Comparative analyses of health traits from regional projects for genetic improvement of dairy health

K.F. Stock[1], D. Agena[1], S. Spittel[2], R. Schafberg[3], M. Hoedemaker[2], F. Reinhardt[1]

[1]Vereinigte Informationssysteme Tierhaltung w.V., Heideweg 1, 27283 Verden / Aller, Germany; [2]University of Veterinary Medicine Hannover, Clinic for Cattle, Bischofsholer Damm 15, 30173 Hannover, Germany; [3] Martin-Luther-University Halle-Wittenberg, Institute of Agricultural and Nutritional Sciences, Theodor-Lieser-Strasse 11, 06120 Halle / Saale; Germany

In the context of increasing importance of functional traits in dairy, a comprehensive key for health data recording has been implemented in different herd management software in Germany, facilitating standardized analyses. However, recording conditions differ considerably between farms, with yet unknown influences on genetic evaluations for health traits. Comparative analyses were therefore performed using two sources of data: In the project GKuh dairy farmers started health data recording with intense expert support. In large dairy farms in Thuringia (THU) routine recording of health events has been practiced for years without specific expert support. Considering health data from 2010-2011 in GKuh (49 farms; 14,307 females) and 2009-2011 in THU (18 farms; 43,668 females), patterns of lactation incidences were similar. Genetic analyses were performed separately in repeatability linear animal models, revealing univariate heritabilities (REML) of 0.02-0.06 in GKuh and 0.03-0.08 in THU. Correlation analyses were based on estimated breeding values (EBV) for health traits and EBV from routine genetic evaluation. Of the 1,709 German Holstein bulls with daughters in the health data only 213 were represented in both datasets. Moderately positive correlations were found between corresponding bull EBV from GKuh and THU (r≤0.4; closer for metabolic and claw diseases than for mastitis) and between EBV for health traits and EBV for longevity and specific functional traits (r=0.4-0.8). Results indicate that combined use of owner-recorded data from different sources will facilitate improvement of functionality of dairy cattle via genetic evaluation for health traits.