Assessing Genotype by Environment interactions in Dutch dairy farms: Impacts of Farming System, Feeding Regime, and Nitrogen Use Efficiency on Milk Production Traits

E.L.P. Guennoc[1], M.G.J. Edens[2], M.S. Gilbert[2], J. Dijkstra[2], H. Bovenhuis[1]

[1] Wageningen University & Research, Animal Breeding and Genomics, Droevendaalsesteeg 1, 6700 AH Wageningen, The Netherlands

[2] Wageningen University & Research, Animal Nutrition, De Elst 1, 6708 WD Wageningen, The Netherlands

As dairy farming transitions towards more sustainable practices, including reduced feed-food competition and improved nitrogen use efficiency (NUE), future farm managements may differ from currently prevailing practices, potentially leading to genotype-by-environment interactions (G×E). This study analysed G×E between organic (OF) and conventional (CF) dairy farming systems using a bivariate model, and across a range of feeding and NUE environments using reaction norm models. Data was available on 974 Dutch dairy farms (2016-2021), including data on farming system (OF or CF) and herd-level average values of dietary concentrate proportion (% of total dry matter (DM)), net energy for lactation (NEL) content of the diet, and NUE (% of N intake retained in milk). Records on 305-d milk yield, fat- and protein content from first lactation Holstein Friesian cows were included, resulting in 6,126 records on OF and 96,015 on CF. Heritability for milk yield was 0.36±0.04 in OF and 0.44±0.01 in CF. Genetic correlations between OF and CF were high for all three traits (0.94±0.03 to 0.99±0.03). Heritability for milk yield increased from 0.17±0.02 at a dietary concentrate level of 13% to 0.54±0.01 at a concentrate level of 43%. Similarly, heritability for milk yield increased from 0.10±0.02 at 6.14 MJ NEL/kg DM to 0.59±0.02 at 7.21 MJ NEL/kg DM, and from 0.11±0.02 at a NUE of 20% to 0.53±0.01 at a NUE of 30%. These changes in heritability were primarily due to changes in additive genetic variance. In contrast, smaller differences in heritability were observed across the same ranges of environments for fat content (0.66±0.01 to 0.74±0.01) and protein content (0.71±0.01 to 0.74±0.01). Moreover, high genetic correlations (> 0.84) were found across environments for all three traits. To conclude, the change in genetic variance across environments indicates a scaling effect. However, this study provides little evidence of genotype re-ranking across environments, suggesting no need for separate breeding programs.