



LOGIX
NEWS
2022



The skeleton of an aurochs, the ancestor of domesticated cattle

Credit: Katrina van Grouw: *Unnatural Selection* Princeton University Press (2018)

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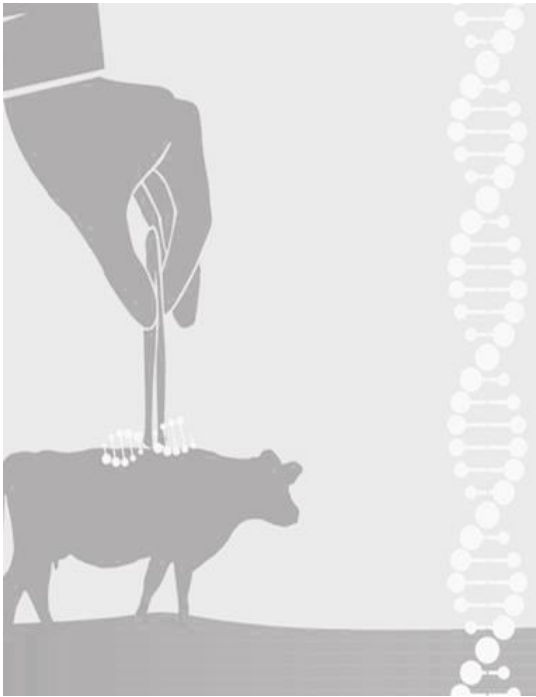


Gene Action 19

No Questions = No Change

Japie van der Westhuizen

To discover the value of a good wine the cork must first be removed.



The need for consistent change is appreciated by inquisitive minds. Although curiosity might get under the skin of some people, it is these inquisitive that drive of new inventions and especially how they are utilised in a way to be of benefit. The Human Genome project is still being hailed as the “world’s largest collaborative biological project” (2011; Batelle Technology Partnership Practice: Economic Impact of the Human Genome Project; How a \$3.8 billion investment drove \$796 billion in economic impact, created 310 000 jobs and launched a genomic revolution). The idea was conceived in 1984, the project launched in 1990, and although declared “essentially complete” in 2003 only 85% of the human genome was mapped. The final gaps were only completed in January 2022. (Main source Wikipedia.org).

The first main spinoff for livestock breeders was the Bovine Genome Project that involved 300 scientists from 25 countries to map the genome that contains over 3 billion (thousand million) base pairs with the code for an estimate 22 000 genes (sharing a whopping 80% with humans).

The final value of the outcome from the questions asked before 1983 is possibly not calculable, but mind boggling.

Being industry owned and driven, SA Stud Book and our staff do not shy away from difficult questions. It is in the nature of a good scientist to welcome questioning and to dig even deeper into the mysteries of science for answers for the needs underpinning such questions.

South African breeders and the broader livestock industry are also the beneficiaries of the original goals and outcomes of the Human Genome Project and the genome mapping of domestic animals that followed over the years. The manner in which Stud Book participated in the Beef and Dairy Genomic Programs was key in allowing the local livestock industry to reap these benefits. The unique combination of this industry owned Association, driven by the needs (and questions) of its members and maintaining the capacity to address those needs, based on sound scientific principles, comes very close to a winning recipe.

A continuous source of questioning can be compared to learning as described by Charlotte Mason (1842 – 1923):

“Teach from a flowing stream, not from a stagnant pool” (*The Story of Charlotte Mason*, p. 288).

Double Muscling in SA Stud Book Beef Cattle Breeds: Where are we now?

Dr Helena Theron

The double muscling syndrome was first documented in 1804 in English Shorthorn cattle. It is nowadays found in many beef cattle breeds all across the world, as well as in South Africa. So far, only 3 variants of the gene that causes double muscling have been found in South African breeds. These are nt821 and Q204X, both of which cause severe double muscling, as well as F94L, which is regarded as less severe. Only one out of the 8 breeds that have already genomically tested many animals through SA Stud Book, had no double-muscling variants. Two breeds have only one variant; three breeds have two variants and all three variants occur in three of the breeds.

Double Muscled Animals (Severe variants nt821 and Q204X)

'Double-muscled animals are generally dysfunctional in most environments.'



Top: Double-muscled animals are overly muscled, and have a high tail setting.

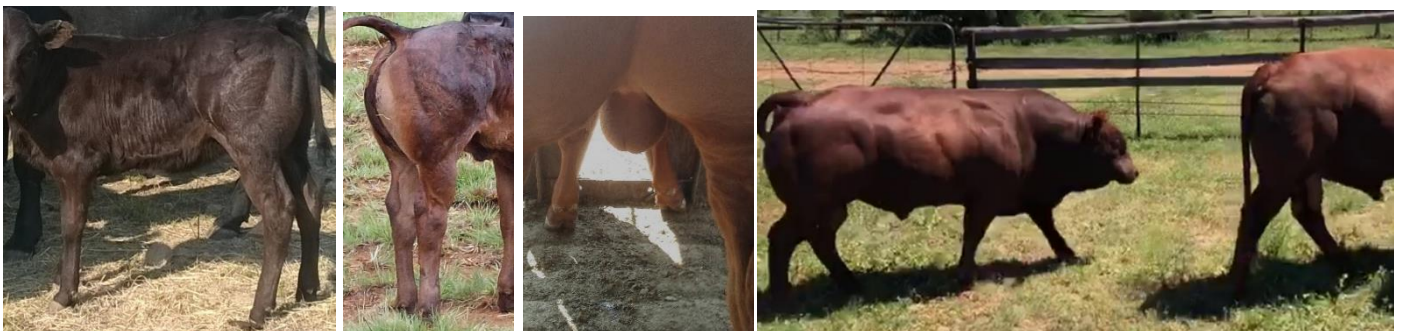


Above: Large double-muscled calves at birth increase the risk of dystocia (difficult calving) and still-born calves.



Above: 'Dry muscling' or less fat on a live animal.

Above: Double-muscled animals have a higher dressing % due to more muscle (meat) and less fat and bone on the carcass. Fat is however an energy store for cows: less fat is detrimental to cow fertility, fitness and survival under extensive conditions.



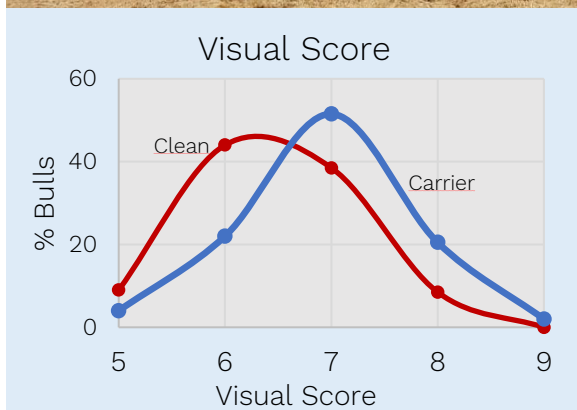
Top left to right: Other effects of the detrimental myostatin variants that may be apparent to different degrees: thin, fine bone structure, straight hocks, underdeveloped scrotum and poor growth, due to underdeveloped organs like the rumen and lungs ('pencil-gut').

Carriers of the double-muscling gene

It is better to test than to guess!



The effect of the gene in carriers of the detrimental myostatin variants Q204X (top) and nt821 (left), may or may not be visible (recessive or partially recessive) due to unknown reasons. It is probably due to interaction with other genes or the environment.



Left: A group of bulls were visually scored and then tested for double-muscling status. It seems that carriers tend to score higher in visual scoring, possibly due to slightly better muscling in carriers than normal animals. This indicates that when the status of the animal is unknown, there might be a selection benefit for carriers, which caused the gene frequency to increase. Note that DM free animals also scored high, indicating that it is possible to select for high-scoring animals without the double-muscling gene.



Normal looking carrier dams (Q204X left and nt821 right) with their double-muscled calves.

Inheritance of Double Muscling

Double muscling is caused by a genetic mutation in the Myostatin (MSTN) gene. In double-muscled animals, the Myostatin gene is defective and produces defective myostatin protein, which causes increased muscle growth in the fetus and young calf to the detriment of other organs, fat and bone in the body, resulting in a dysfunctional animal.

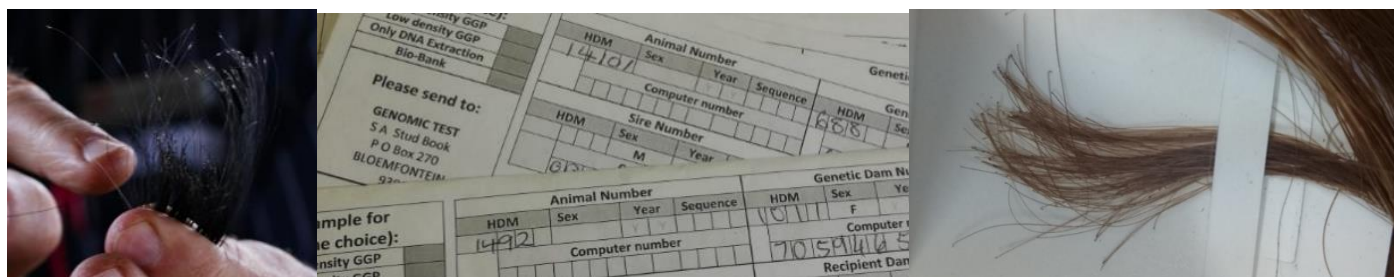
Animals inherit two copies of each gene, one each from their sire and dam respectively. If the animal for example inherits detrimental variants from both parents, he will not have fully active myostatin proteins, which will result in a double-muscled animal. The carrier or heterozygote has one gene that produces active myostatin, and one gene that is unable / partially able to produce active myostatin, depending on the variant. Most myostatin variants are recessive or partially recessive. This means that some heterozygous individuals express double-muscling while others do not, and that expression therefore varies between animals that appear normal to animals that may show some symptoms of double-muscling. The reason for this variation is not known, but it is thought that it may be caused by interaction with other genes in the breed / animal, interaction with the environment, or a combination of both.



Terminology

Free <i>Normal</i> 0  An animal with two normal Myostatin genes is normal, indicated by 0.	Carrier <i>Heterozygote</i> 1  An animal with one normal and one defective Myostatin gene, may or may not be affected.	Double-muscled <i>Affected</i> 2  An animal with two defective Myostatin genes is double-muscled.
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Genetic testing and reports



As genetic testing for myostatin variants is available, the occurrence of double-muscling in a herd can be managed. The Logix genomic test uses DNA from hair roots and semen straws and tests for 9 detrimental / less detrimental (of which 3 occur in SA) and 5 silent Myostatin variants. Contact Elsa at Studbook (elsa@studbook.co.za) in this regard.

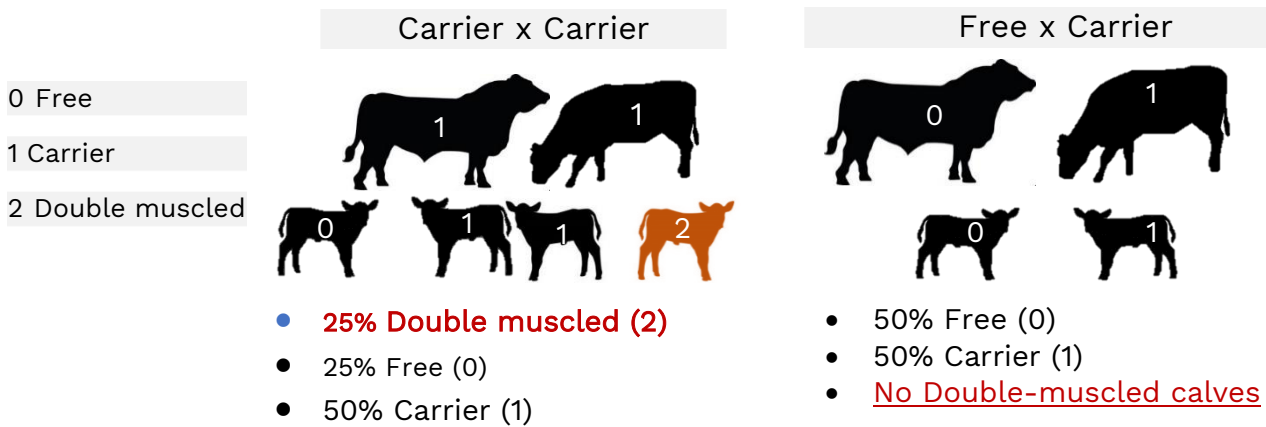
The Logix Genomic Report reports the following:

- Variants that are classified as 'detrimental' as symptoms tend to be more severe. Thus far only nt821 (5 breeds) and Q204X (3 breeds) have been found in Stud Book breeds.
- Variants that tend to be less severe are classified as 'less detrimental'. F94L has been found in low to very low numbers in 6 Stud Book beef breeds. Animals carrying two alleles of this mutation are reported to have higher meat quality and no negative effects like dystocia, although some studies indicate lowered fertility and longevity.
- The variants that are found in the inactive parts of the gene, do not cause double muscling. These variants are known as 'silent' variants. They are found in all breeds.



Top: Bulls with F97L

Management of double muscling



Advantages:

Double-muscled animals: No advantages in SA.

Carrier: Possibly a better looking (more muscular) animal. Some animals may have a higher dressing percentage.

Free: Normal risk for difficult births; Cows have normal fat for fertility and survival, especially during droughts. No need to plan matings and test offspring.

Disadvantages:

Double-muscled animals: Animal is dysfunctional and cannot be used for stud breeding.

Carrier: Higher risk of difficult births and some cows may have lower fat which is detrimental to fertility and survival, especially during droughts. Management is more difficult: Have to keep testing progeny and have to keep planning matings (no carrier x carrier matings), to prevent double-muscled calves.

Free: No disadvantages, especially in cow herd.

If a double-muscled calf is born, both parents are carriers. If one of the parents is free of double-muscling, no double-muscled calves will be born, regardless of the status of the other parent.

- The easiest way to prevent the birth of double-muscled calves in a herd with carrier cows, is to use bulls that are free from double-muscling.
- If free bulls are used, it is not necessary to test the cows. However, if some cows are unknown carriers, the mating may result in a carrier calf, and offspring selected for breeding should therefore be tested.
- **Only free bulls should be used on heifers, to reduce the risk of dystocia (difficult birth).** Carrier bulls may be used on older (free) cows, as the risk of dystocia is smaller.

How to breed a herd free of double muscling

If the cow herd is free of double muscling, cows have normal fat for fertility and survival, as well as a normal risk for more difficult calving. If all sires and dams are free from double-muscling, there is no need to test offspring.

However, some herds already have high frequencies of double muscling. There is however no need to cull all carriers. Initially test the bulls and use only free bulls (especially on heifers). Only heifers tested as free should be retained in the herd over the next few years. Eventually, all the cows will be free and there is no need to test anymore.

The use of carrier bulls

Carrier bulls can indeed be used, especially if the animals' status is known and they are managed so that carrier frequency in the herd is low. Carrier bulls can be used in older, free cows, and if the progeny is not going to be retained for breeding anyway, the progeny does not need to be tested. Double muscling with carrier bulls can be managed by mating them only to free cows to ensure no double muscling calves are born. *It is also not necessary to over-react, as the chance for a double-muscled calf from a carrier x carrier mating is around 25%, so if the carrier frequency in the cow herd is low, or is kept low, the chance for double-muscled calves is also lower.* The carrier frequency in the cow herd can be kept low by using alternating free and carrier bulls, because carrier bulls tend to increase the gene frequency in the herd, while free bulls tend to decrease the gene frequency. Since there is a 50% chance of further carriers from carrier bulls on free cows, offspring should not be retained, or can be tested if they are retained, so that their status is known.

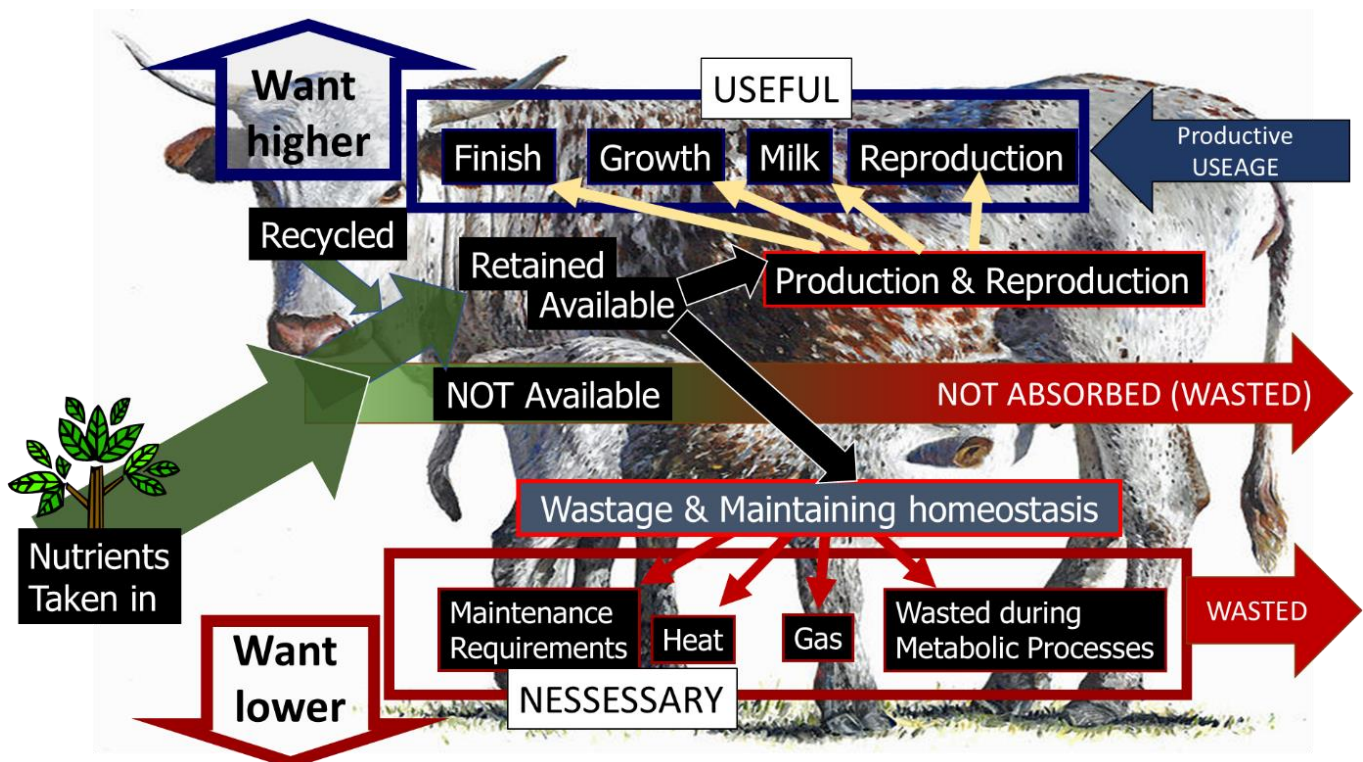
FOUR COWS

Dr Japie van der Westhuizen

“Beyond the joy that your favourite cattle breed brings, any sustainable livestock enterprise must rely on the productivity of the breeding cows.”

No two animals are the same, they all differ, even full sibs. There are many ways to judge which ones are there to carry the burden and which are only in it for the ride. One can even go so far as to simply divide them in different groups, according to their characteristics and how they respond on the physical and production environment they must reproduce and produce in. Irrespective of any decision in defining and describing typical differences, one should be aware that there are fine anatomical and physiological balances at play. A simplified division or grouping is therefore the result of complex sets of genetic differences that govern the anatomy and, more especially, the physiological processes leading to differences in response and even behaviour among animals on the same farm.

The following figure serves as a simplified illustration of the utilisation and channelling of nutrients (especially energy) in a productive beef cow.



In the first place, cows differ in their ability to take in feed above own maintenance requirements. This can simply be due to an unknown inability, limited rumen capacity or because of being unable to properly adapt to environmental constraints, such as walking ability or ill adaptation to weather conditions. Limited intake means limitations in the available energy for productive processes as the major channelling of available nutrients will be for homeostasis (maintaining body functions).

Animals also differ in their ability to absorb roughage at macro level (in the rumen and lower digestive tract). It is known that grasses in the tropical and sub-tropical areas, for example, are less palatable and cause higher heat increments when digested. This, in turn causes slower passage through the digestive tract and generate more digestive heat, raising body temperature in an already hot (and mostly humid) environment. This “negative spiral” causes ill adapted animals to lower their roughage intake even further with less nutrients (especially energy) available for production and reproduction. Ill adapted animals will even waste the available energy with behavioural patterns such

as panting and therefore causing the downward spiral to accelerate (this also happens in extreme cold conditions to animals not adapted to such extremes). Well adapted animals will also have the anatomical (and possibly physiological) mechanisms to rid themselves more easily from an excessive heat increment and also not to be subjected to an additional heat load from the environment. These mechanisms are known to observers, namely, effective sweating (effective sweat glands per surface area, short and smooth hair causing sweat to evaporate directly from the skin, relatively big skin surface ratio to body area), adaptive behavioural patterns (like night time grazing), shiny skin or coat (smooth hair coat, well pigmented skin and sebum secretion), effective respiration (in relation to the heat caused by digestion or the metabolic processes) and even things like selective grazing.

It can therefore be concluded that those animals not thriving under a certain set of environmental constraints will look different and also behave differently to the ones that do. These are the types of observations from pioneers like the late Professor Jan Bonsma that made the headlines and book chapters written 40 to 60 years ago. The well-known diagrams of Professor Bonsma are still used by scholars and serious breeders and it is also amusing that this pioneering work is re-discovered from time to time by some.

The following figures reflect the thought processes by these pioneers.

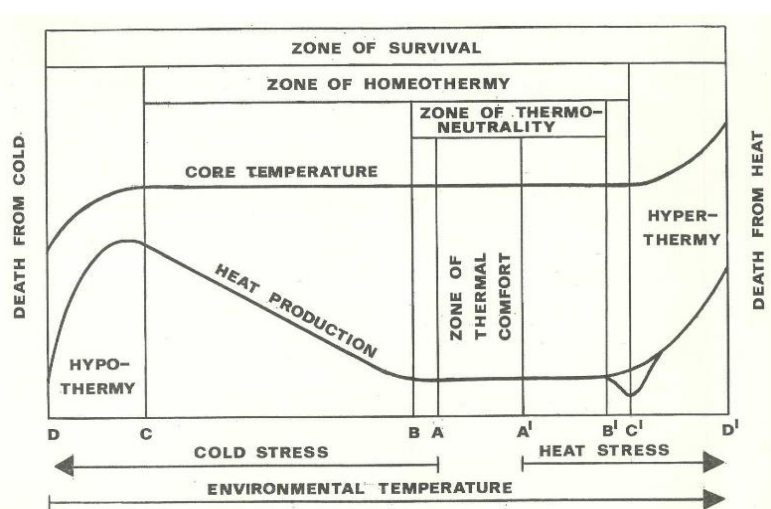


FIG. 7-15. Simplified schematic representation of critical environmental temperatures and the zones embraced by them.

Top From: ESE Hafez. Adaptation of Domestic Animals. Lea & Febiger, 1968.

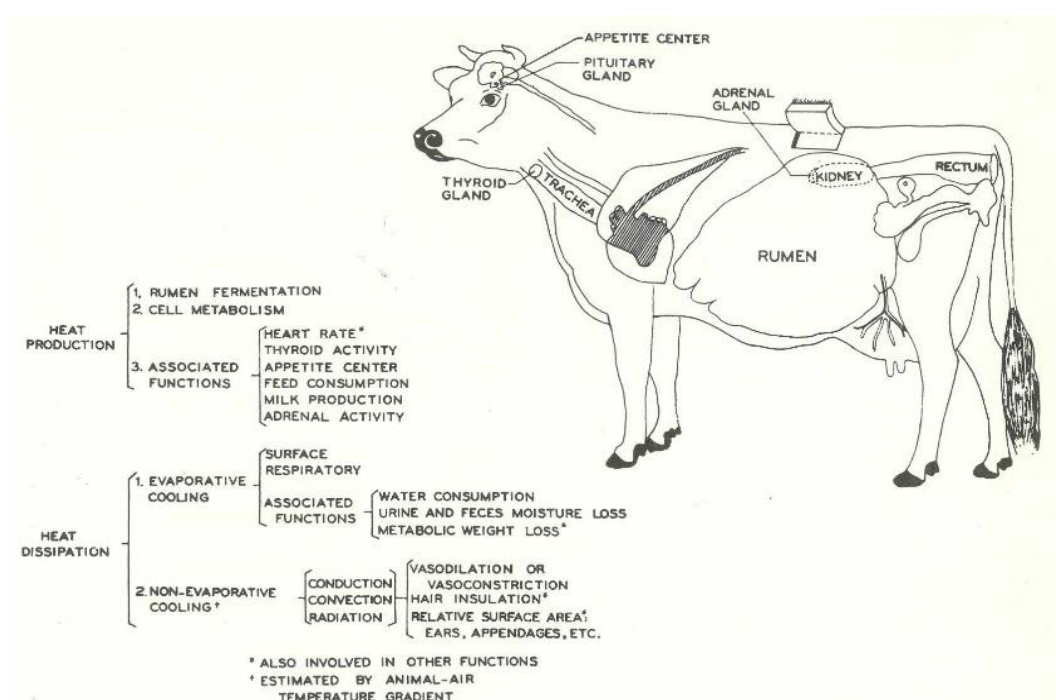


FIG. 17-2. Main sources of heat production and avenues of heat dissipation in cattle.

Top From: ESE Hafez. Adaptation of Domestic Animals. Lea & Febiger,

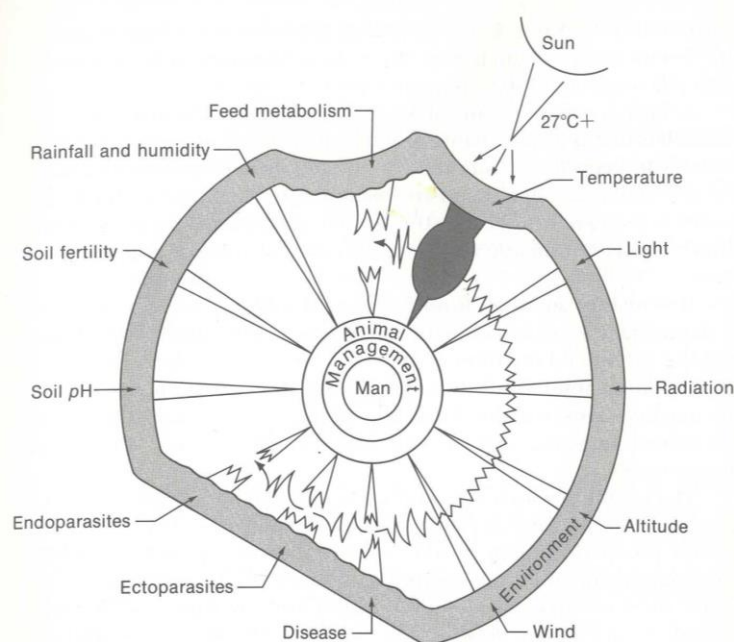


FIGURE 2.2
The probable direct and indirect influences (interaction effects) that 27°C or above air temperature will have on livestock in the N-S 30° latitudes. (From McDowell, 1968).

From: RE McDowell. Improvement of Livestock production in warm climates. WH Freeman and Company, 1972.

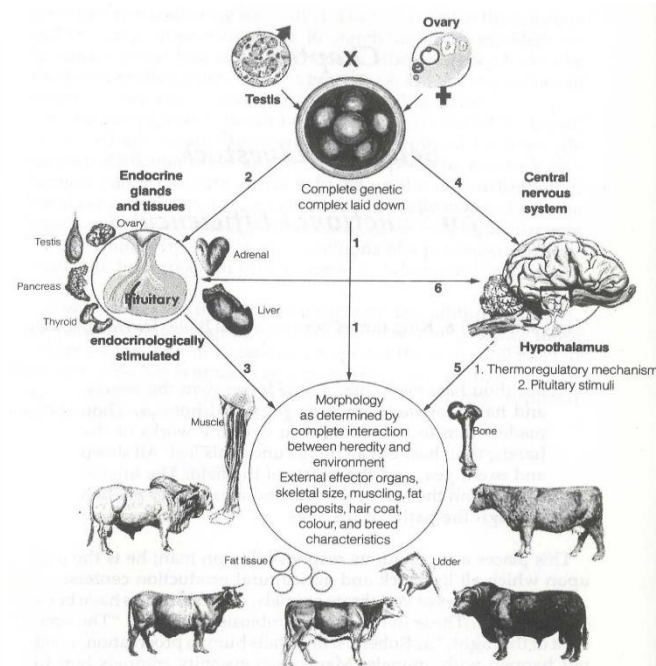


Figure 3.1 The interaction between genes and the phenotype. At the moment of conception the complete genetic potential of the animal is laid down. This determines irrevocably the potential boundaries within which the individual can function, perform or produce during its entire lifetime.

From: J Bonsma. Livestock Production A Global Approach. Tafelberg 1980.

The conclusion is therefore that there is a genetic base causing animals to differ how they make use and respond on environmental factors and the available (feed) resources.

The next important genetic difference among cows is to be found in how they effectively make use of the available nutrients retained for production, reproduction and maintenance of body condition. As in the case of genetic differences in the percentage availability of these nutrients, the channelling of nutrients to these functions differs. These, sometimes unfavourable relationships are well described by the genetic correlations among traits associated with the utilisation of these nutrients (examples of genetic correlations among reproduction, milk/maternal ability, growth rate, maturity age/weight).

Simple solutions, such as selection for cow condition therefore negates all the known facts related to the availability of nutrients on the macro scale and genetic differences in channelling these nutrients for different functions.

On a more practical level

I was taught by one of the star students of the late Professor Bonsma, Dr Herman Venter. He concluded that good observers will recognise four types of cows in herds, irrespective of the production system or other constraints. Obviously, nothing in biology (nature) can be put in boxes or separated in very distinct classes as there will be a continuous or gradual change from one class to the next. Nevertheless, the division can broadly be explained as follows:

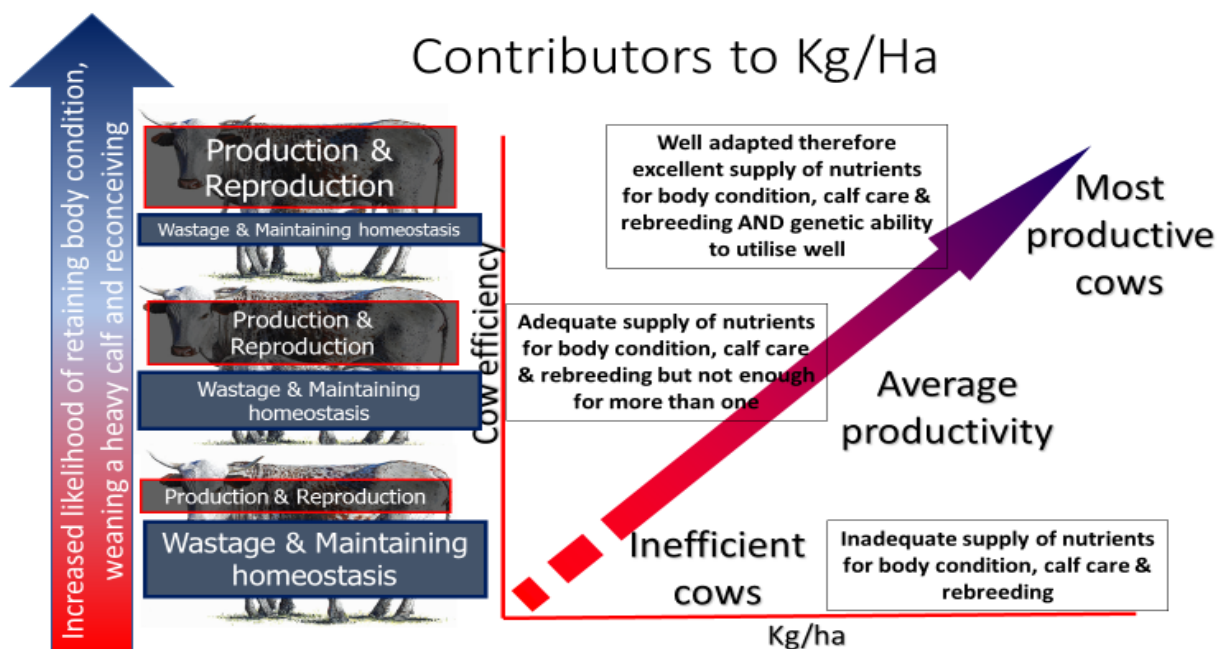


Two heifers from the same farm, each with a calf, and different condition scores.

1. Cow maintaining (or gaining) her body weight and/or condition and weaning a heavy calf.
2. Cow maintaining (or gaining) her body weight and/or condition and weaning a light calf.
3. Cow losing her body weight and/or condition and weaning a heavy calf.
4. Cow losing her body weight and/or condition and weaning a light calf.

Since female reproduction traits can be seen as the prime means of ascertaining suitability and adaptation to the specific set of environmental and management constraints (hence the terms “Natural selection” or even “Survival of the Fittest”) and the dependence on body condition for rebreeding, cows in groups 1 and 2 are more likely to be in calf in the next cycle. Selection for body condition alone will, however favour both these groups of cows, without any distinction.

These differences are illustrated in the next figure:



The bottom line is therefore to be wise and vigilant enough to observe the anatomical differences amongst the breeding cows and to use common sense to only select those or from those that are more likely to produce offspring that will thrive under the climatic conditions and production system favoured. It is also furthermore wise to record the traits that will contribute directly to profit, such as female fertility, mothering ability, pre-weaning growth rate and mature (maintenance) weight. The premise is furthermore that the very first traits that will point out ill adapted females, will be reconception. Selection should therefore concentrate on that. This will advertently lead to selection of well adapted progeny. By adding mothering ability (“milk”) and pre-weaning growth rate, breeders and other beef producers are assured that breeding cows are more efficient in utilising the available nutrients effectively. Where there is fear that maintenance requirements might increase to levels that might cause lower productivity or loss of adaptability, selection against high cow weight can be included the objectives.

Perspective

Based on this background, it can be concluded that any breeder and/or beef producer has two important tools in his or her arsenal to ensure that the breeding cows in the herd are more efficient, and more importantly more efficient cows will be bred. The first important tool is visual assessment, based on knowledge linked to functional efficiency. The second tool is to record traits of economic importance and to use methodologies that clearly point out the genetic differences among the selection candidates. It is known that phenotypes alone only account for a (sometimes small) part of these genetic differences that will be transferrable and therefore distinguishable in performance among progeny. BLUP breeding values is therefore a better tool to point out these genetic differences and should be used wisely as part of a selection objective, together with visual appraisal.

In selecting productive animals:

- Visual appearance should count 100%
- Genetic merit for traits contributing to productivity and efficiency should count 100%
- AND
- Measurement tools should not be confused with selection objectives

DAIRY CATTLE: Logix Genomic Analyses

Based on expression of genes in own environment and population

Dr BE Mostert

The building blocks of any Genomic Analysis are:

- measurements of the population in which the animals' genetics are expressed,
- pedigree information linking relatives' information and
- the genetic variation available in the population.

SA Studbook's Genomic Service is based on all these building blocks.

In 2020, SA Studbook rolled out a Single-Step Genomic Analysis for all the dairy breeds that participate in SA Studbook's Genetic Analyses. This was the first National Genomic Analysis in South Africa for dairy breeds. Single-Step methodology is the latest development in the field of Genomics, where the genomic relationships between genotyped animals are used instead of the theoretical relationships, as is the case in conventional Genetic Analyses. It is therefore possible to know exactly which part of the genome is shared by the genotyped animals. This knowledge is used to predict the breeding values of young, unmeasured animals much more accurately. It is based on measurements of the South African population that spans many generations, as well as the heritability and genetic correlations of South African populations. It stems from the genetic variation caused by many generations of selection intensity and breeding goals. These are the most relevant genomically enriched breeding values that can be predicted for the South African populations. These breeding values are directly comparable within the South African populations as they are estimated in the same Genomic Analysis.

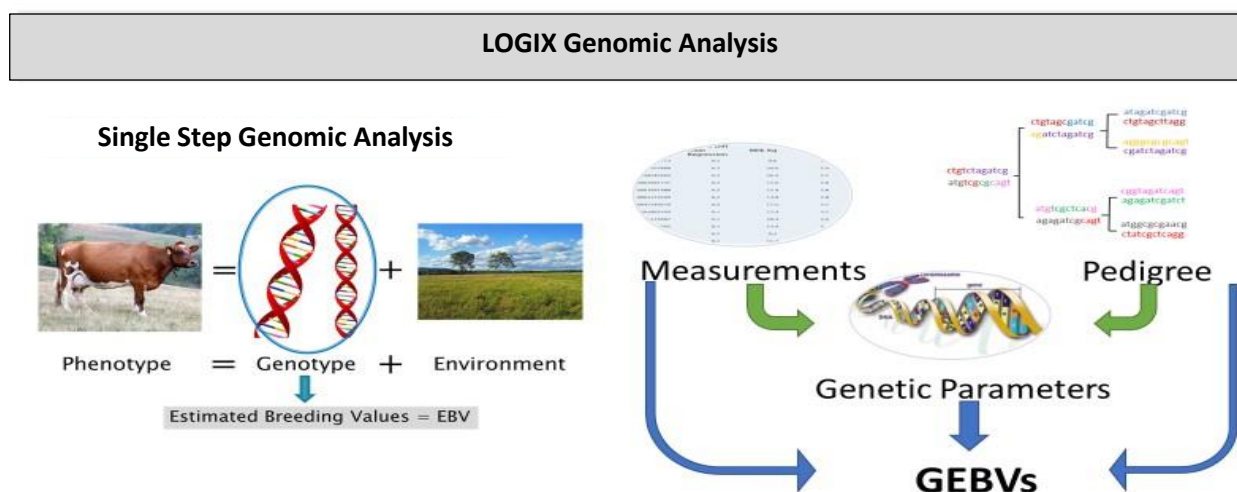


Figure 1: Logix Genomic Analyses are based on gene expression and genetic variation of SA populations and complete genomic and conventional relationships between animals.

The following graphs show the number and distribution over years of birth of the genotyped animals in the Logix Genomic Analyses, as well as the country of origin of the genotyped bulls:

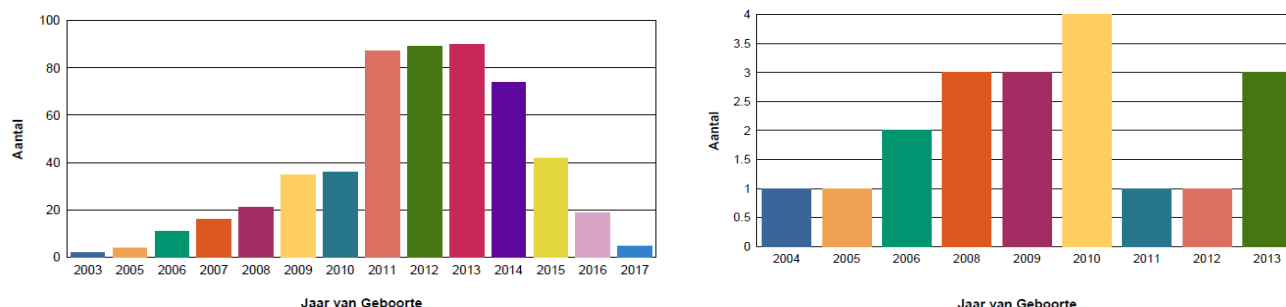


Figure 2: Genotyped Ayrshire cows (left) and bulls (right) per year of birth

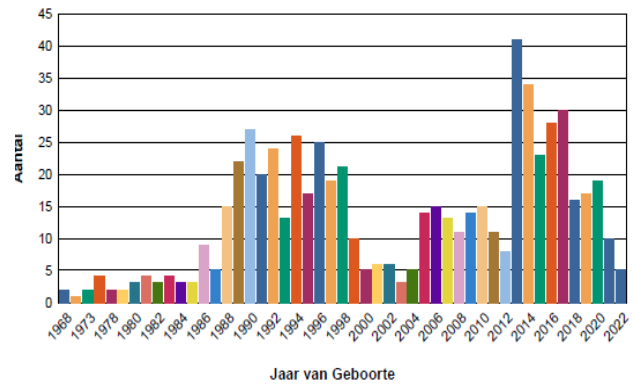
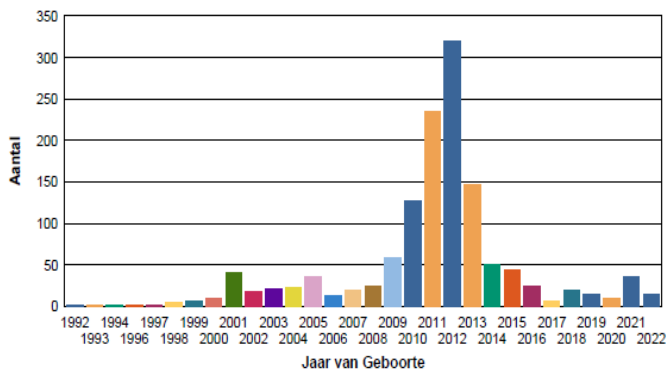


Figure 3: Genotyped Holstein cows (left) and bulls (right) per year of birth

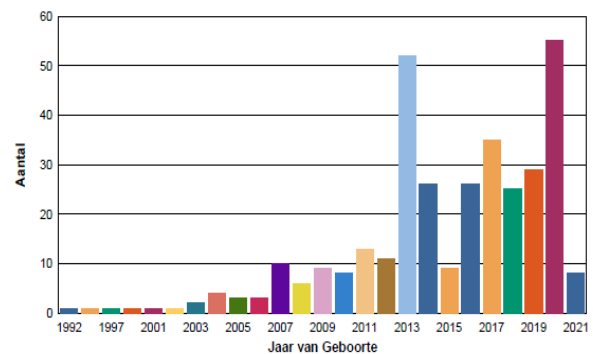
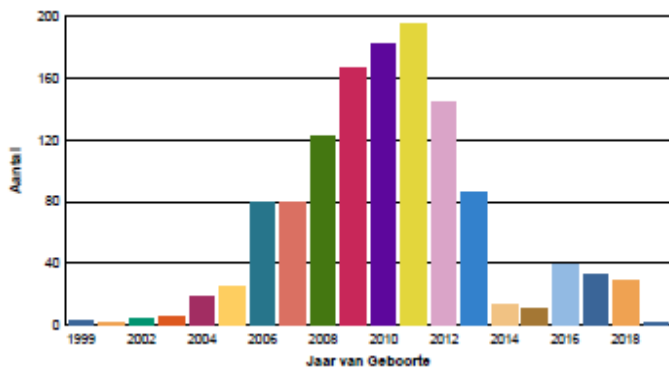


Figure 4: Genotyped Jersey cows (left) and bulls (right) per year of birth

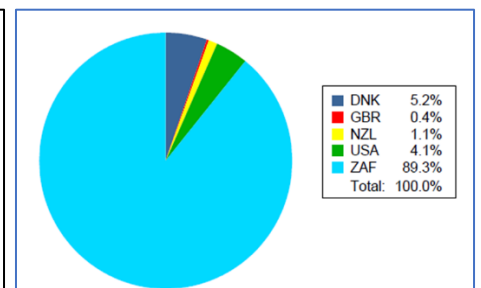
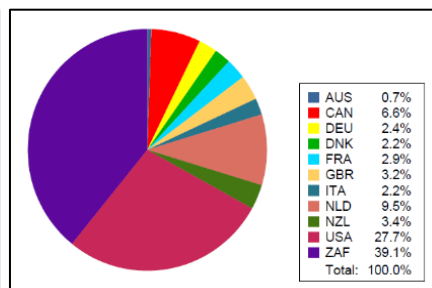
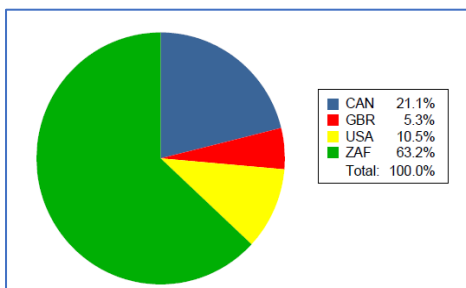


Figure 5: Genotyped bulls per county of birth: Ayrshire (Left), Holstein (middle) and Jersey (right)

SA Studbook's Genomic Selection Service also tests for several single-gene traits. Heterozygotes (carriers of 1 copy of the gene) and homozygotes (carriers of both copies of the gene) have already been identified for DGAT1 in Holstein and Jersey, BLAD and DUMPS (heterozygotes) in Holstein, Yellow Milk Fat carriers in Jersey, carriers of the Celtic polled gene in Jersey, carriers of haplotypes (HH1, HH3, HH5 in Holstein and JH1 in Jersey) and heterozygotes as well as homozygotes for Beta-Casein (A1A2 and A2A2 milk).

The genotypes obtained from SA Studbook's Genomic Service became part of an official, secure Genomic Database for the breed in question, on which valuable, purposeful and applied research can be done in the future for our South African dairy breeds.





There is light at the end of the tunnel!

Suretha Francis

Excitement and disappointment are both parts of farming, whether you like it or not

All good (rain, lower feed price, exciting new bulls) or bad things (your favourite cow is sick, drought, etc.) can affect daily life on the farm. The important part, however, is a long-term plan for the farm, and although small adjustments may be necessary, you should stick to the plan, no matter what happens. Your plan is what keeps you on track. Three essential things can make or break your plan. It is **PLANNING, FOCUS, and EXECUTION**. A well-thought-out plan will ensure that the direction in which the farm is heading, is clear. It sets goals, which show financial survival and the path to success. When it comes to sports, we all know how things can go wrong when a team goes on the field without a well-thought-out plan.

The next point is FOCUS. How often do we see a team lose focus on the field when things go wrong? The things that cause one to lose focus are not necessarily always negative things. It is often the good things that make one lose focus. You think you're in a better position than you are. It is therefore essential to focus on the core factors important for achieving the plan. A good example is, if you start running with the ball without realizing that your back line is not formed properly, it will get you nowhere. Losing focus means removing your eyes from the goal. Stay focused on the end goal.

Execution is the last piece of the puzzle. Nothing can be achieved without the proper execution of the outlined plan. The ability to execute the plan will determine everything. Execution is relatively easy with a proper, focused plan. Without Focus, implementing the plan would be difficult.

Planning, Focus, and Execution go hand in hand. One cannot do one without the other. This is also the case with Purposeful Breeding and Selection. Every breeder must know where they are at the moment in terms of critical factors, to be able to plan where they are going. There can then be a focus on the end goal and the execution of the plan.

Where is your herd headed? It's heading in a specific direction. The answer to the question is twofold. One is to look at the direction in which your herd needs to move to stay relevant and economically efficient. What are the goals you have set for your herd? One such example is to breed fertile and long-living cows, which also have high production.

However, it is important to determine the point of departure. The strict selection of animals, progressive mating practices and the unique characteristics of a breed or herd all play a role in the progress that will be made.

The basic starting point is to know the genetic composition and level of the female animals in your herd. It can then be determined which traits are of economic importance, to compile a plan and set goals to ensure progress. It is important to keep in mind that the results will not be achieved overnight, but only over generations. It is therefore important not to constantly change goals, but to stick to the long-term goal with small adjustments. An example is the establishment of standards that bulls must meet that will be used in the herd. Bulls must be selected with the breeding goal of the herd in mind. The selected bulls should be superior for the specific traits and be able to breed improved progeny. It should also be noted that definitions of certain traits differ between countries and are therefore not directly comparable with each other. SA Dairybulls (www.SADairyBulls.com) is also a platform that is available to compare international bulls on a South African basis. This platform offers breeders the opportunity to establish their purposeful breeding policies, and accelerate genetic progress. It should be borne in mind that a very broad goal will result in slower genetic progress, while a goal to improve specific traits in the herd may result in faster progress.

With new technology at our disposal, selection can be even more purposeful. With genomics, animals can be selected at a younger age with higher accuracy breeding values. By having animals genomically analysed, the breeding values are already more accurate at a younger age, because their genomes can be compared with measured animals in the reference population. A further advantage is testing for single-gene traits, for example A2 milk, infertility haplotypes, coat colour variants, bulldog dwarf gene, horns / polled, kappa casein B and E variants, BLAD and DUMPS, Brachyspina and CVM. Parentage verification is also more accurate and can be done simultaneously if the parents' genomic analyses are available. This can be of great help in multi-sire matings.

It has the advantage that it is also possible to select secondary traits such as health and longevity. However, clear goals will have to be set. It is also of the utmost importance that the breeder will measure the specific traits to be able to determine progress.

It is therefore clear that a very specific breeding goal is of great importance for a herd's survival. Animals that were effective in 1990 are not necessarily effective in 2019. Genetic progress has taken place and traits have been selected. The animals that will be effective in 2030 will also be different from the animals of 2022. So here is an opportunity to start now and focus on the future.

For any further information or assistance in establishing a breeding goal specific to your herd, you are welcome to contact your Studbook advisor or me.



Advantages of Genomics for Small Stock Breeders

Dr Helena Theron

There are several advantages when testing animals genomically, like accurate parentages, detection of single genes, and more accurate breeding values for difficult traits.

Accurate Parentage

While traditional parentage determination with DNA uses only a few markers, thousands of markers are available with genomics, so that even closely related sires (father-son or full brothers) could be differentiated, provided the parents are also genomically tested.

Detection of single genes

A lamb receives two versions of each gene (one from each parent). Some single genes cause wanted or unwanted traits when present in an animal and these single genes can be detected with a genomic test. The genes available for testing on the current chip are listed in Table 1. Note that some genes are recessive, which means the animal must receive the affected genes from both parents to show the trait (homozygous). If the animal has received only one affected gene, it is known as heterozygous and it might or might not show signs of the condition, depending on the specific gene.



Left: The Callipyge gene causes lambs to develop large and muscular rumps and is also known as the 'beautiful buttocks' gene. The lamb second from left is normal. Right: Sheep showing double muscling due to GDF8.



Left: Spider lamb syndrome. Top Right: The Booroola gene causes increased ovulation rates and litter sizes.

Table 1: Single gene traits that could be tested for on the Small Stock Genomic SNP Chip.

NAME	EFFECT
BCO2	Yellow fat
BMP15 Fec Xb Belclare	Increase ovulation rate +1; homozygote infertile
BMP15 FecXG Galway	Increase ovulation rate +0.7; homozygote infertile
BMP15 FecXH Hanna	Increase ovulation rate +1; litter size +0.6; homozygote infertile
BMP15 FecXI Inverdale	Increase ovulation rate +1; litter size +0.6; homozygote infertile
BMP15FecX Gr Grivette	Increase ovulation rate; homozygote not infertile
Booroola	Increase ovulation and litter size
CLN6 Batten disease	Neurodegenerative disease
CLPG	Callipyge gene; causes large, muscular rumps
DGAT1	Increases intra-muscular fat in mutton and fat content in sheep milk
FABP4	Associated with meat tenderness
GDF8	Causes double muscling syndrome
GDF9G8	Causes double muscling syndrome
PYGM	McArdle disease, which causes fatigue and muscle pain - recessive
Spider lamb syndrome	Recessive genetic disorder that causes skeletal deformities

GEBVs

GEBVs (Genomically enhanced EBVs) are estimated by including genomic information in addition to the performance and pedigree information of traditional EBVs. This is especially useful for so-called 'difficult traits' like Fertility, Maternal traits and Longevity, as accuracy increases at a younger age. So even if the animal itself has not yet been measured for the trait, more accurate selection is possible. It also opens the door for estimation of GEBVs for new traits like Adaptability, Disease resistance and Wool & Meat Quality traits.

Other advantages

Genomic analysis can also be used to determine for example breed purity or connectedness between herds. It could also be used to control inbreeding on a genomic level.

Right: A carcass with white fat (normal) and one with Yellow Fat.



Conclusion

Genomic analysis is a new science that opens new possibilities. Breeders are advised to store DNA samples of important animals for future reference.

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Feed Efficiency Tests for Small Stock

A Feed Efficiency Test is a test where a ram's growth (ADG or average daily gain) and feed intake are measured to scientifically determine its genetic potential for growth and feed efficiency. Feed efficiency, also known as Feed Conversion Ratio (FCR), is the amount of feed an animal needs to gain a kg of body weight and is, therefore, an indication of the animal's profitability. It is measured as accurately as possible under commercial conditions and the South African production system.

Individual feed intake and weights of post-wean rams from one or more breeders are recorded in lambing pens on farms, or at specialized test centres. Individual feed intake is measured with an electronic responder. SA Studbook Technical Advisors assist with advice and support and officially ends the test.

To qualify, animals must be registered on Logix, be without structural defects and have weaning weights. Contemporary groups, where the lambs should be the progeny of at least 2 different sires, are formed by grouping the lambs on age (differ less than 30 to 60 days) and weight (less than 15kg). The test begins with a 7 to 14-day adaptation period, followed by a growth period of at least 35 days, but could last up to 56 days, if the animals grew poorly.

Feed Efficiency & Growth Indices for the participating rams are used for breeding more efficient animals, by distinguishing the better animals from the poorer ones. The information is stored on Logix and thus becomes part of the breed's information that is included in genetic analyses for the estimation of genetic merit.

The breeder can rank his animals according to performance for feed conversion ratio (FCR) and ADG. Together with information from the weaning indices, the breeder can select well-balanced, profitable animals. Average and above-average indices are acceptable and these rams can be used for breeding and to genetically improve the herd's efficiency. The growth and feed conversion vary between 200g and 600g and FCR between 3.5 to 8 kg feed for 1kg weight gain. There is therefore a lot of variation available for genetic improvement.

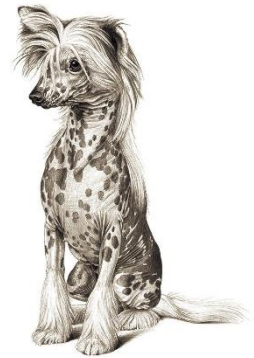
Correlations, heritability and trends over generations: ADG and feed efficiency are moderately heritable traits. Genetic improvement in the progeny is observed when breeders continuously use above-average rams as sires. Progeny will therefore perform better on average in feedlot conditions, with a cost-saving on feed in the feedlot due to improved efficiency.

Benefits: The breeder can make informed decisions and be profitable. Good breeding material can be provided to the commercial breeder by producing lambs that will be more profitable. It is an additional tool to improve the efficiency of the herd and population and thus improve the industry.

For more information see the [Small Stock Feed and Growth Test Guidelines](#).

Gene Action

The book *Unnatural Selection*, (Princeton University Press, 2018) beautifully illustrated by Katrina van Grouw and reviewed by Alison Abbot, (<https://doi.org/10.1038/d41586-018-05689-7>) pays homage to Charles Darwin's *The Variation of Animals and Plants under Domestication* on its 150th anniversary. More than 400 drawings by Katrina van Grouw show how humans has altered the appearance of domestic animals. Here are some examples.



All credits: Katrina van Grouw

Pointed guinea pigs:

The environment can have a big influence on how particular genes are expressed. Cats, rabbits and guinea pigs, for instance, come in 'pointed' varieties, with pale bodies and darker extremities. In these animals, the variant of the gene for the production of melanin is expressed only at low temperatures, distant from core body warmth.

Patterned rabbits:

Cross a brown rabbit with a certain type of white rabbit — each colour being a dominant trait — and both spots and stripes can appear in the offspring. This demonstrates that the hereditary unit is indivisible: in the battle for supremacy between dominant genes, traits don't merge into beige. Instead, there are patches of one trait or the other.

Hairy dogs with bald patches:

Gene dominance is not as black and white as this dog. One gene can be partially dominant with respect to another, and variants of the same gene can be dominant to differing degrees. This Chinese crested dog has one recessive copy of a gene that promotes the growth of a long, silky pelt, and one copy of a partially dominant variant causing hairlessness.



Credits: Katrina van Grouw

Chicken combs:

The fleshy growths on chickens' heads come in all shapes and sizes. Some combs are barely noticeable; others, gloriously elaborate. The genetics of comb shapes are complex, involving different genes and variants, which makes breeding as much a matter of luck as of judgement.