The genetic basis of a domestication trait in the chicken

mapping quantitative trait loci for plumage colour

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Conclusions

The results of this study suggest that appearance of pigmentation in chicken plumage is due to the combined effect of many loci located in different chromosomes and highly influenced by sex.

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Background

Domestication is the process by which animals become adapted to the environment provided by humans. The process of domestication and more specifically the altered selection pressure induced by human has produced a number of correlated behavioural, morphological and physiological changes in animals.

The phenotype that altered during domestication is referred as "domestic phenotype". The most prominent morphological trait that has been changed in the course of domestication is the alteration of plumage colour.

In general, it is believed that chickens were domesticated in South East Asia around 8000 years ago and Red Junglefowl (*Gallus gallus*) is the common ancestor for all domestic chicken.

During domestication of chicken, selection for numerous different colour phenotypes has occurred, giving rise to a wealth of different coloured domestic breeds differing from their wild ancestors.

Several genes have been identified that affect plumage colour in chickens, however many more remain to be identified.

Aim of the study

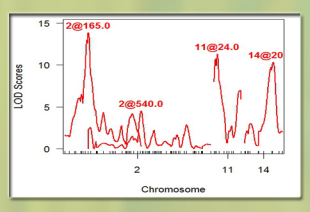
The aim of this study was to identify additional quantitative trait loci (QTLs) and candidate genes responsible for plumage colour variation in chicken.

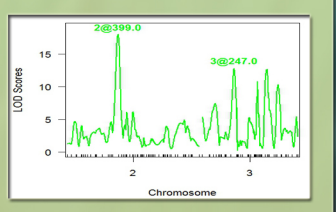
Methods

* 572 F_8 advanced intercross chickens (Red Junglefowl x White Leghorn) were produced.
* Genotyped with 657 molecular markers.
* Chickens were sacrificed at the age of 212 days, wings were separated from the shoulder joint.
* Wings were photographed digitally.
* Colour measurements were done in Adobe Photoshop CS4.
* QTL analyses were done using R/qtl.

Results

* 6 QTLs were detected; 4 for red colour and 2 for metallic green colour.
* 4 pairs of epistatic QTLs were detected; 2 pairs for red colour and 1pair for green colour
* Significant sex interactions were also detected.





Identified QTLs

Trait (Colour)	Chromosome	Locus (cM)	LOD	% variance	Estimated Effect ± SE		Confidence Interval (cM)	P-value
					Additive	Dominance		
Red	2	165	13.84	12.72	10.44±11.49	3.6±12.19	25	3.50e-09***
Red	2	540	4.5	3.89	-8.48±2.5	9.43±3.64	342	6.40e-05***
Red	11	24	11.27	10.19	12.64±7.66	-45.31±12.07	30	7.01e-08***
Red	14	203	10.31	9.26	-26.28±14.21	-13.59±18.21	43	5.86e-08***
Metallic Green	2	399	18.03	14.23	0.2±0.03	-0.1±0.05	21	4.14e-14***
Metallic Green	3	247	12.85	9.9	0.01±0.04	-0.39±0.08	272	1.57e-09***

Experimental Work Flow