

*Chicken phenotypic and
genetic diversity: Where
does it come from ...*

Olivier Hanotte, ILRI

*ACGG 3rd Project Management meeting
Abuja, Nigeria 28-29 November 2016*



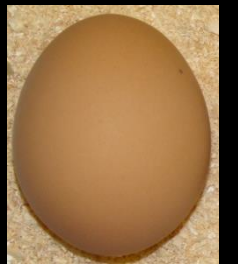
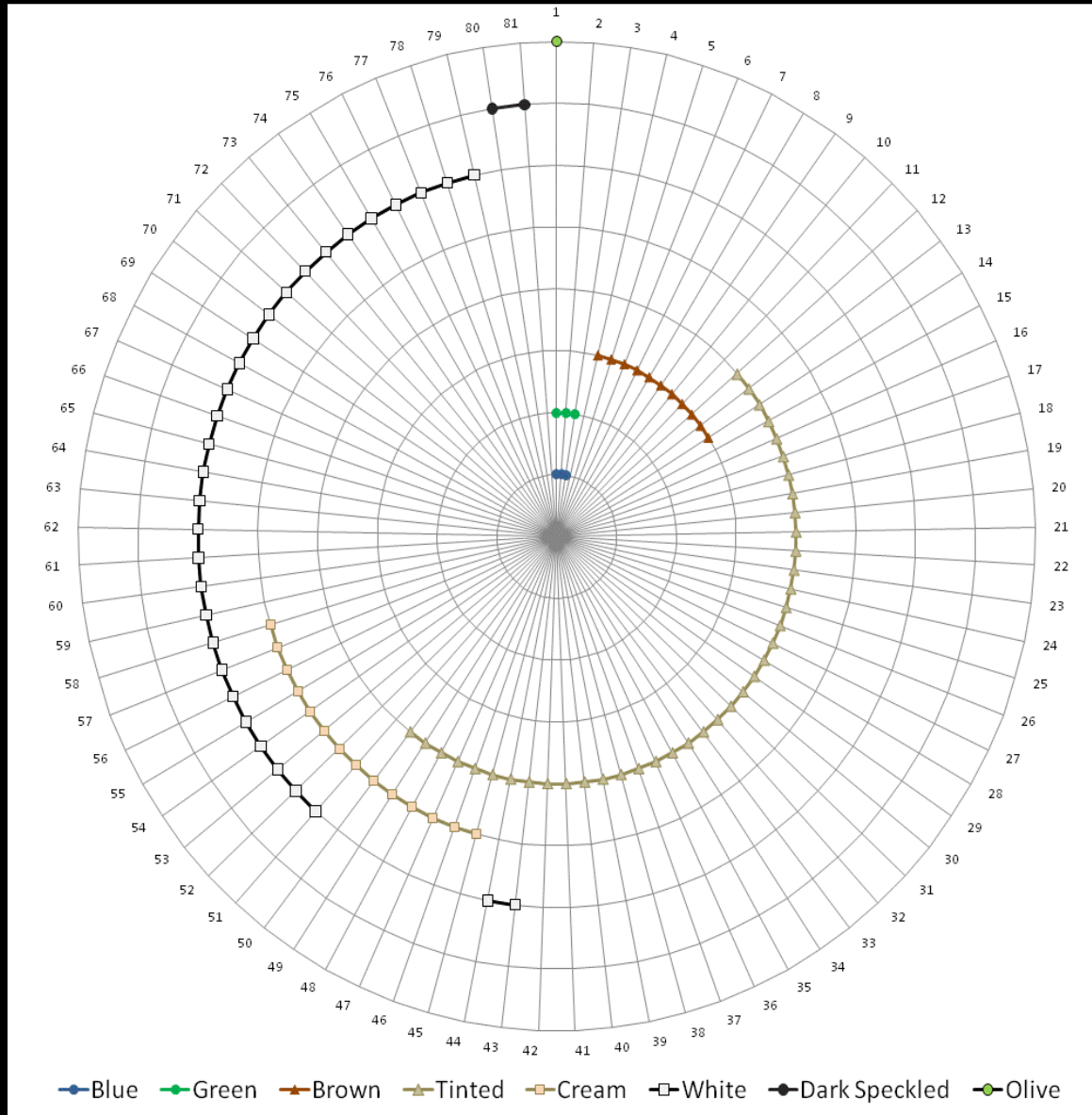
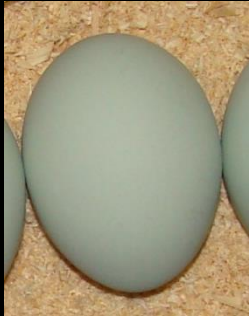




Single comb
Duplex comb

Rose comb
Pea comb
Walnut comb
Strawberry

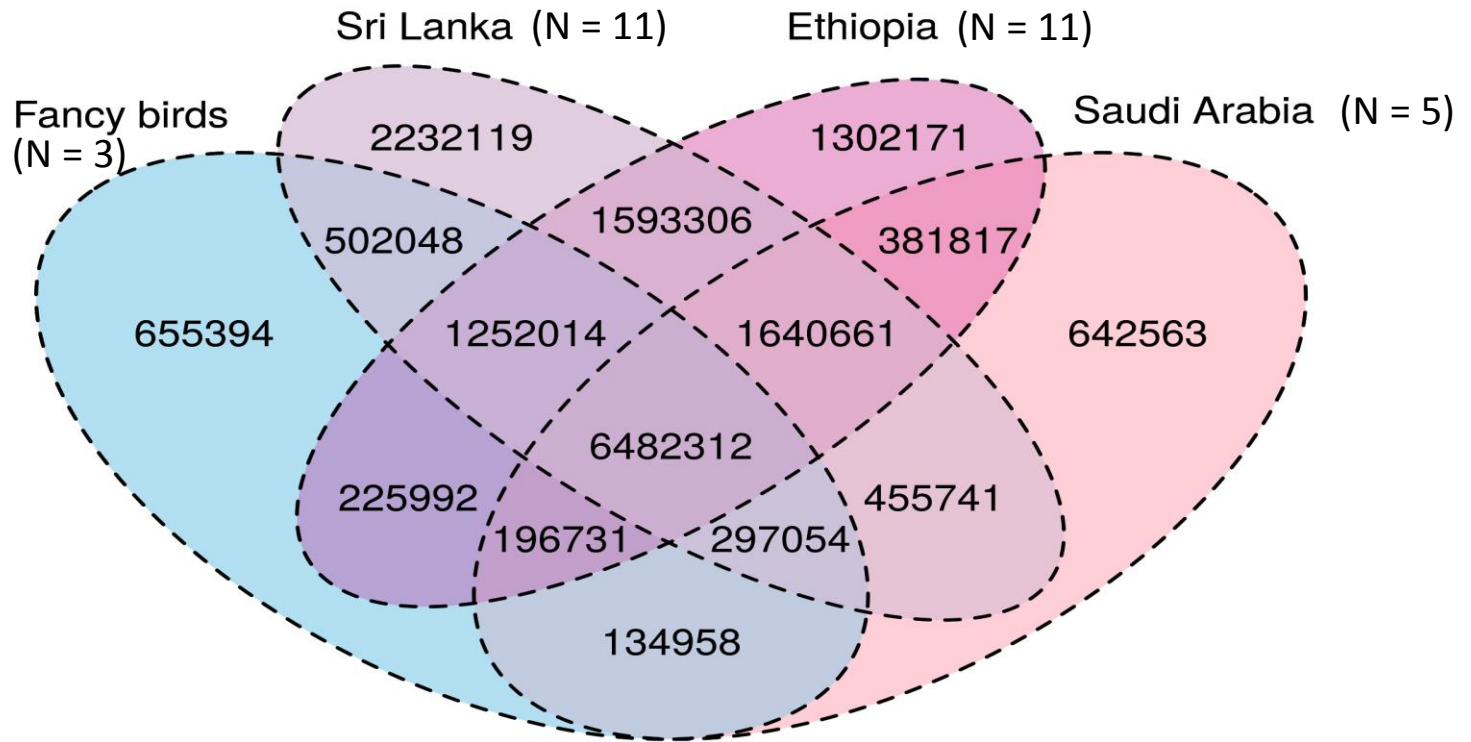
Egg-color phenotypes in 81 fancy chicken breeds



Genome diversity
Comparison with the chicken genome of reference
Galgal 4.0

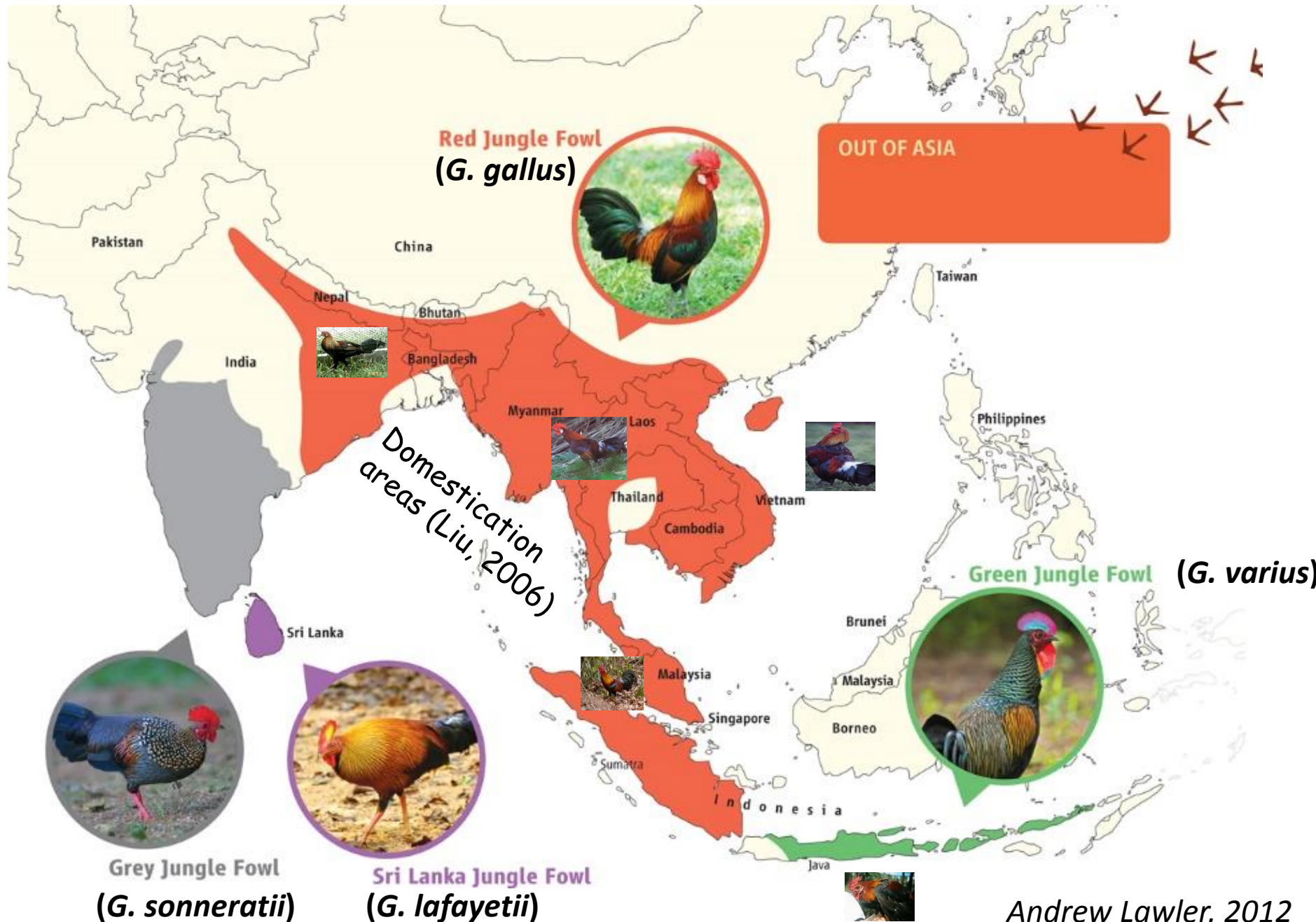
- **Mechelse Koekoek** (parent): 6.96 million differences (Koen Vanmechelen, Library of Collected Knowledge, Arena de Evolucion, Bienal de La Habana (CU), 2015).
- **Mechelse Styrian** (17th generation): 8.40 million differences (Koen Vanmechelen, Library of Collected Knowledge, Arena de Evolucion, Bienal de La Habana (CU), 2015).
- **Ethiopian village chicken**: 6.20 million differences (Lawal Raman, PhD, University of Nottingham).
- **Red junglefowl (wild)**: 7.16 million differences (Lawal Raman, PhD, University of Nottingham).

Shared and unique SNPs across some indigenous chicken population





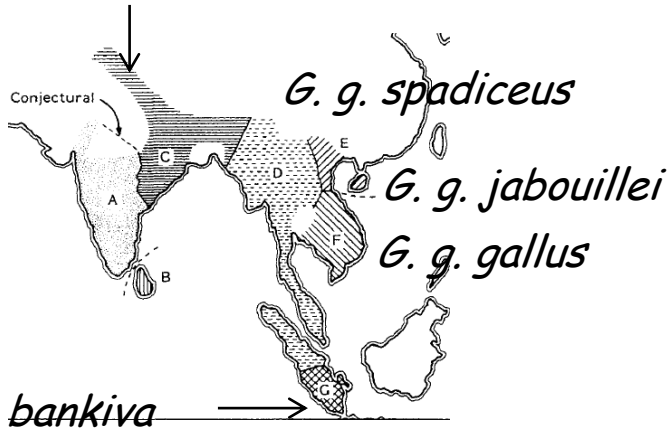
Geographical distribution of the wild junglefowls



Domestic chicken possible ancestors

Gallus sp. Geographic Range

G. g. murghi



Subspecies:

Gallus gallus gallus - E Thailand - Kampuchea, C & S Laos - C & S Vietnam

Gallus gallus spadiceus - S China, Burma, Thailand (not E), peninsular Malaysia and N Sumatra

Gallus gallus bankiva - S Sumatra, Java, Bali

Gallus gallus murghi - N & NE India, Nepal, Bhutan and Bangladesh.

Gallus gallus jabouillei - S China, N Vietnam

Sri Lanka/Ceylon
Junglefowl (*G. lafayetti*)



Grey Junglefowl
(*G. sonneratii*)

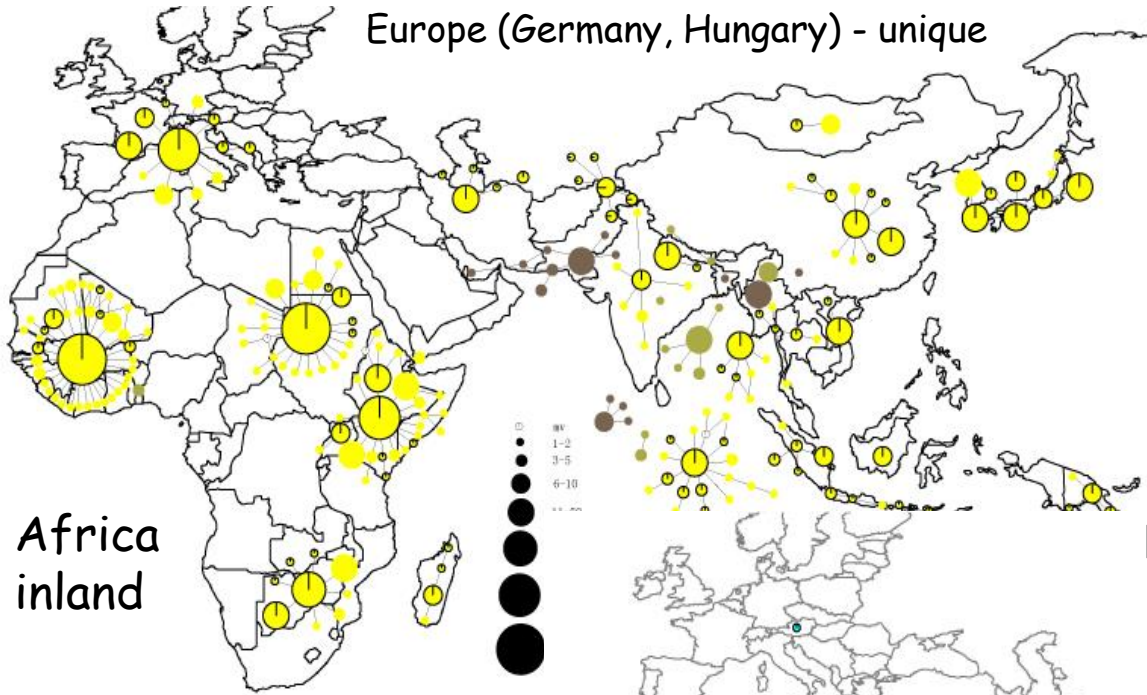


Green Junglefowl
(*G. varius*)

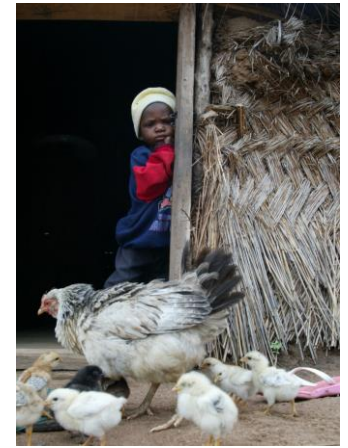


Haplogroup D

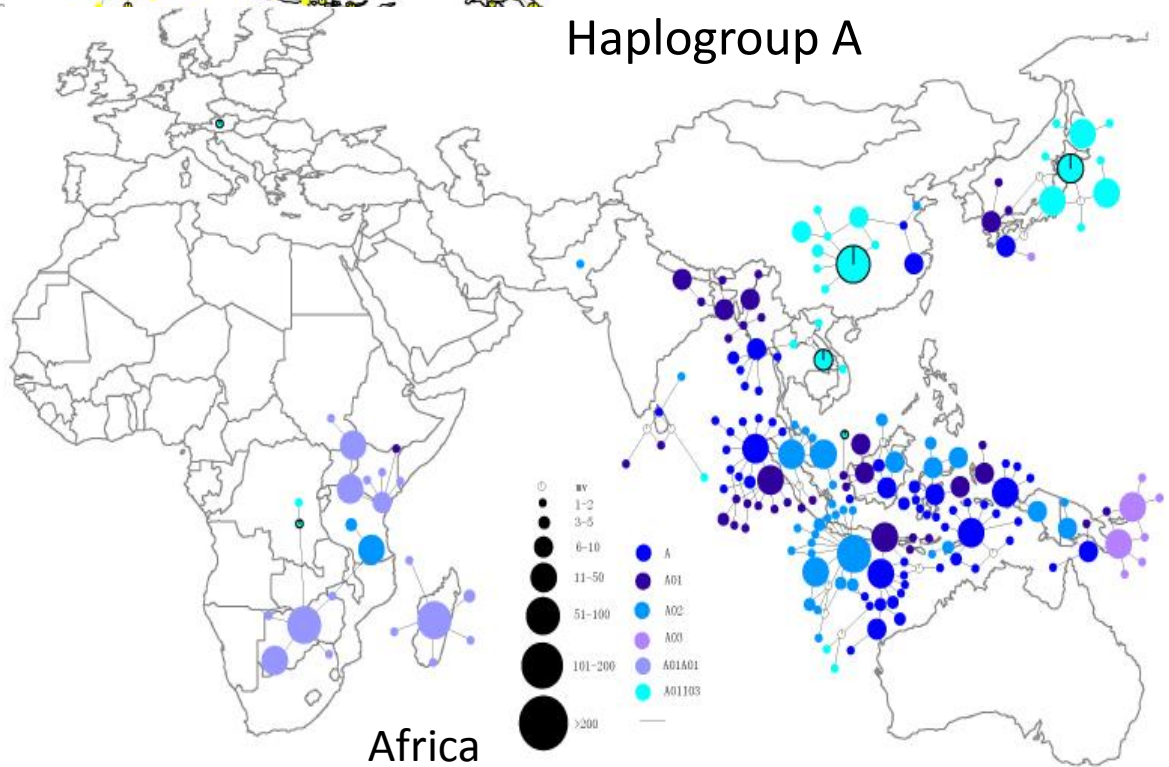
Europe (Germany, Hungary) - unique



Africa inland



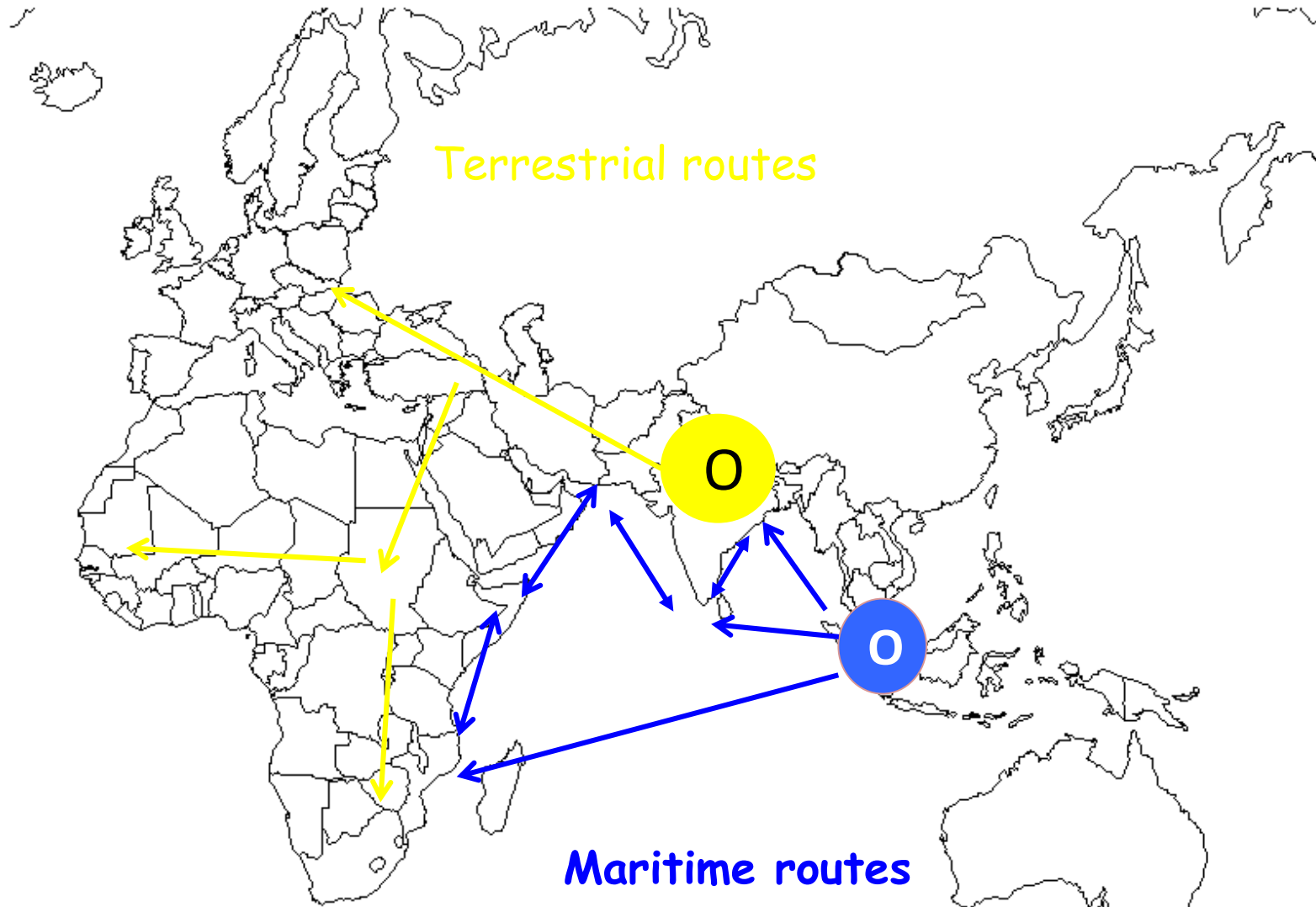
Haplogroup A



Africa coastal

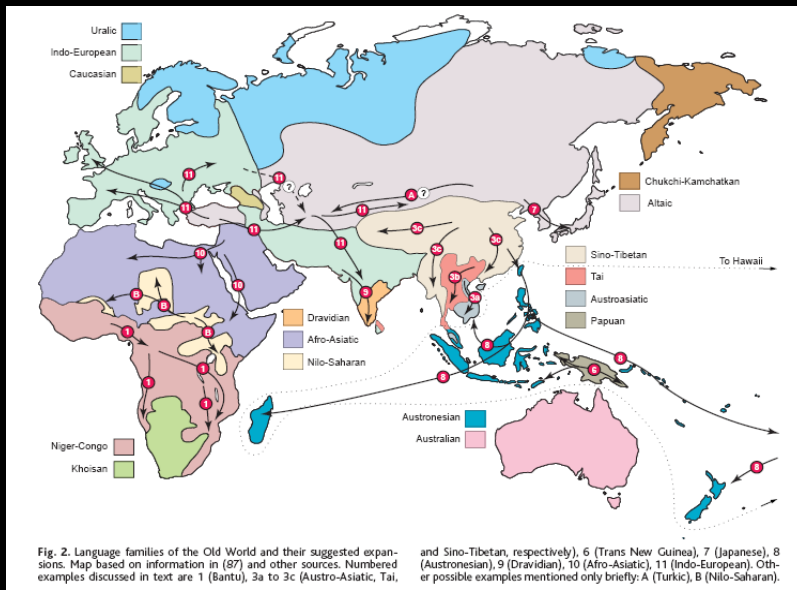


Main origin of African chicken: routes of introduction



J. W. MWACHARO, G. BJØRNSTAD, J. L. HAN and O. HANOTTE (2013). [The history of African chicken: an archaeological and molecular perspective](#). *African Archaeological Review*, 30, 97-114.

Chicken dispersion factors



J. Diamond and P. Bellwood *Farmers and their languages: The first expansions*, *Science* 300, 597 -603

Human migration

Trading

Junglefowl (*Gallus sp.*)



Plate 13. Indian red junglefowl, pair. Painting by H. Jones.



Plate 14. Ceylon junglefowl, pair. Painting by H. Jones.

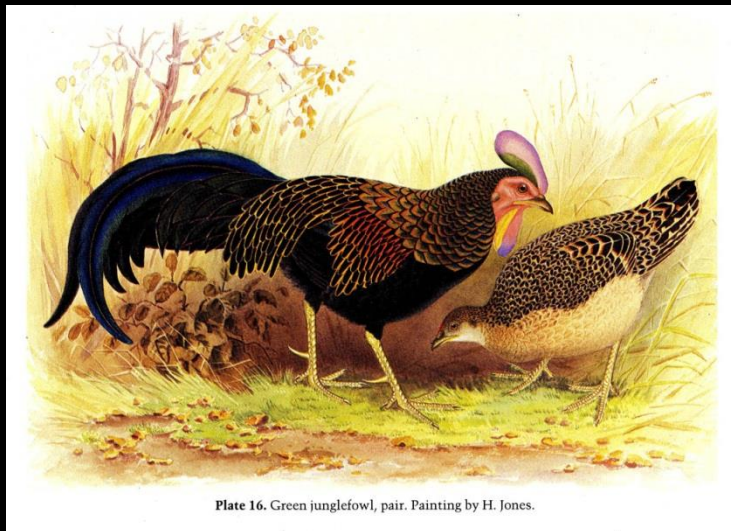
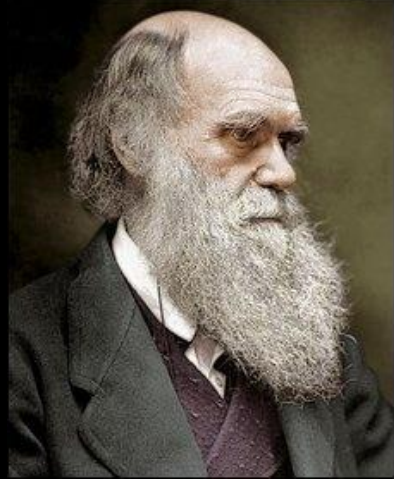


Plate 16. Green junglefowl, pair. Painting by H. Jones.

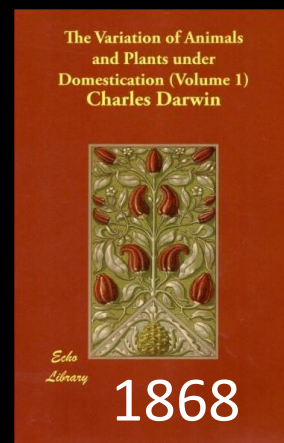


Plate 15. Grey junglefowl, pair. Painting by H. Jones.



Charles Darwin

Red junglefowl only ancestor



... Hence it may be concluded that not only the Game-breed but that all our breeds are probably the descendants of *G. bankiva* *. If so, this species has varied greatly since it was first domesticated; but there has been ample time, as we shall now show ...

* *red junglefowl Gallus gallus*

Nuclear DNA - Autosomal markers

Eriksson *et al.* (2008) Identification of the yellow skin gene reveals an hybrid origin of the domestic chicken *Plos Genetics* vol. 4, 2, e1000010

Author Summary

Many bird species possess yellow skin and legs whereas other species have white or black skin color. Yellow or white skin is due to the presence or absence of carotenoids. The genetic basis underlying this diversity is unknown. Domestic chickens with yellow skin are homozygous for a recessive allele, and white skinned chickens carry the dominant allele. As a result, chickens represent an ideal model for analyzing genetic mechanism responsible for skin color variation. In this study we demonstrate that yellow skin is caused by regulatory mutation(s) that inhibit expression of the beta-carotene dioxygenase 2 (BCDO2) enzyme in skin, but not in other tissues. Because BCDO2 cleaves colorful carotenoids into colorless apocarotenoids, a reduction in expression of this gene produces yellow skin. This study also provides the first conclusive evidence of a hybrid origin of the domestic chicken. It has been



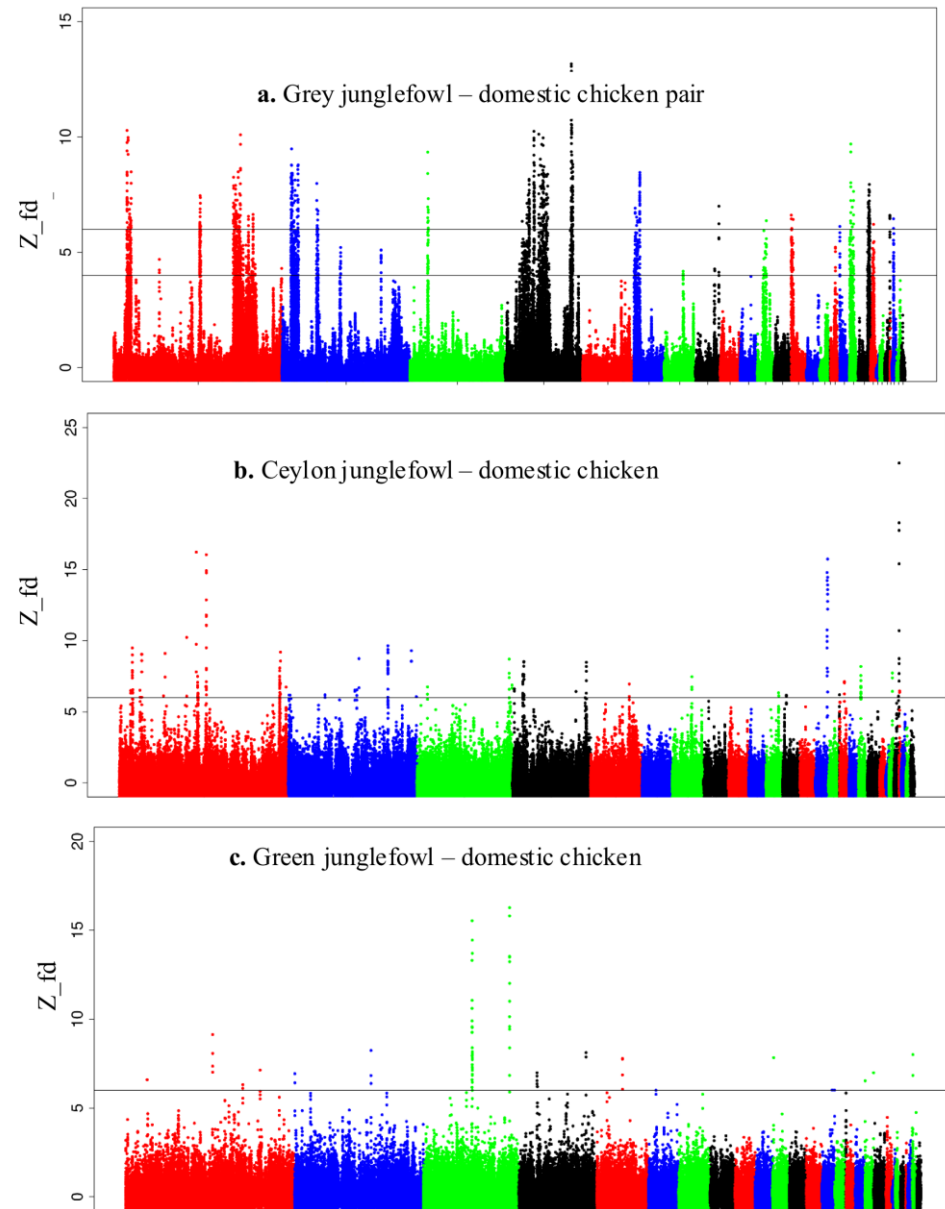
*Junglefowl sp introgression
in domestic chicken
Insight from whole genome
sequences*

*Candidate regions for autosomal
introgression in domestic
chicken*

*grey (n = 41), Ceylon (n = 12),
green (n = 7)*



R. Lawal UoN
PhD thesis
ongoing...



20 kb window with 5 kb overlap along the
autosomes (Chr 1 – 28)

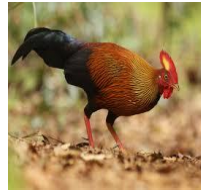


Junglefowl sp introgression in domestic chicken *Insight from whole genome sequences*

R. Lawal UoN PhD thesis ongoing...



◆ Green



◆ Ceylon



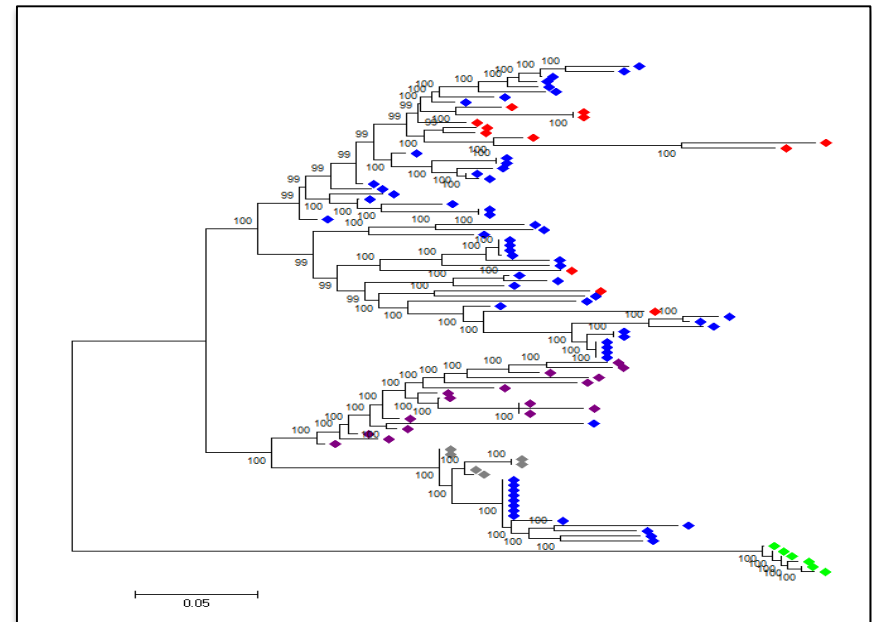
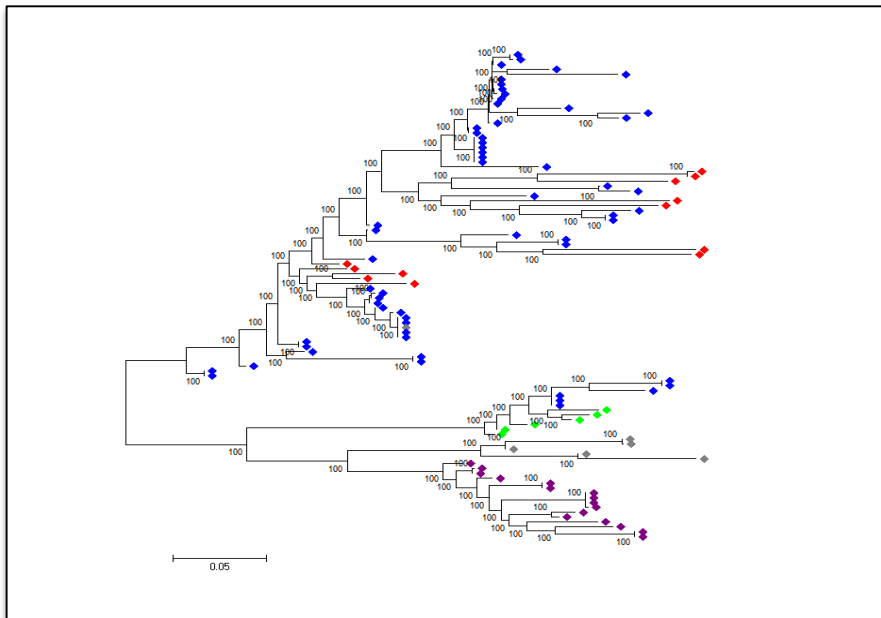
◆ Grey



◆ Red



◆ Domestic



Candidate regions for autosomal introgression in domestic chicken

grey (n = 41), Ceylon (n = 12), green (n = 7)...

RESEARCH ARTICLE

Open Access

Genome-wide analysis reveals the extent of EAV-HP integration in domestic chicken



David Wragg^{1,2*}, Andrew S. Mason³, Le Yu⁴, Richard Kuo³, Raman A. Lawal¹, Takele Taye Desta¹, Joram M. Mwacharo^{1,5}, Chang-Yeon Cho⁶, Steve Kemp⁷, David W. Burt³ and Olivier Hanotte¹

Abstract

Background: EAV-HP is an ancient retrovirus pre-dating *Gallus* speciation, which continues to circulate in modern chicken populations, and led to the emergence of avian leukosis virus subgroup J causing significant economic losses to the poultry industry. We mapped EAV-HP integration sites in Ethiopian village chickens, a Silkie, Taiwan Country chicken, red junglefowl *Gallus gallus* and several inbred experimental lines using whole-genome sequence data.

Results: An average of 75.22 ± 9.52 integration sites per bird were identified, which collectively group into 279 intervals of which 5 % are common to 90 % of the genomes analysed and are suggestive of pre-domestication integration events. More than a third of intervals are specific to individual genomes, supporting active circulation of EAV-HP in modern chickens. Interval density is correlated with chromosome length ($P < 2.31^{-6}$), and 27 % of intervals are located within 5 kb of a transcript. Functional annotation clustering of genes reveals enrichment for immune-related functions ($P < 0.05$).

Conclusions: Our results illustrate a non-random distribution of EAV-HP in the genome, emphasising the importance it may have played in the adaptation of the species, and provide a platform from which to extend investigations on the co-evolutionary significance of endogenous retroviral genera with their hosts.

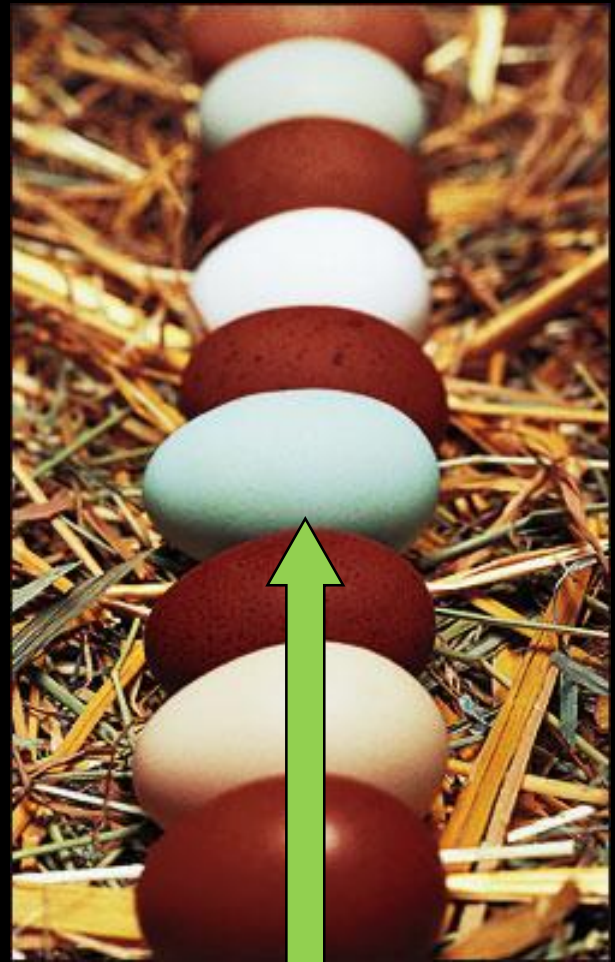
Keywords: Retrovirus, Symbiosis, Adaptation, Immunogenetics, Genetics, NGS, *Gallus*



Chilean – Village chicken



Araucana – Traditional breed



Blue egg

Mendelian inheritance – Dominant
Pigment – Biliverdin

Endogenous Retrovirus EAV-HP Linked to Blue Egg Phenotype in Mapuche Fowl

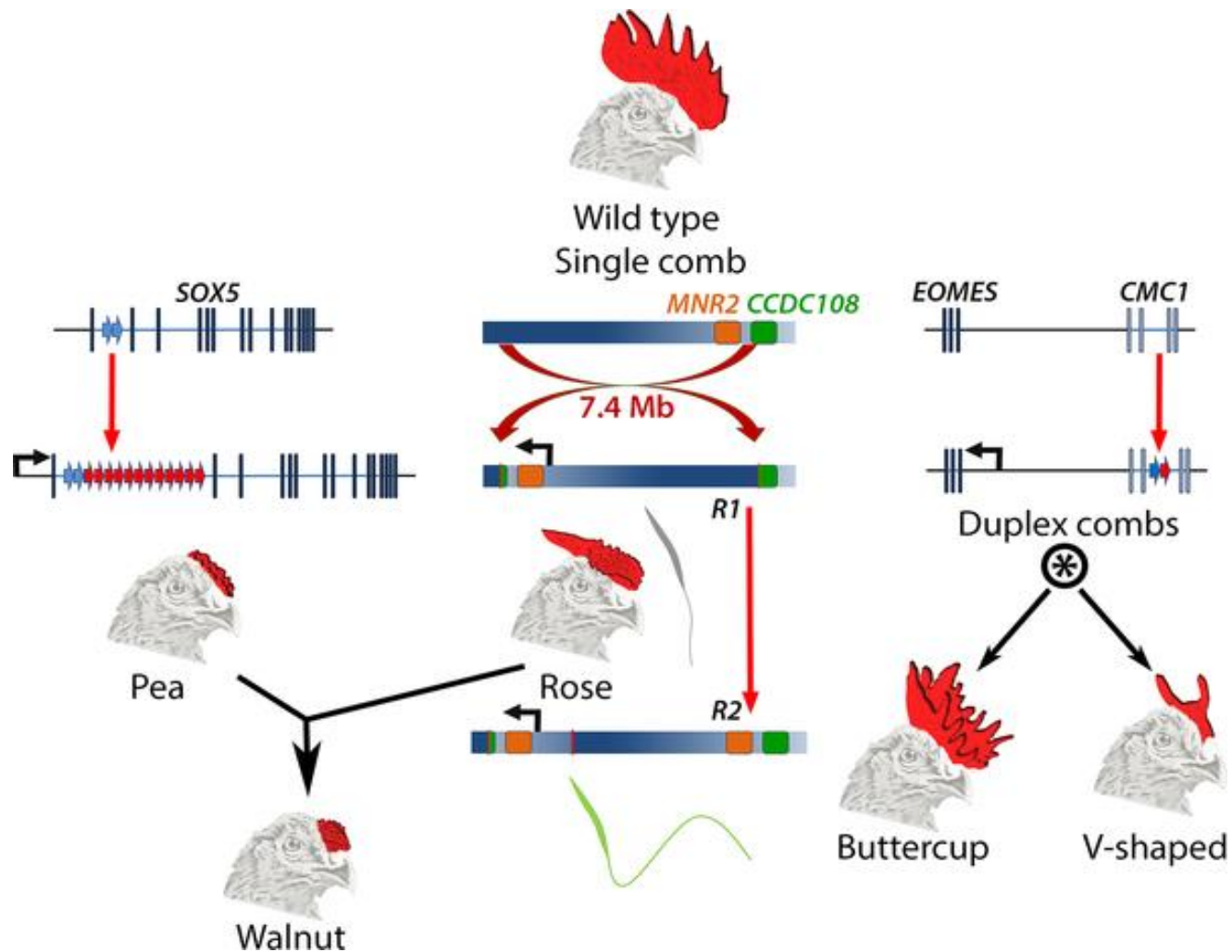
David Wragg¹, Joram M. Mwacharo¹, José A. Alcalde², Chen Wang³, Jian-Lin Han^{3,4}, Jaime Gongora⁵, David Gourichon⁶, Michèle Tixier-Boichard⁷, Olivier Hanotte^{1*}

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Abstract

Oocyan or blue/green eggshell colour is an autosomal dominant trait found in native chickens (Mapuche fowl) of Chile and in some of their descendants in European and North American modern breeds. We report here the identification of an endogenous avian retroviral (EAV-HP) insertion in oocyan Mapuche fowl and European breeds. Sequencing data reveals 100% retroviral identity between the Mapuche and European insertions. Quantitative real-time PCR analysis of European oocyan chicken indicates over-expression of the *SLCO1B3* gene ($P < 0.05$) in the shell gland and oviduct. Predicted transcription factor binding sites in the long terminal repeats (LTR) indicate *AhR/Ar*, a modulator of oestrogen, as a possible promoter/enhancer leading to reproductive tissue-specific over-expression of the *SLCO1B3* gene. Analysis of all jungle fowl species *Gallus sp.* supports the retroviral insertion to be a post-domestication event, while identical LTR sequences within domestic chickens are in agreement with a recent *de novo* mutation.

Fig 1. Major comb variants and their genetic basis.



Headon D (2015) Morphological Mutations: Lessons from the Cockscomb. PLoS Genet 11(3): e1004979. doi:10.1371/journal.pgen.1004979
<http://127.0.0.1:8081/plosgenetics/article?id=info:doi/10.1371/journal.pgen.1004979>

Chicken diversity.....



- Large geographic distribution of the red junglefowl -multiple centers of origins and introgression of local populations followed by dispersion and crossbreeding
- Introgression from other *Gallus* species, grey junglefowl, Ceylon junglefowl, green junglefowl
- Retroviral insertion and circulation
- Mutation (points mutation, chromosomal rearrangements, indel.....)

To be continued

