



Centre for
Tropical Livestock
Genetics and Health

On Phenomics in Animal Breeding Programmes

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Lecture Outline

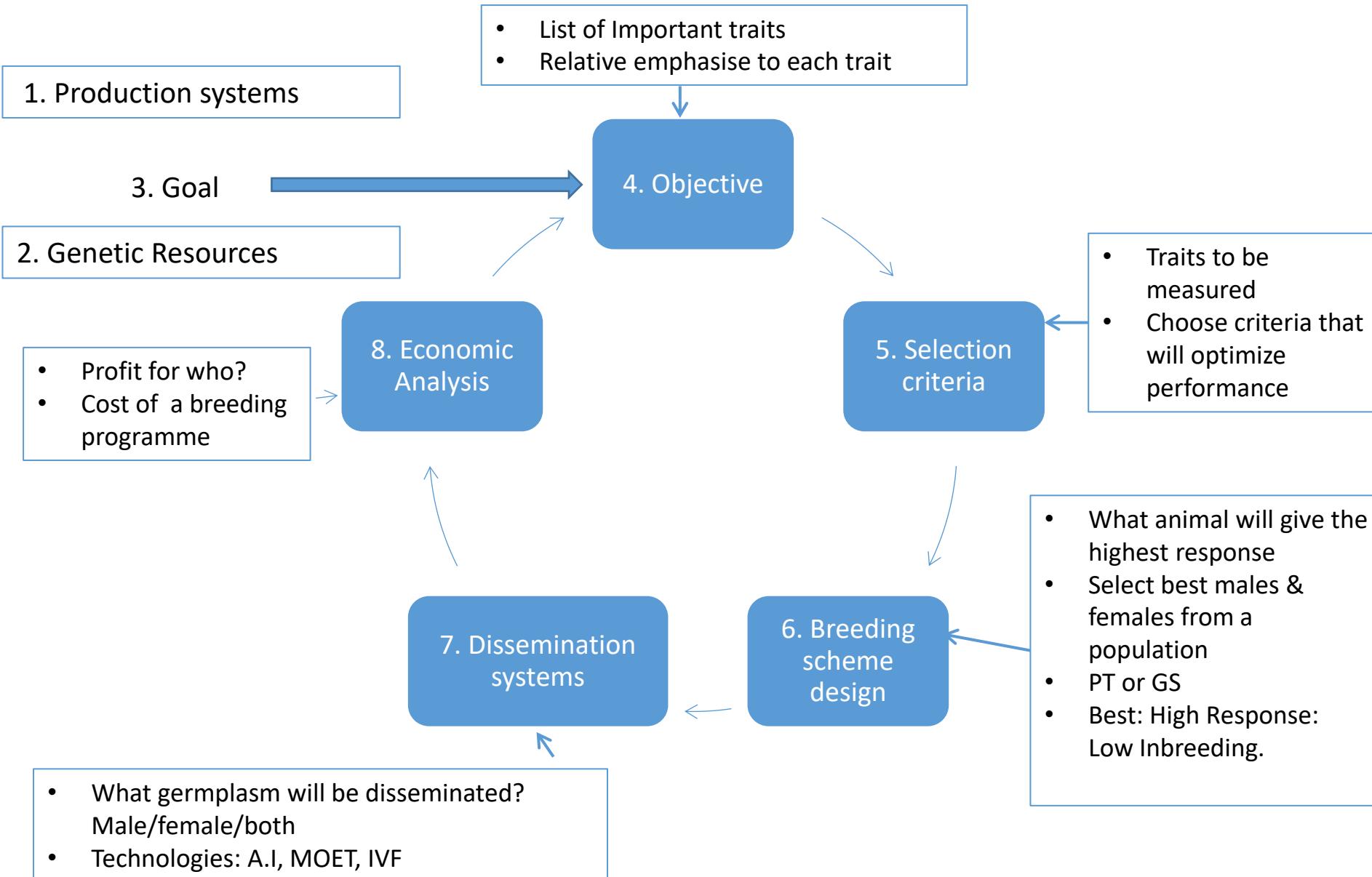
- Recap on Animal Breeding: What is the point about animal breeding?
- Traits and Phenotypes
- Phenomics



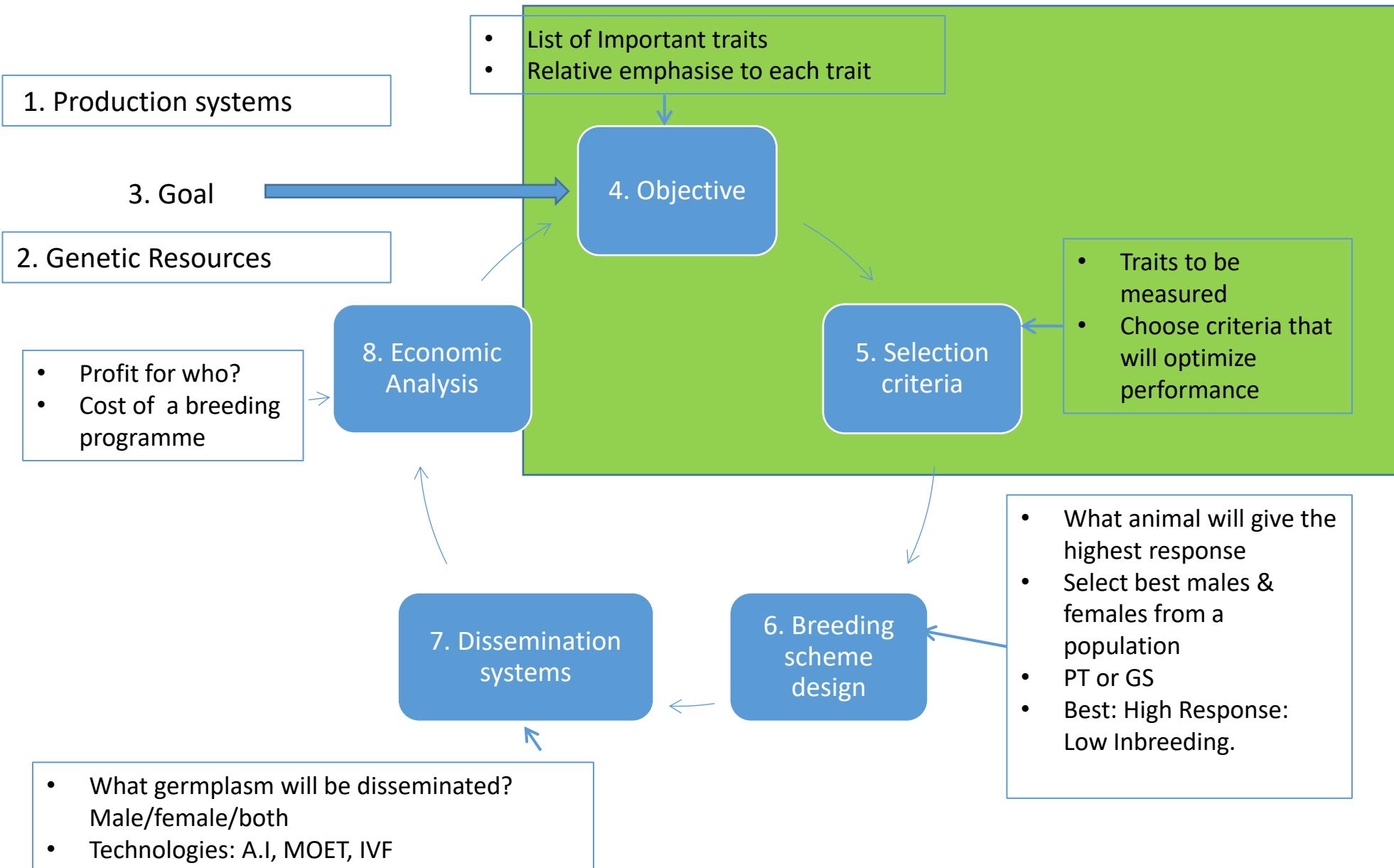
Recap on Animal Breeding: What is the point about animal breeding?

- Animal breeding is a tool to develop livestock populations
 - economical sound
 - animal welfare
- to enable
 - sustainable production of products
 - in the required quality (Herold, 2017)
- Animal breeding is a future oriented measure, the breeding objectives have to be oriented at future environmental conditions.
- (according to Simianer, 2002)

A systematic approach to the design and enhancement of breeding programs



A systematic approach to the design and enhancement of breeding programs



Data categories in animal breeding

Data types

- Production System
- Animal Performance
- Pedigree
- Genomic

Data source

- Surveys, documentation, expert opinion
- Animal lever Performance records
- Animal Level records
- Samples, lab analysis

But then we select individual animals: Estimated Breeding Values (EBVs)

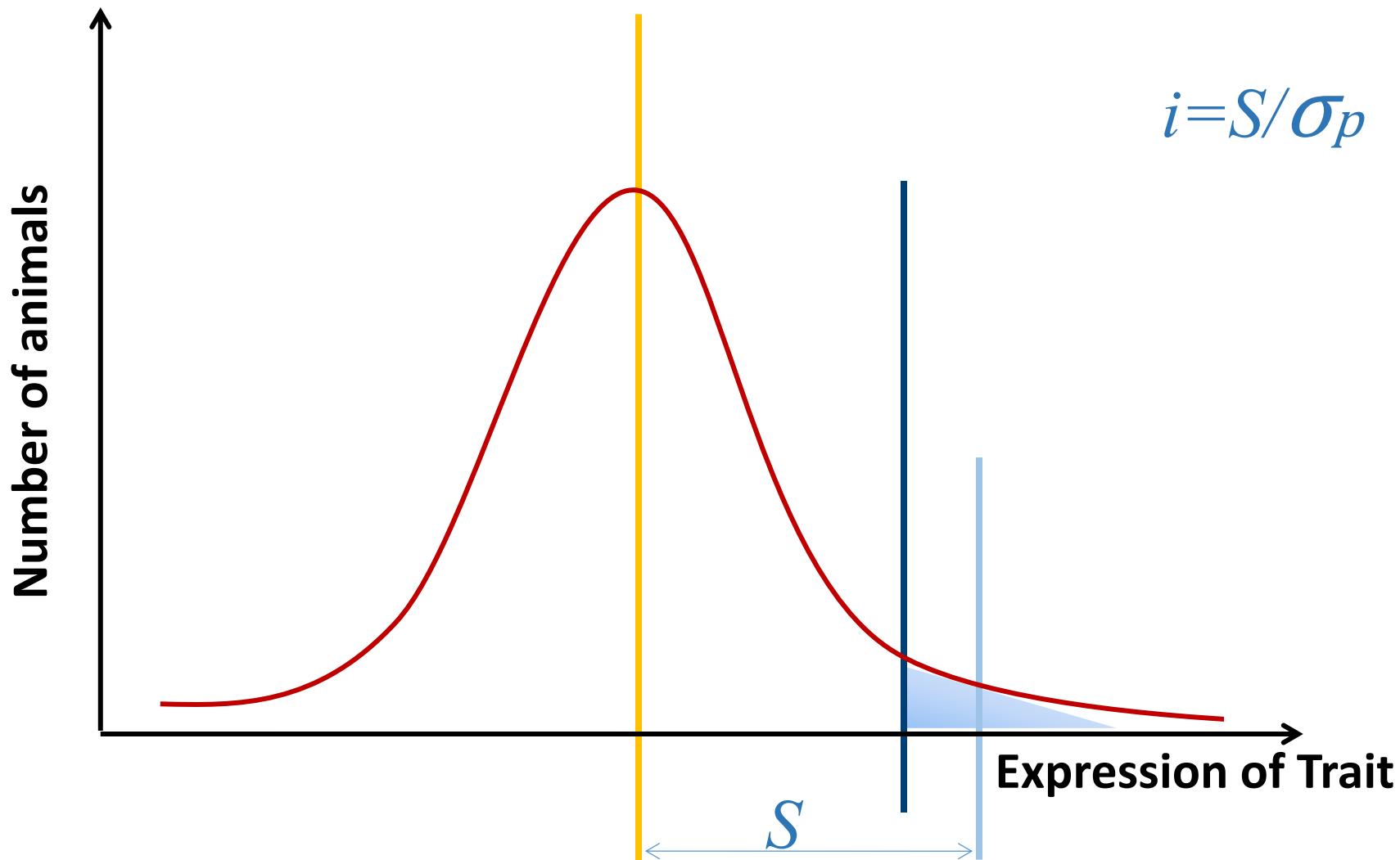
- An animal's breeding value is its genetic merit, half of which will be passed on to its progeny.
- Estimates are called Estimated Breeding Values (EBVs)
- EBVs are expressed in the units of measurement for each particular trait.
- Can only be used to compare animals analysed within the same analysis
- **Accuracy (%)** is based on the amount of performance information available on the animal and its close relatives



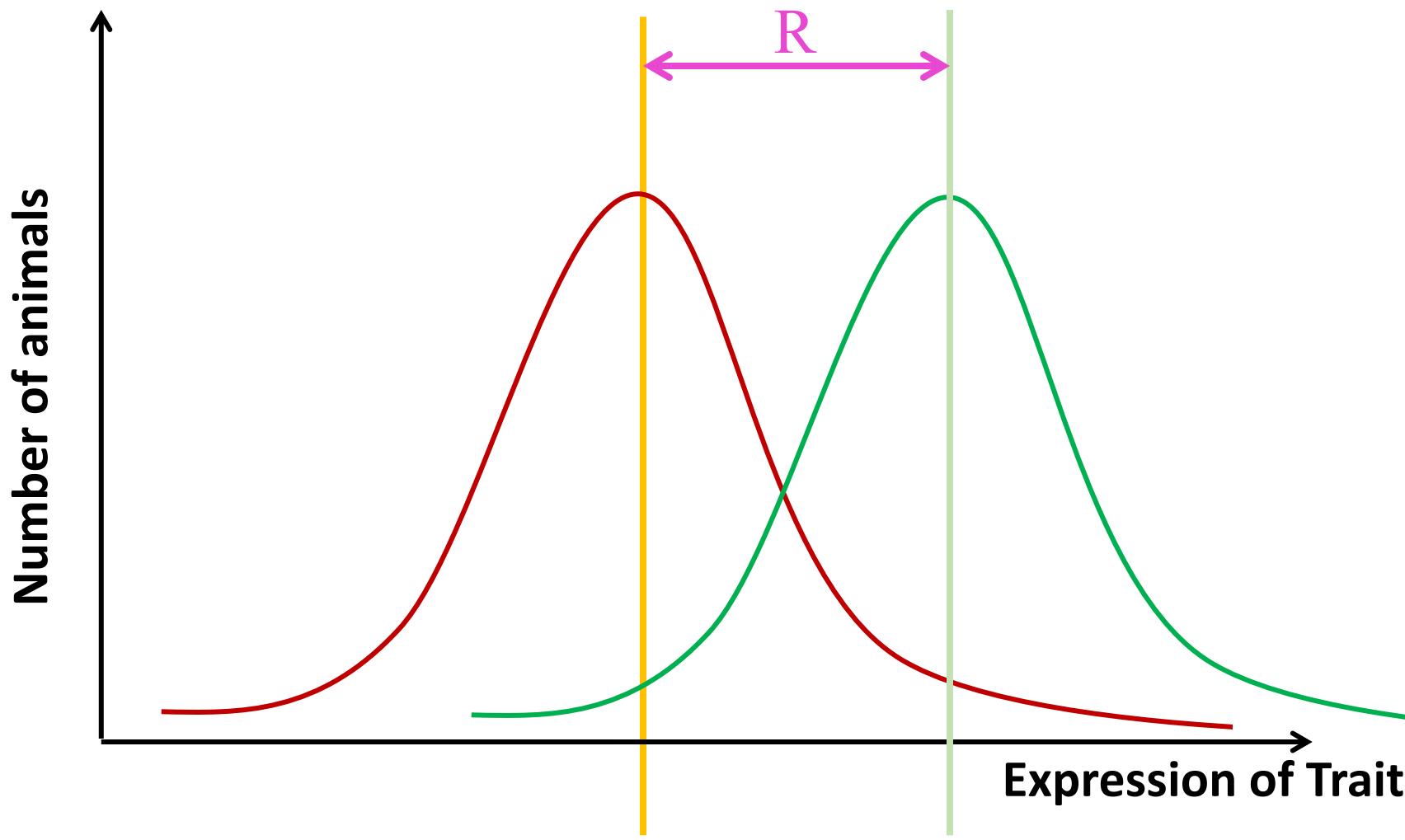
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Animal Breeding aims for progress

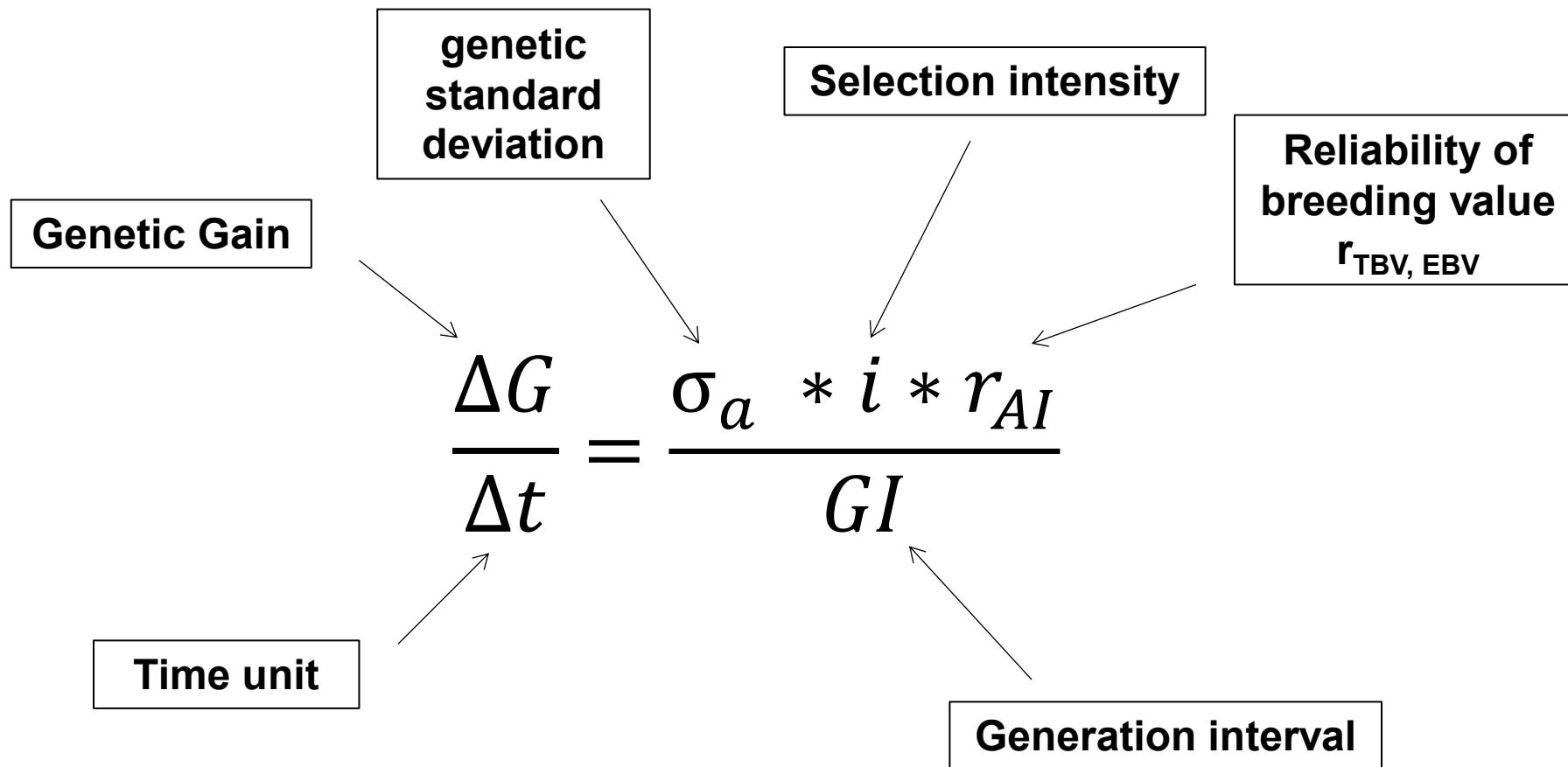
Selection intensity, Selection differential



Response to selection



Breeders equation /Rendel-Robertson-Formula



Determining Economic weight of traits



Selection index or aggregate breeding value

$$ABV = \sum w_i A_i = w_1 A_1 + w_2 A_2 + \dots + w_m A_m$$

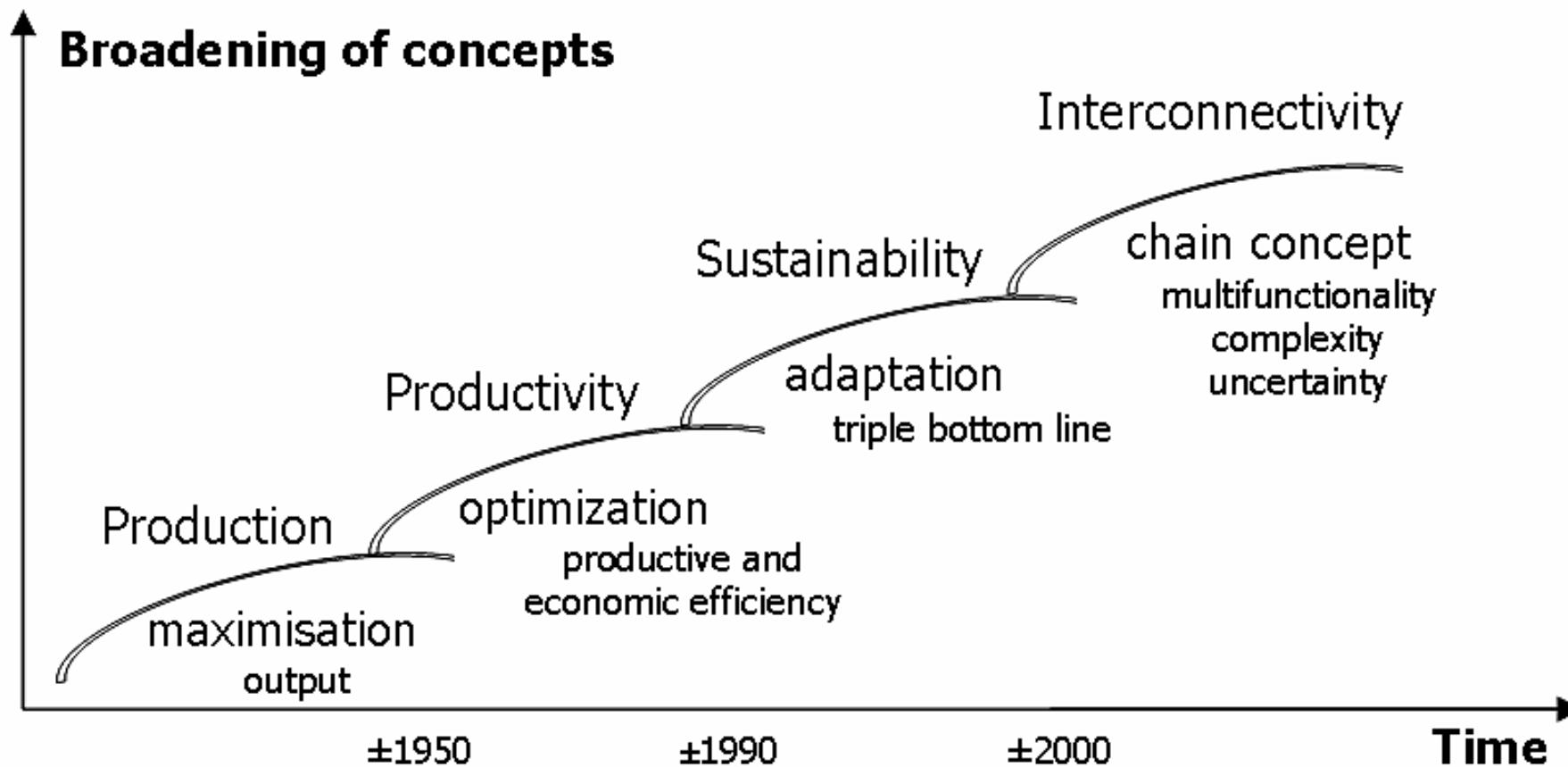
with ABV aggregate breeding value

 m number of traits within aggregate breeding value

w_i economic coefficient for trait i ($i = 1-m$)

A_i breeding value for trait i ($i = 1-m$)

Changes in priorities over time



Source: Siegmund-Schultze et al. (2010) based on Sorensen and Kristensen (1992) and Pearson (2004).



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Traits and Types of Traits

What are traits?

- The ensemble of observable characteristics or traits displayed by an organism
- Phenotypic value: the value observed when the character is measured on an individual (Falconer and Mackay, 1989)
- Traits have dimensions and can be defined in space and state

Traits

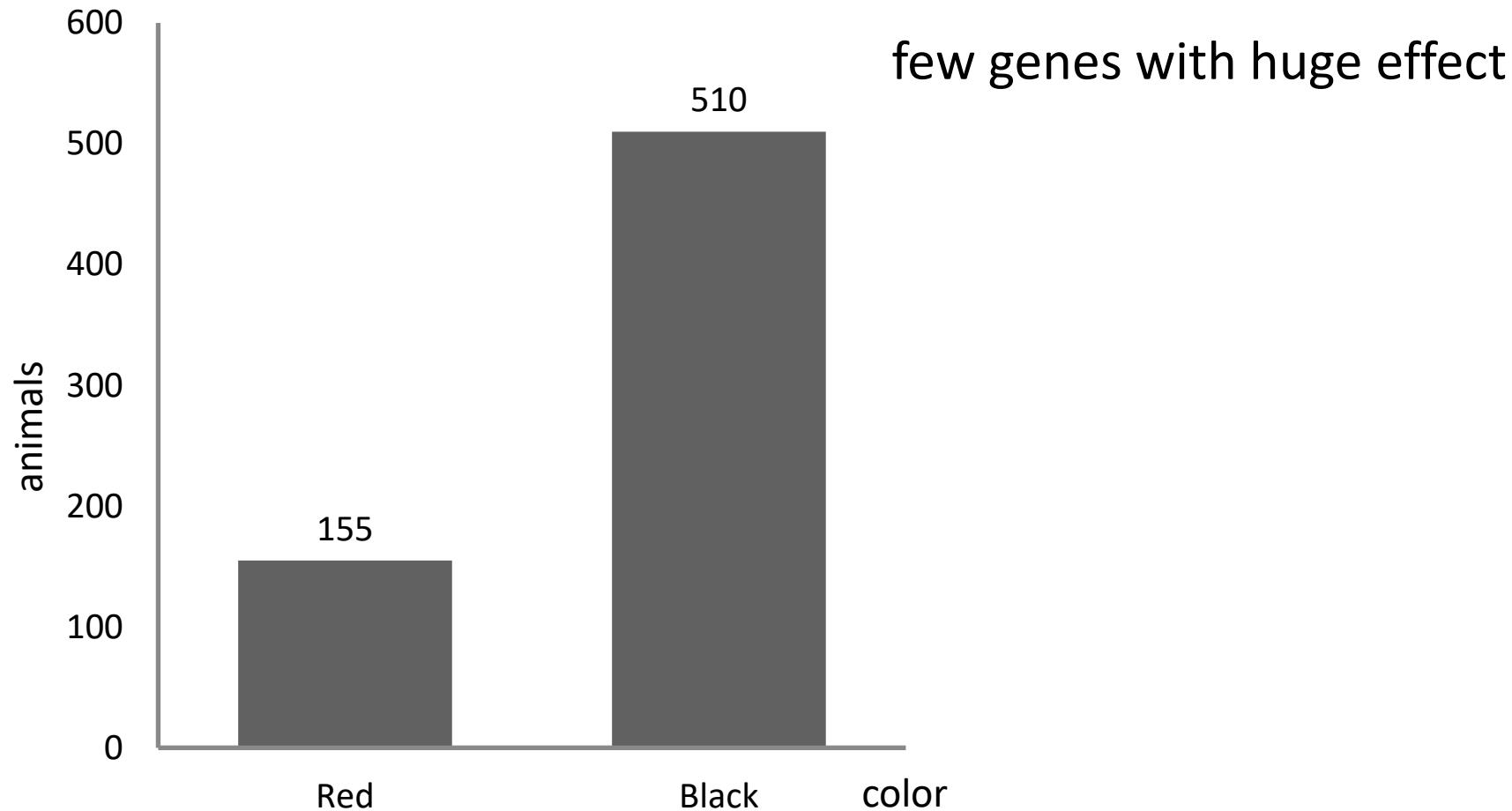
Traits should be

- Heritable (h^2); Genotype should influence phenotype
- Easy to measure, handy
- Have variation around them
- Ascertainable (derived in young age of the animal)
- Helpful if normally distributed
- Not correlated with undesired traits

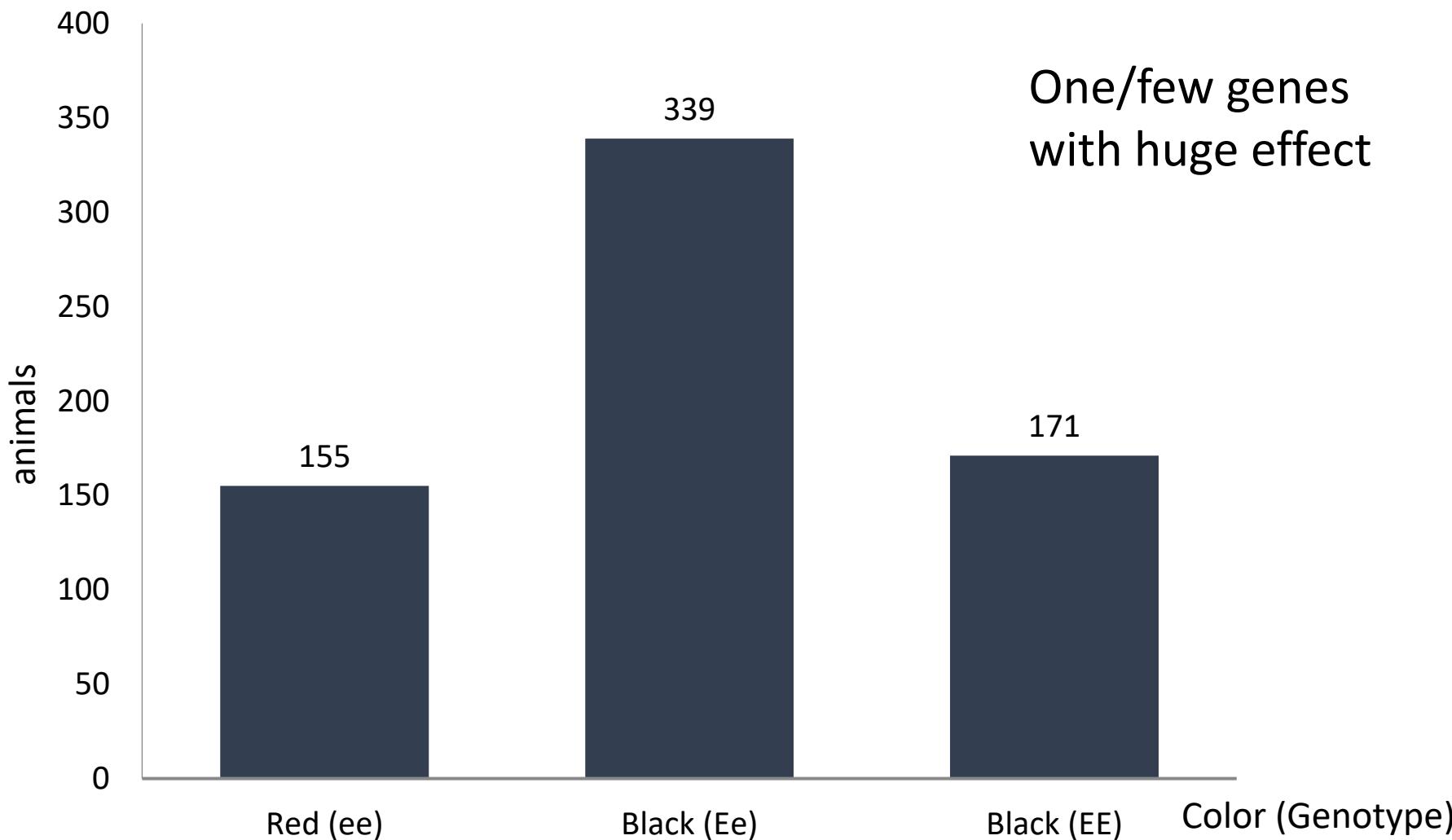
They can be tested

- Directly, on the animal
- Indirect, on relatives of the animal
- via helper traits

Qualitative Traits - *Phenotypic distribution*

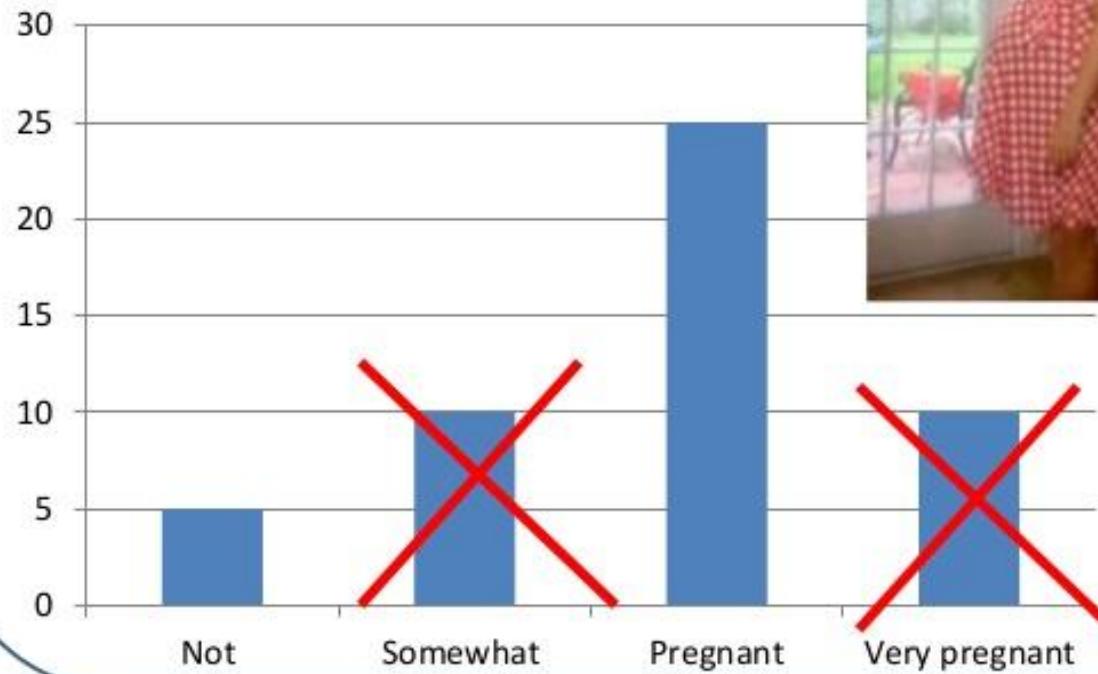


Qualitative Traits - *Genetic distribution*



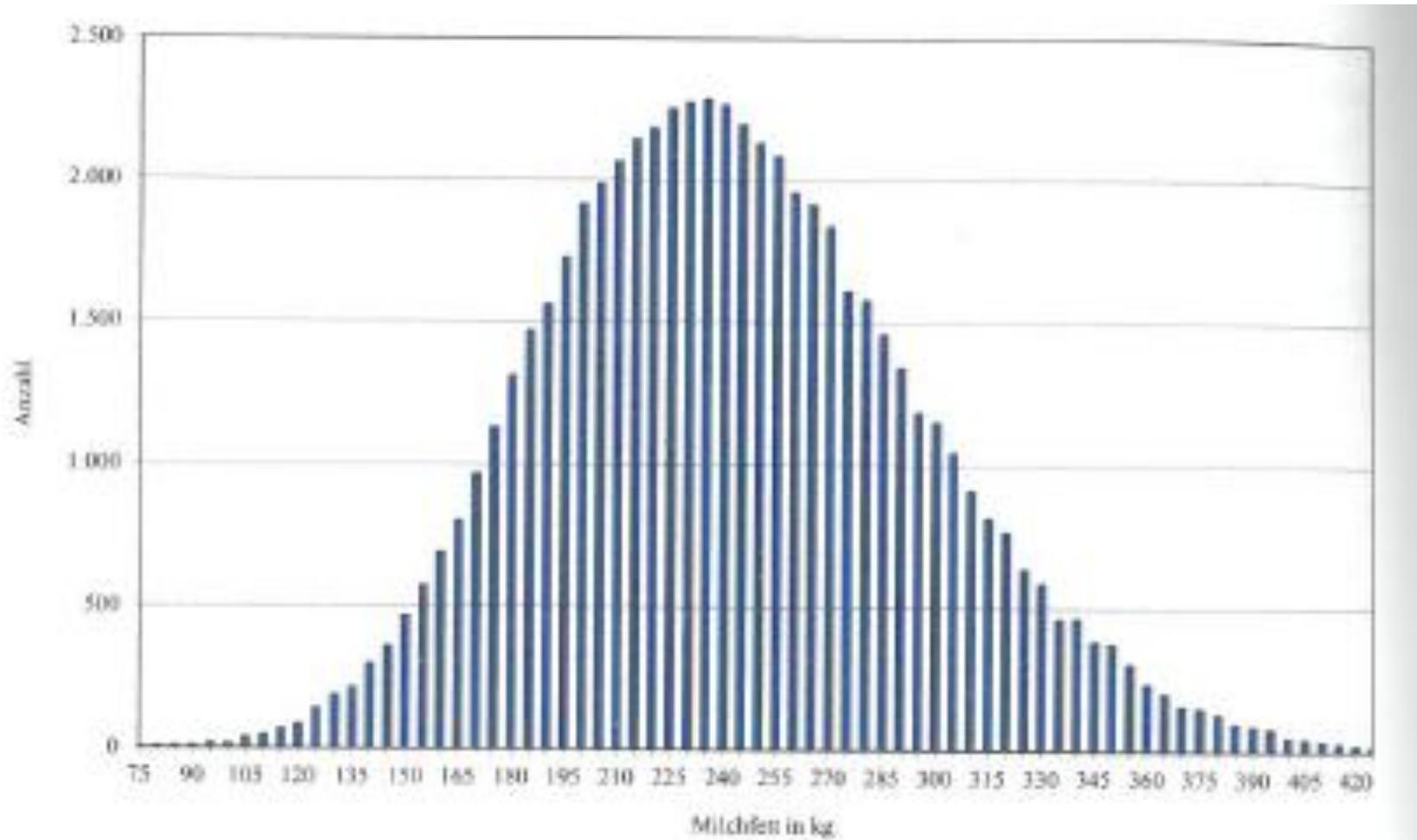
Qualitative traits

– Not “a bit pregnant”



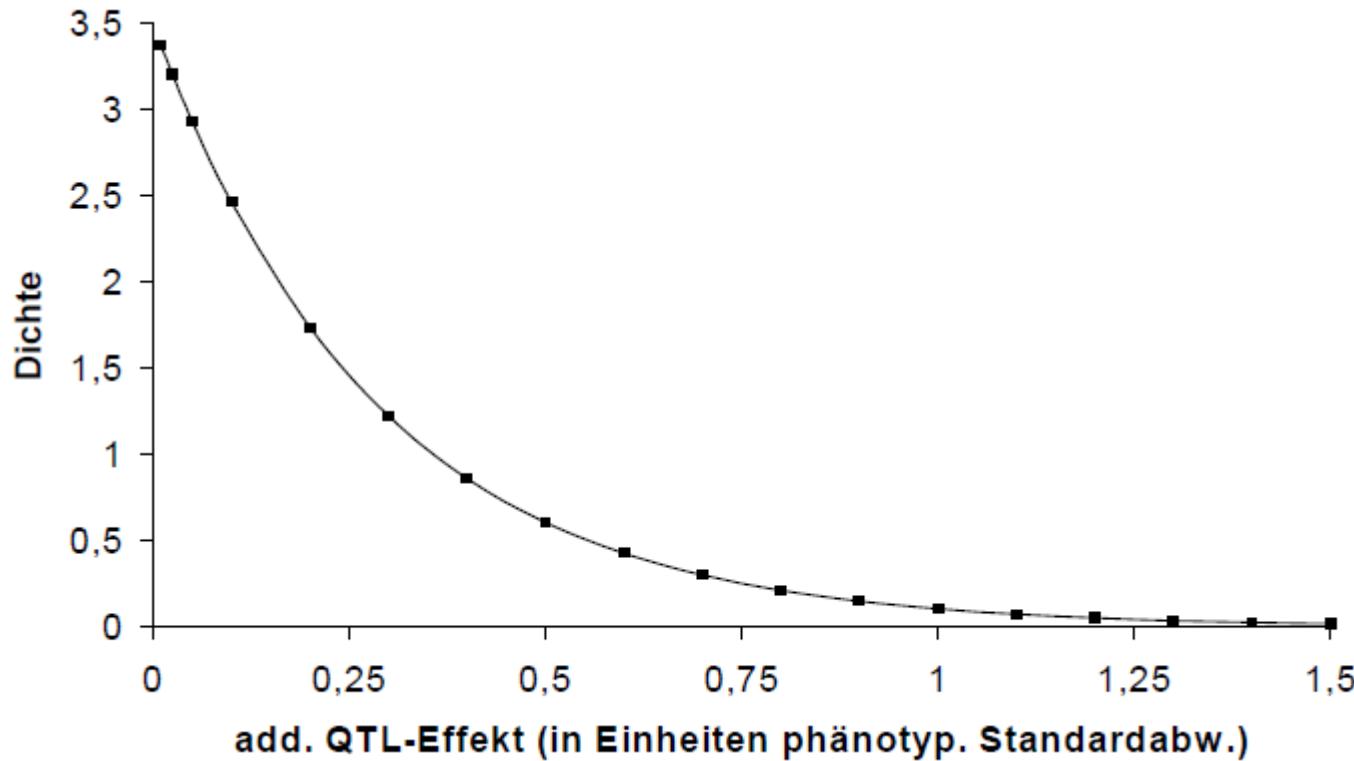
Quantitative Traits

– Phenotypic distribution



Quantitative Traits

– *Genetic Influence on phenotypic distribution*



Quelle: Bennewitz and Meuwissen, 2010

few genes/ QTL with big influence, many with small

Heritability- h^2

→ if you select, you should get response

$$h^2 = \frac{R}{S}$$

When is a trait heritable?

- If it is genetically influenced

$$P = G + E + GxE + e$$

$$h^2 = \frac{\sigma_a}{\sigma_p} = \frac{\sigma_a}{\sigma_a + \sigma_e}$$

Heritability- h^2

- Only valid for the specific population
- Only an estimation

Not heritable: 0

Low h^2 : 0.01 - 0.15

Moderate: 0.15 - 0.40 (-0.50)

High: 0.50 – 0.07

(Qualitative traits: 1)

Heritability- examples

Low: litter size (pig), hatching capability (chicken),
Non-return-rate (cattle)

Moderate: daily gain (cattle, pig), milk yield (cattle),
wool weight (sheep)

High: withers height (cattle), body length (pig)
body weight (chicken)

Heritability- examples

Low: → Fitness traits, fertility traits

Moderate: → classic performance traits

High: → skeletal traits, carcass traits

Traditional traits

- For centuries, farmers in the traditional sector everywhere in the world have used, for selective breeding, phenotypic features, such as:
 - Physical characteristics
 - Measures of yield
 - Product quality; and
 - Adaptive attributes
- For some time, animal breeding has been based on such phenotypes

Latent traits

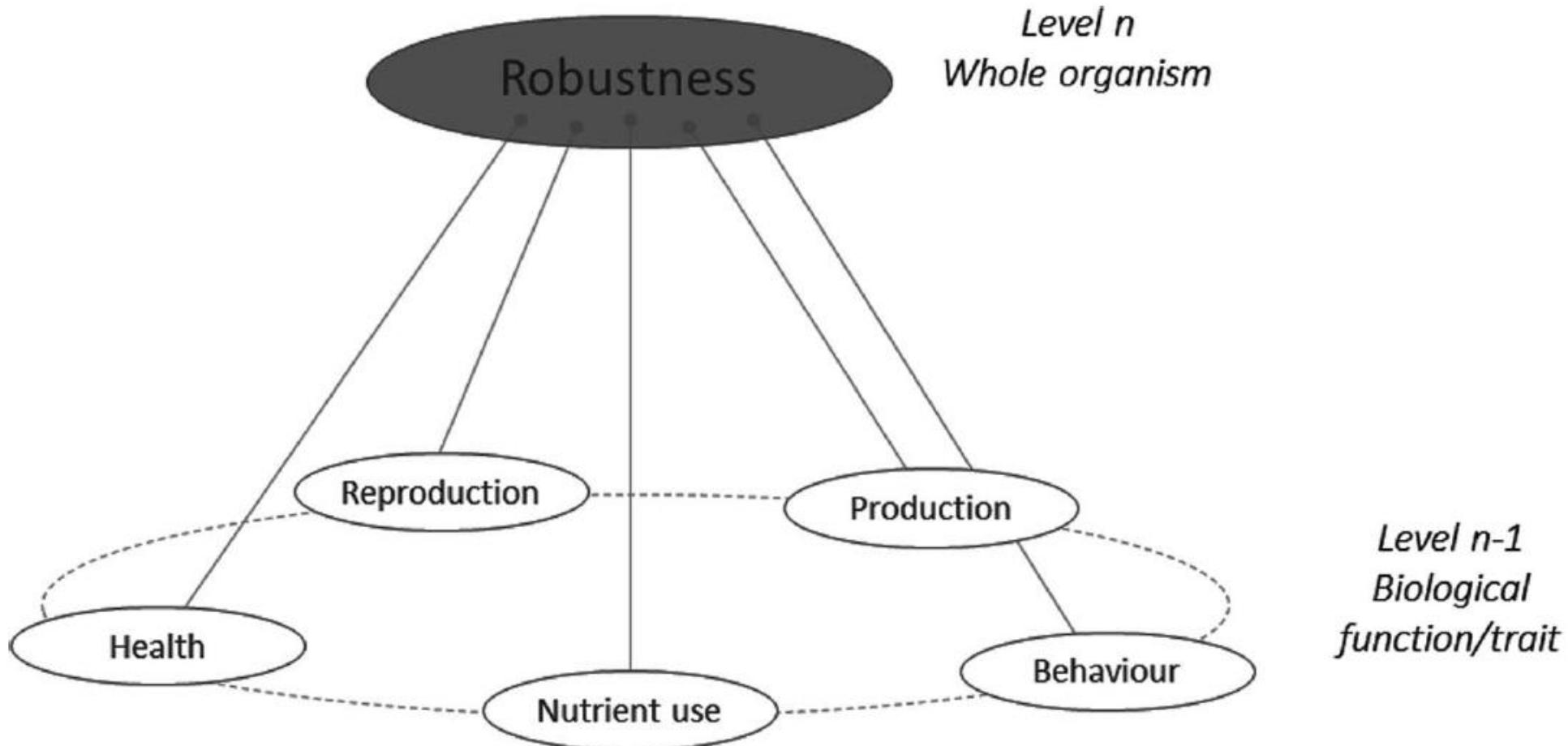
Why should we care about latent traits?

- Until now, most animal breeding programmes have used Direct Traits: those that can be measured, observed the individuals
- Latent traits: those that can be inferred from other observations
- Some indicators traits are easy to measure while their relationships with the traits of interest are so strong
- Proxies for difficult to measure traits
- Increases the accuracy of direct traits when used in combination
- Some parameters account for environmental effects
- Allow to account for traits such as maintenance in a selection index

Enablers of use of latent traits

- Developments in –omics which include elucidation of the mechanisms of genetic inheritance and epigenetic modification in key biological pathways
- Availability of genomic data
- Data from on-farm sensors that facilitate precision management
- More application of mathematical approaches and modelling techniques in animal sciences

Schematic example

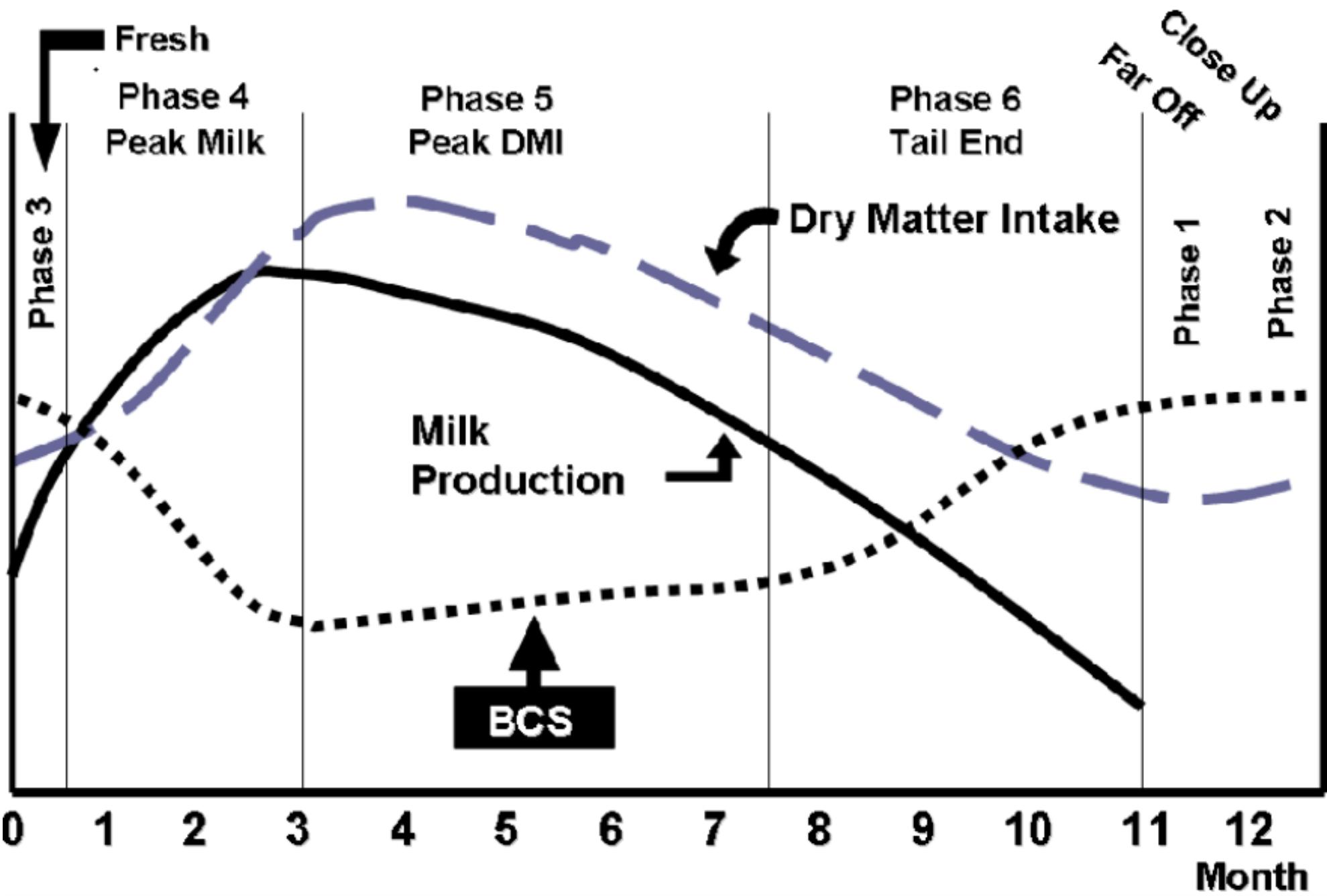


*Level n
Whole organism*

*Level n-1
Biological
function/trait*

Example of other latent traits

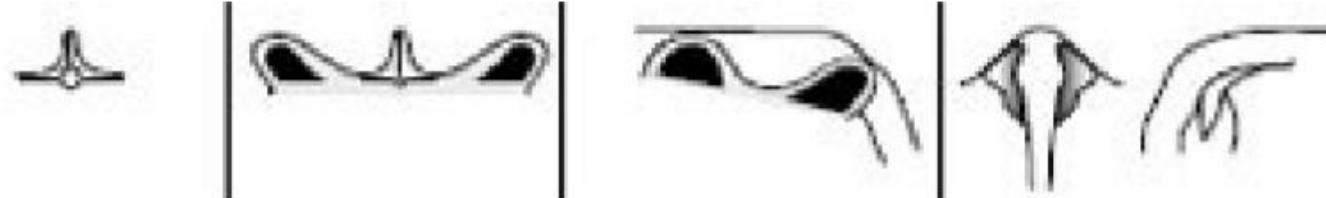
- Body condition score as a proxy for body energy content
- Feed utilisation efficiency
- Luteolysis



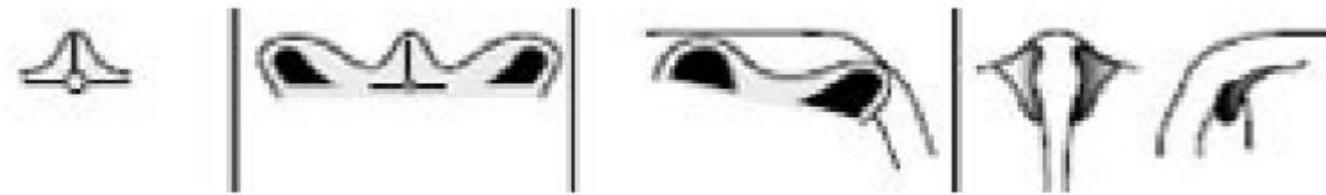
Anglart, D., 2014

	the middle of the back	(cross section) of the hook bones	the line between the hook and pin bones	tail head and pin bone Rear view and angled view
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1.
Severe under-conditioning



2.
Frame
obvious



3.
Frame and covering well

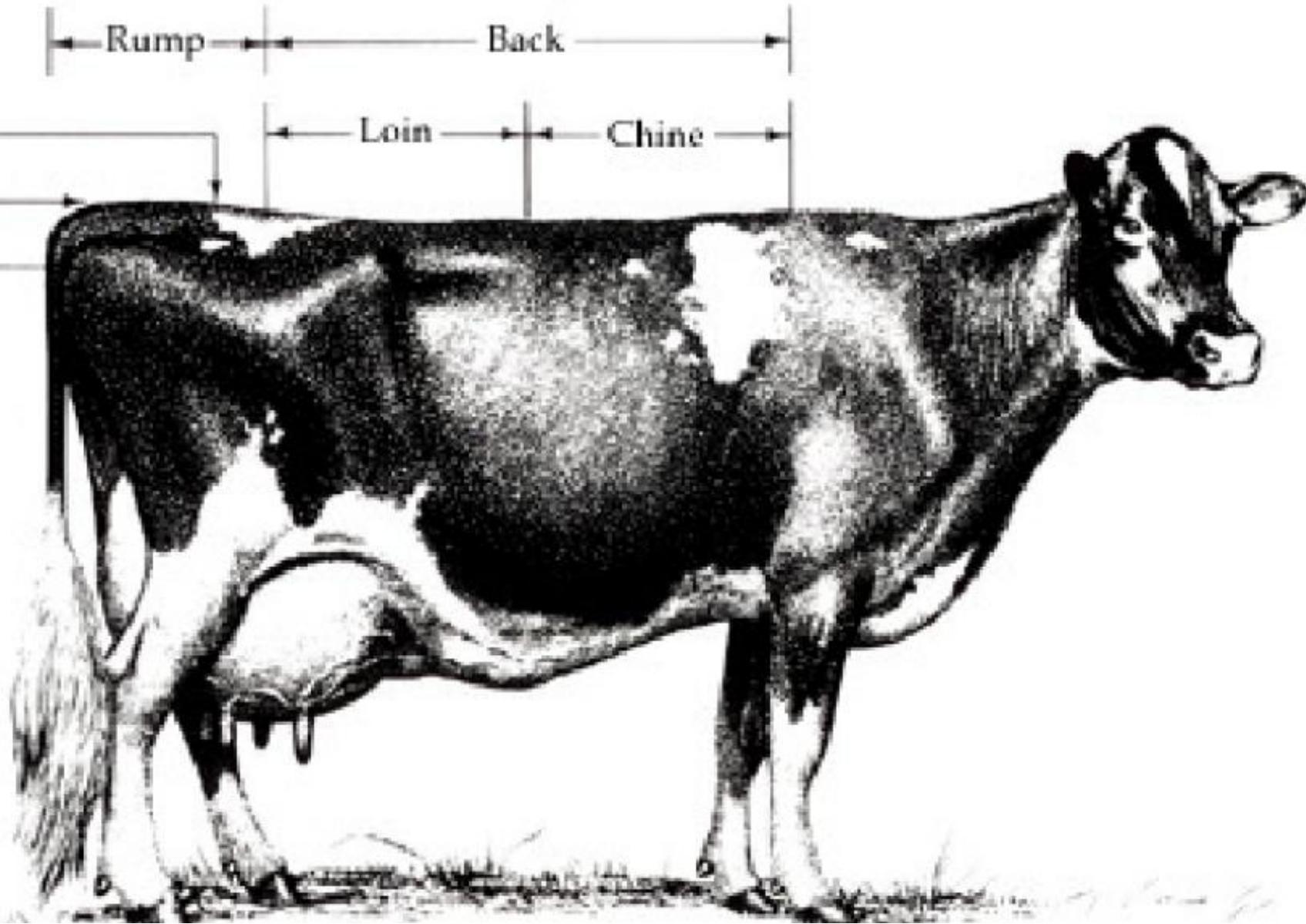


4.
Frame not as visible as
covering



5.
Severe over-conditioning





Anglart, D., 2014



Figures 3.1: View from the back (left) and side (right) of the cow. Only the back view was finally used in the project.

Anglart, D., 2014

Body Energy Content in Dairy Cattle

Calculation of daily energy content (EC)

Estimated BP and BL were combined to predict daily EC (MJ) using the following formula (National Research Council, 2001):

$$EC = [(9.4 \times BL) + (5.7 \times BP)] \times 4.1868$$

Daily body lipid (BL, kg) and protein (BP, kg) weights were then calculated as follows (National Research Council, 2001):

$$BL = (0.037683 \times BCS) \times EBW$$

$$BP = [0.200886 - (0.0066762 \times BCS)] \times EBW$$

where BCS is expressed on a 1 to 9 scale; in our data, cows were scored on a 0 to 5 scale that was converted to $[(BCS - 1) \times 2 + 1]$ and then rescaled to 1 to 9.

Body energy content can be calculated using standard equations using weekly BW and BCS (Banos et al., 2006).

Feed efficiency

Feed Utilisation Efficiency

$$\% \text{ Efficiency} = \frac{\text{Useful Energy Out}}{\text{Useful Energy In}} \times 100$$

- Feed intake
- Methane emissions
- Microbiome analysis

Other feed efficiency traits

- **Feed saved index**

An index for Saved Feed, comprises maintenance and metabolic efficiency.

Maintenance, is based on breeding values for metabolic body weight (MBW).

$$MBW = BW^{0.75}$$

- The trait residual feed intake models the metabolic efficiency
- In order to improve the gross efficiency of milk production not only the residual feed intake is important, but also to which shares feed energy is allocated by the cow towards milk production and body maintenance.

Luteolysis

- In domestic animals, luteolysis is initiated by the hormones prostaglandin F_{2alpha} and oxytocin.
- Degradation of the corpus luteum will result in reduced levels of progesterone, promoting an increase in follicle-stimulating hormone (FSH) secretion by the adenohypophysis, which will trigger the development of a new follicle on the ovary.
- If pregnancy occurs, the placental hormone chorionic gonadotropin continues to maintain the corpus luteum, but in some species it will eventually degrade sometime during pregnancy.
- Luteolysis caused by increased concentrations of PGF_{2α} leads to pregnancy loss

Animal activity as an indicator of reproduction activity

- Accelerometer technology to map animal movement patterns.
- These include, the proportion of time an animal is lying, standing or active and the number of bouts
- The activity levels are calculated using a proprietary “Motion Index” measure which then indicates if the cow is considered on heat or not.

Activitiy in extensive (grazing) systems

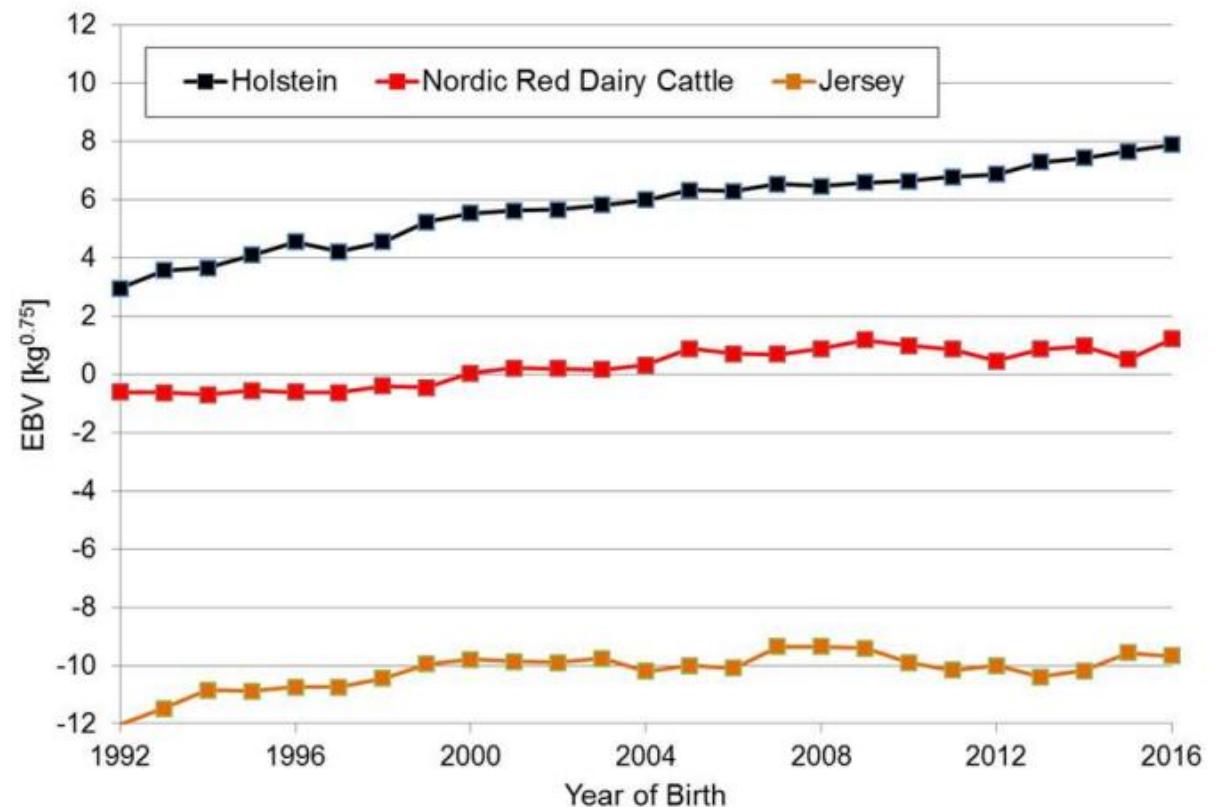
- Bull behavior can influence overall conception rates in multiple sire pastures (Blockey, 1979).
- Libido, the willingness for a bull to breed a cow, and serving capacity have been identified as factors influencing fertility and conception rates in pasture breeding operations (Blockey, 1978; Chenoweth, 1981; Crichton and Lishman, 1988).
- Days to calving is a function of both time from joining to conception and gestation length.
- Automated animal weighing technology (walk over weigh) to estimate calving date of cows under grazing environment (Aldridge et al, 2016)

Some demonstratable results: Genetic trend for metabolic body weight

Metabolic body weight is a latent trait

Genetic trend of combined estimated breeding value (EBV) for metabolic body weight in cows given by year of birth and breed.

Lidauer, et al., 2019





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Phenomics



From Human Medicine

Phenomics

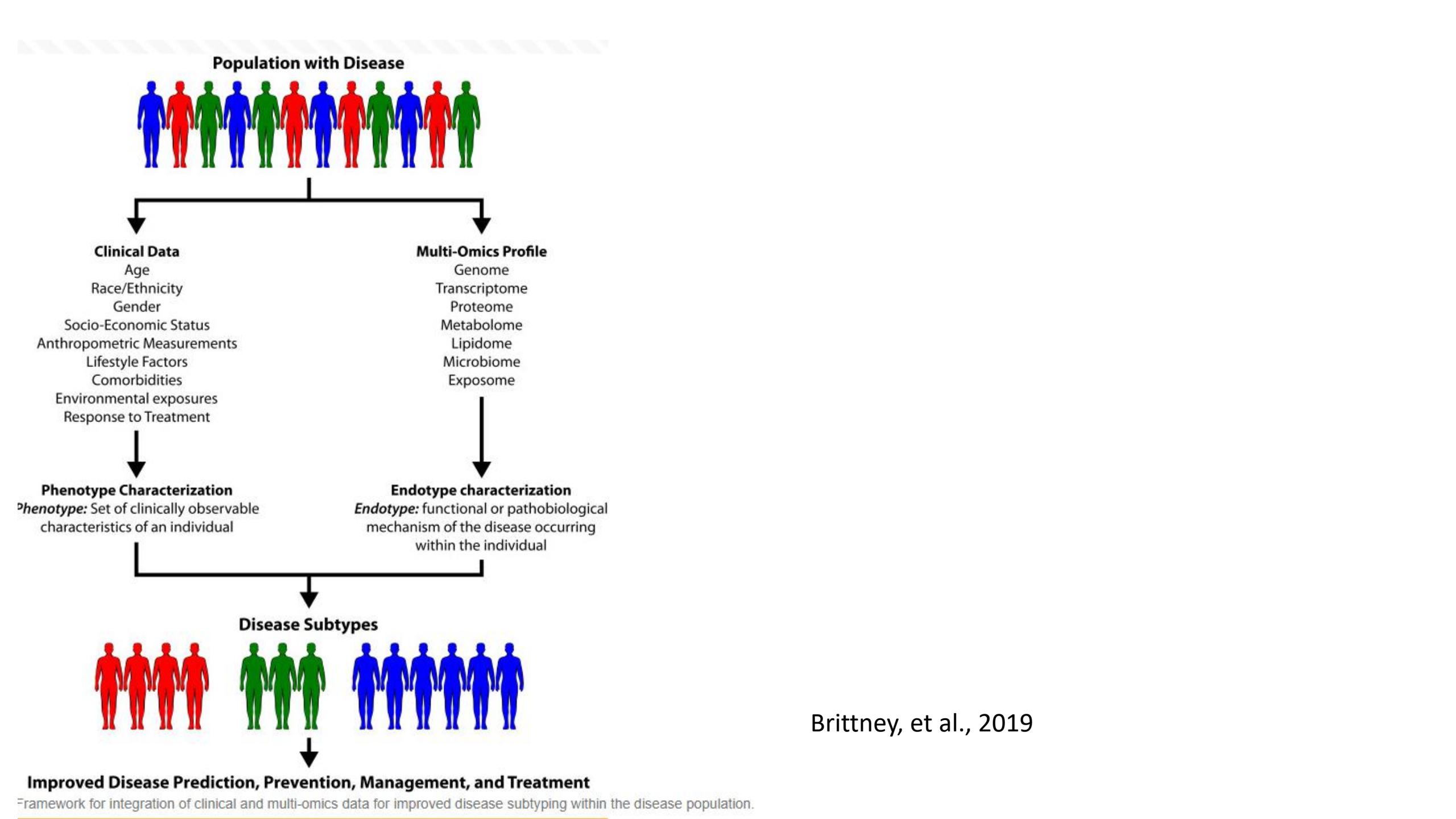
Phenomics is the systematic study of a large set of phenotypes used to describe an organism. In biomedical informatics, the phe-nome is defined as symptoms, physical findings, and disease diagnoses that describe patients for the purposes of medical care. Phenomics can be used to identify and describe disease subtypes or study pleiotropy (ie, multiple phenotypes arising from the same genetic alteration).

Bilder et al., 2009



Use of Phenomics in Human Medicine

- The electronic health record (EHR) is an important resource for the study of human phenomics.
- Compared with observational research cohorts that only capture a prespecified set of phenotypes, the EHR contains information on a vast array of phenotypes that are pertinent to medical care.
- Many health care systems now link EHR and genetic information, obtained through biospecimen collection, which has led to the development of genome-wide association studies (PheWAS).
- Although originally designed to study the relationship between a large set of human phenotypes and a single genetic variant, PheWAS applications have since broadened to assess associations between phenotypes to identify comorbidities, subtypes, or health service outcomes (eg, length of hospital stay and treatment-related complications) related to a specific disease.



Phenomics in Animal Breeding

- The current usage of the word ‘phenome’ to refer to the phenotype as a whole is due to the evolutionary biologist Michael Soulé.
- Phenomics is defined as the acquisition of high-dimensional phenotypic data on an organism-wide scale.
- Phenomic-level data are necessary:
 1. to understand which genomic variants affect phenotypes
 2. to understand pleiotropy and,
 3. to furnish the raw data that are needed to decipher the causes of complex phenomena, including health, yields, disease and evolutionary fitness.

Need for phenotypic information

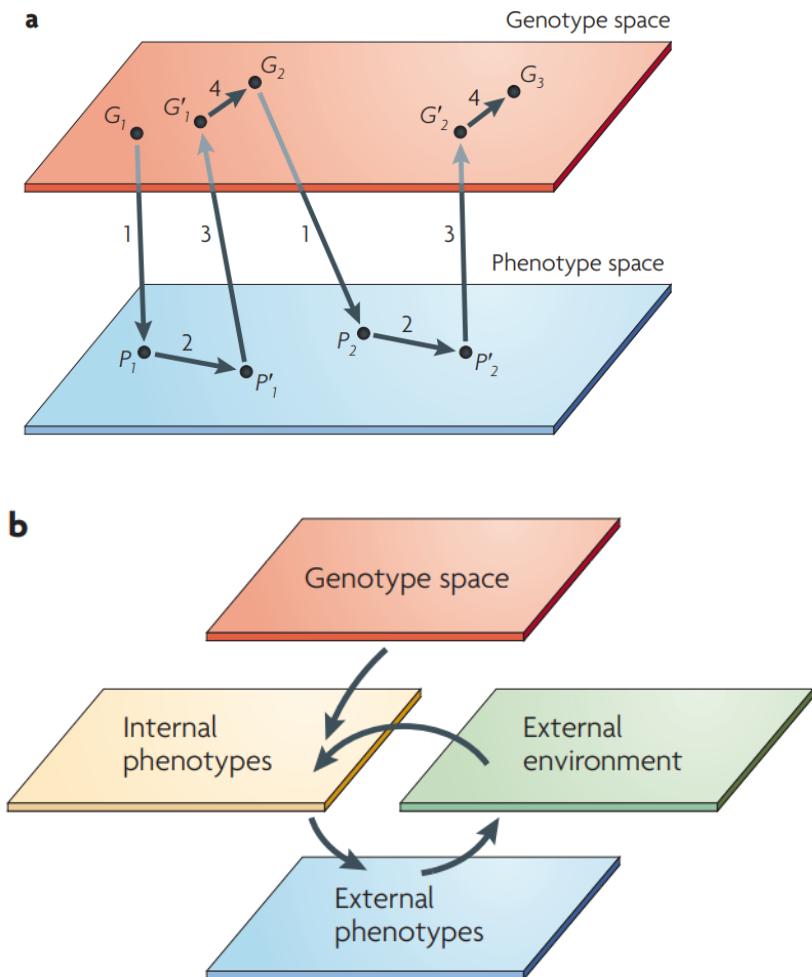
- Phenotypic information may be more informative to the farmer and the policy-maker than a list of genetic associations.
- The simplest justification for phenomics is that the characteristics of organisms of greatest interest to most biologists are phenotypes rather than genotypes.
- Examples of some crucial phenotypes include morbidity, mortality, reproduction, yield, efficiency, resistance to pests, parasites and disease; and the ability of species to adapt to human- and induced changes.

Phenome relative to the Genome

Although analyses of genomic data have been successful at uncovering biological phenomena, they are — in most cases — supplementing rather than supplanting phenotypic information

(Source: Houle et al, 2010)

Genotype-Phenotype map



- We can come close to completely characterizing a genome but not a phenotype, because the information content of phenomes dwarves those of genomes
- Phenotypes vary from cell to cell and from moment to moment and therefore can never be completely characterized.

The analogy between phenomics and genomics

- Although phenomics is defined in analogy to genomics, the analogy is misleading.
- Phenomics will always involve prioritizing what to measure and a balance between exploratory and explanatory goals.
- Continuous measurement of phenotypes generate data, a lot of data, big data
- Big data is not just about volumes but also about dimensions including time series data
- Question is? Can this be useful for animal breeding?

Opportunities

- First, technologies for high-throughput phenotyping are becoming increasingly available.
- Second, conceptual, analytical and bioinformatics approaches that enable the use of very high-dimensional data are advancing rapidly.
- Third, dynamic models that link phenomena across levels — from genes to cells, to organs and through to the whole organism — are in reach.
- Finally, in most cases, phenotypic data continue to be the most powerful predictors of important biological outcomes, such as fitness, disease and mortality.

(Source: Houle et al, 2010)

Feed intake equipment



Animal activity as an indicator of reproduction activity





Pleiotropic traits

- A situations where a single gene influences multiple phenotypic traits
- Example is where a gene affects growth rate and carcass quality, meaning that selecting for increased growth could also inadvertently impact the quality of the meat produced
- Other examples include genes impacting milk production and fertility, or those affecting body size and temperament.

Impact on breeding programs:

- Understanding pleiotropy is crucial for effective cattle breeding programs as selecting for one trait can unintentionally affect other related traits due to the influence of a single gene.

Challenges with New data in breeding programmes

- High volumes of time series data
- The application of information and communications technology, mobile phones, and other digital innovations has shown some promising results but reliable internet connectivity still poses a challenge
- Danger of double counting (when characteristics are correlated)
- Magnitude of genetic correlation between latent traits and acquisition traits may depend on the environment



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Conclusion

Understanding the phenotypes that you are dealing with, in the context that they operate is very vital if we are going to make any genetic improvement.

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