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Genotype by temperature-humidity index interactions on production in the Montbeliarde cattle breedA. Vinet¹, S. Mattalia², R. Vallée², C. Bertrand³, P. Bertuzzi⁴, E. Venot¹ and D. Boichard¹¹Université Paris Saclay, INRAE, AgroParisTech, GABI, Domaine de Vilvert, 78350 Jouy-en-Josas, France, ²Idele, UMTeBIS, MNE, 75012 Paris, France, ³INRAE, CTIG, Domaine de Vilvert, 78350 Jouy-en-Josas, France, ⁴INRAE, AGROCLIM, Domaine Saint Paul, Site Agroparc, 84914 Avignon, France; aurelie.vinet@inrae.fr

Global warming has already caused an increase in average temperature and heat peaks and this phenomenon is expected to continue in the coming decades. This trend will affect European cattle with an expected decrease in welfare and overall performances. The objective of the study was to estimate the magnitude of genotype-by-environment interactions on milk production in Montbeliarde dairy cattle breed for a range of temperature-humidity index (THI). The French genetic database was combined with the Safran database from Météo-France. This database provides daily estimated meteorological measurements since 1958 on a grid of 9,892 8×8 km squares. Both databases were merged according to the commune code of each farm. First lactation test-day records from 2015-2016 were associated with the THI of the day and with the average THI of the 3, 4, and 7 days before the test day. These years were selected according to their contrasted climatic conditions. In total, 266,094 test-day records from 33,296 cows in 1,292 herds were analysed. The 3-day mean THI presented the strongest effect on milk yield and was considered subsequently. Milk yield was analysed with a mixed model including fixed (herd-year, days in milk, age at calving, length of gestation, and THI) and random effects (additive genetic and permanent environmental (PE) effect of the cows). Milk yield was highest around 50 (i.e. ~7-13 °C), with a slope of +0.02 kg and -0.10 kg/THI unit below and above 50. Individual response to THI was estimated by a reaction norm model. This random regression model included THI Legendre polynomials for both genetic and PE random effects. This model estimates a set of regression coefficients for each animal and thus provides genetic variances all along the THI trajectory as well as genetic correlations between THI conditions. Météo-France is acknowledged for the Safran database, and Apis-Gene for funding the CAICalor project.

Long-term impacts of selecting for resilience: combined genetic and systemic modellingM. Kargo¹, C. Bengtsson², N.C. Friggens³, F. Ramirez-Agudelo³, M. Slagboom¹, J.R. Thomasen² and L. Puillet³¹Aarhus University, Blichers Alle, 8830 Tjele, Denmark, ²Viking Genetics, Ebeltoftvej 16, 8960 Randers, Denmark, ³INRAE, UMR MoSAR, 16 Rue Claude Bernard, 75005 Paris, France; morten.kargo@mbg.au.dk

Breeding for economically efficient farm animals has been the cornerstone of livestock sector strategies. This objective is challenged by the need for more resilient animals, able to cope with changing and more extreme environments. Breeding for both resilience and economic efficiency implies dealing with complex biological traits that interact dynamically and depend on diverse environmental conditions. The challenge is to predict long-term effects of selection without unwanted side effects and to ensure that breeding goals are successful in various environments. To tackle this issue, we need to make the best use of knowledge from different disciplines. The objective of this talk is to present the benefits from combining a systemic model (AQAL), which incorporates the biological relationships between efficiency and resilience at animal level, with a stochastic model (ADAM), which incorporates the evolution of traits depending on selection strategy at population level. AQAL integrates parameters of feed resource acquisition and allocation to biological functions as base traits and simulates phenotypic trajectories, depending on potential trade-offs and environmental constraints. Simulations generate different levels of functional traits and resilience of cows, depending on acquisition and allocation. Combined with a simple genetic module, it showed that both changing the genetic (co) variance structure of the base traits and the environmental constraints changed the genetic parameters for the traditional traits. For simulations of breeding schemes including resilience traits the stochastic program ADAM was used. These simulations showed that resilience can be included in the breeding scheme via indicator traits such as SCS or milk yield variation, without harming the overall economic gain too much. Next step is to combine AQAL and ADAM to test different breeding strategies where impacts of selection on allocation and acquisition is modelled for both traditional and resilience traits given different environmental constraints.