

# Overview of the Mendelian Sampling Variance Test Pilot Study

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## Abstract

A software for calculating the Mendelian sampling variance has been developed by MTT for Interbull service users. In 2013 the software and its methodology was approved by the Interbull Technical Committee to be tested in a pilot study with real countries data. Countries were asked to test the software on two different group of traits: a group of traits with medium-high heritability (protein, stature and somatic cells score) including results for both males and females; two traits of their choice with heritability lower than 0.1 with results restricted only to males. A total of 21 countries participated in the pilot study. Data received were mostly related to the Holstein breed, and for low heritable traits countries chose most commonly direct longevity and fertility related traits. Overall, 50 (26%) country-breed-trait combinations failed the test. Some more investigations will be needed to better understand the reasons behind their failure.

The following paper presents an overview of the data received by countries and of the trend test results.

**Key words:** Mendelian sampling, trend validation, dairy cattle, international evaluation

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## Introduction

Following the work done by Tyrisevä *et al.* (2011 and 2012) on developing a test methodology to observe possible trends in genetic variance, the Interbull Technical Committee decided to test the methodology on real country data (Interbull meeting, 2013).

The following paper presents an overview of the data received by countries participating to the pilot study and a summary of the trend test results.

## Data Call and Data Requirements

A data call was sent out to all Interbull users asking to apply the Mendelian sampling variance test on the following traits:

- Protein
- Somatic Cells Score
- Stature
- Two traits of their choice with heritability lower than 0.1

As a requirement, the national genetic evaluation model for the requested traits should have been based on an Animal Model

evaluation. A further requirement for the first three traits with medium to high heritability (protein, somatic cells score and stature) was to apply the test using both bulls' and cows' data. For the low heritable traits instead, countries were required to apply the software only on bulls' data. The reason for it was a software requirement of a minimum value of Mendelian sampling reliability of 0.1 (Tyrisevä *et al.*, 2012).

## Results

### *Data Received*

A total of 21 countries participated to the pilot study (Figure 1) for a total of 208 country-breed-trait available combinations. Almost all countries supplied results for Holstein breed; only few of them supplied also results for the other breeds evaluated internationally (Figure 1 and 2).

Overall, the three mandatory traits (protein, somatic cells score and stature) were as expected the ones more represented (Figure 3); the low heritable traits showed a wider selection of traits although the ones more

represented were direct longevity and fertility traits.

Given the enormous amount of data received, detailed results are shown for the two most represented breeds, Holstein and Brown Swiss for the three mandatory traits. Results related to the optional traits will be restricted to the two most represented ones, direct longevity and lactating cows ability to conceive (cc2) only for the Holstein breed, given the few records available for the other breeds (Figure 4).

### **General Trend Results**

There were a total of 208 country-breed-trait combinations sent to Interbull Centre. In 13 cases the total number of animals for some specific years was too low and the trend and regression could not be performed. The overall results showed in Table 1 referred to the remaining 195 valid results, including bulls' and cows' data for all breeds.

**Table 1.** Overall trend results, including bulls' and cows' data, all breeds.

<b>Trend outcome</b>	<b>N</b>	<b>%</b>
Did not deviated sign. from 0	82	42
Deviated sign. from 0 but within $\pm$ 2%	63	32
Deviated sign. from 0 and above $\pm$ 2%	50	26
Tot. PASSED	145	74
Tot. FAILED	50	26
Total	195	100

### **Trend Results for Protein**

A total of 18 and 4 countries provided results for Holstein and Brown Swiss breeds, respectively (Figure 1). For Holstein, all countries provided results for protein on bulls' data and 17 of them provided results on cows' data. In both cases, there was one instance in which the total number of animals for some

specific years was too low and the trend and regression could not be calculated, leaving valid results for 17 and 16 countries, respectively.

All data provided for Brown Swiss for both bulls and cows were considered.

**Table 2.** Trend results for Holstein and Brown Swiss protein, bulls and cows' data.

<b>Trend outcome Holstein</b>	<b>N</b>		<b>%</b>	
	<b>M</b>	<b>F</b>	<b>M</b>	<b>F</b>
Did not deviated sign. from 0	7	0	41	0
Deviated sign. from 0 but within $\pm$ 2%	3	11	18	69
Deviated sign. from 0 and above $\pm$ 2%	7	5	41	31
Tot. PASSED	10	11	59	69
Tot. FAILED	7	5	41	31
Total	17	16	100	100

<b>Trend outcome Brown Swiss</b>	<b>N</b>		<b>%</b>	
	<b>M</b>	<b>F</b>	<b>M</b>	<b>F</b>
Did not deviated sign. from 0	3	0	75	0
Deviated sign. from 0 but within $\pm$ 2%	0	4	0	100
Deviated sign. from 0 and above $\pm$ 2%	1	0	25	0
Tot. PASSED	3	4	75	100
Tot. FAILED	4	0	25	0
Total	1	4	100	100

### **Trend Results for Somatic Cells Score**

A total of 16 and 4 countries provided information for Holstein and Brown Swiss somatic cells score, respectively. Holstein cows' data was based on results from 14 countries. Data for Holstein cows were based on 14 countries. There was 1 case for bulls and 3 cases for cows' data for which the total number of animals for some specific years was too low and the trend and regression could not be calculated, leaving 15 and 11 valid results for males and females, respectively.

**Table 3.** Trend results for Holstein and Brown Swiss somatic cells score, bulls' and cows' data.

<b>Trend outcome Holstein</b>	<b>N</b>		<b>%</b>	
<b>Somatic Cells Score</b>	<b>M</b>	<b>F</b>	<b>M</b>	<b>F</b>
Did not deviated sign. from 0	11	0	73	0
Deviated sign. from 0 but within±2%	4	11	27	100
Deviated sign. from 0 and above±2%	0	0	0	0
Tot. PASSED	15	11	100	100
Tot. FAILED	0	0	0	0
Total	15	11	100	100

<b>Trend outcome Brown Swiss</b>	<b>N</b>		<b>%</b>	
<b>Somatic Cells Score</b>	<b>M</b>	<b>F</b>	<b>M</b>	<b>F</b>
Did not deviated sign. from 0	4	0	100	0
Deviated sign. from 0 but within±2%	0	3	0	75
Deviated sign. from 0 and above±2%	0	1	0	25
Tot. PASSED	4	3	100	75
Tot. FAILED	0	1	0	25
Total	4	4	100	100

### *Trend Results for Stature*

A total of 15 and 4 countries provided information for Holstein and Brown Swiss stature. For Holstein, all 15 countries provided results on bulls' data and 13 on cows' data. For bulls' data, there was 1 case for which the total number of animals for some specific years was too low and the trend and regression could not be calculated, leaving 14 and 13 valid results for males and females, respectively.

**Table 4.** Trend results for Holstein and Brown Swiss stature, bulls' and cows' data.

<b>Trend outcome Holstein</b>	<b>N</b>		<b>%</b>	
<b>Stature</b>	<b>M</b>	<b>F</b>	<b>M</b>	<b>F</b>
Did not deviated sign. from 0	11	1	79	8
Deviated sign. from 0 but within±2%	3	8	21	61
Deviated sign. from 0 and above±2%	0	4	0	31
Tot. PASSED	14	9	100	69
Tot. FAILED	0	4	0	31
Total	14	13	100	100

<b>Trend outcome Brown Swiss</b>	<b>N</b>		<b>%</b>	
<b>Stature</b>	<b>M</b>	<b>F</b>	<b>M</b>	<b>F</b>
Did not deviated sign. from 0	4	2	100	50
Deviated sign. from 0 but within±2%	0	2	0	50
Deviated sign. from 0 and above±2%	0	0	0	0
Tot. PASSED	4	4	100	100
Tot. FAILED	0	0	0	0
Total	4	4	100	100

### *Trend Results for Direct Longevity and Lactating Cow's Ability to Conceive (cc2)*

Direct longevity and lactating cow's ability to conceive were two of the optional traits provided by participating countries with heritability below 0.1 for which results were based only on bulls' data. A total of 4 countries provided information for Holstein direct longevity, there was 1 case for which the total number of animals for some specific years was too low and the trend and regression could not be calculated, leaving 3 valid results for males. A total of 5 countries provided results for Holstein cc2 bulls (Table 5).

**Table 5.** Trend results for Holstein direct longevity and CC2, based on bulls' data only.

<b>Trend outcome Holstein</b>	<b>N</b>	<b>%</b>
<b>Direct Longevity</b>		
Did not deviated sign. from 0	0	0
Deviated sign. from 0 but within±2%	1	33
Deviated sign. from 0 and above±2%	2	67
Tot. PASSED	1	33
Tot. FAILED	2	67
Total	3	100
<b>CC2</b>		
Did not deviated sign. from 0	1	20
Deviated sign. from 0 but within±2%	1	20
Deviated sign. from 0 and above±2%	3	60
Tot. PASSED	2	40
Tot. FAILED	3	60
Total	5	100

### Additional Information

Additional information about the above traits was also requested together with the data call. Information requested pertained to the type of evaluation applied for each trait (single or multi-trait evaluation), if there was an adjustment for inbreeding and heterogeneous variance and the kind of method applied to calculate female reliabilities. Information collected from the participating countries showed that all Holstein traits were mostly estimated through a single trait evaluation, the only exception being the fertility trait cc2 for which all the six participating countries applied different types of evaluation.

In Brown Swiss, a single trait evaluation was the preferred one for protein and stature while somatic cells score was mostly evaluated via a multi-trait evaluation together with milk, fat and protein.

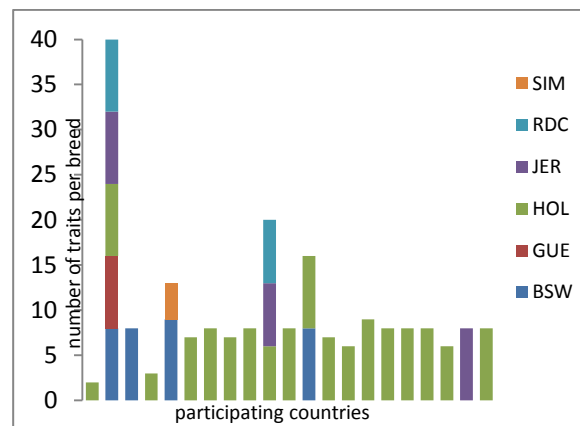
Adjustment for heterogeneous variance was taken into account by the majority of countries participating with Holstein protein and somatic cells score data. It was, instead, mostly ignored for the other Holstein traits (stature, direct longevity and cc2). In Brown Swiss, adjustment for heterogeneous variance was taken into account by the majority of countries for protein; for somatic cells score, out of 4 countries, 2 countries applied it and 2 not; while for stature the majority of countries did not apply such adjustment.

In both breeds and for all the traits considered, the majority of countries did not apply a correction for inbreeding.

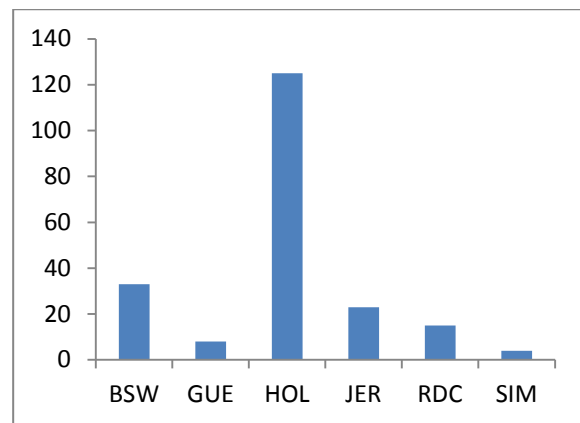
The most common methods for calculation of female reliabilities appeared to be the approximate reliability source method developed by K. Meyer (1987) followed by the methodology developed by Misztal and Wiggans (1988).

### Conclusion

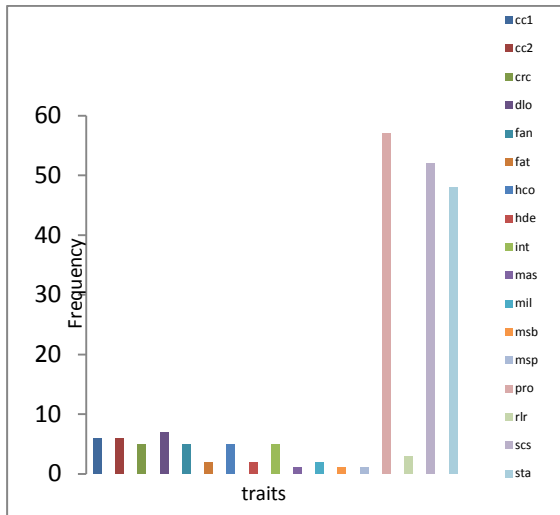
The software was found easy to use by the participating countries. Results look promising, on average 75% passed and 25% failed; therefore the test has sensitivity to detect trends in variance. Anyhow, further investigations are needed to better understand the reasons behind such failings.



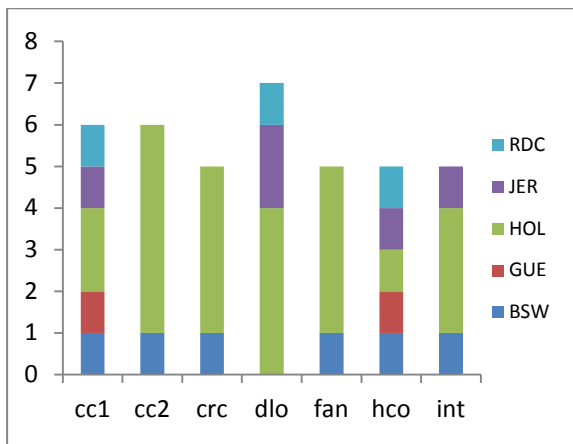
**Figure 1.** Information received by countries participating to the pilot study as function of breed and number of traits submitted: *sim*=Simmental; *rdc*=Red Dairy Cattle; *jer*=Jersey; *hol*=Holstein; *gue*=Guernsey; *bsw*=Brown Swiss.



**Figure 2.** Overall data available per breed. *sim*=Simmental; *rdc*=Red Dairy Cattle; *jer*=Jersey; *hol*=Holstein; *gue*=Guernsey; *bsw*=Brown Swiss.



**Figure 3.** Distribution of traits provided by countries: *cc1*=lactating cow’s ability to conceive (1); *cc2*=lactating cow’s ability to conceive (2); *cc3*=cow recycling; *dlo*= direct longevity; *fan*=foot angle; *fat*= fat yield; *hco*= heifer conception; *hde*= heel depth; *int*= fertility interval traits; *mas*=mastitis; *mil*=milk yield; *msb*=maternal stillbirth; *msp*=milking speed; *pro*=protein yield; *rlr*=rear leg rear view; *scs*=somatic cells score; *sta*=stature.



**Figure 4.** Distribution of optional traits provided by countries per breed: *cc1*=lactating cow’s ability to conceive (1); *cc2*=lactating cow’s ability to conceive (2); *cc3*=cow recycling; *dlo*= direct longevity; *fan*=foot angle; *hco*= heifer conception; *int*= fertility interval traits.

## Acknowledgment

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