

Economic impact of the usage of AI bulls on Finnish dairy farms

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AI bulls in the Nordic dairy breeding program are selected mainly on Nordic Total Merit (NTM) where the traits are weighted based on economic importance. Most AI bulls used in Finland are of Nordic origin but the amount of imported semen has increased. The aims of this study were to investigate (1) the variation and economic impacts of the usage of AI bulls among Finnish dairy herds, and (2) its association with herd characteristics. Data consisted of 104,670 insemination records of 1,279 Ayrshire (AY) herds and 544 Holstein (HOL) herds from 2015, estimated breeding values (EBV) of AI bulls (176 AY and 232 HOL) and farm characteristics. Herds' breeding profile was defined as the mean of the EBVs of the AI bulls used in a herd, weighted by the number of inseminations per bull. AI bulls were grouped according to their EBVs and herds to their breeding profile using cluster analysis, for both breeds. The economic implications of breeding choices were estimated, based on the traits 'genetic standard deviation' and 'economic value in Finland'. The result was compared to the expected response to the NTM based selection. Four bull and herd clusters in both breeds were identified. Herd clusters were named according to the main focus in the breeding choices; Pure AY herds: Yield and functionality (452 herds), Longevity, fertility and health (393), All-rounders (377), Conformation (57); Pure HOL herds: Longevity, health and fertility (280), Production (169), Yield, conformation and longevity (48), Conformation (47). The bull clusters followed mainly the same pattern. Conformation bulls were mostly from North America. In the first three herd clusters of both breeds, their average herd breeding profiles were close to the NTM based selection implicating that the vast majority of farmers followed NTM in their breeding decisions. In the Conformation clusters, the traits other than conformation were almost neglected, which expectedly lead to poorer economic result. The conformation focused herds were in a minority, while they were large herds with recent investments.

On-farm genomics in the Netherlands

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In the last decade, genomics has been introduced for Holstein in The Netherlands, first, by in-house genotyping within breeding companies to improve the breeding programs, followed by the introduction of genomic young bulls onto the Dutch-Flemish market. Nowadays, genomic young bulls dominate the national top lists, and their semen sales have an ever rising market share. Herdbooks have adopted genomic information for genetic defects and parentage identification. The CRV Holstein genomic system entails a training population of ~36,000 bulls for 75 traits, and aims at a turnaround time of 21 days from first genotyping requests to results. Reliabilities of genomic breeding values range between 60 and 75%. Farmers adopt the new technologies and incorporate these into their daily management. CRV has launched a new management tool to support their farmers in using genomic data to create an optimal farm-specific management. This includes advice on young stock selection, strategic mating advice for carrier matings (e.g. beta casein or polled), monitoring the genetic and phenotypic performance of the herd and advice how to optimize the two to reach full potential, and benchmarking of farm performance, both within-herd and against national data. Of course, the management tool also includes individual cow test results, genomic breeding values, tracking of individuals in the process of genotyping, a notification function for new test results, and the ranking on a farm-specific breeding goal, tied directly to the mating advice service for improved bull choices and semen sales based on genomic data. Continuous effort is on: (1) increasing genomic reliabilities by extending the training population with bulls and cows and by improved calculation methods; (2) improving chain control by a Track&Trace system that facilitates fast intervention when a sample drops out because of bad sample quality (new sample), failed DNA extraction (re-try), too low call-rate (re-run chip), or pedigree errors (automatic correction of database); (3) optimizing time needed between request and results, which is already down from 28 to 21 days, and is further enhanced by two lab-batches a week; and (4) improving the translation of genomic information into hands-on advice to increase herd profitability.