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Selecting by the Genome: Applications in Farm and Pet Animal Breeding

*Deepti Sinha

PhD, ICAR- National Dairy Research Institute, Karnal, India

*Corresponding Author's email: deeptisinha1122@gmail.com

Animal breeding has quietly gone through a revolution over the past two decades, and genomic selection sits right at the centre of it. Instead of waiting years to see how an animal's offspring turn out, breeders can now read an animal's DNA and get a fairly accurate picture of its genetic worth almost from birth. The idea rests on a simple but powerful principle: thousands of markers scattered across the genome tend to sit close to the actual genes controlling a trait, so by tracking these markers, breeders can estimate an animal's genomic estimated breeding value (GEBV) without ever needing a single progeny record. This has been especially valuable for traits that are notoriously hard to improve through conventional selection, things like fertility, disease resistance, and longevity, which show up late in life or are only weakly tied to any one gene. The approach has already reshaped dairy cattle breeding, where it has largely replaced the slow, expensive process of progeny testing, and it is steadily making its way into beef cattle, sheep, goats, pigs, poultry, and even companion animals such as dogs and horses. That said, genomic selection isn't without its costs and complications. Genotyping remains expensive, reliable predictions demand large and well-maintained reference populations, and the intensity of selection it enables can quietly erode genetic diversity if left unchecked. This review walks through how genomic selection works, why it has proven so useful, where it is being applied, and what still needs to be worked out before it can be used responsibly and sustainably across a wider range of species.

Keywords: Companion animal breeding, Genetic diversity, Livestock breeding, Marker-assisted selection, Reference population, Single nucleotide polymorphism (SNP)

Introduction

For most of the twentieth century, improving livestock genetically meant playing a long, patient game. Breeders would record how an animal performed, note its pedigree, wait for its offspring to grow up and start producing, and only then decide whether it was worth breeding from again. This worked, but it was slow, and traits that only showed up late in life, or depended on dozens of genes each contributing a little, were especially hard to improve quickly. Genomic selection changed that equation. The core idea is straightforward once you see it: if you scatter enough genetic markers across an animal's genome, some of them will sit close enough to the actual genes influencing a trait that they effectively "tag" those genes through linkage disequilibrium. Track the markers, and you're indirectly tracking the genes. This means an animal's genetic merit can be estimated the moment it's genotyped, no need to wait for it to grow up, reproduce, or show symptoms of disease resistance under real conditions.

From Pedigree Books to Gene Chips: How Breeding Has Evolved

Traditional breeding leaned almost entirely on two things: how an animal itself performed, and how closely it was related to other good performers, captured in estimated breeding values built from pedigree data. Both approaches share the same weakness, they need time. A

dairy bull, for instance, cannot be properly evaluated until his daughters have calved and started lactating, a process that can eat up several years. Genomic selection sidesteps this delay almost entirely. Because it works from genotype alone, breeders can evaluate a calf, a lamb, or a piglet within weeks of birth, well before any phenotype has had the chance to express itself. The practical effect of this is a shorter generation interval, and a shorter generation interval means more rounds of selection can be packed into the same number of years, which in turn means faster genetic progress. On top of that, because genotyping is cheap enough to apply to large numbers of candidates, breeders can also afford to be more selective, keeping only the very best animals and pushing selection intensity higher than progeny testing alone ever allowed.

None of this works without a solid foundation, though. Genomic selection depends on something called a reference population, a group of animals that have both detailed phenotypic records and genome-wide genotype data. This population is used to work out how much each marker contributes to a trait, and those estimates are then applied to any new, unrecorded animal based purely on its genotype. The quality of these predictions hinges on a few things: how many animals are in the reference population, how densely the genome has been sampled with markers, and how strong the linkage disequilibrium is between those markers and the genes actually doing the work.

How Genomic Selection Actually Works

At a technical level, genomic selection unfolds in three stages. First, a reference population is assembled, animals with known genotypes and known phenotypes. Second, statistical models, commonly genomic best linear unbiased prediction (GBLUP) or various Bayesian approaches, are used to estimate how much each marker across the genome contributes to variation in the trait of interest. Third, those marker effects are applied to any new candidate that has been genotyped, generating a genomic estimated breeding value even though that animal has no performance record of its own yet. This is a meaningfully different approach from older marker-assisted selection, which focused on a handful of markers known to sit near genes of large effect. Genomic selection instead throws a much wider net, using thousands of markers regardless of whether each one, on its own, reaches statistical significance. That breadth is exactly why it works so well for traits like milk yield or litter size, which are shaped by many genes each nudging the outcome slightly rather than one dominant gene controlling everything. One quiet vulnerability in the system is that linkage disequilibrium between markers and the actual causal genes tends to erode over generations as recombination reshuffles the genome. If a reference population isn't periodically refreshed with new genotype and phenotype data, prediction accuracy can drift downward over time. Keeping the reference population current is, in that sense, less a one-time investment and more an ongoing commitment.

Why It's Worth the Investment

The advantages genomic selection brings to a breeding programme are fairly concrete. Selection decisions become more accurate, particularly for young animals with no performance history to lean on. Generation intervals shrink, because animals no longer need to wait for progeny records before being evaluated. Traits that were previously difficult to select for, fertility, disease resistance, feed efficiency, longevity, become tractable, since genomic prediction doesn't require direct, repeated phenotypic measurement of the animal itself. And because many economically important traits can be folded into a single selection index, breeders can chase balanced improvement across production, health, and welfare simultaneously, rather than optimizing one trait at the expense of another.

Where It's Being Used

Dairy and beef cattle: Genomic selection has arguably had its biggest impact here, effectively replacing traditional progeny testing in many dairy breeding programmes worldwide. It has

accelerated genetic gains in milk yield, milk composition, fertility, and udder health, and in beef cattle, has been applied to growth rate, feed efficiency, and carcass quality.

Sheep and goats: In small ruminants, genomic tools are being used to improve prolificacy, wool characteristics, and the ability to cope with harsh or resource-poor environments, an especially valuable trait as climate variability increases.

Pigs and poultry: These species benefit from genomic selection almost naturally, since their short generation intervals and high reproductive rates mean genetic gains spread through the population quickly once superior animals are identified. Improvements have shown up in feed conversion efficiency, growth performance, and disease resistance.

Companion animals: The same logic is now reaching dogs and horses. In dogs, genomic tools help reduce the incidence of inherited diseases and can support selection for behavioural and working traits in service and working breeds. In horses, genomic information is being used to refine selection for speed, endurance, and temperament in performance and sport horses.

Health, Resilience, and a Changing Climate

Beyond raw productivity, genomic selection is proving useful for animal welfare in a fairly direct way. By identifying genetic variants tied to stronger immune function, breeders can build populations less prone to disease, which in turn reduces how often antibiotics or other interventions are needed. The same genomic tools are also being turned toward heat tolerance and stress resilience, traits that are becoming increasingly relevant as breeding programmes have to account for a warming, less predictable climate.

New Technologies Feeding Into the System

Genomic selection doesn't stand still. Whole genome sequencing is pushing resolution down to the level of individual causal variants rather than just nearby markers. Machine learning is helping researchers make sense of genomic datasets that have grown too large and complex for older statistical methods to handle efficiently. Digital phenotyping tools, sensors, imaging systems, and similar technologies are improving how accurately traits are measured in the first place, which naturally feeds back into better predictions. And gene editing tools like CRISPR are beginning to be discussed not as a replacement for genomic selection, but as a potential complement to it.

The Genetic Diversity Trade-Off

Here's the catch that comes with all this progress: genomic selection is very good at concentrating genetic gain, which means it's also very good at concentrating genetic risk. Evidence from French dairy cattle populations, for instance, shows that genomic selection sped up genetic improvement considerably, largely by improving selection accuracy and shortening generation intervals, but it also encouraged heavier reliance on a small number of elite sires. Fewer sires contributing to more offspring means a smaller effective population size, and a smaller effective population size means inbreeding tends to creep up faster than it would under more conventional selection.

There's a subtler effect too. Genomic selection doesn't erode genetic diversity evenly across the genome. Regions carrying strongly favoured alleles can experience what's called a selective sweep, where diversity nearby collapses as that allele rapidly spreads through the population, even while overall genome-wide diversity looks fine on paper.

The encouraging part is that genomic tools cut both ways here. Because genomic relationship matrices give a far more precise picture of how related two animals actually are than pedigree records ever could, breeders can design mating strategies, such as optimal contribution selection, that deliberately cap inbreeding while still capturing most of the available genetic gain. Used thoughtfully, genomic selection doesn't have to trade diversity for progress; it can do both, but only if diversity is actively managed rather than assumed to take care of itself.

Challenges Still on the Table

None of this comes free. Genotyping infrastructure and the sheer scale of data involved carry a real upfront cost, one that can be genuinely limiting for smaller or resource-constrained breeding programmes. Reference populations need to be large to be useful, and building one from scratch is neither quick nor cheap. Selection pressure, if left unmanaged, can tip over into unwanted inbreeding. There's also a subtler risk of breeding programmes narrowing their focus too tightly onto production traits, at the cost of fitness, robustness, and welfare. And running the statistical models themselves increasingly demands genuine bioinformatics expertise, not just animal science knowledge.

Where This Is Headed

The next stage for genomic selection looks less like a single technology and more like an integration project. Genomics is expected to increasingly sit alongside transcriptomics, proteomics, and metabolomics, giving breeders a fuller biological picture of how complex traits actually come together. Artificial intelligence and large-scale data analytics are likely to keep improving prediction accuracy, and international collaboration on shared genomic databases could extend these benefits to species and breeds that currently lack the scale to build strong reference populations on their own.

Conclusion

Genomic selection has fundamentally changed how animal breeding works, not by replacing the underlying science of quantitative genetics, but by giving breeders a far faster, more precise way to apply it. It has already reshaped dairy cattle breeding and is steadily extending its reach into beef cattle, small ruminants, pigs, poultry, and companion animals, delivering real gains in productivity, health, and resilience along the way. The challenges it brings, cost, data demands, and the quiet risk of narrowing genetic diversity, are real, but they are also manageable with the right breeding strategies. As sequencing costs keep falling and analytical tools keep improving, genomic selection seems set to remain one of the most important tools available for building healthier, more productive, and more sustainable animal populations.

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