



A linkage disequilibrium study in layers and broiler commercial chicken populations

Frédéric Hérault, Florian Herry, Amandine Varenne, Thierry Burlot, David Picard–Druet, Julien Recoquillay, Camille Macé, Frédéric Fagnoul, Sophie Allais, Pascale Le Roy

► To cite this version:

Frédéric Hérault, Florian Herry, Amandine Varenne, Thierry Burlot, David Picard–Druet, et al.. A linkage disequilibrium study in layers and broiler commercial chicken populations. 11. World Congress on Genetics Applied to Livestock Production (WCGALP), Feb 2018, Auckland, New Zealand. hal-01791806

HAL Id: hal-01791806

<https://hal.science/hal-01791806>

Submitted on 14 May 2018

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License

A Linkage disequilibrium study in layers and broiler commercial chicken populations.

F. Hérault¹, F. Herry¹⁻², A. Varenne², T. Burlot², D. Picard-Druet¹, J. Recoquillay³, C. Macé³, F. Fagnoul³, S. Allais¹ and P. Le Roy¹.

¹ PEGASE, INRA, Agrocampus Ouest, 16 Le Clos 35590 Saint-Gilles, France

frederic.herault@inra.fr (Corresponding Author)

² NOVOGEN, Mauguierand 22800 Le Foeil, France

³ HUBBARD, Mauguierand 22800 Le Foeil, France

Summary

Knowledge of the linkage disequilibrium (LD) pattern is useful in animal genetic studies as it underlies mapping studies and genomic selection. Recently, the availability of the high density 600K Affymetrix® Axiom® HD SNP genotyping array allows to assess a higher resolution of the LD structure in chicken genome. In this study, we analysed genotypes of 1541 animals from layers and broiler commercial populations to characterize their LD pattern. LD was measured by the average r^2 value at a given physical distance between SNP. LD extends over a larger region for layers line than for broiler line. Most differences between lines appeared at small interval distance ($< 0.5\text{Mb}$). LD extent and decay differed considerably between chromosome categories. Average r^2 values were higher for Z chromosome than for macro, intermediates and microchromosomes. The extent of useful LD observed for autosomal chromosomes is at least tenfold longer for layers line than for broiler. Finally, this study shed light on high LD for the Z chromosome. The differences in LD pattern observed between chromosomes and chicken lines should be taken into account to define an economically efficient genotyping strategy.

Keywords: layer, broiler, linkage disequilibrium.

Introduction

Accurate knowledge of the linkage disequilibrium (LD) pattern is important in domestic animal genetic studies as it underlies mapping studies and genomic selection. Using thousands of genetic markers, association studies rely on LD extent to identify markers in high LD with causal polymorphisms and to achieve fine mapping of a QTL. LD extent is also one of the parameters which affect the genomic evaluation accuracy. Consequently, accurate characterization of LD structure is needed to achieve reliable prediction for genetic selection candidates and to maximise the genetic gain in selection (Meuwissen et al., 2001). LD extent is also an important parameter for the selection of markers in the design of low density SNP array which are crucial to define large scale genotyping strategy.

Since 2013, the availability of the high density 600K Affymetrix® Axiom® HD SNP genotyping array (Kranis et al., 2013) allows a higher resolution assessment of the LD structure in chicken genome. This SNP genotyping array was constructed using 24 chicken lines (experimental, commercial broiler and layer lines) to ensure a uniform distribution of SNP based on genetic map distance for broiler and layer lines, and to allow hundreds of thousands of informative SNP per line.

The chicken genome is organized in 38 autosomes and one pair of sex chromosomes. Chicken autosomes are characterized by their organisation in five large chromosomes spanning from 40 to 200 Mb (macrochromosomes, GGA1 to GGA5), five intermediate size chromosomes spanning from 20 to 40 Mb (GGA6 to GGA10) and 28 small size chromosomes <20 Mb (microchromosomes, GGA11 to GGA38). Recombination rate and gene density are higher for microchromosomes than for others (International Chicken Genome Sequencing Consortium, 2004).

The aim of the present study was to assess a high resolution of the LD pattern in chicken genome using the 600K Affymetrix® Axiom® HD SNP genotyping array to characterize LD structure according to chromosomes length in layers and broiler commercial lines.

Material and Methods

Genotype data

The three populations studied consisted of a total of 1541 animals from layers and broiler commercial lines. Two layers lines, a white egg laying chickens (Leghorn (L)) and a brown egg laying chickens (Rhode-Island (RI)) selected by the NOVOGEN breeding company (Le Foail, France) and a broiler line (Shaver Yellow Cornish (SYC)) selected by the HUBBARD breeding company (Le Foail, France) were genotyped using the 600K Affymetrix® Axiom® HD genotyping array. The RI line was constituted of 447 chickens, the L line was constituted of 711 chickens, and the SYC line was constituted of 383 chickens. Blood samples were collected from brachial veins of individuals and DNA was extracted and hybridized on the high density genotyping array which contains 580,961 SNP that were distributed over chromosomes 1 to 28, chromosome 33, a linkage group (LGE64) and the two sex chromosomes, along with 3724 markers of unknown location based on Gallus gallus - 5.0 reference assembly.

Within each breed, genotype filtration was performed using PLINK software (PLINK version 1.9; www.cog-genomics.org/plink/1.9/) (Chang et al., 2015). SNP with genotype call rate <95%, MAF <0.05 and Hardy–Weinberg equilibrium deviation P-value <0.0001 were filtered out. For the purpose of this study, we used only SNP with assigned chromosome location. SNP located on chromosome W, 16 and 33 as well as SNP located on linkage group LGE64 were discarded from this study as these chromosomes did not include enough markers. All individuals used in this study had genotype call rate greater than 95%.

Estimation of linkage disequilibrium

LD was calculated as pairwise r^2 values using PLINK software between each pair of SNP within a chromosome for each population. LD extent and decay were estimated for each chromosome category according to the classification used by the International Chicken Genome Sequencing Consortium: macro, intermediate and microchromosomes and Z chromosome. For Z chromosome r^2 calculation was limited to males. LD pattern for each breed and each chromosome category was estimated as the average r^2 value at a given inter markers physical distance.

Results and discussion

Markers

As shown in Table 1, most of the SNP have been eliminated because of the minor allele frequency. Clearly, layer lines exhibit a higher proportion of low MAF SNP than the broiler line. The L line had the smallest number of informative SNP, and SYC broiler line had the highest number of SNP in use. These results are consistent with previous studies (Megens et al., 2009; Qanbari et al., 2010). Although the number of informative SNP differed considerably between lines, estimated genome coverage for each line was nearly the same and the average adjacent distance between markers was below 5kb.

Table 1. Descriptive summary of SNP used for each population.

	Layers		Broilers
	L	RI	SYC
Total number SNP	580,961	580,961	580,961
SNP Call rate < 95%	2,530	7,541	4,274
MAF ¹ < 5%	327,452	258,772	181,584
HWE ² < 0.0001	3,857	12,538	6,664
Remaining located SNP	245,669 (42%)	300,362 (52%)	386,187 (66%)
Genome coverage (Mb)	1,017	1,017	1,019
Mean adjacent marker spacing (kb)	4.1	3.4	2.6

¹ MAF: number of SNP with minor allele frequency <0.05

² HWE: number of SNP with Hardy–Weinberg equilibrium deviation P-value <0.0001.

Linkage disequilibrium analyses

LD extent and decay were estimated for each line as a function of physical distance between SNP (Table 2). For all studied populations, LD decline as the pairwise distance between SNP increase, to reach 0.02 between 3 and 10 Mb depending on the population. At small interval distance (< 0.5Mb), observed LD strength varied considerably between lines. The L line and the SYC broiler line had the highest and lowest average LD, respectively.

Table 2. Strength of LD versus physical distance between SNP for each population.

	Layers		Broilers
	L	RI	SYC
Distance (Mb) ¹	Mean ± SD	Mean ± SD	Mean ± SD
0.0-0.025	0.62 ± 0.37	0.52 ± 0.38	0.34 ± 0.33
0.025-0.05	0.53 ± 0.37	0.46 ± 0.37	0.28 ± 0.29
0.05-0.075	0.49 ± 0.36	0.43 ± 0.36	0.25 ± 0.28
0.075-0.12	0.44 ± 0.35	0.39 ± 0.35	0.23 ± 0.26
0.12-0.2	0.39 ± 0.34	0.35 ± 0.33	0.2 ± 0.24
0.2-0.5	0.29 ± 0.3	0.27 ± 0.29	0.15 ± 0.2
0.5-1.5	0.16 ± 0.22	0.15 ± 0.21	0.08 ± 0.14
1.5-3.0	0.07 ± 0.14	0.07 ± 0.14	0.04 ± 0.09
3.0-5.0	0.04 ± 0.09	0.04 ± 0.09	0.02 ± 0.05
5.0-10.0	0.02 ± 0.05	0.02 ± 0.05	0.01 ± 0.02

¹ Distance (Mb): based on Gallus gallus - 5.0 reference assembly.

LD extent and decay were also estimated according to chromosome category for each population. As shown on Figure 1, LD extent and decay differed considerably between chromosome categories. The levels of LD were higher and extended over longer distance for Z chromosome than for macro, intermediate and microchromosomes for all populations.

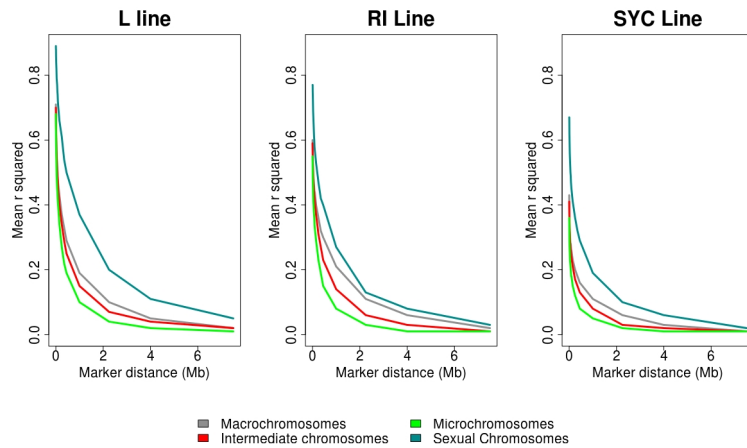


Figure 1. Decay of linkage disequilibrium with distance between SNP in different populations according to chromosome category.

It is generally considered that an average r^2 value stronger than 0.3 is sufficient to be useful for association studies or genomic selection (Ardlie et al., 2002; Calus et al., 2008). Considering the extent of useful LD for autosomal chromosomes, there is a great similarity between the two layers line compared to SYC broiler line. The extent of useful LD for large chromosomes is tenfold longer for layers line than for broiler. The difference of extent of useful LD between layers and broiler is substantially higher for the microchromosomes. It should be noted that a slight difference was observed between the two layers lines for the microchromosomes. This difference may be explained by the higher gene density and recombination rate observed for these chromosomes. Finally, the extent of useful LD was longer and more similar between layers and broiler lines for Z chromosome than for macrochromosome, intermediate or microchromosome. (Table3).

Table 3. Extent of useful LD ($r^2 > 0.3$).

	Layers		Broilers
	L	RI	SYC
Genome	200-300 kb	200-300 kb	20-30 kb
Macrochromosomes	300-400 kb	400-500 kb	30-40 kb
Intermediate chromosomes	200-300 kb	200-300 kb	20-30 kb
Microchromosomes	100-200 kb	90-100 kb	5-7.5 kb
Z chromosome	500-1500 kb	400-500 kb	300-400 kb

Conclusion

In this study we have characterized the LD pattern of three chicken populations. The strength and extent of LD varied considerably between breeds and chromosome categories. On one

hand, the LD extent observed over large region for Chromosome Z and macrochromosome is an advantage for finding association between a phenotype and a marker even with a sparse SNP map. On the opposite, it will make fine mapping more challenging. On the other hand, on microchromosomes, the fast decay of LD requires a denser marker map to identify association between marker and phenotype, but will be useful for high resolution mapping of causal polymorphisms. These differences in LD pattern should be taken into account to define an economically efficient genotyping strategy.

Acknowledgements

This research project was partly supported by the French national research agency “ANR” within the framework of project ANR-10-GENOM_BTV-015 UtOpIGe”.

List of references

- Ardlie, K.G., Kruglyak, L., Seielstad, M., 2002. Patterns of linkage disequilibrium in the human genome. *Nat. Rev. Genet.* 3, nrg777. <https://doi.org/10.1038/nrg777>
- Calus, M.P.L., Meuwissen, T.H.E., de Roos, A.P.W., Veerkamp, R.F., 2008. Accuracy of Genomic Selection Using Different Methods to Define Haplotypes. *Genetics* 178, 553–561. <https://doi.org/10.1534/genetics.107.080838>
- Chang, C.C., Chow, C.C., Tellier, L.C., Vattikuti, S., Purcell, S.M., Lee, J.J., 2015. Second-generation PLINK: rising to the challenge of larger and richer datasets. *GigaScience* 4, 7. <https://doi.org/10.1186/s13742-015-0047-8>
- International Chicken Genome Sequencing Consortium, 2004. Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* 432, nature03154. <https://doi.org/10.1038/nature03154>
- Kranis, A., Gheyas, A.A., Boschiero, C., Turner, F., Yu, L., Smith, S., Talbot, R., Pirani, A., Brew, F., Kaiser, P., Hocking, P.M., Fife, M., Salmon, N., Fulton, J., Strom, T.M., Haberer, G., Weigend, S., Preisinger, R., Gholami, M., Qanbari, S., Simianer, H., Watson, K.A., Woolliams, J.A., Burt, D.W., 2013. Development of a high density 600K SNP genotyping array for chicken. *BMC Genomics* 14, 59. <https://doi.org/10.1186/1471-2164-14-59>
- Megens, H.-J., Crooijmans, R.P., Bastiaansen, J.W., Kerstens, H.H., Coster, A., Jalving, R., Vereijken, A., Silva, P., Muir, W.M., Cheng, H.H., Hanotte, O., Groenen, M.A., 2009. Comparison of linkage disequilibrium and haplotype diversity on macro- and microchromosomes in chicken. *BMC Genet.* 10, 86. <https://doi.org/10.1186/1471-2156-10-86>
- Meuwissen, T.H.E., Hayes, B.J., Goddard, M.E., 2001. Prediction of Total Genetic Value Using Genome-Wide Dense Marker Maps. *Genetics* 157, 1819–1829.
- Qanbari, S., Hansen, M., Weigend, S., Preisinger, R., Simianer, H., 2010. Linkage disequilibrium reveals different demographic history in egg laying chickens. *BMC Genet.* 11, 103. <https://doi.org/10.1186/1471-2156-11-103>