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From the 50K chip to the HD: Imputation efficiency in 9 French dairy cattle breeds

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Since 2008, genomic selection based on the Bovine SNP50 BeadChip® (50K) is implemented in France for the three main dairy breeds. The major challenge for the other breeds is to build large reference populations. New perspectives are offered with the BovineHD BeadChip® (HD). Indeed the density of this chip (1 Single Nucleotide Polymorphism per 4 kilobases) should be high enough to detect conserved linkage disequilibrium across breeds and therefore combine reference population with an appropriate methodology.With this aim, 2102 bulls from 9 breeds (52 to 551 per breed) were genotyped with the HD chip in the ANR-APISGENE funded GEMBAL project. 549 Holstein bulls genotyped in EUROGENOMICS consortium were added to this population leading to a total of 2651 bulls genotyped on the HD chip. This sample will be used to impute the 50K-genotypes from the national databases. Imputation error rates were computed in each breed with a validation set of 20% of the animals, selected either by age (youngest cohort) or by randomly choosing complete families. Markers were masked for validation population in order to mimic 50K genotypes. Then, imputation was done using the Beagle 3.3.0 software. Mean allele imputation error rates ranged from 0.34% to 5.1% depending on the breed. Results were better for large breeds than for regional French breeds due to differences on effective population size and, above all, on number of animals HD-genotyped. Accuracies were lower in Brown Swiss and Simmental because foreign ancestors were not genotyped; they could be improved through genotypes exchange s. Multi-breed imputation may also be a way to improve efficiency of imputation for related breeds.