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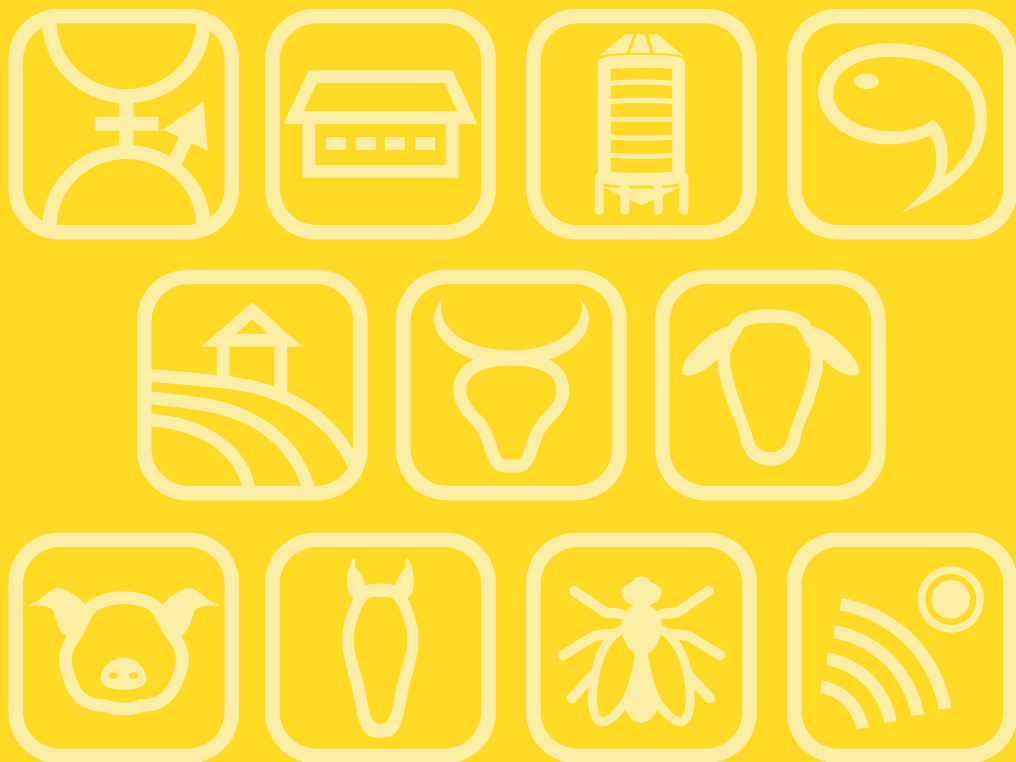
Can we breed cattle with more efficient rumen microbiome?

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Milk and meat from ruminants have reduced malnutrition and improved prosperity in many societies. However, ruminant production is facing significant challenges in terms of improving feed efficiency (FE) and reducing its environmental footprint. Recent research has revealed that variations in the composition and function of the rumen microbiome can directly and/or indirectly influence several phenotypic traits in cattle such as FE, methane emissions, metabolic health, milk and meat quality. This presents an opportunity for rumen microbiome interventions to improve productivity, health and reduce the environmental footprint of cattle production. More and more evidence revealed the individualized rumen microbiome and host genetics could be one of the factors influencing the colonizing of selective rumen microbes. Here, we reported the identified heritable rumen bacteria in both beef and dairy cattle. Some of the traits of the host that influence the composition and function of the rumen microbiome appear to be heritable. The extent of this heritability is also influenced by host genetics and has implications for cattle production-related traits. Moreover, we showed that heritable rumen bacteria exhibited a high degree of maternal similarity as compared to those that were nonheritable. Our findings illustrated that both the host and rumen microbiome cattle production and such traits associated with the rumen microbiome could be passed from parents to offspring. The identified genotypes may potentially serve as markers for breeding cattle for optimal rumen function.

Characterization of physiological responses in Rasa Aragonesa ewes under water restriction

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The aim of this study was to characterise the effect of water restriction on ewes. Two hundred and two Rasa Aragonesa ewes were subjected to total water restriction for 5 days. Intake, body weight (BW) and body condition score (BCS) were measured daily during the 5 days of restriction, as well as temperature and percent humidity. Blood samples were collected just prior to the challenge (0d), and at the end of the study (5d) for haematological and metabolite measurements. Wool samples were taken at day 0 and 4 weeks later (28d). Variation in blood and wool traits was also calculated for each animal. Dry matter intake, BW and BCS were decreased during the trial. Mixed model statistical analysis indicated that all haematological and metabolite levels changed during the water restriction period except for plasma cortisol. Principal component analysis (PCA) and hierarchical clustering were performed with variation traits between 0d and 5d (blood samples) and 0d and 28d (wool samples) to identify different responses among ewes. Four clusters were identified: 1) fat mobilization ewes (n= 56; wool cortisol increase and low increase neutrophils-to-lymphocytes ratio (NLR)) with low dehydration but highest fat mobilization; 2) high-stressed ewes (n= 9; very high plasma cortisol increase) with low dehydration; 3) low-stressed ewes (n= 106; low plasma cortisol and low NLR increase) with minor fat mobilisation but high dehydration; 4) stressed ewes (n= 31; high NLR increase) with higher dehydration. In general, the Rasa aragonesa ewes exhibit a high tolerance to water stress (C1 & C3 = 162 ewes; 80%) but with different adaptation responses.