



# Reliability of genomic prediction using low density chips

D.Segelke\* †, J.Chen\*, Z.Liu\*, F. Reinhardt\*, G.Thaller †, R.Reents\*

\*Vereinigte Informationssysteme Tierhaltung vit, Heideweg 1, 27283 Verden (Aller), Germany

† Institute of Animal Breeding and Husbandry, Christian-Albrechts-University, 24098 Kiel, Germany

## Conclusions:

The accuracy of genotype imputation from the low-density chips Illumina 3K & BovineLD to the BovineSNP50 BeadChip was investigated for 3 different data sets using the imputation programs Findhap & Beagle. Allele error rate of Findhap was almost 3 times higher than Beagle. The 6K chip was twice as accurate as the 3K chip. Using Findhap & the 3K Chip reduce the reliability of genomic prediction about 5%. Beagle and the 6K chip had a reliability loss of round 1%. The low-density chip BovineLD 6K could be used routinely

for large-scale genotyping.

## Introduction:

With the availability of dense SNP marker chips, genomic evaluation was implemented in many countries. But for an average dairy breeder genotyping his whole herd is still too expensive. Therefore there was a demand to develop low density chips to reduce genotyping costs.

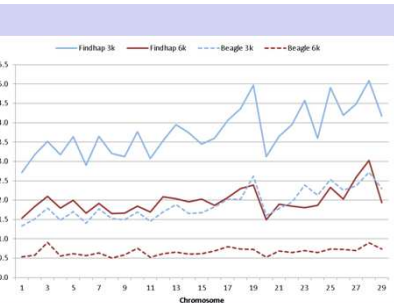


Figure 1. Mean allele error rate by chromosome when using EuroGenomics data set II.

## Results:

Allele imputation error rates depended on the size of the reference population, imputation programs, chip density and relationship between reference and validation animals. Allele error rate for the EuroGenomics data set II was 3.3% for Findhap 3K, 1.6% for Beagle 3K, 1.7% for Findhap 6K and 0.6% for Beagle 6K, respectively.

Reliability of the genomic prediction decreased on average about 5.3% for Findhap 3K, 2.6% for Beagle 3K, 1.9% for Findhap 6K and 1.0% for Beagle 6K averaged over 12 selected traits, in comparison to those of using original genotypes. Differences in GEBV of original and imputed genotypes were largest for Findhap 3K, whereas Beagle 6K had the smallest difference.

## Materials & Methods:

To study the accuracy of low density chips, Illumina Bovine3K BeadChip (3K) and BovineLD BeadChip (6K), were simulated using Illumina marker maps. Accuracy of imputing was investigated by using the software packages Beagle and Findhap. **Three** different genotype data sets were used: EuroGenomics data set with **14,405** reference bulls, smaller EuroGenomics data set with **11,670** older reference bulls and a data set containing **31,597** genotyped German Holstein animals. For validation, 1,374 bulls for the EuroGenomics data set, 534 bulls for the smaller EuroGenomics data set and 2,205 animals of the genotyped German Holstein data set, their imputed genotypes were compared to their original genotypes to calculate allele error rate.

Additionally reliability loss by using imputed instead of original genotypes was computed. Furthermore the difference in combined genomic-enhanced breeding values (GEBV) between original and imputed genotypes were calculated.

Trait	Reliability using real 50K genotypes	Reductions in reliability			
		Findhap 3K	Beagle 3K	Findhap 6K	Beagle 6K
Milk, kg	35.1	6.6	1.1	1.8	0
Fat, kg	34.6	7.8	3.8	1.6	1.1
Protein, kg	25.8	7.0	1.3	1.3	0
SCS	43.6	8.2	4.1	2.2	1.5
Days open	18.1	2.6	0.0	3.2	0
NR56 heifer <sup>1</sup>	13.7	3.4	1.1	1.5	0.9
Angularity	26.1	2.2	1.7	2.1	0.5
Stature	37.0	7.3	3.8	2.1	1.8
Chest width	26.6	3.6	2.6	1.6	1.6
Front teat length	44.9	5.1	4.9	1.2	2.3
Udder depth	46.9	8.0	6.3	3.1	2.2
Udder support	23.3	1.6	0.5	0.7	0.1
Average	31.3	5.3	2.6	1.9	1.0

<sup>1</sup>NR = Non-return rate

Table 1. Reliabilities (%), expressed as  $(R^2_{\text{GEBV}} - R^2_{\text{im}})$  reliability, of the original 50K genotypes and the reduction in reliabilities when using the imputed 50 K genotypes.



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