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Guinea fowl domestication : new insights from the first whole genome assembly and the pool sequencing of wild and domestic populations.

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II Joint Congress on Evolutionary Biology – Montpellier 2018



- **Village poultry in Africa**, intensive livestock farming for meat production in **Europe** (mostly France and Italy).

- **Natural range in sub-Saharan Africa**, 8 subspecies.
- **Domestication** may have occurred **about 2,000 years BP** in Mali and Sudan, archaeozoological and artistic data (Larson and Fuller, 2014).
- Food supply, farm keeper and parasite / snake hunter.
- **Diffused** in the Mediterranean world during the Roman Empire, and throughout the world **from the 16th century**.
- **Genetic diversity** studied from mtDNA (Walker *et al*, 2004; Adeola *et al*, 2015) or microsatellites (Kayang *et al*, 2010; Weimann *et al*, 2016).

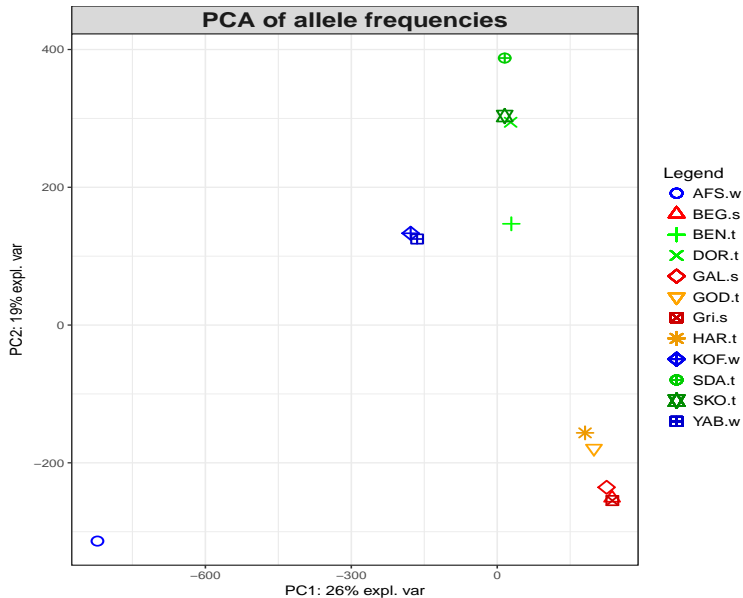
- **Sequencing** of a male sample on Illumina HiSeq 2500, at about 70X coverage (3 and 8kb paired-end reads).
- **Assembled** using ALLPATHS2 (Maccallum *et al*, 2009)
 - Male genome of **1.04Gb**
 - **2,739 scaffolds (N50 7.8Mb)**
- **Alignment to the chicken genome** (Galgal5) + known **cytogenetic rearrangements** (Shibusawa *et al*, 2002)
 - 29 autosomes + Z + mtDNA + linkage group LGE64.
- Assembly quality comparable to that of other Galliformes (chicken, quail, common duck).

Pool-sequencing of 12 samples

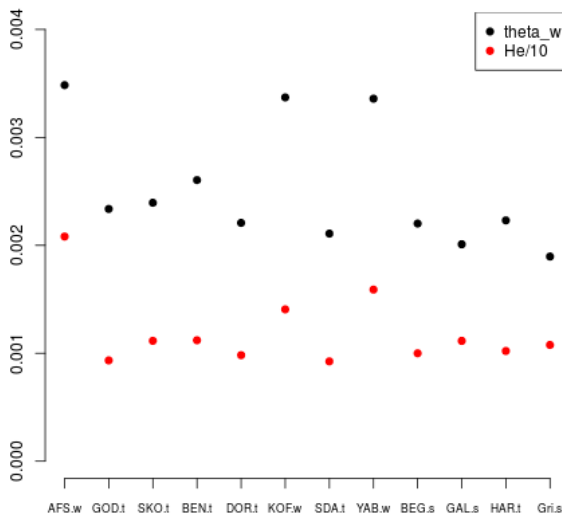
- **Africa, wild** : **AFS-w** (South Africa, $n = 3$, 14X), **KOF-w**, **YAB-w** (Burkina Faso, $n = 8$, 20X).
- **Africa, domestic** : **SDA-t**, **SKO-t**, **DOR-t** (Burkina Faso, $n = 5$, 10X), **BEN-t** (Bénin, $n = 15$, 16X).
- **Europe, domestic** : **GOD-t**, **HAR-t** (Hungaria, $n = 30$, 17X).
- **Europe, selected** : **BEG-s** (France, $n = 12$, 15X), **GAL-s** (France, $n = 29$, 37X), **GRI-s** (France, $n = 20$, 38X).

→ **80 million SNPs** with allele frequency called in all pools and $\text{MAF} \geq 0.05$.

Genetic structure reflects sub-species and domestication

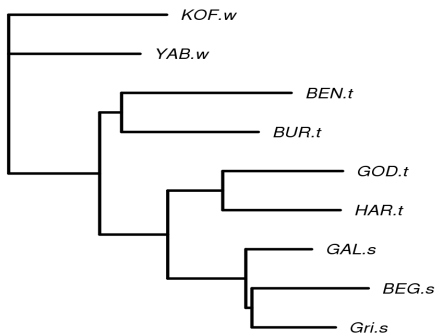


Reduced diversity in domestic populations



Population tree confirms genetic structure and diversity

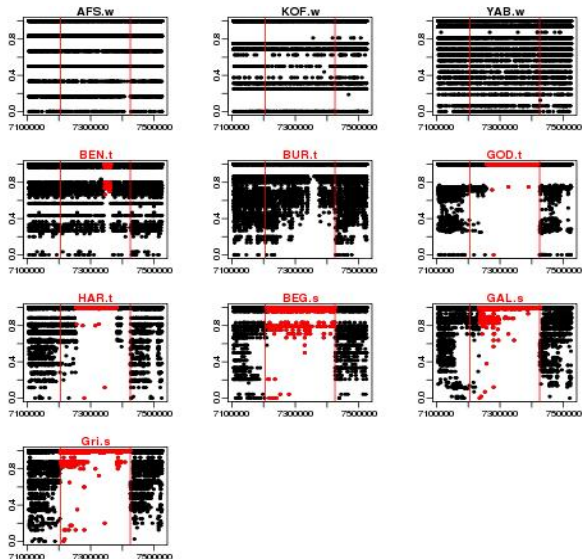
Whole Genome tree



- Estimated by FLK (Bonhomme *et al*, 2010) from allele frequencies at ≈ 8.9 million SNPs.
- Domestic samples from Burkina-Faso merged (**BUR-t**), AFS-w used as outgroup.

- **Selective sweep** signatures detected **within each population** using Pool-HMM (Boitard *et al*, 2012; 2013).
→ thousands of candidate regions.
- 5 regions related to **domestication** : detected in 6 out of 7 domestic populations, undetected in wild populations.
- 31 regions specific to **Europe**, 64 to **intensive meat production**.
- Combining candidates from the 3 categories leads to 0.6% of the genome, including 223 genes (**2-fold enrichment**).

Domestication candidate region



Candidate genes and mutations

- Within the 5 domestication regions, **30 genes in total** (from 1 to 16 per region).
- **29** of these genes **include candidate variants**:
allele frequency ≥ 0.75 in all domestic populations and ≤ 0.25 in all wild populations.
- **2** of these genes include **1 candidate variant with functional effect (missense)** : *PAPPA2* and *EDNRB*.

Example 1 : *PAPPA2*

- **Only gene** in a **candidate region** of 21 kb, at position 7.3 Mb on chromosome 7.
- *PAPPA2* (Pregnancy-Associated Plasma Preproprotein-A2) is a **modulator of IGF-I** (Fujimoto *et al*, 2017).
- Mutations associated to **body size** in at least 3 vertebrate species: mice (Christians *et al*, 2006), humans (Lango Allen *et al*, 2010) and cows (Bouwman *et al*, 2018).

Example 2 : *EDNRB*

- Expressed in **melanocytes deriving from the neural crest** → potential domestication gene (Wilkins *et al*, 2014).
- Mutations associated to **white spotted patterns** in chickens (Kinoshita *et al*, 2014) and **pigmentation disorders** in other species (Dang *et al*, 2011; Ayala-Valdovinos *et al*, 2016).
- In our African samples, **strong pigmentation differences between wild** (left) **and domestic** (right) animals.



- **White spotted** patterns found among **village chickens in Benin**, said to be associated with luck and wealth (Chrysostome *et al*, 2013).
- **Selection for tameness via *EDNRB***?
- **11 other genes in the candidate region** of *EDNRB*, 175 kb long at 11.1-11.3 Mb on chromosome 8.
- **Two of them associated to behavioral traits:** *VAMP7* (mice, Danglot *et al*, 2012) and *TMLHE* (humans, Ziats *et al*, 2015; quails, Fariello *et al*, 2017).

- **Genome assembly of the Guinea fowl.**
- First **study of genetic diversity** in this species **based on genome-wide data.**
- **Domestic** populations **cluster together**, and have **reduced genetic diversity.**
- **Domestication** likely occurred **in Western Africa.**
- Domestication **candidate genes** and mutations, related to body size, pigmentation or behaviour.

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