

International genetic evaluations of fertility traits considering more than one trait per country

M.A. Nilforooshan, W.F. Fikse, H. Jorjani

Interbull Centre, Department of Animal Breeding & Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden

Mohammad.Nilforooshan@hgen.slu.se

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Outline

- 1. Introduction**
- 2. Structure of the analyses**
- 3. The choice of traits and changes of international evaluations**
- 4. The reasons of changes**
- 5. Results**
- 6. Conclusion**

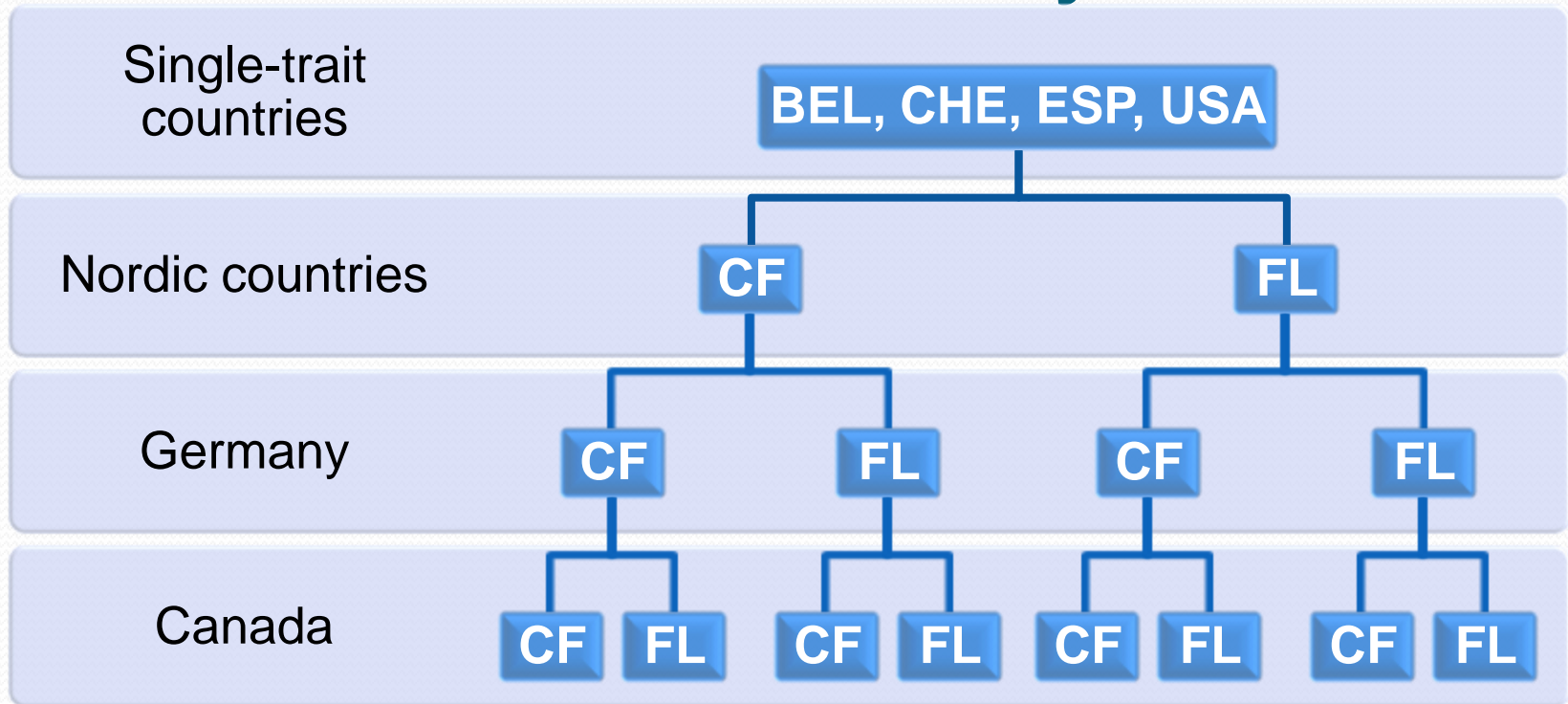
Methods

- National genetic evaluation systems alone cannot be very efficient without an international genetic evaluation system
- ST-MACE (Schaeffer, 1994) is the current method of evaluation in use in Interbull centre
- No residual covariances among daughter groups
- Multiple measures are available for some biological traits
- MT-MACE is proposed by Schaeffer (2001); it can handle non-zero residual covariances among country-traits

Past experiences

- MT-MACE in simulation study (Sullivan et al., 2005)
- MT-MACE tested on field data (Mark and Sullivan, 2006)
- Jorjani (2006) studied female fertility traits having multiple data from some countries
- The **aim** of this study is to find the effect of including more than one trait from a country in a well established methodology (ST-MACE)

Structure of the analyses



BEL (DO); CHE (CF); ESP (DO); USA (DO)

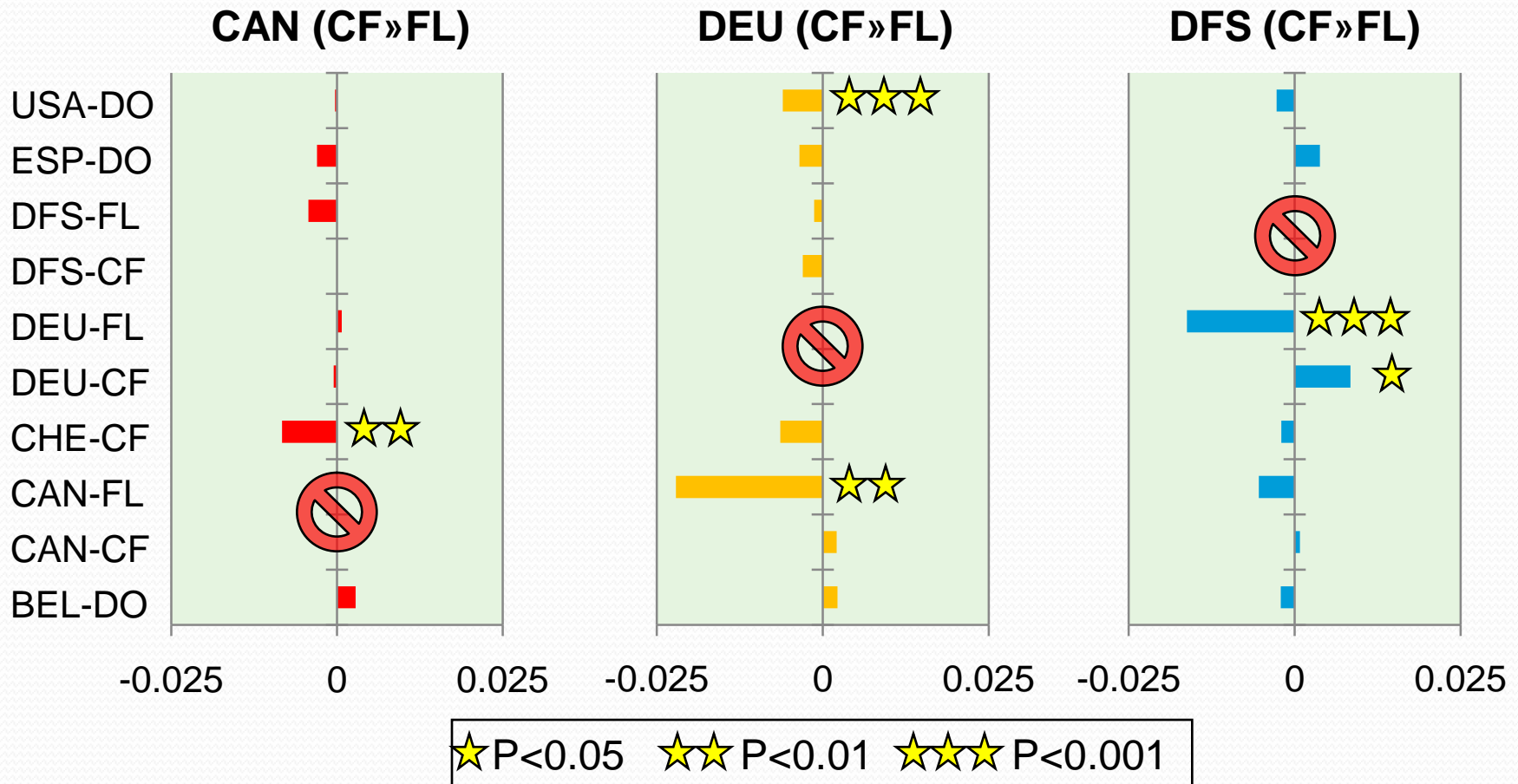
DO= Days open

CF= Calving to first service

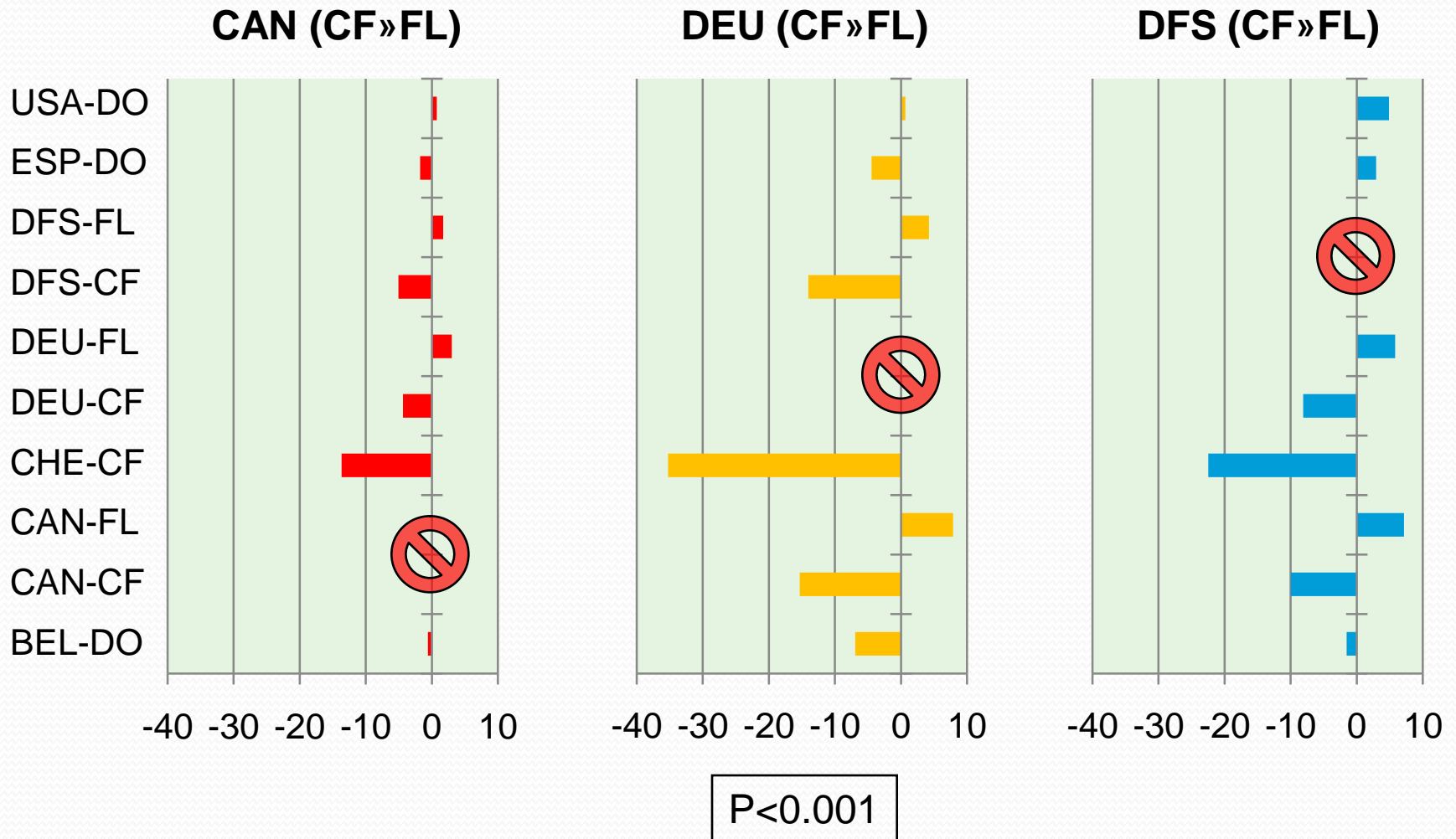
FL= First to last insemination

Changes in between-country genetic correlations

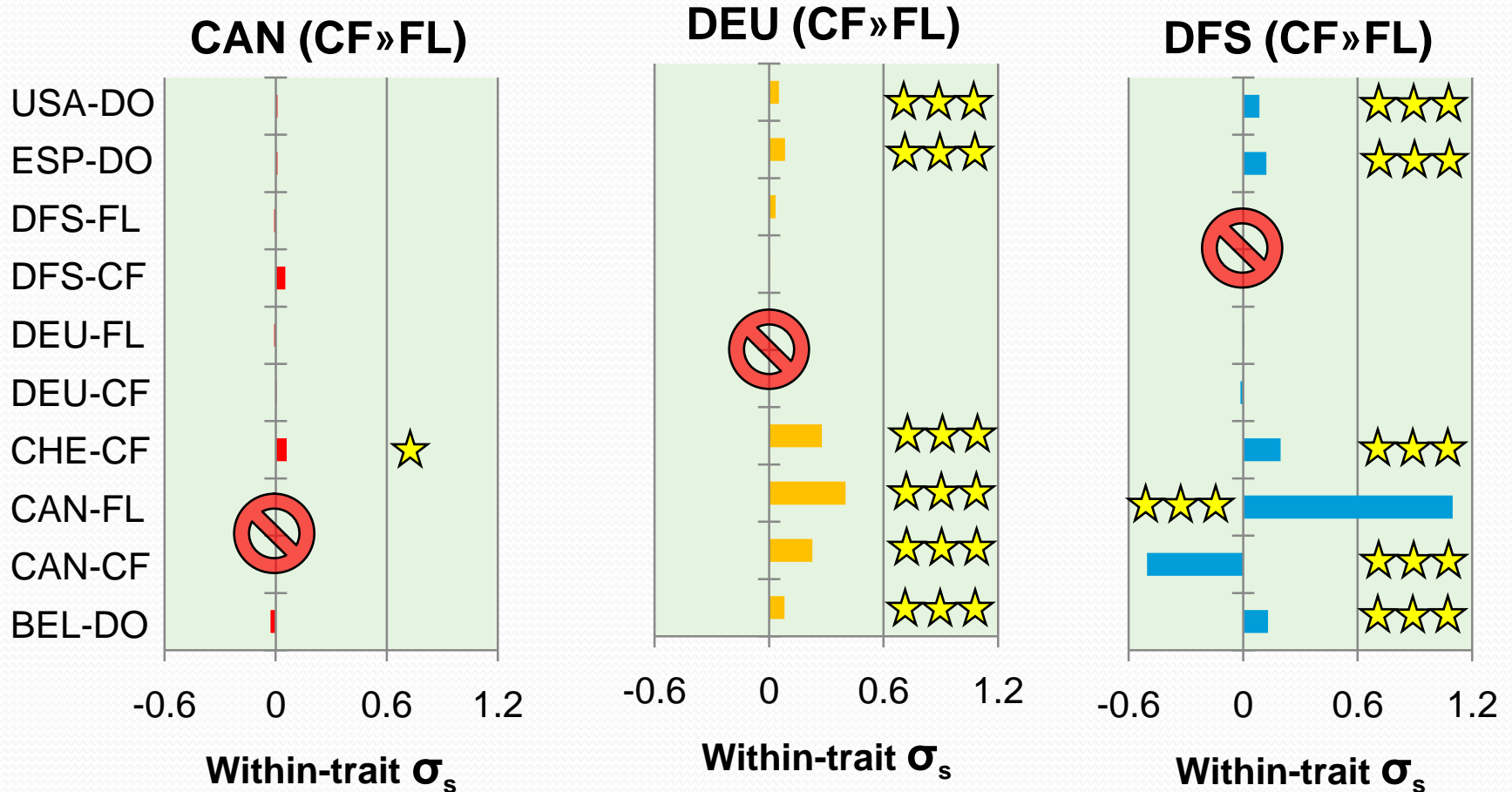
$\mathbf{rg}_1 \rightarrow \mathbf{rg}_2$ from a two-trait country \Rightarrow Changes in the rest?



Changes of international reliabilities



Changes of international EBVs



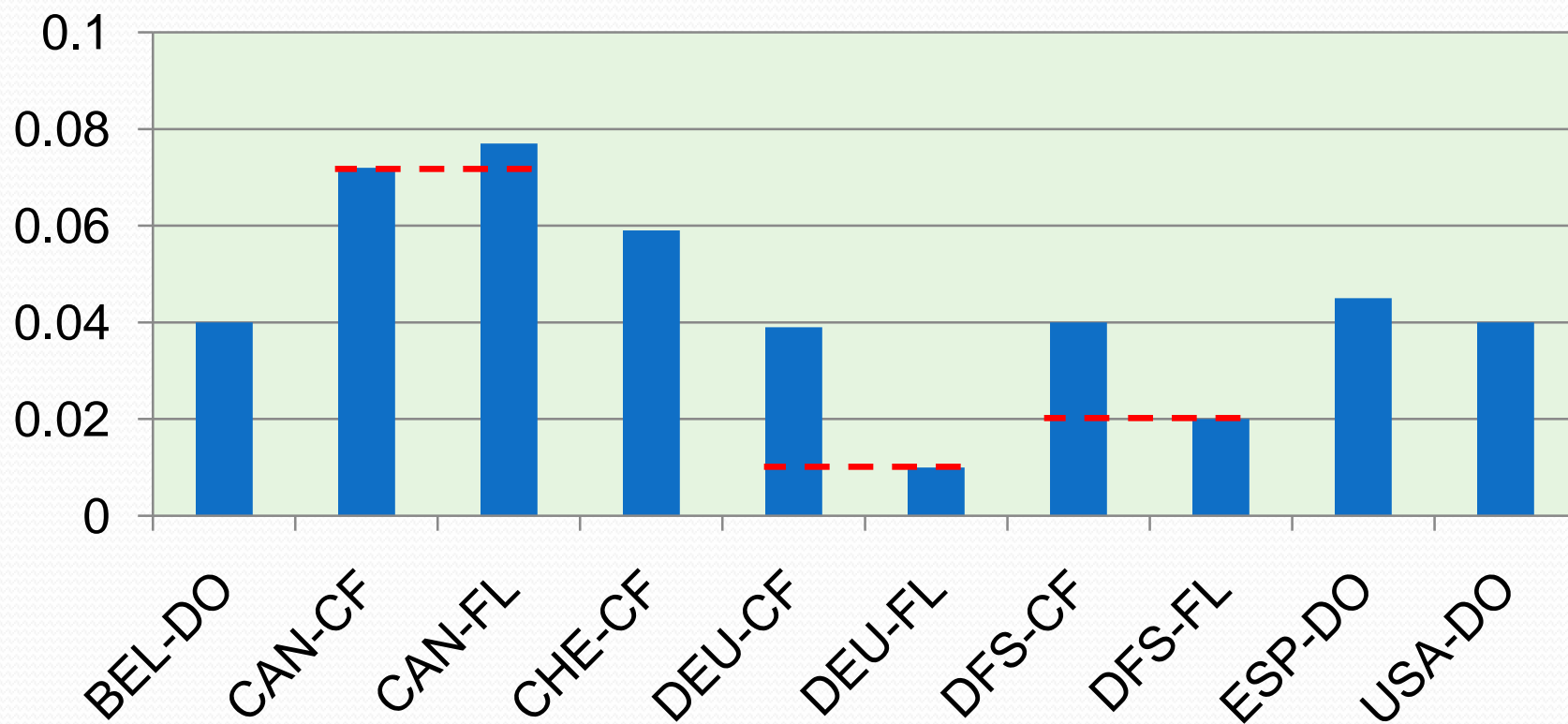
★ $P < 0.05$ ★★★★★ $P < 0.001$



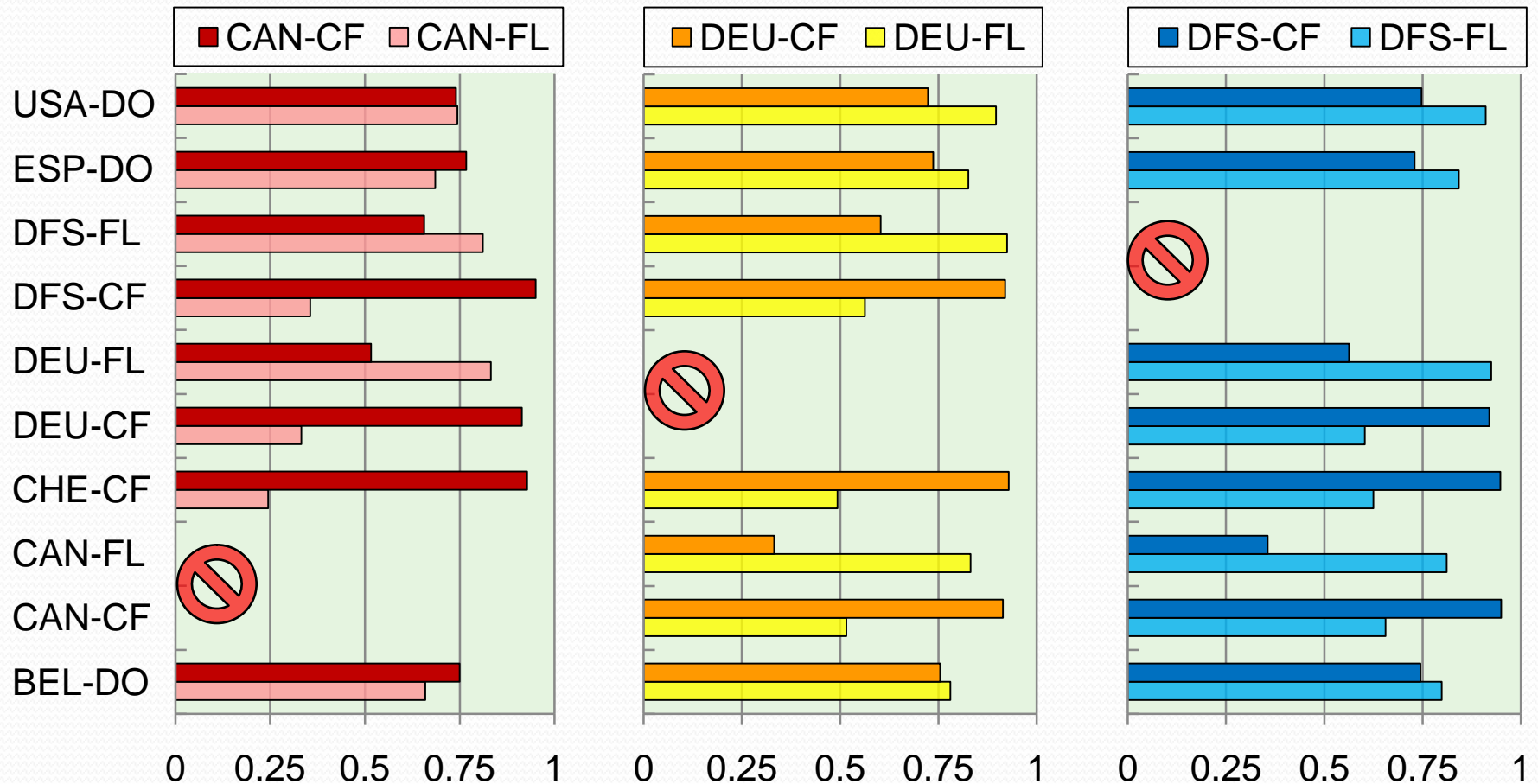
What are the important underlying reasons behind these changes?

Heritabilities

h^2

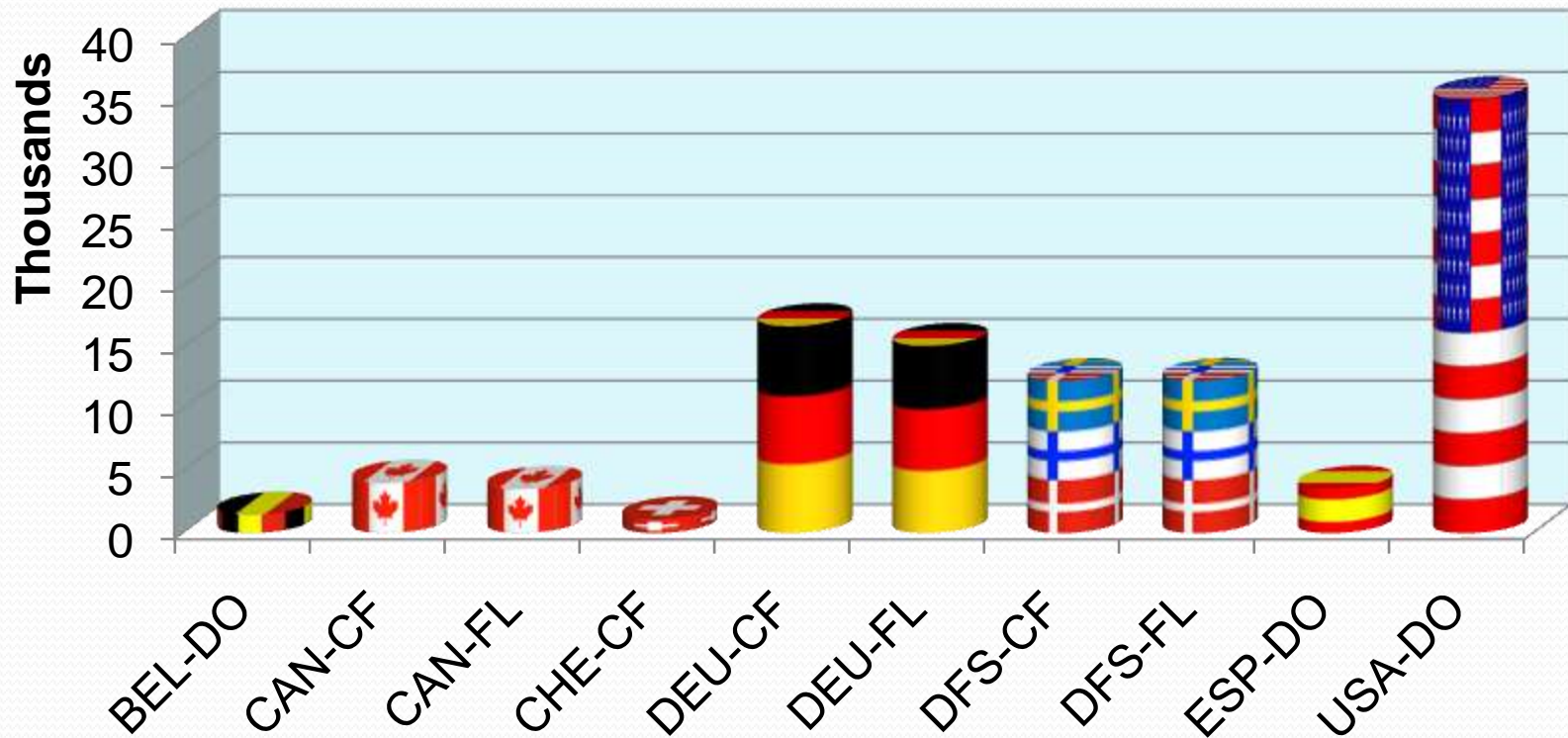


Differences in the genetic correlations



Population size

no. of bulls



Changes of international evaluations due to the choice of alternative traits

Partial correlation coefficients

Variable	h^2_i	$h^2_2-h^2_1$	rg_2-rg_1	Log n. bulls
Δrg	-0.211	-0.019	-0.410*	0.034
$\Delta Rel.$	0.193	0.586**	0.836***	0.480*
$\Delta EBV $	0.767***	0.116	0.597**	0.0002

Conclusion

- The results provided a range of reasonable genetic correlations for multi-country multi-trait genetic evaluations
- In most cases, $\mathbf{rg}_{i,j1} \leftrightarrow \mathbf{rg}_{i,j2}$ had no effect on $\mathbf{rg}_{i,k}$ ($j \neq k$)
- International breeding values changed for some country-traits, especially for small populations due to the choice of alternative traits
- Reliabilities were expectedly affected by the choice of traits
- Applying this method provides a firm base for comparisons between the current well-defined method (ST-MACE) and the coming results of MT-MACE