



# Improved ssGTBLUP for single-step genomic evaluation



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## Conclusions:

- ❖ **ssGTBLUP** computationally less demanding and time consuming than ssGBLUP
- ❖ **GBVs and genetic trends** from the ssGBLUP and ssGTBLUP with QP transformation were the same
- ❖ Without QP transformation convergence of both ssGBLUP and ssGTBLUP was poor > **GBVs might not be reliable**

## Introduction

Single step GTBLUP (ssGTBLUP) was developed to overcome computational challenges due to increasingly large number of genotyped animals in the “traditional” ssGBLUP. In ssGTBLUP,  $\mathbf{G}^{-1}$  matrix is expressed through product of two rectangular matrices, and  $(\mathbf{A}_{22})^{-1}$  matrix through sparse matrices. In practice, ssGTBLUP has the same convergence properties in PCG iteration as the original single-step MME but lower computing costs (Mäntysaari et al. 2017).

**The aim:** Compare ssGBLUP and ssGTBLUP in realistic models having: 1) residual polygenic effect (RPG), and 2) unknown parent groups (UPG). The UPG by QP transformation included  $(\mathbf{G}^{-1} - (\mathbf{A}_{22})^{-1})$ . The approaches were applied to a Nordic Holstein 305 days milk, protein and fat production model for three lactations (9 traits). The data had 10 million pedigree animals of which 7.3 million had observations. The genomic information was from ca. 140 000 animals.



## Studied single-step approaches

- ssGBLUP<sub>w30</sub> (**G30**)  
”Traditional” ssGBLUP, (w=) 30% RPG.
- ssGTBLUP<sub>w30</sub> (**T30**)  
 $\mathbf{G}^{-1}$  replaced by  $\mathbf{C}^{-1}\mathbf{T}'\mathbf{T}$ , where the  $\mathbf{T}$  matrix in the ssGTBLUP approach with  $\mathbf{C} = w\mathbf{A}_{22}$ . RPG (w=) 30%.
- ssGBLUP\_QP<sub>w30</sub> (**QPG30**)  
Like a), QP transformation included  $(\mathbf{G}^{-1} - (\mathbf{A}_{22})^{-1})$
- ssGTBLUP\_QP<sub>w30</sub> (**QPT30**)  
Like c), QP transformation included  $(\mathbf{G}^{-1} - (\mathbf{A}_{22})^{-1})$

Method	Peak memory (GB)	Matrix (GB)	Time form matrix	Seconds/Iteration	Number of Iterations
<b>EBV</b>				10.2	2189
<b>G30</b>	304.6	36.2	16h 47min	22.3	~9000
<b>T30</b>	118.7	24.1	4h 1min	17.3	~9000
<b>QPG30</b>	304.9	36.3	20h 28min	23.0	2240
<b>QPT30</b>	271.9	24.1	7h 53min	20.9	2101

\* Convergence criterion Cr=1.0e-7 was not met properly

