Three years ago, genotyping arrays of approximately 50 thousands (50K) markers were developed i
These tools allowed the breeders to apply genomic selection but also to implement fine-mapping
much more rapidly. In 2010, chips having much more markers (600K-1000K) are expected to be laun
cattle, which will likely impact the cost of older 50K chips. In parallel, whole genome sequencing c
steadily decreasing. Further, low density marker panels for screening larger portions of the cattle po
at lower costs are under development. This paper will compare the properties of these different
panels in terms of cost and genome coverage (measured as the linkage disequilibrium with unge
SNPs). Both costs and prediction accuracy of missing markers (imputation) when using lower
panels determine which marker panel would be the most cost effective in genomic selection. With
marker panels (60K) it is possible to obtain an allelic imputation error rate close to 0.5% and resul
that error rates further decrease with higher marker densities. On the contrary, allelic imputation er
increase when using lower marker density panels: ~3% with 3,000 SNPs. The error rate is a functio
relationship between the animals genotyped on the lower density panels and the animals genotype
the markers. With both parents genotyped, allelic imputation error rates are close to 0.5%, even wi
3,000 SNPs (and still lower at increasing densities). Finally, the precision of genomic selection for
genotyped on different chips will also be presented.