

Single Step is a new method to calculate breeding values for Dairy breeds

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STØTTET AF
Mælkeafgiftsfonden

SEGES
INNOVATION

Traditional evaluation

Input:

Phenotype (milk, type score, etc.), y

Fixed effects (calving month, etc), fix

Pedigree (traditional pedigree), a

Genetic model: $y = \text{fix} + a + e$

Single step evaluation

Input:

Phenotype (milk, type score, etc.), y

Fixed effects (calving month, etc), fix

Pedigree (traditional and genomic combined), $t+g$

Genetic model: $y = \text{fix} + (t+g) + e$

Pedigree in single step

- Combination of traditional and genomic pedigree is difficult
 - Need to be combined optimally
 - Ressource demanding - extra calculation time and computer capacity
- Influences genetic trend (inflation) - if not done right

Improvement in Single Step

- Change in combination of traditional and genomic pedigree
- Exclusion of genomic information for animals born before 2009
 - Traditional pedigree and phenotype is kept

Why change?

- Higher reliability
- Break-down of assumptions = risk of bias
 - Influence on genetic trend

Time plan

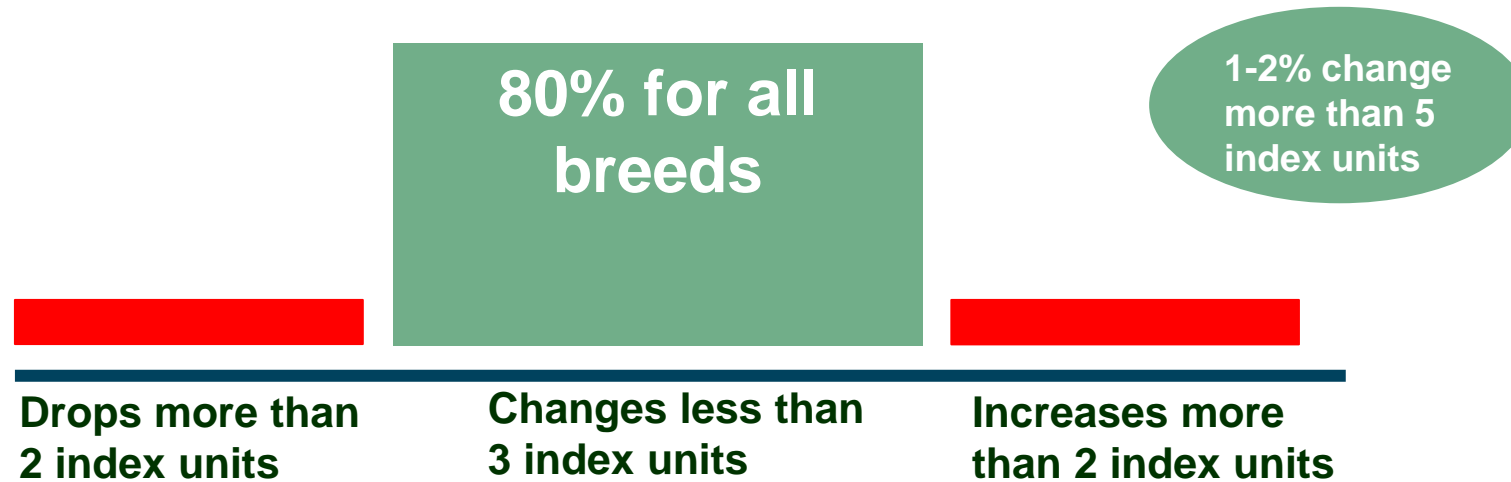
Trait	Actual and expected implementation
Metabolic efficiency in Saved feed	2020
Type traits	November 2022
Claw health	2023
Other traits in NTM	Will follow

Type traits

- Single traits and combined indices
- Changes depends on animal group and breed

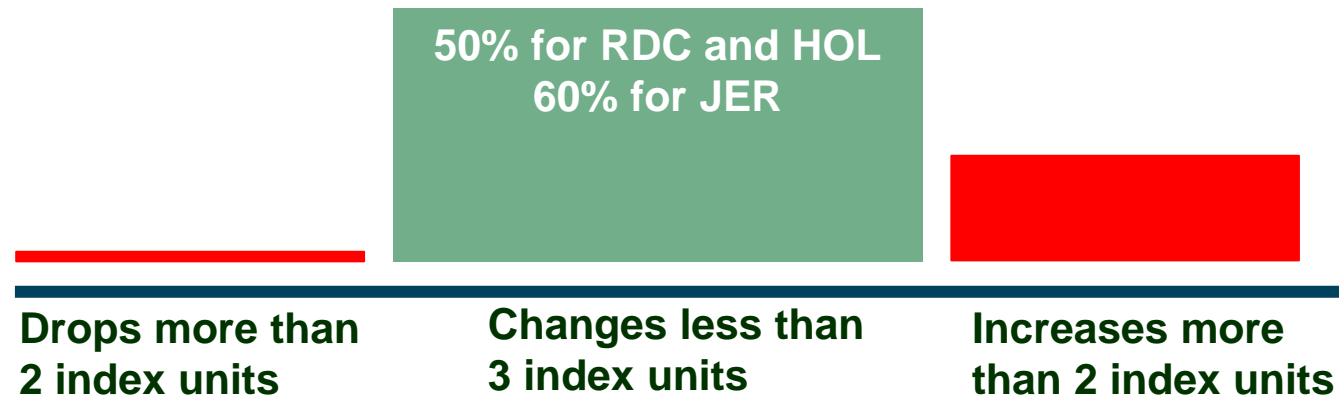
Proven bulls

- Almost no changes for all breeds
- Unchanged ranking within birth year
- Bit steeper trend – 1-3 index units in 7 years



Young bulls

- Minor changes for all breeds
- Minor reranking within birth year
- In general 1-3 index units increase



Non-genotyped females

- Almost no changes for all breeds
- Unchanged ranking within birth year



Genotyped females

- Minor changes for all breeds
- Minor reranking within birth year
- In general 1-2 index units increase

