



SPOTLIGHT NOTABLE RESULTS

downside risk in BOR, CON, SOU, and UPL directly in year t and also a delayed effect on the year $t+1$ for CON (table 5). The effect of drought is more ambiguous in NA and WA as in the current year it appears to lessen the economic downside risk whilst it has a negative effect in the year $t+1$. Heat is significantly and negatively associated with economic downside risk across all classes.

Table 4. Drought and heat effect on technical efficiency across climatic classes.

Climatic class	NAT	WAT	BOR	CON	SOU	UPL
Drought effect	+	-	-	(not sign.) ¹	-	-
Delayed drought effect	-	(not sign.)		(not sign.)		
Heat effect	-	-	-	(not sign.)	-	(not sign.)

1 Not significant.

Table 5. Drought and heat effect on economic downside risk across climatic classes

Climatic class	NAT	WAT	BOR	CON	SOU	UPL
Drought effect	+	-	-	(not sign.) ¹	-	-
Delayed drought effect	-	(not sign.)		(not sign.)		
Heat effect	-	-	-	(not sign.)	-	(not sign.)

To conclude, this study confirms that European dairy farms are technically highly efficient. A significant effect of drought stress on efficiency was shown in most of the classes. The delayed effect of drought observed in the NAT class could be due to a shortage of forage stock in the subsequent year, potentially causing an increase in feed costs per cow. A shortage of forage may lead to a reduced proportion of forage in the diet, which may affect production levels. In terms of the heat stress, a significant effect was observed on

efficiency across four out of six climatic classes. The lack of a significant heat effect on efficiency for UPL was somehow expected as this class grouped upland farms, located above 600 m of altitude, where heat waves are less frequent and intense compared to lowland classes.

The downside economic risk was also clearly affected by drought and heat stress across classes. However, an unexpected significant positive effect of drought was found in NAT and WAT. This finding may indicate a negative role played by excessive rainfall, as NAT and WAT are two of the three most humid classes present in the analysis, with an average daily precipitation level of 2.99 and 2.27 mm over 2007-2013, respectively.

Ruminal microbiota is associated with feed efficiency phenotype of fattening bulls fed high-concentrate diets

By: Sandra Costa-Roura; Daniel Villalba (UDL), Mireia Blanco; Isabel Casasús (CITA), Joaquim Balcells; Ahmad Reza Seradj (UDL).

Improving feed efficiency in livestock production is of great importance to cut down on nutrition costs. Our assay aimed to examine the relationship between ruminal microbiota and variation in feed efficiency in beef cattle fed concentrate-based diets.

Residual feed intake of 389 fattening bulls, supplied with corn-based concentrate and forage ad libitum, was used to estimate animals' feed efficiency. Bulls' concentrate intake was recorded on a daily basis, and their body weight (BW) was





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measured at least once a week. Feces and ruminal fluid samples were collected, at mid-growing (159 d of age and 225 kg BW) and mid-finishing periods (266 d of age and 434 kg BW), from 48 bulls chosen at random to estimate their forage intake and to characterize their apparent digestibility, ruminal fermentation and microbiota.

Within the 48 sampled bulls, only those animals with extreme values of feed efficiency (high-efficiency [HE, n=12] and low-efficiency [LE, n=13]) were subjected to further comparisons. No differences in dry matter intake were found between the two categories of feed efficiency (P=0.699); however, HE animals had higher

Growing phase: 159 d of age and 225 kg

Finishing phase: 266 d of age and 434 kg

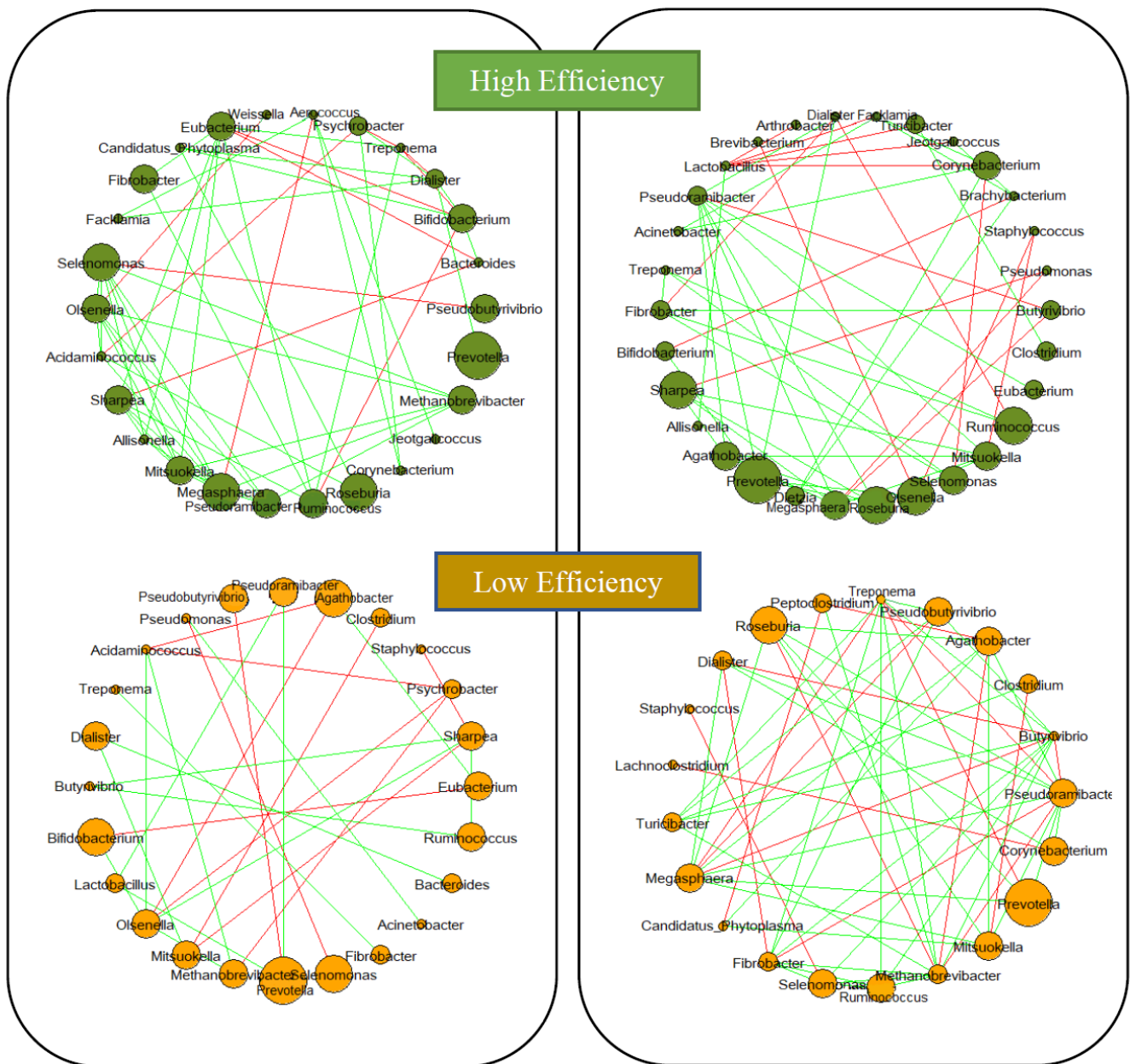


Figure 7. Microbial genera network in the rumen high-efficiency and low-efficiency. Networks were generated based on those genera establishing significant correlations ($r > 0.60$ and $P < 0.05$). Green and red edges indicate positive and negative correlations, respectively. Node size is proportional to genus abundance in ruminal fluid.





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apparent digestibility of dry matter ($P=0.002$), organic matter ($P=0.003$) and crude protein ($P=0.043$). Volatile fatty acids concentration remained unaffected by feed efficiency ($P=0.676$) but butyrate proportion increased with time in LE animals ($P=0.047$).

Ruminal microbiota was different between HE and LE animals ($P=0.022$): both alpha biodiversity ($P=0.005$ for Shannon index and $P=0.020$ for Simpson index) and genera network connectance (Figure 7) increased with time in LE bulls; which suggests that LE animals hosted a more robust ruminal microbiota. Methanobrevinacter, Roseburia, Agathobacter, Butyrivibrio, Pseudobutyrvibrio, Ruminococcus and Selenomonas genera are usually related to high energy loss through methane production and were found to establish more connections with other genera in LE animals' rumen than in HE ones (Figure 7). Microbiota function capability suggested that methane metabolism was decreased in HE finishing bulls. In conclusion, rumen microbiota was found to be associated with feed efficiency phenotypes in fattening bulls fed concentrate-based diets. Our results also highlighted a possible trade-off between animal feed efficiency and ruminal microbiota robustness that should be taken into account for the optimization of cattle production, especially in systems with intrinsic characteristics that may constitute a disturbance to rumen microbial community.

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Genomic prediction using purebred and crossbred individuals

By: Emre Karaman; Guosheng Su (QGG AU), Iola Croue (ALLICE), Mogens S. Lund (QGG AU)

Crossbreeding is an efficient strategy in dairy cattle breeding, to achieve better productivity and robustness at the animal and herd level. Crossbreeding systems, e.g. ProCROSS system (<https://www.procross.info>) yield crossbred animals with different proportions of genome segments coming from the pure breeds included in the system. Genomic evaluations in dairy cattle are generally carried out separately for each pure breed, and neither crossbred data is used, nor do they get evaluations. Genetic evaluation for crossbreds requires methods which can efficiently handle data from purebred and crossbred individuals. In WP4 (Task 4.1) of the GenTORE project, we provided and tested a model which can handle data from purebred and crossbred individuals, allowing for simultaneous evaluation of purebred and crossbred animals. The proposed model includes a genomic component for each pure breed in the gene pool. It relies on the accurate determination of breed origin of each genome segment. Models using breed origin of alleles (BOA) are generally referred to as BOA models.

Accuracies for within-, across- and multi-breed predictions using standard genomic prediction models were compared with BOA models, using simulated data sets. Genotypic data (~13K SNPs, 5 chromosomes) from real dairy populations, i.e. Danish Holstein (H), Swedish Red (R) and Danish

