



Effect of animal diet on the taste persistency of dairy products by High-Resolution Mass Spectrometry

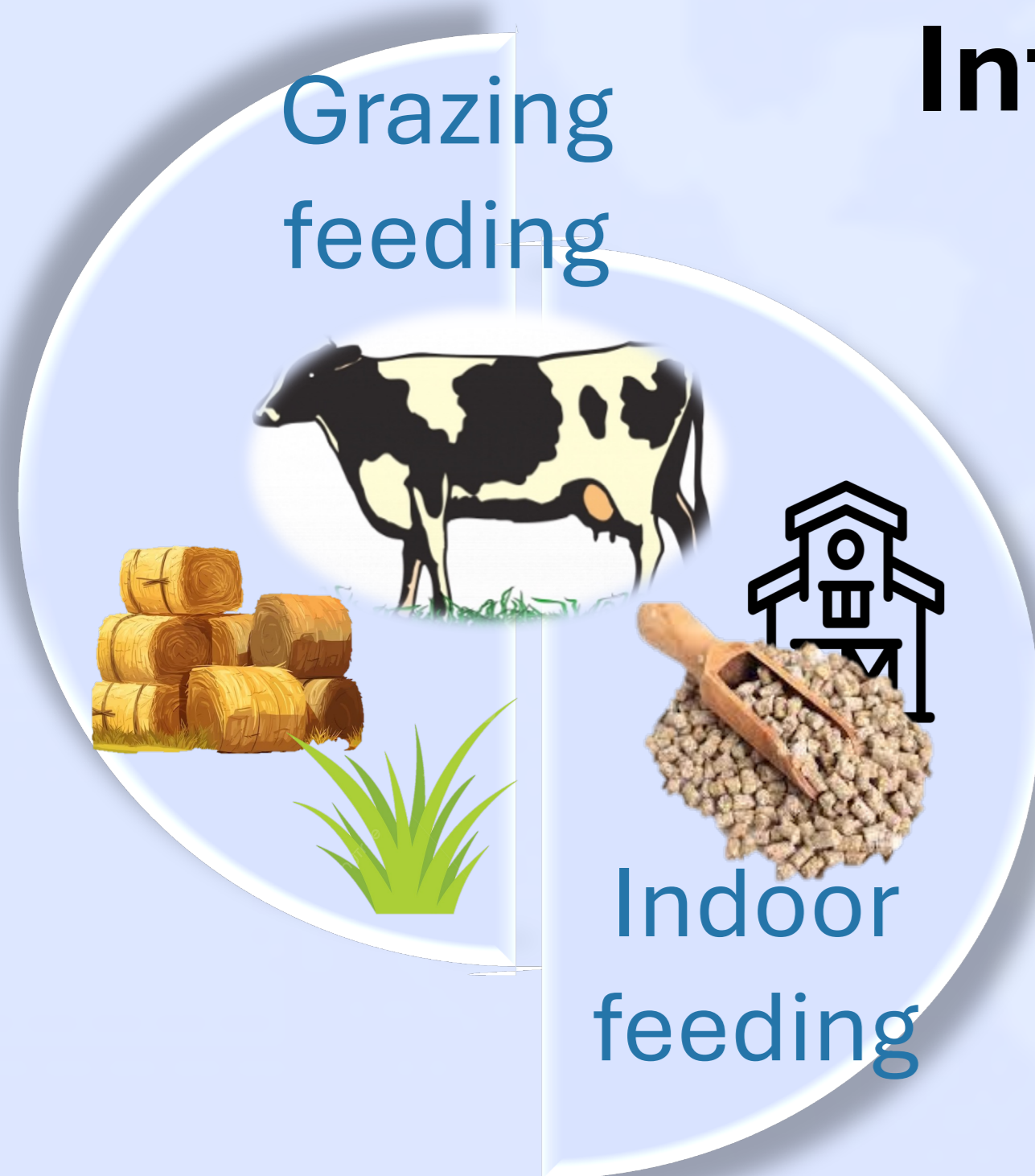
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Introduction

Raw materials for food manufacturing are often considered similar in the whole agricultural world, as the parameters commonly employed to evaluate their quality are mostly connected to standard guidelines required by law. Among all the different raw materials employed for food production, milk plays an important role as it is considered a sustainable food worldwide. Different factors such as the animal species, farm and feeding conditions, as well as the location where cows are reared, can affect the milk quality as well as dairy products¹. Here, an untargeted LC-MS metabolomic approach was applied to investigate the molecular complexity of milk obtained from cows fed under different regimen with the aim to find a correlation between metabolic fingerprint with their food quality.



Methodologies

During spring 2022 and spring 2023, milk samples were collected from different dairy farms located in Basilicata region, Italy. Dairy farms were divided in grazing farms (group A, 23 samples) and indoor farms (group B, 24 samples). 10 mL of each milk sample were extracted according to the protocol of Zha et al.² Analysis on the sample extracts were carried out by Zamboni group at the ETH Zurich using a Q-Exactive HF-X Mass Spectrometer (Thermo Fisher Scientific) coupled to a Vanquish Autosampler – HPLC (Thermo Fisher Scientific) and data processed using SLAW approach³. MetaboAnalyst⁴ and Phyton were used for data visualization and figures.

Results

Unsupervised principal component analysis revealed differences between the two feeding systems, i.e. indoor system cows and grazing regimen (**Figure 1**). A lower clusterization was observed for the grazing system, thus reflecting the heterogeneity of the feeding conditions (i.e. soil, water, location). Van Krevelen diagrams were used to visualize the different metabolic classes to whom each identified compound belonged (**Figure 2**). Discriminant metabolites mainly were polyphenols and lipids (**Figure 3**).

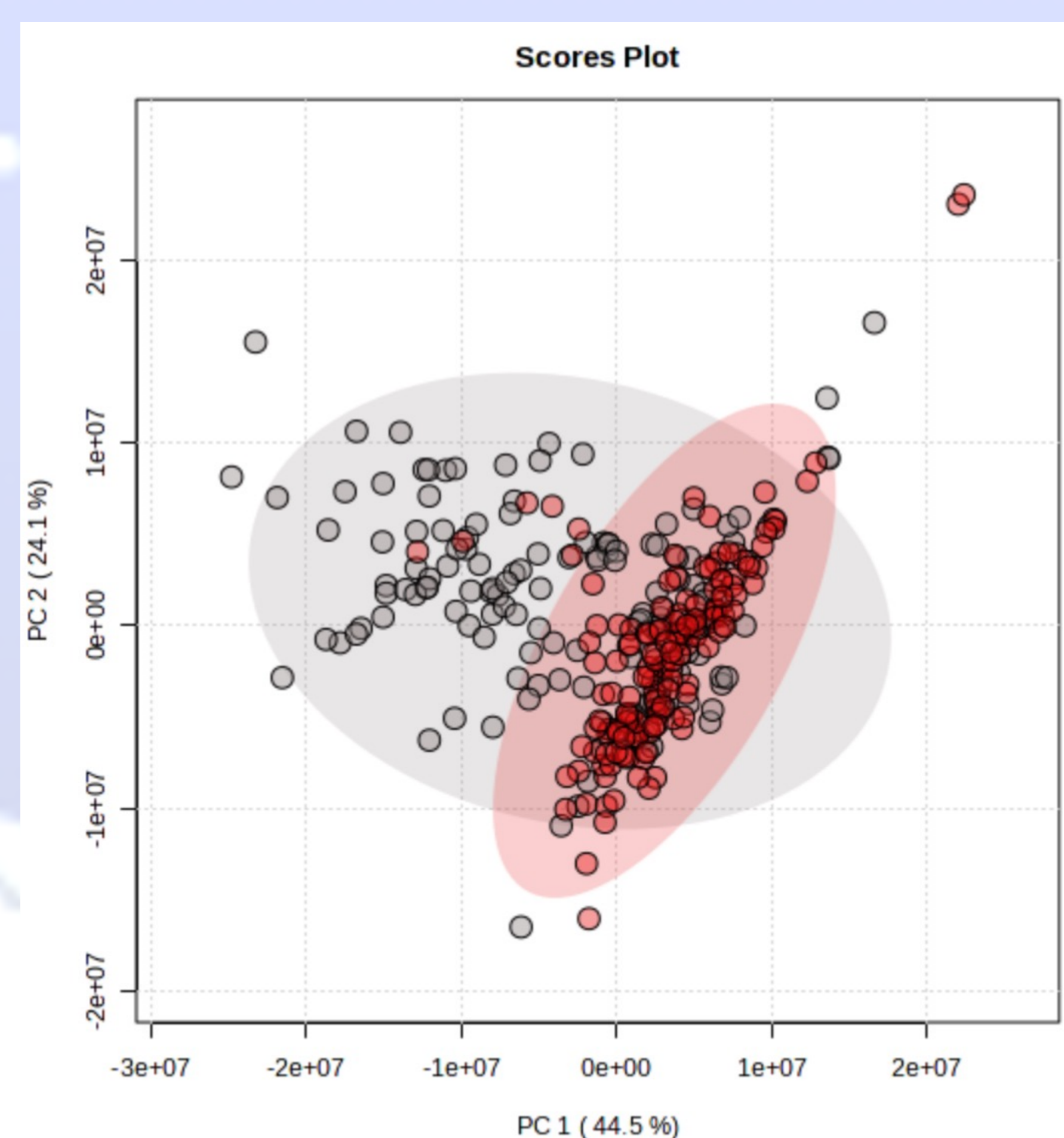


Figure 1. Unsupervised principal component analysis (PCA) of milk samples from cows under different feeding system.

Green dots: indoor system cows. Pink dots: grazing feeding.

Figure 3. Number of discriminant metabolites in milk distinguished by class of compounds.

Red bar indoor system cows. Black bar grazing feeding.

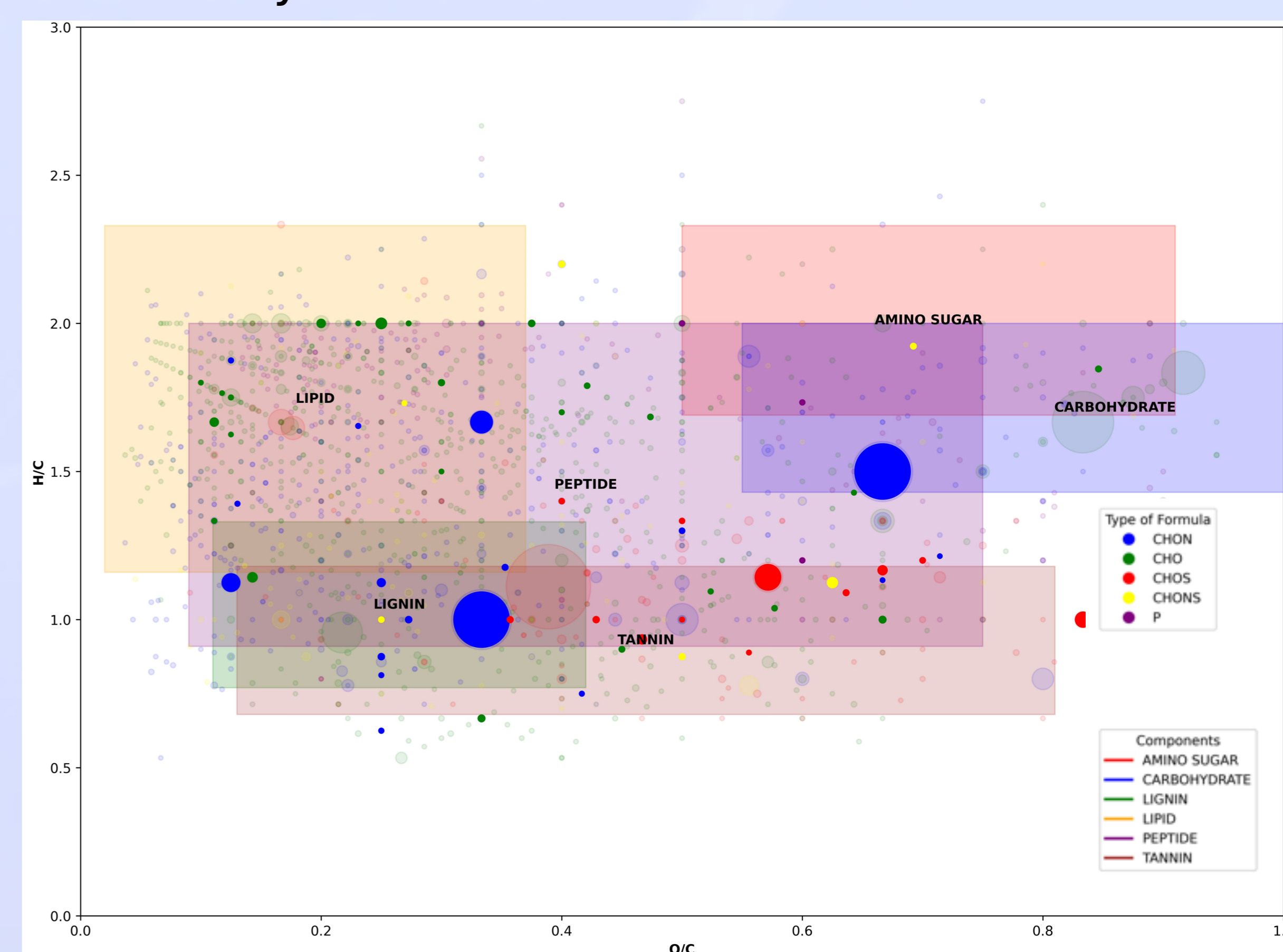
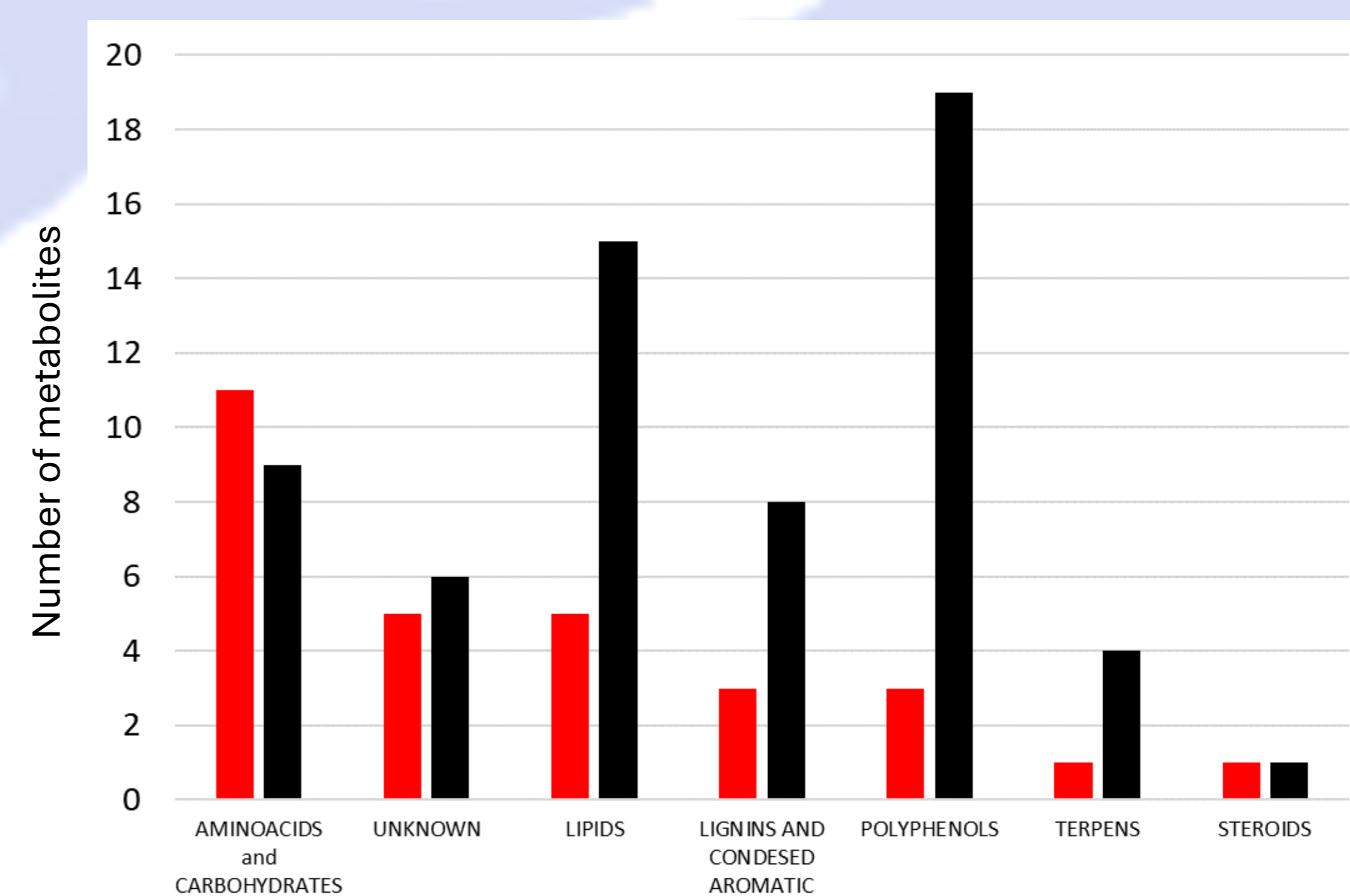


Figure 2. Van Krevelen diagram of a representative milk sample from grazing feeding. In bold the discriminant molecular formulae compared to indoor feeding regimen.



Conclusions

The untargeted LC-MS metabolomic approach allowed to establish the molecular complexity of milk obtained from cows fed under different regimen. Preliminary results showed that the different quality of dairy products can be related to polyphenols and lipids, mostly present in milk from grazing regimen.

References

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