

# RECENT DEVELOPMENTS IN THE USE OF NEAR INFRA-RED SPECTROSCOPY FOR THE EVALUATION OF GRASS SILAGE

N.W. Offer, D.S. Percival and C.Thomas.

Scottish Agricultural College, Auchincruive, Ayr, UK, KA6 5HW

## ABSTRACT

This work assessed the potential of near infra-red spectroscopy (NIRS) to predict the voluntary intake and fermentation characteristics of grass silage. NIRS spectra were obtained from dried milled (Dry) or fresh samples by two methods (Wet1 - vertical transport mechanism and Wet2 - rotating cup drawer). Prediction errors (SECV as a percentage of mean values) were 5.5, 6.5 and 2.5 for Dry, Wet1 and Wet2 respectively for intake by dairy cows (n=28). Corresponding values were 10.3, 16.1 and 10.9 for lambs (n=88). The Wet2 method gave more accurate predictions than Wet1 except for predictions of ADF and unfermentable metabolisable energy (UFME) and was more accurate than the Dry sample method for the prediction of intake by dairy cows, TDM and UFME. However, the Dry sample technique performed best for OM, NDF, ADF, pH, sugar, lactic acid and VFA. NIRS has the potential to replace all the current advisory analytical methods..

## KEYWORDS

Silage, evaluation, near infra-red, dairy cows, lambs, intake, fermentation

## ACRONYMS

**ODM** - oven dry matter, **TDM** - ethanol-corrected toluene dry matter, **UFME** - unfermentable metabolisable energy, **ET** - electrometric titration, **OMD** - organic matter digestibility, **DG5** protein degradability at 5 %/h outflow rate, **SECV** - standard error of cross-validation as a percentage of mean.

## INTRODUCTION

The importance of accurate prediction of silage intake potential and characterisation of silage fermentation has been recognised (Thomas et al. 1996) yet there is a strong need to improve the cost-effectiveness of silage analysis. The achievement of these objectives demands that manual processing of silage samples should be minimised. Near infrared spectroscopy (NIRS) is in widespread use in the UK for the prediction of silage digestibility and crude protein but most laboratories also use a range of other measurements. The following measurements are made for advisory silage analysis at the Scottish Agricultural College (SAC): ODM, ash, fermentation characteristics by ET and crude protein and OMD by NIRS on 100°C dried samples. This paper explores the possibility of using NIRS to replace all routine silage measurements.

## MATERIALS AND METHODS

Eighty eight silages (predominantly perennial ryegrass) have been evaluated over a period of four years to develop methods of predicting silage intake (Percival et al., 1996). The following analytical methods have been applied to all silages: ODM, TDM and ash, ET (Moisio and Heikonen, 1989; Offer et al. 1994), HPLC (Rooke et al. 1990), NDF and ADF (Goering and Van Soest, 1970). UFME was calculated according to AFRC (1993) using HPLC values for the fermentation end products and measured oil values. Silages showed a wide range of composition (ranges for TDM, OMD and ammonia were 107-333 g/kg, 0.60-0.83 and 10-353 gN/kg TN respectively). Voluntary intakes were measured for all silages using lambs (as sole feed), and for 28 with early-lactation dairy cows receiving 7 kg/d of concentrate. DG5 was measured for 28 silages using the *in situ* technique of Orskov and McDonald (1979). All samples were scanned by NIRS (1100-

2500nm) using the following three methods: after drying at 100°C using a NIR Systems 6500 (Dry); scanned fresh using a similar instrument fitted with a vertical transport mechanism (Wet1) and scanned fresh in a Bran and Luebbe 500 fitted with a rotating cup drawer (Wet2). All models used second derivative (2:10:10:1) mathematics. The Dry scans were subject to standard normal variate transformation and detrend before derivatisation. This process yielded 84 (Wet) or 76 (Dry) segment values which were examined using stepwise multiple linear regression (MLR). The statistics presented were obtained using partial least squares applied to those segments which proved significant ( $P \leq 0.05$ ) in MLR models (typically less than 20).

## RESULTS AND DISCUSSION

NIRS gave more accurate predictions than current SAC advisory methods with the exception of TDM and VFA (Table 1). NIRS predicted OM, NDF, ADF and pH with errors of less than 6% of mean values, whilst errors were higher for neutralising value (13.2%) and sugar (29.4%). The Wet2 scanning method performed better than the Wet1 method with the exception of ADF and UFME. Generally, the differences were not great, although the Wet2 method gave a substantially more accurate prediction of intake by dairy cows (SECV 2.5 and 6.5% for Wet2 and Wet1 respectively). The Wet2 method proved more accurate than the Dry method for the prediction of intake by dairy cows, TDM and UFME. However, the Dry technique performed best for OM, NDF, ADF, pH, sugar, lactic acid and VFA. Both Wet2 and Dry gave similar predictions of intake by lambs, ODM/TDM (silage volatiles), protein degradability and neutralising value.

It is concluded that NIRS has the potential to replace all the current advisory analytical methods. For the Dry method, measurement of ODM would be needed but would present little additional work. The Wet method appears a cost-effective choice for silage analysis but clearly scanning method is an important variable.

## ACKNOWLEDGEMENT

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	Prediction Method							
	Current <sup>a</sup>		Dry		Wet1		Wet2	
	R <sup>2</sup>	SECV	R <sup>2</sup>	SECV	R <sup>2</sup>	SECV	R <sup>2</sup>	SECV
intake by dairy cows	0.82	6.7	0.88	5.5	0.83	6.5	0.97	2.5
intake by lambs	0.60	14.7	0.81	10.3	0.53	16.1	0.78	10.9
TDM	0.99	2.3	0.65	13.7	0.87	8.2	0.88	7.7
ODM/TDM	0.50	2.2	0.45	6	0.32	2.9	0.52	2.4
organic matter	-	-	0.84	1.2	0.58	2.0	0.66	1.8
NDF	-	-	0.90	4.8	0.71	7.7	0.76	7.4
ADF	-	-	0.84	5.6	0.78	6.7	0.77	6.7
UFME	0.51	13.9	0.69	11.9	0.76	10.4	0.75	10.7
DG5	0.73	2.2	0.96	0.9	0.95	1.0	0.96	0.9
pH	-	-	0.92	2.2	0.74	3.9	0.76	3.7
neutralising value	-	-	0.82	13.7	0.84	13.2	0.83	13.2
sugar (by ET)	-	-	0.81	29.4	0.73	35.5	0.72	36.4
lactic acid (by HPLC)	0.85	17.2	0.91	13.2	0.82	18.9	0.88	15.1
VFA (by HPLC)	0.93	22.1	0.85	33.0	0.46	63.8	0.71	46.0

Current<sup>a</sup> SAC advisory method using ODM, OMD, crude protein, NDF and ET.