

Finding the Best Animals in a Large Herd

How to Succeed in Breeding When the Farm Manager No Longer Knows Every Cow Personally

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In the past, breeding was a matter of observation. The farm manager knew every cow, knew which family was consistent, which line caused problems, and which animal reliably produced good daughters despite unremarkable statistics. With 200, 500, or 1,000 cows, this approach to breeding can no longer be sustained—simply observing each animal individually is no longer sufficient. Nevertheless, decisions must be made: Which animals are valuable for breeding? Which heifers belong in the purebred program? Which are suitable for embryo transfer, sexed semen, or targeted elite mating? Which animals must be consistently removed from the purebred program? The answer does not lie in abandoning the breeder's eye. It lies in making it systematic—with genomics as the first filter, the phenotype as a reality check, and the cow's family as the benchmark for repeatability.

When the eye can no longer take in the entire herd

In smaller herds, breeding relies on personal knowledge. The farm manager sees every cow daily, knows the mothers, grandmothers, and usually the great-grandmothers as well. Weaknesses are noted in passing, and strengths are refined over the years. In this scenario, the breeder himself is the most important selection tool on his farm—and that's excellent. It's also not scalable.

With 500 or 1,000 animals, a person reaches a biological limit. Even attentive farm managers can reliably remember about 50 to 80 animals—the newly milked cows, the top cows that are most important economically, a few problematic outliers, and influential cow families. The remaining 90 percent of the herd remain undifferentiated. This is not a failure, but reality. Anyone who still wants to engage in breeding work on this scale needs a method that complements—not replaces—individual animal assessment. This is precisely what a systematic selection program achieves, in which genomic data, phenotypic recording, and line classification work together.

Someone with 1,000 cows doesn't know 1,000 cows—they know the 50 on which they base the system.

Key point: *The breeder managing a large herd does not have to lose sight of the individual animal. They must make their approach scalable.*

Breeding does not start with the best animal, but with a clear breeding goal

The most common mistake in larger herds isn't a lack of genomics. It's a lack of prioritization. Those who sort animals solely by the highest total breeding value will indeed find animals with good numbers—but not necessarily the animals that are a good fit for their own farm. A high-quality breeding program therefore doesn't start with the question of which cow has the highest values, but with a simpler one: Which cow should be the backbone of this farm in five to ten years?

For most larger dairy farms, the answer will not be the cow with the most extreme index scores. Rather, it will be a long-lived, fertile, healthy, functional cow with good production, a stable udder, correct conformation, low somatic cell count, high persistence, and as little management effort as possible. It is precisely this shift in breeding goals—away from a one-sided focus on maximum performance toward robustness, health, and efficiency—that Boichard and Brochard (2012) describe, as do Miglior et al. (2017) in their comprehensive review article for the *Journal of Dairy Science*, which looks back over the past century. De Vries (2020) also demonstrates that a longer productive lifespan is not only a matter of animal welfare but also a key economic consideration.

Breeding does not begin with the best animal, but with the clearest question.

Key statement: *Those who do not define a breeding goal adopt the breeding goals of others—usually that of the available index.*

From gut feeling to a selection system: a multi-stage approach

In a large herd, animal selection must not wait until the heifer has already calved. By then, a great deal of money has already been spent on rearing, insemination, and management. The better approach is a multi-stage selection process that begins as early as possible and is gradually refined.

First stage: All female calves are genotyped early on. This transforms an anonymous group of offspring into a sortable genetic population. Pryce and Hayes (2012) describe the advantages of this approach in their widely cited review article for *Animal Production Science*: Genomic information from young female animals allows selection decisions to be made with significantly greater certainty than is possible with estimates based solely on parental averages. Vit Verden also explicitly points out in the context of the KuhVision program that DNA analysis of female animals forms the central basis for genomic herd management.

Second step: The animals are ranked according to a farm-specific index. Not every animal with a high RZG, TPI, or total index is automatically the right animal for the farm. The key is to weight these factors according to the farm's breeding goals: milk yield, fat/protein content, longevity, fertility, udder health, hooves, conformation, udder, calving ease, suitability for robotic milking, and show potential. A farmer operating a robotic milking system will prioritize teat placement and milkability differently than a

carousel operation. Those who sell breeding stock pay closer attention to conformation and pedigree than a pure dairy producer.

Third Level: The herd is divided into four breeding groups. The top 5 to 10 percent form the elite group for embryo transfer (ET), sexed semen, targeted elite mating, and—depending on the business model—the sale of embryos or breeding stock. The next 30 to 40 percent constitute the purebred group for high-quality female offspring. The middle group is used selectively as needed, often with conventional semen or selected beef breeds. The bottom group is consistently excluded from further purebred breeding—either for beef-on-dairy or sale. This four-tiered differentiation is the true driving force behind genomic herd management: it allocates the genetic investment to those animals that truly justify it.

In large herds, breeding progress does not result from luck. It results from consistent selection.

Key point: *Not every cow needs to become a mother of the next generation. In large herds, this is the most important insight.*

Genomics reveals potential—but not automatically the best cow

Genomic scores are not a beauty contest. They indicate genetic potential—not management performance. This is a major advantage because an animal's value can be estimated as early as the calf stage, long before the farm has invested in rearing or artificial insemination. However, it also has its limitations. A heifer with a high genomic score may underperform in a poor rearing system. A cow with average scores can perform significantly above her genomic expectations through excellent management.

In their methodological review, Hayes et al. (2009) made it clear that genomic predictions represent probabilities—not certainties. For an individual animal, any prediction may be off the mark; within a herd, however, the predictions are statistically reliable. The analyses from the German KuhVision program demonstrate precisely this effect: In larger comparison groups, genomic differences between animals correspond to subsequent phenotypic differences—such as in milk yield, somatic cell count, and non-return rate. At the individual animal level, genomics remains fallible; at the herd level, it is a powerful selection tool.

Genomics reads the cards—it doesn't play them.

Key point: *At the individual animal level, genomics is not infallible. At the herd level, it is indispensable.*

The phenotype remains the incorruptible reality check

A high-quality breeding program needs both: genotype and phenotype. The genotype answers the question of what the animal possesses genetically. The phenotype answers the question of what the animal actually exhibits under real

conditions. In large herds, phenotypic assessment must be systematic—otherwise, the farm manager’s subjective perception becomes an unreliable basis for evaluation.

Standardized phenotypic recording includes linear description or classification, udder type and attachment, teat placement, legs and hooves, movement, body capacity, strength, milk flow and milkability, cell count trends, fertility, insemination effort, calving interval, health events such as mastitis, hoof problems, metabolic disorders, or afterbirth behavior—supplemented by behavioral data from the milking system, feed intake, and general robustness. ICAR and the World Holstein Friesian Federation emphasize that the linear conformation description replaces the subjective overall impression with a series of individually defined traits—thereby making it comparable across farms, classifiers, and generations.

The phenotype doesn’t lie. It’s just quieter than the index.

Key point: Without a standardized phenotype, any index comparison in a large herd becomes mere speculation.

The best breeding cow isn't always the one with the highest index

In practice, it’s worth taking a two-step approach. First, genomic sorting is performed—this is fast, consistent, and reproducible. Then, the best animals are evaluated phenotypically. In this process, animals from the top genomic group are often eliminated: weak conformation, unfavorable udder placement, insufficient body capacity, conspicuous behavior, or a cow family that produces high numbers but doesn’t perform well in everyday management.

Conversely, animals with index scores that aren’t quite extreme are often very interesting from a breeding perspective if they offer a strong overall package: a solid family background, a functional body, a trouble-free start to lactation, high nutrient content, stable health, and suitable bloodlines. An Excel ranking alone is therefore insufficient for a high-quality breeding program. It requires a regular breeding conference on the farm: evaluating data, inspecting animals in the barn, reviewing families, and planning matings. In large herds, this breeding conference is the counterpart to the traditional breeder’s evening barn round.

The best breeding cow is the one that ranks at the top and produces in the barn.

Key point: Those who merely sort will find the highest number. Those who sort and evaluate will find the right cow.

The cow family is becoming more important again—but in a different way than before

One of the surprising developments of the genomic era is the renaissance of the cow family. Genomics hasn’t done away with the family—it has made it verifiable. In the past, a cow family was a story: “Good cows come from this line.” Today, this story can be verified with data: performance across multiple generations, service life, conformation scores, somatic cell count trends, fertility, genomic stability, and recurring strengths and weaknesses.

A family is of breeding value when it produces not just individual outliers, but consistently high-performing animals. This consistency is also scientifically grounded. In their work on Mendelian sampling and selection limits, Cole and VanRaden (2011) demonstrated that there is significant leeway within a family—but that this leeway is also clearly bounded. A strong family not only produces a strong daughter; it reliably produces a distribution with a high median. That is the true family value.

This repeatability is particularly crucial for ET candidates. A heifer with a high genomic value but without a proven family poses a different risk than a heifer from a line that has combined performance, conformation, and fitness over generations. The genomic value tells you what cards you have in your hand. The family tells you how those cards are typically played in that line.

A family is not just one cow. It is a distribution—and a distribution is less likely to lie.

Key point: *Genomics does not make the cow's family obsolete. It makes it more reliable.*

Embryo Transfer as an Amplifier, Not a Fix

ET is not a corrective program for unbalanced animals. ET is an enhancer. It amplifies what an animal brings to the table—both the positive and the problematic traits. That is why, before every ET decision, it must be very clearly defined what exactly is being enhanced. In the Cabi literature review, Mapletoft and Bó (2016) classify embryo transfer as the most effective breeding tool, provided it is applied to animals that are genuinely superior from a breeding perspective; Hansen (2020) expands on the methodological maturity and success factors of modern reproductive technologies in the *Annual Review of Animal Biosciences*.

Based on consulting practice and the literature, a clear minimum profile emerges for ET candidates: They should be in the upper genetic segment of the herd, offer clear breeding value, and show no serious weaknesses in fertility, cell count, conformation, or udder. The cow's family line should be promising or, at the very least, robust; the bloodline should be appropriate; the phenotypic appearance should be compelling; and there should be no known genetic risks. Those who honestly assess these points avoid the classic ET misinvestments—and significantly accelerate breeding progress on the farm.

ET amplifies strengths—but unfortunately also weaknesses. Being aware of both is the first step.

Key point: *ET candidates are not "high-potential." They are "complete."*

Inbreeding and genetic defects must be the focus

The greater the genetic progress, the more important it becomes to monitor genetic diversity. Those who consistently use the same popular bull lines produce high scores in the short term, but in the long term, they narrow the breeding window. Doekes et al. (2018) documented for the Dutch Holstein-Friesian population that the annual increase in genomic inbreeding has accelerated since the beginning of the genomic era. Mäki-Tanila and Toro (2014) place this development within the broader

context of diversity regulation in livestock populations and advocate for conscious management rather than passive drift.

Every high-quality breeding program therefore includes established routines: inbreeding checks for every mating, screening for haplotypes and recessive genetic defects, monitoring dominant bloodlines, the deliberate use of outcross bulls, avoiding close repeat matings, and the willingness to occasionally exclude animals from the top index if they are genetically too closely related to the herd. As part of its breeding value estimation, vit Verden explicitly highlights the added value of genomic information for inbreeding management and the detection of recessive traits—an aspect that goes far beyond simple “ranking optimization.”

Inbreeding progress is like compound interest. It works quietly—and takes time to show results.

Key point: *In large herds, inbreeding control is not a secondary issue—it is part of the actual breeding work.*

The breeder's role: from animal expert to system expert

The modern breeder managing a large herd no longer needs to know every cow by heart. But he must know his system. He doesn't have to calculate every number himself. But he must understand which numbers are important. He doesn't have to look at every animal every day. But he must know which animals need to be examined today—and why. This is the new art of breeding: making the right animals visible within a large herd.

This shift is not trivial. It requires a different kind of attention—less blanket and more targeted and informed. It also requires discipline, because the system is only as good as its consistent maintenance: regular genotyping, well-maintained phenotype data, clearly defined breeding groups, and an honest breeding conference held at regular intervals. From a consulting perspective, it is precisely this discipline that many large herds struggle with. The tools are available; their consistent use makes all the difference.

He doesn't have to know every cow. He has to know which cow he should know.

Key takeaway: *In a large herd, the breeder becomes an expert in the system—without losing sight of the individual animals.*

Five Tools for Breeding Work in Large Herds

The following five tools translate the system into immediately actionable barn practices. They work individually, but their full strength is realized when used in combination.

□□ Tool 1 — The 5-Step Filter for Elite Animals

From an anonymous calf to a targeted elite asset

Step 1 — Genomic Pre-Filter:

- Top animals based on the farm's own index, not on a blanket total breeding value

Stage 2 — Exclusion Criteria:

- excessive inbreeding, known genetic defects, poor somatic cell count predisposition,
- low fertility, problematic calving traits

Stage 3 — Phenotypic Check:

- Udder, legs and hocks, body conformation, milkability, behavior, rearing performance

Stage 4 — Check the cow's family:

- Does the family persist over several generations?
- Are there long-lived cows—or just a few high individual scores?

Step 5 — Determine usage:

- ET, sexed semen, targeted purebred breeding, normal insemination,
- or a deliberate decision not to produce female offspring

Practical Benefits

Consistently identified elite animals instead of random sorting by index.

Tool 2 — Four breeding groups for a large herd

Treating all animals the same distributes breeding progress randomly

Top 5–10% – Elite group:

- ET, sexed semen, targeted elite mating
- Embryo and breeding animal sales, if applicable

Next 30–40% – Purebred:

- High-quality female offspring
- Sexed semen as needed

Mid-range:

- Conventional semen or selected beef breeds
- depending on the need for replacement stock

Lower group:

- Consistently beef-on-dairy or for sale
- do not produce female offspring

Practical Benefits

Breeding progress is targeted—and rearing costs are directed toward the right genetics.

Tool 3 — Breeding Program Timeline

From calf to first lactation—when things happen

Birth to 3 months:

- Collect a DNA sample, verify pedigree
- Retrieve genomic scores, initial grouping

3 to 8 months:

- Monitor growth and development
- Document health events, identify weaknesses

Age at insemination:

- Final classification into Elite, Purebred, Normal, Beef-on-Dairy

Before first calving:

- Assessment of development, legs and hooves, pelvis, body, and family information

After first calving:

- Phenotypic reality check: udder, milkability, somatic cell count,
- fertility, persistence

After 100–150 days of lactation:

- Decision on breeding enhancement: ET, targeted mating,
- embryo transfer, or sale of offspring

Practical Benefits

Breeding work becomes routine—not improvisation.

□□ Tool 4 — ET Criteria Check

ET is an amplifier, not a repair

Minimum requirements:

- Upper genetic segment on the farm
- Clear breeding value
- No serious weaknesses in fertility, cell count,
- conformation, or udder
- interesting or solid cow family
- Suitable bloodline
- marketable pedigree
- Convincing phenotypic impression
- No known genetic risk factors

Mnemonic

If you have a weak point, don't duplicate it twelve times—that's embryo transfer in a nutshell.

□□ Tool 5 — Inbreeding and Genetic Defect Routine

Genetic diversity is an investment—not a sacrifice

Mandatory for every large herd:

- Inbreeding control for each mating (typically a 6–8% limit)
- Screening for haplotypes and recessive genetic defects
- Monitoring of dominant bloodlines
- Deliberate use of outcross bulls
- Avoidance of close repeat matings

- Willingness to occasionally forego top index scores
- if the kinship is too close

Practical benefits

Protection against silent inbreeding drift—and preservation of genetic flexibility for the next generation.

Conclusion: You don't just find the best animals—you filter them out

In large herds, elite animals do not emerge because the farm manager happens to discover a special cow by chance. They emerge because the farm has a system that identifies exceptional animals early on. Genomics provides the first powerful filter. The phenotype provides the reality check. The cow's family provides the repeatability. The breeding goal provides the direction. And in the end, the farm manager makes the decision—based on data that he alone could never have compiled.

The future of breeding on large dairy farms does not belong to algorithms alone. Nor does it belong to old-fashioned gut instinct alone. It belongs to farms that combine both—data that sorts, eyes that inspect, and breeders who decide. This is more demanding than any one of these three approaches. But it is also the only approach that truly does justice to large herds.

Data sorts. Eyes inspect. Breeders decide—in this order, breeding in large herds becomes robust.

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About the Author

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