



Detecting beer intake by unique metabolic patterns

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Slide 1 Date: 16/09/2016

Alcoholic beverages

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→ ?

Alcohol content **OR**

Specific components

Assessment of intake specific alcoholic beverages



Self reported questioners

Biomarkers



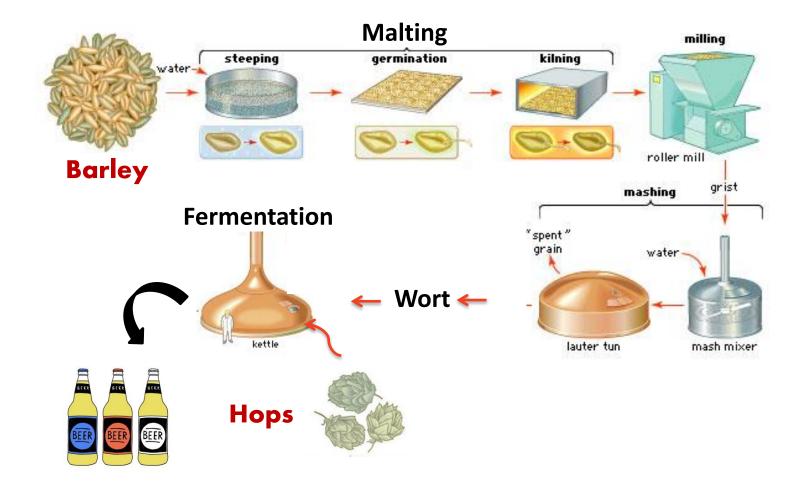
- Endogenous metabolites
- Beer components and biotransformation products



Slide 2 Date: 16/09/2016



Beer components





Slide 3 Date: 16/09/2016



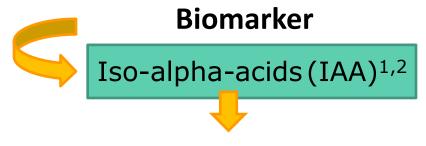
Hops

flavoring and stability agent in beer

- Alpha-acids (AA)
 Cohumulone, humulone and adhumulone
- Beta acids
- Flavonoids

Iso-xanthohumol³

Biomarker



Storage induced degradation

Variable rate of biotransformation to 8-prenylnaringenin

- 1. Rodda, L.N., et al. (2015b). Forensic Sci Int. 250, 37-43.
- 2. Rodda, L.N., et al. (2013). Anal Bioanal Chem. 405, 9755-9767.
- 3. Quifer-Rada, P. et al. (2014) J Nut. 4, 484-488.



AIM

Metabeer

Beer intake



- to identify the plasma and urinary metabolites
- to discover biomarkers



Pilotbeer

Validation of biomarker of beer intake with small scale meal study



Slide 5 Date: 16/09/2016

Metabeer - TEST DRINKS

Test Drinks	Iso-alpha-acids (mg/l)	Alcohol Content
Control drink (C) Sports Drink	×	×
Light/alcohol-free Beer (LB)	19.3	×
Regular Pilsner (RB)	22.9	4.6%
Strong Pilsner (SB)	38.3	8%



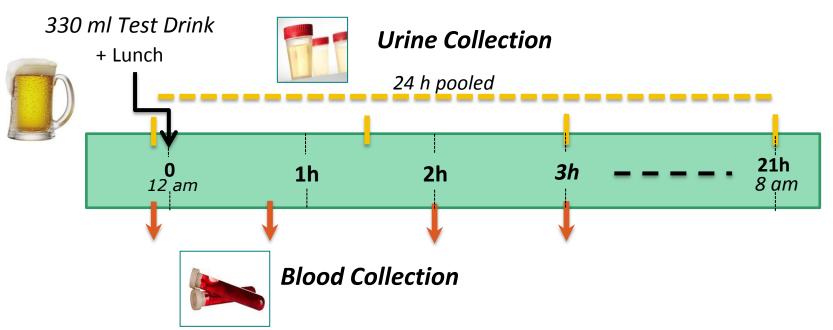
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METABEER: STUDY DESIGN AND SUBJECTS

- √ 4-way, cross-over, single-blinded intervention study
- √ 18 healthy men and women in the age group of 18-60

Test Day

No alcohol consumption 2 days prior





Slide 7 Date: 16/09/2016

Sample and Data Analysis

UPLC-QTOF







Data Analysis

- ASCA to isolate effect of test drinks
- PLS-DA to extract metabolites associated with beer intake
- VIP



Slide 8 Date: 16/09/2016

Sample and Data Analysis

UPLC-QTOF







- Test beers
- Hops
- Beer Wort



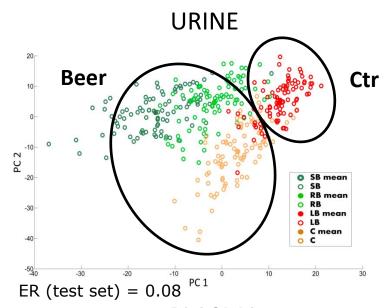


- Hops (present in hops and beer)
- Barley/malting (present in wort and beer)
- Fermentation (present in only in beer)
- Human metabolism
 (not present in beer, hops or wort)



Slide 9 Date: 16/09/2016

Metabolites Associated with Beer Intake



PLASMA	
12 0	
Beer	
86 80 80 80 80 80 80 80 80 80 80 80 80 80	
(° ° °) Ct	r
-5 PC 1	
ER (test set) = 0.25	

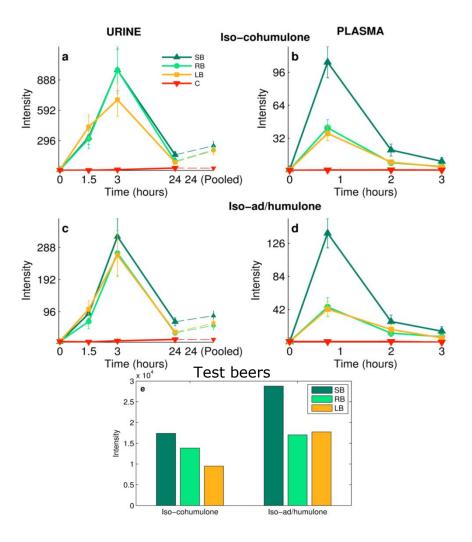
Slide 10

	Plasma	Urine
Total number of features	1503	8935
Beer markers	6	52
Hops	2	15
Barley/malting	4	15
Fermentation	-	2
Human metabolism	-	20



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Hops originating metabolites



Iso-alpha-acids (IAAs)

- Early excreted metabolites
- Beer specific
- Detected in both plasma and urine

Can we use IAAs as biomarker of beer intake??



Date: 16/09/2016

Slide 11

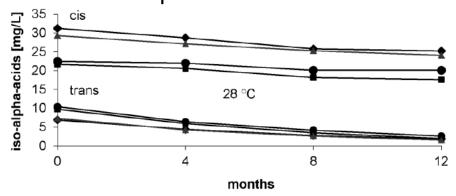
Hops originating metabolites

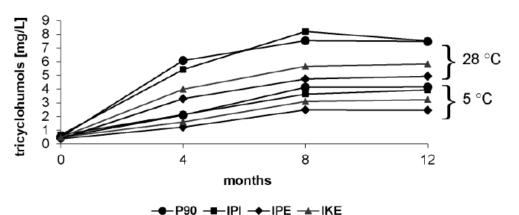
Storage induced degradation of IAAs

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- Tri- and tetra-cyclohumols
- Hydroxlated humulones

Effect of storage on iso-alpha-acid concentrations





Human metabolism associated metabolites

- NO or CH₂O conjugate of IAAs
- NO₂ or CH₂O₂ conjugate of IAAs
 - Cysteine conjugates
- Phase II metabolites

Specific to beer intake



Slide 13 Date: 16/09/2016

Barley/Malting and Fermentation originating metabolites

m/z	RT	Annotation	Suggested Compound (identification level)	Biofluid	Source
365.10	0.88	[M+Na] ⁺	Maltose ²	Urine	Malting/Mashing
225.08 227.10	1.93	[M-H] ⁻ [M+H] ⁺	Pyroglutamyl proline ¹	Urine Plasma	Heat treatment during malting
182.08 132.10	0.78 0.91	[M+H] ⁺ [M+H] ⁺	Tyrosine ¹ Iso/Leucine ¹	Plasma Plasma	Barley Barley
166.12 230.05 232.06	1.13 1.01	[M+H] ⁺ [M-H] ⁻ [M+H] ⁺	Hordenine ¹ N-methyl Tyramine sulfate ²	Urine Urine	Barley Barley
161.04	1.79	[M-H]-	2-ethyl malate ²	Urine	Fermentation

^{*}identification level



Slide 14 Date: 16/09/2016

Single Biomarker of Beer Intake

Specificity Stability

Hops originating metabolites





Barley/malting and fermentation originating metabolites





Aggregated beer biomarkers

Representative of beer raw materials and production process.

Criteria for selection:

- Identified metabolites
- Significant up-regulation after beer intake



Slide 15 Date: 16/09/2016

Selected metabolites for the aggregated beer biomarker

Compound	Source	Specificity
IAAs + Tricyclohumols	Hops	✓
N-methyl Tyramine Sulfate	Barley	*
Pyro-glutamyl Proline	Barley/malting	×
2-ethyl malate	Fermentation	×



Slide 16 Date: 16/09/2016

VALIDATION of aggregated beer biomarker PILOTBEER study



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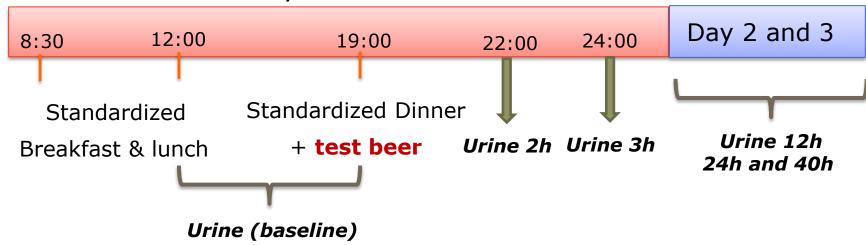
PILOTBEER: Study design

Cross-over study 4 healthy subjects (age 28-60)

Test Drinks	Iso-alpha Acids (mg/l)	Alcohol Content
Low hops Pilsner	8	7-8%
High hops Pilsner	31	4.8%

two days before No alcohol consumption







Slide 18 Date: 16/09/2016

Sample and Data Analysis

UPLC-QTOF



4 metabolites samples **Metabeer samples Test** 4 metabolites Urine 24 h pooled urine **PLSDA** Before Cal VS model After beer intake Beer VS Ctr

Pilotbeer samples

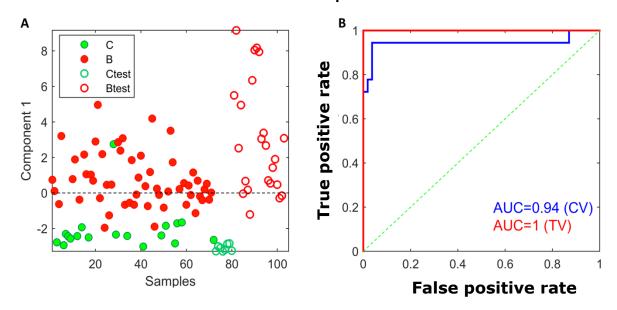


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Results: Validation

Metabeer: Pooled 24 h urine

Pilot beer: Urine collected up to 12 h.



Pilot beer: urine collected 12 to 24 h after beer intake are wrongly classified as controls.

metabolites associated with beer intake were already excreted at 12 h



Slide 20 Date: 16/09/2016

Conclusions

Slide 21

- Beer intake is associated with increase in a number of metabolites in plasma and urine.
- The metabolites are grouped according to their origin: hops, wort, fermentation, and human metabolism.
- The majority of beer-specific compounds are originated from hops, but many of these are chemically unstable limiting their usefulness as single biomarkers.
- Wort and fermentation products, in combination with one or more hopsspecific marker provided a biomarker model for compliance.
- Biomarker model based on a set of three or four of these signature biomarkers was able to completely discriminate between samples collected after beer intake in an independent study with high sensitivity and specificity.



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Limitations/Future Perspectives

Validation study was a controlled study with low number of subjects and limited beer types

Further interventions with other types of beers (stout, ale, wheat, rice, etc.) is required to test whether additional markers are needed.

The sensitivity and specificity of the aggregated biomarker of beer intake still needs to be validated in an observational study.



Slide 22 Date: 16/09/2016



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ALL PARTICIPANTANTS OF THE STUDIES

THANK YOU FOR YOUR ATTENTION





Slide 23 Date: 16/09/2016