Quantitative Genetics in Comparison:

Statistical and Genomic Practices across Biomedicine, Behavioural Science and Agriculture

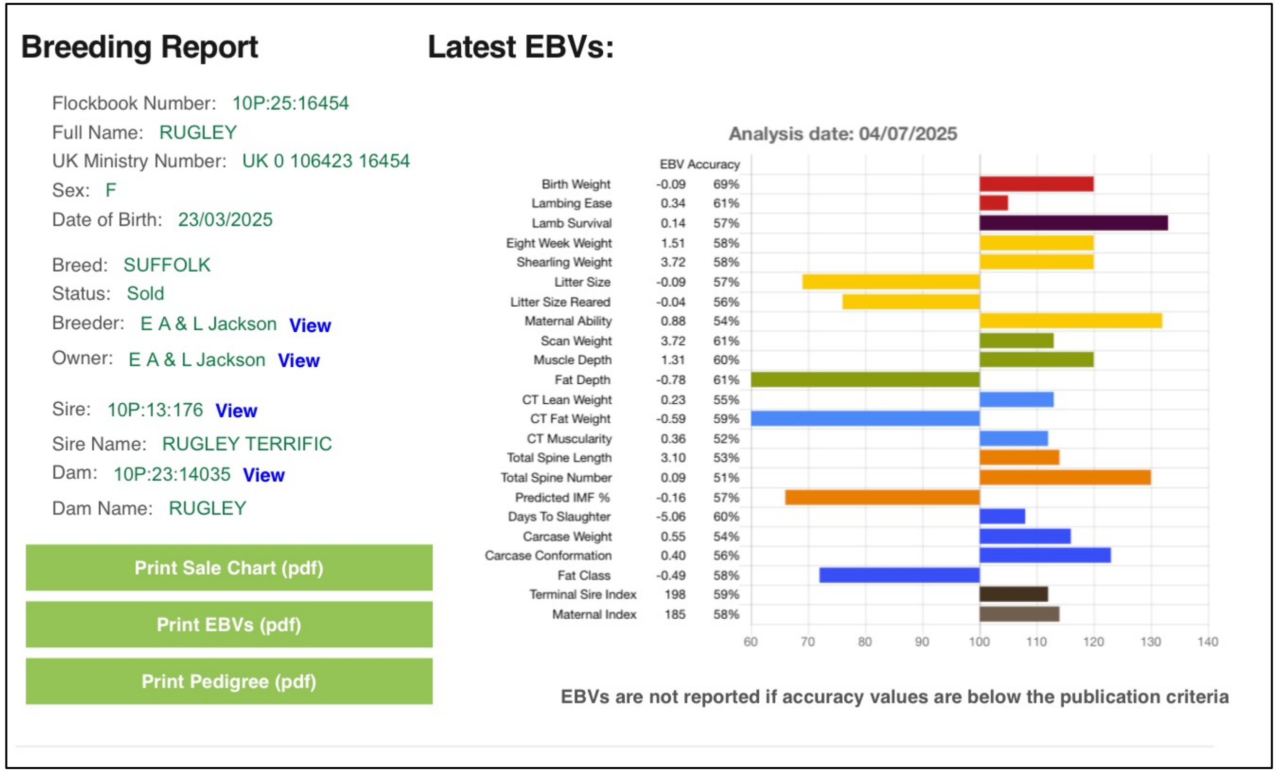
21 July 2025

ISHPSSB, Porto, Portugal

ISHPSSB25PORTO

Session Plan

1. Welcome and introduction (Hugh Williamson)
2. Human quantitative genetics: A brief introduction (Davide Serpico)
3. The field of indicators: Quantitative genetic repertoires in animal and plant breeding (Hugh Williamson)
4. Quantitative genetic practices in animal breeding (James Lowe)
5. What is so special, if anything, about genetic prediction of human complex diseases? (Davide Serpico)
6. General discussion



Breeding Report

Flockbook Number: 10P:25:16454
Full Name: RUGLEY
UK Ministry Number: UK 0 106423 16454
Sex: F
Date of Birth: 23/03/2025

Breed: SUFFOLK
Status: Sold
Breeder: E A & L Jackson **View**
Owner: E A & L Jackson **View**

Sire: 10P:13:176 **View**
Sire Name: RUGLEY TERRIFIC
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The Field of Indicators:
Quantitative Genetic Repertoires in Animal and Plant Breeding

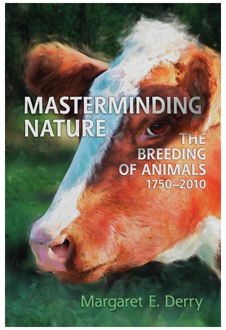
Hugh F. Williamson (Technical University of Munich)

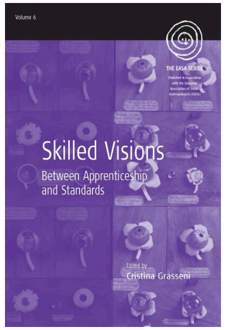
Overview

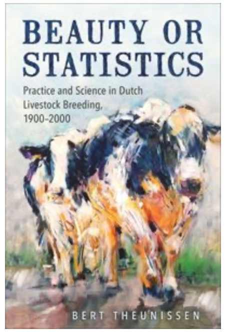
1. Current work on quantitative genetics in animal and plant breeding
2. Quantitative genetics as production of indicators
3. Three key indicators: Heritability, breeding values, genetic gain
4. Exchanging repertoires between animal and plant breeding
5. Reframing critical issues in breeding via indicators

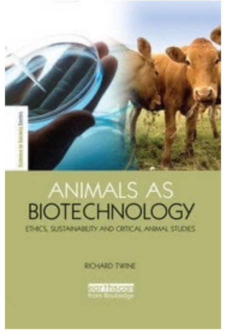
Quantitative Genetics in Plant and Animal Breeding

- Minimal literature, primarily **social sciences** and **history**, very little **philosophy**
- Almost exclusively on **animal** rather than **plant breeding**









Two key issues in critical literature:

1. Contestations over data-driven vs skilled expertise
2. Quantitative genetics as biopower over animals

Literature still not very good on defining and analysing quantitative genetics as a technical and scientific field

- e.g. Gibbs et al. (2009) simplistically equate quantitative genetics with classical genetics

Quantitative Genetics as Production of Indicators

Quantitative genetics in breeding as **production of numerical indicators** through statistical methods

- Part of wider field of indicator practices
- E.g. **material** and **visual** indicators also contribute to production of numerical indicators

Reframing critical issues around indicators:

1. Expertise issues concern breeding values in animal breeding, e.g. trust and reliability
2. Biopower issues circulate around selection index design
3. **Plus:** ambiguities around role of environment and GxE interactions

What is an Indicator?

Porter (2015: 34) on indicators:

- “Indicators detect, point or measure, but do not explain”, rather they “indicate as a guide to action”.
- Indicators “typically cannot measure the very thing of interest”—the phenomenon—"but in its place something whose movements show a consistent relationship to that thing”.

Morgan (2020: 106) on indicators:

- Indicators are “numbers that are not conceived as direct measurements of the concepts they relate to (such as the business cycle, or the health status, of a country), but are understood to be indicators for characteristics relevant for those concepts (such as, respectively, industrial production or infant mortality).”

Indicators in Quantitative Genetics

Indicators measure and analyse phenomena that have consistent relationships to the target phenomena

- In case of quantitative genetics, **target phenomena** are **genes**
- **Measured phenomena** are primarily **numerical phenotypic data**, at population level

- However, recent advances are introducing additional **proxies** for phenotypic data
    - **Molecular markers**, e.g. SNPs
    - Computer vision-driven **imaging** of phenotypes as proxy for marker profiles

“In conventional quantitative genetics, the importance of Mendelism is not that individual genes can be tracked from one generation to the next – quantitative genetics does not do this – but that Mendelian assumptions let us work out what phenotypes […] will appear in the next generation as a function of the phenotypes in the previous generation.” (Griffiths and Stotz 2013: 132)

Indicators in Breeding

Production and use of numerical indicators in breeding is focused on their assembly into **ordinal rankings** to facilitate **decision making** in breeding program design and selection of parents

Three key indicators:

I. Heritability
II. Breeding values
III. Genetic gain

These indicators are **linked** in practice, e.g. heritability values are used to calculate both breeding values and genetic gain

Indicators in Breeding: I. Heritability

Heritability expresses “the reliability of the phenotypic value as a guide to the breeding value” (Falconer and Mackay, 1996: 160)

Pragmatically, provides an indication of whether a given trait is **tractable as a target of breeding** through quantitative genetic methods.

- Without sufficient heritability, selection on a trait will not lead to consistent and reproducible (i.e. genetic) change in the breeding population

Heritability is always **relative** to specific populations, environmental conditions and phenotypic measurement methods (Falconer and Mackay 1996: 161)

Image: Sheep Ireland

Indicators in Breeding: II. Breeding Values

Value of an individual as a parent, relative to (offspring) performance for a particular trait

Used to rank individuals when selecting parents for breeding

Can be calculated for one trait, or for a set of traits via a **selection index**

- Selection indexes combine breeding values for multiple traits and **weight** them for relative value, producing one **index value**

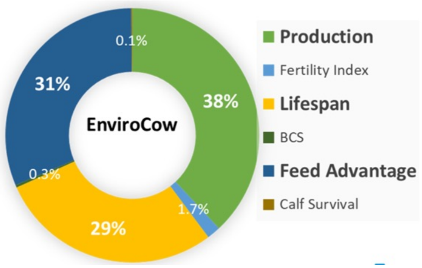


Image: British Cattle Breeders Club

Typically calculated using phenotypic data from relatives of a given individual

- **Genomic Selection** allows prediction from individuals’ genotypes (genome-wide marker panels)
- **Phenomic Selection** allows prediction of genotypes from high-throughput imaging
- Accuracy depends on **training models** with phenotypic, genomic marker and phenomic data from large, **related** populations

Indicators in Breeding: II. Breeding Values

AKA Estimated Breeding Values (EBVs) or Expected Progeny Difference (EPD) – varies with industry

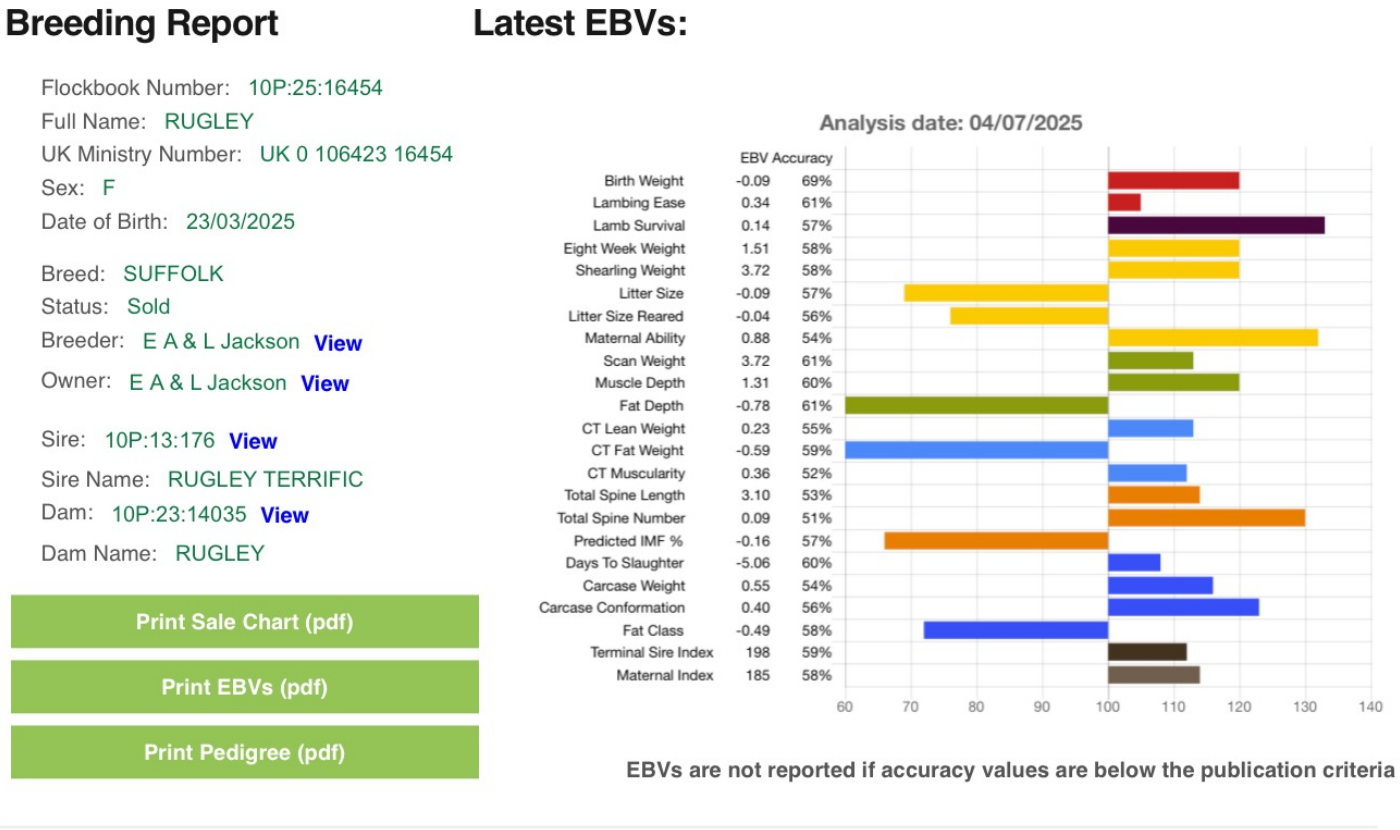


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Image: Signet Sheep Breeding

Indicators in Breeding: III. Genetic Gain

Rate of genetic gain, AKA response to selection

Indicator of the change in a trait within a population owing to genetic effects, and thus selection practices

Can be calculated as **realised** change, between historical and present populations, or **estimated** for future populations

- Realised genetic gain may be used to **evaluate the success** of prior breeding programs and is increasingly adopted as a **key performance indicator** for breeding
- Estimations are used to **compare different potential breeding program designs**, informing choice of design

Quantitative Genetic Repertoires

Repertoires: “the well-aligned assemblages of skills, behaviors, and material, social, and epistemic components that groups may use to practice certain kinds of science” (Ankeny and Leonelli 2016: 20)

Quantitative genetic repertoires in breeding:

- Three indicators, plus…
- Statistical models (mixed models, machine learning), coding skills
- Databases (phenotypic, genomic, pedigrees), data access arrangements
- SNP chips + relationships with biotech companies
- Skill in judging and using indicators in breeding decisions
- Knowledge of how to construct reliable selection indexes

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Sub-repertoires:

- **Genomic Selection**

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- Knowledge of how to construct reliable selection indexes
- **Imaging technologies and techniques?**

Sub-repertoires:

- Genomic Selection
- **Phenomic Selection**

Quantitative Genetics in Animal Breeding

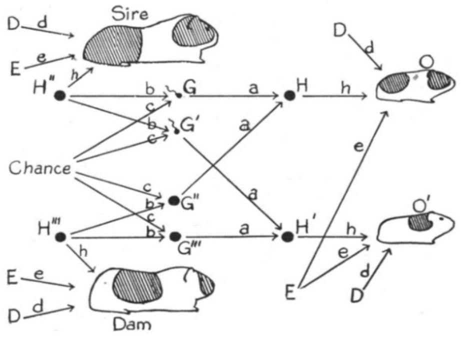
Strong history of innovation in animal breeding context

Origins via Sewall Wright & J.L. Lush

Later advances in statistical modelling:

- Henderson & BLUP models
- Meuwissen et al. & Genomic Selection

Collection of animal population data at scale: artificial insemination and INTERBULL



Wright (1920)

Image: Wikipedia

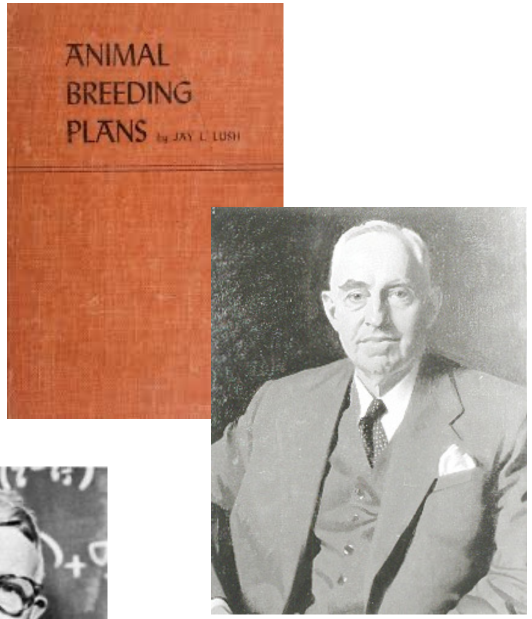


Image: Iowa State University

Quantitative Genetics in Plant Breeding

20th century plant breeding – limited interest in quantitative genetics

Most applications in maize breeding

e.g. Illinois Long-Term Selection Experiment

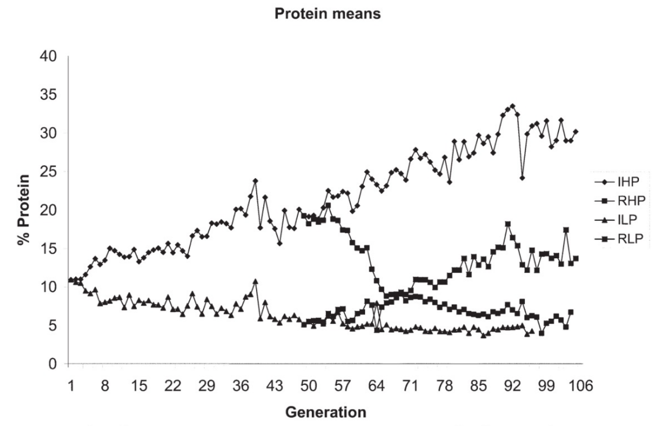
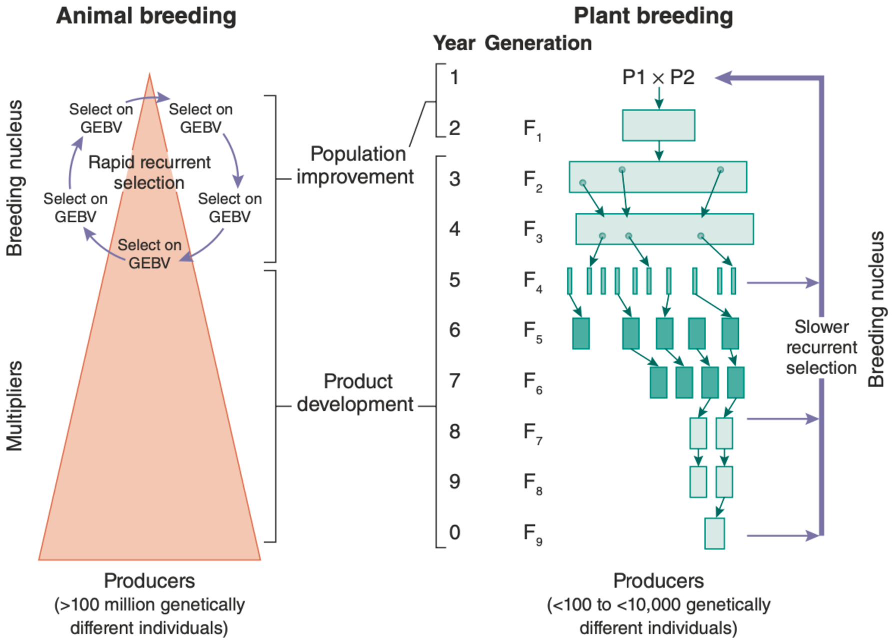


Figure 2. Plot of mean protein concentration against generation for Illinois High Protein (IHP), Reverse High Protein (RHP), Illinois Low Protein (ILP), and Reverse Low Protein (RLP).

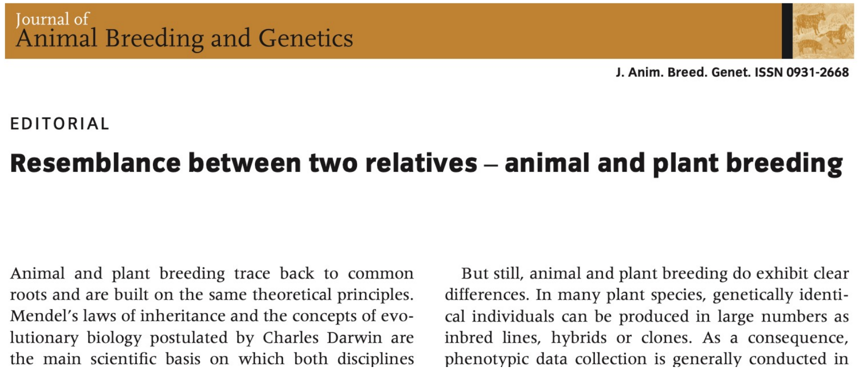
Dudley et al. 2007

Image: Illinois Farm Bureau Partners



Hickey et al. 2017

Convergence across Domains?



Journal of
Animal Breeding and Genetics

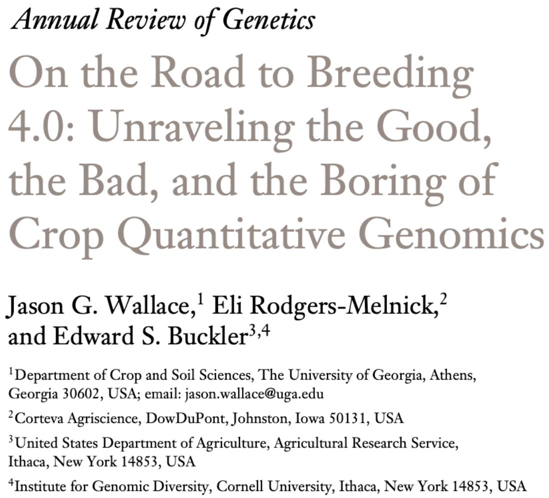
J. Anim. Breed. Genet. ISSN 0931-2668

EDITORIAL

Resemblance between two relatives – animal and plant breeding

Animal and plant breeding trace back to common roots and are built on the same theoretical principles. Mendel's laws of inheritance and the concepts of evolutionary biology postulated by Charles Darwin are the main scientific basis on which both disciplines

But still, animal and plant breeding do exhibit clear differences. In many plant species, genetically identical individuals can be produced in large numbers as inbred lines, hybrids or clones. As a consequence, phenotypic data collection is generally conducted in



Annual Review of Genetics

On the Road to Breeding 4.0: Unraveling the Good, the Bad, and the Boring of Crop Quantitative Genomics

Jason G. Wallace,[1] Eli Rodgers-Melnick,[2] and Edward S. Buckler[3,4]

[1]Department of Crop and Soil Sciences, The University of Georgia, Athens, Georgia 30602, USA; email: jason.wallace@uga.edu

[2]Corteva Agriscience, DowDuPont, Johnston, Iowa 50131, USA

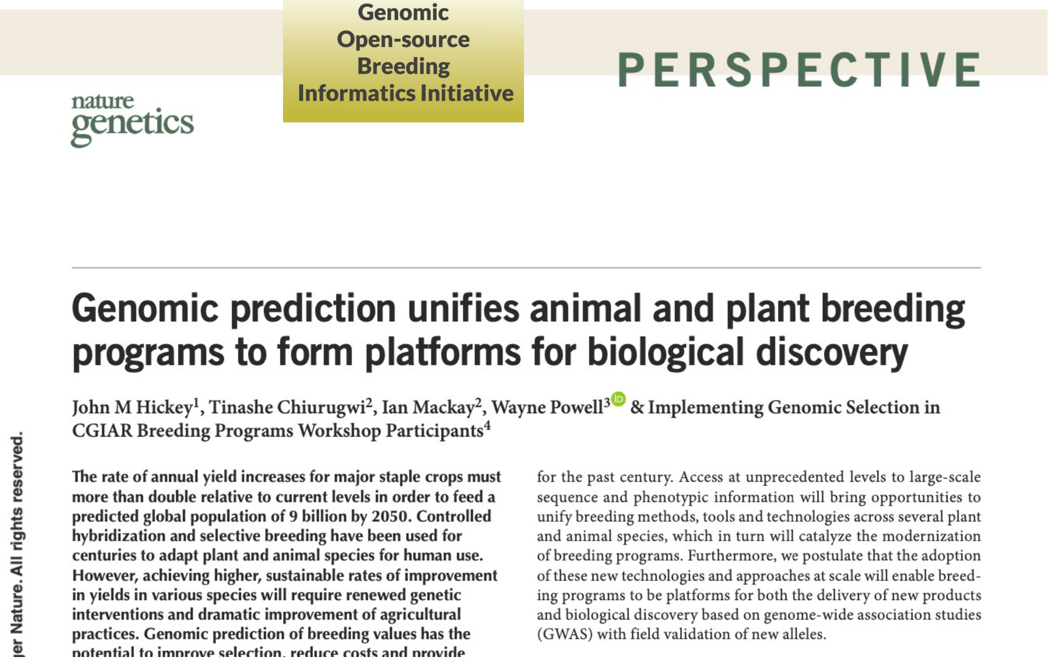
[3]United States Department of Agriculture, Agricultural Research Service, Ithaca, New York 14853, USA

[4]Institute for Genomic Diversity, Cornell University, Ithaca, New York 14853, USA

BILL & MELINDA GATES *foundation*

GOBii

Genomic Open-source Breeding Informatics Initiative



PERSPECTIVE

nature genetics

Genomic prediction unifies animal and plant breeding programs to form platforms for biological discovery

John M Hickey[1], Tinashe Chiurugwi[2], Ian Mackay[2], Wayne Powell[3] & Implementing Genomic Selection in CGIAR Breeding Programs Workshop Participants[4]

The rate of annual yield increases for major staple crops must more than double relative to current levels in order to feed a predicted global population of 9 billion by 2050. Controlled hybridization and selective breeding have been used for centuries to adapt plant and animal species for human use. However, achieving higher, sustainable rates of improvement in yields in various species will require renewed genetic interventions and dramatic improvement of agricultural practices. Genomic prediction of breeding values has the potential to improve selection, reduce costs and provide

for the past century. Access at unprecedented levels to large-scale sequence and phenotypic information will bring opportunities to unify breeding methods, tools and technologies across several plant and animal species, which in turn will catalyze the modernization of breeding programs. Furthermore, we postulate that the adoption of these new technologies and approaches at scale will enable breeding programs to be platforms for both the delivery of new products and biological discovery based on genome-wide association studies (GWAS) with field validation of new alleles.

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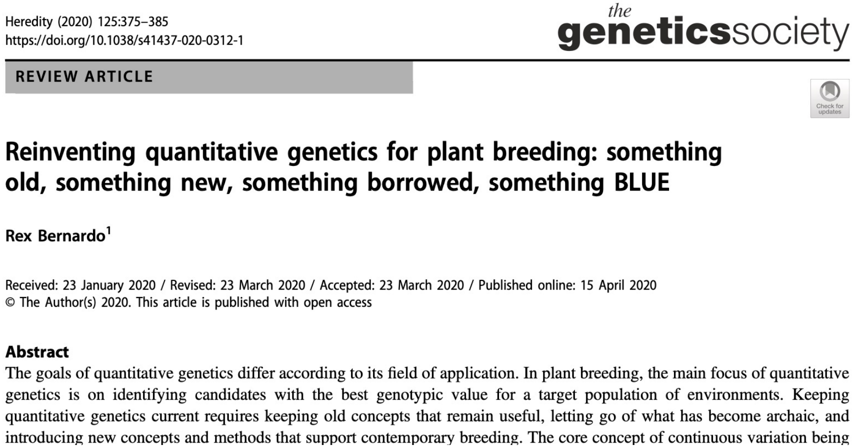

Heredity (2020) 125:375–385
https://doi.org/10.1038/s41437-020-0312-1

the genetics society

REVIEW ARTICLE

Reinventing quantitative genetics for plant breeding: something old, something new, something borrowed, something BLUE

Rex Bernardo[1]

Received: 23 January 2020 / Revised: 23 March 2020 / Accepted: 23 March 2020 / Published online: 15 April 2020
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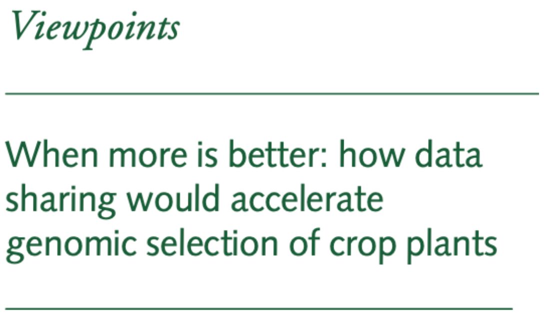
Abstract

The goals of quantitative genetics differ according to its field of application. In plant breeding, the main focus of quantitative genetics is on identifying candidates with the best genotypic value for a target population of environments. Keeping quantitative genetics current requires keeping old concepts that remain useful, letting go of what has become archaic, and introducing new concepts and methods that support contemporary breeding. The core concept of continuous variation being

Exchanging Repertoires

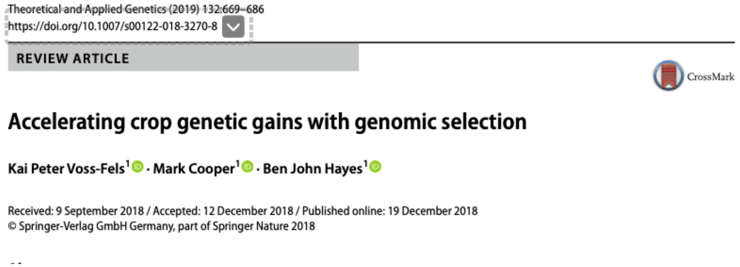
Animal breeding —> Plant breeding

- Enthusiastic uptake of **Genomic Selection** repertoire and population improvement



Viewpoints

When more is better: how data sharing would accelerate genomic selection of crop plants



Theoretical and Applied Genetics (2019) 132:669–686
https://doi.org/10.1007/s00122-018-3270-8

REVIEW ARTICLE

Accelerating crop genetic gains with genomic selection

Kai Peter Voss-Fels[1] · Mark Cooper[1] · Ben John Hayes[1]

Received: 9 September 2018 / Accepted: 12 December 2018 / Published online: 19 December 2018
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Plant breeding —> Animal breeding

- Emerging movement of **phenomics** and **Phenomic Selection** repertoires to animal breeding

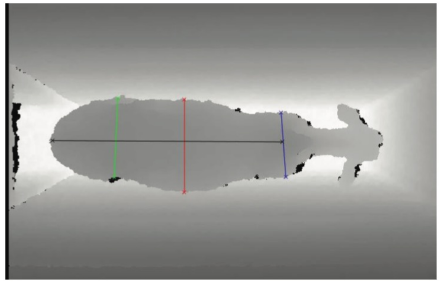


Figure 1. An example of body measurements taken from a Nellore calf using the Microsoft Kinect tool.

Ventura (2020)

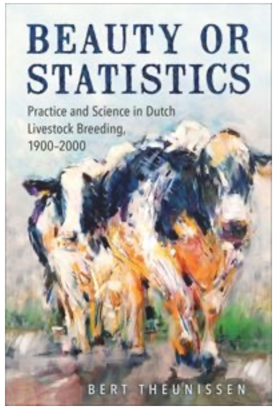
Exchange often motivated by discourses of ‘grand challenges’ such as climate change adaptation and global food security

Reframing Critical Issues

How does a focus on indicators refine our understanding of critical issues in plant and animal breeding?

Reframing Critical Issues: Expertise

1. Contestations over appropriate kinds of expertise in breeding


BEAUTY OR STATISTICS

Practice and Science in Dutch Livestock Breeding, 1900-2000

BERT THEUNISSEN

Perception of a fundamental clash between data-driven breeding and ‘skilled vision’

- Visible versus invisible characteristics; sustained performance vs show ring culture

In practice, animal breeders sensitive to ambiguities – numbers as tool, not imperative

Farmer-breeders have legitimate concerns over reliability of indicators

- E.g. environmental context, measurement methods

Plant breeding expertise often removed from working farms – different issues

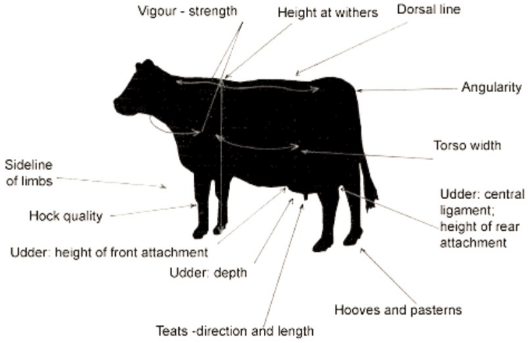


Figure 2. Sketch of a Milking Cow Highlighting the Traits Evaluated.

Grasseni (2005)

Reframing Critical Issues: Biopower

2. Quantitative genetics as wielding biopower over animals

Biopower issues can be focused in particular on design and use of selection indexes

Especially choice of traits and weightings — who decides? (Cole et al. 2021)

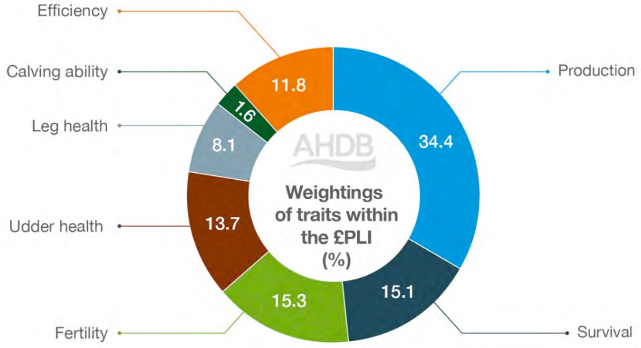
Fundamental ethical questions of what purpose particular indexes serve

- Animal welfare vs instrumentalist use of animals

But also epistemic challenges

- E.g. number of traits affecting reliability—limits range of possibility

Cf. eugenic concerns in human genetics



Source: AHDB[779]

Reframing Critical Issues: Environments

3. Exchange of repertoires highlights neglected role of environments

GxE acknowledged but poorly addressed in animal breeding – ‘contemporary groups’

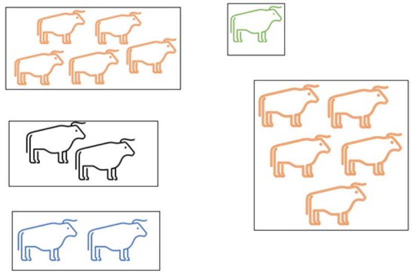


Image: Simbra

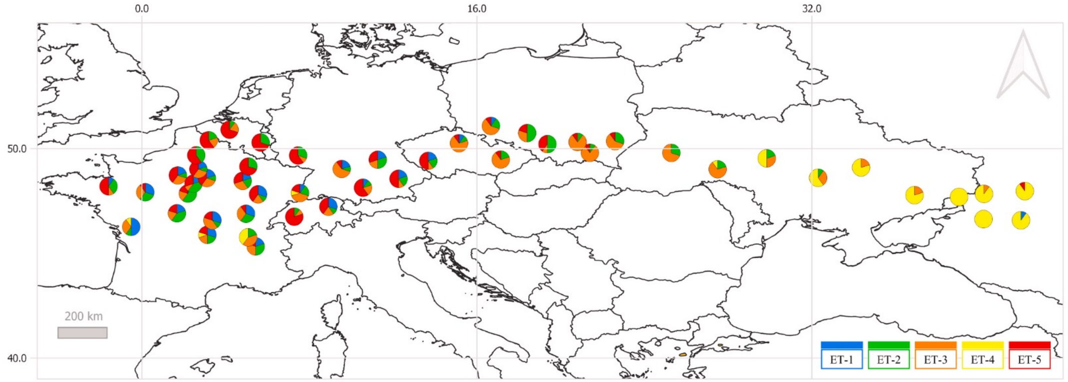
More systematic approach in plant breeding

- Target Population of Environments (TPE) & Multi-environment trials (METs)
- Emphasis on genetic gain in environmental context

But still issues around how genetic gain is calculated

- Speed of breeding over environmental adaptation?

(Williamson & Leonelli 2022)



Elmerich et al. 2023

Conclusion

- Quantitative genetics in breeding can be understood as production of statistical indicators
- Indicators used for ordinal ranking to support breeding decisions (selection, program design)
- Three key indicators: Heritability, breeding values, genetic gain
- Increasing convergence of plant and animal breeding around genomic practices
- Major critical issues linked to indicators:
    1. Contested expertise in breeding linked to epistemic issues
    2. Selection indexes can apply biopower over animals
    3. Environmental variation not yet sufficiently addressed

Acknowledgements

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