DataGene
Solutions for Herd Development

Younger bulls deliver gains thanks to genomics

Genomics has led dairy farmers and breeding companies to use younger sires, contributing to the almost doubling of genetic gain in the past nine years.

This was one of the findings University of Queensland Professor Ben Hayes presented as part of a genomic 'score card', comparing results with predictions.

Since the introduction of genomic Australian Breeding Values (ABVgs) the average age of both Holstein and Jersey artificial insemination bulls used by dairy farmers to breed their cows had dropped from 7.5 years to 4.5 years.

The most dramatic drop was the age of sires used to breed the next generation of AI bulls. This reduced from 7.5 years to 2-3 years in Holsteins and 3-4 years in Jerseys.

Ben said this demonstrated AI companies were intensively selecting sires of sons using genomic breeding values. It also closed the breeding generation gap, an important factor for increasing the rate of genetic gain for dairy farmers, which is on an upward trajectory due to many changes in breeding.

University of Queensland's Professor Ben Hayes.

In a paper he co-authored with Gert Nieuwhof from Agriculture Victoria Research Centre for AgriBioscience in Melbourne as well as DataGene, Ben said the greatest gains from genomic selection were for traits that were previously difficult to select for, such as fertility.

"With genomics we should have a much wider range of animals with reliable breeding traits to select, so traits like fertility should go up faster rate than overall index," he said.

Following the launch of ABV(g)s in 2010, the trend for fertility in Holsteins and Jerseys increased significantly. Large-scale projects were already in place to focus on declining Holstein fertility, including a move by the dairy industry to place more weight on fertility in its Balanced Performance Index.

Due to this multi-pronged approach to tackling fertility decline, Ben said genomics could not claim all the fertility gains, but it contributed to it.

Genomic advances

Ben discussed future breeding technologies, including Invitro Breeding (IVB), which is being trialled at the University of California. He said IVB was a tool in the pipeline and it would shake-up traditional perceptions of breeding.

"What they are proposing is to skip, at least for a few generations, making cows and bulls entirely," he said.

Ben said the concept would begin with an IVF program to produce embryos but instead of implanting these to produce calves, they are genotyped to discover the best ones. Cells from these are differentiated into both sperm and eggs. They are then run through another round of selection by genotyping to produce genomic breeding values, and then fertilise the eggs with the sperm you

More than 230 people attended Herd '19 held in Bendigo in March. Held every two years, the Herd conferences have become a 'must attend' event for people involved at all levels in herd improvement. The program features leading scientists and farmers from around the world, but equally important is the spirit of learning and collaboration among the attendees who may not otherwise meet in person very often.

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have made and produce more embryos. At that stage you either implant the embryos (to produce calves) or keep going through this cycle. The generation interval is about 3-4 months.

Ben said his colleagues at the University of California in the US were "on the cusp of making this work".

Performance records

Maintaining and building a reference-set of on-farm data was essential to the success of this new technology, he stressed. He said it would ensure animal performance could keep pace with the generation gains from the new technology. Without this, the reliability of breeding values would erode, which could happen "alarmingly quickly". Ben said "an awful lot" of data would need to keep coming into the system.

Phenotypes – the performance records of a trait – maintain the reliability of genomic predictions. Examples of phenotypes include cow production or fertility records. DataGene's Ginfo Project collects farm records to contribute to the reliability of Australian genomic breeding values, but all farms that herd record help maintain a strong database. "Just getting DNA information on animals, and lots of animals, doesn't get you anywhere. You need those really good trait records, large and continually updated reference populations," Ben said.

Health traits, such as mastitis resistance, will be vital in future breeding technological developments.

"If you are going to run something like this, turnover five or six generations without seeing a cow, we have to make really sure we have got really good genomic breeding values for not just production but also health traits," Ben said. "The last thing you want to do is crank through the cycles, with your health traits deteriorating as you go. You need really good genomic breeding values across a range of traits."

Ben said this type of technology – that allowed a fast advancement in generation intervals – could also assist with developing new lines of cattle. For example, improving the heat tolerance. "You could (develop) highly heat-tolerant cows by cranking through multiple cycles and selecting hard on the heat tolerance ABV(g)," he said.

Another future technology example included, a hand-held 'whole genome sequencer'. Resembling a USB stick which would be plugged into a computer, Ben said it's used in hospitals and produces a sequence "really quickly" for patients who are admitted with a bacterial infection. It checks, on-the- spot, if the bacteria is resistant to antibiotics.

Ben's group is developing this technology, which will eventually enable 'crush-side' genotyping of cattle. DNA from an ear punch or tail-hair is fed into the genome sequencer and "within minutes" it would provide a genotype and then genomic breeding values.