Estimation of Haplotype Diversity and Recombination Rate on Chromosomes 5 and 15 in Layer Chickens

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Ziqing Weng, Graduate Student; Anna Wolc, Adjunct Assistant Professor, Department of Animal Science;
Jesus Arango, Petek Settar, Janet E. Fulton, Neil P. O'Sullivan, Poultry Geneticists, Hy-Line International;
Rohan Fernando, Jack Dekkers, Dorian Garrick, Professors, Department of Animal Science
Iowa State University

Summary and Implications

The objectives of this study were to compare the performance of different haplotype reconstruction approaches, characterize haplotype diversity and identify recombination hotspots on chromosomes 5 and 15 in layer chicken. BEAGLE, DAGPHASE, and fastPHASE software recognized fewer haplotypes than two other methods. In total, 10 and 2 recombination hotspots were identified on chromosomes 5 and 15, respectively. Further study is needed to confirm these regions with high recombination rate and high haplotype diversity.

Introduction

Various approaches have been developed to phase and reconstruct haplotypes from genotype data using family and/or population information. Quantitative trait loci and their surrounding markers tend to be inherited together in haplotype blocks. Recombinations at meiosis separate haplotype blocks, and create new haplotypes. Reconstructing haplotype blocks and quantifying recombination rate are valuable for genomic analysis.

Materials and Methods

The study population included 1,200 purebred birds representing 7 generations that were genotyped with an Affymetrix 600K single nucleotide polymorphisms (SNP) panel. Missing genotypes (~0.006%) were imputed using FImpute. SNP with call rate <0.9, Mendelian error rate >0.05, and minor allele frequency <0.0001 were removed. After quality control, only 173,224 segregating SNPs remained. Recombination events were identified within parent-offspring pairs using LINKPHASE. The average size of 492 half-sib families was 3.0±3.0. Different approaches were applied to reconstruct haplotypes: findhap3.0, BEAGLE4.0, DAGPHASE2.5, AlphaPhase1.1, and fastPHASE1.2. The haplotype diversity and recombination rate within each non-overlapping 1Mb window were assessed on chromosomes 5 (physical length of 62Mb) and 15 (physical length of 13Mb). Only haplotypes with a frequency greater than 1% were counted because phasing errors can result in erroneous low frequency haplotypes.

Results and Discussion

Figure 1 uses chromosome 5 as a representative example of the number of haplotypes (including haplotypes with frequencies <1%) detected by different approaches. fastPHASE only uses population information, while other methods combine family and population information. BEAGLE, DAGPHASE, and fastPHASE identified much lower numbers of haplotypes than the other two methods. These three approaches use Hidden Markov models to cluster haplotypes. AlphaPhase uses a long-range phasing algorithm, whereas findhap applies both long and short segments to close relatives and distant ancestors. Computationally, findhap was much faster than the other approaches, while fastPHASE was the slowest. After removing low frequency haplotypes, all the approaches yielded similar haplotype diversity (Table 1). There were 1,008 and 202 recombination events identified from 1,348 parent-offspring pairs on chromosomes 5 and 15, respectively. Ten recombination hotspots, and twelve cold-spots, were identified on chromosome 5. On chromosome 15, 2 hotspots and 5 cold-spots were found. Windows with recombination rates greater than 0.025 (≥1.5 SD from the mean) were considered to be hotspots, while windows with zero recombination were cold-spots. The haplotype diversity increased with increases in recombination rate. The number of haplotypes in hotspots and cold-spots were 8.5±1.7 and 1.9±0.9 on chromosome 5 and 10.5±4.9 and 2.6±1.3 on chromosome 15.

Further study is needed to confirm these regions with high recombination rate and high haplotype diversity.

Acknowledgments

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Table 1. The average number of common haplotypes (±SD) detected within 1 Mb windows using different methods.

Chromosome	Average # of SNPs per 1 Mb	findhap	BEAGLE	DAGPHASE	AlphaPhase	fastPHASE
5	173.2±50.7	5.8±4.0	4.7±2.6	4.7±2.6	9.0±6.4	4.7±2.6
15	253.3±83.3	5.8±4.3	4.7±3.8	4.7±3.8	7.9±7.0	4.5±3.7

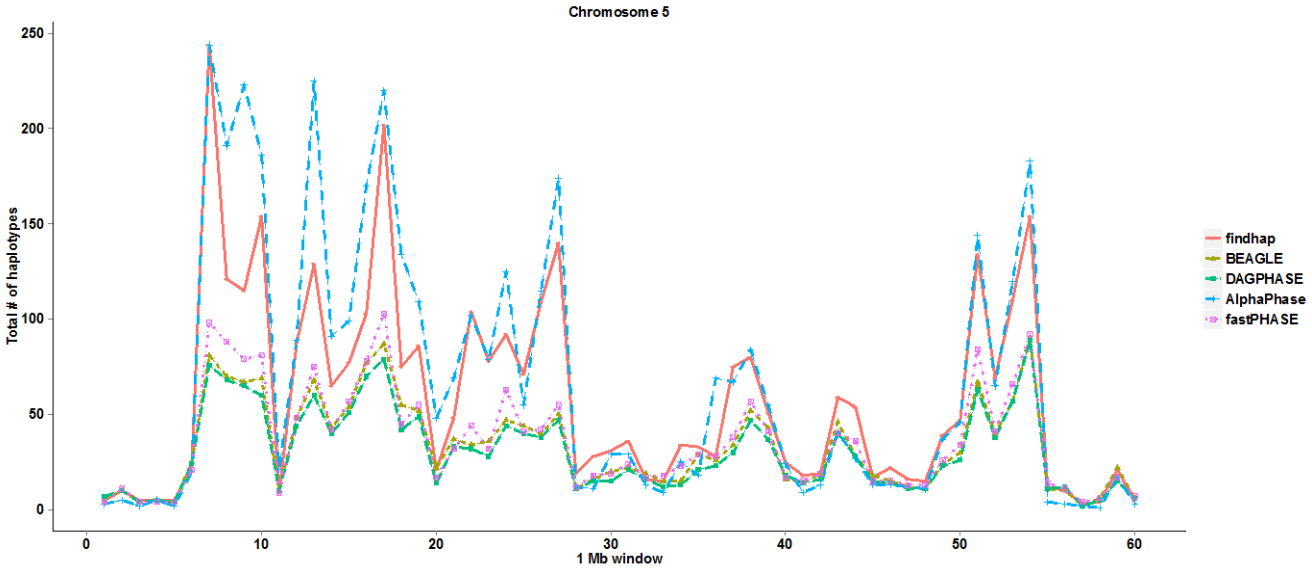

Figure 1. The number of raw haplotypes within 1 Mb window on chromosome 5 using different approaches.