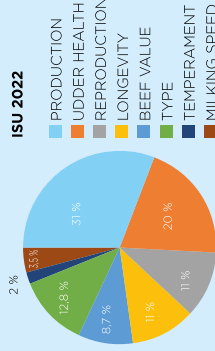


Revision of the Montbeliarde ISU

The last ISU revision was in 2012. A reform of a breed proof was necessary for the selection objectives to correspond to the economic conditions of the Montbeliarde herds, the genetic progress of the breed, and to integrate new available traits.

Major changes in the new ISU

- > Affirms body capacity and beef value of the Montbeliarde breed
- > Gives more weight to functional traits: longevity and udder health
- > Rebalances the fat & protein % in the production category
- > Integrates selection for improved temperament



PRODUCTION

For production, the former INEL changes its name to **DAIRY SYNTHESIS**. The composition changes with more importance given to fat production.

$$\text{DAIRY SYNTHESIS} = 0.76 \times (\text{Pkg} + 0.51 \text{ Fkg} + 0.15\text{F}\% + 0.52\text{P}\%)$$

TYPE

The emphasis placed on various conformation traits has changed. A noticeable change is the new breeding value for body capacity which combines Body & Rump. Furthermore, the new trait, «rear teat placement» has been added to the udder breeding value.

> BODY

The body capacity breeding value combines the former Body & Rump breeding values.

Body = 30% CHEST WIDTH + 20% CHEST DEPTH + 25% THURL WIDTH + 25% RUMP LENGTH
 The traits **BODY DEPTH & RUMP WIDTH** are no longer assessed because they are strongly related to **CHEST DEPTH & THURL WIDTH**.

The traits **STATURE & RUMP ANGLE** are still evaluated but are not included in the Body Capacity breeding value.

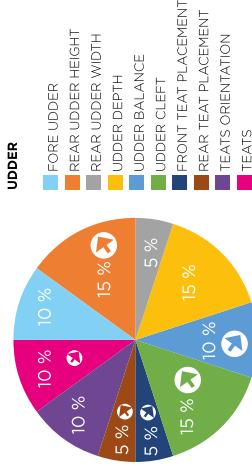
> FEET & LEGS

HOCK THICKNESS is no longer assessed.

> UDDER

The new trait **REAR TEAT PLACEMENT** now has a 5% emphasis in the UDDER breeding value. Values higher than 100 indicate wider spacing of the rear teats. On the contrary, values under 100 indicate closer spacing.

REAR UDDER HEIGHT and **UDDER CLEFT** are given more weight in the UDDER breeding value. **UDDER BALANCE, FRONT TEAT PLACEMENT** and the **TEATS** are given less weight.



NEW CALVING EASE SCORES

- > Beginning of Single Step method > Values are more spread on a bigger scale
- > The mode of expression in % of births with easy calvings on heifers has been kept

Calving Ease Meaning	CE Score with New Method	CE Score with Old Method
Very Difficult	From 48 to 50	Below 84
Difficult	From 51 to 77	From 85 to 86
Average / Normal	From 78 to 88	From 87 to 88 / Normal
Easy	From 89 to 94	From 89 to 90
Very Easy	From 95	From 91 and above/Easy

How to pick a bull

- > **To use on HEIFERS**
 - For Pure Breeding : SELECT a bull with Calving Ease score from 89 and above
 - However for Crossbreeding , SELECT a bull with Calving Ease score from 90 and above
- > **To use on COWS**
 - For Pure Breeding : SELECT a bull with Calving Ease score from 78 avec above
 - However for Crossbreeding , SELECT a bull with Calving Ease score from 89 and above

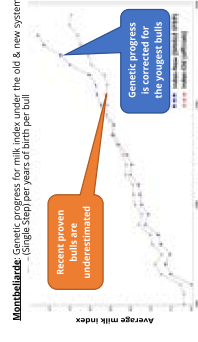
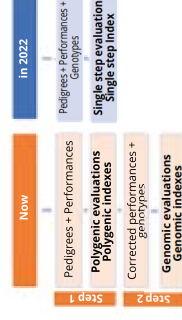
New genetic calculation method: the SINGLE STEP

Starting with the April 2022 proofs, a new calculation method called SINGLE STEP is used. It has been implemented broadly by all our partners: IDELE, GENEVAL, ALLICE and INRAE within the UNIGENO project and is used in the genetic estimation of all French breeds using genomic information. This method is also used internationally.

Why a new indexing method?

For several years, the percentage of genotyped animals have increased. Thanks to this tool, animals with poor performance predictions are culled before they go into production, both males and females. Thus, only the best animals are given an opportunity to contribute performance data, which leads to an **overestimation of the reference population** (those animals with genomic testing + performance information) and an **underestimation of the indexed animals** (the whole population): this concept is called **pre-selection bias**.

The objective of the single step method is to correct this pre-selection bias by considering all the information available for all animals simultaneously, whether they enter production or not. With the single step, noticeable information increases, particularly in the evaluations of young animals, now corrected for the pre-selection bias.



SINGLE STEP, what are the main evolutions?

- > Change from two steps to one: single step means all pedigree, performance, and genotype data are evaluated simultaneously
- > All genotypes are considered in the reference population
- > A method that now fairly compares genotyped and non-genotyped animals
- > Correction of the pre-selection bias