

Note – Economical value of Metabolic efficiency

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To ensure a smooth and elegant implementation for breeding values of metabolic efficiency (**ME**), breeding values for ME is standardized to the same level as breeding values for maintenance. This have 2 advantages (1) the effect of 1 index unit ME and maintenance are equal - easier to explain in practice and (2) the current Saved feed weight in NTM can be used - means when breeding values for ME are published and included in Saved feed, they have effect on NTM. The description on how to standardize the ME breeding values towards the level of maintenance breeding values are described below.

Assumptions genetic evaluation:

The breed specific assumptions made for the genetic evaluation is presented below (Table 1). Here it is assumed the heritability and the percentage of permanent environmental variance are the same for all breeds.

Table 1. Breed specific assumptions for the genetic evaluation of RFI (metabolic efficiency). Variances are on daily basis.

| | HOL | RDC | JER |
|--|-----------|-----------|-----------|
| Phenotypic SD ¹ | 1.65 | 1.84 | 3.0 |
| Heritability, % (% PE) | 15% (25%) | 15% (25%) | 15% (25%) |
| Genetic SD for RFI | 0.64 | 0.71 | 1.165 |
| Genetic SD for MBW on RFI scale ² | 0.287 | 0.347 | 0.235 |

¹Phenotypic SD used for MiX99 (SD value from standardization of RFI phenotypes)

²The genetic SD for MBW on the same scale as RFI, meaning the genetic SD are 1:1 for RFI and MBW

It has to be noted that the genetic SD for RFI is estimated with relatively high standard error. It is therefore needed to discuss how to come up with realistic assumption when combining EBV for maintenance efficiency and metabolic efficiency. One way to do that is to compare the genetic SD for RFI with the genetic SD for MBW on the RFI scale. The applied additive variance for RFI in the genetic evaluation is 2-5 times higher than for MBW depending on breed. How to handle that in the standardization is covered below.

How to handle different genetic SD over the lactation and low reliability for RFI

Genetic SD for RFI is for RDC estimated at research farms to be 0.71 kg DMI/day (Table 1). If we simply calculate the genetic SD per lactation by summing over 305 day, we assume the trait is genetically the same over lactation. But that is not correct, since the genetic correlation for RFI has been found to be significantly below one between lactation stages, from studies on research farm data. Studies has indicated the genetic correlation between parts of the lactation might be even negative. It is therefore suggested to set RFI and MBW additive variances to 1:1 in the standardization, instead of using the solutions where the applied additive variance estimates from research farms are 2-5 times higher than the MBW evaluation.

Another thing we have to deal with is to ensure that we do not overestimate the effect on RFI since we have an expected low GEBV reliability for candidates at 3%.

Assumptions in standardization:

The assumptions needed for standardization of RFI phenotypes can be found in table 2. The aim for this standardization is to - standardize RFI GEBVs to the same level as the maintenance evaluation. That means 1 index unit RFI contains the same amount of DMI as 1 index unit MBW. Here it is important to note that RFI solutions is on daily basis.

Table 2. Breed specific assumptions for the standardization of breeding values for RFI (metabolic efficiency).

| | HOL | RDC | JER |
|--|-------|-------|-------|
| Genetic SD for RFI using MBW SD ¹ | 0.287 | 0.347 | 0.235 |
| Standardization value for RFI (SD _{MBW_RFI}) ² | 0.269 | 0.323 | 0.219 |
| Expected EBV SD on candidates ³ expressed in DMI on daily basis | 0.05 | 0.06 | 0.04 |
| SD RFI solutions from bull candidates born from 2017-2019 | 0.115 | 0.198 | 0.397 |
| Factor used to standardize solutions ⁴ | 0.432 | 0.303 | 0.103 |

¹Genetic SD for MBW in kg DMI on daily basis = (((SD value MBW / accuracy MBW) x 17.8 kg DMI/kg MBW in a lactation) / 365 days) x (365/305)

²SD_{MBW_RFI}: Genetic SD RFI x sqrt(reliability MBW)

³Genetic SD RFI x sqrt(0.03)

⁴Factor = Expected SD of candidates divided by obtained SD for bull candidates born in 2017-2019

Description of standardization

The standardization if done in 2 steps:

1. Solutions from MiX99 is multiplied with the Factor from Table 2 and -1 to turn the scale around – meaning positive solution values now are favorable to select for.
2. Standardized breeding values are calculated as:

$$RFI\ BV_{100} = 10 \times \frac{EBV_{raw} - \mu_{EBV\ rollingbase}}{SD_{MBW_DMI}} + 100$$

Where

EBV_{raw} is the solution from step 1

$\mu_{EBV\ rollingbase}$ is in this case set to candidates born from 2017-2019 since we only have few cows with data

SD_{MBW_DMI} is the standardization value for RFI (values are presented for the different breeds in table above).

Since we would like to put RFI on the same scale as MBW, we should use the value from the MBW evaluation.