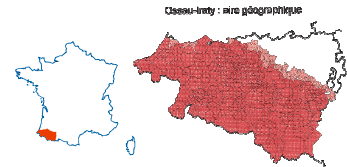


Microbiological composition and lactofermentation capacity of ewe raw milk produced in farmhouses located in PDO Ossau-Iraty cheese area

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Aim : To evaluate the microbiological variability in milk with respect to the functional capacity of lactofermentation combining the individual quantitative microbial group counts with an Relative Index* that represented the global microbial balances between some major dairy microbial groups within milk .

Material & Methods



71 ewe's milk samples obtained from 12 farmhouses (5 to 6 samples from each farmhouse between April and June – milk from morning milking – one milking)

71 microbiological analyses by culture dependent methods to quantify 4 major groups of dairy micro-organisms



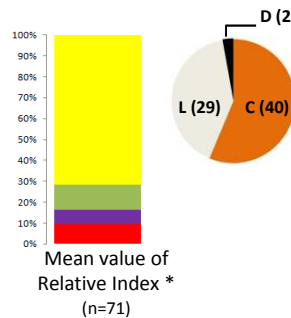
71 lactofermentation tests from each milk – 37°C/24 hours

Micro-organisms	Media and culture condition
Ripening Bacteria (RB)	CRBM ⁽¹⁾ – 25°C/5 days
Lactic Acid Bacteria (LAB)	MRS ⁽²⁾ + natamycin + nalidixic acid – 30°C/3 days
Yeasts and Molds (YM)	OGA ⁽³⁾ – 25°C/3 days
Gram Negative Bacteria (GNB)	PCA ⁽⁴⁾ with skimmed milk + Gram ⁺ ATB inhibitors (crystal violet + vancomycin) – 30°C/3 days
FMAR	PCA ⁽⁴⁾ – 30°C/3 days

Results

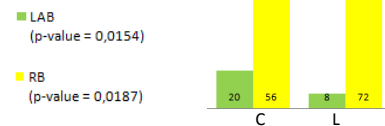
Quantification and relative proportion of some major groups of dairy micro-organisms according to a Relative Index* for each analyzed milk

Ripening bacteria were dominant in 79% of the 71 analyzed milk samples (40 to 97% of the total counts - 3.9×10^2 to 8.4×10^4 UFC.mL⁻¹). Lactic acid bacteria never appeared as dominant.

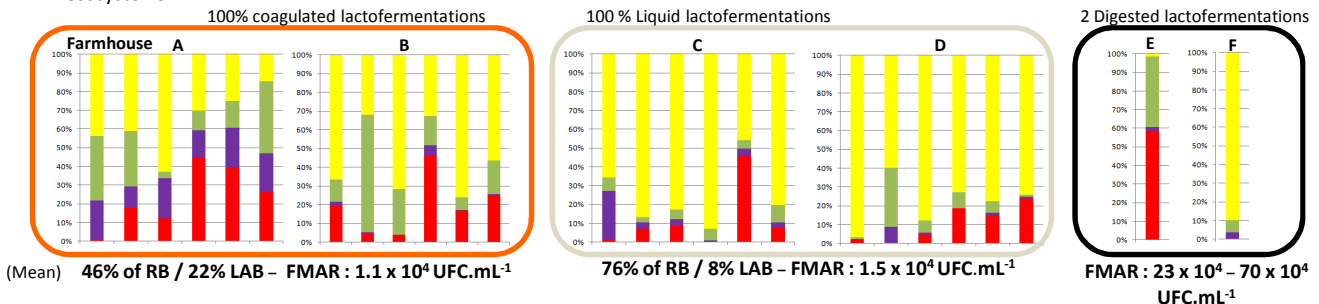


Lactofermentation tests (37°C) respect to the state of milk ; L : liquid ; C : coagulated, D : digested (n)

The state C and L of the lactofermentation tests can be explained by the proportion of two majors dairy groups (Mean % ; ANOVA followed by Tukey Contrasts test)



Farmhouse seems to be the major discriminating factor (X-squared test ; p-value = 0,004) on lactofermentation state suggesting that environment, practices overall milk production could interact both in the microbiological and physicochemical composition and participate to the creation of unique milk ecosystems.



Such tool could be useful for the farmer and/or cheese-maker to monitor the microbial variability of the milk and to try modulating the practices linked to the cheese-making and/or to the management of his herd which can affect the milk composition.

* index developed in a French research program (FlorAcQ 2011-2014) ; (1) Denis C., Gueguen M., Henry C., Levert D., 2001. New media for the numeration of cheese surface bacteria. Le Lait, 81 (3), 365-379; (2) De Man, J.C., Rogosa, M., and Sharpe, M.E., 1960. A medium for the cultivation of lactobacilli. J. App. Bacteriol., 23, (1): 130-135; (3) Mossel D.A.A., Kleynen-Semmeling A.M.C., Vincantie H.M. 1970. Oxytetracycline-Glucose-Yeast Extract Agar for selective enumeration of moulds and yeasts in foods and clinical materials. J. App.Bact., 33, 454-457; (4) Marshall, R.T. (ed.). 1992. Standard methods for the microbiological examination of dairy products, 16th ed. American Public Health Association, Washington, D.C