







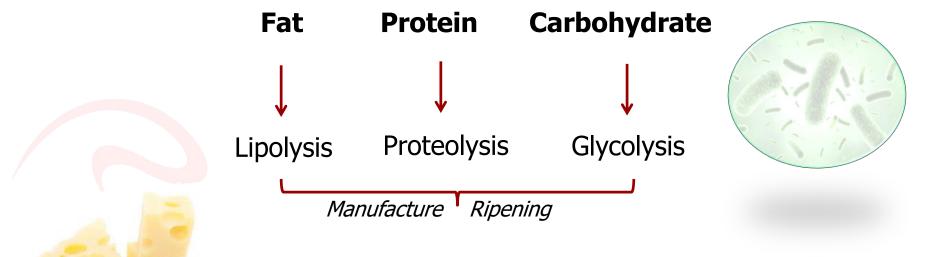
Genome-wide association and biological pathway analysis of cheese volatilome in dairy cattle

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Research Hypothesis



Cheese volatile organic compounds (VOCs)



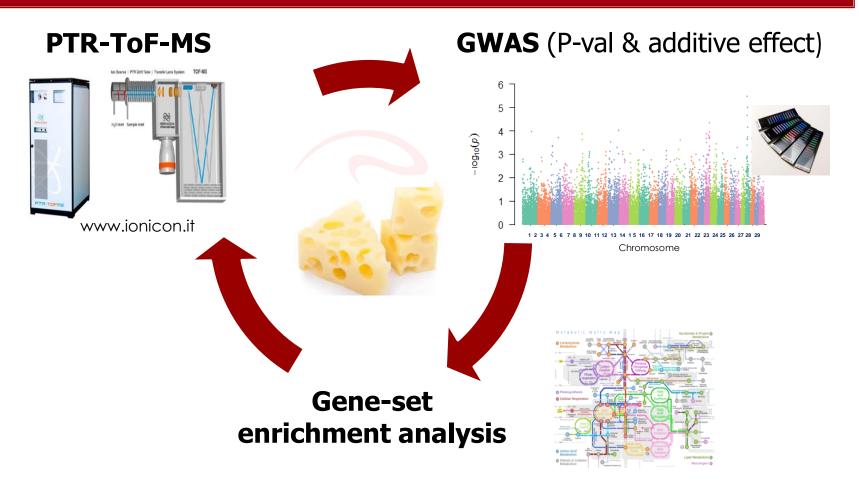


Cheese flavour





Aim of the study



Genomic regions and **biological functions** potentially contributing to the **synthesis** of **cheese VOCs**





Cowability/Cowplus projects





Individual model cheeses







Cowability Cowplus











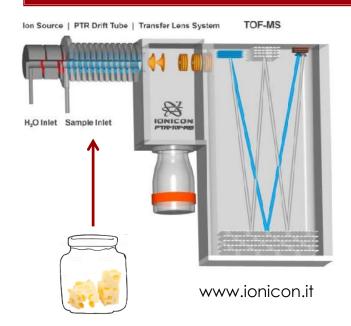
1,075 Brown Swiss cows

60d ripening





Methods-PTR-ToF-MS analysis



- 8863.64 8000-7000-2000-1000-
- **1. Data transformation:** ln [(peak fraction +1) * 10⁶]
- **2. Quality filtering:** peaks <1 ppbv, interfering ions and isotopologues (*r*>0.95, *P*<0.001)
- 3. Tentative association to cheese VOCs



- Direct injection
- > Short analysis time
- High sensitivity

128 unknown peaks + 45 peaks associated to cheese VOCs





Methods-GWAS and pathway analysis

Dataset

-Phenotypes: 173 cheese VOCs +

milk and cheese composition

-Genotypes: 1,011 animals and

37,568 SNPs (Illumina Bovine SNP50)









GWAS

Single marker regression: DIM, parity, herd as fixed factors, *P*<5*10⁻⁵ (*Genabel R package*)



Pathway analysis

SNP selection: SNP-to-gene distance

<15 kb, *P*<0.05 (*BiomaRt R package*)

Gene-set enrichment: GO and KEGG

databases, FDR < 0.05 (goseq R package)





Results - GWAS

Carbohydrate metabolism

BTA3 (~ 106.61 Mb): GLUT1 BTA8(~ 75.00 Mb)*: B4GALT1* BTA18 (~ 16.12 Mb): PHKB

186 significant SNPs for 120 traits

Fat metabolism

BTA14 (~ 44.03 Mb): *FABP4*

BTA19 (~ 48.93 Mb): **GH1** and **FASN**

BTA28 (~ 46.15 Mb): **ALOX5**

Protein metabolism

BTA4 (~ 13.15 Mb)*: ASNS*

BTA6 (~ 81.65-88.07 Mb): **CSNs** and *GnRH*

BTA5 (~ 88.31 Mb): **BCAT1**

BTA16 (~77.29-77.47 Mb): *HSD11B1*





Results-VOCs correlations based on additive effect

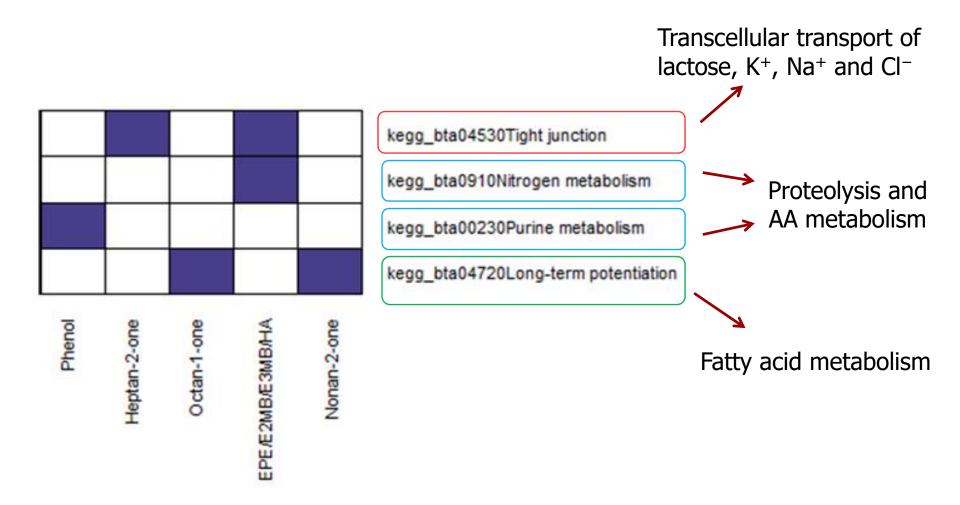
ketones and Subnet 2 aldehydes **Subnet 3 Subnet 1** esters **Subnet 7 Subnet 8 Subnet 5** Subnet 6 **Subnet 4**

acetate ester fragment/acetic acid, acetoin and butanoic acid





Results — Pathway analysis







Conclusions & Challenges



Does cow's genetic background contribute to cheese flavour?



Integration of PTR-ToF-MS, GWAS and pathway analysis

More accurate identification of VOCs

Improvement of genome annotation

Cow's genes related to **protein**, **fat** and **carbohydrate** metabolism

influence cheese VOCs















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