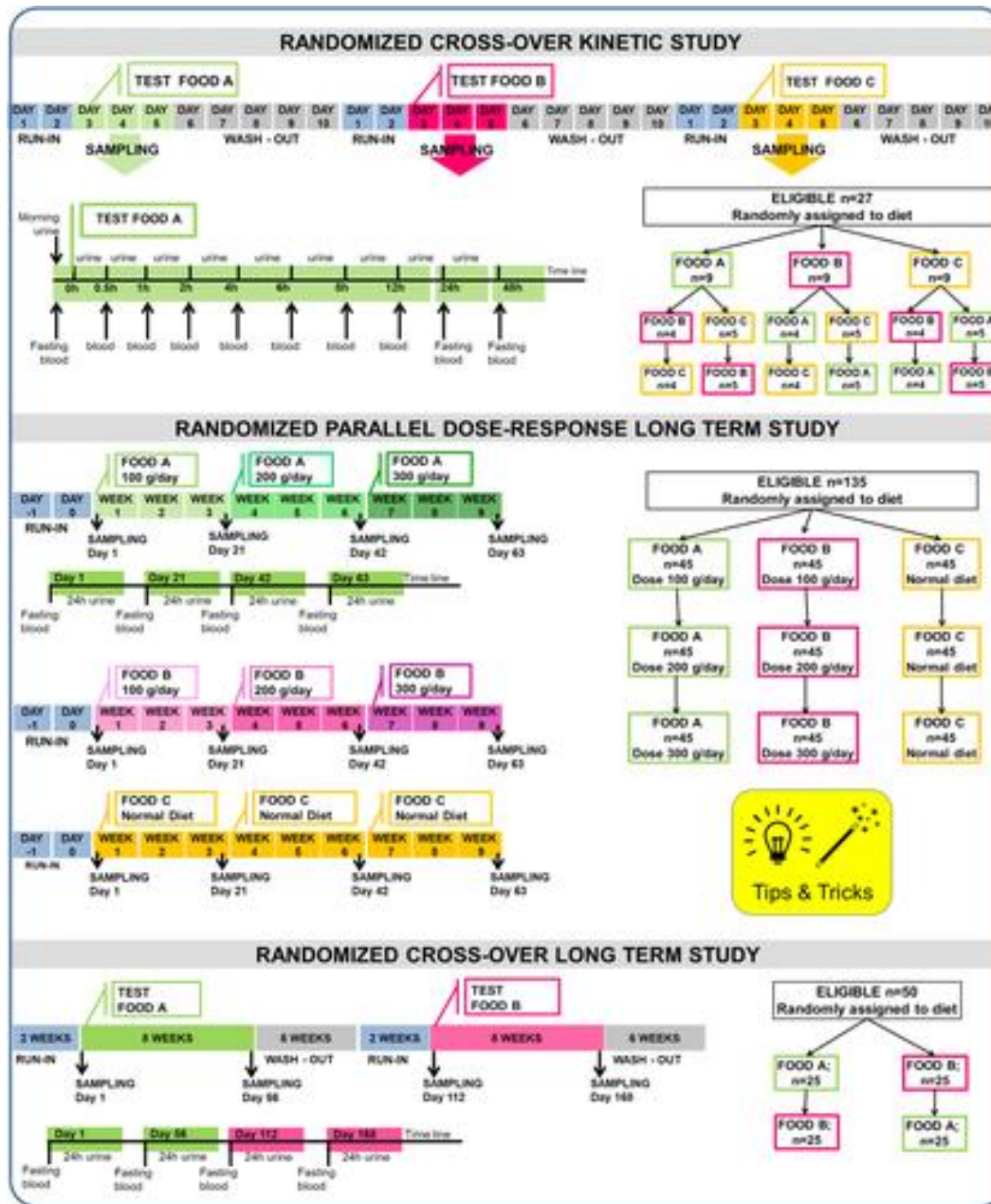


Nutrimetabolomics: An Integrative Action for Metabolomic Analyses in Human Nutritional Studies

*Marynka M. Ulaszewska, Christoph H. Weinert, Alessia Trimigno, Reto Portmann, Cristina Andres Lacueva, René Badertscher, Lorraine Brennan, Carl Brunius, Achim Bub, Francesco Capozzi, Marta Cialiè Rosso, Chiara E. Cordero, Hannelore Daniel, Stéphanie Durand, Bjoern Egert, Paola G. Ferrario, Edith J.M. Feskens, Pietro Franceschi, Mar Garcia-Aloy, Franck Giacomoni, Pieter Giesbertz, Raúl González-Domínguez, Kati Hanhineva, Lieselot Y. Hemeryck, Joachim Kopka, Sabine E. Kulling, Rafael Llorach, Claudine Manach, Fulvio Mattivi, Carole Migné, Linda H. Münger, Beate Ott, Gianfranco Picone, Grégory Pimentel, Estelle Pujos-Guillot, Samantha Riccadonna, Manuela J. Rist, Caroline Rombouts, Josep Rubert, Thomas Skurk, Pedapati S. C. Sri Harsha, Lieven Van Meulebroek, Lynn Vanhaecke, Rosa Vázquez-Fresno, David Wishart, and Guy Vergères**

Qual o desenho experimental?

Nutrimetabolomics: An Integrative Action for Metabolomic Analyses in Human Nutritional Studies



Amostras?



Spot urine sample



24 h urine sample



Sarstedt®
MarketLab®

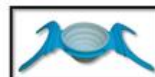
URINE COLLECTION

Wide-mouth plastic bag and a plastic container



FECES COLLECTION

Stool specimen collection units



Fecotainer®

Freezing toilet at -30°C



Toilet type T-1970, Gisebo;
Privetti® Pikkuvihrea



collection of 24h urine sample requires **an instruction for volunteer.**



avoid stool contamination with water, urine or other materials (e.g. toilet paper).
An instruction for volunteer is required.

Samples should be transferred/delivered to laboratory as soon as possible for further storage (< 2h).


In contrast to serum/plasma, urine and feces require sample specific normalization. Volume and weight of urine and feces and thus the overall concentration of metabolites may vary drastically. Information such as volume and weight for both matrices should be collected at sample arrival to the laboratory, before samples aliquotiation.

Preparação de amostras


Table 2. Overview of commonly used solvents for microbial metabolite extraction.

Method	Organism	Ref.
<i>For general extraction of different chemical classes</i>		
80:20 methanol:water	<i>Escherichia coli</i>	[103–105]
50:50 methanol: water	<i>Schizosaccharomyces pombe</i>	[106]
60:40 methanol:water	<i>Streptomyces coelicolor</i>	[33]
72:28 methanol	<i>Saccharomyces cerevisiae</i>	[107]
30:30:20 methanol:water:chloroform	<i>Corynebacterium glutamicum</i>	[108]
60:20:20 methanol:water:chloroform	<i>Leishmania donovani</i>	[80]
40:40:20 acetonitrile:methanol:water	<i>S. cerevisiae</i>	[31]
with 0.1% formic acid	<i>E. coli</i>	[66]
40:40:20 acetonitrile:methanol:water	<i>Mycobacterium tuberculosis</i>	[109]
	<i>E. coli</i>	[110]
	<i>S. cerevisiae</i> CEN.PK 113–7D	[61]
Boiling HEPES-buffered ethanol solution (75:25 v/v ethanol:water; pH=5.2)	<i>Methylobacterium extorquens</i>	[111]
60:40 ethanol:water	<i>Staphylococcus aureus</i>	[58]
Pure cold methanol	<i>E. coli</i>	[66,71,72,112]
Boiling ethanol	<i>S. cerevisiae</i> CEN.PK 113–7D	[61]
	<i>E. coli</i> , <i>B. subtilis</i> , <i>S. cerevisiae</i>	[49]
	<i>S. cerevisiae</i>	[60,69,113–115]
	<i>Pichia pastoris</i>	[116]
<i>For specific classes of compounds</i>		
Alkaline extraction (for basic molecules)	<i>M. extorquens</i>	[111]
Acid extraction (for organic acids)	<i>M. extorquens</i>	[111]
Bligh–Dyer method (for lipids)	<i>Trypanosoma brucei</i>	[117]


Nutrimetabolomics: An Integrative Action for Metabolomic Analyses in Human Nutritional Studies



Tips & Tricks



**PLASMA/
SERUM**











URINE

PRE-STORAGE PREPARATION

Plasma/serum (top layer) should be decanted as aliquots into micro tubes pre-labelled according to their destination using a transfer pipette, homogenized by vortexing and then aliquoted.


Centrifugation of urine is a necessary step in order to remove human cells/bacteria, as well as other non-cellular components and materials in suspension. Selected volumes of urine should be transferred into appropriate centrifuge tubes and centrifuged at 1800 x g for 10 min at 4°C. After that the supernatant should be aliquoted.

ALIQUOTING

 <p>For GC-MS 3 replicates 150-300 µL each</p>	 <p>For GC-MS 3 replicates 150-300 µL each</p>
 <p>For LC-MS 3 replicates 150-300 µL each</p>	 <p>For LC-MS 3 replicates 150-300 µL each</p>
 <p>For NMR 3 replicates 150-300 µL each</p>	 <p>For NMR 3 replicates 150-300 µL each</p>
 <p>+ Pooled QC 50-300 µL from each sample, splitted into few vials</p>	 <p>+ Pooled QC 50-300 µL from each sample splitted into few vials</p>

PRE-STORAGE PREPARATION

FECES




HOMOGENIZATION OF STOOL SAMPLE:

- automatic homogenization of a whole plastic bag in stomacher or blender
- stirring of fresh sample with a sterile spatula directly in delivery bag/container
- collecting multiple aliquots of i.e. 20 mg from the same area below the surface of the stool

PREPARATION OF SAMPLE AFTER HOMOGENIZATION:


- a. fresh feces freezing at -80° C
- b. centrifuging of fresh feces with or without portions of extracting agent (ice-cold PBS, 95% ethanol, etc.) and collection of supernatants (fecal water)
- c. feces freeze-drying (fecal powder)



Tips & Tricks

ALIUQUOTING


Fresh feces freezing



For GC-MS
3 replicates 10-50 g each

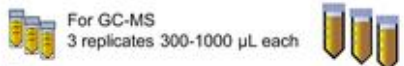
For LC-MS
3 replicates 10-50 g each

For NMR
3 replicates 10-50 g each



+ Pooled QC
0.5-10g from
each sample
splitted into
several vials


Fresh feces centrifuging: fecal water



For GC-MS
3 replicates 300-1000 µL each


For LC-MS
3 replicates 300-1000 µL each

For NMR
3 replicates 300-1000 µL each



+ Pooled QC
50-200 µL from
each sample
splitted into
several vials


Feces freeze-drying: fecal powder




For GC-MS
3 replicates 50-400 mg each

For LC-MS
3 replicates 50-400 mg each

For NMR
3 replicates 50-400 mg each




+ Pooled QC
approx. 30-100 mg
from each sample
splitted into
several vials



Fecal powder is hygroscopic, weigh with caution. Verify the weight of one spatula of fecal powder, and fill eppendorf tube/vial with only approximative amount (i.e. ca 50 mg or 100mg). Take note of exact weight on the sample label.


Nutrimetabolomics: An Integrative Action for Metabolomic Analyses in Human Nutritional Studies



Tips & Tricks

SERUM

Clot for 30 min at room temperature, centrifuge 10 min at 4°C and 2,500 × g



spray-coated silica


PLASMA


Mix with anticoagulant, centrifuge 10 min at 4°C and 2,500 × g


Li/ Na
Heparin


K₂EDTA


Na Citrate


 Serum samples can show features of polymeric material, peptides, and xanthines (the latter ones probably from clot).


 Higher content of peptides and protein fragments


 Incubation affects analyte peak area less in serum than in plasma, what may result in reduced peak areas of plasma amino acids, and carbohydrates with GC-MS detection


 Metabolite concentrations were found generally higher in serum, yet still highly correlated with plasma


 Anticoagulants may interfere with NMR signals and MS analysis


 Presence of anticoagulant cations can cause problems in metabolomic and lipidomic analysis by binding to negatively charged phospholipids and causing ion enhancement.


 Lithium ions from heparin can exacerbate matrix effects by increasing the signals of plastic polymers from vacutainer container

 EDTA was poorly suited for the analysis of polar metabolites. Sodium citrate can cause problems in determining citric acid and its derivatives

 Sodium and potassium formate ion clusters from K-EDTA, Na Citrate creates adducts in MS spectra

 Presence of anticoagulant residues may affect further extraction processes including derivatization efficiency in case of GC-MS analysis

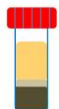
 Isolation of plasma yields a greater sample volume per volume of whole blood drawn

 Absence of platelet microparticles and postcoagulation protein fragments

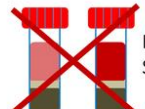
HEMOLYSIS PROBLEM:

The breakdown of blood cells strongly alters metabolic profiles of blood-derived samples, by increasing the concentrations of numerous metabolites coming from the intracellular space as well as by inducing the degradation of some compounds by the action of released enzymes

NORMAL SAMPLE



~~HEMOLYSIS SAMPLES~~



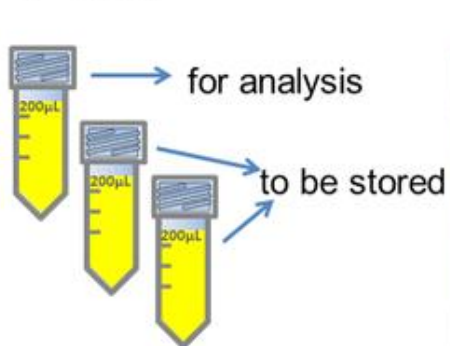
HEMOLYSIS SAMPLES

HEMOLYZED SAMPLES SHOULD BE AVOIDED IN METABOLOMIC STUDIES

Qual abordagem analítica?

UNTARGETED ANALYSIS

- LC-MS: polar and medium-polar metabolites (i.e., polyphenols and its metabolites, amino acids)
- LC-MS: non-polar metabolites (i.e., lipidomics)
- GC-MS: volatile metabolites
- GC-MS: metabolites after derivatization
- NMR



**MINIMUM
REQUIREMENT**

3 ALIQUOTS FOR ONE TYPE OF ANALYSIS (i.e., GC-MS)

TARGETED ANALYSIS

- LC-MS (kits, etc)
- GC-MS quantitative analysis with/without derivatization (i.e., SCFA, sugars etc.)
- Clinical analysis (multiple choices)

In general multiple aliquots of smaller volume (i.e., 200 µL) are recommended, rather than few aliquots of high volume.

Higher number of aliquots is recommended, which allows for additional analysis (i.e., additional analytical technique that arises in the future)



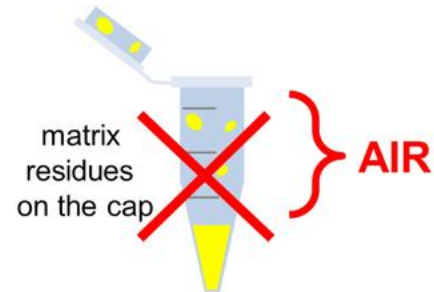
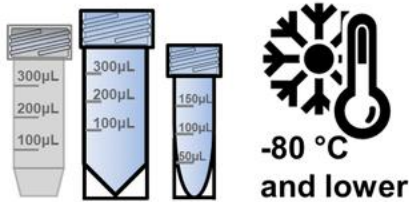
Nutrimetabolomics: An Integrative Action for Metabolomic Analyses in Human Nutritional Studies

Use containers adapted for the volume of matrix that will be stored. Matrix should fill possibly 80%-90% of container with minimum amount of air above its surface. Use containers with low adherence in the interior of the tube, and twisted caps that avoid splashing while opening

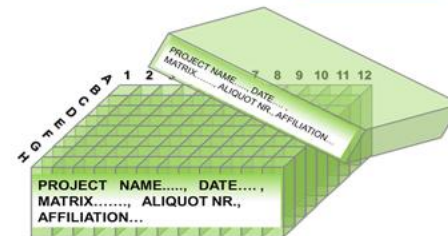
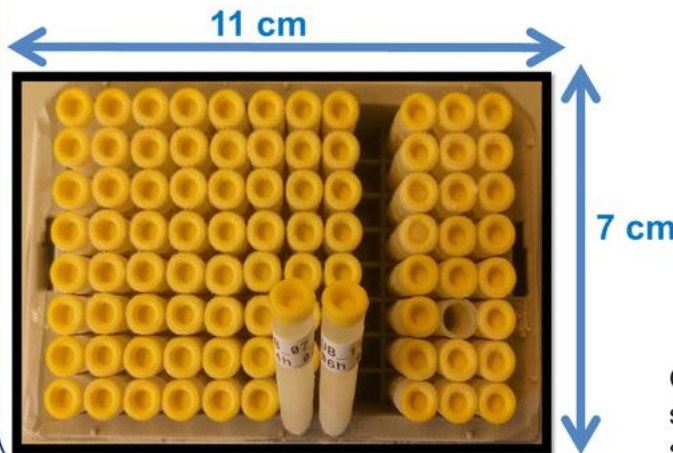


Conical/skirted vials for better recovery of matrix, twisted caps.

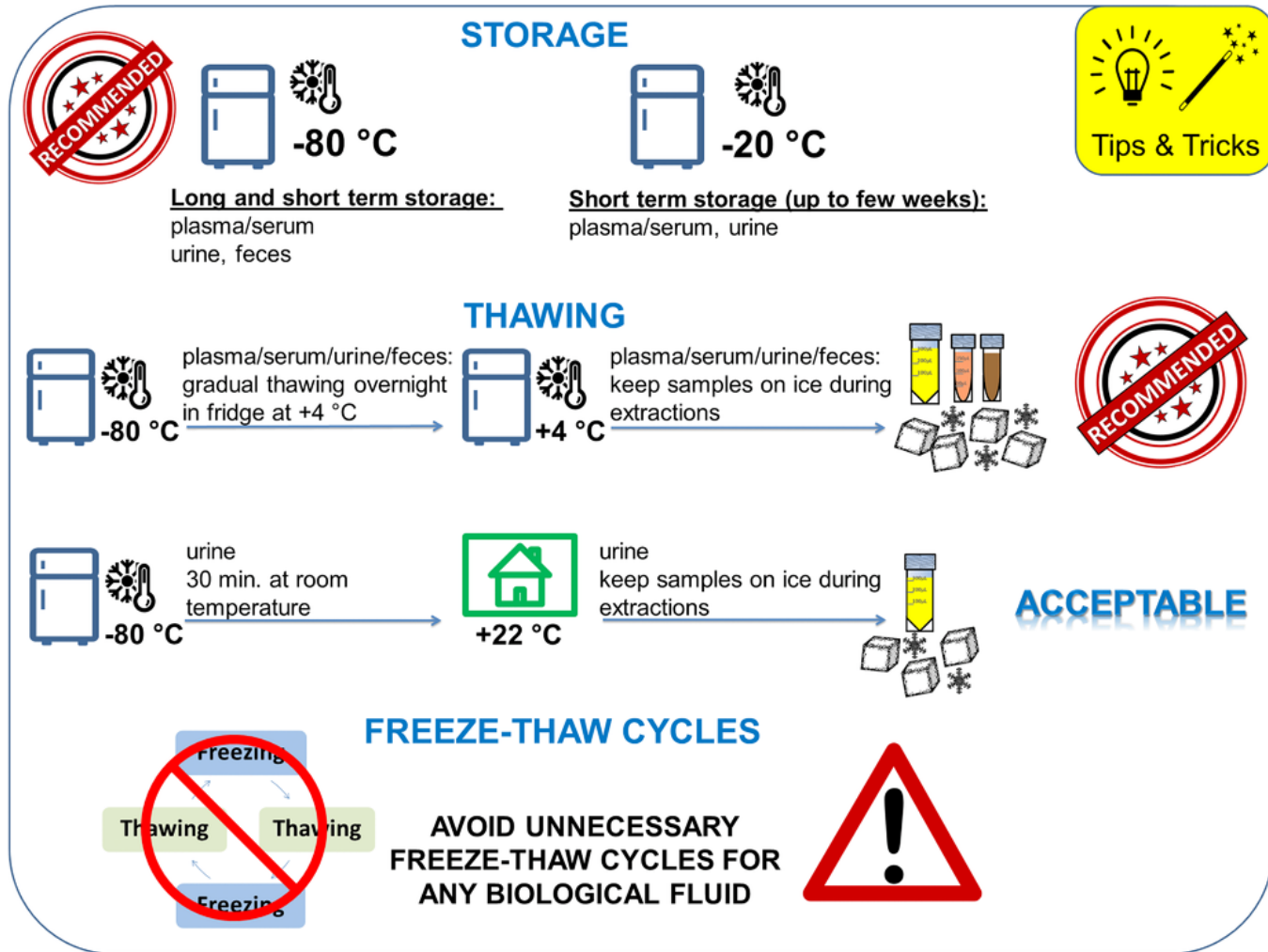
Recommended cryovial




DON'T STORE AIR




Optimization of storage capacity in freezers of small aliquotes in tight boxes. Avoid long term storage in paper boxes.



Nutrimetabolomics: An Integrative Action for Metabolomic Analyses in Human Nutritional Studies



QUALITY CONTROL



Tips & Tricks

**Extraction with 96 well plate,
preparation of ca. 200 samples/day for LC-MS**

	1	2	3	4	5	6	7	8	9	10	11	12
A	Blank											
B												
C												
D												
E												
F												
G												
H												

	1	2	3	4	5	6	7	8	9	10	11	12
A	Blank											
B												
C												
D												
E												
F												
G												
H												

	1	2	3	4	5	6	7	8	9	10	11	12
A	Blank											
B												
C												
D												
E												
F												
G												
H												

	1	2	3	4	5	6	7	8	9	10	11	12
A	Blank											
B												
C												
D												
E												
F												
G												
H												

Blank Blanks of extraction process

QC pooled sample extracted for evaluation of well plate performance

Real samples in random order


QC pooled sample, extracted multiple times

QCs extracts are combined in one **QC pooled vial**, and injected multiple times along injection queue. This quantity is sufficient to cover injections of full sample set at least twice – in both ionization modes. It is recommended to split this QC pooled vial into smaller aliquots.

Example of injection queue, with double QCs injections incorporated every 10 samples. Depending on chromatography time duration, QCs can be incorporated more or less frequently.

Examples: Run time is 12 min: double QCs every ca. 8/10 injections
Run time is 5 min: double QCs every ca. 20 injections

RANDOMIZATION



**IT'S
A MUST
!!!**

EXAMPLE OF AN INJECTION QUEUE in LC-MS

DAY 1

- x001_solvent
- x002_solvent
- x003_QC equilibration_run
- x004_QC equilibration_run
- x005_QC equilibration_run
- x006_QC equilibration_run
- x007_QC equilibration_run
- x008_Blank1
- x009_Blank2
- x010_Blank3
- x011_solvent
- x012_QC pooled
- x013_QC pooled
- x014_QC pooled
- x015_QC pooled
- x016_urine
- x017_urine
- x018_urine
- x019_urine
- x020_QC_plate1_1
- x021_urine
- x022_urine
- x023_urine
- x024_urine
- x025_urine
- x026_solvent
- x027_QC pooled
- x028_QC pooled
- x029_urine
- x030_urine
- x031_urine
- ...
- x137_urine
- x138_urine
- x139_solvent
- x140_QC pooled
- x141_QC pooled
- x142_urine
- x143_urine
- x144_QC_plate2_3
- x145_urine
- x146_urine

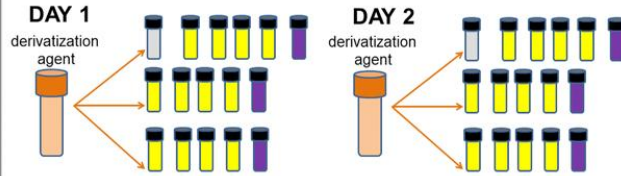
DAY 2

- x147_urine
- x148_urine
- x149_urine
- x150_urine
- x151_solvent
- x152_QC pooled
- x153_QC pooled
-
-

Nutrimetabolomics: An Integrative Action for Metabolomic Analyses in Human Nutritional Studies



Extraction with derivatization, preparation of ca. 15/20 samples/day for GC-MS

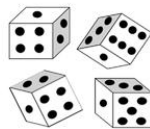


- Blanks of extraction process
- QC pooled sample extracted every day few times (i.e., 3)
- Real samples in random order

Time-consuming extraction methods such as derivatization procedures in GC-MS require a different strategy for sample organization. Preparation of one large QC pooled extract is not recommended due to low stability of derivatized extracts.

Every day, a blank, and series of QC samples must be extracted together with randomized study samples. Fresh samples should be analysed within 24-36 h. In the reported queue example, given a run time of ca. 70-75 min, double QCs samples are injected every 4 samples.

RANDOMIZATION

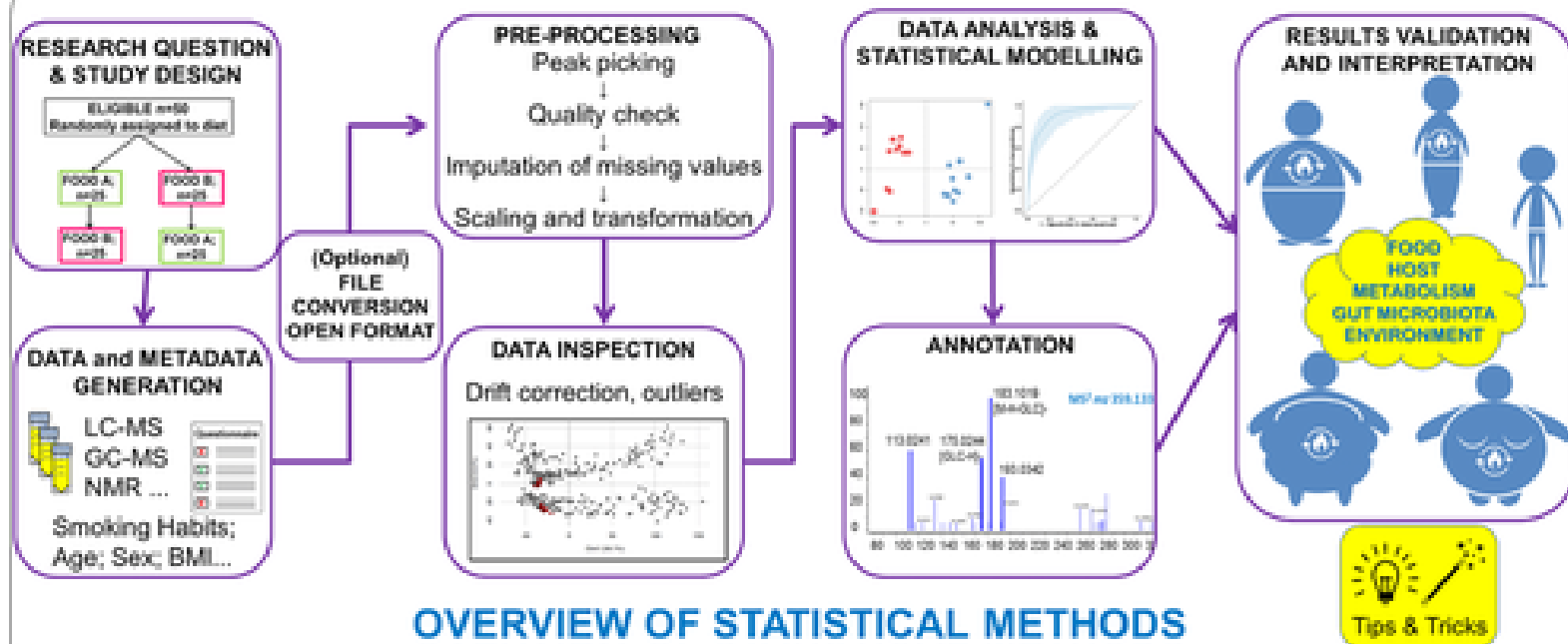


EXAMPLE OF AN INJECTION QUEUE in GC-MS

DAY 1	x001_QC equilibration_run
	x002_QC equilibration_run
	x003_QC equilibration_run
	x004_QC equilibration_run
	x005_QC equilibration_run
	x006_Blank01
	x007_QC
	x008_QC
	x009_urine
	x010_urine
	x011_urine
	x012_urine
DAY 2	x013_QC
	x014_QC
	x015_urine
	x016_urine
	x017_urine
	x018_urine
	x019_QC
	x020_QC
	x021_urine
	x022_urine
	x023_urine
	x024_urine
	x025_QC
	x026_QC
	x027_Blank02
x028_QC	
x029_QC	
x030_urine	
x031_urine	
x032_urine	
x033_urine	
x034_QC	
x035_QC	
x036_urine	
x037_urine	
x038_urine	
x039_urine	
x040_QC	
x041_QC	
x042_urine	
x043_urine	
x044_urine	
x045_urine	
x046_QC	
x047_QC	

Qual análise estatística?

DATA ANALYSIS AND STATISTICAL MODELLING FLOW

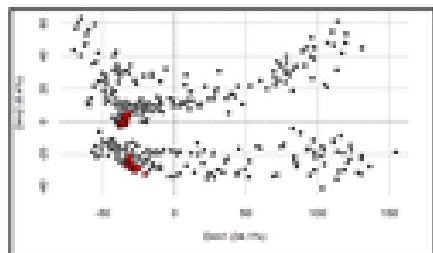


OVERVIEW OF STATISTICAL METHODS

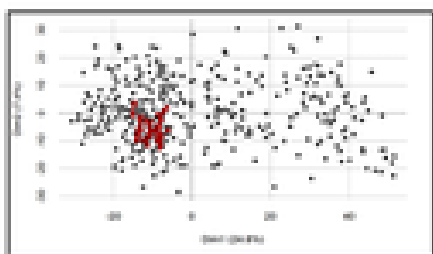
	Visualisation	Regression	Independent 2-group test	Dependent 2-group test	Multiple factors	Time series
Parametric	Plot	Linear models	t-test	Paired t-test	ANOVA Mixed models	Repeated measures
Non-parametric	Rank plot	Rank regr. Kernel LOESS	MW U-test	Wilcoxon signed-rank	Kruskal-Wallis Friedman rank ANOVA	Friedman rank-repeated
Multivariate	PCA	PLS; RF; SVM	PLS-DA; RF; SVM	ML-PLS; ML-RF; ML-SVM	ANOVA decomposition	ANOVA decomposition

VERIFICATION OF QUALITY CONTROL SAMPLES AND OUTLIERS WITH PCA

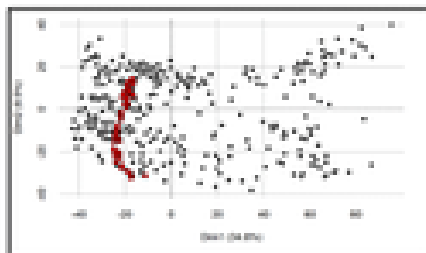
Example of Batch Effect – samples divided into two clouds due to a prompt problem during injections (RAW, not normalized data)



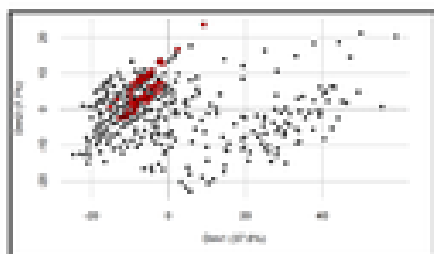
The same sample set normalized by:
1) median of each feature/plate = 1
2) Intensity of creatinine *m/z* feature



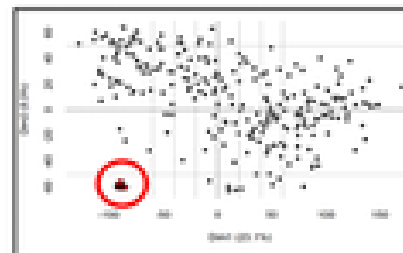
Example of Drift due to loss of signal intensity– Samples and QCs suffered from drop in the signal intensity during injections (RAW, not normalized data)



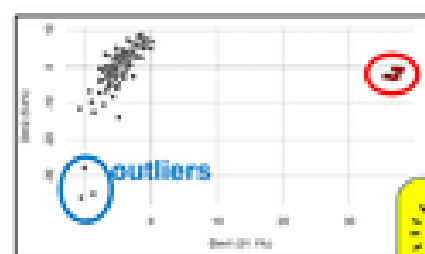
The same sample set normalized by:
1) median of each feature/plate = 1
2) Intensity of creatinine *m/z* feature



Example of QC prepared from study samples – a tight QCs cloud is located nearby a wide cloud of real samples (RAW, not normalized data)



Example of QC prepared from commercial biological fluid (i.e. plasma)– a tight QCs cloud is located far from a wider cloud of real samples (RAW, not normalized data). Three samples (outliers) are separated from the rest of samples (blue circle)



● QC samples ● Study samples ○ Outliers samples



Exemplos



Universidade Federal do Ceará
Departamento de Engenharia Química



UNIVERSITY OF COPENHAGEN



inct
institutos nacionais
de ciência e tecnologia

^1H NMR spectroscopy and chemometrics evaluation of non-thermal processing of orange juice

Amostra: Suco laranja

Processamento: Plasma e O_3

Análise: RMN ^1H

Quimiometria: PCA e quantificação ($q\text{NMR}$)

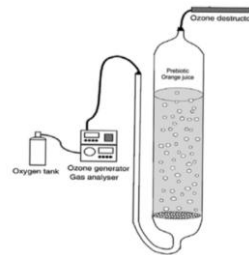
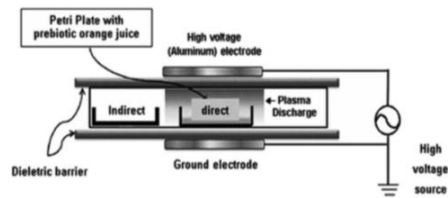
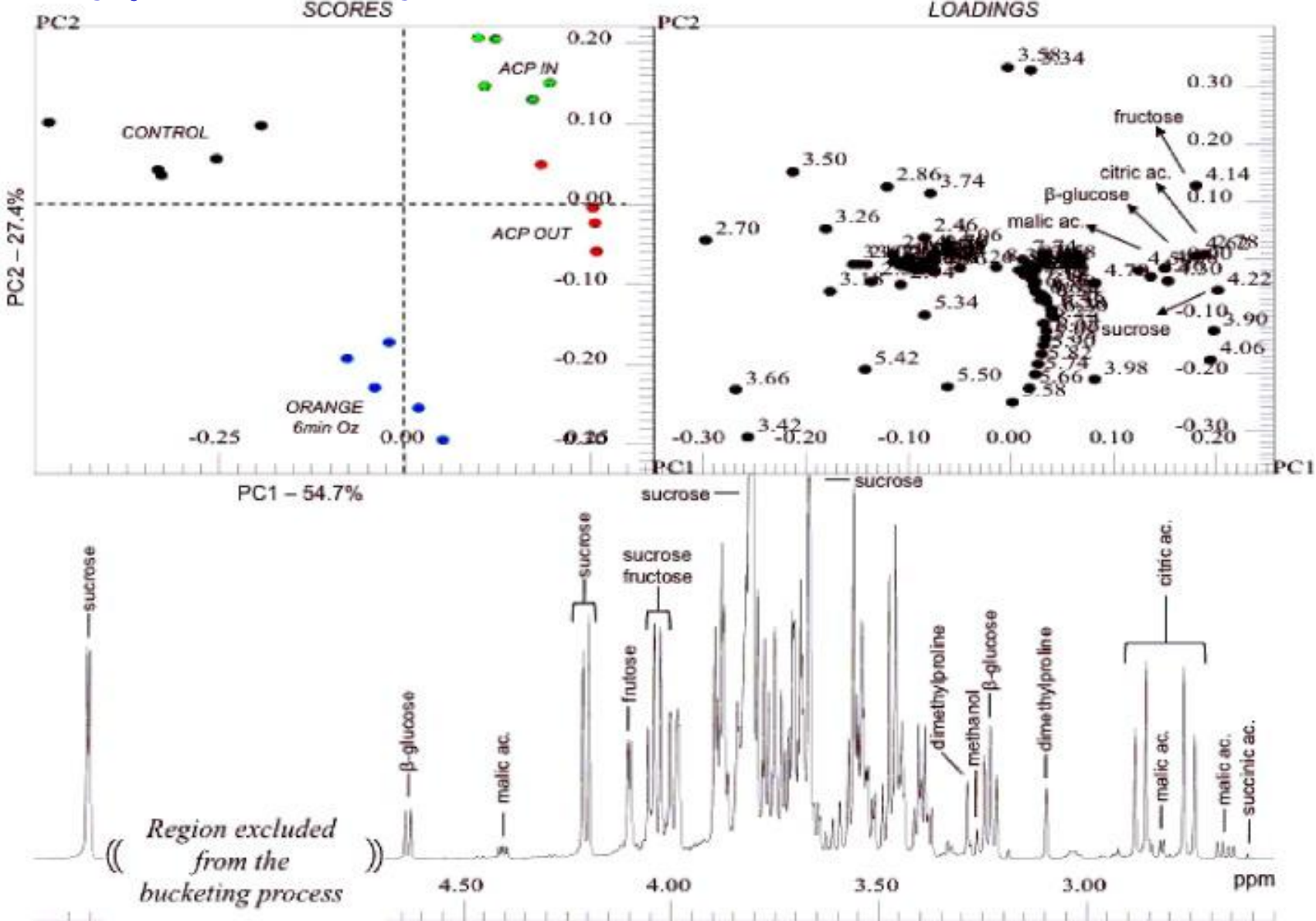
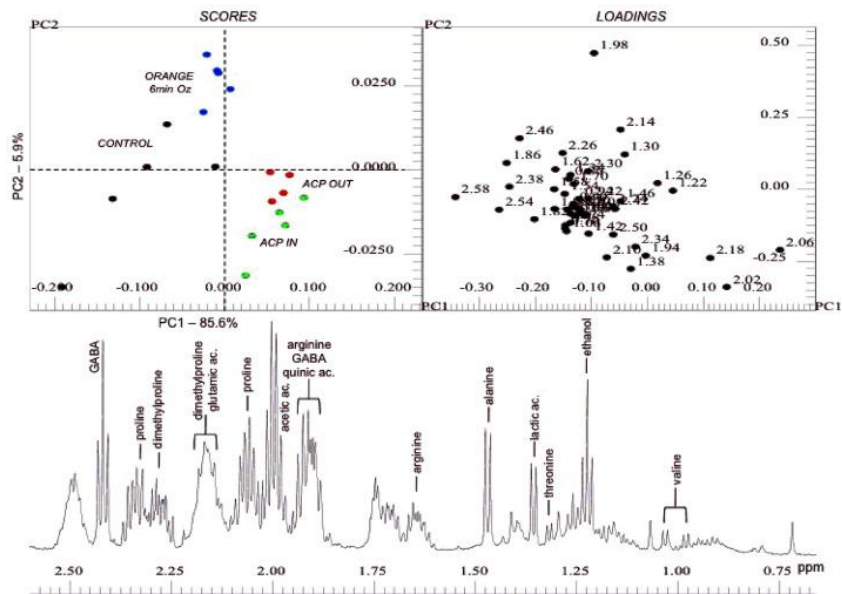


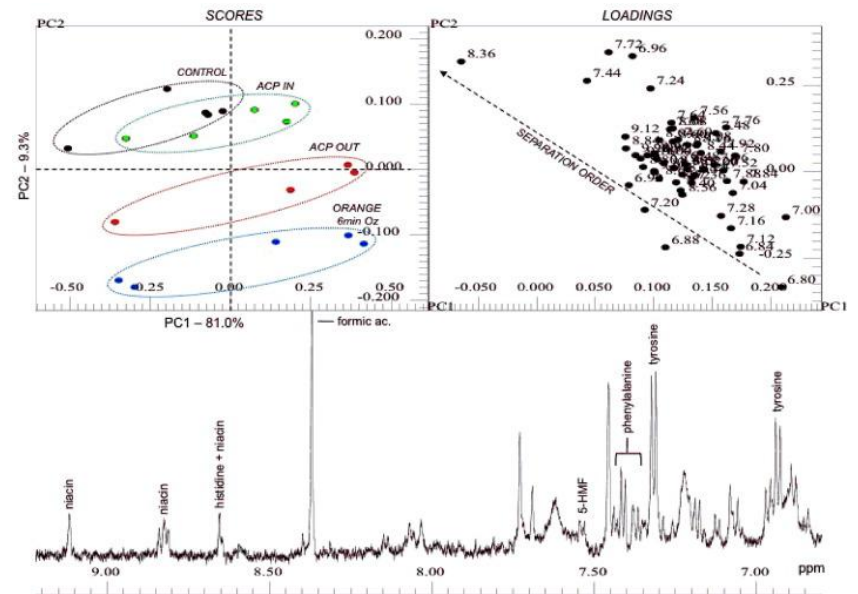
Fig. 1. ^1H NMR spectrum (C), PC1 vs. PC2 scores (left side – A) and loadings (right side – B) coordinate system for the orange juice submitted to different processing: control – black; 0.230 mg O_3 mL $^{-1}$ – blue; ACP IN – green; ACP OUT – red



Região alifáticos



Região aromáticos



- The processes promoted slight variation in concentration of primary metabolites.
- The variations did not result in significant changes in orange juice composition.
- Plasma and ozone are suitable non-thermal alternatives for orange juice processing.

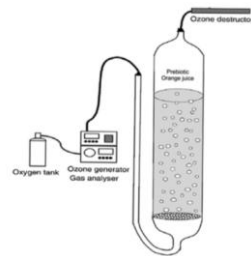
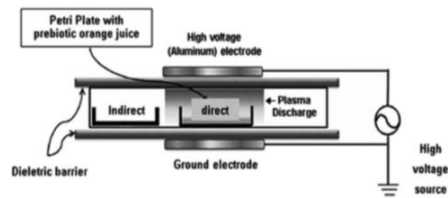
An untargeted chemometric evaluation of plasma and ozone processing effect on volatile compounds in orange juice

Amostra: Suco laranja

Processamento: Plasma e O₃

Análise: GC-MS

Quimiometria: análise hierárquica + PCA



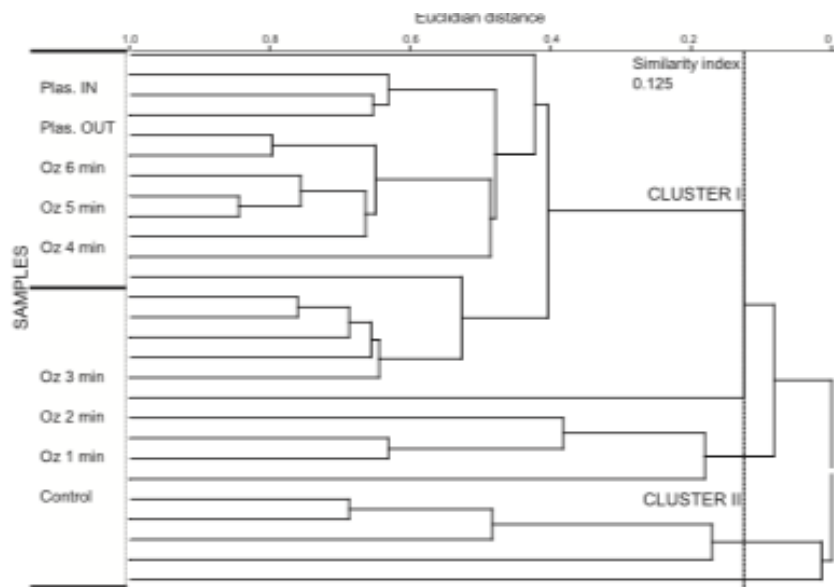


Fig. 2. Dendrogram representing chemical composition similarity relationships among orange juices to whose cluster it belongs: I) plasma IN, plasma OUT, and 4–6 min ozone; II) control, and 1–3 min ozone.

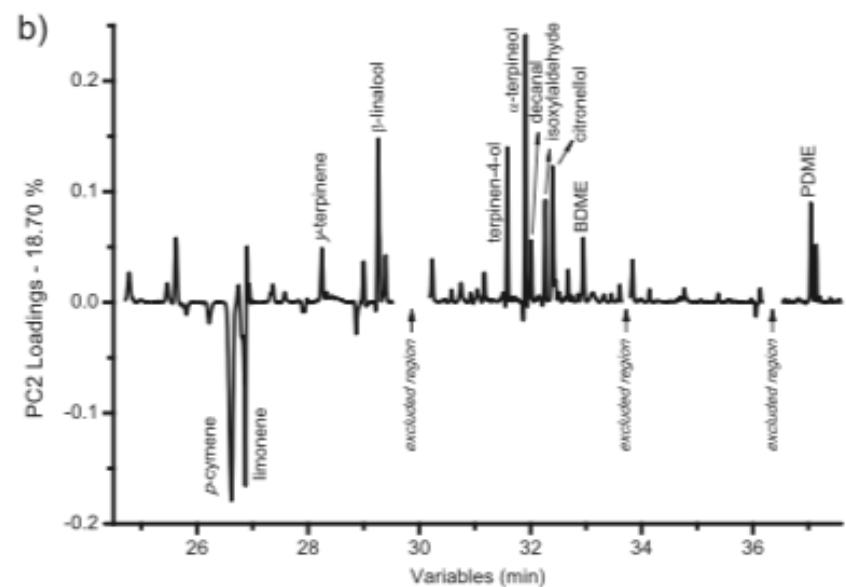
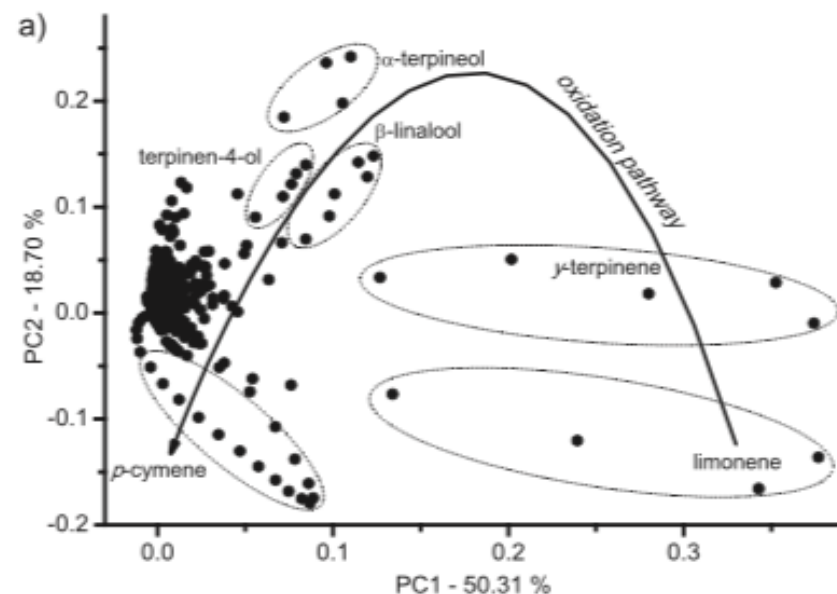
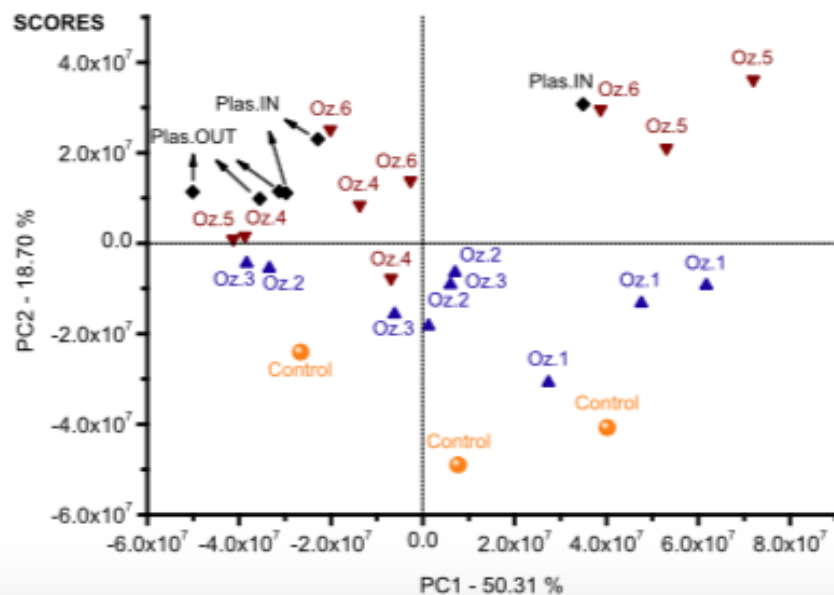


Fig. 4. PC1 vs PC2 loadings plotted in two dimensions (a); and PC2 plotted in line (b). The excluded regions reflect interfering signals removed for chemometrics.

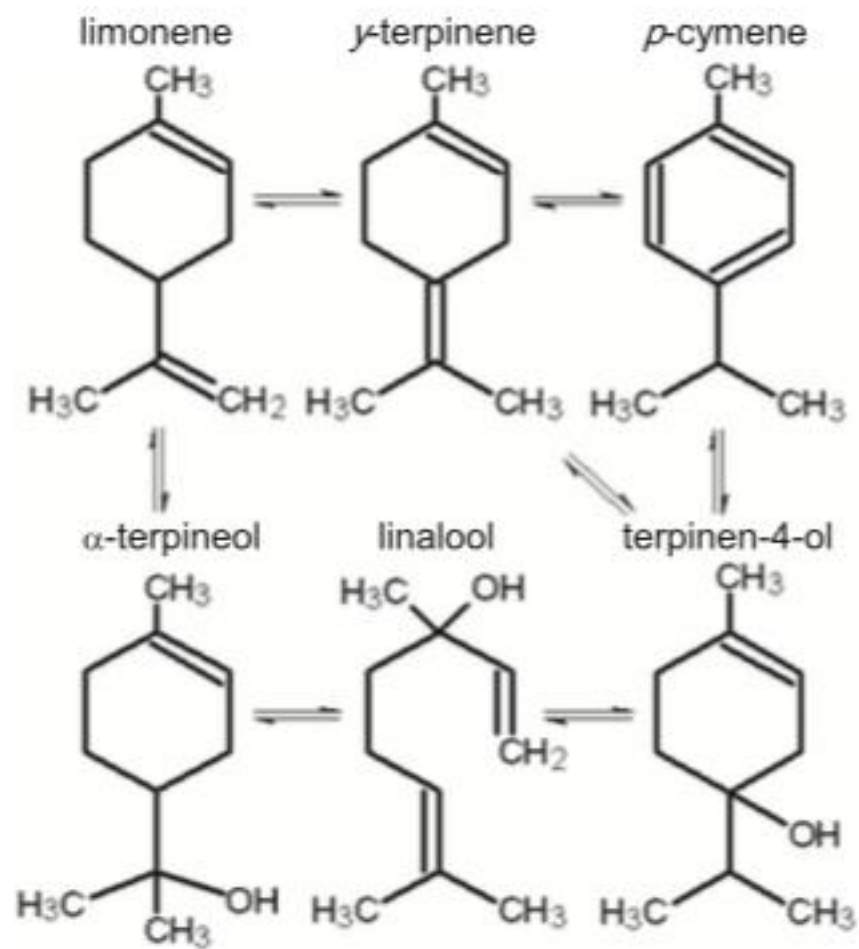


Fig. 5. Proposed oxidation, hydrolysis and reduction of terpenes under plasma and ozone processing of orange juice.

NMR spectroscopy and chemometrics to evaluate different processing of coconut water

Amostra: água de coco

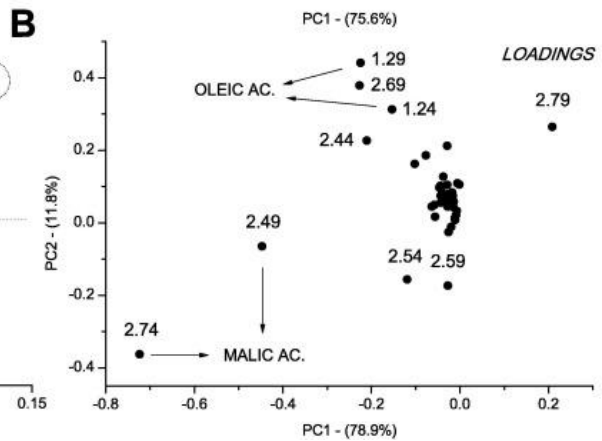
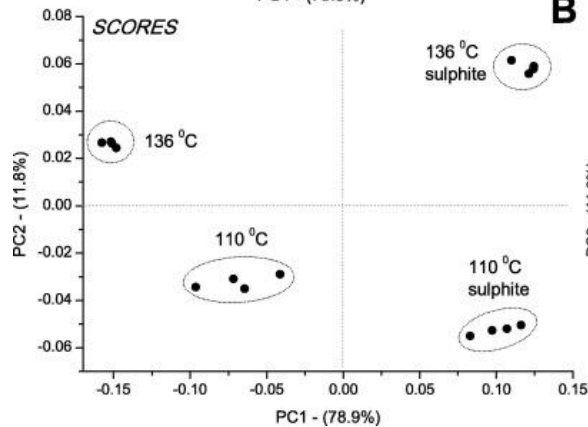
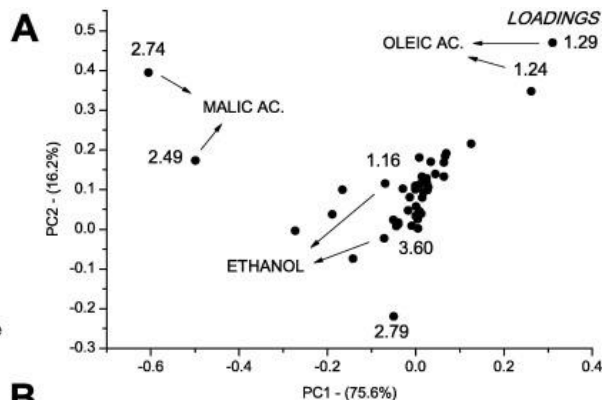
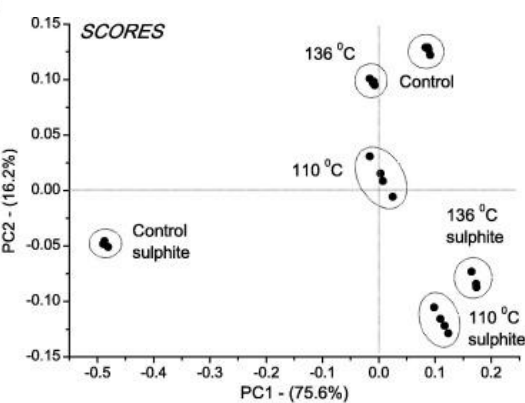
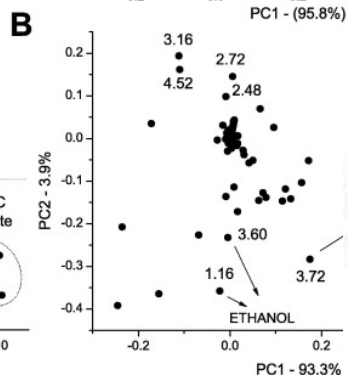
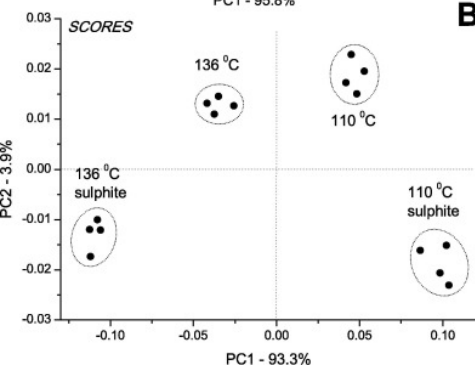
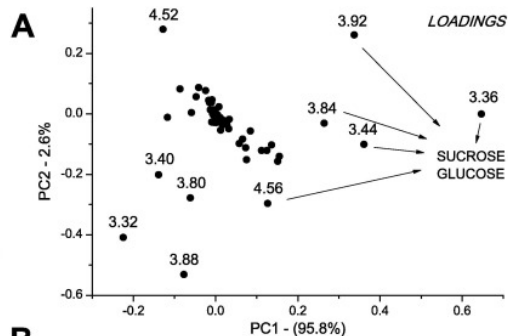
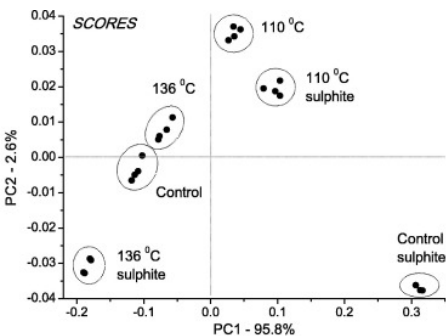
Processamento: térmico (UHT) + com/sem SO₂

Análise: RMN ¹H

Quimiometria: PCA e quantificação (*q*NMR)



Completo



Alifático

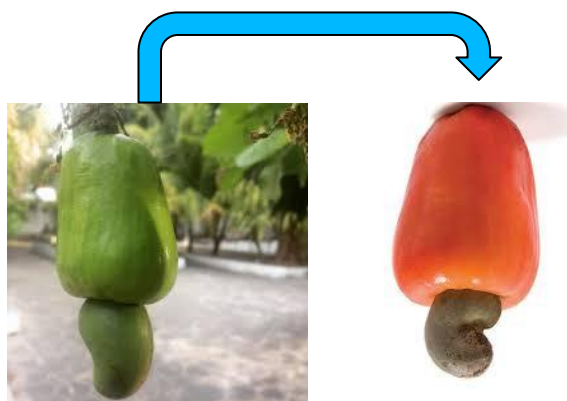
UPLC–qTOF-MS/MS-based phenolic profile and their biosynthetic enzyme activity used to discriminate between cashew apple (*Anacardium occidentale* L.) maturation stages

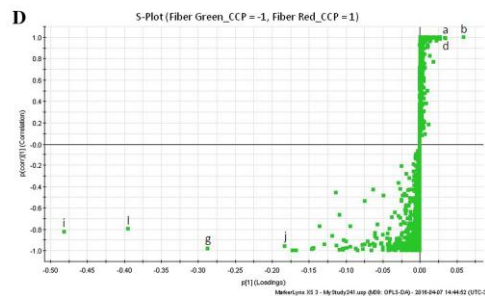
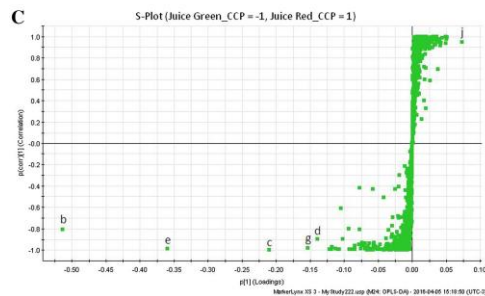
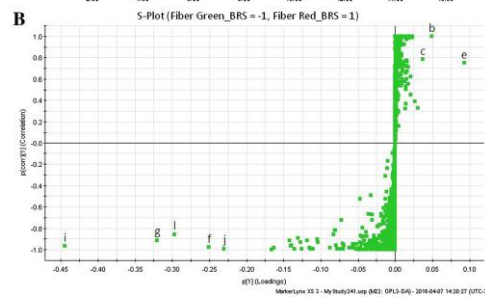
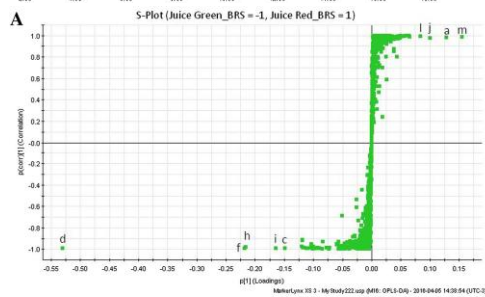
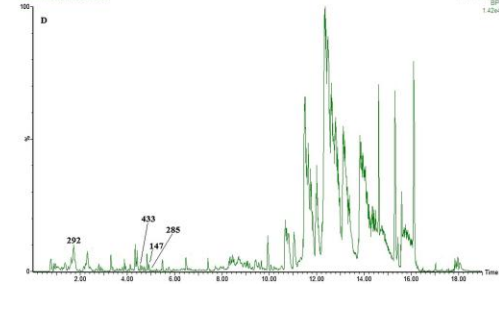
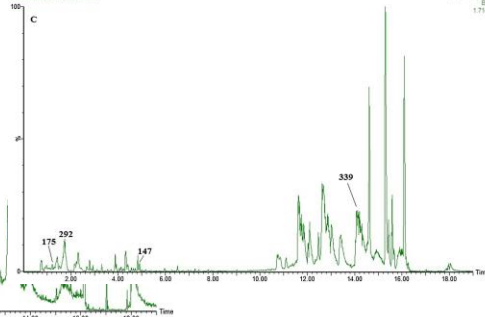
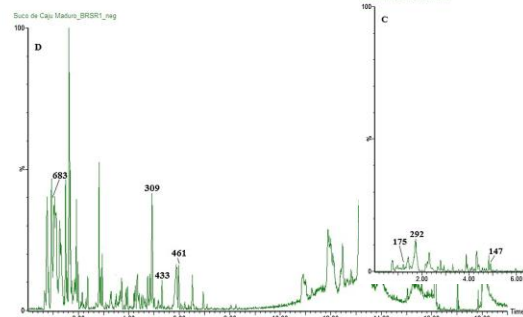
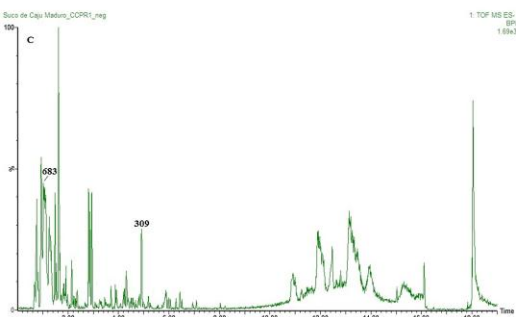
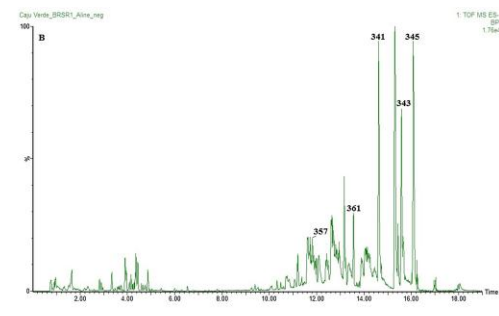
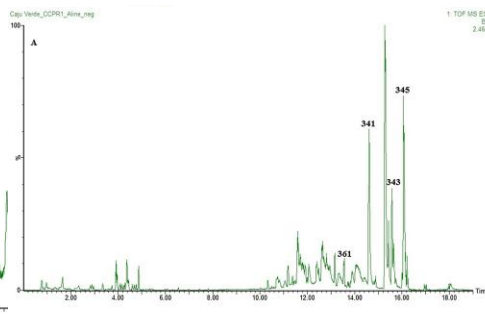
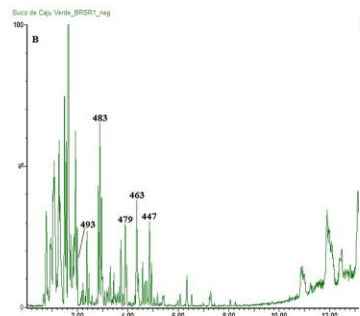
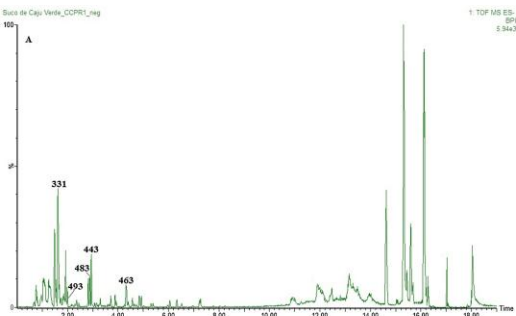
Amostra: caju

Processamento: diferentes estádios de maturação

Análise: LC-MS

Quimiometria: PCA e OPLS-DA





cinnamoyl [glucoside](#) may be used as a chemical [marker](#) stage 7-ripe juice [samples](#), while monogalloyl diglucoside (c) and digalloyl [glucoside](#) (d) as chemical markers of stage 2-green juice samples from both cashew clones. Meanwhile, four compounds could be used as markers for stage 2-green [fiber](#) of both clones, [anacardic acids](#) (i, j and l) and GA₁₉ (g) which have low [solubility](#) in [aqueous solutions](#) due to their chemical natures as phenolic [lipids](#) and a [diterpenoid](#) acid, respectively.

The evaluation of enzymes of phenolic [biosynthetic pathway](#) in juice samples showed that PAL activity decreased significantly during the [development](#) of cashew apple clones, despite of which, it was much higher in ripe CCP 76 cashew apple. UGT activity differed between clones, however its main product, cinnamoyl glucoside was the most characteristic compound, thus a chemical marker of ripe juice samples from both clones. FLS showed the highest specific activity in both cashew clones and its product, [flavonols](#) (glycosylated probably due to UGT action), were identified in cashew apple at immature and ripe stages. LAR activity was not detected during the development of cashew apple from clones BRS 189 and CCP 76 agreeing with previous publications [\[12\]](#), [\[13\]](#) which found no LAR substrates, flavan-3-ols or proanthocyanidins in cashew apples.

Chemical profiling of guarana seeds (*Paullinia cupana*) from different geographical origins using UPLC-QTOF-MS combined with chemometrics

^1H quantitative nuclear magnetic resonance and principal component analysis as tool for discrimination of guarana seeds from different geographic regions of Brazil

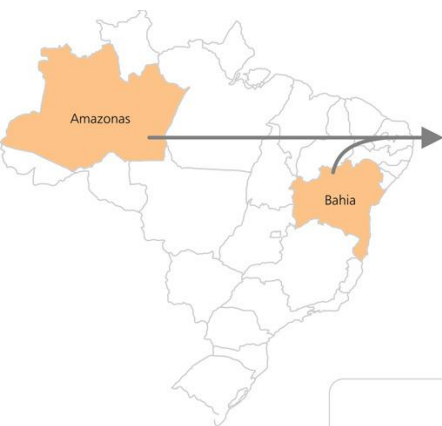
Amostra: guaraná

Processamento: diferentes origens

Análise: LC-MS e RMN ^1H

Quimiometria: PCA e quantificação

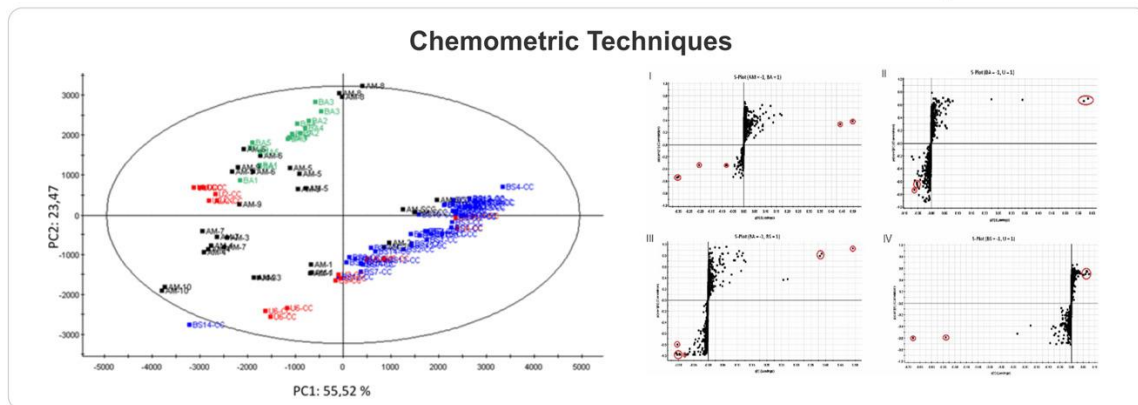
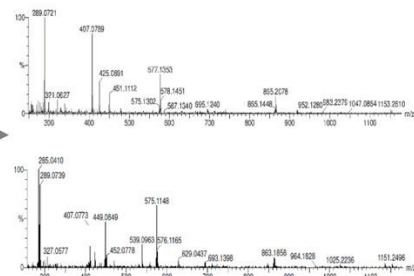


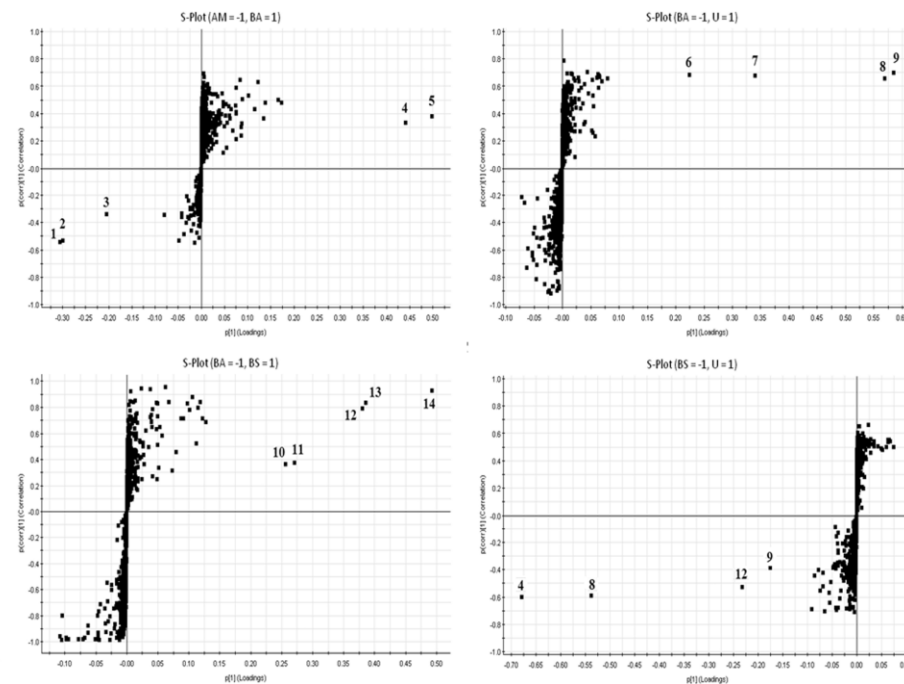
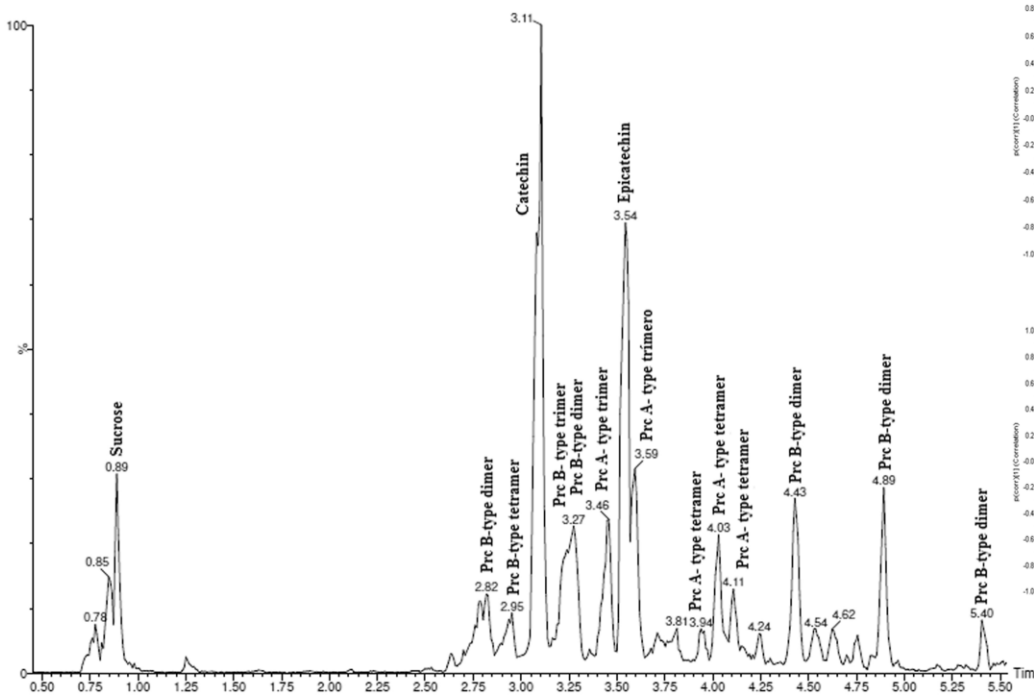
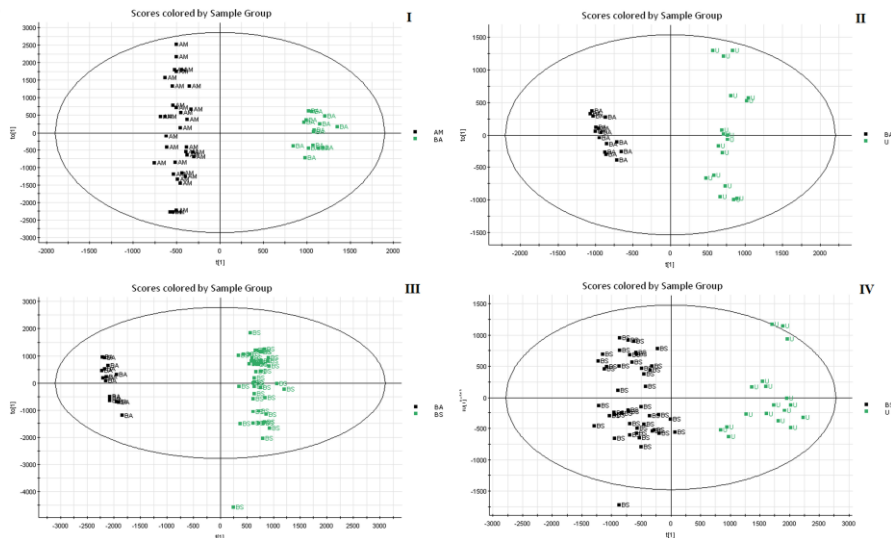
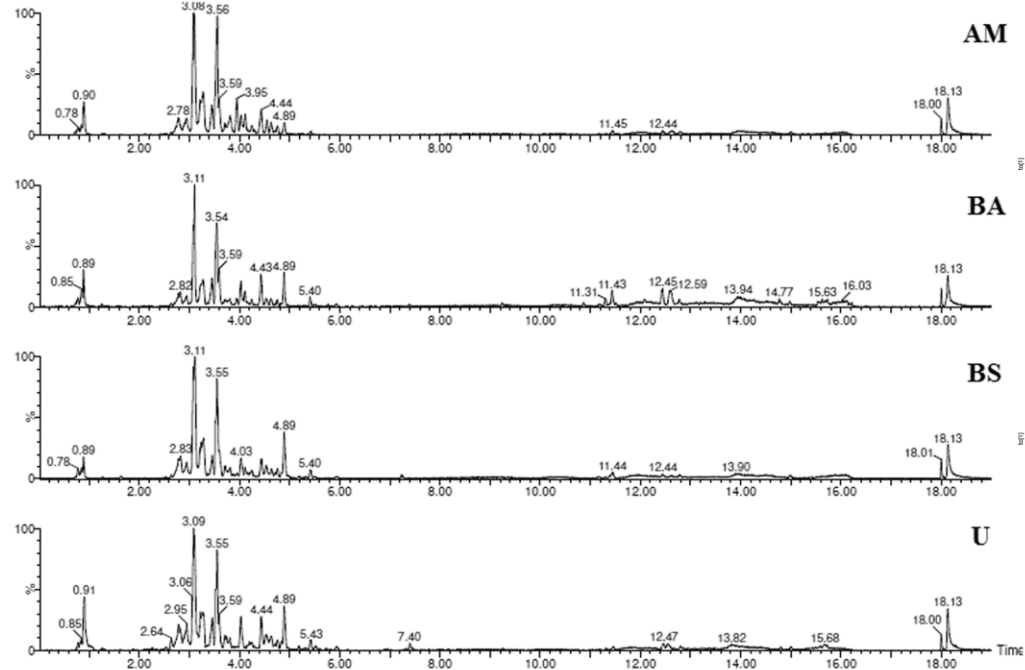


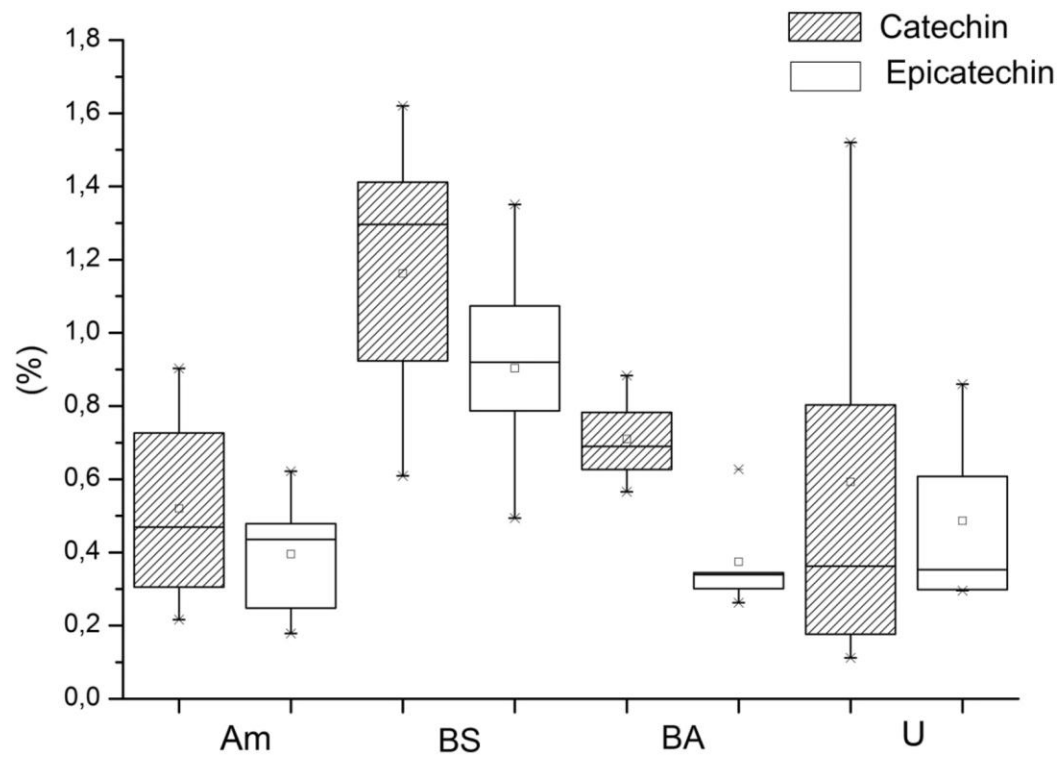
Paullinia cupana



UPLC-QTOF-MS







Genotype evaluation of cowpea seeds (*Vigna unguiculata*) using ^1H qNMR combined with exploratory tools and solid-state NMR

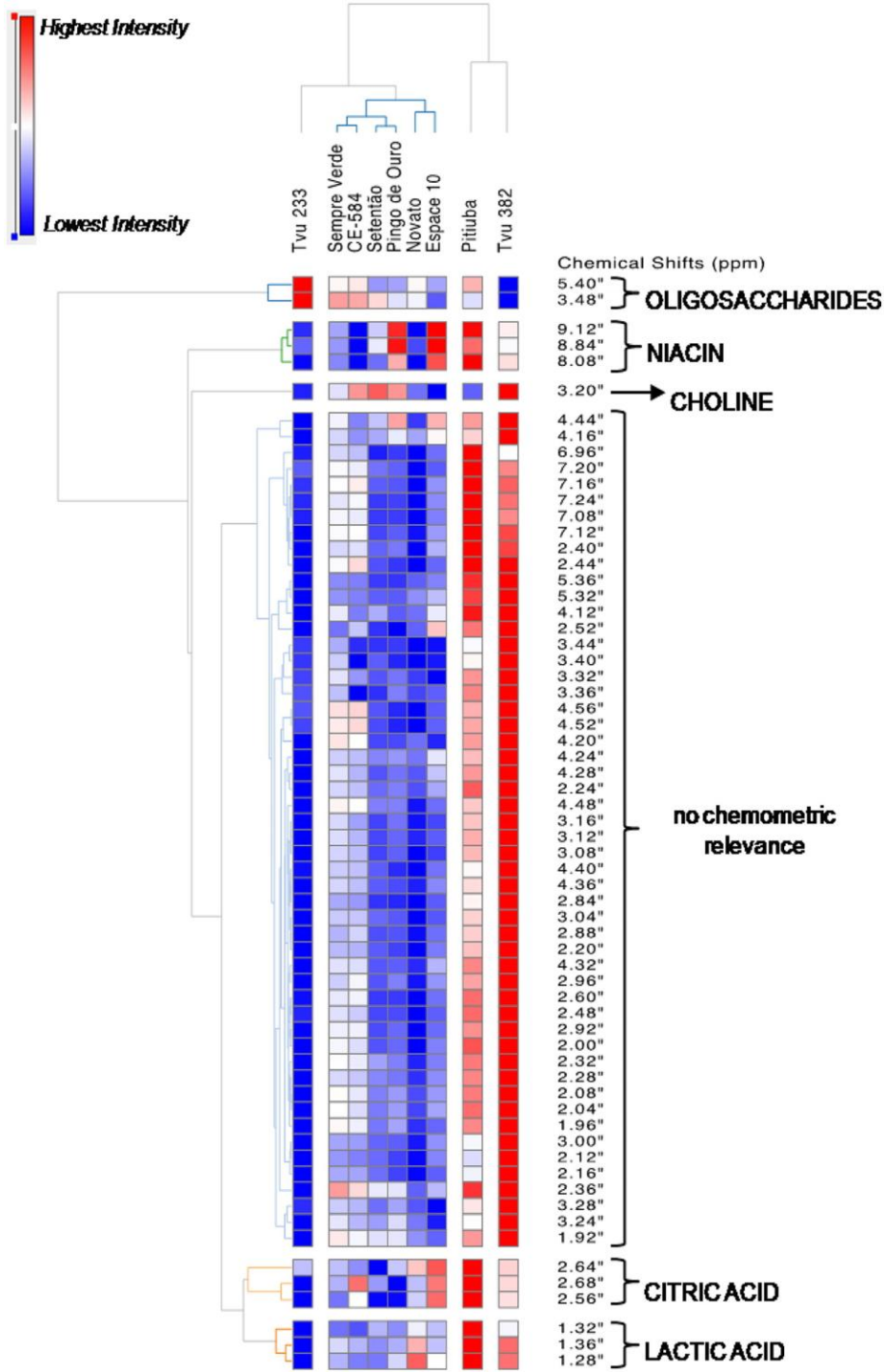
Amostra: feijão caupi

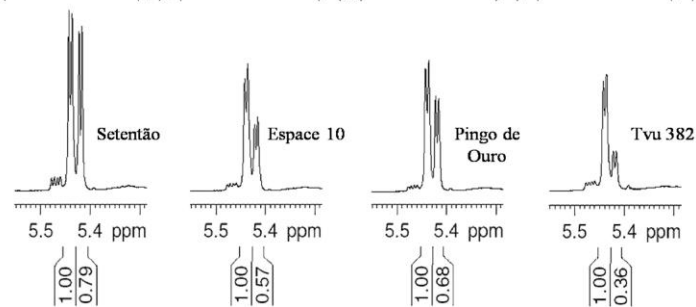
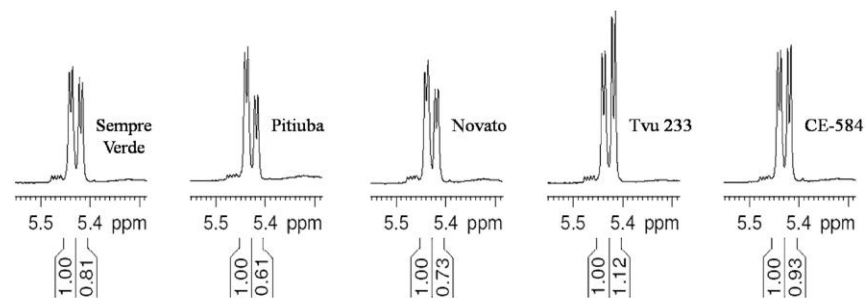
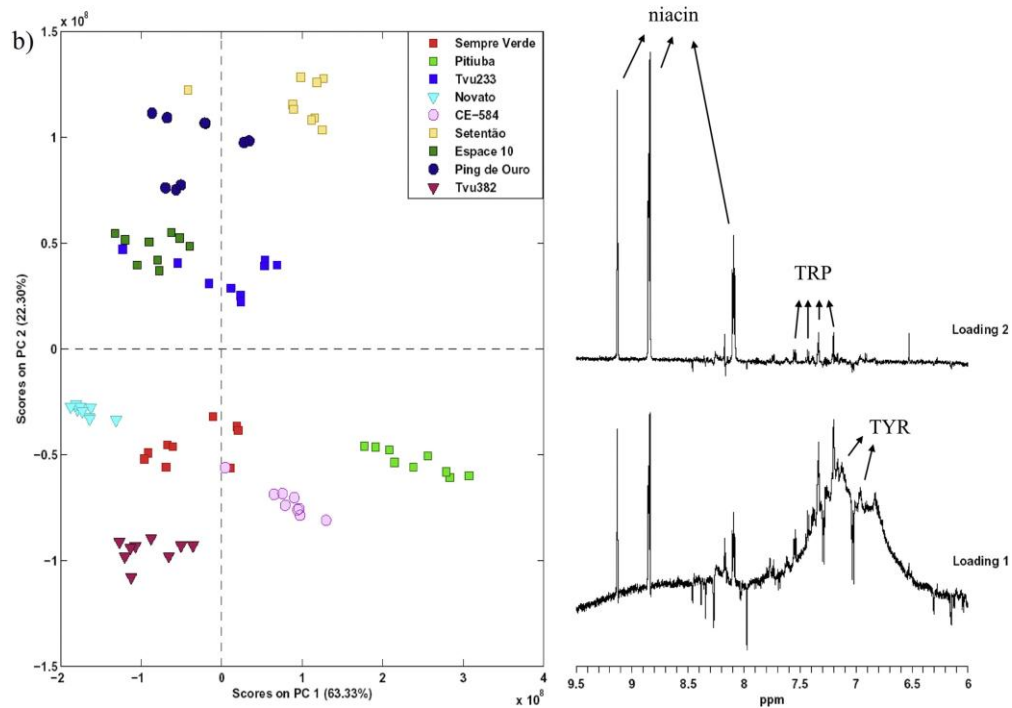
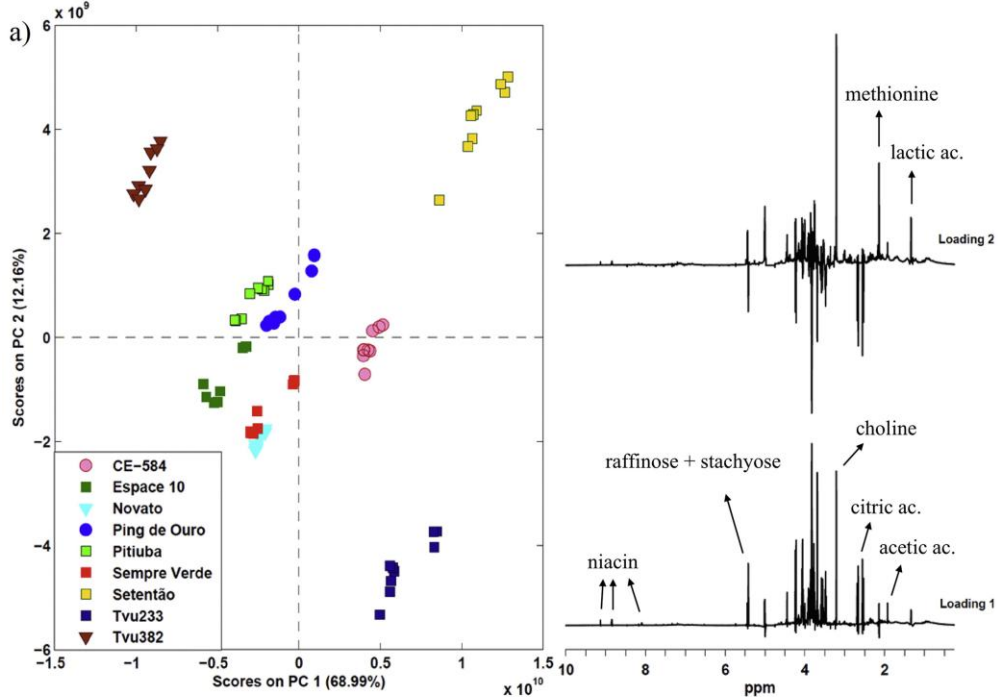
Processamento: (9 genótipos)

Análise: RMN ^1H

Quimiometria: PCA e quantificação (qNMR)







Tracking thermal degradation on passion fruit juice through Nuclear Magnetic Resonance and chemometrics

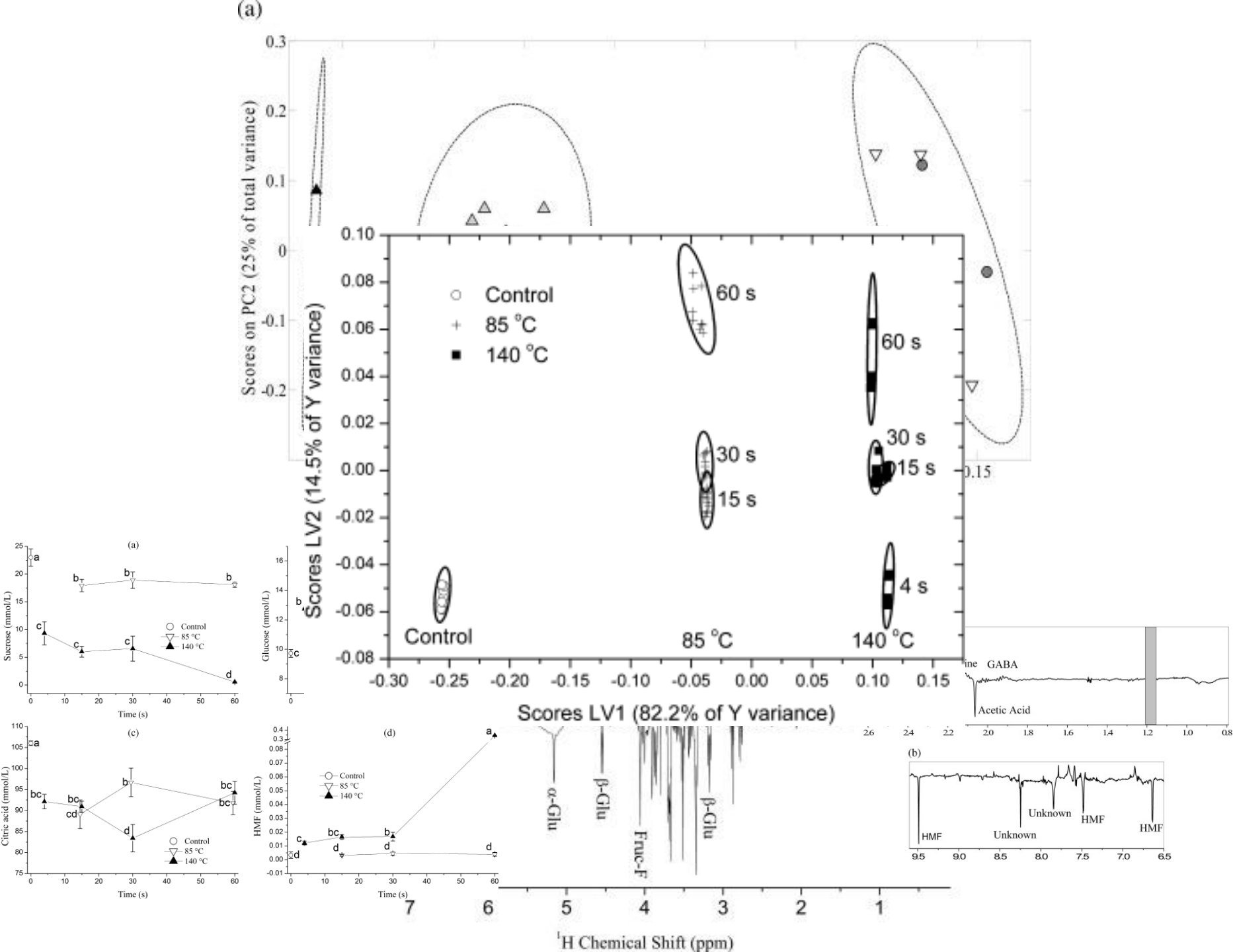
Amostra: suco maracujá

Processamento: térmico UHT e HTST

Análise: RMN ^1H

Quimiometria: PCA e quantificação ($q\text{NMR}$)





Chemometric evaluation of the volatile profile of probiotic melon and probiotic cashew juice

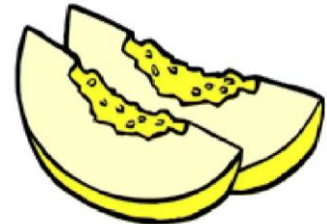
Amostra: suco melão e caju

Processamento: probiótico + térmico UHT e HTST

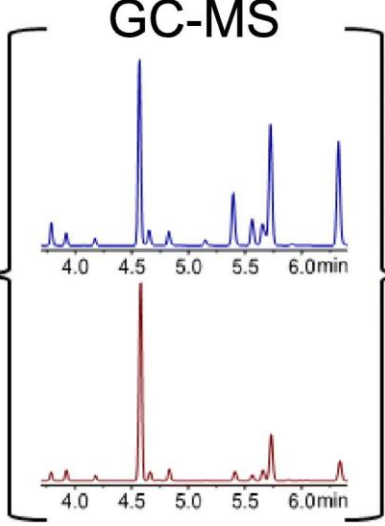
Análise: GC-MS

Quimiometria: PCA e quantificação (q NMR)

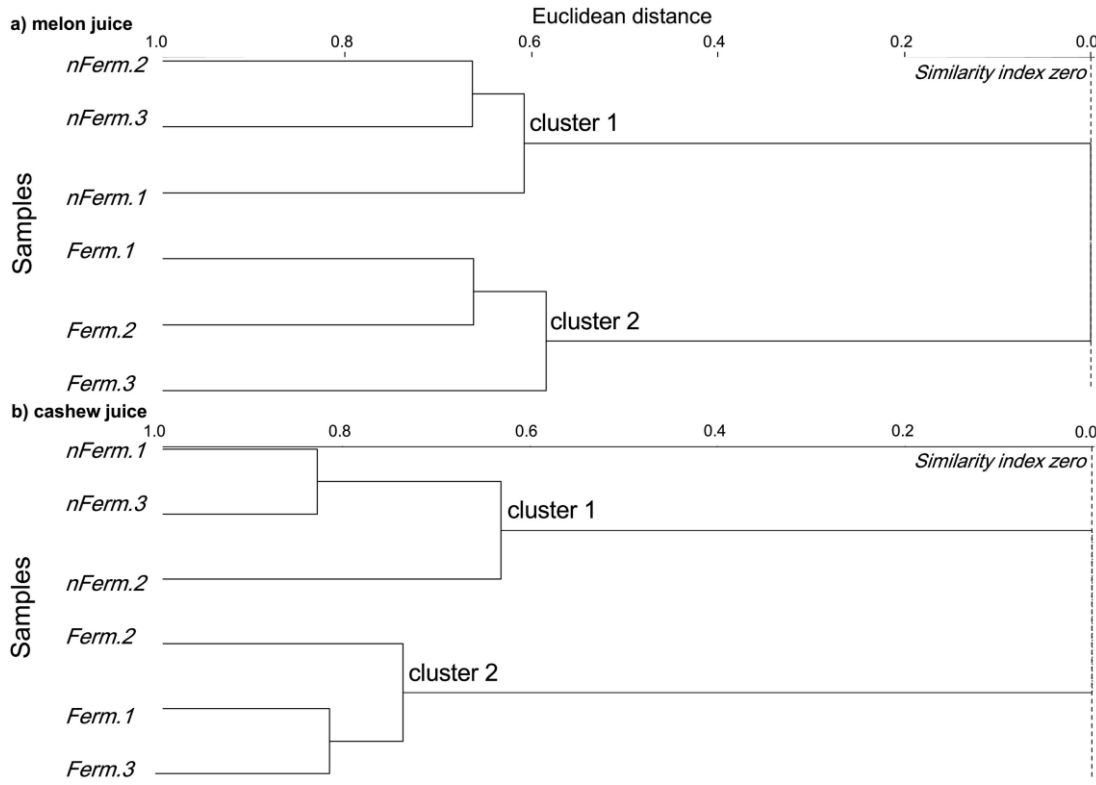
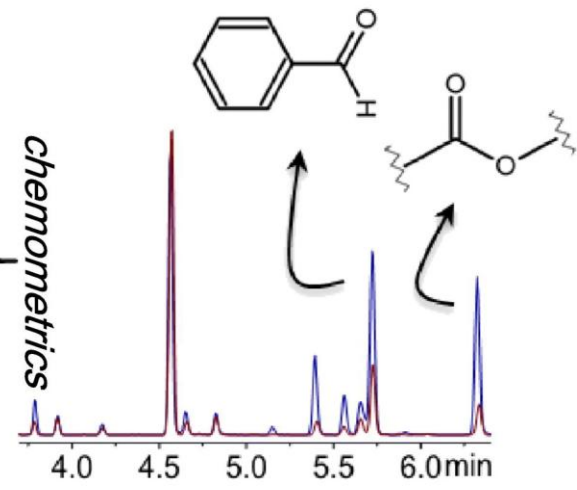


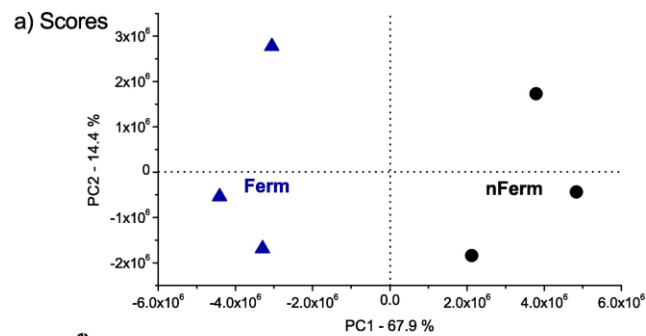


Lactobacillus casei

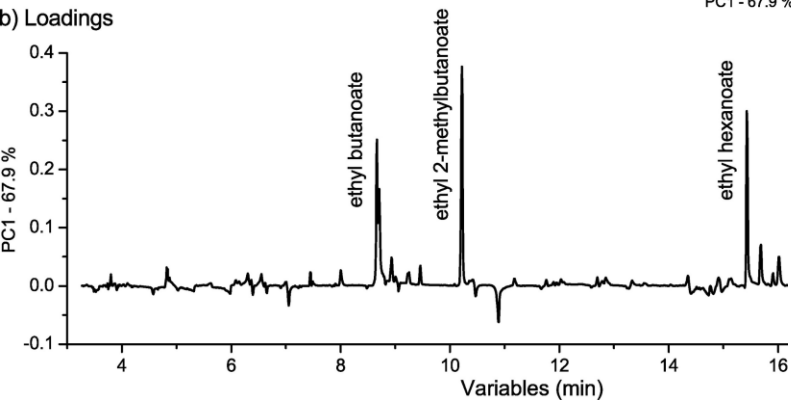


chemometrics

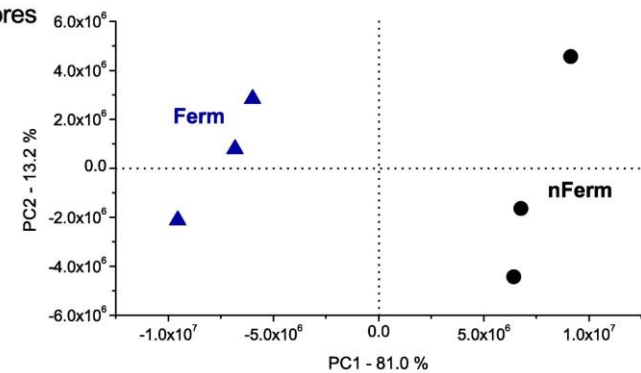




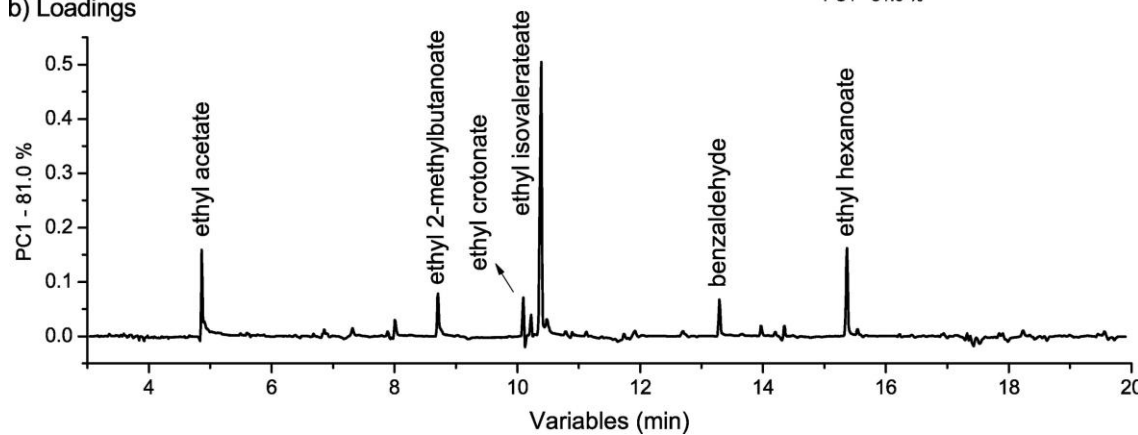
b) Loadings

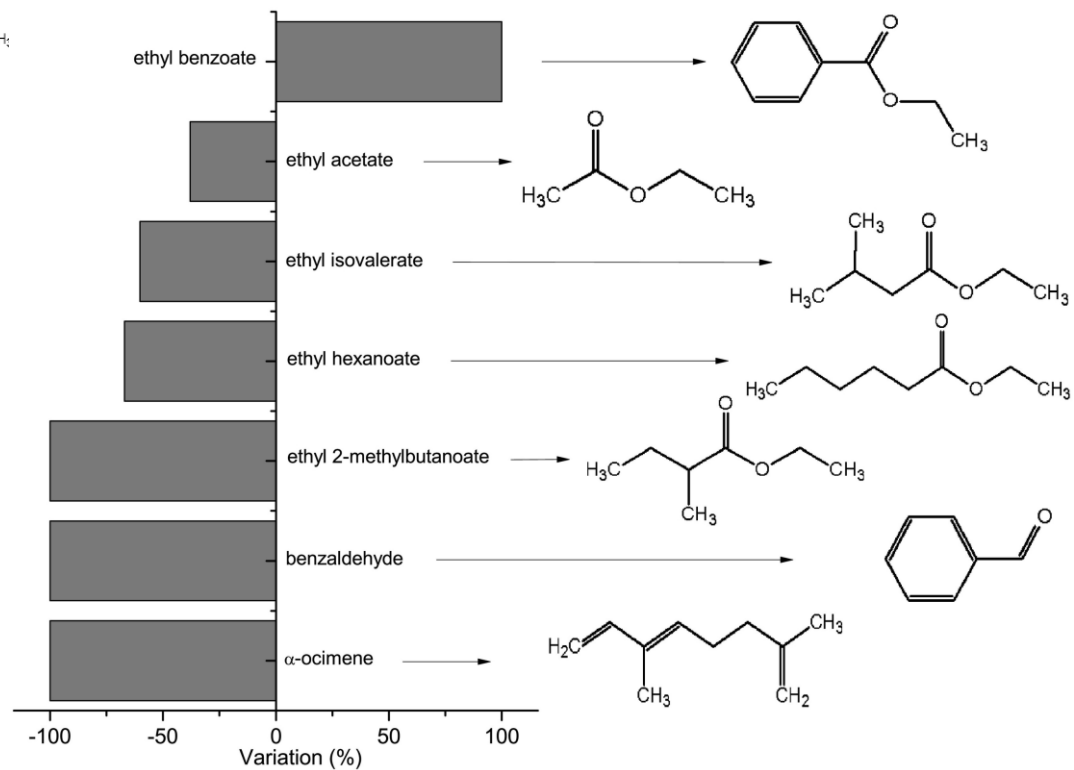
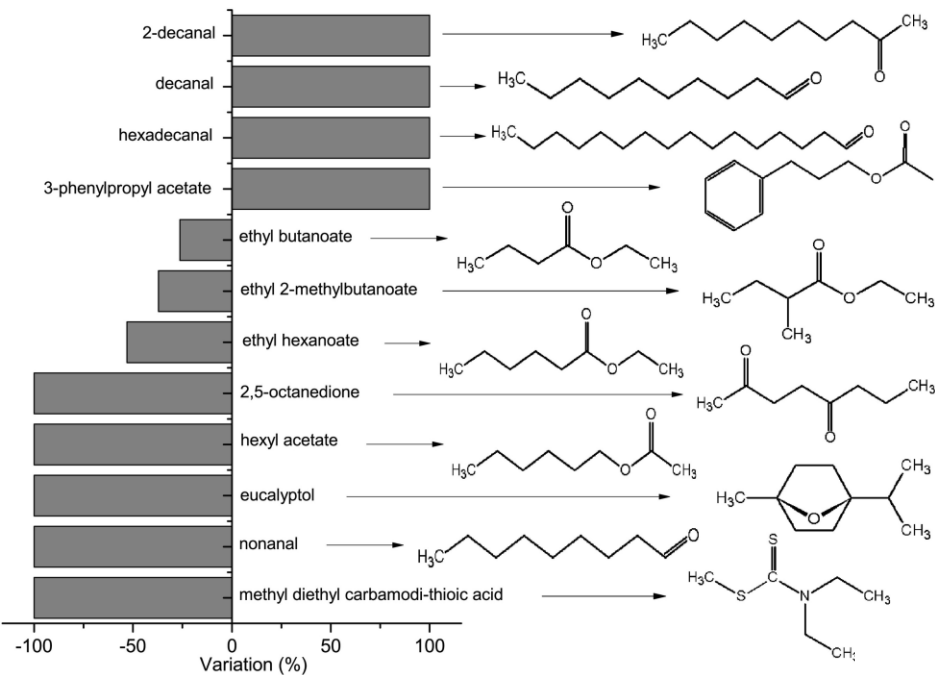


a) Scores



b) Loadings





Evaluation of thermal and non-thermal processing effect on non-prebiotic and prebiotic acerola juices using ^1H qNMR and GC-MS coupled to chemometrics

Amostra: suco acerola

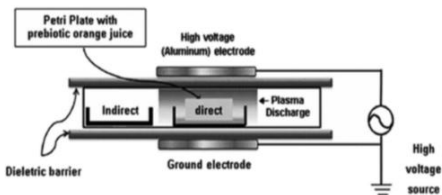
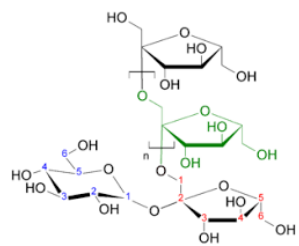
Processamento: prébiotico + térmico UHT e HTST + US+ Plasma

Análise: RMN ^1H + GC-MS

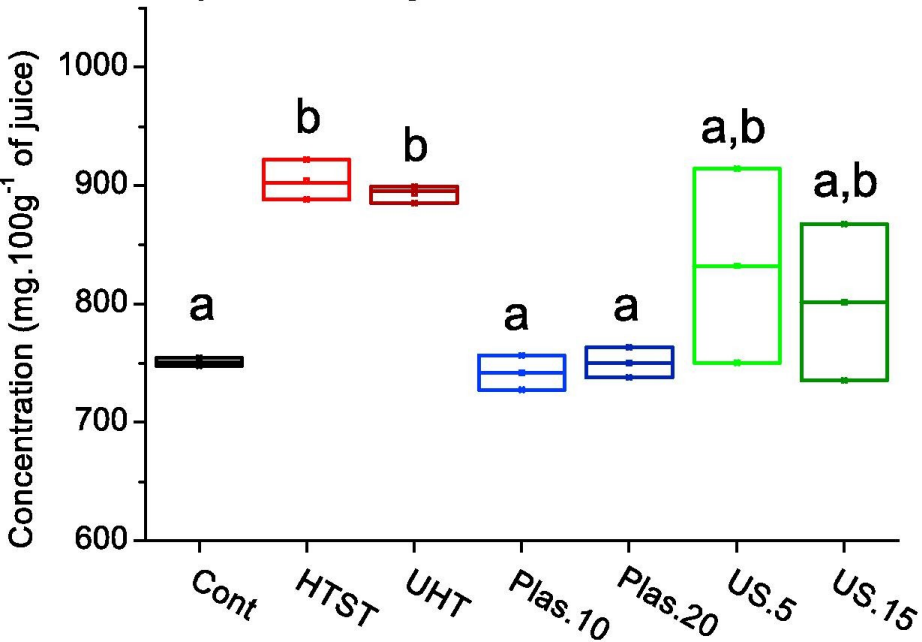
Quimiometria: PCA e quantificação (qNMR)



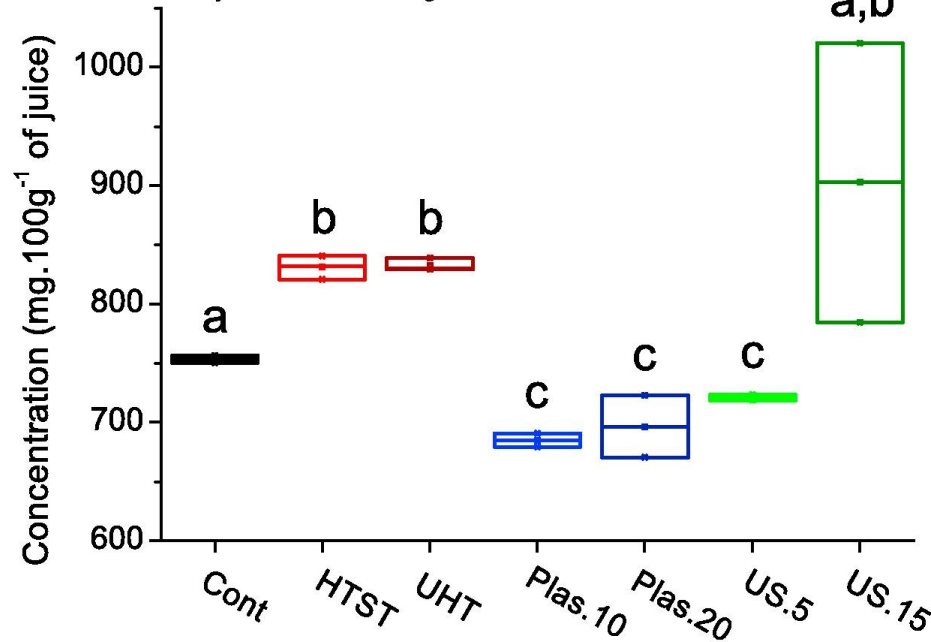
+



a) acerola juice

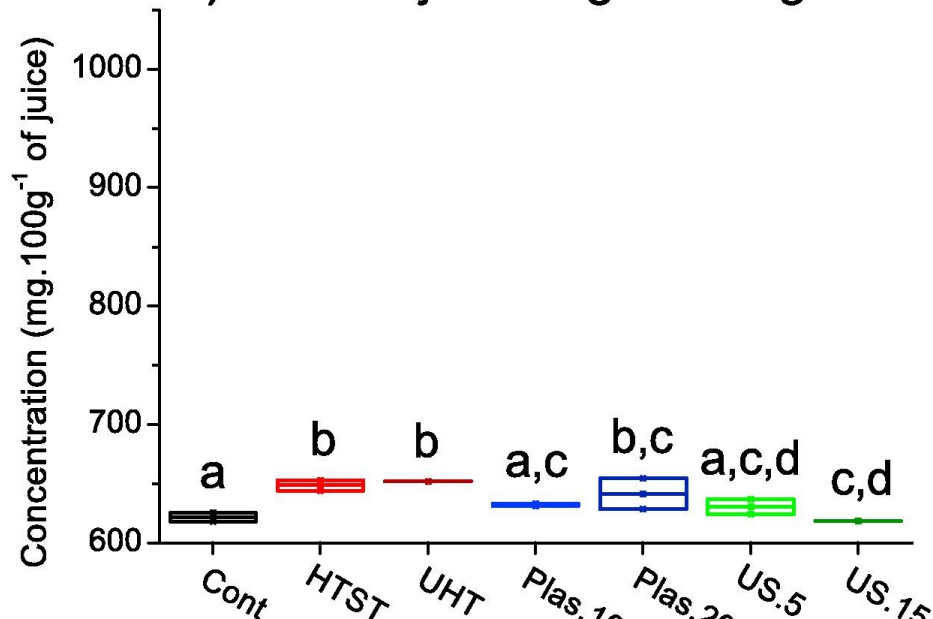


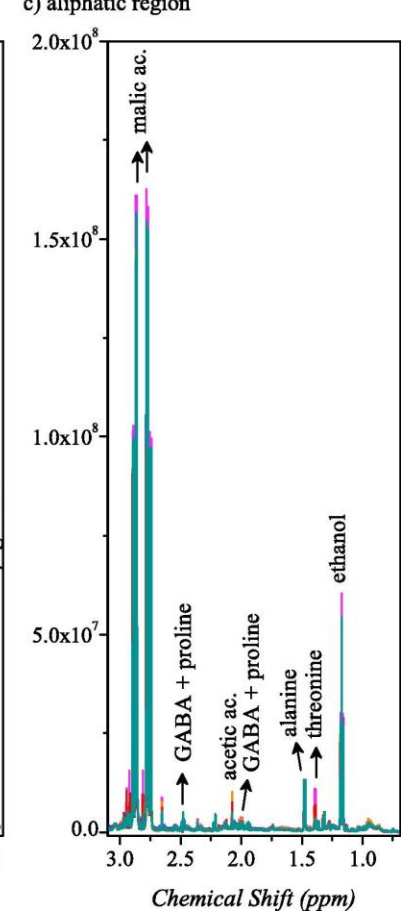
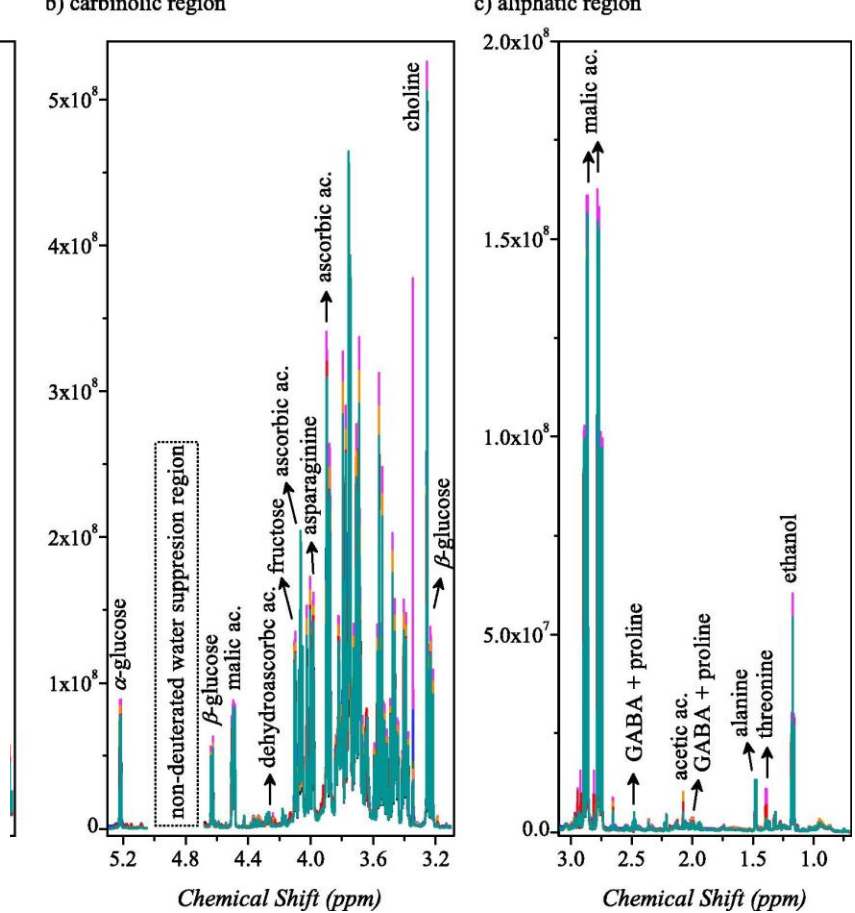
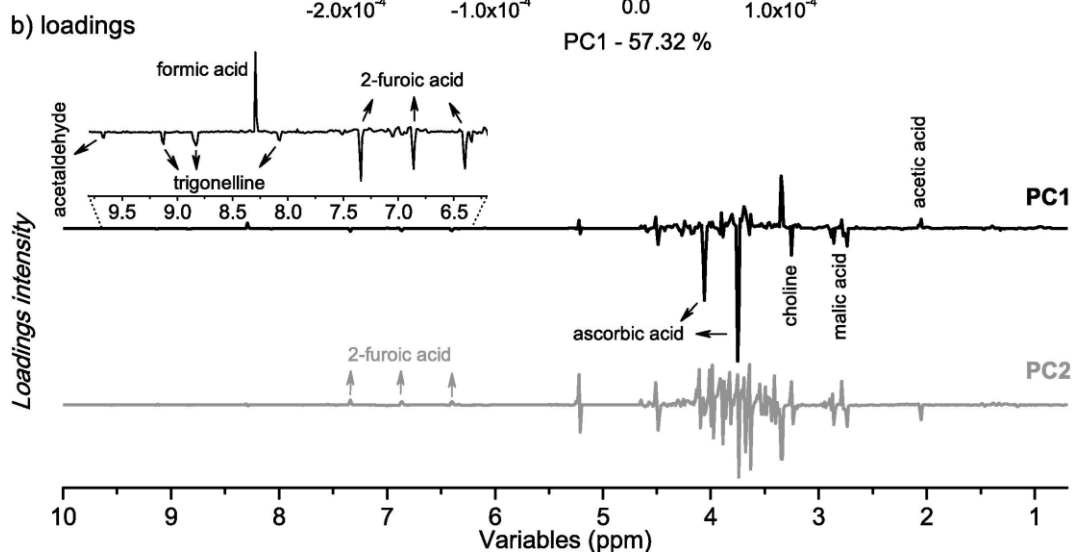
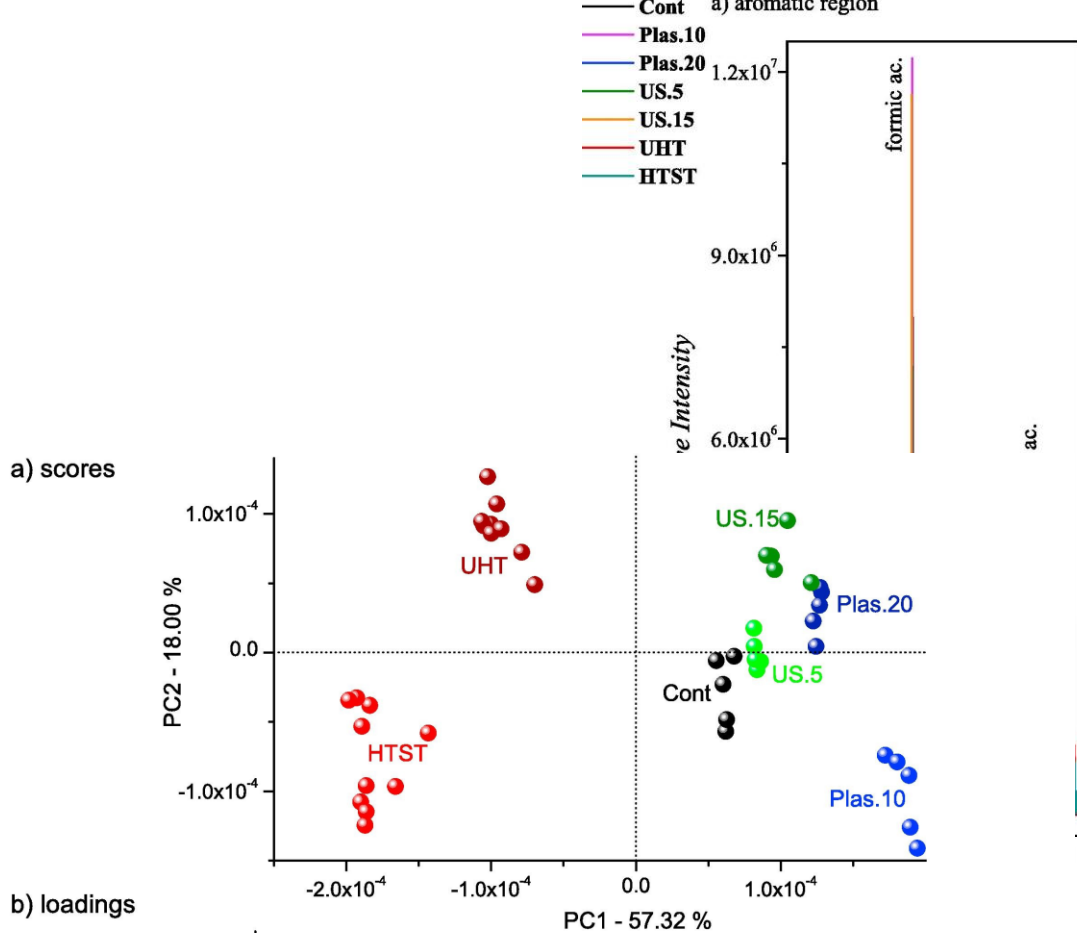
b) acerola juice + inulin

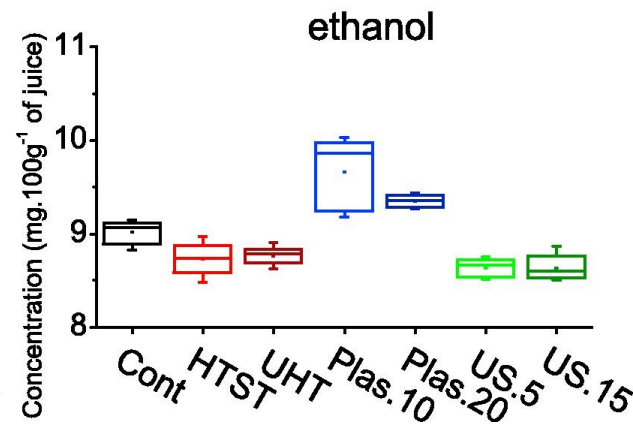
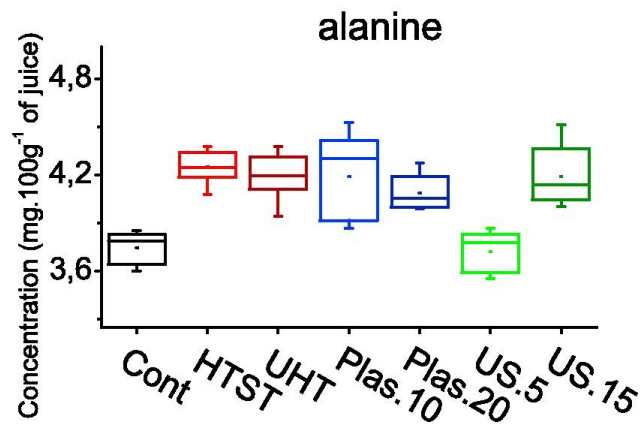
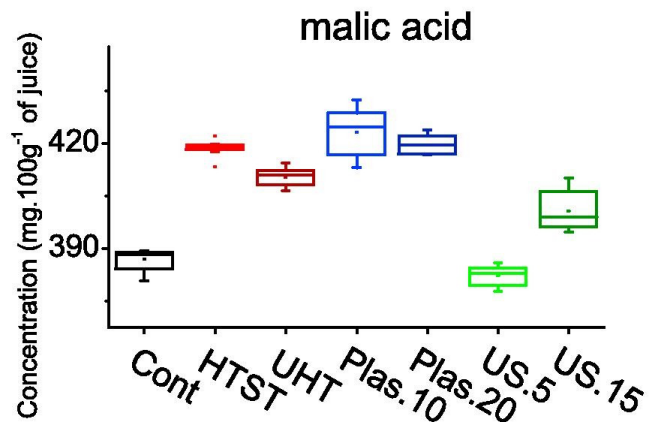
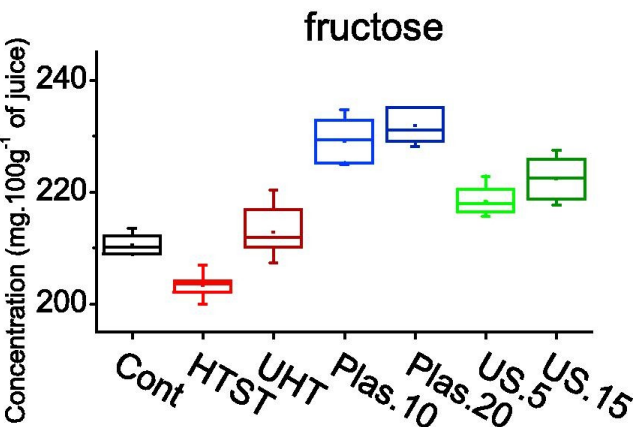
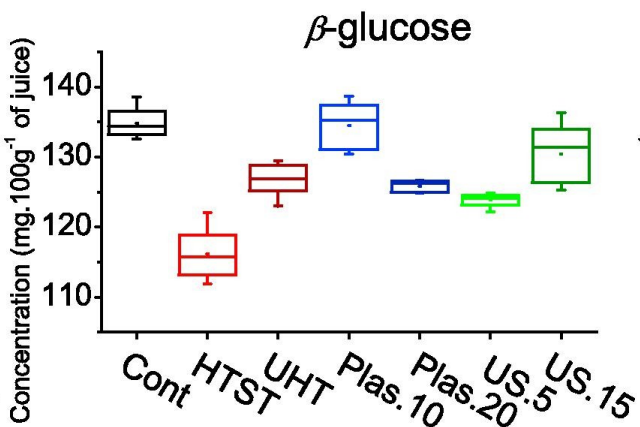
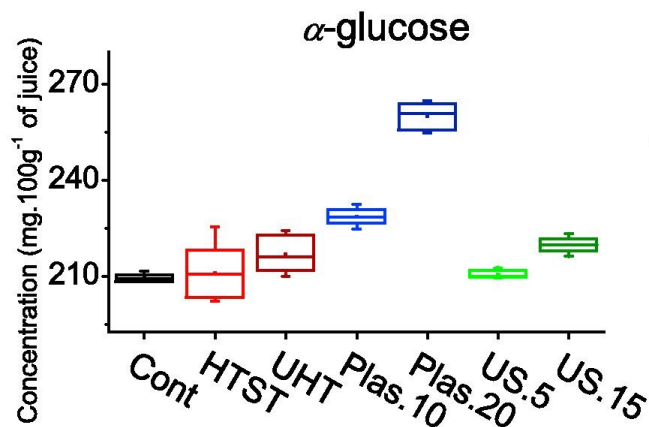
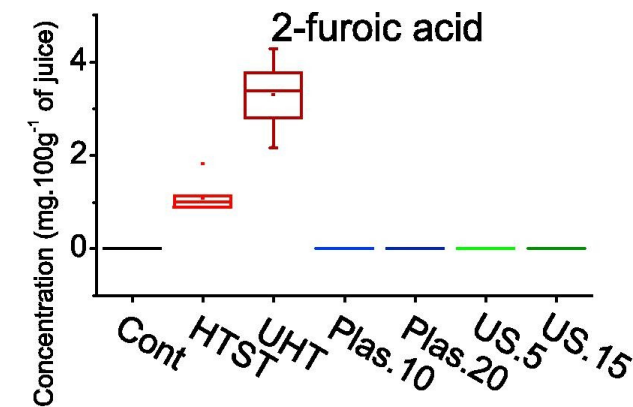
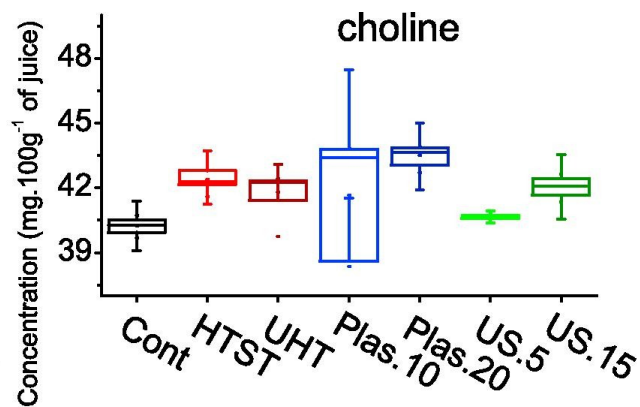
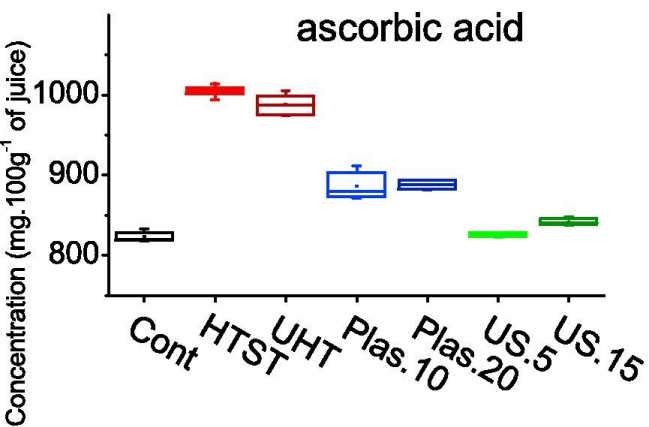


Vitamina C

c) acerola juice + gluco-oligosaccharides

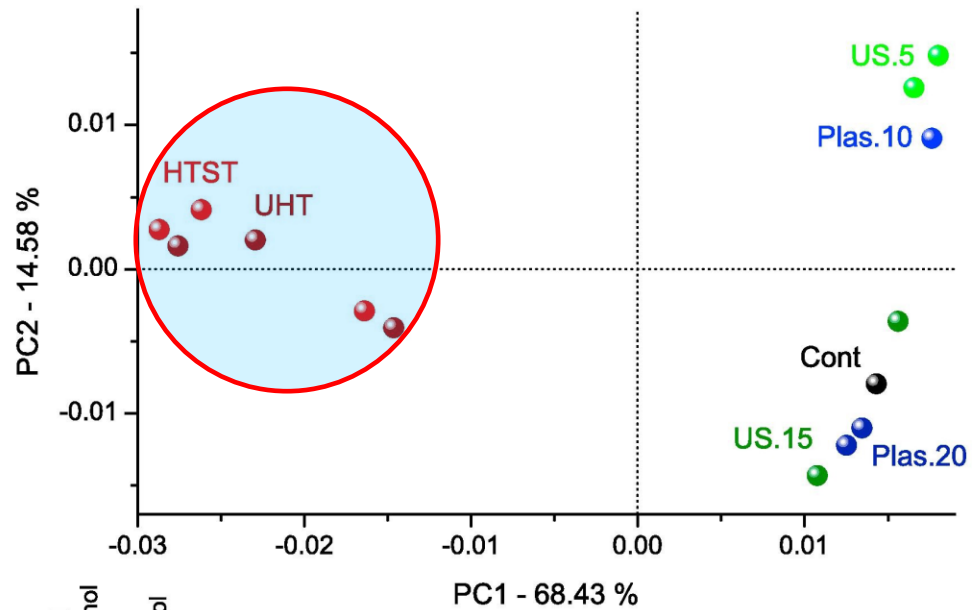






voláteis

a) scores



b) loadings

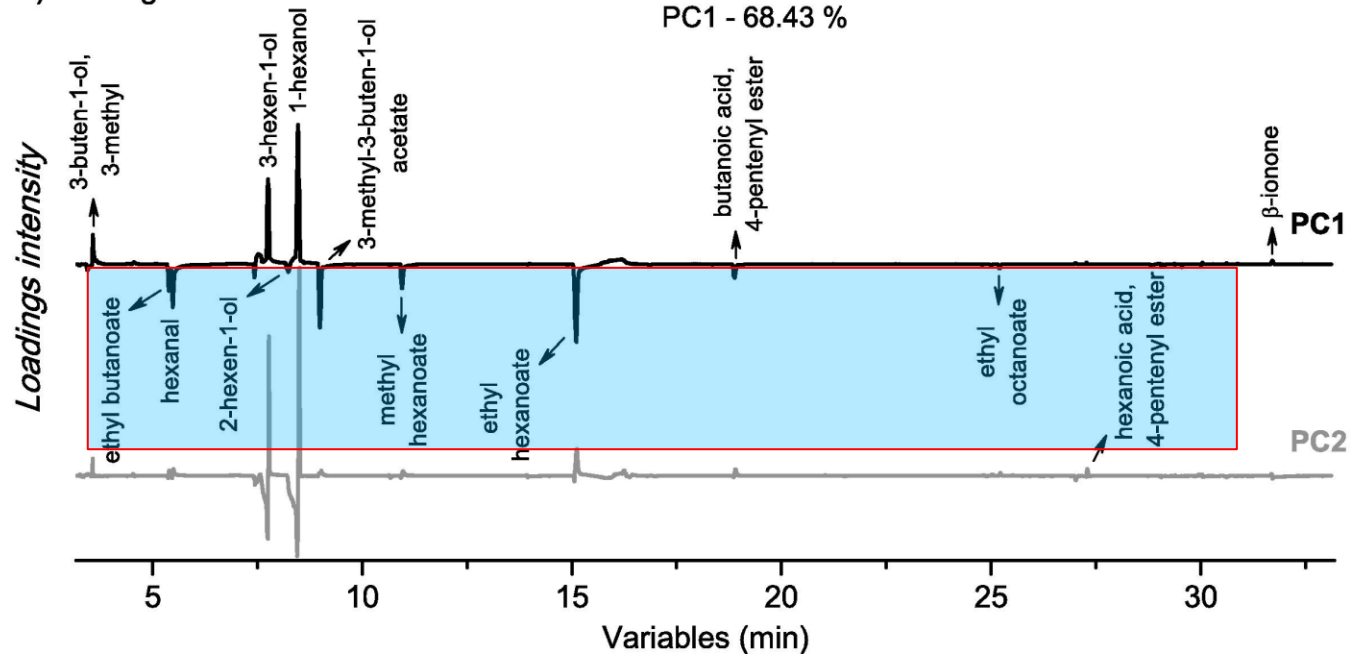


Table 1

Structures of the relevant volatile flavor components detected in acerola juices according to PCA, with respective retention times (RT), experimental and reference retention index (RI), major *m/z* peak, and percentage (%) of match.

RT (min)	Compound name	Structure	RI ¹ exp.	RI ¹ refer.	Major <i>m/z</i>	Match (%)
3.577	3-methyl-3-buten-1-ol		727	723 ²	41	94
5.384	hexanal		801	801 ²	44	86
5.479	ethyl butanoate		804	802 ²	43	92
7.706	3-hexen-1-ol		856	850 ²	41	97
8.021	2-hexen-1-ol		864	859 ²	57	95
8.431	1-hexanol		873	871 ²	56	94
8.972	3-methyl-3-buten-1-ol, acetate		886	880 ²	43	95
10.957	methyl hexanoate		926	921 ²	74	94
15.086	ethyl hexanoate		1001	997 ²	88	95
18.897	butanoic acid, 4-pentyl ester		1067	1064 ²	68	84
25.208	ethyl octanoate		1199	1196 ²	94	88
27.310	hexanoic acid, 3-methyl-2-butenyl ester		1268	1267 ¹	88	68
31.670	β -ionone		1490	1487 ²	177	92

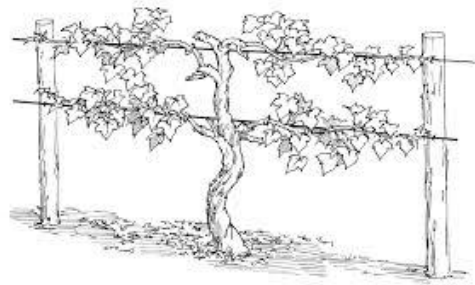
^1H NMR and LC-MS-based metabolomic approach for evaluation of the seasonality and viticultural practices in wines from São Francisco River Valley, a Brazilian semi-arid region

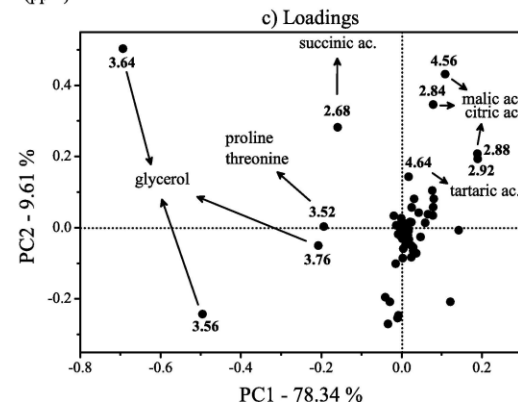
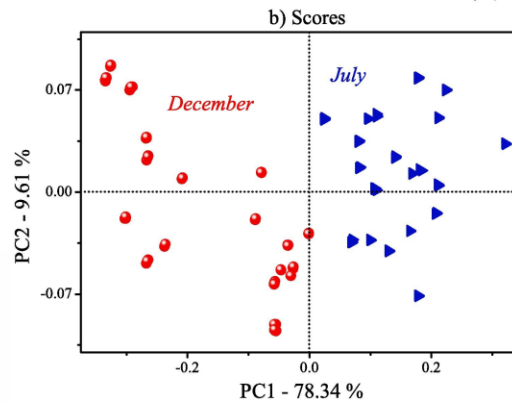
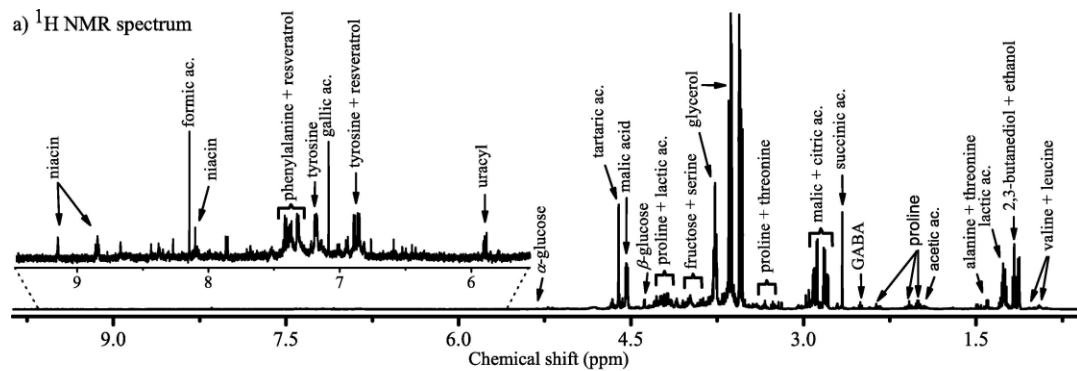
Amostra: vinho

Processamento: prébiotico + térmico UHT e HTST + US+ Plasma

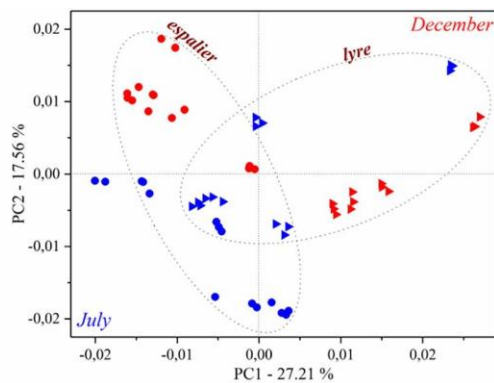
Análise: RMN ^1H + LC-MS

Quimiometria: PCA e quantificação ($q\text{NMR}$)

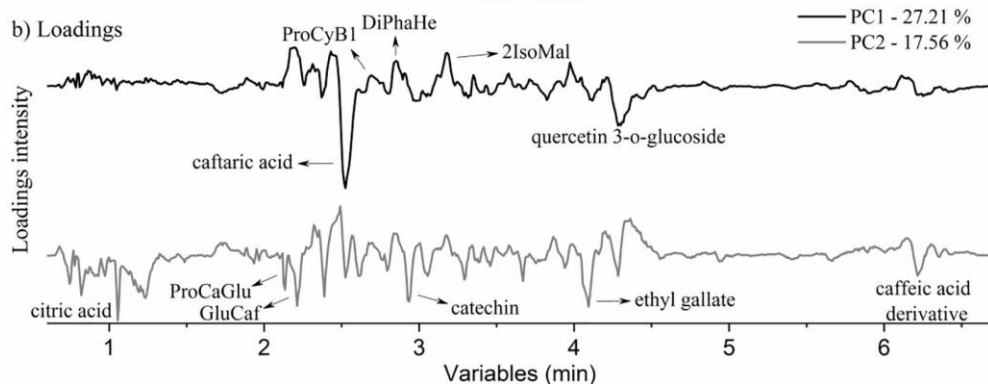


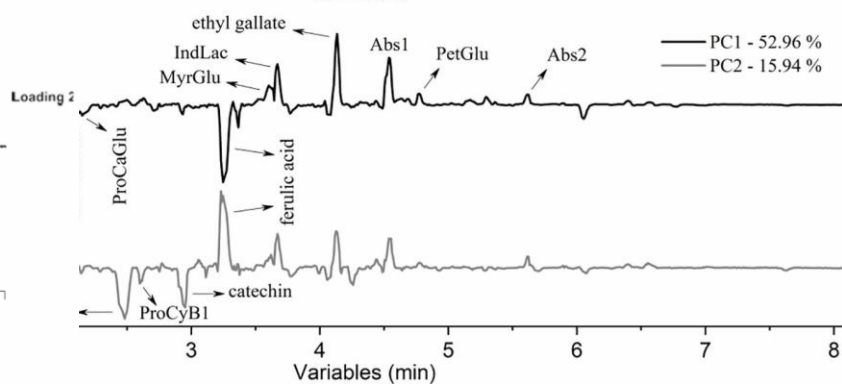
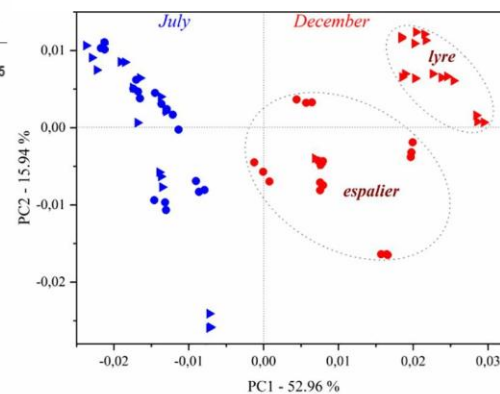
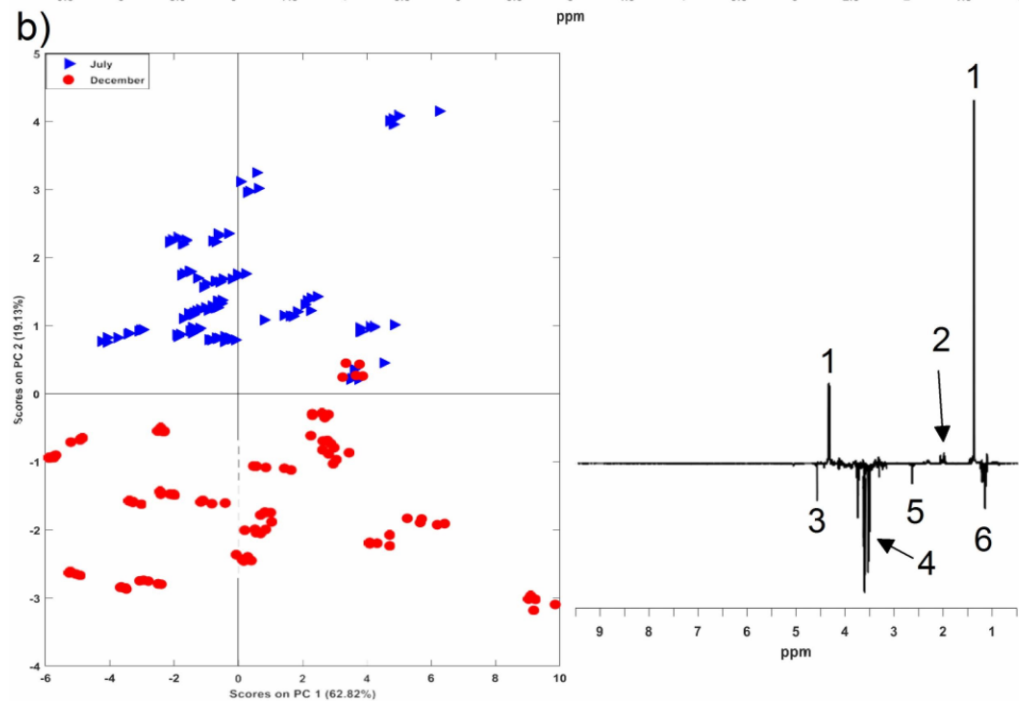
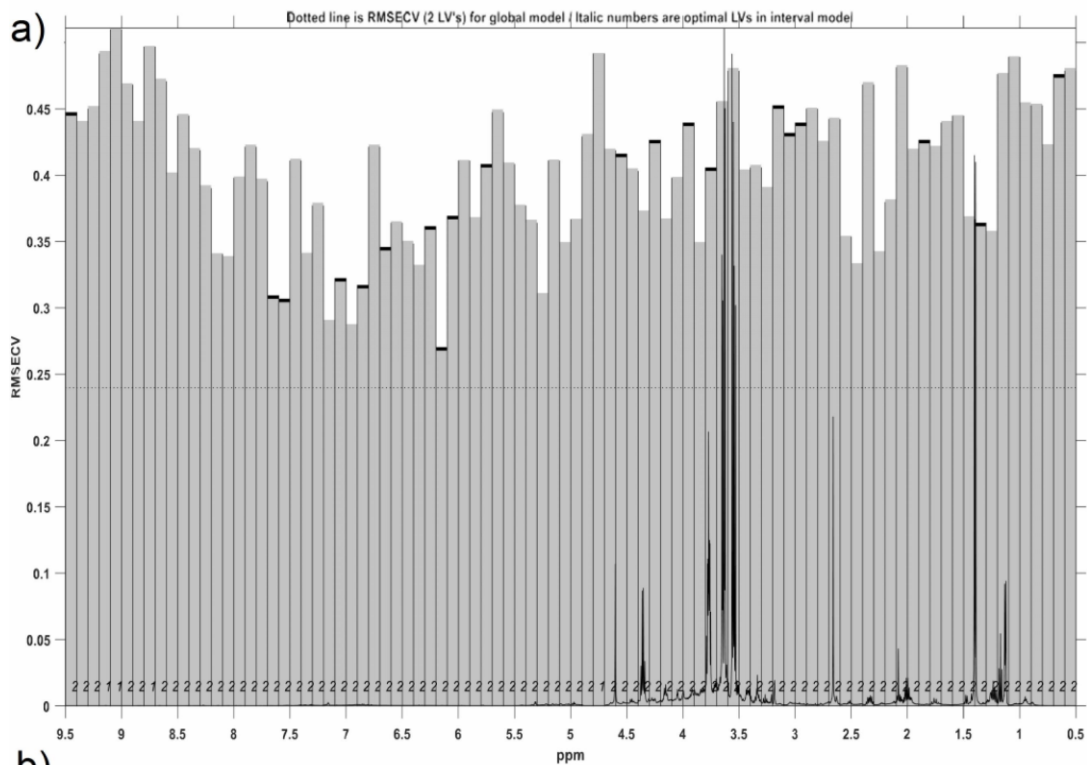


a) Scores



b) Loadings





PAPER



Cashew apple fiber prevents high fat diet-induced obesity in mice: an NMR metabolomic evaluation†

Cite this: *Food Funct.*, 2019, **10**, 1671

Diana Valesca Carvalho,^a Lorena Mara Alexandre Silva,^b Elenilson Godoy Alves Filho,^b Flávia Almeida Santos,^a Renan Pereira de Lima,^a Ana Flávia Seraine Custódio Viana,^a Paulo Iury Gomes Nunes,^a Said Gonçalves da Cruz Fonseca,^a Tiago Sousa de Melo,^c Daniel de Araújo Viana,^d Maria Izabel Gallão^a and Edy Sousa de Brito^{b,*}



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Bioactive Carbohydrates and Dietary Fibre

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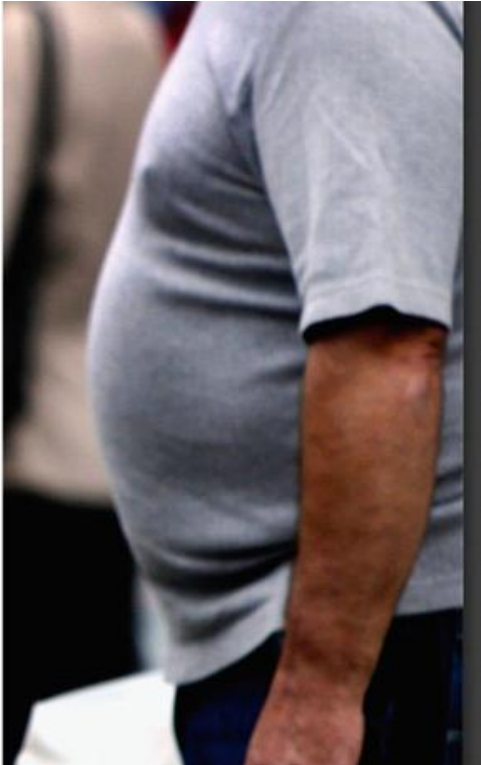
Influence of low molecular weight compounds associated to cashew (*Anacardium occidentale* L.) fiber on lipid metabolism, glycemia and insulinemia of normal mice

Diana Valesca Carvalho^a, Flávia Almeida Santos^b, Renan Pereira de Lima^c, Ana Flávia Seraine Custódio Viana^b, Said Gonçalves Cruz Fonseca^d, Paulo Iury Gomes Nunes^b, Tiago Sousa de Melo^e, Maria Izabel Gallão^f, Edy Sousa de Brito^{g,*}



Brasil

53,8%



EXCESSO DE PESO

* $\text{IMC} \geq 25\text{kg/m}^2$

18,9%



* $\text{IMC} \geq 30\text{kg/m}^2$

(Vigitel, 2017)

Bagaço de frutas – fonte alternativa de fibra alimentar

- » Subproduto produção de sucos
- » Geralmente descartado no meio ambiente
- » Fibra e compostos fenólicos ligados à matriz da fibra
- » Caju: Importância sócio-econômica/riqueza em nutrientes



Fonte: Siqueira, de Brito. Foto: Cláudio de Norões Rocha

Preparação da ração dos camundongos

Metabolismo normal



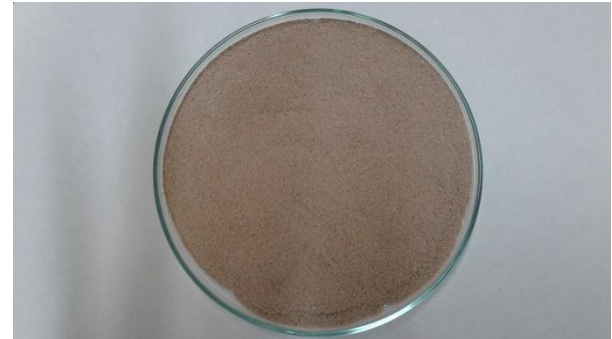
FcI (10%)



Dieta Normal (ND)
– Ração comercial



ND-FcI



FcSM (10%)

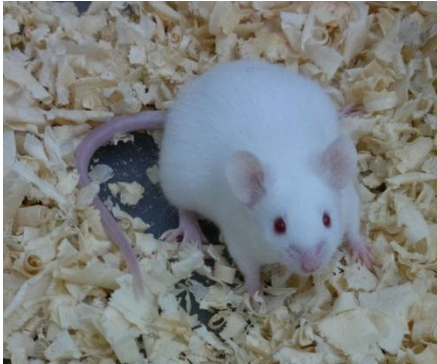


Dieta Normal (ND)
– Ração comercial



ND-FcSM





(p:19-25g)

**(CEPA/UFC
21/15)**

Dietas

Dieta Normal (ND)
n=10

ND-FcI (10%)
n=10

ND-FcSM (10%)
n=10

Dieta Normal (ND)
n=10

HFD
n=10

HFD-FcSM (10%)
n=10

**Metabolismo
normal**

Obesidade

**Alimentados durante 15
semanas; ração e água *ad
libidum***

Peso animal

**Consumo de ração e
água 2x/semana**

Coleta de amostras

14^a semana



Fezes

Obesidade

15^a
semana

Jejum de 6h



Sangue

Eutanásia

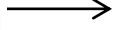
Metabolismo
normal e
Obesidade



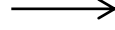
Fígado



Tecido adiposo
branco
abdominal



Soro



- **Glicose**
- **Colesterol total, HDL, LDL, triglicerídeos**
- **Enzimas hepáticas (AST, ALT)**
- **Enzimas digestivas (amilase, lipase)**
- **Hormônios (Insulina, leptina, grelina)**
- **Citocinas (IL-6 e TNF- α , adiponectina)**



• **Peso**

Peso

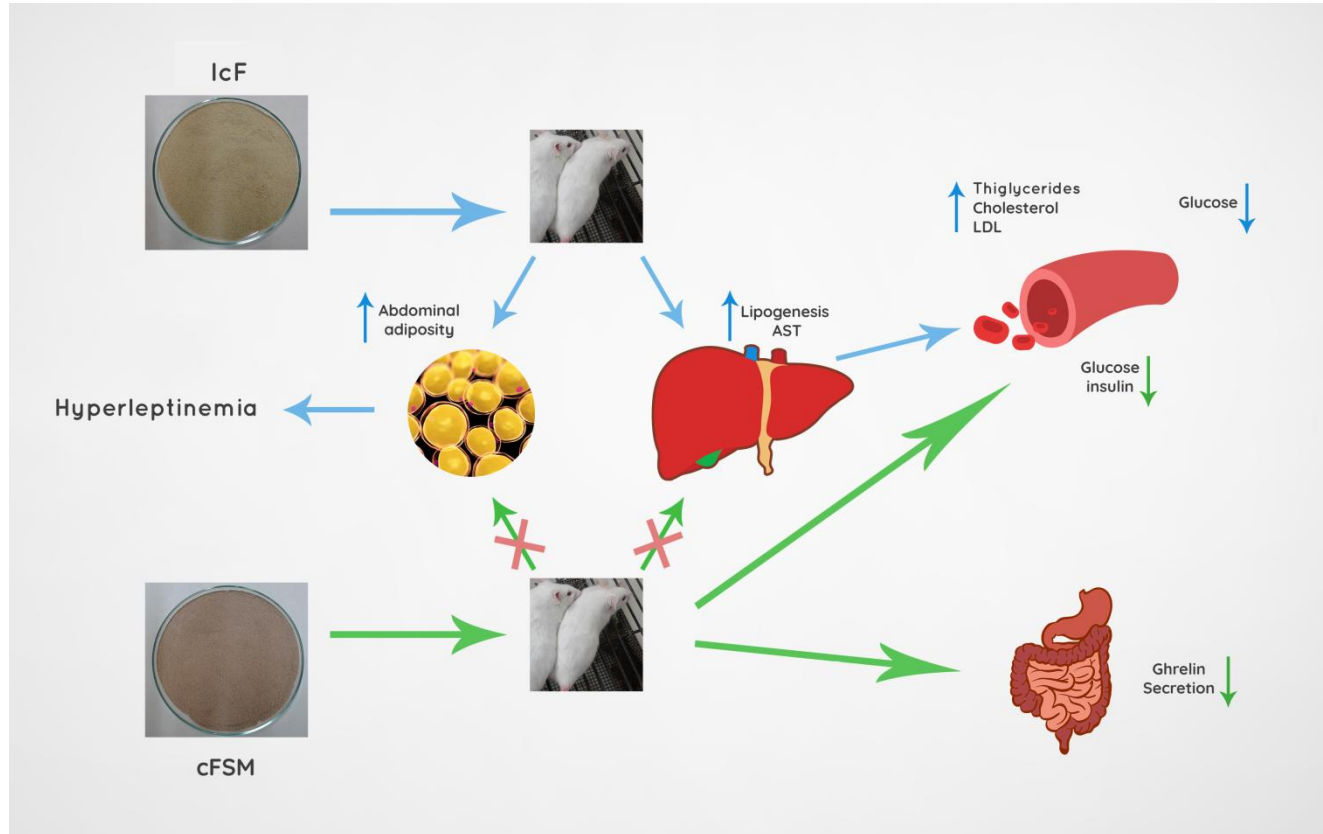
• **MDA**

• **NP-SH**

• **Colesterol**

• **Histologia**

Metabolismo normal

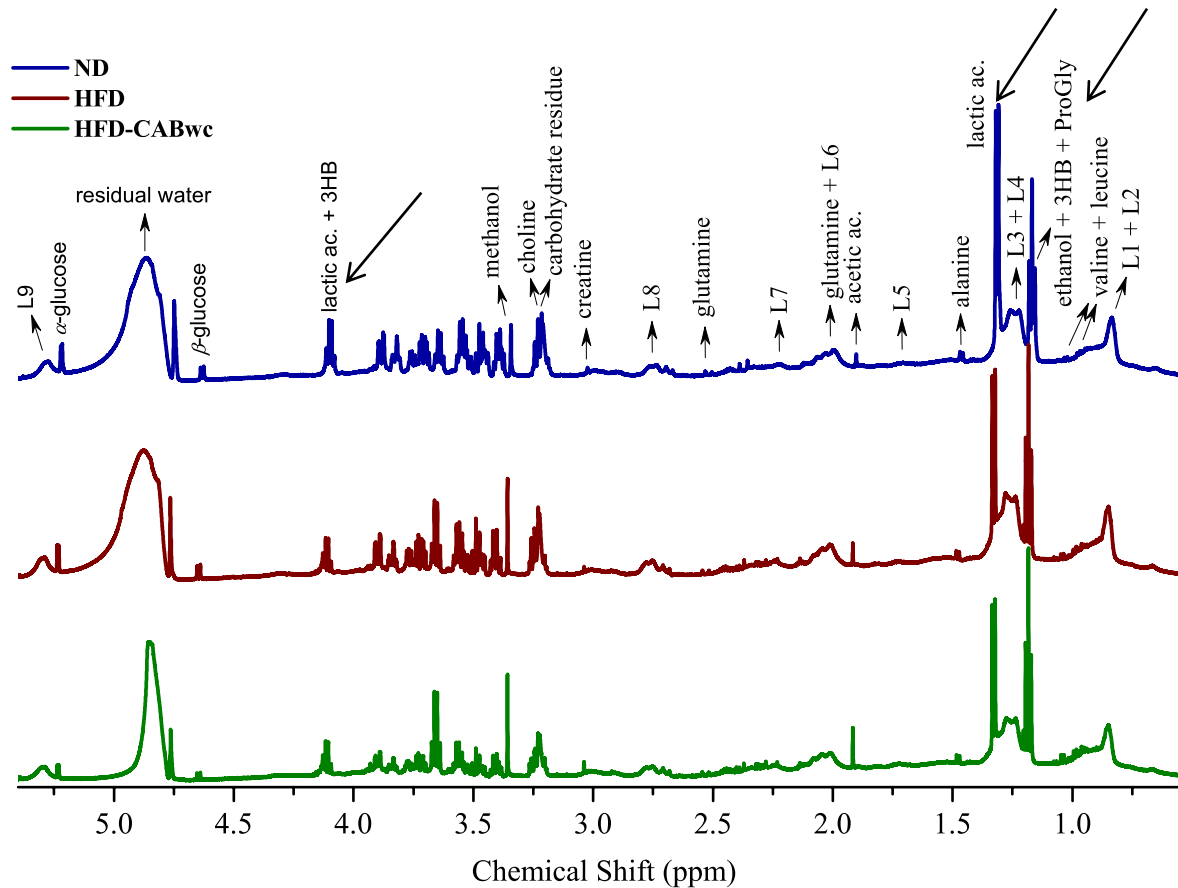


Ingestão alimentar e energética: sem diferença

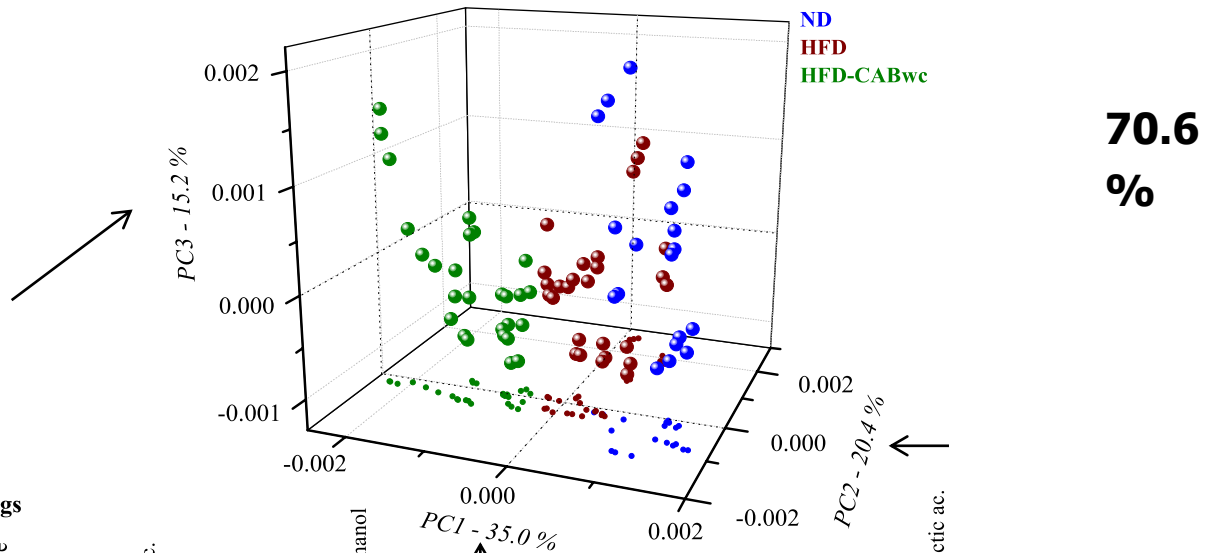
Ingestão de água: elevada FcSM

Peso corporal: sem diferença

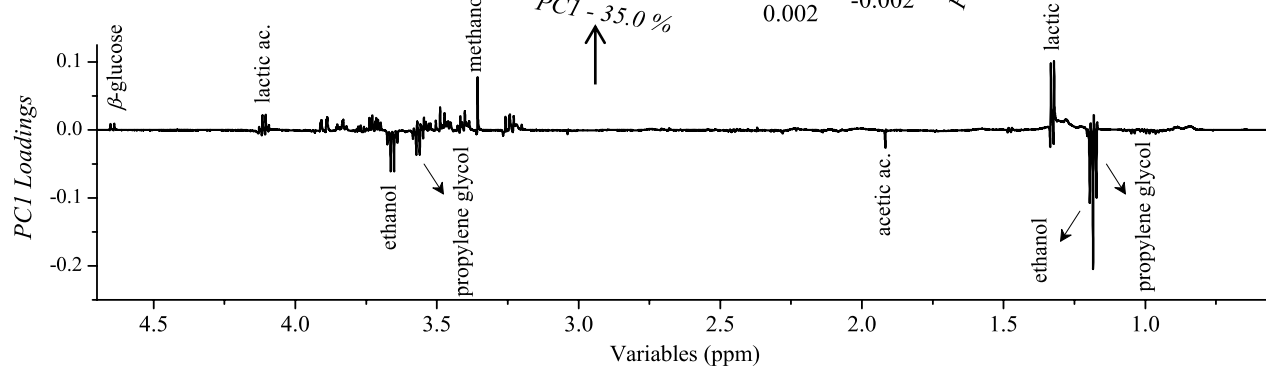
Perfil do soro dos camundongos através de RMN acoplado a quimiometria



a) Scores

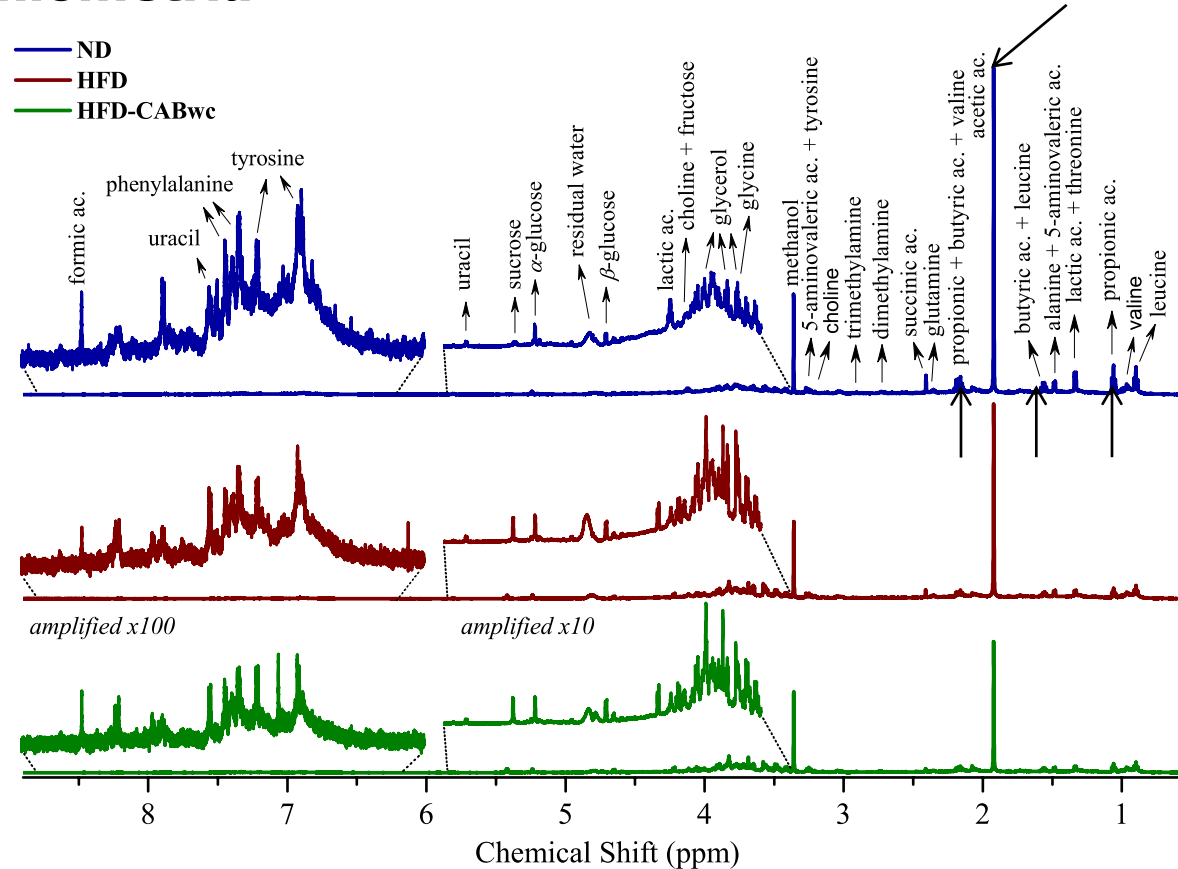


b) Loadings



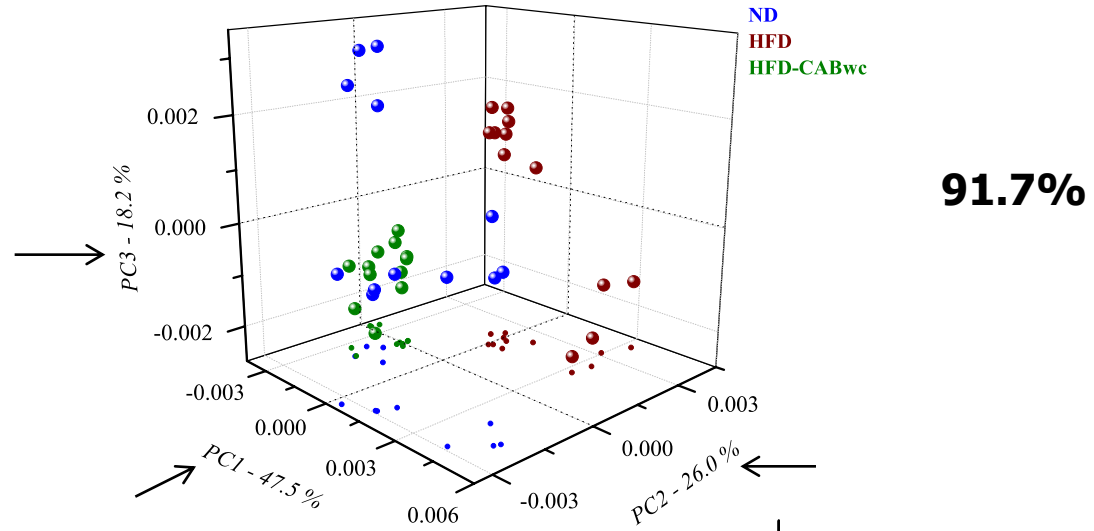
» etanol pode ser produzido por microrganismos intestinais sob diferentes condições nutricionais (Elshaghabee et. al, 2016).

Perfil das fezes dos camundongos através de RMN acoplado a quimiometria

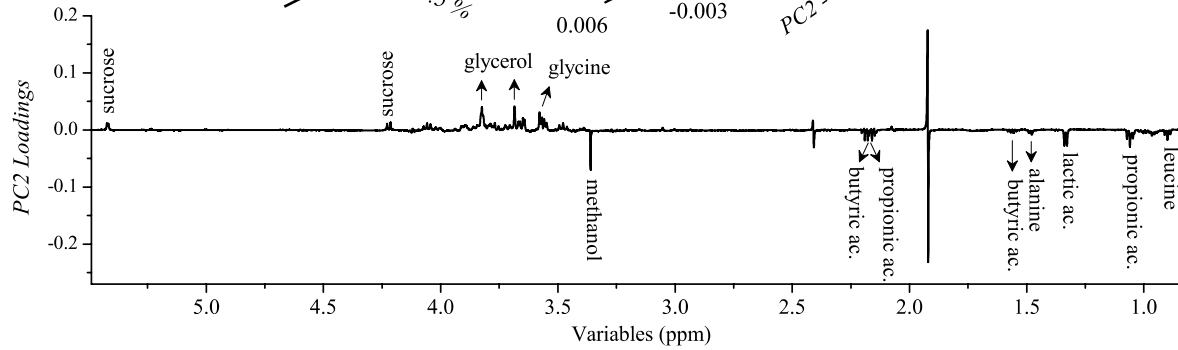


A comparação entre os espectros mostrou que as fezes são principalmente compostos de ácidos orgânicos de cadeia curta (acético, propiônico, butírico, láctico, succínico e fórmico), aminoácidos (leucina, alanina, uracila, tirosina e fenilalanina), açúcares (sacarose, glicose e frutose) e metanol.

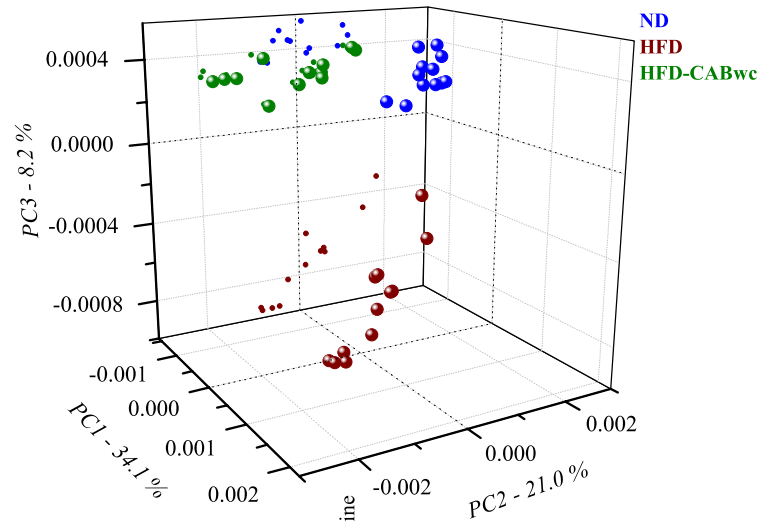
a) Scores



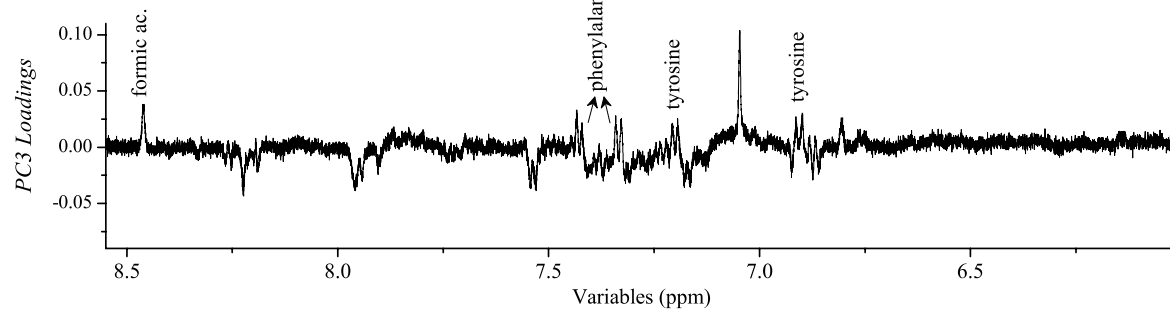
b) Loadings



a) Scores



b) Loadings



A presença desses aminoácidos está possivelmente relacionada às atividades metabólicas das bactérias intestinais do gênero *Adlercreutzia*, *Anaerostipes*, *Coprococcus* da família Lachnospiraceae (Lin et. al, 2016).

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Universidade Federal do Ceará
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MINISTÉRIO DA
AGRICULTURA, PECUÁRIA
E ABASTECIMENTO



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