

## **Design of a low density SNP chip for genomic selection in layer chicken**

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The main goal of selection is to choose breeders of the next generation among a set of selection candidates. In genomic selection, the choice of breeders rests on the use of information on DNA polymorphisms, in particular SNP, in addition of performance measures. Since 2013, a commercial high density genotyping chip (600 000 markers) for chicken allowed the implementation of genomic selection in layer and broiler breeding. However, genotyping costs with this chip still remain high for a routine use on a large number of selection candidates. Consequently, the current aim of genomic selection is to develop, at a lower cost, low density genotyping chips (LD chips). To do so, a set of SNP markers has to be selected to enable an imputation (prediction) of missing genotypes on a high density chip (HD chip).

In this perspective, various simulation studies were conducted to choose the best strategy for low density genotyping of laying hen lines. Different genotyping densities, several population scenarios and two imputation programs (FImpute V2.2 and Beagle V4.1) were tested. Low density genotyping chips were designed according to two strategies: a choice of SNP depending on a clustering based on linkage disequilibrium threshold or a choice of SNP at regular intervals. Three criteria of imputation accuracy were compared: genotyping error rate, allelic error rate and correlation. It appears that genotyping error rate as a criterion is more discriminating than the two others. FImpute software is preferred to Beagle software because FImpute is a better compromise between imputation accuracy and calculation time. The study of different low density genotyping chips shows that imputations improve with SNP density, when the LD threshold increases and when SNP with low MAF (Minor Allele Frequency) are considered. Population studies show that imputations are better when the size of the reference population increases. The influence of kinship degree between reference population and target population, and the impact on accuracy of genomic evaluations still remain to be deepened.

These studies will be extended to a second laying hens line to see if a shared low density genotyping chip can be created for both lines.

**Keywords:** Imputation accuracy ; layer chickens ; SNP density ; reference population, genomic evaluation