Genomic revolution in dairy cattle breeding: PROMISES and pitfalls

by **Dr Japie van der Westhuizen**

Dairy cattle breeding has fully embraced the genomic era. Traditional methods, which relied on recording pedigree records and physical traits alone – especially progeny testing – have been replaced by DNA-based genomic selection. By using thousands of genetic markers through affordable single nucleotide polymorphism (SNP) chips, breeders can predict a calf's potential for milk yield, fertility, disease resistance, and more long before it enters the milking parlour or considered as an artificially inseminated sire.

This approach has shortened generation intervals, allowing young bulls to be selected at 18–24 months instead of waiting years for performance, particularly progeny, data. There are many examples where genomic tools have sped up annual genetic gains in meeting selection goals. This applies equally to full-ration, high-output systems and grass-fed systems. When used wisely, this technology is hailed as a game-changer for the efficiency and sustainability of dairy cattle breeding.

Realistically, however, there are pitfalls that could undermine this success. Using genomics is not foolproof, and mistakes can lead to financial losses, poorer herd health, and slower progress.

Promises versus reality in imported genomic data

The globalisation of genomic services can create the first major pitfall. Dairy farmers in developing countries such as South Africa, often send biological samples overseas to laboratories in the United States or Europe for analysis. These laboratories either use their own data or services of the country in question to predict genomic breeding values and even rank animals by genetic merit. The appeal is obvious – access to innovative technology without having local infrastructure. However, this cross-border approach overlooks a fundamental truth that breeding values are population-specific.

Genomic breeding values are based on reference populations from the exporting country. For example, United States Holsteins are generally raised in temperate climates and fed high-grain diets. When these values are applied to South African herds – where heat stress, tick-borne diseases, and pasture-based systems are common – the original rankings can be misleading. A bull that scores highly in United States models for milk yield or other selection indices might perform poorly in South Africa's subtropical conditions, showing lower fertility, weaker disease resistance, and a shorter lifespan.

Research from the International Livestock Research Institute has shown that genomic predictions can lose accuracy by as much as 20%–30% when applied across different environments. This drop in accuracy is caused by genotype-by-environment (GxE) interactions. As a result, farmers may select animals that fail to thrive locally, wasting money on imported semen and veterinary costs.

Worse still, these predictions often overlook region-specific breeding objectives. In exporting countries, breeding goals may focus on producing large milk volumes, supported by relatively low feed costs and higher milk prices, or by payment systems that reward milk solids differently. In South Africa, however, where feed costs can consume up to 60% of profits and droughts are common, breeding objectives should prioritise feed efficiency, heat tolerance, and longer functional herd life.

Relying on foreign genomic breeding values means animals are ranked according to mismatched economic conditions, ignoring local feed costs and market returns. This mismatch can erode profitability. A 2023 analysis by the University of Pretoria, in collaboration with the Agricultural Research Council, found that South African dairies lost up to 15% in net margins when using unadjusted United States genomic evaluations without recalibration.

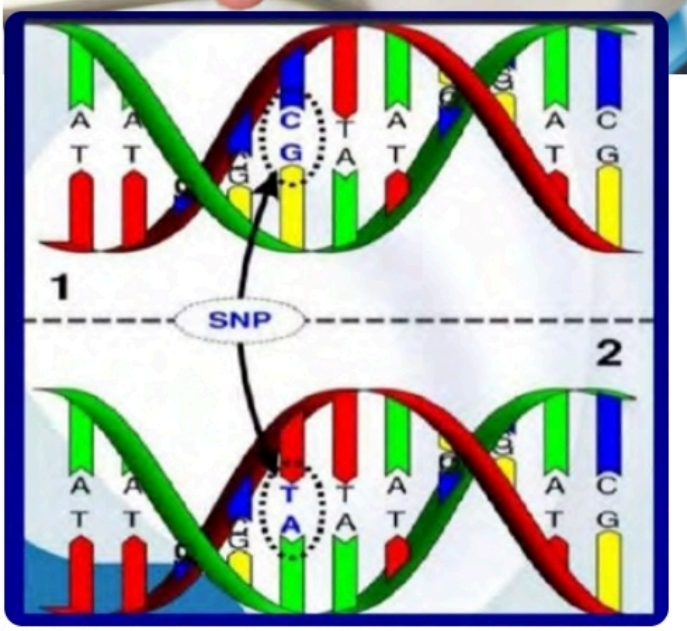
Environmental differences – such as varying parasite pressures and seasonal rainfall patterns – make direct comparisons using foreign estimated breeding values (EBVs) even more problematic, particularly because traits like parasite resistance are often not well represented in foreign reference data.

Leveraging local expertise: South Africa's SA Stud Book system and international models

Fortunately, South Africa has a scientifically grounded alternative. SA Stud Book operates a comprehensive, internationally certified breeding value prediction system using the advanced genomic single-step method for major dairy breeds, including Holstein/Friesian types, Jerseys, and Ayrshires. This single-step method integrates genomic data directly into EBVs, combining pedigree, performance, and genomic information in one process to produce accurate, locally relevant rankings while reducing bias and improving precision for South African conditions.

SA Stud Book also offers tailored selection indices, developed with local dairy breeders' societies and producers. These include SAINET and the Logix Merit Index, which adapt global concepts – similar to the United States Net Merit Index – to South African realities. Each index weights traits according to local economics: SAINET emphasises net income through milk solids, fertility, and longevity, while the Logix Merit Index ranks females for overall efficiency, incorporating production, health, and sustainability. Additional tools, such as the Fluid Merit Index and Cheese Merit Index, cater to specific processing needs, ensuring selections align with regional market demands and cost structures.

The system is linked to the International Bull Evaluation Service, managed by the INTERBULL Centre, which serves over 30 countries. INTERBULL's multiple across-country evaluation (MACE) converts national EBVs into internationally comparable values, accounting for genetic correlations and genotype-by-environment differences. For genomic data, genomic MACE (GMACE) includes young sires by incorporating SNP information, achieving reliabilities of 70–80%. This partnership provides access to converted genomic EBVs (gEBVs) comparable to local standards and available via SADairyBulls.com, minimising the risks of using unadjusted foreign data while



harmonising international genetics with South African breeding goals, such as improved feed efficiency and resilience.

SA Stud Book's recognition by the International Committee for Animal Recording (ICAR) for incorporating SNP data – not just for parentage verification but also for genetic discovery – adds to its other international certifications for milk recording, technical services, and genetic merit prediction. This science-based framework allows South African farmers to make informed decisions without over-reliance on overseas systems. A similar success story is Ireland's Cattle Breeders Federation (ICBF), whose national genotyping programme has genotyped over 520 000 dairy calves across 4 300 herds (by 2024). By aligning genomic tools with locally relevant breeding goals, focusing on fertility, sustainability, and low-emission traits for grass-based systems, the ICBF has accelerated genetic gains, shortened generation intervals, improved herd management, and reduced greenhouse gas emissions, demonstrating the economic and environmental benefits of region-specific genomic programmes.

Commercial strings attached

Another pitfall is the bundling of genomic services with commercial incentives. Some companies offer 'free' or discounted genotyping, but only on the condition that farmers also buy their other products, such as semen, vaccines, remedies, or feed additives. This creates potential conflicts of interest, as breeding decisions may be influenced by company catalogues rather than the farm's actual needs.

In South Africa, where semen imports dominate, farmers may overlook locally bred sires in favour of heavily promoted international bulls – or even select artificially inseminated bulls that are wrongly ranked for local conditions. Critics of these practices, including the Food and Agriculture Organization (FAO), have warned that such commercial pressures can stifle innovation in developing countries like South Africa and lead to higher long-term costs.

Ultimately, these practices delay the adoption of truly adaptive genetics, as marketing hype overshadows evidence-based selection.

Inbreeding and a narrowed gene pool

Genomics speeds up genetic progress, but if used incorrectly it carries the risk of inbreeding depression. When breeding decisions focus only on top-ranked animals from a limited population, herds can lose valuable genetic diversity. In some dairy cattle populations, inbreeding rates have risen by as much as one percent per year since the adoption of genomics, resulting in weaker immunity and higher calf mortality.

If these rapid increases go unchecked, fertility problems could emerge in future generations. To counter this, tools such as genomic relationship matrices – or the inbreeding predictor available on the SADairyBulls.com platform – can help monitor and manage inbreeding levels.

In the long term, a narrowing gene pool poses a serious threat to herd resilience, especially as climate change brings new environmental stresses.

Navigating the pitfalls: A balanced approach

To avoid these challenges, experts recommend hybrid strategies. Invest in national genomic programmes – such as South Africa's SA Stud Book and Ireland's ICBF – to build locally relevant reference populations and indices. Use multi-trait indices reflecting local economics, weighting traits by profit impact through tools such as SAINET and the Logix Merit Index.

Diversify semen sources and insist on transparent services, ensuring genomic testing is not tied to product sales. Combine genomics with on-farm data – phenotypic records capturing real animal performance –because without proper recording, genomics lose value. Regular herd audits can also validate predictions and guide future selections.

Genomics holds great promise for sustainable dairy breeding, but blind adoption, especially of foreign systems, can have unintended consequences. The key is context-specific application – using South Africa's certified, INTERBULL-integrated system as a model.

The future of dairy breeding lies not in DNA alone, but in smart, local use of genomic tools that turn genetic progress into real-world productivity, resilience, and profitability. tdm