Mapping linkage disequilibrium in breeds of *Gallus gallus*

Reuben J. Pengelly[1], Almas A. Gheyas[2], David W. Burt[2], Andrew Collins[1] & Sarah Ennis[1]

1. Human Genetics & Genomic Medicine, Faculty of Medicine, University of Southampton, UK; 2. Roslin Institute, University of Edinburgh, UK.
Contact: R.J.Pengelly@soton.ac.uk

Introduction

- Many breeds of *G. gallus* have been selected for traits beneficial for meat and egg production (broiler & layer breeds respectively). As the process of selective breeding is predominantly phenotype led, the genes under selection are often not known.
- Linkage disequilibrium (LD) patterns are shaped by many factors, including recombination, selection pressures and population history, such as bottlenecks.
- LD maps constructed according to the Malécot model incorporate information from genetic and haplotypic diversity of a population to produce a genetic map in LD units (LDU), analogous to a pedigree-based genetic map in Morgans, though produced instead from population data and thus incorporating the additional factors beyond recombination [1].
  - 1 LDU represents the distance over which LD descends to background levels.
- Comparison of LD patterns will allow for the identification of regions under selection, as well as fine-mapping of recombination.

Objectives

1. Generate LD maps from genotype data for three breeds.
2. Evaluate LD maps for pan-genomic population differences.

Materials & Methods

- High density array derived genotyping data [2] for broilers and brown and white egg layers (BEL & WEL respectively) were filtered for common, high quality SNP markers (counts in Table 1).

	Broilers	BEL	WEL
Founders	123	52	46
SNPs	606,769	636,071	327,756

Table 1: Genotype data used for LD map generation

- An LD map for each chromosome was constructed from the genotype data using the software LDMAP [1].

Results

- LD maps show consistent gross topography between breeds, and with previous linkage maps for chromosome 2 (Figure 1) [3].
  - Similarity between LD and linkage maps for chromosome 2 confirms recombination as a predominant driving force behind LD structure, as is seen in human populations [1].
  - LD map length is proportional to the haplotypic diversity within the population, the short map for WEL therefore mirrors the limited diversity due to a recent population bottleneck.

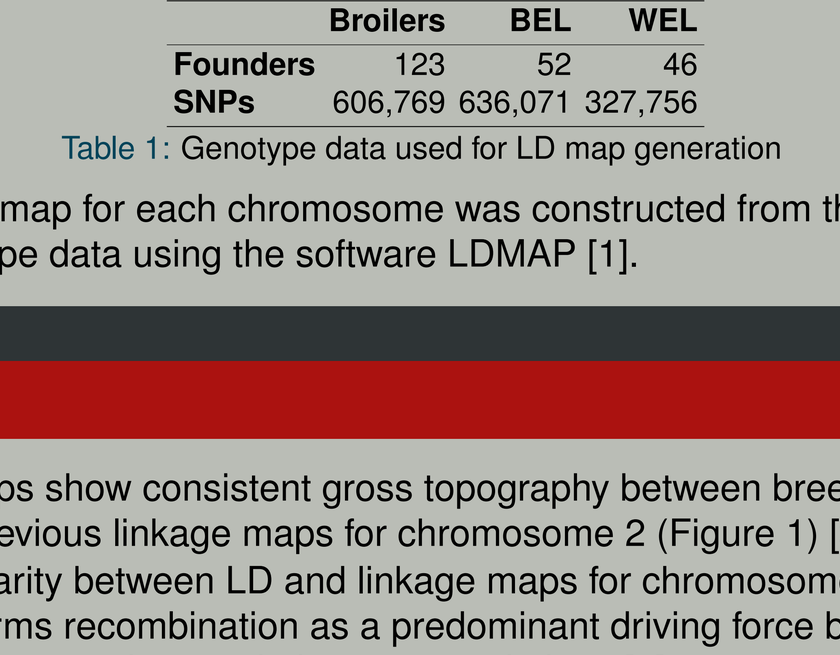

Figure 1: LD and linkage maps for chromosome 2

- There is a strong correlation between the physical and cM with LDU length of the 28 autosomes for all breeds (Figure 2) [3].
  - Correlation with physical length of chromosome is far stronger than with genetic length in cM.

Results contd.

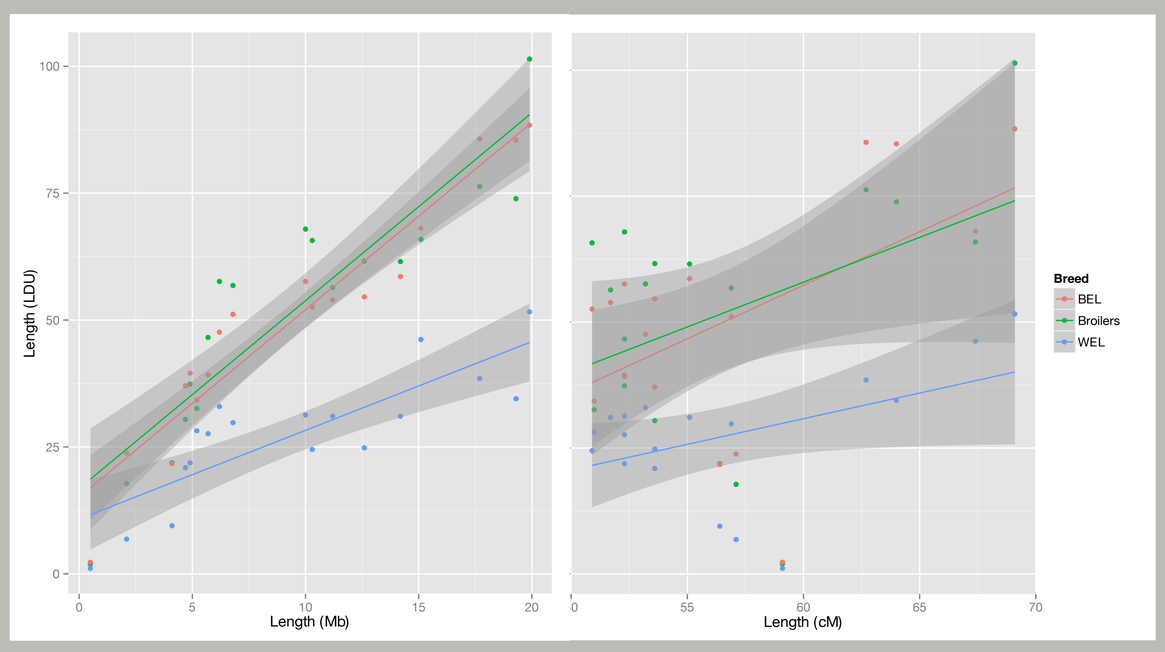

Figure 2: Relationship between Mb and cM with LDU for chromosomes 11–28

- There is negligible correlation of fine scale LD structure between breeds ($r^2 \ll 0.10$ in all pairwise comparisons).
  - The low correlation in LD structure indicates that the profiles of recombination vary significantly between breeds.
  - This LD structure variation is highlighted in plots of LDU/sliding window (Figure 3).

Figure 3: LDU spans of 40 kb sliding windows for chromosome 2

Conclusion

- LD maps provide similar information to linkage maps.
  - We have generated LD maps with 15–30-fold greater resolution than existing linkage maps.
- There is much variation in LD patterns between breeds.
  - LD pattern variation between breeds greatly exceeds that seen between outbred human populations [4].
- Mapping the specific LD patterns in breeds will aid mapping of selection and interpretation of GWAS results.
- Whole-genome sequencing of populations would provide the best possible resolution for LD mapping [4].

References

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