acetate, propionate, total VFA, or ammonia concentration or the relative abundance of the Firmicutes and Bacteroidetes phyla ($P < 0.5$). A number of associations occurred for D-lactate, L-lactate, and total lactate concentration and the acidosis eigenvectors at all time points before d 21 ($P < 0.05$). Ten associations were found at one time-point only for butyrate and valerate concentrations ($P < 0.05$). A number of associations were found with the Actinobacteria, Chloroflexi, Euryarchaeota, Fibrobacteres, Proteobacteria, and Tenericutes phyla at one or more time points ($P < 0.05$). Gene-wide associations with the metabolome and microbiome were present despite the small population size and suggest the presence of markers for ruminal acidosis. Qualitative trait loci and candidate gene analysis is being conducted.

Key Words: genome wide association, lactic acid, ruminal acidosis

BREEDING AND GENETICS SYMPOSIUM: RESILIENCE OF LIVESTOCK TO CHANGING ENVIRONMENTS

0401 Production, biological, and genetic responses to heat stress in ruminants and pigs.

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Heat stress (HS) compromised efficient animal production and reduced livestock output during the summer was traditionally thought to result from decreased nutrient intake. Our data from ruminants and monogastrics challenge this dogma and indicate that heat-stressed animals utilize homeorhetic strategies to modify metabolic and fuel selection priorities independently of feed intake. Systemic shifts in bioenergetics are characterized by increased basal and stimulated circulating insulin. Hepatocytes and myocytes also show clear differences in glucose production and metabolic flexibility, respectively, during HS. Intriguingly, HS animals do not mobilize adipose tissue despite being in both a negative energy balance and catabolic state. The origin of the aforementioned metabolic changes may lay at the gastrointestinal tract. For a variety of reasons, HS compromises intestinal integrity. Increased permeability to luminal contents results in local and systemic inflammatory responses. Consequently, heat-stressed animals are simultaneously confronted with life-threatening hyperthermia and endotoxemia. Determining how these systems are homeostatically and homeorhetically coordinated to prioritize acclimation and survival vs. agriculturally productive purposes would presumably reveal mechanisms amenable to manipulation. Interestingly, thermoregulatory and production responses to HS are only marginally related. In other words, increases in body temperature indices poorly predict the decrease in both milk yield and growth. Further, HS-induced decreased feed intake is also an inaccurate predictor of milk yield or growth during HS. This suggests that traits associated with production and thermoregulation during HS may be governed by separate genomic loci and potentially interdependent biological mechanisms. Thus, selecting animals with a “tolerant” phenotype based solely or separately on thermoregulatory capacity or production may not ultimately increase HS resilience. Therefore, the variation of multiple phenotypes and genotypes needs to be accounted for to generate a more comprehensive heat tolerant animal. In summary, HS is one of the primary hurdles to efficient animal production. Defining the physiological mechanisms through which HS and other environmental factors influence complex, multifactorial traits, is critical for developing approaches to ameliorate current production issues and is a prerequisite for generating future strategies (genetic, managerial, nutritional, and pharmaceutical) to maximize livestock efficiency.

Key Words: heat stress, genetics, insulin, tolerance

0402 Breeding for resilience to heat stress effects: A comparison across dairy ruminant species.

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Dairy animals are more susceptible to heat stress (HS), because milk production results in a large metabolic heat strain. As a consequence, selection for increased milk production will tend to decrease animals’ tolerance to increasing heat loads. A comprehensive approach to characterize HS effects on dairy production and to develop breeding tools to select for heat tolerance (HT) was followed by making use of available milk recording information, climatological data and genomic information on three dairy ruminant populations, Holstein cattle and local breeds Manchega sheep and Florida goats raised in the warm southern regions of Spain. Heat stress thresholds were around 55/63 (15/18) and 63/65 (19/20) for average daily values of THI (°C temperature) for fat/protein yields in Holstein and Manchega, respectively. For goats, HS thresholds could not be clearly identified. Sufficient genetic variability was observed in productive response to heat to consider this trait for selection in the three populations. Genetic antagonism between milk production and HT (ability to maintain milk production under high heat loads) was found for the three populations but stronger for cattle and goats. Several selection criteria including eigen-components of the response variability (looking for tolerance criteria independent of production level) were compared and slopes of the genetic response curves in the HS region were recommended. Estimated genetic correlations between production under cold and comfort or heat conditions was different from unity in all species (down to 0.3 in cattle), indicating the different genetic mechanisms involved in heat and cold tolerance. Genome-wide association studies using slopes of polynomial curves of response as pseudo-phenotypes have been performed. Beside genomic regions related to fat metabolism (e.g., ACSL3), regions highlighting the effect of HS on the regulatory activity of transcription factors (TBL1XR1, DCHAU1), a number of genes involved in basic processes related to proteins transport and intracellular signal transduction (CNIH3 and CNIH4 ubiquitines and chaperones such as NVL from the chaperone-like AAA-ATPase family) showed signinficant signals. Although the use of milk recording and weather data has been proven useful to identify HT animals, the use of finer phenotypes together with genomic information are deemed important to succeed in selecting HT animals while maintaining productivity.

Key Words: heat tolerance, selection, dairy ruminants

0403 Climate change and selective breeding in aquaculture.

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Aquaculture is an important sector that strengthens food security. Based on FAO, aquaculture production has to increase up to 42.9% to meet the global population demand in 2020. According to the reports by IPCC and FAO, climate change may result in global warming, sea-level rise, changes of ocean productivity, water shortage, and more frequent extreme climate events. Climate change may affect aquaculture directly and indirectly, depending on climatic zones, aquaculture activities, and farmed species. Climate change may introduce opportunities—rise of temperature may increase growth and open up new farming opportunities due to aquatic species migration—as well as several challenges to aquaculture. First, genotype-by-environment interactions (GxE) may increase because aquatic animals may expose to more fluctuating rearing environments. Rainbow trout (*Oncorhynchus mykiss*), the most popular farmed salmonid worldwide, has a very narrow range of optimal temperature to grow. The magnitudes of GxE, i.e., average genetic correlation (r_g), from 1964–2013 were reviewed across 38 species. The review revealed strong re-ranking for growth of rainbow trout in different temperatures ($r_g = 0.36$), indicating lower-than-expected production in suboptimal rearing temperature when selecting for growth based only on optimal rearing temperature. Second, it can be hypothesized that climate change may increase environmental variance in sensitive genotypes. Third, climate change may facilitate an outbreak of (new) pathogens or parasites, increasing mortality and hence reducing production. Fourth, 20% reduction of ocean productivity worldwide has been predicted, implying a decline of fishmeal and fish oil supplies and hence the replacement of the raw materials may become more important in the future. Finally, reduction in biodiversity may threaten genetic variation and the ecosystems of wild stocks. Furthermore, this may imply a lack of founder populations for breeding in the future. To ensure the food security, the impacts of climate change have to be addressed through resource management, reduction of environmental impacts, and selective breeding strategies. Breeding goals may change toward "resilience," i.e., stability of performance under fluctuating rearing environments or toward new trait mean. The breeding goals may include disease resistance or tolerance for emerging pathogens and parasites. Anyhow, more research is needed to better understand the opportunities of selective breeding for resilient animals in aquaculture under climate change. To avoid any loss of biodiversity in wild stocks, an international gene bank of the wild stocks may store genetic resources of founder populations for future breeding programs.

Key Words: climate change, genotype-by-environment interaction, selective breeding

0404 Introgression of genes conveying resistance to heat stress into cattle populations using the "Slick" genetic variant as a model.

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There are ~270 million dairy cows globally and over 75% of these are found in hot climates and most of these have not undergone intensive, genetic selection. The ability to integrate genetically-improved cows into tropical cattle populations will underpin improvement of production performance.

The main impediment to the introduction of genetically-improved, high producing dairy cattle, typically from temperate countries, into tropical climates is the relatively poor heat tolerance and low tick resistance of the cattle breeds common in temperate climes. The concept of using gene introgression to improve heat tolerance and tick resistance was given momentum more than 15 yr ago following the identification of "slick," a major, dominant, gene for heat tolerance (and likely, tick resistance), segregating in the Senepol beef breed.

Our discovery, in 2013, of the "slick" causal mutation, a truncation of the prolactin receptor, provided the impetus to embark on crossbreeding of NZ dairy cattle with Senepol to enhance dairy performance in the tropics. A further advantage of the Senepol is that it is a *Bos taurus* breed, avoiding the potential disadvantages of *Bos indicus* crossbreds, which includes poor milk let down and late age at first calving.

The "slick" mutation is an enabling genetic variation which provides the necessary physiological traits (notably sweating ability) to improve animal welfare and performance in hot climates. The characteristics of NZ dairy breeds provide fertility, grazing ability and lactation performance on high roughage diets.

The primary objective of the breeding program is to produce homozygous "slick" bulls that have 75% NZ dairy genetics. The (5 yr) breeding program requires crossbreeding to produce 50% dairy F1 daughters; using these animals as egg donors through JIVET to produce 75% dairy F2 offspring and then inter-crossing the lines to generate homozygous sires. Gene editing of the "slick" mutation directly into dairy sires is not a practical option in NZ at the current time.

Further improvements in tropical dairy cow development are possible if more genetic variations associated with heat tolerance are found, although introgression of additional variations (for example, coat color) will be challenging in a breeding program such as that outlined here.

Key Words: Senepol, thermoregulation, dairy

0405 Genetic solutions to infertility caused by heat stress.

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Reproductive function in mammals is very susceptible to disruption by heat stress. In lactating dairy cows, for example, pregnancy rates per insemination can be as low as 10–15% in the summer vs. 25–40% in cool weather. Reduced fertility is caused by a combination of (1) the negative consequences of the physiological adjustments engaged to minimize hyperthermia during heat stress and (2) direct deleterious effects of elevated body temperature on the gamete and embryo (i.e., heat shock). There is genetic variation body temperature regulation during heat stress as well as in cellular resistance to elevated temperature. Thus, opportunities exist for improving reproduction during heat stress by modifying livestock genetically to improve body temperature regulation and cellular resistance to heat shock. Genetic improvement can be achieved by identifying genetically superior animals within a breed (heritability for rectal temperature during heat stress is 0.17) as well as by transferring genes from thermotolerant breeds to thermosensitive ones. A successful example of gene transfer is for a mutation in *PRLR* causing the slick hair phenotype. Holstein cattle inheriting this mutation have increased ability to regulate body temperature during heat stress and are less likely to experience a decrease in milk yield during summer than other Holsteins. Among the genes conferring cellular resistance to heat shock is a mutation in the promoter of *HSPA1L* identified in cattle. Selection for the beneficial allele of this gene, as well as other genes controlling cellular resistance to heat shock, might reduce the damage to the oocyte and embryo caused by elevated body temperature.

Key Words: heat stress, infertility, reproduction, body temperature

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0406 Resilience and lessons from studies in genetics of heat stress.

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Production environments are expected to change, mostly to hotter climates but also possibly more extreme and drier. This raises a question whether the current generation of farm animals can cope with the changes or should they be specifically selected for changing conditions. In general, genetic selection produces animals with smaller environmental footprint but also with smaller environmental flexibility. Some answers are coming from heat stress research across species, with heat tolerance partly understood as a greater environmental flexibility. Specific studies in various species show complexities of defining and selecting for heat tolerance. In Holsteins, the genetic component of heat stress on production approximately doubles in second and quadruples in third parity. Best production under heat stress is by cows with elevated body temperature, probably at a risk of increased mortality. In hot but less intensive environments, the effect of heat stress on production is minimal although the negative effect on fertility remains. Mortality peaks under heat stress and increases with parity. In Angus, the effect of heat stress is stronger only in selected regions, probably due to adaptation of calving seasons to local conditions and crossbreeding. Genetically, while the direct effect shows variability due to heat stress, the maternal does not, probably due to dams shielding calves from environmental challenges. In pigs, the effect of heat stress is strong in commercial but almost none in nucleus farms. This is partly due to lower pig density and better heat abatement in nucleus farms. Under intensive management, heat stress is less evident in drier environments because of more efficient cooling. A genetic component of heat stress exists but it is partly masked by improving management and selection based on data from elite farms. Genetic selection may provide superior identification of heat-tolerant animals but a few cycles may be needed for clear results. Also simple traits exist that are strongly related to heat stress, e.g., slick hair in dairy and shedding intensity in Angus. Defining resilience/robustness may be difficult especially when masked by improving environment. Under climate change, the current selection may be adequate if it (1) is accompanied by constantly improving management, (2) uses commercial data and (3) includes traits important under climate change such as mortality.

Key Words: G x E interaction, animal stress, robustness