Methods: Two groups of Japanese quail were mated, 1 male to 4 females, and housed in groups of 16, but assigned either at random (RG) or as half-sib groups (KIN). Birds were selected for increased 6 week weight based on traditional animal model BLUP for 25 cycles.
Results: Birds selected in RG resulted in a negative response to selection for body weight at 6 weeks of age (BW) (-.074±.26g/generation), in contrast, birds selected in KIN significantly increased BW (.749±.21g/generation). Similarly, mortality increased with RG (.3±.2/generation) but decreased with KIN (-.2±.2/generation).
Conclusions: These results show that competitive effects can be easily addressed in commercial breeding operations using traditional animal model BLUP, but with animals housed as families rather than at random.

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TOWARDS GENOMIC PREDICTION FROM GENOME SEQUENCE DATA AND THE 1000 BULL GENOMES PROJECT

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Using full genome sequence data in genomic prediction could be advantageous in at least three situations. If linkage disequilibrium between SNP on standard arrays and causative mutations affecting the quantitative trait is incomplete, accuracy of prediction could be improved by including the causative mutations in the data set. Secondly, if genomic predictions are made across breeds, using full sequence data is likely to be particularly advantageous, as there is no longer the need to rely on marker-associations which may not persist across breeds. Thirdly, persistence of accuracy of genomic predictions across generations should be improved with full sequence data. Unfortunately the cost of sequencing is such that it is unlikely that the entire reference population will be sequenced. An alternative strategy is to sequence key ancestors of the population, then impute the genotypes for the sequence variants into much larger reference sets with phenotypes and SNP panel genotypes. The 1000 Bull Genomes Project aims to build this database of sequenced key ancestor bulls for the bovine research community. Thus far the data set consists of 133 full genome sequences of Holstein and Fleckvieh bulls, sequenced at an average of 11.3 fold coverage. There were 17.4 million filtered sequence variants detected in the sequences, including 15.8 million SNP and 1.6 million insertion-deletions. Agreement of sequence genotypes to genotypes from a SNP array in the sequenced bulls was excellent at 98.8%. This increased to 99.7% when the genotypes were imputed given the probability of the genotypes from all sequences. This project will provide a strong opportunity to identify the most important causative variants. As a consequence, it will help to understand the biology, to differentiate shared causative variants across breeds from within breed variants. Finally, examples are given of genomic predictions for quantitative traits using imputed sequence data.