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French regional genetic collaborative projects to improve welfare and resilience of dairy cows

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Two collaborative projects, GENOSANTE and MO3SAN, considering Holstein (HOL) and Normande (NOR) breeds on the one hand, and Montbéliarde (MON) breed on the the other hand, bring together French companies (AI cooperatives, milk recording and herd support organizations in HOL and NOR; AI cooperatives, milk recording and herd support organizations and Livestock health protection groups (GDS) in MON) and research organizations (INRA, ALLICE, and IDELE). They aim at providing selection tools for new traits to improve dairy herd profitability and cow welfare. The two projects focus on three areas of research: ketosis, claw disorders and heath data through events recorded by farmers.

Ketosis is one of the most common disorders in dairy cows due to energy deficit in early lactation. Its prevalence reaches 4% for its clinical form and 12-20% for the subclinical form. Analysis of beta-hydroxybutyrate (BHB) and acetone through MIR spectrum in milk collected since 2012, from 7 to 120 days in milk, were used. Heritability estimates of acetone were 0.12 in HOL, 0.15 in NOR and 0.10 in MON and 0.10, 0.16 and 0.12 for BHB. Genetic and genomic breeding values for ketosis have been estimated routinely since 2016 in HOL and NOR and are under development in MON.

Claw lesions are the 3rd most important health issue in dairy cattle, after mastitis and fertility issues. They impact herds both economically and in terms of animal welfare. 21 lesions are routinely recorded by professional trimmers on touch screens. Seven lesions (Digital Dermatitis (DD), Heel Horn Erosion (HHE), Interdigital Hyperplasia (IH), Sole Hemorrhage Circumscribed (SHC), Sole Hemorrhage Diffused (SHD), Sole Ulcer (SU) and White Line Fissure (WLF)), with prevalence ranging from 8 to

45% on trimmed cows (depending on the trait and breed), were studied. Heritabilities ranged from 0.02 to 0.08 in HOL, 0.04 to 0.22 in NOR and 0.05 to 0.11 in MON. Genetic correlations revealed two distinct genetic groups for claw lesions: infectious (DD, HHE, and IH) and noninfectious (SHC, SHD, WLF, and SU) lesions. Genetic correlations among lesions of the same group were moderate to high. Genetic evaluation for claw health was implemented late 2017 in HOL, and is under development in NOR and MON.

Common health disorders registered on farm (metritis, retained placenta, milk fever...) are currently under study in HOL.

All these developments aim at improving dairy cow welfare and resilience through genetic and management and are only possible with efficient data flows from phenotype collection in herds to tools for breeders and include genetic pipelines. Keywords: dairy cow, ketosis, claw, health, genomic evaluation