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

Chiara Evangelista-Marco Milanesi-Daniele Pietrucci-Federica Gabbianelli-Giovanni Chillemi
Department of Innovation in Biological, Agri-food and Forestry Systems (DIBAF), University of Tuscia, 01100 Viterbo, Italy

Introduction

In accordance with the PhD thesis project previously described (Evangelista, 2022), in this poster I reports the main results of the second activity concerning:
(A) Results on the chemical-physical composition of previously collected samples (ration, feaces and milk);
(B) The characterization of metagenomic profiles of buffalos in different farms and influencing factors on the microbiome in feaces.

Material & method

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 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). 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. The results on the composition of faeces, TMR and milk are presented in tables 1,2 and 3, respectively. Feaces samples for microbiome analyses were collected and stored in DNA/RNA Shield™ Lysis Tubes at -80°C. A selection of the samples from which to extract the DNA was made using the R program taking into consideration the chemical composition of feaces and TMR, and composition of milk. DNA extraction for sequencing according to the NGS (next generation sequences) technique, has been made using Quick-DNA^{TM} Faecal Microbe Miniprep Kit (Zymo Research Corporation, USA). The extracted DNA was quantified and stored at -20°C.

Results & Discussion

Table 1 shows the results relating to the composition of the 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 and physical composition of the ration supplied to the animals.

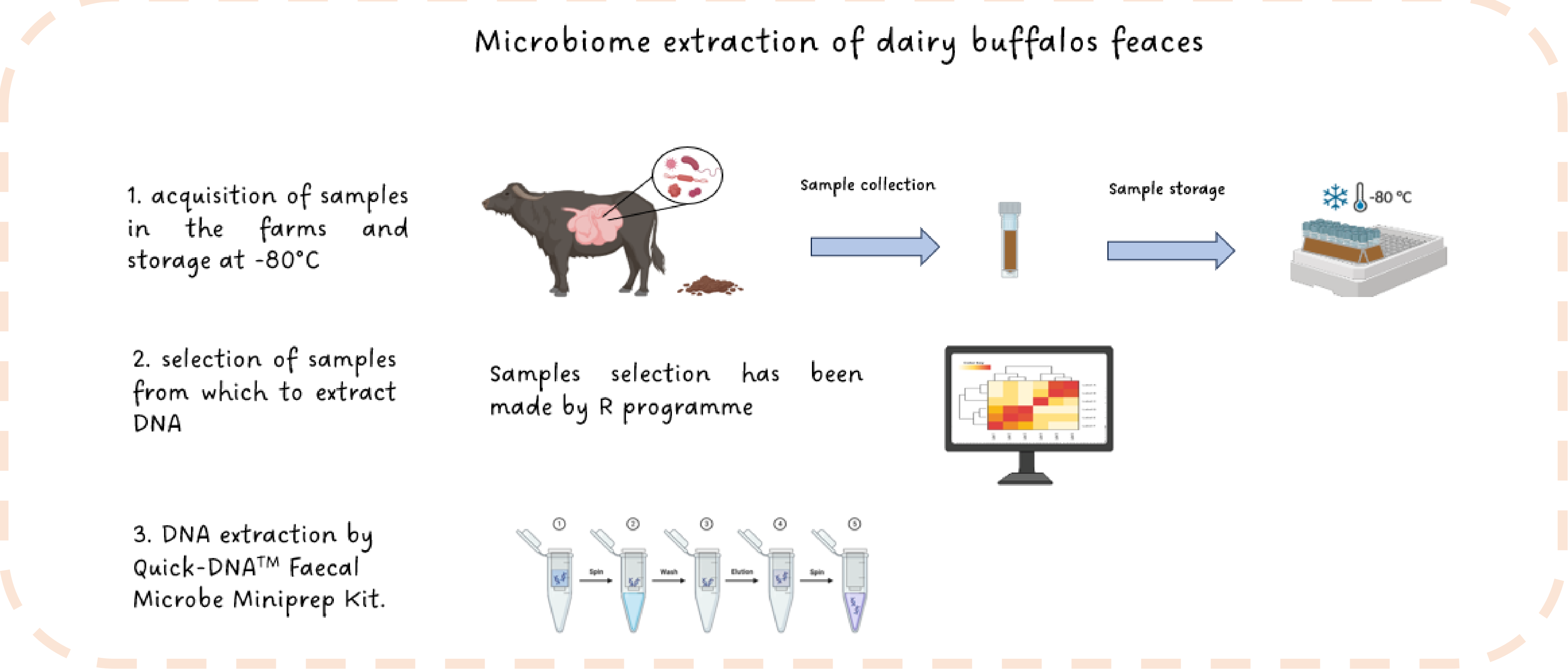
	DM (%)	Ash (%)	CP (%)	EE (%)	aNDF (%)	ADF (%)	ADL (%)	Starch (%)	Upper (%)	Middle (%)	Lower (%)	Bottom (%)
Means (±SD)	52.12 (±6.47)	6.80 (±0.88)	11.87 (±1.98)	2.48 (±0.43)	46.61 (±5.32)	31.10 (±3.80)	6.13 (±0.95)	13.66 (±2.69)	21.64 (±15.45)	25.16 (±9.89)	28.46 (±8.46)	24.82 (±6.06)
Max	67.32	10.76	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.

	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.


Microbiome extraction of dairy buffalos feaces

1. acquisition of samples in the farms and storage at -80°C

2. selection of samples from which to extract DNA

Samples selection has been made by R programme

3. DNA extraction by Quick-DNA^{TM} Faecal Microbe Miniprep Kit.

Formulation of the research program for the following year

The next phase involves the analysis and study of the results obtained from NGS on the faecal microbiome. Research of relationships between the microbiota composition and the diet, its digestibility, and the quality of the productions.
The next step, in the next year, foresees 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.

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