DESIGN OF A LOW DENSITY SNP CHIP FOR GENOMIC SELECTION



IN LAYER CHICKENS

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INTRODUCTION

Since 2013, a commercial high-density SNP chip of 600 000 SNP for chicken is available and enables the implementation of genomic selection in layers production. However, genotyping costs still remain high for a routine use on a large number of selection candidates. Combining genotyping on lowdensity SNP chip, at a lower cost, and genotype imputation should be considered on a large number of selection candidates. Thus, the definition of SNP panel is the milestone of this approach.

The main objective of this study is to choose the best strategy for low density genotyping of laying hen lines in order to optimize selection scheme.

■ MATERIALS AND METHODS

Study populations: Study of two different lines of Rhode Island (RI) and Leghorn (L) from Novogen, genotyped on HD SNP chip (Table 1). After quality control, respectively 300 351 and 245 667 SNP are retained and distributed for Rhode Island and Leghorn lines on the genome.

| Line | Rhode Island | Leghorn |
|-----------------------------|--------------|---------|
| Number | 1027 | 1474 |
| Sires | 1027 ♂ | 561 ♂ |
| Dams | 0 ♀ | 913 ♀ |
| Generation 0 (G0) | 447 | 711 |
| Generation 1 (G1) | 580 | 763 |
| Table 1 : Study populations | | |

Low density SNP chips:

Simulation of low-density SNP chip according to two intrachromosomes methodologies (Table 2):

- « Equidistant » methodology: Selection of SNP at regular
- « Linkage Disequilibrium » methodology: Selection of SNP according to the LD between SNP.

Imputation strategies: Use of Fimpute (Sargolzaei et al., 2014) to impute G0 from G1. From low density SNP chips designed, study of the effect of:

- SNP density,
- LD threshold used to designed low density SNP chips,
- the type of chromosome (macro-chromosomes (1 to 5), intermediate chromosomes (6 to 10), microchromosomes (11 to 33) and sexual chromosome Z,
- MAF (Minor Allelic Frequence) of SNP,
- the methodology used to designed low-density SNP chips.

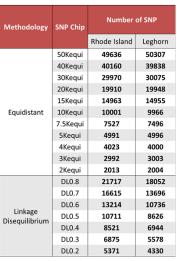


Table 2: Summary of SNP chips studied

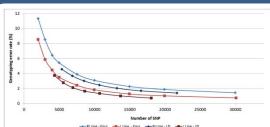


Figure 2 : Evolution of genotyping error rate as a function of the

RESULTS AND DISCUSSION

Influence of SNP density:

- ➤ Decrease of genotyping error rate with an increase in the number of SNP (Figure 2).
- > Valid for both methodologies.

Influence of LD threshold:

- Decrease of genotyping error rate with an increase in LD threshold (Figure 3).
- > By increasing LD threshold, the number of SNP on low density SNP chip increases. The increase of LD threshold also makes it possible to choose a SNP still more representative of its group.



Choice of the methodology:

- « Equidistant » methodology: Number of SNP proportional to the size of chromosome (Figure 4).
- « LD » methodology: Consideration of the particular structure of chicken species' LD and of the lower persistence of LD on micro-chromosomes than on macro-chromosomes.
 - → Necessity of a greater number of SNP on micro-chromosome to cover the whole chromosome (Figure 4).
- « LD » methodology seems to be the most appropriated to get good imputations.

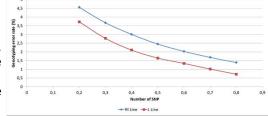


Figure 3: Evolution of genotyping error rate as a function of LD threshold

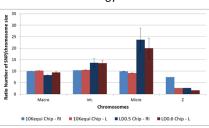


Figure 4: Evolution of the ratio Number of SNP/Chromosome size as a function of the type of chromosome.

Influence of Minor Allelic Frequencies (MAF):

- > Variability of genotyping error rate higher with equidistant methodology than with LD methodology (Figure 5).
- Lower genotyping error rates obtained with LD methodology, except for SNP with high MAF.
- Decrease of genotyping error rates for SNP high MAF with equidistant methodology.
- Valid for both lines.

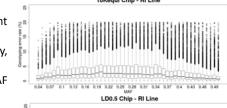


Figure 5: Evolution of genotyping error rate according to the MAF for Rhode Island Line



According to the MAF, lower genotyping error rates obtained with LD methodology, excepted for SNP with high MAF.









