# Easy implementation of QP transformation in ssGTBLUP

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The increasing amount of genomic information in the single-step evaluations has caused problems in the convergence of iterative solving. This can be due to incorrectly accounting genetic groups in the computations if genetic groups are included in the mixed model equations (MME) through QP transformation in full pedigree relationship matrix (**A**) but not in the pedigree ($\mathbf{A}_{22}$) and/or genomic (**G**) relationship matrices for the genotyped animals. Often this problem can be solved by properly accounting for the contributions of the genotyped animals to the genetic groups. In practice, this means that for each genetic group, the elements in the row of $\mathbf{H}_{+}^{22}=\mathbf{G}^{-1}-(\mathbf{A}_{22})^{-1}$ corresponding to an animal are weighted by the proportions of genes the animals received from the group (**Q**-matrix), i.e., product $\mathbf{H}_{+}^{22}\mathbf{Q}$. With ssGTBLUP, the QP transformation is possible to do by including new columns (**TQ**) into the original **T** matrix. The contribution due to the $\mathbf{A}_{22}^{-1}$ matrix is as easy by including the "phantom parents" to the set of genotyped animals.

We applied single-step test-day (TD) model to Nordic Holstein data where unknown parent group coefficients were accounted in a) ssGTBLUP $\mathbf{A}^{-1}$, b) ssGBLUP with $\mathbf{H}_{+}^{22}$, c) ssGTBLUP with $\mathbf{H}_{+}^{22}$, and d) ssGTBLUP $\mathbf{A}_{22}^{-1}$. The TD data included 8.4 million cows with records, 10.4 million animals in the pedigree, and 178177 genotyped animals. To reduce over-dispersion, 30% of the residual polygenic effect was included in **G**. All MME were solved with MiX99 software. Methods b), c), and d) gave the same results: correlations between GEBVs of both genotyped and non-genotyped bulls were 0.999. Also, the genetic trends, as well as standard deviations of the GEBVs by birth year, were the same. The central observation was that case a) i.e., single-step ignoring QP transformation both in **G** and $\mathbf{A}_{22}$ did not converge in a reasonable time. Thus, we conclude that 1) QP transformation is needed in **G** and/or $\mathbf{A}_{22}$ for good convergence of the single-step model, 2) different methods to make QP transformation to genotyped animals give similar results, and 3) QP transformation is easy to implement also in the ssGTBLUP which with large genomic data is computationally efficient.

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