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Genetic Considerations for the Conservation of the Red Junglefowl

By

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ABSTRACT:

The undomesticated wild populations of our domestic species deserve heightened consideration when it comes to their conservation. Not only do they carry significant socio-cultural and economic roles, but they offer an exceptionally unique case study for population genetics. The red junglefowl (*Gallus gallus*) of southern and south-eastern Asia is considered to be the living ancestor and progenitor of the domestic chicken. This literature review examines how published research has evaluated its genetic relationship with the chicken and implications for its conservation. A special emphasis is given to the threat of genetic introgression with domestic and feral chicken populations from hybridizations along the wild-domestic interface.

INTRODUCTION:

The red junglefowl (*Gallus gallus*) is a gallinaceous bird found extensively throughout the tropical and subtropical forests of southern and south-eastern Asia. Its range stretches from north of India and Nepal towards the eastern coasts of China and Vietnam, it is also found throughout the Philippines, Malaysia, Indonesia, and the islands of Sumatra and Java (Johnsgard, P. A. 1999; Gill, F., Donsker D. & Rasmussen P. 2023).

There are currently five recognized subspecies of the red junglefowl: *G.g. bankiva*, *G.g. gallus*, *G.g. jabouillei*, *G.g. murghi*, and *G.g. spadiceus*, with each occupying different regions along its distribution. Researchers have previously investigated whether a potential sixth subspecies, *G.g. philippensis* merits its own classification, but genetic and morphological evidence was not sufficient to make that determination. Instead it appears that red junglefowl

found in the Philippines are of the subspecies *G.g. gallus* (Nishida et al. 1985; Compendio & Nishibori 2021).

Of all the subspecies of red junglefowl, it has been shown that *G.g. spadiceus* specifically shares the greatest degree of genetic similarity with the domestic chicken. This finding is most likely due to the extensive range occupied by these populations of red junglefowl in India and Nepal, and a greater population census size when compared with the other subspecies (Sambandam et al. 2012).

The domestic chicken holds a vital role throughout historic and contemporary societies. Not only does it maintain a significant socio-cultural presence around the world, but it is also economically indispensable as a widely available and affordable source of food, and as a model organism in the research and development of pharmacological and genomic applications. During 2022, the number of chickens produced for meat in the U.S. alone exceeded the entire human population on Earth. In fact, this has been true of U.S. broiler chicken production every year since 1990 (National Agricultural Statistics Service 2022). This argument alone justifies extensive and continued research into the red junglefowl as an extension to the study of genetic potential in the chicken. The future of poultry production may rely on advantages gained from red junglefowl populations serving as reservoirs of potential solutions to the yet to be discovered problems.

THE GENETIC RELATIONSHIP BETWEEN THE RED JUNGLEFOWL AND THE
DOMESTIC CHICKEN

Although it was hypothesized from morphological similarities that the domestic chicken was a relative of the red junglefowl, the exact nature of their relationship was initially unclear. Some of the earliest phylogenetic studies of the chicken used blood and protein loci polymorphisms to establish shared ancestry between red junglefowl and some domestic chicken breeds of Japan (Okada et al. 1984).

But this research didn't carry the same degree of conclusivity that later phylogenetic constructions using mitochondrial and nuclear genomic analyses did. Using mtDNA a phylogeny was constructed of the genus *Gallus* which established a clear matrilineal relationship between the red junglefowl and the chicken (Fumihito et al. 1994, 1996). This was corroborated with additional studies using DNA fingerprinting (Yamashita et al. 1994; Ponsuksili et al. 1998; Ponsuksill et al. 1999), microsatellite analysis (Romanov & Weigend 2001; Rosenberg et al. 2001), and mtDNA D-loop sequencing (Niu et al. 2002).

Additional research seeking to further elucidate the relationships between the different species of junglefowl found evidence for historic inter-species hybridizations between the red junglefowl and the grey junglefowl (*Gallus sonneratii*) (Nishibori et al. 2005). This determination was also supported by the discovery that the yellow skin allele found in domestic chicken breeds was likely acquired through hybridization with the grey junglefowl early on in the domestication process as it is present in the grey junglefowl and chicken but absent in the red junglefowl (Eriksson et al. 2008).

An investigation into the genetic landscape of red junglefowl populations throughout India highlighted some key discoveries. Northeastern populations of red junglefowl displayed the greatest heterozygosity when compared to the other red junglefowl distributions sampled. This

regional population also shares the greatest genetic similarity to the domestic chicken, which supports the claim that this region may be a major historic site of domestication (Sambandam et al. 2012). It also indicated a high likelihood of historic and contemporary gene flow with domestic and feral chicken populations in the area. Which also implies a much lower frequency of gene flow among the other populations of Indian red jungle and domestic chickens.

Understanding the intricacies of the chicken genome is complicated by historic and contemporary gene flow between feral chicken populations and red junglefowl, as well as the intentional crossbreeding of domestic chickens by local farmers (Singchat et al. 2022). This poses a unique challenge for the conservation of the red junglefowl. On one hand there is the threat of genetic introgression which may lead to the loss of some potentially advantageous allele frequencies that could prove important in future commercial poultry production endeavors. But on the other hand, frequent monitoring of red junglefowl and feral chicken populations without interfering may give researchers the opportunity to study the populations genetics of a unique system with complex gene flow interactions along the wild-domestic interface.

Frequent genotyping of red junglefowl, and domestic or feral chicken populations reveals a rich and complex life history that is very distinct from the life histories of other wild-domestic conspecifics. It is important to continue sampling individuals from these populations to keep a record of genotype frequencies and their changes over time. This benefits the collaboration between researchers who continue contributing data for longitudinal genomic analysis and future studies.

LOSS OF GENETIC VARIATION THROUGH INTROGRESSION

One of the major considerations regarding the conservation of the red junglefowl would be the threat of genetic introgression via hybridization with domestic and feral chicken populations resulting in a loss of genetic diversity and heterozygosity. This has been observed with historical comparative analyses using museum specimens (Wu et al. 2023). But, it can also be examined in extant populations of red junglefowl and chicken as well, such as on the island of Kauai in Hawaii (Martin Cerezo et al. 2023)

Another piece of information to take into account is that phenotype may not be an accurate representation of genetic purity in red junglefowl, examples of this would be the presence of an eclipse plumage in males, or small comb sizes in hens. When crossed with the domestic chicken, phenotypic characteristics of the red junglefowl persist or may disappear after a few generations, which may be misleading for demographic studies that rely on morphological evidence to determine ancestry rather than genetic comparisons (Brisbin & Peterson 2007). This is an important consideration when comparing demographic studies and the assumed purity of sampled individuals. Even museum specimens indicated to be of pure red junglefowl stock were determined to contain genes derived from their domestic conspecific (Peterson & Brisbin 1998).

There is another important distinction to make when comparing the genetic conservation of the red junglefowl with other wild-domestic conspecifics. Many of the remaining wild populations of our domestic species, such as the African wild ass (*Equus africanus*) or wild water buffalo (*Bubalus arnee*) are endangered and declining in population size at an alarming rate, yet this is not currently a concern of the red junglefowl (Smith et al. 2022). One of the challenges regarding small population densities is the potential loss of genetic variation and heterozygosity through allelic fixation or genetic drift. This can result in the accumulation of deleterious allele frequencies and/or a loss of potentially adaptive genetic variation which puts a population at risk

for extirpation. A concern which is amplified by the added pressures of habitat loss and climate change (Fred W. Allendorf et al. 2022). Because the populations of the red junglefowl are well-distributed and sizable, the species is not considered at risk for genetic drift like highly isolated populations of few individuals would be (Sambandam et al. 2012).

CONCLUSION:

It is difficult to discern where the line separating a red junglefowl from the domestic chicken really lies when their genetic relationships are so inextricably linked. The conservation of the red junglefowl is not necessarily an argument to sustain genetically pure populations of this bird in the wild, but rather to maintain a diligent and prolonged study of the processes of gene flow along the wild-domestic interface so that we may continue to examine the nuances between domestication and evolution over time.

As it currently stands, the red junglefowl is not considered a threatened species. Indeed, it may even be considered one of the most successful domesticates in human history by sheer numbers alone - not to mention its immense cultural and economic value. Truly, this bird serves as an excellent model organism for investigating the intricate complexities of the population genetics of our beloved domestic animals.

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