Development of strategies for the adaptation of the livestock sector to the new climate regime with machine learning and artificial intelligence methods

Chiara Evangelista (chiara.evangelista@unitus.it)
Dept. for Innovation in biological, agri-food and forestry systems, University of Tuscia, Viterbo, Italy
Tutor: Prof. Giovanni Chillemi

The first activity was concluded with the identification by ML (Machine Learning) methods of a narrower range of wavelengths in the near infrared for the identification of DM (Dry matter), aNDF (neutral detergent fibre); ADF (acid detergent fibre) and ADL (acid detergent lignin). The second activity is based on the study of metagenomics from the faeces of dairy buffaloes to identify correlations with nutrition and its digestibility.

Sviluppo di strategie per l'adattamento del settore zootecnico al nuovo regime climatico con metodiche di machine learning ed intelligenza artificiale

La prima attività si è conclusa con l'identificazione, tramite metodi ML (Machine Learning), di un intervallo più ristretto di lunghezze d'onda nel vicino infrarosso per l'identificazione di parametri quali: Sostanza secca (DM), fibra neutro detersa (aNDF), fibra acido detersa (ADF), e lignina (ADL). La seconda attività si basa sullo studio della metagenomica dalle feci di bufale da latte al fine di individuare delle correlazioni con l'alimentazione e la digeribilità di questa.

Key words: precision feeding; feaces; microbiome; buffalo**.**

1. Introduction

In accordance with the PhD thesis project previously described (Evangelista, 2022), in this poster reports the main results of the second activity concerning:

(A) The characterization of metagenomic profiles of different buffalo farms and the influencing factors on the microbiome in feaces

2. Materials and Methods

Faecal samples were collected in 10 dairy buffalo herds representative of the Amaseno valley, in the Lazio region. The samples were collected from each company once a month, from June to November 2022 for a total of 6 samplings. The faeces were collected approximately 2-3 hours after the distribution of the morning feed on a representative sample of animals (about 8-10 buffaloes per farm) directly from the rectal ampoule. In addition, samples of TMR (Total Mixed Ration) and bulk milk were collected for each farm. A total of 60 TMR, 60 of faeces, and 60 bulk milks were collected and analysed.
The analyses conducted on TMR, and faeces were: Dry matter (DM) was measured after oven drying at 65°C to constant weight. Then, TMR and feaces samples were ground through a mill (Retsch Müller, Germany) to pass a 1 mm screen and then sealed polyethylene containers were used to store prepared samples. Samples were analysed for crude protein (AOAC, 2005), ash (AOAC, 1990), ethereal extract (AOAC, 2000), and starch (AOAC, 2005) using a K-TSTA assay kit (Megazyme International, Bray, Ireland), and neutral detergent fibre (aNDF), acid detergent fibre (ADF), and acid detergent lignin (ADL) were analysed using an Ankom200 Fiber Analyzer (Ankom Technology, Macedon, NY) according to Van Soest et al. (1991). Furthermore, the pH was determined on the faeces by means of a portable pH-meter ("XS Tester", Giorgio Bormac, Italy). Chemical data are reported as percentages on a dry matter basis. MIlk analyzes were conducted by Experimental Zooprophylactic Institute of Rome.
DNA extraction for sequencing according to the NGS (next generation sequences) technique, the kit was used: Quick-DNATM Faecal/Soil Microbe Miniprep Kit (Zymo Research Corporation, USA).

3. Results and Discussion

3.1 Determination of chemical composition of feceas, TMR and bulk milk

Table 1 shows the chemical composition of buffalo faeces (Mean ± SD).

Table 1 Chemical composition of faeces.

	DM (%)	Ash (%)	CP (%)	EE (%)	aNDF (%)	ADF (%)	ADL (%)	Starch (%)	pH
Means (±SD)	13.76 (±1.39)	12.16 (±1.26)	14.12 (±1.27)	1.29 (±0.31)	56.50 (±3.84)	43.88 (±3.25)	14.78 (±2.24)	1.71 (±1.19)	6.34 (±0.22)
Max	19.14	15.55	17.96	2.43	64.24	50.51	20.40	8.34	6.73
Min.	11.34	9.67	11.16	0.83	43.38	35.11	10.49	0.78	5.73

DM: dry matter; ash; crude protein; ethereal extract; aNDF (neutral detergent fibre); ADF (acid detergent fibre); ADL (acid detergent lignin); and starch are on DM basis.

Table 2 shows the results relating to the chemical-physical composition of the TMR (Mean ±SD).

Table 2 Chemical-physical composition of the TMR.

	DM (%)	Ash (%)	CP (%)	EE (%)	aNDF (%)	ADF (%)	ADL (%)	Starch (%)	Upper (%)	Middle (%)	Lower (%)	Bottom (%)
Means (±SD)	52.12 (±6.47)	6.80 (±0.88)	11.87 (±1.98)	2.48 (±0.43)	46.61 (±5.32)	31.10 (±3.80)	6.13 (±0.95)	13.66 (±2.69)	21.64 (±15.45)	25.16 (±9.89)	28.46 (±8.46)	24.82 (±6.06)
Max	67.32	10.76	15.48	3.78	57.70	43.34	8.50	17.80	61.20	43.90	44.90	37.30
Min.	40.98	5.23	6.13	1.70	36.79	23.94	3.20	5.83	1.00	6.30	13.60	12.70

DM: dry matter; ash; crude protein; ethereal extract; aNDF (neutral detergent fibre); ADF (acid detergent fibre); ADL (acid detergent lignin); and starch are on DM basis; Upper = % of ration retained by a sieve with holes of 19 mm; Middle = % of the ration retained by a sieve of 8 mm; Lower = % of the ration retained by a sieve of 4 mm; bottom =Bottom of ration with dimensions <4 mm.

Table 3 shows the results relating to the chemical composition of the bulk milk (Mean ± SD).

Table 3 Chemical composition of buffalo bulk milk.

	Fat (%)	Protein (%)	Lactose (%)	Casein (%)	Urea (mg/dl)	pH	Acidity (°SH/100)	SCC (*1000/ml)	RCT (min.)	K_{20} (min.)	A_{30} (min.)
Means (±SD)	8.31 (±0.56)	4.73 (±0.16)	4.57 (±0.06)	3.86 (±0.18)	41.81 (±5.45)	6.76 (±0.10)	7.83 (±0.58)	265.50 (±155.13)	21.23 (±5.25)	4.63 (±2.84)	23.12 (±10.27)
Max	9.67	5.23	4.68	4.32	54.2	6.94	9.98	699	36.37	21	45.10
Min.	7.09	4.46	4.38	3.40	29.50	6.19	6.50	78	4.37	2.30	2.90

SCC: somatic cell count; RCT: rennet coagulation time, min; k_{20}: curd firming time, min; a_{30}: curd firmness, mm.

DNA extractions from faeces samples have just been completed. The DNA will be sequenced in the coming months.

The results on the composition of the ration and faeces show a wide variability mainly due to the different feed management adopted by the 10 farms. From the results of the NGS analysis we therefore expect to have a microbial variability within the faeces. In this way we will try to understand how diet influences the microbial composition of faeces.

3.2 Formulation of the research program for the following year

The next phase involves the analysis and study of the results obtained from the NGS on the faeces microbiome. The following step involves an in vivo study to test the ability of a supplement based on cellulolytic bacteria to improve the digestive efficiency of the fiber in dairy buffaloes.

4. References

AOAC: Official Method of Analysis, 18th ed.; Association of Official Analytical Chemists: Washington, DC, USA, 2005.

AOAC: Official Methods of Analysis, 15th ed.; Association of Official Analytical Chemists: Washington, DC, USA, 1990.

AOAC: Official Method of Analysis, 17th ed.; Association of Official Analytical Chemists: Washington, DC, USA, 2000.

Evangelista C. Development of strategies for the adaptation of the livestock sector to the new climate regime with machine learning and artificial intelligence methods. In Proc.s of the 26th Workshop on the Developments in the Italian PhD Research on Food Science and Technology, Asti (Italy), 19-21 September, 2022, pp. 85-86.

Van Soest, P.J.; Robertson, J.B.; Lewis, B.A. Methods for dietary fiber, neutral detergent fiber, and nonstarch polysaccharides in relation to animal nutrition. J. Dairy Sci. 1991, 74, 3583–3597.