SO'DIFF: Identification of quality markers from Tomme de Savoie to support selection of indigenous microorganisms

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1. Context

Tomme de Savoie is a raw milk semi hard cheese granted with Protected Geographical Indication.

Microorganisms are key factors for aromatic richness development in fermented products, such as cheeses. Over the last decades, the abundance of microorganisms in raw milk and in the cheese making environment decreased, particularly due to intensive increase in hygienic conditions because of concerns about human health.

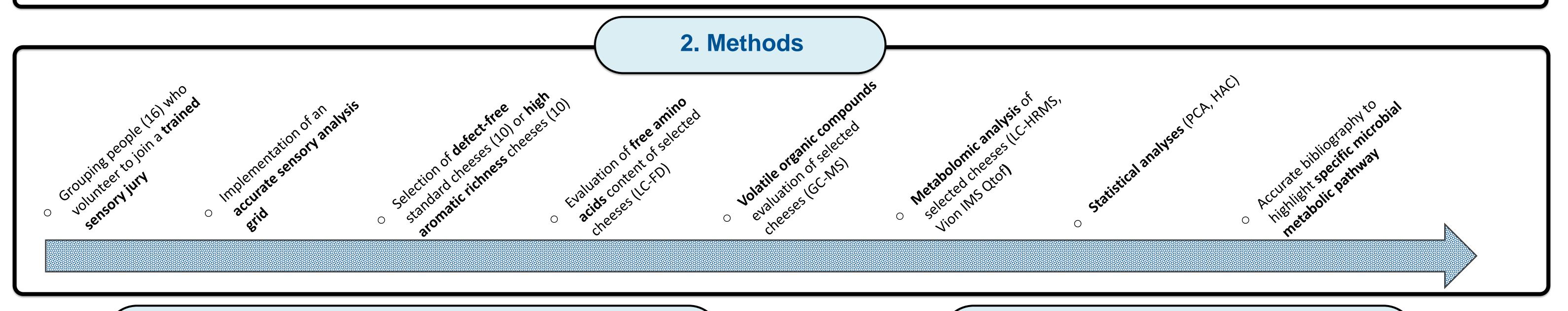
Aware of this challenge for a long time, Tomme de Savoie cheese makers contribute to the collect of several hundreds of indigenous microorganisms since the 1980s which are now grouped together in a specific microbial collection.

Cheese makers are now willing to develop Tomme de Savoie aromatic richness, in particular using microorganism's abilities. The project aims at:

- identifying the quality markers responsible for aromatic richness,
- supporting the selection of indigenous microorganisms of interest for cheese making.



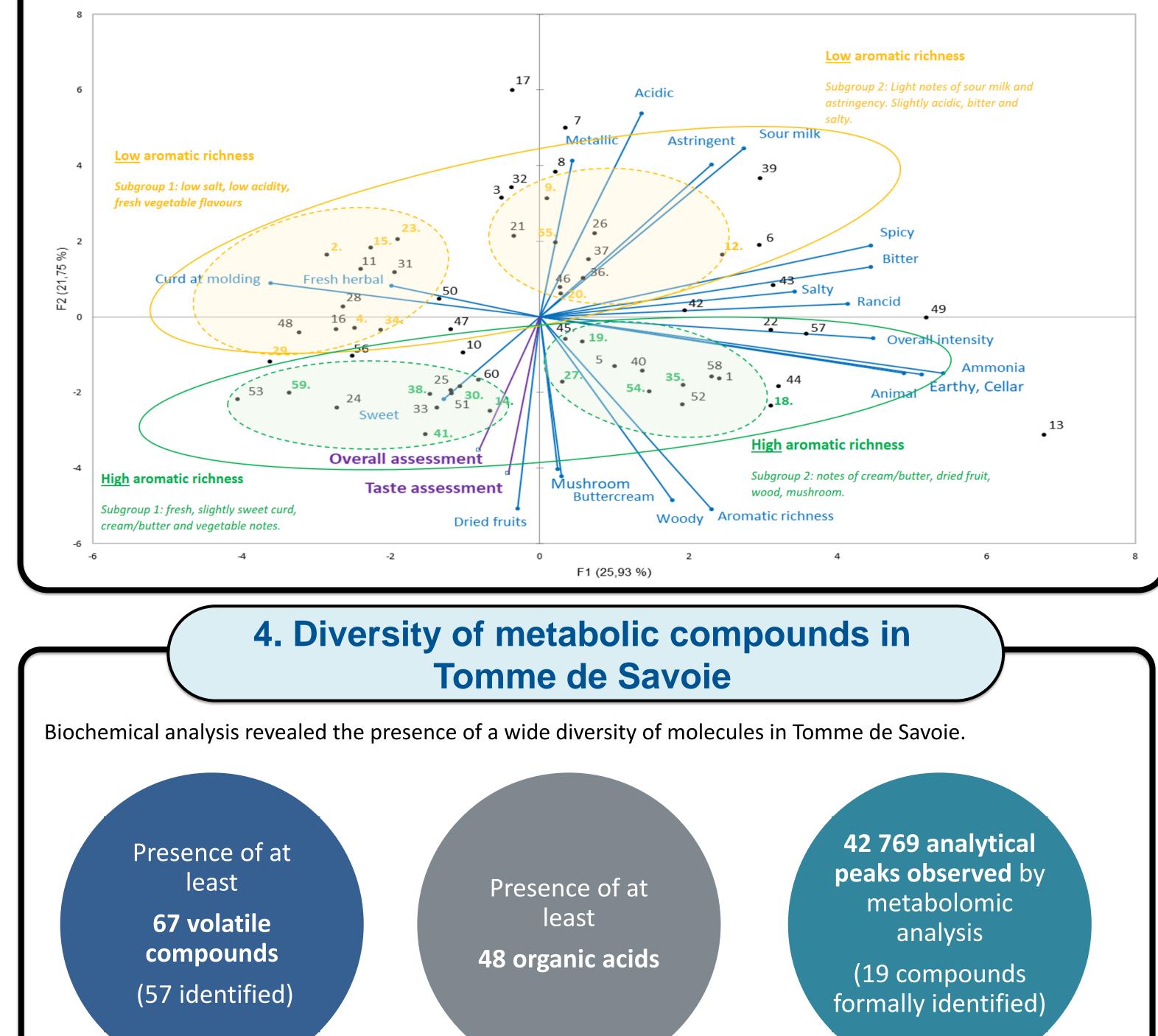




3. Sensory criteria linked to aromatic richness in **Tomme de Savoie**

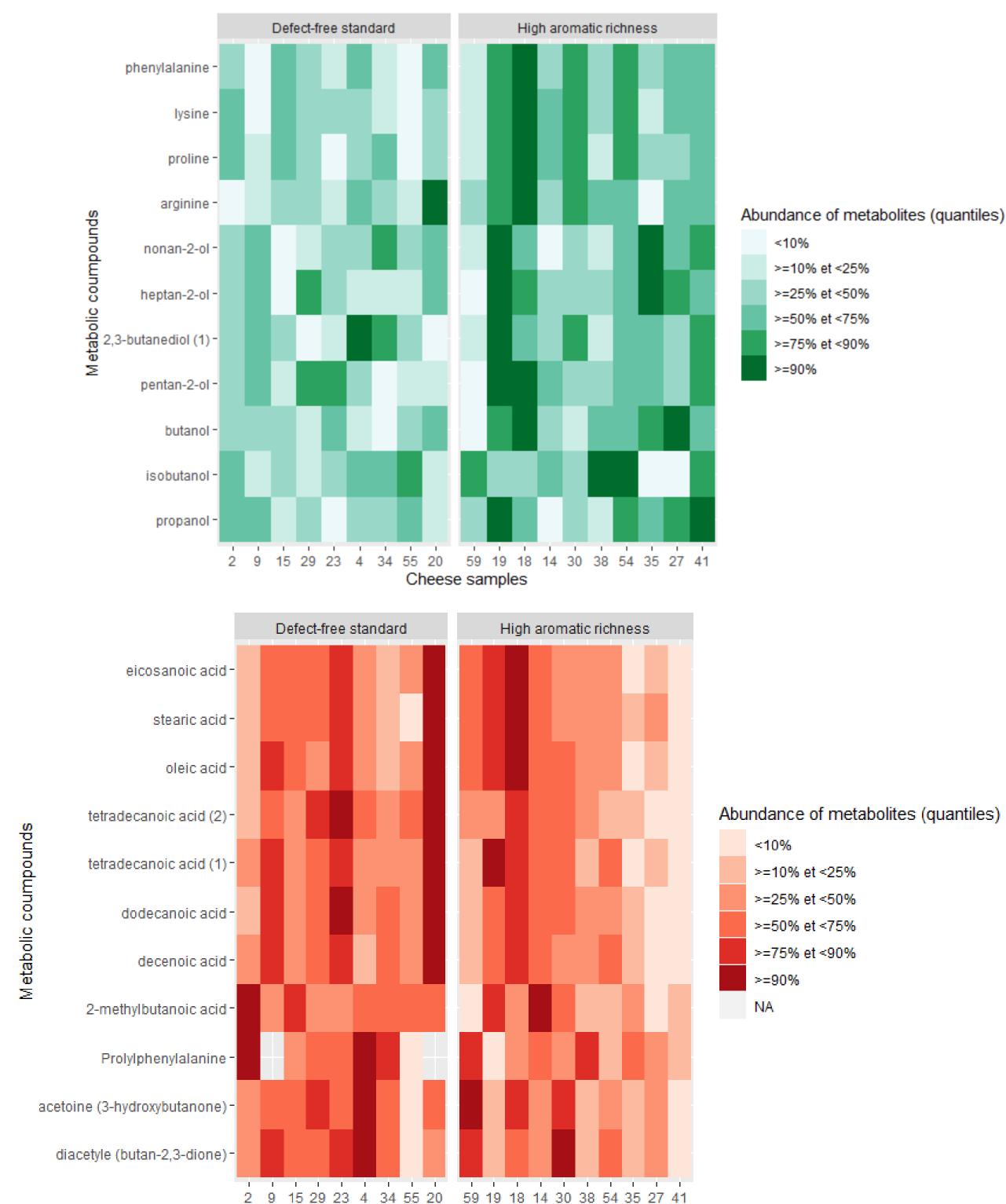
- ▶ 27 sensory descriptors have been established by the trained sensory jury.
- Sensory analysis revealed that aromatic richness is correlated to taste of slightly sweet curd and/or cream/butter, with notes of dried fruits, oak and mushroom.
- ▶ This work led to the selection of 10 defect-free standard and 10 high aromatic richness cheeses.

Biplot (axes F1 et F2 : 47,68 %)



5. Quality markers of Tomme de Savoie

Tomme de Savoie aromatic richness appeared to be positively or negatively correlated with the abundance of 22 molecules.



In particular, Tomme de Savoie has a high content in compounds as various as myristic acid, stearic acid, oleic acid, leucine, phenylalanine, glutamic acid, butyric acid, caproic acid, 2,3-butanediol, acetoin, butan-2-one, heptan-2-one, ethyl benzene, ethyl acetate, secondary alcohols (propan-2-ol, pentan-2-ol, heptan-2-ol), acetic acid, etc.

Cheese samples

Litterature revealed that the abundance of these molecules relies on:

- lipolysis (degradation of long chains fatty acids, production of secondary alcohols),
 - proteolysis (amino acids release, prolylphenylalanine cleavage, production of primary alcohols),
- and glycolysis (degradation of acetoin and diacetyl in 2,3-butanediol).

Perspectives / conclusion

Aromatic richness appeared to be correlated with the abundance of 22 molecules, whose production relies on several steps of glycolysis. Notably, corresponding metabolic pathways led to the production of some primary and secondary alcohols.

Further investigation revealed that ripening microorganisms including lactobacilli, non-starter acid lactic bacteria, yeasts and molds are highly likely to play a central role.

These results will support the selection and characterization of indigenous microorganisms in order to improve the aromatic richness of Tomme de Savoie. The methodology developed in this project could be further used for the improvement of other cheeses and dairy products.

