



## Session 22

## Theatre 7

### **Increasing duration of feed restriction: performance ranking and variability of beef cows' response**

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Animal resilience and robustness are two traits of importance for livestock systems and genetic selection. Their phenotyping is essential to evaluate the adaptation of different genotypes to changing environments. The objective was to characterise productive and metabolic responses of primiparous Charolais cows to two feed restrictions (FR) of different duration. After calving, 13 cows (39±2 mo old, 680±42 kg BW at calving) were fed hay *ad libitum* supplemented with concentrate to fulfil their energy and protein requirements. At 55±6 d post calving, cows underwent a succession of FR (50% of their energy requirements) and *ad libitum* intake: 4 d FR (FR4), followed by 17 d *ad libitum* intake, a second 10 d FR (FR10) followed by 18 d *ad libitum* intake. Individual milk yield (MY; weight-suckle-weight method), BW, BCS and plasma non-esterified fatty acids (NEFA), β-OH butyrate, glucose and urea concentrations were measured before, during and after each FR. Among all measured parameters, MY and NEFA concentrations showed the most pronounced dynamic changes. MY and NEFA returned to their initial levels within 3±1 d, independently of FR duration (SAS Proc Mixed with repeated measures analysis). Functional data analysis was applied to MY and NEFA responses to obtain parameters describing deviation and recovery trajectories in response to FR. FR duration did not change the ranking of animal responses, i.e. responder cows in FR4 remained responders in FR10 (P<0.03 to 0.07) as shown by the linear correlations between deviation and recovery trajectories after FR. Individual variability of MY and NEFA was, however, higher during FR10 than FR4 (Levene test, P<0.05). Altogether 1/ parameters derived from MY and NEFA dynamics accounted for individual differences in responses to FR perturbations and 2/ cow differences appeared to be stable when similar FR are applied for a longer period. Further research is warranted to test these parameters as proxies of animal resilience and robustness and if relevant used to improve future breeding strategies. Gentore (H2020) project funded this study.



## Session 22

## Theatre 8

### **Identification of longevity predictors in French dairy cattle**

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Resilient animals are able to maintain the normal processes when confronted with environmental perturbations, reducing, in the long term, the risk to be culled. Thus, longevity can be proposed as a proxy of resilience. The length of productive life (LPL), defined as the time between the date of the first calving and the date of culling, is the most popular measure for longevity. It requires a long time to be observed and the identification of its predictors is of high interest. The aim of this study was to investigate the effect of production, reproduction, morphology and health traits on LPL, in order to identify predictors of longevity. Data included 278,237 lactations from 122,470 Holstein Friesian cows reared in 640 herds. Two different longevity traits were investigated: true longevity (TL), defined as the ability to avoid any culling, and functional longevity (FL), that is the aptitude to avoid culling for reasons other than production. Survival analysis was performed using a Weibull proportional hazard model including several non-genetic factors, such as herd-year, year-season, herd size variation, and age at the first calving, with or without adjustment for milk production (i.e. to evaluate FL and TL). The investigated traits were added to this model and tested distinctly from the others. Our study revealed that insemination status, calving ease, mastitis, somatic cell count, body condition score, body depth and udder depth had significant relationships with TL and FL and they can be used as predictors of longevity. In addition, we found differences in estimation of risk of culling between TL and FL, suggesting that milk production plays an important role in culling decisions. The identified longevity predictors can be validated extending the methodology used in this study to other bovine production contexts. In addition, they can be exploited to develop a multi-trait model for genetic and genomic evaluation for resilience.

