Bull ranking and results of genetic evaluations

One of the most important projects implemented in 2017 by Centre for Genetics was the creation of a website presenting results of genetic evaluations for bulls. This service aims at easy and intuitive presentation of breeding values. The website contains both the results of national and international evaluations. It is also worth noting that bull cards also contain positions in rankings of countries that are members of the EuroGenomics Cooperative. The basic criterion that motivated the creators of this website was the ease and speed of searching for bulls. The website allows to search for animals by number or name. It is also possible to search by partial numbers or names. For example, a bull Cyrano with ID DE066847135 can be found by typing in the search engine its full ID along with country code or using only part of its ID, i.e. 666847135. The search engine automatically recognizes whether the query concerns bull ID or name.

Bull ranking can be easily sorted based on traits that are important for cattle breeders. For example, using appropriate filters, one can prepare a ranking of bulls with the best breeding value for feet and legs whose PF index is greater than 140 points. This allows for selection of top bulls with the best conformation. Custom ranking can be prepared based on a list of traits which includes: PF index and all sub-indices together with their main components.
The bull card contains a “clickable” pedigree, which gives quick access to information about ancestors of a given bull. Breeding values are grouped into separate tabs based on sub-indices. After expanding each tab, users get access to information about the type of evaluation (MACE - international conventional, GMACE - international genomic, EBV - domestic conventional, GEBV – domestic genomic), graphical representation of bull’s position in the population (graph where population average is indicated by a red bar and a blue bar indicates bull’s breeding value, which is below or above the average) and accuracy is shown with three colours (only red - low accuracy, red and yellow - moderate accuracy; red, yellow and green - high accuracy). Apart from that bull card also contains a tab with “international ranking”. It contains breeding values based on evaluations in EuroGenomics member countries. The international ranking includes position in rankings and breeding values expressed on Dutch (gN-VI), French (gISU), Nordic (gNTM) and Spanish (gICO) scale. The last element included in bull’s card is the “Offspring” tab, which contains a list of individuals sired by a given bull. Such a list can be easily filtered using birth date, name and range of PF index. Thanks to this, it is possible to see what was the highest PF index of individuals sired by a given bull.

The website prepared by the Centre for Genetics also allows for comparison of selected bulls. This tool allows for a quick and easy comparison of breeding values for selected bulls.

The website prepared by CGen has been optimized for tablets and mobile phones. Thanks to this, it has very good readability on mobile devices, so that every breeder or inseminator can have the current bull ranking “in their pocket”. We encourage everyone to use this new website, which is available at www.cgen.pl/index/evaluation/bull/ranking.
Pedigree index

In 2017, the Centre for Genetics launched a new service designed to calculate and present pedigree index for heifers and young bulls.

By default the ranking contains 100 heifers or young bulls. This number can be increase up to 5000 using a drop down menu. Animals with low pedigree index (rPF) and therefore low position in the ranking (lower than 5000) will not appear on the website.

Both in the case of young bulls and heifers, separate rankings were created for HO and RW breeds. The rankings have been divided into three age categories: up to 6 months, between 6 and 12 months, and between 12 and 24 months. It is also possible to create a ranking for animals from a selected voivodeship and district. The ranking can be narrowed down only to heifers that qualify for genotyping. Such heifers fulfil the conditions necessary for inclusion in genomic evaluations.

The website also allows to submit requests for genotyping heifers by filling out a form available in the heifers card. The heifers card presents basic information such as ID and name together with the rPF index and pedigree information. Pedigree is presented in a “clickable” form. One can click a selected ancestor in order to see its card with breeding values. It is worth noting that a new ranking based on pedigree index is published every week on Tuesday. This makes the results for newly registered heifers and young bulls available as soon as possible.

In 2017, the average rPF per voivodeship was between 108 and 114 for the HO breed and between 101 and 108 for the RW breed. Detailed results broken down into voivodships are presented in Figures 1 and 2.

![Graph showing mean rPF per voivodeship](image)

**Figure 1.** Mean pedigree index per voivodship for heifers of HO breed.
Another service that has been recently made available on the CGen website is a ranking of the best herds based on pedigree index of heifers. This ranking is updated three times a year in accordance with the schedule of official genetic evaluations in Poland. The ranking includes only herds with a minimum of 5 heifers.

Assessing the level of inbreeding in a population is a multi-stage and complex process. The first step is to perform quality control of the pedigree. Pedigree completeness is calculated as one of the first measures of data quality. The pedigree completeness, expressed as the number of full generations of ancestors available for a given animal, directly affects the accuracy of inbreeding coefficient in the population. Lack of pedigree information leads to underestimation of inbreeding of a given individual, which in turn leads to underestimation of its relationship with the population and loss of an important part of information about the animal.

Additionally, matings between bulls and cows in the Polish population were simulated in order to calculate future inbreeding. This can be translated into mean inbreeding of bull’s future daughters (Figure 3). The number of common ancestors between the bull and the population of cows, has a direct influence on the inbreeding coefficient of future daughters. Comparison of observed and future inbreeding can show whether breeders tend to mate closely related animals.
Analysis performed by CGen showed that the annual inbreeding rate in the Polish population was low with values below 0.10% per year in years 2010-2016 (Figure 4). This means that the inbreeding rate is maintained at a safe level not exceeding 1% per generation (about 4 years). This may be due to the relatively low intensity of selection and high import of quite diverse genetic material. The experience of countries that use genomic selection more intensively indicates that in the era of genomic revolution, the rate of inbreeding is increasing.

It should be emphasized that the results of the project were presented at the international conference (EAAP 2017) in Tallinn (Estonia) where dr Ewa Sell-Kubiak received an award for presenting results based on the analysis of inbreeding in the Polish Holstein-Friesian cattle.

Currently inbreeding is estimated by CGen on a weekly basis and results are published online at www.cgen.pl/index/evaluation/bull/ranking.

![Inbreeding level in the Polish Holstein-Friesian cattle](image-url)

*Figure 3. Inbreeding level in the Polish Holstein-Friesian cattle*
In 2017, CGen began developing a system for genetic evaluations. This involves both conventional (based on pedigree and phenotypes) as well as genomic (using additional information about the genotype of animals). A database enabling efficient data flow between CGen and the Symlek system became the key element of the newly created system. Numerous procedures have been created to enable efficient data import and export as well as quality control in key stages. Backup infrastructure constitutes an important element of the system. This is to ensure the safety of collected data and prevent their loss.

First pipeline for genetic evaluation was prepared for production traits and somatic cell count. It is based on new estimates of variance components and contains restructured phantom parent groups. At the end of 2017, CGen contacted Interbull and obtained permission to proceed with validation of the developed models.

CGen also initiated work on models for genetic evaluation of fertility and inclusion of new traits, such as conception rate, calving ease, and lactation persistence. Statistical models were developed for these traits and genetic parameters were estimated. Further work in 2018 is going to be focused on validation of the new models by Interbull and introduction into routine evaluations.
Analysis of genomic inbreeding based on data from EuroGenomics Cooperative

In 2017 the Centre for Genetics received genotypes of 22,262 bulls as part of a research project carried out in cooperation with the EuroGenomics Cooperative. An important stage of this project was quality control and consolidation of genotypes from all members of the EuroGenomics Cooperative. A system for genotype imputation was created that makes it possible to use genomic information from SNP chips of various sizes. This allows for simultaneous use of genotypes from low density (10K) and medium density (50K) chips. These data will be used to analyse genomic inbreeding.

Parentage verification and discovery

Centre for Genetics in cooperation with the Laboratory of Cattle Genetics created an application for parentage verification using markers from SNP chips. The application has been developed in accordance with ICAR standards and recommendations. Parentage verification is carried out using a set of 200 SNP markers, which are divided into a core set of 100 SNPs and 100 backup SNPs. According to the latest ICAR recommendations, the entire set of 200 SNPs is used simultaneously to verify parentage of a given individual. This set of 200 SNPs can be reduced by removing markers excluded by the ICAR DNA Working Group. The first stage of parentage control consists of separate tests where the individual in question is compared with its sire and then with its dam. Only SNPs for which both the subject and the parent are homozygous (genotypes AA or BB) are compared. Then the number of conflicts is counted, i.e. cases when the compared individuals are opposite homozygotes (i.e. the offspring is AA while the parent is BB). If the number of conflicts does not exceed 2, parentage is confirmed. If the number of conflicts is between 3 and 5, it is doubtful, and when the number of conflicts exceeds 5, parentage is excluded. If in the first stage the genotypes of both sire and dam are consistent with the individual in question, a second phase of comparison is performed, where SNPs for which the parents are homozygotes and the subject is heterozygous are compared. Conflict occurs when parents are homozygous for the same allele (i.e. sire and dam are both AA or both BB) while the subject is heterozygous (genotype AB). If the number of conflicts does not exceed 3, parentage is accepted. In the case of 4 to 7 conflicts the result is doubtful, and with more than 7 conflicts parentage is excluded.
Parentage discovery is done using 554 SNP markers from a panel developed by Interbull called GenoEx-PSE. This panel contains the same 200 markers used for parentage verification together with additional SNPs on chromosomes 1 to 29 (75 SNPs) and on chromosomes 1, 2, 3, 5, 7, 8, 11, 13, 19 and 21 (279 SNPs). Such arrangement of markers on chromosomes is to enable efficient parentage discovery and at the same time prevent genotype imputation. When looking for potential parents, attention should be paid to the age of the subject and potential parent. This is to eliminate cases when the potential parent is younger than the subject because in reality he/she is his/her descendant. The application also verifies if the potential parent is female or male.

The first stage of parentage discovery consists of independent tests for potential sires and dams. The minimum number of common markers in the compared animals is 350 out of 554. If the percentage of conflicts between the subject and its potential parent does not exceed 1%, it can be concluded that the search was successful. However, when the percentage of conflicts is between 1 and 3%, the result is doubtful, and when it exceeds 3%, the parent is excluded. If parentage discovery provides both a potential sire and dam, then the second phase of discovery is conducted. It looks similar to the second phase of parentage verification (comparison of trios: individuals-sire-dam). If the percentage of conflicts in this comparison is below 1.5%, then the discovered parents are consistent. When the percentage of conflicts is between 1.5 and 4.0% the result is doubtful, and with more than 4% of conflicts parents are excluded.
"CGen trimming" project

"CGen trimming" project is focused on claw health improvement. The basic target in 2017 was to begin recording data on prevalence of claw diseases on Polish farms.

CGen developed a web-based application to record results of hoof trimming. It was made available for free to members of the project. Consultations with hoof trimmers and breeders enabled to determine the scope of information summarizing a given hoof trimming visit and the way of presenting the historical data. The application contains a system for reporting diseases and treatment. There is also a possibility to include information about cows’ housing system, which will allow for more accurate analyses of the prevalence of claw diseases. The application owes its success to:

- automatic data transfer from Symlek,
- fast data recording during hoof trimming,
- easy claw disease recording,
- possibility to input interventions (application of bandage on a claw),
- access to historical information per cow recorded by people working on the farm,
- possibility to get summary reports after hoof trimming visit.

A manual for the application and a list of claw diseases’ synonyms were created to make it easier to work with the application. The members of the project have positive opinion about the application. More and more hoof trimmers are joining the project. The application is being constantly refined considering their suggestions.

Application “CGen trimming” is an element of the data recording system for genetic analyses and to start genetic evaluation of claw health. A system was established that allows for communication between the Symlek system, application “CGen trimming” and the members of the project. A clear data protection policy was established to protect breeders’ information. Breeders need to authorize access to data for contractors working on their farm who are not the employees of PFHBiPM (hoof trimmers, vets). Searching for cows in the application is possible by using four digits from cow’s ear tag. There is no need to input the whole tag number to find the right cow and record the hoof trimming result. That is why hoof trimmers need less time to input data to the application and the risk of making a mistake is lower. Sending reliable information about hoof health to domestic database is very important. Reliable data has to properly relate the diagnosis of the disease with the right cow to create a full history of claw health with information about treatment. It allows to monitor permanently the claw health and evaluate the effectiveness of the treatment. The application can only be used after a contract is signed with a breeder. Overall 124 breeders joined the “CGen trimming” project in 2017.
One of the targets of the “CGen trimming” project is the implementation of claw health genetic evaluation in Poland. For this reason CGen placed the emphasis on the hoof trimmers’ knowledge. They are responsible for recording the data and correct identification of diseases is the key element of the project. That is why CGen organized two training sessions for them. Lectures were given by prof. Johann Kofler (University of Veterinary medicine Vienna, Austria) who is a co-author of “ICAR Claw Health Atlas”. Additionally the lecturer gave a workshop on therapeutic hoof trimming during the practical part of the training session in the Uniwersyteckie Centrum Medycyny Weterynaryjnej (Poznan University of Life Sciences). What is more, CGen started a cooperation with Kurt Bach – veterinarian from Denmark. Kurt Bach gave a lecture on claw anatomy, causes of diseases, possible therapy and methods of prevention for breeders. Biosecurity and the role of hoof trimmers in reducing the spread of infectious diseases between farms was also discussed.

After the workshops, 26 hoof trimming firms joined the “CGen trimming” project and got access to the application to collect data. Moreover, world-known specialists came to evaluate the manual skills of hoof trimmers. Piet Kloosterman (respected examiner of the 5-step Dutch method of hoof trimming) appreciated the willingness to learn of the participants during the workshop and positively evaluated their manual skills. They had an opportunity to discuss individual disease units and solidify the knowledge about therapeutic cutting and removing load from a claw.
CGen employees took part in many events and conferences which gave a lot of opportunities to meet breeders and hoof trimmers. It was a great to exchange experience and talk about the need to reduce the prevalence of claw diseases. The topic was getting more and more popular and as the result more breeders were joining the “CGen trimming” project. Permanent cooperation with hoof trimmer, his regular visits on the farm and monitoring of the claw health with the information collected in the application will help breeders to manage the farm in a more effective way.

The “ICAR Claw Health Atlas” poster.
The Polish version of the “ICAR Claw Health Atlas” was made available to spread the knowledge about claw diseases. Short descriptions were added to the photos for better recognition of the diseases. What is more, working with the “CGen trimming” application during hoof trimming on the farm was shown in a film which is available online at www.cgen.pl/korekcja.

**Economic selection index**

In 2017 CGen started working on development of the first Polish economic index for Holstein-Friesian cattle. The index will allow to maximise profits from genetic gain. This project is conducted in cooperation with AbacusBio. Experts from AbacusBio are experienced in implementing economic indexes worldwide.

Development of a new tool to support breeders in making important decisions about their herd requires a lot of analyses. At the beginning there is a need to get to know breeders’ preferences. That is why CGen created a survey in which breeders make simple choices while deciding which trait is more important for them. The economic selection index will be based on the information gathered in the survey to meet the expectations of Polish breeders.

The weight given to each traits included in the index will be given based on the economic conditions in Polish farms. CGen created an economic survey to collect data about production costs and profits which will be useful to estimate economic weights for traits included in the index. What is important, information is needed from different farms located across Poland. That is why, in 2018 CGen will rely on cooperation with Polish breeders.

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