



ASPA 23rd Congress Book of Abstracts

Fulvia Bovera

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P075

Fuel consumption for TMR preparation and distribution in different dairy farms

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The aim of the study was to evaluate the diesel fuel consumption (DFC) of a mixer wagon during feeds loading and mixing phases, and TMR distribution in dairy farms. In this work, the operating performance of a horizontal self-propelled TMR mixer wagon (Gulliver 6014, Sgariboldi, Codogno, Italy) with desilage conveyor arm, cutting slasher and mixer tank of 14 cubic metre capacity with paddle technology were analysed. The mixer wagon was equipped with a 100 kW turbo-diesel engine with a displacement of 3.6 L and it was characterised by hydrostatic transmission. Four different dairy farms located in the northern part of Italy (Lombardy) were involved in the study. All the farms had a corn and grass silage-based diet and a dietary content of hay from 2 to 16%. Fuel consumption was recorded as well as the duration of the different preparation and distribution phases, accounting for the amount of TMR produced in each farm and to the NDF content. Data were statistically analysed using simple linear regression.

The results showed a statistically significant correlation ($R^2=0.90$) between the amount of TMR produced and the consumption of diesel fuel. The relation between the NDF content of the TMR and the DFC had a coefficient of determination equal to 0.69, showing a higher consumption of fuel with the increase of the fibre contained in the ration. This is probably explainable with a greater absorption of power during loading due to a greater use of the cutting slasher to cut the fibrous parts. The relationship between increasing preparation and distribution times and fuel consumption showed, as expected, a high correlation ($R^2=0.98$). The hourly DFC of the three work phases analysed (loading, mixing and distribution) were similar over the four dairy farms involved in the study, with average values of 13.19 ± 0.33 kg/h, 13.75 ± 0.18 kg/h and 12.73 ± 0.47 kg/h, respectively. The average operating times measured were respectively of 25.06 ± 6.79 min for the loading phase (including the transfer time between the different feed storages in the dairy farm), 7.18 ± 1.39 min for mixing and 3.96 ± 0.9 min for the distribution, highlighting as the loading phase is the one requiring the most energy expenditure. This suggests the need – for the dairy farms – to optimise the internal logistics and the location of the feed storages.

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P076

Evolution of gastrointestinal microbiota structure in sheep: dietary and age effects

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The aim of this work was to study and describe the colonisation and evolution of microbiota from gastrointestinal tracts (GIT) in Sarda dairy sheep raised indoor from birth to 20 months of age (at middle of the first lactation). Since the day of 75 from conception, the sheep were divided into two groups and respectively exposed to two different dietary regimes. One group was fed a glucogenic diet with a high content of starch and sugars (starch) and the second was fed a lipogenic diet with a high content of high digestible fibre from soyhulls and beet pulp (fibre). Samples from different GIT of male lambs (rumen, ileum and rectum content) at birth and weaning were collected post-mortem. In addition, samples of rumen liquid and faeces were collected, *in vivo*, from female replacement lambs at birth, at weaning, at 6 months, gestation and first lactation phases. Samples were immediately frozen until DNA extraction, and microbial groups and structure were analysed by quantitative real-time PCR and DGGE. Metagenomic analyses of 16S-RNA were carried out on samples collected at birth and weaning, and are in progress for rest of the samples. Preliminary results showed that: – at birth (even before suckling) the GIT of lambs is characterised by a heterogeneous microbiota; – at weaning the microbiota is already structured, with developed mature microbial functions, that are dietary driven even maintaining the large individual differences observed at birth; – the adult-like composition of microbiota is reached around 1 year of age; – from prepuberal to first lactation the number of bacteria, protozoa and fungi increased significantly ($p < .05$). The number of fungi, *Fibrobacter succinogenes*, *Treponema saccharophilum* and *T. bryantii* were higher in sheep exposed to fibre vs. starch diets ($p < .05$). The number of protozoa increased with age ($p < .05$) and tended to be higher in fibre fed ewes ($p < .01$). This work confirmed that diet was the first driver of the rumen microbial colonisation and its microbiota structure. However, during the last-trimester of pregnancy, the effect of diet